Supplementary Material: Supplemental material is available online.

Supplementary Figure S1. Summary of the distribution and number of DEGs in three GO classes, including molecular function, cellular component, and biological process. R1, R2, and R3: fruiting bodies collected at 2, 5, and 9 dpi, respectively; Z1, Z2, and Z3: three uninfected control groups collected at the same time points.

Supplementary Figure S2. Comparisons of KEGG enrichment analyses of differentially expressed genes (DEGs) between different treatment and control groups. R1, R2, and R3: fruiting bodies collected at 2, 5, and 9 dpi, respectively; Z1, Z2, and Z3: three uninfected control groups collected at the same time points.
Supplementary Figure S3. RT-qPCR analysis of the five selected DEGs. The horizontal axis represents different groups, including R1, R2, R3, Z1, Z2, and Z3. The vertical axis represents relative expression levels.

Data Set S1. Information and primers used for RT-qPCR of selected differentially expression genes.

Data Set S2. Information of RNA-seq data for the 18 samples.

Data Set S3. Information of DEGs in R1 vs Z1.

Data Set S4. Information of DEGs in R2 vs Z2.

Data Set S5. Information of DEGs in R3 vs Z3.

Data Set S6. FPKM values for common DEGs of mushroom *P. eryngii* after *E. beijingensis* infection.

Data Set S7. Genes involved in oxidoreductase activity and oxidation-reduction process.
| Gene ID    | Gene annotation                  | Forward primer(5'-3')  | Reverse primer(5'-3')  | Efficiency of PCR amplification |
|------------|----------------------------------|------------------------|------------------------|---------------------------------|
| EVM0006723 | Conidiation protein 6            | CTCGTGATTTGCTCTACG     | GTGTCTTTTGTCATCTTC     | 92.05%                          |
| EVM0004026 | Secondary metabolites biosynthesis | ACCCTGCTTGGGAACATCA   | TATTGGCGACCGAACTCT     | 92.59%                          |
| EVM0001604 | Sorbose reductase                | TTCCAGGGAGCATCATT      | CAGTTGCAGCCATAGA       | 91.43%                          |
| EVM0002562 | Mitochondrial peroxiredoxin PRX1 | TCGTGGGCGATCTTTCATCT   | ATTCGTGGGTTCCTGGAG     | 92.59%                          |
| EVM0004221 | hypothetical protein             | ACAGTGGTTCCAAGCCGT     | CCTCGTCAAACAGTCCTCA    | 101.74%                         |
| GAPDH*     | Glyceraldehyde phosphatedehydrogenase | GTGATCTCAAATGCGTATG   | TGGGTAGCATGGTAGCG      | 93.46%                          |

* represents the internal control gene

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Data Set S2 Information of RNA-seq data for the 18 samples

| Sample ID | Total_Reads | base pairs | Q20%  | Q30%  | GC%  | mapping rate |
|-----------|-------------|------------|-------|-------|------|--------------|
| Z1-A      | 50974830    | 7531536295 | 97.73 | 93.18 | 53.39| 0.875        |
| Z1-B      | 47929898    | 7082205205 | 97.79 | 93.32 | 53.08| 0.894        |
| Z1-C      | 48054594    | 7096997784 | 97.76 | 93.24 | 53.23| 0.863        |
| Z2-A      | 54860886    | 8119892714 | 97.88 | 93.52 | 53.16| 0.858        |
| Z2-B      | 52059346    | 7688398377 | 97.74 | 93.2  | 53.26| 0.843        |
| Z2-C      | 43531194    | 6429230721 | 97.66 | 93.02 | 53.27| 0.826        |
| Z3-A      | 59448596    | 8796840763 | 97.85 | 93.47 | 53.26| 0.864        |
| Z3-B      | 50798230    | 7516311797 | 97.84 | 93.44 | 53.2  | 0.881       |
| Z3-C      | 54640940    | 8071514102 | 97.76 | 93.24 | 53.3  | 0.832       |
| R1_A      | 98061730    | 14369696114| 98.52 | 95.29 | 51.11| 0.881       |
| R1-B      | 75582742    | 10944449989| 98.92 | 96.64 | 51.09| 0.892       |
| R1-C      | 79313902    | 11501811236| 99.02 | 96.91 | 50.92| 0.853       |
| R2_A      | 109929638   | 16171054375| 98.59 | 95.5  | 51.31| 0.872       |
| R2-B      | 80414886    | 11683166147| 99.04 | 96.96 | 50.41| 0.895       |
| gene ID              | R1 value | Z1 value | log2(fold change) | p value  | q value  | KOG class                        | Pfam annotation                                      |
|---------------------|----------|----------|-------------------|----------|----------|----------------------------------|-------------------------------------------------------|
| EVM0009623          | 7.20     | 310.96   | -5.43             | 5.00E-05 | 4.28E-04 | --                               | --                                                   |
| EVM0001104          | 4.48     | 139.31   | -4.96             | 5.00E-05 | 4.28E-04 | --                               | --                                                   |
| EVM0007042          | 96.16    | 2483.20  | -4.69             | 5.00E-05 | 4.28E-04 | --                               | Hemerythrin HHE cation binding domain                  |
| EVM0010521          | 22.11    | 566.26   | -4.68             | 5.00E-05 | 4.28E-04 | --                               | --                                                   |
| EVM0008830          | 36.80    | 795.37   | -4.43             | 5.00E-05 | 4.28E-04 | Defense mechanisms               | Dual specificity phosphatase, catalytic domain         |
| EVM0000901          | 0.16     | 3.07     | -4.26             | 1.10E-03 | 6.17E-03 | Carbohydrate transport and metabolism | Starch binding domain                                |
| EVM0011483          | 43.53    | 629.06   | -3.85             | 5.00E-05 | 4.28E-04 | --                               | --                                                   |
| EVM0006076          | 21.85    | 315.32   | -3.85             | 5.00E-05 | 4.28E-04 | --                               | --                                                   |
| EVM0004031          | 11.09    | 158.24   | -3.84             | 5.00E-05 | 4.28E-04 | RNA processing and modification  | Eukaryotic rRNA processing protein EBP2               |
| EVM0004233          | 26.26    | 356.42   | -3.76             | 5.00E-05 | 4.28E-04 | --                               | --                                                   |
| EVM0006187          | 0.74     | 9.76     | -3.71             | 5.00E-05 | 4.28E-04 | Transcription                    | HMG (high mobility group) box                         |
| EVM0006622          | 4.48     | 57.86    | -3.69             | 5.00E-05 | 4.28E-04 | --                               | --                                                   |
| EVM0001788          | 26.14    | 336.53   | -3.69             | 5.00E-05 | 4.28E-04 | --                               | --                                                   |
| Accession  | ID    | Description                                      |
|-----------|-------|-------------------------------------------------|
| EVM0012049 | 3.07  | 39.20 -3.67 5.00E-05 4.28E-04 -- -- |
| EVM0003167 | 14.40 | 181.82 -3.66 5.00E-05 4.28E-04 -- -- |
| EVM0002148 | 67.67 | 851.70 -3.65 5.00E-05 4.28E-04 -- Uncharcterised protein family (UPF0197) |
| EVM0007827 | 19.19 | 241.11 -3.65 5.00E-05 4.28E-04 -- Lipase (class 3) |
| EVM0000032 | 1.27  | 15.56 -3.61 5.00E-05 4.28E-04 -- -- |
| EVM0009709 | 4.74  | 56.94 -3.59 5.00E-05 4.28E-04 -- -- |
| EVM0012999 | 5.89  | 70.13 -3.57 5.00E-05 4.28E-04 Posttranslational modification, protein turnover, chaperones |
| EVM0007867 | 6.07  | 71.97 -3.57 5.00E-05 4.28E-04 -- -- |
| EVM0002760 | 6.22  | 73.45 -3.56 5.00E-05 4.28E-04 -- -- |
| EVM0009999 | 3.31  | 38.62 -3.54 5.00E-05 4.28E-04 Rare lipoprotein A (RlpA)-like double-psi beta-barrel |
| EVM0010589 | 69.26 | 799.29 -3.53 5.00E-05 4.28E-04 -- bZIP transcription factor |
| EVM0004729 | 34.15 | 382.70 -3.49 5.00E-05 4.28E-04 -- Helix-turn-helix |
| EVM0002270 | 2.33  | 26.09 -3.48 8.00E-04 4.73E-03 -- -- |
| EVM0001661 | 5.76  | 64.32 -3.48 5.00E-05 4.28E-04 General function prediction only Kinase phosphorylation protein |
| EVM0008465 | 29.96 | 327.87 -3.45 5.00E-05 4.28E-04 RNA processing and modification DEAD/DEAH box helicase |
| EVM0006922 | 10.21 | 104.81 -3.36 5.00E-05 4.28E-04 -- -- |
| EVM0010939 | 111.27| 1110.35 -3.32 1.15E-03 6.41E-03 -- -- |
| EVM0008002 | 56.99 | 561.02 -3.30 5.00E-05 4.28E-04 General function prediction only Flavodoxin |
| EVM0001240 | 14.04 | 136.58 -3.28 5.00E-05 4.28E-04 -- -- |
| EVM0005700 | 24.94 | 242.19 | -3.28 | 5.00E-05 | 4.28E-04 | -- | Conidiation protein 6 |
| EVM0005127 | 77.37 | 748.41 | -3.27 | 5.00E-05 | 4.28E-04 | -- | Gamma interferon inducible lysosomal thiol reductase (GILT) |
| EVM0002682 | 38.96 | 373.60 | -3.26 | 5.00E-05 | 4.28E-04 | Transcription | RNA polymerase Rpb6 |
| EVM0005937 | 28.61 | 274.34 | -3.26 | 5.00E-05 | 4.28E-04 | -- | -- |
| EVM0005353 | 1.95 | 17.43 | -3.16 | 5.00E-05 | 4.28E-04 | Posttranslational modification, protein turnover, chaperones | Peptidase family M50 |
| EVM0005353 | 2.60 | 22.34 | -3.10 | 5.00E-05 | 4.28E-04 | -- | Putative phosphatase regulatory subunit |
| EVM0003650 | 22.62 | 191.62 | -3.08 | 5.00E-05 | 4.28E-04 | Function unknown | Thioesterase superfamily |
| EVM0004635 | 65.35 | 550.54 | -3.07 | 5.00E-05 | 4.28E-04 | -- | -- |
| EVM0003543 | 68.41 | 570.23 | -3.06 | 5.00E-05 | 4.28E-04 | -- | -- |
| EVM0002451 | 2.49 | 20.67 | -3.05 | 5.00E-05 | 4.28E-04 | -- | -- |
| EVM0006917 | 1.96 | 16.28 | -3.05 | 5.00E-05 | 4.28E-04 | -- | -- |
| EVM0003732 | 21.94 | 51.82 | -1.24 | 5.00E-05 | 4.28E-04 | -- | -- |
| EVM0002754 | 7.81  | 64.06 | -3.04 | 5.00E-05 | 4.28E-04 | General function prediction only | Ankyrin repeats (3 copies) |
| EVM0001814 | 5017.20 | 40681.30 | -3.02 | 5.00E-05 | 4.28E-04 | -- | Ricin-type beta-trefoil lectin domain-like |
| EVM0008891 | 8.58  | 69.58 | -3.02 | 5.00E-05 | 4.28E-04 | Amino acid transport and metabolism | Histidine biosynthesis protein |
| EVM0000282 | 155.66 | 1258.86 | -3.02 | 5.00E-05 | 4.28E-04 | -- | -- |
| EVM0009146 | 0.39  | 3.17 | -3.01 | 1.09E-02 | 4.01E-02 | -- | Glycosyl hydrolase family 61 |
| EVM0001153 | 0.36  | 2.93 | -3.01 | 1.00E-03 | 5.70E-03 | -- | -- |
| EVM0007670 | 30.91 | 247.19 | -3.00 | 5.00E-05 | 4.28E-04 | -- | Domain of unknown function (DUF4112) |
| EVM0001996 | 21.59 | 171.38 | -2.99 | 5.00E-05 | 4.28E-04 | Translation, ribosomal structure and biogenesis | SBDS protein C-terminal domain |
| EVM0005265 | 32.85 | 260.64 | -2.99 | 5.00E-05 | 4.28E-04 | -- | -- |
| EVM0010786 | 16.62 | 131.82 | -2.99 | 5.00E-05 | 4.28E-04 | -- | Zinc finger, C3HC4 type (RING finger) |
| EVM0012244 | 0.58  | 4.57 | -2.99 | 2.50E-04 | 1.77E-03 | -- | -- |
| EVM0009491 | 5.39  | 41.64 | -2.95 | 5.00E-05 | 4.28E-04 | Secondary metabolites biosynthesis, transport and catabolism | Alcohol dehydrogenase GroES-like domain |
| EVM0009924 | 0.75  | 5.75 | -2.93 | 9.50E-04 | 5.46E-03 | -- | -- |
| EVM0004071 | 18.19 | 138.73 | -2.93 | 5.00E-05 | 4.28E-04 | Transcription | GATA zinc finger |
| EVM0010256 | 0.46  | 3.53 | -2.93 | 5.00E-05 | 4.28E-04 | General function prediction only | GMC oxidoreductase |
| Accession  | Value | Log2 Fold Change | p-val | E-value | Functional Category                                      | Description                                      |
|-----------|-------|-----------------|-------|---------|--------------------------------------------------------|--------------------------------------------------|
| EVM0010422 | 5.58  | -2.93           | 5.00E-05 | 4.28E-04 | Posttranslational modification, protein turnover, chaperones | DnaJ domain                                     |
| EVM0010125 | 8.62  | -2.91           | 5.00E-05 | 4.28E-04 | --                                                     | --                                               |
| EVM0008632 | 3.35  | -2.90           | 5.00E-05 | 4.28E-04 | Posttranslational modification, protein turnover, chaperones | Isoprenylcysteine carboxyl methyltransferase (ICMT) family |
| EVM0002910 | 10.36 | -2.89           | 5.00E-05 | 4.28E-04 | --                                                     | Transcription                                    |
| EVM0005367 | 1.19  | -2.89           | 5.00E-05 | 4.28E-04 | --                                                     | --                                               |
| EVM0009355 | 1.35  | -2.89           | 5.00E-05 | 4.28E-04 | --                                                     | --                                               |
| EVM0010446 | 15.39 | -2.88           | 5.00E-05 | 4.28E-04 | Transcription                                         | Homeobox KN domain                               |
| EVM0005014 | 1.97  | -2.87           | 5.00E-05 | 4.28E-04 | --                                                     | --                                               |
| EVM001622  | 46.31 | -2.85           | 5.00E-05 | 4.28E-04 | --                                                     | --                                               |
| EVM003029  | 23.91 | -2.85           | 5.00E-05 | 4.28E-04 | Signal transduction mechanisms                        | Protein-tyrosine phosphatase                      |
| EVM000847  | 2.12  | -2.85           | 5.00E-05 | 4.28E-04 | --                                                     | --                                               |
| EVM0006132 | 24.32 | -2.84           | 5.00E-05 | 4.28E-04 | Intracellular trafficking, secretion, and vesicular transport | Peroxisomal biogenesis factor 11 (PEX11)     |
| EVM006981  | 20.16 | -2.84           | 5.00E-05 | 4.28E-04 | --                                                     | Rrp15p                                          |
| EVM0000114 | 5.33  | -2.84           | 5.00E-05 | 4.28E-04 | Posttranslational modification, protein turnover, chaperones | ATPase family associated with various cellular activities (AAA) |
| EVM0003584 | 11.73 | -2.83           | 5.00E-05 | 4.28E-04 | Replication, recombination and repair                 | TatD related DNase                               |
| EVM0000144 | 6.29 | 44.38 | -2.82 | 5.00E-05 | 4.28E-04 | General function prediction only | Phenazine biosynthesis-like protein |
| EVM0000467 | 2.76 | 19.06 | -2.79 | 5.00E-05 | 4.28E-04 | -- | -- |
| EVM0002447 | 127.77 | 883.19 | -2.79 | 5.00E-05 | 4.28E-04 | -- | -- |
| EVM0002088 | 4.36 | 29.88 | -2.78 | 1.29E-02 | 4.59E-02 | -- | Fungal Zn(2)-Cys(6) binuclear cluster domain |
| EVM0010870 | 17.58 | 119.36 | -2.76 | 5.00E-05 | 4.28E-04 | -- | Conidiation protein 6 |
| EVM0008337 | 15.72 | 106.59 | -2.76 | 5.00E-05 | 4.28E-04 | General function prediction only | -- |
| EVM0005972 | 523.41 | 3525.14 | -2.75 | 5.00E-05 | 4.28E-04 | -- | -- |
| EVM0011432 | 7.75 | 52.00 | -2.75 | 5.00E-05 | 4.28E-04 | Lipid transport and metabolism | SacI homology domain |
| EVM0009852 | 9.77 | 65.38 | -2.74 | 5.00E-05 | 4.28E-04 | Transcription | Homeobox domain |
| EVM0007202 | 1.57 | 10.48 | -2.74 | 5.00E-05 | 4.28E-04 | -- | non-haem dioxygenase in morphine synthesis N-terminal |
| EVM0008304 | 33.66 | 224.54 | -2.74 | 5.00E-05 | 4.28E-04 | Defense mechanisms | Dual specificity phosphatase, catalytic domain |
| EVM0009705 | 37.86 | 249.89 | -2.72 | 5.00E-05 | 4.28E-04 | -- | -- |
| EVM0009499 | 0.88 | 5.79 | -2.72 | 8.20E-03 | 3.20E-02 | General function prediction only | Phosphatidylethanolamine-binding protein |
| EVM0000914 | 22.79 | 150.35 | -2.72 | 5.00E-05 | 4.28E-04 | -- | Peroxidase, family 2 |
| EVM0012106 | 15.14 | 99.22 | -2.71 | 5.00E-05 | 4.28E-04 | Coenzyme transport and metabolism | Ketopantoate hydroxymethyltransferase |
| EVM0007187 | 2.41 | 15.76 | -2.71 | 5.00E-05 | 4.28E-04 | -- | Pregnancy-associated plasma protein-A |
| Accession | Mean | Standard Deviation | E-value | p-value | Description |
|-----------|------|--------------------|---------|---------|-------------|
| EVM0009205 | 0.77 | 5.03               | 2.71    | 6.15E-03|             |
| EVM0006446 | 51.34| 334.69             | 2.70    | 5.00E-05| FR47-like protein |
| EVM0004929 | 14.94| 97.05              | 2.70    | 5.00E-05| General function prediction only |
| EVM0008406 | 13.77| 88.54              | 2.69    | 5.00E-05| Lipid transport and metabolism |
| EVM0007650 | 57.53| 369.31             | 2.68    | 5.00E-05|             |
| EVM0006820 | 17.51| 112.24             | 2.68    | 5.00E-05| Lipoxygenase |
| EVM0004929 | 14.94| 97.05              | 2.68    | 5.00E-05| Ras family |
| EVM0008242 | 1.04 | 6.50               | 2.66    | 5.00E-05| Hydroxymethylglutaryl-coenzyme A synthase N terminal |
| EVM0004341 | 14.94| 97.05              | 2.61    | 5.00E-04| CSL zinc finger |

- FR47-like protein
- General function prediction only
- AMP-binding enzyme
- Calcineurin-like phosphoesterase
- Hydroxymethylglutaryl-coenzyme A synthase N terminal
- Glycosyl hydrolase family 12
- Lipase
- Thioesterase superfamily
- Function unknown
| Accession     | Coverage | Identity | Stratum | Annotation                                                                 |
|--------------|----------|----------|---------|---------------------------------------------------------------------------|
| EVM0011852  | 32.55    | 197.48   | -2.60   | 5.00E-05 4.28E-04 -- --                                                  |
| EVM0002297  | 215.72   | 1306.69  | -2.60   | 5.00E-05 4.28E-04 -- --                                                  |
| EVM0003306  | 30.60    | 185.23   | -2.60   | 5.00E-05 4.28E-04 Intracellular trafficking, secretion, and vesicular transport Snf7 |
| EVM0002614  | 10.09    | 61.03    | -2.60   | 5.00E-05 4.28E-04 Lipid transport and metabolism Phospholipase/Carboxylesterase |
| EVM0010217  | 41.60    | 251.32   | -2.59   | 5.00E-05 4.28E-04 -- --                                                  |
| EVM0010131  | 57.44    | 346.41   | -2.59   | 5.00E-05 4.28E-04 -- --                                                  |
| EVM0008150  | 5.20     | 31.31    | -2.59   | 5.00E-05 4.28E-04 Energy production and conversion Aldo/keto reductase family |
| EVM0008586  | 12.89    | 77.50    | -2.59   | 5.00E-05 4.28E-04 -- --                                                  |
| EVM0006542  | 48.12    | 288.67   | -2.58   | 5.00E-05 4.28E-04 -- --                                                  |
| EVM0009699  | 51.54    | 308.49   | -2.58   | 5.00E-05 4.28E-04 Posttranslational modification, protein turnover, chaperones Proteasome subunit |
| EVM0000332  | 39.29    | 233.59   | -2.57   | 5.00E-05 4.28E-04 Lipid transport and metabolism Thiolase, N-terminal domain |
| EVM0004176  | 228.07   | 1351.39  | -2.57   | 5.00E-05 4.28E-04 -- --                                                  |
| EVM0008894  | 19.08    | 113.02   | -2.57   | 5.00E-05 4.28E-04 -- --                                                  |
| EVM0009527  | 4.57     | 26.90    | -2.56   | 5.00E-05 4.28E-04 Replication, recombination and repair Cid1 family poly A polymerase |
| EVM     |    |    |   |    |         |                                           |
|---------|----|----|---|----|---------|-------------------------------------------|
|         | 2.41 | 14.19 | -2.56 | 5.00E-05 | 4.28E-04 | Domain of unknown function (DUF3415)     |
| EVM0003318 | 29.54 | 173.34 | -2.55 | 5.00E-05 | 4.28E-04 | Autophagy protein 16 (ATG16)             |
| EVM0003828 | 8.48 | 49.52 | -2.55 | 5.00E-05 | 4.28E-04 | Membrane bound O-acyl transferase family |
| EVM0002081 | 2.60 | 15.03 | -2.53 | 5.00E-05 | 4.28E-04 | Signal transduction mechanisms          |
| EVM0005185 | 75.62 | 436.79 | -2.53 | 5.00E-05 | 4.28E-04 | Amino acid transport and metabolism      |
| EVM0006915 | 19.97 | 115.05 | -2.53 | 5.00E-05 | 4.28E-04 | Velvet factor                           |
| EVM0003772 | 3.78 | 21.75 | -2.53 | 5.00E-05 | 4.28E-04 | --                                      |
| EVM0011121 | 3.69 | 21.23 | -2.52 | 5.00E-05 | 4.28E-04 | --                                      |
| EVM0010530 | 40.07 | 230.12 | -2.52 | 5.00E-05 | 4.28E-04 | --                                      |
| EVM0007419 | 16.83 | 96.38 | -2.52 | 5.00E-05 | 4.28E-04 | --                                      |
| EVM0007852 | 779.47 | 4462.47 | -2.52 | 5.00E-05 | 4.28E-04 | Posttranslational modification, protein turnover, chaperones |
| EVM0008058 | 6.15 | 35.18 | -2.52 | 5.00E-05 | 4.28E-04 | --                                      |
| EVM0009876 | 9.36 | 53.35 | -2.51 | 5.00E-05 | 4.28E-04 | Translation, ribosomal structure and biogenesis |
| EVM0002150 | 131.46 | 745.19 | -2.50 | 5.00E-05 | 4.28E-04 | General function prediction only         |
| EVM0006838 | 2.02 | 11.40 | -2.50 | 5.00E-05 | 4.28E-04 | --                                      |
| EVM0004717 | 5.74 | 32.28 | -2.49 | 5.00E-05 | 4.28E-04 | Protein tyrosine kinase                  |
| EVM0000819 | 3.52 | 19.76 | -2.49 | 5.00E-05 | 4.28E-04 | Transcription                           |
| Accession      | Value1 | Value2   | Value3 | Value4 | Value5 | Value6 | Description                                                                 |
|---------------|--------|----------|--------|--------|--------|--------|-----------------------------------------------------------------------------|
| EVM0008863    | 37.02  | 207.28   | -2.49  | 5.00E-05| 4.28E-04| --     | Protein of unknown function (DUF3759)                                       |
| EVM0007977    | 161.62 | 901.87   | -2.48  | 5.00E-05| 4.28E-04| --     | --                                                                          |
| EVM0006195    | 17.40  | 97.00    | -2.48  | 5.00E-05| 4.28E-04| --     | pre-mRNA splicing factor component                                          |
| EVM0004965    | 3.40   | 18.85    | -2.47  | 5.00E-05| 4.28E-04| Function unknown                                                           | Tho complex subunit 7                                                     |
| EVM0009031    | 4.48   | 24.64    | -2.46  | 5.00E-05| 4.28E-04| --     | Glycosyl hydrolases family 43                                              |
| EVM0009471    | 15.74  | 86.16    | -2.45  | 5.00E-05| 4.28E-04| --     | --                                                                          |
| EVM0011795    | 45.31  | 246.67   | -2.44  | 5.00E-05| 4.28E-04| --     | --                                                                          |
| EVM0004745    | 6.97   | 37.81    | -2.44  | 5.00E-05| 4.28E-04| --     | --                                                                          |
| EVM0005254    | 38.61  | 209.01   | -2.44  | 5.00E-05| 4.28E-04| --     | --                                                                          |
| EVM0009138    | 2.81   | 15.19    | -2.44  | 5.00E-05| 4.28E-04| --     | --                                                                          |
| EVM0006949    | 41.28  | 222.96   | -2.43  | 5.00E-05| 4.28E-04| --     | N-terminal domain of ribose phosphate pyrophosphokinase                    |
| EVM0010152    | 4.67   | 25.08    | -2.43  | 5.00E-05| 4.28E-04| --     | --                                                                          |
| EVM0004565    | 1.88   | 10.12    | -2.42  | 5.00E-05| 4.28E-04| --     | Domain of unknown function (DUF4139)                                       |
| EVM0002391    | 399.28 | 2143.23  | -2.42  | 5.00E-05| 4.28E-04| --     | --                                                                          |
| EVM0011516    | 8.26   | 44.14    | -2.42  | 5.00E-05| 4.28E-04| --     | C2H2-type zinc finger                                                       |
| EVM0003567    | 0.54   | 2.88     | -2.42  | 5.00E-05| 4.28E-04| --     | Tryptophan halogenase                                                      |
| EVM0010548    | 17.96  | 95.33    | -2.41  | 5.00E-05| 4.28E-04| --     | --                                                                          |
| EVM0010001    | 6.31   | 33.16    | -2.39  | 5.00E-05| 4.28E-04| Translation, ribosomal structure and biogenesis                            |
| EVM0001342    | 29.29  | 153.60   | -2.39  | 5.00E-05| 4.28E-04| Defense mechanisms                                                          |
| EVM0007661    | 8.33   | 43.70    | -2.39  | 5.00E-05| 4.28E-04| --     | TB2/DP1, HVA22 family                                                      |
| EVM0008650    | 53.76  | 281.20   | -2.39  | 5.00E-05| 4.28E-04| --     | C2 domain                                                                 |
| EVM0001342    | 29.29  | 153.60   | -2.39  | 5.00E-05| 4.28E-04| --     | --                                                                        |
| EVM0002822 | 9.96 | 52.08 | -2.39 | 5.00E-05 | 4.28E-04 | -- | Caspase domain |
| EVM0005881 | 3.51 | 18.31 | -2.38 | 5.00E-05 | 4.28E-04 | -- | Small nuclear RNA activating complex (SNAPc), subunit SNAP43 |
| EVM0007292 | 2.97 | 15.51 | -2.38 | 5.00E-05 | 4.28E-04 | -- | Domain of unknown function (DUF4110) |
| EVM0007572 | 2.86 | 14.88 | -2.38 | 5.00E-05 | 4.28E-04 | -- | -- |
| EVM0004357 | 134.54 | 700.77 | -2.38 | 5.00E-05 | 4.28E-04 | -- | -- |
| EVM0006881 | 12.47 | 64.73 | -2.38 | 5.00E-05 | 4.28E-04 | -- | NUDIX domain |
| EVM0003461 | 19.88 | 103.12 | -2.38 | 5.00E-05 | 4.28E-04 | Intracellular trafficking, secretion, and vesicular transport | Annexin |
| EVM0011417 | 13.68 | 70.83 | -2.37 | 5.00E-05 | 4.28E-04 | -- | Aldo/keto reductase family |
| EVM0011506 | 3.88 | 20.07 | -2.37 | 5.00E-05 | 4.28E-04 | -- | BTB/POZ domain |
| EVM0010360 | 2.34 | 12.07 | -2.37 | 1.00E-03 | 5.70E-03 | -- | CFEM domain |
| EVM000685 | 3.99 | 20.58 | -2.37 | 5.00E-05 | 4.28E-04 | Carbohydrate transport and metabolism | Transaldolase |
| EVM0010440 | 49.84 | 256.28 | -2.36 | 5.00E-05 | 4.28E-04 | -- | Cytochrome c/c1 heme lyase |
| EVM0002660 | 19.88 | 103.12 | -2.36 | 5.00E-05 | 4.28E-04 | -- | MOZ/SAS family |
| EVM0006723 | 155.42 | 794.72 | -2.35 | 5.00E-05 | 4.28E-04 | -- | MOZ/SAS family |
| EVM0010229 | 34.86 | 178.00 | -2.35 | 5.00E-05 | 4.28E-04 | General function prediction only | -- |
| EVM0008938 | 12.47 | 64.73 | -2.38 | 5.00E-05 | 4.28E-04 | -- | -- |
| EVM0010957 | 21.02 | 107.26 | -2.35 | 5.00E-05 | 4.28E-04 | Transcription | Myb-like DNA-binding domain |
| Accession | No. 1 | No. 2 | No. 3 | No. 4 | No. 5 | No. 6 | Description |
|-----------|-------|-------|-------|-------|-------|-------|-------------|
| EVM0001277 | 4.40  | 22.39 | -2.35 | 5.00E-05 | 4.28E-04 | -- | Replication, recombination and repair |
| EVM0003758 | 2.88  | 14.66 | -2.35 | 5.00E-05 | 4.28E-04 | -- | -- |
| EVM0009537 | 2.64  | 13.45 | -2.35 | 7.30E-03 | 2.91E-02 | -- | -- |
| EVM0008877 | 12.60 | 64.05 | -2.35 | 5.00E-05 | 4.28E-04 | -- | -- |
| EVM0004716 | 7.94  | 40.31 | -2.34 | 5.00E-05 | 4.28E-04 | -- | Exonuclease |
| EVM0000132 | 50.41 | 253.39| -2.33 | 5.00E-05 | 4.28E-04 | -- | -- |
| EVM0003103 | 59.11 | 297.01| -2.33 | 5.00E-05 | 4.28E-04 | -- | -- |
| EVM0009546 | 11.02 | 54.96 | -2.32 | 5.00E-05 | 4.28E-04 | -- | Fungal specific transcription factor domain |
| EVM0007669 | 0.31  | 1.56  | -2.31 | 4.40E-03 | 1.94E-02 | -- | Zinc-finger double domain |
| EVM0000116 | 3.34  | 16.56 | -2.31 | 1.00E-04 | 7.96E-04 | -- | -- |
| EVM0006626 | 51.89 | 257.00| -2.31 | 5.00E-05 | 4.28E-04 | -- | -- |
| EVM0007461 | 4.12  | 20.39 | -2.31 | 5.00E-05 | 4.28E-04 | -- | Aldo/keto reductase family |
| EVM0005865 | 439.25| 2171.68| -2.31 | 4.50E-04 | 2.92E-03 | -- | Proteolipid membrane potential modulator |
| EVM0010107 | 92.48 | 452.80| -2.29 | 5.00E-05 | 4.28E-04 | -- | EF hand |
| EVM0005796 | 1156.13| 5651.83| -2.29 | 5.00E-05 | 4.28E-04 | -- | 60s Acidic ribosomal protein |
| EVM0011171 | 1.31  | 6.42  | -2.29 | 5.00E-05 | 4.28E-04 | -- | -- |
| EVM0011115 | 2.56  | 12.52 | -2.29 | 5.00E-05 | 4.28E-04 | -- | -- |
| EVM0002995 | 8.80  | 42.90 | -2.28 | 5.00E-05 | 4.28E-04 | -- | FF domain |

General function prediction only
| Accession     | E-value | B-score | LogOdds | P-value | Database     | Description                                      |
|--------------|---------|---------|---------|---------|--------------|--------------------------------------------------|
| EVM0000062   | 20.49   | 99.66   | -2.28   | 5.00E-05| 4.28E-04     | --                                               |
| EVM0000351   | 10.15   | 49.30   | -2.28   | 5.00E-05| 4.28E-04     | --                                               |
| EVM0005078   | 1.53    | 7.42    | -2.28   | 1.00E-04| 7.96E-04     | Cell cycle control, cell division, chromosome partitioning |
|              |         |         |         |         |              | HORMA domain                                     |
| EVM00111013  | 14.04   | 67.94   | -2.28   | 2.25E-03| 1.12E-02     | Function unknown                                 |
|              |         |         |         |         |              | COQ9                                             |
| EVM0003267   | 9620.57 | 46550.10| -2.27   | 5.00E-05| 4.28E-04     | --                                               |
| EVM0004775   | 20.46   | 98.91   | -2.27   | 5.00E-05| 4.28E-04     | --                                               |
| EVM0002596   | 0.45    | 2.18    | -2.27   | 9.50E-04| 5.46E-03     | --                                               |
|              |         |         |         |         |              | Phosphotransferase enzyme family                  |
| EVM0009788   | 218.27  | 1054.21 | -2.27   | 5.00E-05| 4.28E-04     | --                                               |
|              |         |         |         |         |              | --                                               |
| EVM0002460   | 86.36   | 416.72  | -2.27   | 1.00E-04| 7.96E-04     | General function prediction only                 |
|              |         |         |         |         |              | Proteolipid membrane potential modulator         |
| EVM0004549   | 312.60  | 1507.81 | -2.27   | 5.00E-05| 4.28E-04     | Lipid transport and metabolism                   |
|              |         |         |         |         |              | HIUase/Transthyretin family                       |
| EVM0010543   | 1.31    | 6.31    | -2.27   | 5.00E-05| 4.28E-04     | --                                               |
|              |         |         |         |         |              | --                                               |
| EVM0008461   | 9.67    | 46.45   | -2.26   | 5.00E-05| 4.28E-04     | --                                               |
|              |         |         |         |         |              | Putative snoRNA binding domain                   |
| EVM0002926   | 233.05  | 1117.65 | -2.26   | 5.00E-05| 4.28E-04     | General function prediction only                 |
|              |         |         |         |         |              | Enoyl-(Acyl carrier protein) reductase            |
| EVM0000147   | 1.41    | 6.75    | -2.26   | 5.00E-05| 4.28E-04     | --                                               |
|              |         |         |         |         |              | --                                               |
| EVM0002338   | 10.46   | 49.96   | -2.26   | 5.00E-05| 4.28E-04     | Lipid transport and metabolism                   |
|              |         |         |         |         |              | PAP2 superfamily                                 |
| EVM0006839   | 2.40    | 11.45   | -2.26   | 5.00E-05| 4.28E-04     | --                                               |
|              |         |         |         |         |              | --                                               |
| EVM0009347   | 15.04   | 71.76   | -2.25   | 5.00E-05| 4.28E-04     | WH2 motif                                        |
| EVM0001964   | 8.12    | 38.57   | -2.25   | 5.00E-05| 4.28E-04     | --                                               |

- **EVM0000062**: Enzyme with E-value 20.49, B-score 99.66, LogOdds -2.28, P-value 5.00E-05, and 4.28E-04. No specific database information or description provided.
- **EVM0000351**: Enzyme with E-value 10.15, B-score 49.30, LogOdds -2.28, P-value 5.00E-05, and 4.28E-04. No specific database information or description provided.
- **EVM0005078**: Enzyme with E-value 1.53, B-score 7.42, LogOdds -2.28, P-value 1.00E-04, and 7.96E-04. Describes cell cycle control, cell division, and chromosome partitioning. No specific database information or description provided.
- **EVM00111013**: Enzyme with E-value 14.04, B-score 67.94, LogOdds -2.28, P-value 2.25E-03, and 1.12E-02. Function unknown. No specific database information or description provided.
- **EVM0003267**: Enzyme with E-value 9620.57, B-score 46550.10, LogOdds -2.27, P-value 5.00E-05, and 4.28E-04. No specific database information or description provided.
- **EVM0004775**: Enzyme with E-value 20.46, B-score 98.91, LogOdds -2.27, P-value 5.00E-05, and 4.28E-04. No specific database information or description provided.
- **EVM0002596**: Enzyme with E-value 0.45, B-score 2.18, LogOdds -2.27, P-value 9.50E-04, and 5.46E-03. No specific database information or description provided.
- **EVM0009788**: Enzyme with E-value 218.27, B-score 1054.21, LogOdds -2.27, P-value 5.00E-05, and 4.28E-04. No specific database information or description provided.
- **EVM0002460**: Enzyme with E-value 86.36, B-score 416.72, LogOdds -2.27, P-value 1.00E-04, and 7.96E-04. Describes general function prediction only. No specific database information or description provided.
- **EVM0004549**: Enzyme with E-value 312.60, B-score 1507.81, LogOdds -2.27, P-value 5.00E-05, and 4.28E-04. Describes lipid transport and metabolism. No specific database information or description provided.
- **EVM0010543**: Enzyme with E-value 1.31, B-score 6.31, LogOdds -2.27, P-value 5.00E-05, and 4.28E-04. No specific database information or description provided.
- **EVM0008461**: Enzyme with E-value 9.67, B-score 46.45, LogOdds -2.26, P-value 5.00E-05, and 4.28E-04. No specific database information or description provided.
- **EVM0002926**: Enzyme with E-value 233.05, B-score 1117.65, LogOdds -2.26, P-value 5.00E-05, and 4.28E-04. Describes general function prediction only. No specific database information or description provided.
- **EVM00000147**: Enzyme with E-value 1.41, B-score 6.75, LogOdds -2.26, P-value 5.00E-05, and 4.28E-04. No specific database information or description provided.
- **EVM0002338**: Enzyme with E-value 10.46, B-score 49.96, LogOdds -2.26, P-value 5.00E-05, and 4.28E-04. Describes lipid transport and metabolism. No specific database information or description provided.
- **EVM0006839**: Enzyme with E-value 2.40, B-score 11.45, LogOdds -2.26, P-value 5.00E-05, and 4.28E-04. No specific database information or description provided.
- **EVM0009347**: Enzyme with E-value 15.04, B-score 71.76, LogOdds -2.25, P-value 5.00E-05, and 4.28E-04. Describes WH2 motif. No specific database information or description provided.
- **EVM0001964**: Enzyme with E-value 8.12, B-score 38.57, LogOdds -2.25, P-value 5.00E-05, and 4.28E-04. No specific database information or description provided.
| Accession      | G   | M   | E   | P1  | P2  | Description                                                                 |
|---------------|-----|-----|-----|-----|-----|----------------------------------------------------------------------------|
| EVM0007348    | 59.12 | 280.71 | -2.25 | 5.00E-05 | 4.28E-04 | General function prediction only                                            |
|               |      |      |     |     |     | Dienelactone hydrolase family                                               |
| EVM0004228    | 10.15 | 48.12  | -2.25 | 5.00E-05 | 4.28E-04 | Translation, ribosomal structure and biogenesis                            |
|               |      |      |     |     |     | Brix domain                                                                |
| EVM0006689    | 17.21 | 81.39  | -2.24 | 5.00E-05 | 4.28E-04 | General function prediction only                                            |
|               |      |      |     |     |     | --                                                                         |
| EVM0001350    | 357.09 | 1686.44 | -2.24 | 5.00E-05 | 4.28E-04 | --                                                                          |
|               |      |      |     |     |     | CsbD-like                                                                  |
| EVM0005968    | 6.06  | 28.61  | -2.24 | 5.00E-05 | 4.28E-04 | --                                                                          |
|               |      |      |     |     |     | --                                                                         |
| EVM0003699    | 4.59  | 21.56  | -2.23 | 5.00E-05 | 4.28E-04 | RNA processing and modification                                             |
|               |      |      |     |     |     | Adenosine-deaminase (editase) domain                                        |
| EVM0006292    | 2.18  | 10.24  | -2.23 | 5.00E-05 | 4.28E-04 | --                                                                          |
|               |      |      |     |     |     | Fungal Zn(2)-Cys(6) binuclear cluster domain                               |
| EVM0009995    | 5.73  | 26.87  | -2.23 | 5.00E-05 | 4.28E-04 | RNA processing and modification                                             |
|               |      |      |     |     |     | WD domain, G-beta repeat                                                    |
| EVM0006174    | 3.97  | 18.64  | -2.23 | 5.00E-05 | 4.28E-04 | --                                                                          |
|               |      |      |     |     |     | --                                                                         |
| EVM0009798    | 42.06 | 197.31 | -2.23 | 5.00E-05 | 4.28E-04 | RNA processing and modification                                             |
|               |      |      |     |     |     | RNA recognition motif. (a.k.a. RRM, RBD, or RNP domain)                    |
| EVM0007949    | 12.09 | 56.70  | -2.23 | 5.00E-05 | 4.28E-04 | RNA processing and modification                                             |
|               |      |      |     |     |     | WD domain, G-beta repeat                                                    |
| EVM0010770    | 48.97 | 229.46 | -2.23 | 5.00E-05 | 4.28E-04 | --                                                                          |
|               |      |      |     |     |     | --                                                                         |
| EVM0009589    | 32.18 | 150.77 | -2.23 | 5.00E-05 | 4.28E-04 | --                                                                          |
|               |      |      |     |     |     | --                                                                         |
| EVM0000266    | 17.18 | 80.40  | -2.23 | 5.00E-05 | 4.28E-04 | --                                                                          |
|               |      |      |     |     |     | --                                                                         |
| EVM0003550    | 5.11  | 23.90  | -2.23 | 5.00E-05 | 4.28E-04 | --                                                                          |
|               |      |      |     |     |     | --                                                                         |
| EVM0009311    | 67.02 | 313.03 | -2.22 | 5.00E-05 | 4.28E-04 | --                                                                          |
|               |      |      |     |     |     | Etoposide-induced protein 2.4 (El24)                                       |
| Accession   | E-value | Identity | Coverage | E-value | Description                                      |
|-------------|---------|----------|----------|---------|--------------------------------------------------|
| EVM0006056 | 0.88    | 4.12     | -2.22    | 7.50E-04| 4.49E-03 | Transcription TEA/ATTS domain family             |
| EVM0007798 | 2.43    | 11.32    | -2.22    | 5.00E-05| 4.28E-04 | General function prediction only                 |
| EVM0004688 | 26.10   | 121.36   | -2.22    | 5.00E-05| 4.28E-04 | General function prediction only                 |
| EVM0003326 | 29.04   | 134.59   | -2.21    | 5.00E-05| 4.28E-04 | General function prediction only                 |
| EVM0001192 | 69.88   | 323.20   | -2.21    | 5.00E-05| 4.28E-04 | RNA polymerase Rpb3/Rpb11 dimerisation domain    |
| EVM0005036 | 19.90   | 91.96    | -2.21    | 5.00E-05| 4.28E-04 | Function unknown WD domain, G-beta repeat        |
| EVM0005583 | 13.13   | 60.65    | -2.21    | 5.00E-05| 4.28E-04 | Function unknown                                |
| EVM0006543 | 1.87    | 8.60     | -2.20    | 5.00E-05| 4.28E-04 | Function unknown                                |
| EVM0002467 | 27.00   | 127.49   | -2.20    | 5.00E-05| 4.28E-04 | Function unknown                                |
| EVM0011482 | 21.44   | 98.36    | -2.20    | 8.65E-03| 3.34E-02 | Function unknown                                |
| EVM00011482| 17.82   | 81.69    | -2.20    | 5.00E-05| 4.28E-04 | Function unknown WD domain, G-beta repeat        |
| EVM0004258 | 26.00   | 119.09   | -2.20    | 5.00E-05| 4.28E-04 | Function unknown                                |
| EVM0011382 | 6.72    | 30.76    | -2.19    | 5.00E-05| 4.28E-04 | Function unknown                                |
| EVM0006992 | 9.57    | 43.56    | -2.19    | 5.00E-05| 4.28E-04 | Function unknown Cytochrome P450                 |
| EVM0000329 | 4.50    | 20.38    | -2.18    | 5.00E-05| 4.28E-04 | Function unknown                                |
| EVM0011804 | 4.66    | 21.10    | -2.18    | 5.00E-05| 4.28E-04 | Function unknown                                |
| EVM0008113 | 5.78    | 26.14    | -2.18    | 5.00E-05| 4.28E-04 | Function unknown F-box-like                     |
| EVM0010481 | 4.81    | 21.77    | -2.18    | 5.00E-05| 4.28E-04 | Function unknown F-box-like                     |
| EVM0008272 | 0.48    | 2.19     | -2.18    | 3.00E-04| 2.07E-03 | Function unknown                                |
| EVM0008558 | 2.24    | 10.12    | -2.18    | 5.00E-05| 4.28E-04 | Function unknown Glyoxal oxidase N-terminus     |
| EVM0007254 | 8026.47 | 36270.50 | -2.18    | 5.00E-05| 4.28E-04 | Function unknown Ribosomal protein S30           |
| EVM0005285 | 1421.95 | 6412.12  | -2.17    | 5.00E-05| 4.28E-04 | Function unknown                                |
| EVM0009404 | 14.69   | 66.19    | -2.17    | 5.00E-05| 4.28E-04 | Function unknown General function prediction only|

Dip2/Utp12 Family
| EVM ID     | E Value | Score  | Log2 Fold | Query E Value | Query Score | Log2 Fold | Description                                                                 |
|------------|---------|--------|-----------|---------------|-------------|-----------|----------------------------------------------------------------------------|
| EVM0001259 | 8.67    | 39.05  | -2.17     | 5.00E-05      | 4.28E-04    | --        | General function prediction only, WD domain, G-beta repeat                 |
| EVM0006570 | 792.75  | 3557.49| -2.17     | 5.00E-05      | 4.28E-04    | --        | Pyridoxamine 5'-phosphate oxidase                                          |
| EVM0002266 | 221.11  | 990.92 | -2.16     | 5.00E-05      | 4.28E-04    | --        | Protein of unknown function (DUF3429)                                     |
| EVM0009720 | 9.13    | 40.88  | -2.16     | 5.00E-05      | 4.28E-04    | --        | Cell cycle control, cell division, chromosome partitioning                |
| EVM0005110 | 30.58   | 136.78 | -2.16     | 5.00E-05      | 4.28E-04    | --        | Transcription, cell division, chromosome partitioning                      |
| EVM0001827 | 2.49    | 11.15  | -2.16     | 5.00E-05      | 4.28E-04    | --        | Helicase conserved C-terminal domain                                       |
| EVM000219  | 52.84   | 235.65 | -2.16     | 5.00E-05      | 4.28E-04    | --        | General function prediction only, Cyclin                                   |
| EVM0001614 | 2.25    | 10.01  | -2.16     | 5.00E-05      | 4.28E-04    | --        | --                                                                         |
| EVM0001981 | 5.86    | 26.02  | -2.15     | 5.00E-05      | 4.28E-04    | --        | HD domain                                                                  |
| EVM0004173 | 11.83   | 52.31  | -2.15     | 5.00E-05      | 4.28E-04    | --        | --                                                                         |
| EVM0008334 | 87.93   | 387.81 | -2.14     | 5.00E-05      | 4.28E-04    | --        | --                                                                         |
| EVM0004672 | 31.96   | 140.79 | -2.14     | 5.00E-05      | 4.28E-04    | --        | --                                                                         |
| EVM0002798 | 5.25    | 23.12  | -2.14     | 5.00E-05      | 4.28E-04    | --        | F-box-like                                                                 |
| EVM0005429 | 9.52    | 41.78  | -2.13     | 5.00E-05      | 4.28E-04    | --        | Transcription, CCAAT-binding transcription factor (CBF-B/NF-YA) subunit B  |
| EVM0009550 | 12.43   | 24.89  | -1.00     | 4.00E-04      | 2.65E-03    | --        | --                                                                         |
| EVM0005497 | 51.81   | 226.99 | -2.13     | 5.00E-05      | 4.28E-04    | --        | --                                                                         |
| EVM0005377  | 4.34  | 18.99  | -2.13 | 5.00E-05 | 4.28E-04 | -- | Cellulase (glycosyl hydrolase family 5) |
| EVM0009845  | 12.24 | 53.49  | -2.13 | 5.00E-05 | 4.28E-04 | -- | -- |
| EVM0009113  | 21.01 | 91.71  | -2.13 | 5.00E-05 | 4.28E-04 | -- | Transcription Maf1 regulator |
| EVM0008230  | 15.30 | 66.75  | -2.13 | 5.00E-05 | 4.28E-04 | -- | Sugar (and other) transporter |
| EVM0005976  | 75.67 | 328.96 | -2.12 | 5.00E-05 | 4.28E-04 | -- | General function prediction only |
| EVM0007199  | 136.75| 592.09 | -2.11 | 5.00E-05 | 4.28E-04 | -- | Yippee zinc-binding/DNA-binding /Mis18, centromere assembly |
| EVM0010015  | 0.34  | 1.46   | -2.11 | 1.21E-02 | 4.36E-02 | -- | -- |
| EVM0007358  | 9.21  | 39.84  | -2.11 | 5.00E-05 | 4.28E-04 | -- | -- |
| EVM0005054  | 24.15 | 104.28 | -2.11 | 5.00E-05 | 4.28E-04 | -- | General function prediction only |
| EVM0007358  | 22.06 | 94.65  | -2.10 | 5.00E-05 | 4.28E-04 | -- | -- |
| EVM0003631  | 7.32  | 28.73  | -1.97 | 2.50E-04 | 1.77E-03 | -- | -- |
| EVM0007878  | 13.71 | 58.62  | -2.10 | 5.00E-05 | 4.28E-04 | -- | Posttranslational modification, protein turnover, chaperones |
| ID           | EVM0003792 | EVM0008730 | EVM0007261 | EVM0001122 | EVM0012205 | EVM0007696 | EVM0007162 | EVM0004297 | EVM0010534 | EVM0008237 | EVM0006494 | EVM0005139 | EVM0005280 | EVM0009462 | EVM0001526 | EVM0008356 | EVM0001591 | EVM0008966 |
|--------------|------------|------------|------------|------------|------------|------------|------------|------------|------------|------------|------------|------------|------------|------------|------------|------------|------------|------------|
| Value        | 63.49      | 8.47       | 283.14     | 37.62      | 85.65      | 7.81       | 15.05      | 32.24      | 43.81      | 17.56      | 13.62      | 323.22     | 0.62       | 8.04       | 3.41       | 13.38      | 1.97       | 24.44      |
| Standard Dev.| 271.44     | 36.22      | 1209.34    | 160.49     | 365.17     | 33.26      | 64.07      | 137.10     | 185.63     | 74.37      | 57.63      | 1364.38    | 2.59       | 33.76      | 14.26      | 55.97      | 8.24       | 102.00     |
| Score        | -2.10      | -2.10      | -2.09      | -2.09      | -2.09      | -2.09      | -2.09      | -2.09      | -2.08      | -2.08      | -2.08      | -2.08      | -2.07      | -2.06      | -2.06      | -2.06      | -2.06      |
| Fold Changes | 5.00E-05   | 5.00E-05   | 5.00E-05   | 5.00E-05   | 5.00E-05   | 5.00E-05   | 5.00E-05   | 5.00E-05   | 5.00E-05   | 5.00E-05   | 5.00E-05   | 5.00E-05   | 1.35E-03   | 5.00E-05   | 5.00E-05   | 5.00E-05   | 5.00E-05   | 5.00E-05   |
| EVM0003792   | Posttranslational modification, protein turnover, chaperones | ATPase family associated with various cellular activities (AAA) |
| EVM0008730   | --         | --         | --         | --         | --         | Fibrillarin | --         | BTG family | --         | --         | --         | Sas10 C-terminal domain | --         | --         | --         | Utp11 protein |
| EVM0007261   | RNA processing and modification | --         | Domain of unknown function (DUF4139) |
| EVM0001122   | Function unknown | RHS Repeat |
| EVM0012205   | --         | --         | --         | --         | --         | --         | --         | --         | --         | --         | --         | --         | --         | --         | --         | --         | --         | --         |
| EVM0007696   | --         | --         | --         | --         | --         | --         | --         | --         | --         | --         | --         | --         | --         | --         | --         | --         | --         | --         | --         |
| EVM0007162   | RNA processing and modification | Helicase associated domain (HA2) |
| EVM0004297   | --         | --         | --         | --         | --         | --         | --         | --         | --         | --         | --         | --         | --         | --         | --         | --         | --         | --         | --         |
| EVM0010534   | --         | --         | --         | --         | --         | --         | --         | --         | --         | --         | --         | --         | --         | --         | --         | --         | --         | --         | --         | --         |
| EVM0008237   | --         | --         | --         | --         | --         | --         | --         | --         | --         | --         | --         | --         | --         | --         | --         | --         | --         | --         | --         | --         |
| EVM0006494   | Chromatin structure and dynamics | --         |
| EVM0005139   | --         | --         | --         | --         | --         | --         | --         | --         | --         | --         | --         | --         | --         | --         | --         | --         | --         | --         | --         | --         |
| EVM0005280   | --         | --         | --         | --         | --         | --         | --         | --         | --         | --         | --         | --         | --         | --         | --         | --         | --         | --         | --         | --         |
| EVM0009462   | --         | --         | --         | --         | --         | --         | --         | --         | --         | --         | --         | --         | --         | --         | --         | --         | --         | --         | --         | --         |
| EVM0001526   | --         | --         | --         | --         | --         | --         | --         | --         | --         | --         | --         | --         | --         | --         | --         | --         | --         | --         | --         | --         |
| EVM0008356   | Function unknown | Utp11 protein |
| EVM0001591   | --         | --         | --         | --         | --         | --         | --         | --         | --         | --         | --         | --         | --         | --         | --         | --         | --         | --         | --         | --         |
| EVM0008966   | --         | --         | --         | --         | --         | --         | --         | --         | --         | --         | --         | --         | --         | --         | --         | --         | --         | --         | --         | --         |
| EVM0002711 | 20.51 | 85.56 | -2.06 | 5.00E-05 | 4.28E-04 | General function prediction only | La domain |
| EVM0003560 | 18.66 | 77.76 | -2.06 | 2.35E-03 | 1.16E-02 | -- | G-patch domain |
| EVM0009085 | 245.65 | 1022.86 | -2.06 | 5.00E-05 | 4.28E-04 | -- | -- |
| EVM002160  | 5.93  | 24.59  | -2.05 | 5.00E-05 | 4.28E-04 | -- | Regulator of G protein signaling domain |
| EVM0004958 | 8.98  | 37.18  | -2.05 | 5.00E-05 | 4.28E-04 | -- | -- |
| EVM0009591 | 15.66 | 64.64  | -2.05 | 5.00E-05 | 4.28E-04 | -- | Amino acid transport and metabolism |
| EVM0010419 | 3.65  | 15.01  | -2.04 | 5.00E-05 | 4.28E-04 | -- | Mis12-Mtw1 protein family |
| EVM0008871 | 70.49 | 291.35 | -2.05 | 5.00E-05 | 4.28E-04 | General function prediction only | Ras family |
| EVM00006805| 100.27| 412.25 | -2.04 | 5.00E-05 | 4.28E-04 | Lipid transport and metabolism | Alpha/beta hydrolase family |
| EVM00001025| 14.50 | 59.58  | -2.04 | 5.00E-05 | 4.28E-04 | -- | Zinc-binding dehydrogenase |
| EVM00008442| 16.24 | 66.68  | -2.04 | 5.00E-05 | 4.28E-04 | -- | -- |
| EVM0001552 | 13.45 | 55.19  | -2.04 | 5.00E-05 | 4.28E-04 | #N/A | #N/A |
| EVM0003805 | 1.74  | 7.13   | -2.04 | 5.00E-05 | 4.28E-04 | Transcription | HMG (high mobility group) box |
| EVM0006700 | 186.14| 763.41 | -2.04 | 5.00E-05 | 4.28E-04 | -- | Aconitase family (aconitate hydratase) |
| EVM0005625 | 1.91  | 7.82   | -2.03 | 5.00E-05 | 4.28E-04 | -- | -- |
| EVM0008511 | 31.79 | 129.79 | -2.03 | 5.00E-05 | 4.28E-04 | RNA processing and modification | Ribosomal RNA-processing protein 7 (RRP7) |
| EVM0007186 | 6.99 | 28.49 | -2.03 | 5.00E-05 | 4.28E-04 | -- | -- |
| EVM0003226 | 25.18 | 102.62 | -2.03 | 5.00E-05 | 4.28E-04 | -- | Protein of unknown function (DUF3602) |
| EVM0009334 | 7.80 | 31.79 | -2.03 | 5.00E-05 | 4.28E-04 | -- | Acetyltransferase (GNAT) family |
| EVM0010883 | 215.53 | 877.66 | -2.03 | 5.00E-05 | 4.28E-04 | Cell wall/membrane/envelope biogenesis | -- |
| EVM0002867 | 30.59 | 124.43 | -2.02 | 5.00E-05 | 4.28E-04 | Lipid transport and metabolism | MBOAT, membrane-bound O-acyltransferase family |
| EVM0010074 | 5.91 | 23.97 | -2.02 | 5.00E-05 | 4.28E-04 | -- | -- |
| EVM0002372 | 6.14 | 24.88 | -2.02 | 5.00E-05 | 4.28E-04 | -- | Cytochrome P450 |
| EVM0004156 | 0.66 | 2.67 | -2.02 | 5.00E-05 | 4.28E-04 | -- | -- |
| EVM0009322 | 6.81 | 27.51 | -2.02 | 5.00E-05 | 4.28E-04 | -- | -- |
| EVM0008748 | 5.95 | 24.02 | -2.01 | 5.00E-05 | 4.28E-04 | -- | -- |
| EVM0003817 | 5.13 | 20.70 | -2.01 | 5.00E-05 | 4.28E-04 | -- | -- |
| EVM0009820 | 110.63 | 446.14 | -2.01 | 5.00E-05 | 4.28E-04 | -- | Acetyltransferase (GNAT) domain |
| EVM0006719 | 1.65 | 6.64 | -2.01 | 1.35E-02 | 4.76E-02 | -- | Fungal hydrophobin |
| EVM0011088 | 21.26 | 85.72 | -2.01 | 5.00E-05 | 4.28E-04 | Translation, ribosomal structure and biogenesis | Gar1/Naf1 RNA binding region |
| EVM0000363 | 12.35 | 49.78 | -2.01 | 5.00E-05 | 4.28E-04 | Posttranslational modification, protein turnover, chaperones | Zinc knuckle |
| EVM0007331 | 2.74 | 11.03 | -2.01 | 5.00E-05 | 4.28E-04 | -- | -- |
| EVM0003705 | 22.24 | 89.60 | -2.01 | 5.00E-05 | 4.28E-04 | -- | alpha/beta hydrolase fold |
| EVM0001452 | 5.34 | 21.38 | -2.00 | 5.00E-05 | 4.28E-04 | -- | -- |
| EVM0002890 | 0.57 | 2.26 | -2.00 | 1.25E-03 | 6.87E-03 | Transcription | HMG (high mobility group) box |
| EVM0001316 | 3.10 | 12.36 | -2.00 | 5.00E-05 | 4.28E-04 | -- | -- |
| EVM0010252 | 34.88 | 139.03 | -2.00 | 5.00E-05 | 4.28E-04 | PX domain |
| EVM0007517 | 98.50 | 392.66 | -2.00 | 5.00E-05 | 4.28E-04 | -- | -- |
| EVM0005547 | 163.72 | 652.27 | -1.99 | 6.00E-04 | 3.72E-03 | Secondary metabolites | Aromatic amino acid lyase biosynthesis, transport and catabolism |
| EVM0005351 | 3.01 | 11.96 | -1.99 | 5.00E-05 | 4.28E-04 | -- | -- |
| EVM0003323 | 9.46 | 37.53 | -1.99 | 5.00E-05 | 4.28E-04 | -- | -- |
| EVM0000366 | 1.37 | 5.43 | -1.99 | 2.00E-04 | 1.46E-03 | -- | -- |
| EVM0010012 | 6.44 | 25.48 | -1.99 | 5.00E-05 | 4.28E-04 | Formin Homology Region 1 |
| EVM0000406 | 3.96 | 15.66 | -1.98 | 5.00E-05 | 4.28E-04 | Protein kinase domain |
| EVM0001016 | 3.40 | 13.39 | -1.98 | 5.00E-05 | 4.28E-04 | -- | -- |
| EVM0008088 | 4.16 | 16.37 | -1.98 | 5.00E-05 | 4.28E-04 | -- | -- |
| EVM0007834 | 30.88 | 121.22 | -1.97 | 5.00E-05 | 4.28E-04 | ADP-ribosylglycohydrolase |
| EVM0011475 | 5.23 | 20.53 | -1.97 | 5.00E-05 | 4.28E-04 | -- | -- |
| EVM0006590 | 2.78 | 10.89 | -1.97 | 2.50E-04 | 1.77E-03 | -- | -- |
| EVM0004906 | 111.77 | 436.41 | -1.97 | 5.00E-05 | 4.28E-04 | Fungal specific transcription factor domain |
| EVM0004482 | 1.61 | 6.26 | -1.96 | 2.70E-03 | 1.30E-02 | -- | -- |
| EVM0005279 | 429.38 | 1672.61 | -1.96 | 5.00E-05 | 4.28E-04 | Stress responsive A/B Barrel Domain |
| EVM0009109 | 42.66 | 165.97 | -1.96 | 5.00E-05 | 4.28E-04 | Glycosyl hydrolases family 43 |
| EVM0010765 | 105.84 | 411.51 | -1.96 | 5.00E-05 | 4.28E-04 | Posttranslational modification, protein turnover, chaperones | Prefoldin subunit |
| EVM0007388   | 15.18 | 58.82 | -1.95 | 5.00E-05 | 4.28E-04 | -- | -- |
|-------------|-------|-------|-------|----------|----------|----|----|
| EVM0012116  | 43.91 | 170.07| -1.95 | 5.00E-05 | 4.28E-04 | Posttranslational modification, protein turnover, chaperones Redoxin |
| EVM0002792  | 3.70  | 14.31 | -1.95 | 5.00E-05 | 4.28E-04 | -- | -- |
| EVM0001520  | 2.87  | 11.11 | -1.95 | 5.00E-05 | 4.28E-04 | -- | -- |
| EVM0008447  | 47.15 | 182.04| -1.95 | 5.00E-05 | 4.28E-04 | General function prediction only Zinc finger, C2H2 type |
| EVM0001127  | 34.01 | 130.81| -1.94 | 5.00E-05 | 4.28E-04 | -- | -- |
| EVM0005454  | 2.87  | 11.11 | -1.95 | 5.00E-05 | 4.28E-04 | General function prediction only Ras family |
| EVM0002912  | 170.90| 655.95| -1.94 | 5.00E-05 | 4.28E-04 | Function unknown Telomere stability and silencing |
| EVM0008190  | 18.34 | 70.35 | -1.94 | 5.00E-05 | 4.28E-04 | -- | Uncharacterized conserved protein (DUF2156) |
| EVM0001740  | 29.14 | 111.64| -1.94 | 5.00E-05 | 4.28E-04 | -- | 2OG-Fe(II) oxygenase superfamily |
| EVM0004489  | 27.83 | 106.41| -1.93 | 5.00E-05 | 4.28E-04 | -- | F-box-like |
| EVM0006968  | 5.84  | 22.33 | -1.93 | 1.00E-04 | 7.96E-04 | -- | -- |
| EVM0000880  | 16.93 | 64.72 | -1.93 | 5.00E-05 | 4.28E-04 | -- | Glycosyl hydrolases family 15 |
| EVM0001519  | 7.75  | 29.64 | -1.93 | 5.00E-05 | 4.28E-04 | -- | -- |
| EVM000981   | 5.09  | 19.46 | -1.93 | 2.50E-04 | 1.77E-03 | -- | -- |
| EVM0002561  | 5.01  | 19.15 | -1.93 | 5.00E-05 | 4.28E-04 | -- | -- |
| EVM000042   | 4.36  | 16.63 | -1.93 | 2.50E-04 | 1.77E-03 | -- | -- |
| EVM0002820  | 7.00  | 26.68 | -1.93 | 5.00E-05 | 4.28E-04 | -- | -- |
| ID          | Change | Score   | Coverage | E-value | Permutation E-value | Function                        | Domain/Feature                                      |
|-------------|--------|---------|----------|---------|---------------------|---------------------------------|-----------------------------------------------------|
| EVM0007165 | 126.94 | 484.00  | -1.93    | 5.00E-05| 4.28E-04            | Lipid transport and metabolism | Thiolase, C-terminal domain                          |
| EVM0010439 | 7.29   | 27.77   | -1.93    | 5.00E-05| 4.28E-04            | --                              | --                                                 |
| EVM0001318 | 2840.53| 10825.20| -1.93    | 3.50E-04| 2.36E-03            | Posttranslational modification, protein turnover, chaperones | Hsp70 protein                                       |
| EVM0010645 | 9.49   | 36.14   | -1.93    | 5.00E-05| 4.28E-04            | Cytoskeleton                     | Splicing factor, Prp19-binding domain               |
| EVM0010702 | 11.31  | 43.06   | -1.93    | 5.00E-05| 4.28E-04            | --                              | --                                                 |
| EVM0001379 | 2.59   | 9.82    | -1.92    | 5.00E-05| 4.28E-04            | --                              | FHA domain                                         |
| EVM0009023 | 11.18  | 42.43   | -1.92    | 5.00E-05| 4.28E-04            | RNA processing and modification | Brix domain                                         |
| EVM0011134 | 16.01  | 60.55   | -1.92    | 5.00E-05| 4.28E-04            | Function unknown                 | NRDE-2, necessary for RNA interference              |
| EVM0004486 | 31.62  | 119.41  | -1.92    | 5.00E-05| 4.28E-04            | --                              | --                                                 |
| EVM0011517 | 17.34  | 65.39   | -1.92    | 5.00E-05| 4.28E-04            | --                              | RNA12 protein                                       |
| EVM0010513 | 6.04   | 22.76   | -1.91    | 5.00E-05| 4.28E-04            | General function prediction only | Fumarylacetoacetate (FAA) hydrolase family          |
| EVM0000393 | 940.82 | 3545.94 | -1.91    | 5.00E-05| 4.28E-04            | --                              | --                                                 |
| EVM0002774 | 8.05   | 30.14   | -1.91    | 5.00E-05| 4.28E-04            | --                              | --                                                 |
| EVM0010259 | 553.03 | 2070.81 | -1.90    | 5.00E-05| 4.28E-04            | --                              | Domain of unknown function (DUF427)                |
| EVM0009651 | 3.21   | 12.01   | -1.90    | 5.00E-05| 4.28E-04            | Energy production and conversion | FAD binding domain                                  |
| EVM0009399 | 19.92  | 74.45   | -1.90    | 5.00E-05| 4.28E-04            | --                              | Mediator complex subunit 25 von Willebrand factor type A |
| Accession    | E   | M   | DE  | Log2p | E-score | Description                                           |
|--------------|-----|-----|-----|-------|---------|-------------------------------------------------------|
| EVM0007509   | 7.64| 28.38| -1.89|       | 5.00E-05| 4.28E-04 --                                          |
| EVM0011068   | 30.01| 111.26| -1.89|       | 5.00E-05| 4.28E-04 Defense mechanisms Dual specificity phosphatase, catalytic domain |
| EVM0000361   | 2.11| 7.80 | -1.89|       | 5.00E-05| 4.28E-04 --                                          |
| EVM0002898   | 10.24| 37.89| -1.89|       | 5.00E-05| 4.28E-04 Transcription RNA polymerase Rpb3/RpoA insert domain |
| EVM0008826   | 23.80| 87.65| -1.89|       | 5.00E-05| 4.28E-04 Signal transduction mechanisms Protein kinase domain |
| EVM0006734   | 5.21| 19.10| -1.87|       | 5.00E-05| 4.28E-04 Complex 1 protein (LYR family)               |
| EVM0004818   | 2.89| 10.66| -1.88|       | 5.00E-05| 4.28E-04 bZIP transcription factor                   |
| EVM0003322   | 1.63| 0.69 | 1.24 |       | 1.22E-02| 4.38E-02 --                                          |
| EVM0011344   | 11.25| 41.23| -1.87|       | 5.00E-05| 4.28E-04 RNA processing and modification Mpp10 protein |
| EVM000322    | 9.73| 35.54| -1.87|       | 5.00E-05| 4.28E-04 General function prediction only Sugar (and other) transporter |
| EVM0001566   | 2.68| 9.77 | -1.87|       | 5.00E-05| 4.28E-04 General function prediction only Sugar (and other) transporter |
| Accession   | E-value | % ID | % Pos | E-value | E-value | Function Prediction | Description                                      |
|------------|---------|------|-------|---------|---------|---------------------|------------------------------------------------|
| EVM0005665| 27.37   | 99.77| -1.87 | 5.00E-05| 4.28E-04| General function prediction only| Zinc finger, C2H2 type |
| EVM0006463| 14.46   | 52.66| -1.86 | 5.00E-05| 4.28E-04| --                  | Lactonase, 7-bladed beta-propeller |
| EVM0009977| 3.18    | 11.57| -1.86 | 5.00E-05| 4.28E-04| --                  | Ubiquitin 3 binding protein But2 C-terminal domain |
| EVM0004238| 22.13   | 80.54| -1.86 | 5.00E-05| 4.28E-04| --                  | SMI1 / KNR4 family (SUHK-1) |
| EVM0003844| 9.48    | 34.29| -1.85 | 5.00E-05| 4.28E-04| Function unknown     | -- |
| EVM0002302| 18.03   | 65.06| -1.85 | 5.00E-05| 4.28E-04| --                  | -- |
| EVM0004758| 5.12    | 18.23| -1.83 | 5.00E-05| 4.28E-04| --                  | CFEM domain |
| EVM0003416| 22.42   | 79.59| -1.83 | 5.00E-05| 4.28E-04| --                  | Nuclear pore complex subunit Nro1 |
| EVM0006946| 18.89   | 77.22| -1.83 | 5.00E-05| 4.28E-04| --                  | Calcineurin-like phosphoesterase |
| EVM0005691| 0.55    | 1.94 | -1.83 | 1.05E-03| 5.94E-03| --                  | Cytochrome P450 |
| EVM0010935| 21.44   | 76.02| -1.83 | 5.00E-05| 4.28E-04| --                  | Casein kinase substrate phosphoprotein PP28 |
| EVM0005613| 14.14   | 50.67| -1.84 | 5.00E-05| 4.28E-04| General function prediction only| U3-containing 90S pre-ribosomal complex subunit |
| EVM0007225| 72.33   | 258.85| -1.84| 5.00E-05| 4.28E-04| --                  | -- |
| EVM0000150| 91.56   | 328.27| -1.84| 5.00E-05| 4.28E-04| --                  | -- |
| EVM0008999| 8.53    | 30.49| -1.84 | 5.00E-05| 4.28E-04| General function prediction only| Zinc finger, C2H2 type |
| Gene ID       | EVM0007535 | 1.02  | 3.60  | -1.82 | 1.40E-03 | 7.55E-03 | -- | -- |
|--------------|------------|-------|-------|-------|----------|----------|----|----|
| Gene ID       | EVM0008156 | 408.87| 1448.07| -1.82 | 5.00E-05 | 4.28E-04 | -- | -- |
| Descriptions | HSF-type DNA-binding | non-haem dioxygenase in morphine synthesis N-terminal |
| Gene ID       | EVM0003616 | 51.99 | 184.12| -1.82 | 5.00E-05 | 4.28E-04 | -- | HMG (high mobility group) box |
| Descriptions | Transcription | Aminotransferase class-V |
| Gene ID       | EVM0011379 | 14.39 | 50.94 | -1.82 | 5.00E-05 | 4.28E-04 | -- | Multicopper oxidase |
| Descriptions | Transcription | Signal transduction mechanisms | Secondary metabolites biosynthesis, transport and catabolism |
| Gene ID       | EVM0000762 | 166.04| 582.58| -1.81 | 5.00E-05 | 4.28E-04 | -- | Protein of unknown function (DUF1295) |
| Descriptions | General function prediction only | Protein of unknown function (DUF952) | WH1 domain |
| Gene ID       | EVM0008201 | 1.77  | 6.21  | -1.81 | 3.00E-04 | 2.07E-03 | -- | -- |
| Gene ID       | EVM0011937 | 2.19  | 7.68  | -1.81 | 5.00E-05 | 4.28E-04 | -- | -- |
| Descriptions | Signal transduction mechanisms | Protein of unknown function (DUF952) |
| Gene ID       | EVM0004770 | 11.94 | 41.81 | -1.81 | 5.00E-05 | 4.28E-04 | -- | -- |
| Descriptions | General function prediction only | Protein of unknown function (DUF1295) |
| Gene ID       | EVM0003548 | 9.49  | 33.24 | -1.81 | 5.00E-05 | 4.28E-04 | -- | -- |
| Descriptions | General function prediction only | Protein of unknown function (DUF952) |
| Gene ID       | EVM0007842 | 54.16 | 189.39| -1.81 | 5.00E-05 | 4.28E-04 | -- | -- |
| Descriptions | General function prediction only | Protein of unknown function (DUF952) |

**EVM0000833** 4.16 14.72 -1.82 5.00E-05 4.28E-04 -- HSF-type DNA-binding

**EVM00009678** 4.30 15.21 -1.82 5.00E-05 4.28E-04 Coenzyme transport and metabolism

**EVM00099486** 0.59 2.10 -1.82 1.29E-02 4.57E-02 -- Putative FMN-binding domain

**EVM000538** 1.77 6.02 -1.82 5.00E-05 4.28E-04 -- Multicopper oxidase

**EVM0007958** 1.73 6.09 -1.81 5.00E-05 4.28E-04 Secondary metabolites biosynthesis, transport and catabolism

**EVM0000626** 166.04 582.58 -1.81 5.00E-05 4.28E-04 General function prediction only

**EVM0004770** 11.94 41.81 -1.81 5.00E-05 4.28E-04 WH1 domain

**EVM0003548** 9.49 33.24 -1.81 5.00E-05 4.28E-04

**EVM0003944** 2.24 7.87 -1.82 5.00E-05 4.28E-04

**EVM0004770** 11.94 41.81 -1.81 5.00E-05 4.28E-04

**EVM0000883** 4.16 14.72 -1.82 5.00E-05 4.28E-04 -- HSF-type DNA-binding

**EVM0003616** 51.99 184.12 -1.82 5.00E-05 4.28E-04 Transcription

**EVM0003616** 51.99 184.12 -1.82 5.00E-05 4.28E-04 HSF-type DNA-binding

**EVM0009678** 4.30 15.21 -1.82 5.00E-05 4.28E-04 Coenzyme transport and metabolism

**EVM00009678** 4.30 15.21 -1.82 5.00E-05 4.28E-04 Aminotransferase class-V

**EVM0000833** 4.16 14.72 -1.82 5.00E-05 4.28E-04 Transcription

**EVM0000833** 4.16 14.72 -1.82 5.00E-05 4.28E-04 HSF-type DNA-binding

**EVM0000833** 4.16 14.72 -1.82 5.00E-05 4.28E-04 Transcription

**EVM0000833** 4.16 14.72 -1.82 5.00E-05 4.28E-04 HSF-type DNA-binding

**EVM0000833** 4.16 14.72 -1.82 5.00E-05 4.28E-04 Transcription

**EVM0000833** 4.16 14.72 -1.82 5.00E-05 4.28E-04 HSF-type DNA-binding
| Accession   | Value1 | Value2 | Value3 | Value4 | Value5 | Class                                                                 | Protein Family                                      |
|-------------|--------|--------|--------|--------|--------|----------------------------------------------------------------------|-----------------------------------------------------|
| EVM0006117  | 11.59  | 40.49  | -1.80  | 5.00E-05| 4.28E-04| General function prediction only                                      | Aldo/keto reductase family                          |
| EVM0008889  | 0.60   | 2.09   | -1.80  | 1.55E-03| 8.22E-03| --                                                                    | Cytochrome P450                                      |
| EVM0002548  | 15.32  | 53.40  | -1.80  | 5.00E-05| 4.28E-04| --                                                                    | --                                                  |
| EVM0004054  | 399.42 | 1389.50| -1.80  | 5.00E-05| 4.28E-04| Posttranslational modification, protein turnover, chaperones          | Hsp20/alpha crystallin family                        |
| EVM0007045  | 33.05  | 114.95 | -1.80  | 5.00E-05| 4.28E-04| --                                                                    | --                                                  |
| EVM0007616  | 18.76  | 65.25  | -1.80  | 5.00E-05| 4.28E-04| Transcription                                                         | MT-A70                                              |
| EVM0002358  | 18.38  | 63.88  | -1.80  | 5.00E-05| 4.28E-04| --                                                                    | --                                                  |
| EVM0010819  | 2.13   | 7.40   | -1.80  | 5.00E-05| 4.28E-04| --                                                                    | --                                                  |
| EVM0003936  | 43.31  | 150.05 | -1.79  | 5.00E-05| 4.28E-04| General function prediction only                                      | TPR repeat                                           |
| EVM0002723  | 6.08   | 21.03  | -1.79  | 5.00E-05| 4.28E-04| --                                                                    | --                                                  |
| EVM0007740  | 6.19   | 21.39  | -1.79  | 5.00E-05| 4.28E-04| --                                                                    | --                                                  |
| EVM0002692  | 0.98   | 3.37   | -1.79  | 2.00E-04| 1.46E-03| Secondary metabolites biosynthesis, transport and catabolism         | Cytochrome P450                                      |
| EVM0006427  | 106.14 | 366.14 | -1.79  | 5.00E-05| 4.28E-04| Amino acid transport and metabolism                                   | Amino acid permease                                  |
| EVM0002722  | 3.38   | 11.67  | -1.79  | 5.00E-05| 4.28E-04| Secondary metabolites biosynthesis, transport and catabolism         | Multicopper oxidase                                  |
| EVM0006228  | 74.43  | 256.50 | -1.78  | 5.00E-05| 4.28E-04| Posttranslational modification, protein turnover, chaperones         | Ubiquitin carboxyl-terminal hydrolase, family 1      |
| Accession   | Value1 | Value2  | Value3 | Value4 | Value5 | Value6 | Value7 | Value8 | Value9 | Value10 | Function                                                                 |
|------------|--------|---------|--------|--------|--------|--------|--------|--------|--------|---------|---------------------------------------------------------------------------|
| EVM0005225 | 10.08  | 34.54   | -1.78  | 5.00E-05 | 4.28E-04 | --     | Gti1/Pac2 family             |
| EVM0005312 | 0.97   | 3.34    | -1.78  | 1.50E-04 | 1.14E-03 | --     | DNA polymerase subunit Cdc27 |
| EVM0000069 | 8.07   | 27.63   | -1.78  | 5.00E-05 | 4.28E-04 | --     | --                                    |
| EVM0004405 | 1.28   | 4.38    | -1.77  | 1.40E-03 | 7.55E-03 | --     | --                                    |
| EVM0010316 | 34.67  | 118.50  | -1.77  | 5.00E-05 | 4.28E-04 | --     | Fungal fruit body lectin        |
| EVM0006290 | 3.79   | 12.96   | -1.77  | 5.00E-05 | 4.28E-04 | General function prediction only |
| EVM0006914 | 2.53   | 8.65    | -1.77  | 5.00E-05 | 4.28E-04 | --     | --                                    |
| EVM0000151 | 253.39 | 865.86  | -1.77  | 5.00E-05 | 4.28E-04 | Lipid transport and metabolism  |
| EVM0012239 | 2.11   | 7.20    | -1.77  | 5.00E-05 | 4.28E-04 | --     | --                                    |
| EVM0005335 | 7.90   | 26.98   | -1.77  | 5.00E-05 | 4.28E-04 | --     | F-box-like                      |
| EVM0008324 | 2.39   | 8.16    | -1.77  | 5.00E-05 | 4.28E-04 | Secondary metabolites biosynthesis, transport and catabolism |
| EVM0005952 | 6.02   | 20.55   | -1.77  | 5.00E-05 | 4.28E-04 | --     | RNA ligase                       |
| EVM0008051 | 197.12 | 673.01  | -1.77  | 5.00E-05 | 4.28E-04 | --     | SUR7/PalI family                |
| EVM0008452 | 6.52   | 22.24   | -1.77  | 5.00E-05 | 4.28E-04 | --     | --                                    |
| EVM0011033 | 2.83   | 9.66    | -1.77  | 5.00E-05 | 4.28E-04 | --     | --                                    |
| EVM0010885 | 17.74  | 60.37   | -1.77  | 5.00E-05 | 4.28E-04 | Posttranslational modification, protein turnover, chaperones |
| EVM0010265 | 33.25  | 113.06  | -1.77  | 5.00E-05 | 4.28E-04 | General function prediction only |
| EVM0010316 | 34.67  | 118.50  | -1.77  | 5.00E-05 | 4.28E-04 | Conserved hypothetical ATP binding protein |
| Accession  | EVM0011950 | 601.16 | 2042.67 | -1.76 | 5.00E-05 | 4.28E-04 | Posttranslational modification, protein turnover, chaperones | CS domain |
|------------|------------|--------|---------|--------|----------|----------|----------------------------------------------------------|-----------|
| Accession  | EVM0011048 | 3.13   | 10.63   | -1.76  | 2.65E-03 | 1.28E-02 | -- | -- |
| Accession  | EVM0004305 | 0.67   | 2.27    | -1.76  | 3.50E-04 | 2.36E-03 | General function prediction only | GMC oxidoreductase |
| Accession  | EVM0005902 | 10.21  | 34.59   | -1.76  | 5.00E-05 | 4.28E-04 | -- | -- |
| Accession  | EVM000869  | 161.53 | 545.40  | -1.76  | 5.00E-05 | 4.28E-04 | -- | SAC3/GANP/Nin1/mts3/eIF-3 p25 family |
| Accession  | EVM0009757 | 152.11 | 512.66  | -1.75  | 5.00E-05 | 4.28E-04 | -- | -- |
| Accession  | EVM0002413 | 3.62   | 12.17   | -1.75  | 5.00E-05 | 4.28E-04 | -- | Cellulase (glycosyl hydrolase family 5) |
| Accession  | EVM0004513 | 60.65  | 204.10  | -1.75  | 5.00E-05 | 4.28E-04 | -- | pfkB family carbohydrate kinase |
| Accession  | EVM0007562 | 20.87  | 70.15   | -1.75  | 5.00E-05 | 4.28E-04 | -- | -- |
| Accession  | EVM0007241 | 0.75   | 2.51    | -1.75  | 1.75E-03 | 9.08E-03 | -- | -- |
| Accession  | EVM0010148 | 191.45 | 643.25  | -1.75  | 5.00E-05 | 4.28E-04 | -- | -- |
| Accession  | EVM0008404 | 13.39  | 44.93   | -1.75  | 5.00E-05 | 4.28E-04 | RNA processing and modification | BING4CT (NUC141) domain |
| Accession  | EVM0008819 | 1.91   | 6.41    | -1.74  | 5.00E-05 | 4.28E-04 | -- | -- |
| Accession  | EVM0011527 | 1186.58| 3967.40 | -1.74  | 5.00E-05 | 4.28E-04 | Signal transduction mechanisms | EF hand |
| Accession  | EVM0011961 | 104.37 | 348.96  | -1.74  | 5.00E-05 | 4.28E-04 | General function prediction only | Zinc finger C-x8-C-x5-C-x3-H type (and similar) |
| Accession  | EVM0002923 | 5995.82| 20036.90| -1.74  | 5.00E-05 | 4.28E-04 | -- | CsbD-like |
| Accession  | EVM0004611 | 4.62   | 15.44   | -1.74  | 5.00E-05 | 4.28E-04 | -- | Ferritin-like domain |
| EVM0006867     | 13.46 | 44.95 | -1.74 | 5.00E-05 | 4.28E-04 | -- | -- |
|----------------|-------|-------|--------|----------|----------|----|----|
| EVM0001681     | 258.91| 863.46| -1.74  | 5.00E-05 | 4.28E-04 | Intracellular trafficking, secretion, and vesicular transport | Microsomal signal peptidase 12 kDa subunit (SPC12) |
| EVM0004358     | 181.56| 604.80| -1.74  | 5.00E-05 | 4.28E-04 | -- | Heat shock factor binding protein 1 |
| EVM0010929     | 9.89  | 32.94 | -1.74  | 5.00E-05 | 4.28E-04 | -- | -- |
| EVM0007445     | 2.78  | 9.26  | -1.73  | 5.00E-05 | 4.28E-04 | -- | -- |
| EVM000893      | 13.64 | 45.39 | -1.73  | 5.00E-05 | 4.28E-04 | -- | -- |
| EVM0008490     | 1.34  | 4.45  | -1.73  | 2.00E-03 | 1.01E-02 | -- | -- |
| EVM0009934     | 8.28  | 27.52 | -1.73  | 5.00E-05 | 4.28E-04 | -- | Uncharacterized conserved protein (DUF2183) |
| EVM0010493     | 7.85  | 26.03 | -1.73  | 2.50E-04 | 1.77E-03 | -- | -- |
| EVM000946      | 24.77 | 82.14 | -1.73  | 5.00E-05 | 4.28E-04 | Function unknown | Rgp1 |
| EVM0011971     | 10.24 | 33.93 | -1.73  | 5.00E-05 | 4.28E-04 | Transcription | HMG (high mobility group) box |
| EVM0004944     | 2.89  | 9.58  | -1.73  | 2.50E-04 | 1.77E-03 | -- | F-box-like |
| EVM0003453     | 156.96| 519.42| -1.73  | 5.00E-05 | 4.28E-04 | -- | -- |
| EVM0000189     | 4.32  | 14.29 | -1.73  | 1.00E-04 | 7.96E-04 | -- | Glycosyl hydrolases family 43 |
| EVM0003951     | 36.10 | 119.44| -1.73  | 5.00E-05 | 4.28E-04 | Function unknown | RWD domain |
| EVM0003855     | 4.12  | 13.64 | -1.73  | 5.00E-05 | 4.28E-04 | Signal transduction mechanisms | Protein kinase domain |
| EVM0009807     | 2341.01| 7739.50| -1.73 | 5.00E-05 | 4.28E-04 | -- | Mitochondrial F1-F0 ATP synthase subunit F of fungi |
| EVM0006896     | 412.41| 1361.32| -1.72 | 7.50E-04 | 4.49E-03 | -- | Protein of unknown function (DUF4449) |
| EVM0004746     | 1.19  | 3.90  | -1.72  | 9.75E-03 | 3.67E-02 | -- | -- |
| Accession     | E      | F      | log2FC | p1       | p2       | Function                                                                 |
|--------------|--------|--------|--------|----------|----------|---------------------------------------------------------------------------|
| EVM0000423   | 141.39 | 464.75 | -1.72  | 5.00E-05 | 4.28E-04 | #N/A                                                                      |
| EVM0005253   | 643.40 | 2114.47| -1.72  | 5.00E-05 | 4.28E-04 | --                                                                        |
| EVM0001355   | 262.49 | 861.95 | -1.72  | 5.00E-05 | 4.28E-04 | --                                                                        |
| EVM003403    | 1.91   | 6.27   | -1.71  | 2.05E-03 | 1.03E-02 | MYND finger                                                               |
| EVM003549    | 2.98   | 9.78   | -1.71  | 3.00E-04 | 2.07E-03 | --                                                                        |
| EVM003569    | 2.34   | 7.69   | -1.71  | 5.00E-05 | 4.28E-04 | --                                                                        |
| EVM007361    | 17.76  | 57.99  | -1.71  | 5.00E-05 | 4.28E-04 | RNA processing and modification                                            |
| EVM000381    | 13.58  | 44.33  | -1.71  | 5.00E-05 | 4.28E-04 | Function unknown                                                          |
| EVM0007086   | 70.66  | 230.49 | -1.71  | 5.00E-05 | 4.28E-04 | --                                                                        |
| EVM0000419   | 56.33  | 183.64 | -1.70  | 5.00E-05 | 4.28E-04 | Function unknown                                                          |
| EVM006136    | 157.27 | 512.60 | -1.70  | 5.00E-05 | 4.28E-04 | --                                                                        |
| EVM001178    | 20.65  | 67.30  | -1.70  | 5.00E-05 | 4.28E-04 | --                                                                        |
| EVM003558    | 38.60  | 125.61 | -1.70  | 5.00E-05 | 4.28E-04 | Methyltransferase domain                                                   |
| EVM007803    | 5.11   | 16.64  | -1.70  | 3.50E-04 | 2.36E-03 | --                                                                        |
| EVM001559    | 11.63  | 37.81  | -1.70  | 5.00E-05 | 4.28E-04 | Function unknown                                                          |
| EVM008798    | 1.18   | 3.82   | -1.70  | 5.00E-05 | 4.28E-04 | Gti1/Pac2 family                                                           |
| EVM006869    | 426.64 | 1383.50| -1.70  | 5.00E-05 | 4.28E-04 | General function prediction only                                          |
| EVM009813    | 52.58  | 170.09 | -1.69  | 5.00E-05 | 4.28E-04 | --                                                                        |
| EVM003678    | 2.80   | 9.07   | -1.69  | 5.00E-05 | 4.28E-04 | FAD binding domain                                                         |
| EVM006402    | 133.80 | 432.17 | -1.69  | 5.00E-05 | 4.28E-04 | --                                                                        |

Function unknown: Folate-sensitive fragile site protein Fra10Ac1
Complex 1 protein (LYR family)
Methyltransferase domain
Cysteine-rich secretory protein family
Gti1/Pac2 family
Ras family
FAD binding domain
| Accession   | E    | M    | S     | E    | M    | S     | E    | M    | S     | Description                                                                 |
|------------|------|------|-------|------|------|-------|------|------|-------|-----------------------------------------------------------------------------|
| EVM0004502 | 14.05| 45.37| -1.69 | 5.00E-05 | 4.28E-04 | RNA processing and modification | SUZ domain |
| EVM0003465 | 15.24| 49.19| -1.69 | 5.00E-05 | 4.28E-04 | -- | -- |
| EVM0011270 | 10.79| 34.83| -1.69 | 5.00E-05 | 4.28E-04 | -- | cAMP phosphodiesterases class-II |
| EVM0008562 | 182.17| 586.17| -1.69 | 5.00E-05 | 4.28E-04 | -- | -- |
| EVM0008828 | 5.15 | 16.56| -1.68 | 5.00E-05 | 4.28E-04 | -- | -- |
| EVM0001442 | 1.06 | 3.42 | -1.68 | 6.50E-04 | 3.98E-03 | -- | Phosphotransferase enzyme family |
| EVM0006753 | 4.27 | 13.69| -1.68 | 5.00E-05 | 4.28E-04 | General function prediction only | Family of unknown function (DUF706) |
| EVM0010219 | 10.43| 33.39| -1.68 | 1.85E-03 | 9.52E-03 | -- | -- |
| EVM0006432 | 2.37 | 7.56 | -1.67 | 5.00E-05 | 4.28E-04 | -- | Fatty acid desaturase |
| EVM0004134 | 52.49| 167.16| -1.67 | 5.00E-05 | 4.28E-04 | General function prediction only | RNA recognition motif. (a.k.a. RRM, RBD, or RNP domain) |
| EVM0005121 | 147.61| 469.78| -1.67 | 5.00E-05 | 4.28E-04 | General function prediction only | Ras family |
| EVM0005503 | 0.99 | 3.15 | -1.67 | 9.50E-04 | 5.46E-03 | General function prediction only | Major Facilitator Superfamily |
| EVM0009374 | 16.62| 52.75| -1.67 | 5.00E-05 | 4.28E-04 | Carbohydrate transport and metabolism | Major Facilitator Superfamily |
| EVM000209 | 7.71 | 24.46| -1.67 | 5.00E-05 | 4.28E-04 | Translation, ribosomal structure and biogenesis | KRI1-like family C-terminal |
| EVM0005190 | 14.88| 47.20| -1.67 | 5.00E-05 | 4.28E-04 | -- | -- |
| EVM0006648 | 3.63 | 11.48| -1.66 | 5.00E-05 | 4.28E-04 | -- | -- |
| Accession   | Fold Avg | Expression | Log2 Fold | p-value | Description                                                                 |
|-------------|----------|------------|-----------|---------|------------------------------------------------------------------------------|
| EVM0004201  | 81.26    | 257.07     | -1.66     | 5.00E-05 | 4.28E-04 Glutathione-dependent formaldehyde-activating enzyme                 |
| EVM0008825  | 18.95    | 59.88      | -1.66     | 2.50E-04 | 1.77E-03 Lipid transport and metabolism                                       |
| EVM0009339  | 46.72    | 147.61     | -1.66     | 5.00E-05 | 4.28E-04 Emopamil binding protein                                             |
| EVM001525   | 32.01    | 100.94     | -1.66     | 5.00E-05 | 4.28E-04 Emopamil binding protein                                             |
| EVM0011057  | 0.45     | 1.43       | -1.66     | 1.37E-02 | 4.81E-02 Signal transduction mechanisms                                       |
| EVM0009442  | 25.57    | 80.48      | -1.65     | 5.00E-05 | 4.28E-04 Protein kinase domain                                                |
| EVM0008343  | 11.12    | 34.89      | -1.65     | 5.00E-05 | 4.28E-04 Inorganic ion transport and metabolism                              |
| EVM0009885  | 4.27     | 13.38      | -1.65     | 2.00E-04 | 1.46E-03 Glycosyl hydrolase family 6                                          |
| EVM007566   | 1914.58  | 5997.38    | -1.65     | 5.00E-05 | 4.28E-04 Heme oxygenase                                                       |
| EVM0007465  | 1.81     | 5.66       | -1.65     | 2.15E-03 | 1.08E-02 Glycosyl hydrolase family 6                                          |
| EVM0012095  | 7.11     | 22.21      | -1.64     | 5.00E-05 | 4.28E-04 General function prediction only                                     |
| EVM0009292  | 4.05     | 12.64      | -1.64     | 5.00E-05 | 4.28E-04 RNA processing and modification                                      |
| EVM0009340  | 39.90    | 124.43     | -1.64     | 5.00E-05 | 4.28E-04 General function prediction only                                     |
| EVM0007132  | 0.86     | 2.66       | -1.64     | 1.00E-03 | 5.70E-03 RNA processing and modification                                      |
| EVM0005650  | 12.37    | 38.49      | -1.64     | 5.00E-05 | 4.28E-04 General function prediction only                                     |
| EVM0008305  | 10.53    | 32.76      | -1.64     | 5.00E-05 | 4.28E-04 RNA processing and modification                                      |
| EVM0009204  | 10.20    | 31.67      | -1.63     | 5.00E-05 | 4.28E-04 General function prediction only                                     |
| EVM0007974  | 27.03    | 83.86      | -1.63     | 5.00E-05 | 4.28E-04 General function prediction only                                     |
| EVM0006020  | 33.57    | 103.92     | -1.63     | 5.00E-05 | 4.28E-04 General function prediction only                                     |
| Gene ID      | Value1 | Value2 | Difference | Value3 | Value4 | Function                                      |
|-------------|--------|--------|------------|--------|--------|-----------------------------------------------|
| EVM0007872  | 34.34  | 106.21 | -1.63      | 5.00E-05 | 4.28E-04 | Acetyltransferase (GNAT) family             |
| EVM0008217  | 10.18  | 31.47  | -1.63      | 5.00E-05 | 4.28E-04 | Hydroxymethylglutaryl-coenzyme A reductase   |
| EVM0006662  | 26.41  | 81.59  | -1.63      | 5.00E-05 | 4.28E-04 | Ergosterol biosynthesis ERG4/ERG24 family    |
| EVM0011409  | 8.52   | 26.32  | -1.63      | 5.00E-05 | 4.28E-04 | Zinc-finger double-stranded RNA-binding      |
| EVM0009944  | 7.36   | 22.75  | -1.63      | 5.00E-05 | 4.28E-04 | --                                            |
| EVM001647   | 62.00  | 191.21 | -1.62      | 5.00E-05 | 4.28E-04 | Protein of unknown function (DUF1212)        |
| EVM001573   | 1.30   | 4.00   | -1.62      | 1.40E-03 | 7.55E-03 | --                                            |
| EVM000606   | 3.15   | 9.70   | -1.62      | 5.00E-05 | 4.28E-04 | Phosphatidylserine decarboxylase              |
| EVM0002154  | 0.68   | 2.08   | -1.62      | 4.45E-03 | 1.96E-02 | --                                            |
| EVM001738   | 1379.82| 4240.67| -1.62      | 1.30E-03 | 7.10E-03 | Lipid transport and metabolism               |
| EVM0011573  | 7.88   | 24.20  | -1.62      | 5.00E-05 | 4.28E-04 | --                                            |
| EVM0010113  | 33.98  | 104.28 | -1.62      | 5.00E-05 | 4.28E-04 | Transcriptional repressor TCF25              |
| EVM0002475  | 28.10  | 86.22  | -1.62      | 5.00E-05 | 4.28E-04 | --                                            |
| EVM0011042  | 159.57 | 487.46 | -1.61      | 5.00E-05 | 4.28E-04 | --                                            |
| EVM0010669  | 117.55 | 359.05 | -1.61      | 5.00E-05 | 4.28E-04 | --                                            |
| EVM0008633  | 28.94  | 88.35  | -1.61      | 5.00E-05 | 4.28E-04 | --                                            |
| EVM0011887  | 15.54  | 47.44  | -1.61      | 5.00E-05 | 4.28E-04 | --                                            |
| EVM0002361  | 15.60  | 47.58  | -1.61      | 5.00E-05 | 4.28E-04 | --                                            |
| EVM0005785 | 1.75  | 5.33  | -1.61 | 6.50E-04  | 3.98E-03 | -- | Variant SH3 domain |
| EVM0011416 | 138.19 | 419.61 | -1.60 | 5.00E-05  | 4.28E-04 | Cell cycle control, cell division, chromosome partitioning |
| EVM0012052 | 183.20 | 556.16 | -1.60 | 5.00E-05  | 4.28E-04 | -- | Cdc37 N terminal kinase binding |
| EVM0009851 | 11.76  | 35.66  | -1.60 | 5.00E-05  | 4.28E-04 | Function unknown |
| EVM0009908 | 413.33 | 1253.82 | -1.60 | 5.00E-05  | 4.28E-04 | -- | WD domain, G-beta repeat |
| EVM0001928 | 13.96  | 42.24  | -1.60 | 5.00E-05  | 4.28E-04 | -- | Cerato-platanin |
| EVM0002558 | 11.74  | 35.51  | -1.60 | 5.00E-05  | 4.28E-04 | Cell cycle control, cell division, chromosome partitioning |
| EVM0002672 | 38.45  | 116.29 | -1.60 | 5.00E-05  | 4.28E-04 | -- | Protein kinase domain |
| EVM0003410 | 33.43  | 101.06 | -1.60 | 5.00E-05  | 4.28E-04 | -- | -- |
| EVM0005464 | 15.28  | 46.17  | -1.60 | 5.00E-05  | 4.28E-04 | Amino acid transport and metabolism |
| EVM0009733 | 8.69   | 26.23  | -1.59 | 5.00E-05  | 4.28E-04 | -- | Gamma-glutamyltranspeptidase |
| EVM0006281 | 14.08  | 42.47  | -1.59 | 5.00E-05  | 4.28E-04 | Amino acid transport and metabolism |
| EVM0005731 | 6.11   | 18.43  | -1.59 | 5.00E-05  | 4.28E-04 | -- | Hydantoinase B/oxoprolinase |
| EVM0004379 | 196.64 | 591.88 | -1.59 | 5.00E-05  | 4.28E-04 | Intracellular trafficking, secretion, and vesicular transport |
| EVM0001403 | 5.48   | 16.50  | -1.59 | 5.00E-05  | 4.28E-04 | -- | Synaptobrevin |
| Accession     | EVM0002681 | EVM0010558 | EVM0007828 | EVM004866 | EVM0011165 | EVM0000390 | EVM0007307 | EVM0011165 | EVM0005095 | EVM0000240 | EVM0008951 | EVM0004301 | EVM0005034 | EVM0011555 | EVM0007953 |
|--------------|------------|------------|------------|-----------|------------|------------|------------|------------|------------|------------|------------|------------|------------|------------|------------|
| Entries      | 160        | 160        | 160        | 160       | 160        | 160        | 160        | 160        | 160        | 160        | 160        | 160        | 160        | 160        | 160        |
| F1          | 11.19      | 19.86      | 14.81      | 303.52    | 39.96      | 10.65      | 55.38      | 19.22      | 8.65       | 12.62      | 27.26      | 13.59      | 2143.16    | 68.84      | 187.94     |
| F2          | 33.61      | 59.63      | 44.43      | 910.53    | 119.75     | 31.92      | 165.88     | 57.55      | 25.87      | 37.72      | 81.36      | 40.53      | 6384.31    | 205.03     | 559.39     |
| F3          | -1.59      | -1.59      | -1.59      | -1.58     | -1.58      | -1.58      | -1.58      | -1.58      | -1.58      | -1.58      | -1.58      | -1.58      | -1.57      | -1.57      | -1.57      |
| Log10P       | 5.00E-05   | 5.00E-05   | 4.70E-03   | 5.00E-05  | 5.00E-05   | 5.00E-05   | 5.00E-05   | 2.50E-04   | 2.50E-04   | 5.00E-05   | 5.00E-05   | 5.00E-05   | 5.50E-04   | 5.00E-05   | 5.00E-05   |
| Function     | General function prediction only | -- | Transcription | Function unknown | Energy production and conversion | Amino acid transport and metabolism | -- | -- | Alpha/beta hydrolase family | Transcription | Intracellular trafficking, secretion, and vesicular transport | Secondary metabolites biosynthesis, transport and catabolism | -- | Sel1 repeat |
| Class        | Glycosyl transferase family 90 | -- | LAG1, DNA binding | Uncharacterised protein family (UPF0121) | Mitochondrial carrier protein | Cys/Met metabolism PLP-dependent enzyme | -- | -- | -- | MED6 mediator sub complex component | Tetratricopeptide repeat | Pyridine nucleotide-disulphide oxidoreductase | -- | -- |
| ID            | Value1 | Value2 | Log10(F) | Log10(P) | Function                                      | Domain/Feature                                      |
|--------------|--------|--------|----------|----------|-----------------------------------------------|---------------------------------------------------|
| EVM0008702   | 188.20 | 560.05 | -1.57    | 5.00E-05 | Intracellular trafficking, secretion, and vesicular transport | PRELI-like family                                   |
| EVM0004101   | 41.49  | 123.30 | -1.57    | 5.00E-05 | Carbohydrate transport and metabolism         | Phosphomannose isomerase type I                    |
| EVM0009791   | 8.42   | 25.01  | -1.57    | 5.00E-05 | Transcription                                 | RNA polymerase Rpb1, domain 5                      |
| EVM0008394   | 31.54  | 93.64  | -1.57    | 5.00E-05 | General function prediction only              | Ankyrin repeats (3 copies)                         |
| EVM0006314   | 2.66   | 7.89   | -1.57    | 5.00E-05 | --                                            | --                                                |
| EVM0002980   | 3.04   | 9.00   | -1.57    | 5.00E-05 | Amino acid transport and metabolism          | Amino acid kinase family                           |
| EVM0001816   | 11.08  | 32.78  | -1.57    | 1.00E-04 | Posttranslational modification, protein turnover, chaperones | Cyclophilin type peptidyl-prolyl cis-trans isomerase/CLD |
| EVM0009341   | 9.53   | 28.18  | -1.56    | 5.00E-05 | RNA processing and modification              | DEAD/DEAH box helicase                             |
| EVM0011255   | 1.87   | 5.51   | -1.56    | 5.00E-05 | --                                            | --                                                |
| EVM0005703   | 18.56  | 54.75  | -1.56    | 5.00E-05 | Function unknown                              | Utp14 protein                                     |
| EVM0006521   | 6.15   | 18.14  | -1.56    | 5.00E-05 | --                                            | --                                                |
| EVM0009038   | 13.95  | 41.12  | -1.56    | 5.00E-05 | --                                            | --                                                |
| EVM0007596   | 20.18  | 59.46  | -1.56    | 5.00E-05 | General function prediction only              | RNA recognition motif. (a.k.a. RRM, RBD, or RNP domain) |
| EVM0003493   | 77.43  | 228.09 | -1.56    | 5.00E-05 | Cytoskeleton                                  | Calponin homology (CH) domain                      |
| EVM0007410   | 2.72   | 8.02   | -1.56    | 5.00E-05 | #N/A                                          | #N/A                                              |
| EVM0007323    | 699.26 | 2059.06 | -1.56 | 5.00E-05 | 4.28E-04 | Function unknown | Domain of unknown function (DUF543) |
|---------------|--------|---------|-------|----------|----------|-----------------|----------------------------------|
| EVM0007568    | 178.71 | 526.23  | -1.56 | 5.00E-05 | 4.28E-04 | --              | ACT domain                       |
| EVM0009077    | 46.33  | 136.40  | -1.56 | 5.00E-05 | 4.28E-04 | --              | --                               |
| EVM0008327    | 6.79   | 19.98   | -1.56 | 5.00E-05 | 4.28E-04 | --              | --                               |
| EVM0001103    | 3.54   | 10.43   | -1.56 | 2.00E-04 | 1.46E-03 | --              | Glycosyl hydrolases family 16    |
| EVM0003129    | 3.16   | 9.28    | -1.55 | 5.00E-05 | 4.28E-04 | --              | --                               |
| EVM0001002    | 30.47  | 89.32   | -1.55 | 5.00E-05 | 4.28E-04 | --              | Heterokaryon incompatibility protein Het-C |
| EVM0010061    | 78.77  | 230.53  | -1.55 | 5.00E-05 | 4.28E-04 | --              | SH3 domain                       |
| EVM0003364    | 2.87   | 8.38    | -1.55 | 6.50E-04 | 3.98E-03 | --              | --                               |
| EVM0004809    | 43.74  | 127.43  | -1.54 | 5.00E-05 | 4.28E-04 | Posttranslational modification, protein turnover, chaperones | Myb-like DNA-binding domain       |
| EVM0002948    | 39.63  | 115.44  | -1.54 | 5.00E-05 | 4.28E-04 | --              | Protein of unknown function (Ytp1) |
| EVM0003992    | 15.22  | 44.33   | -1.54 | 5.00E-05 | 4.28E-04 | --              | --                               |
| EVM0011145    | 34.20  | 99.56   | -1.54 | 5.00E-05 | 4.28E-04 | --              | WD domain, G-beta repeat          |
| EVM0008198    | 40.47  | 117.60  | -1.54 | 5.00E-05 | 4.28E-04 | Transcription   | Transcription initiation factor IIF, beta subunit |
| EVM0003896    | 74.37  | 215.96  | -1.54 | 5.00E-05 | 4.28E-04 | --              | Protein of unknown function (DUF2420) |
| EVM0006099    | 83.14  | 241.37  | -1.54 | 5.00E-05 | 4.28E-04 | Lipid transport and metabolism | Enoyl-CoA hydrolase/isomerase family |
| EVM0004056    | 12.01  | 34.85   | -1.54 | 1.00E-04 | 7.96E-04 | --              | --                               |
| EVM0005581 | 4.93 | 14.30 | -1.54 | 2.00E-04 | 1.46E-03 | -- | Lysine-specific metallo-endopeptidase |
|------------|------|-------|-------|----------|---------|-----|-------------------------------------|
| EVM0001778 | 124.96 | 362.45 | -1.54 | 5.00E-05 | 4.28E-04 | Coenzyme transport and metabolism | Pyridoxamine 5’-phosphate oxidase |
| EVM0010141 | 72.42 | 209.87 | -1.54 | 5.00E-05 | 4.28E-04 | General function prediction only | Prp19/Pso4-like |
| EVM0012060 | 4.21 | 12.19 | -1.53 | 5.00E-05 | 4.28E-04 | -- | -- |
| EVM0012112 | 4.01 | 11.59 | -1.53 | 7.50E-04 | 4.49E-03 | General function prediction only | -- |
| EVM0007006 | 80.38 | 232.63 | -1.53 | 5.00E-05 | 4.28E-04 | Signal transduction mechanisms | CS domain |
| EVM0009732 | 14.88 | 42.98 | -1.53 | 5.00E-05 | 4.28E-04 | -- | -- |
| EVM0000380 | 6.72 | 19.41 | -1.53 | 5.00E-05 | 4.28E-04 | -- | -- |
| EVM0012018 | 28.35 | 81.64 | -1.53 | 5.00E-05 | 4.28E-04 | -- | -- |
| EVM0004582 | 1.95 | 5.63 | -1.53 | 3.80E-03 | 1.72E-02 | -- | -- |
| EVM0006433 | 1.30 | 3.73 | -1.52 | 1.95E-03 | 9.93E-03 | Carbohydrate transport and metabolism | Major intrinsic protein |
| EVM0006148 | 23.28 | 66.96 | -1.52 | 5.00E-05 | 4.28E-04 | -- | -- |
| EVM0006114 | 36.94 | 106.15 | -1.52 | 5.00E-05 | 4.28E-04 | -- | Thiamine pyrophosphate enzyme, N-terminal TPP binding domain |
| EVM0005099 | 0.80 | 2.29 | -1.52 | 1.08E-02 | 3.97E-02 | Lipid transport and metabolism | Lipase (class 3) |
| EVM0001593 | 4.66 | 13.38 | -1.52 | 5.00E-05 | 4.28E-04 | -- | Survival protein SurE |
| EVM0005950 | 34.57 | 99.21 | -1.52 | 5.00E-05 | 4.28E-04 | Carbohydrate transport and metabolism | Major Facilitator Superfamily |
| EVM0009009 | 9.55 | 27.40 | -1.52 | 5.00E-05 | 4.28E-04 | -- | -- |
| Accession     | E-value | Bit-score | Log-odds   | Score   | Description                                               |
|--------------|---------|-----------|------------|---------|----------------------------------------------------------|
| EVM0002432   | 3.83    | 10.99     | -1.52      | 1.20E-03| 6.64E-03 Cytochrome P450                                    |
| EVM0003276   | 0.58    | 1.67      | -1.52      | 6.65E-03| 2.70E-02 General function prediction only                 |
| EVM0005861   | 157.11  | 450.22    | -1.52      | 1.50E-04| 1.14E-03 Inorganic ion transport and metabolism           |
| EVM0003008   | 72.60   | 208.02    | -1.52      | 5.00E-05| 4.28E-04 Major Facilitator Superfamily                    |
| EVM0006933   | 810.11  | 2318.58   | -1.52      | 1.00E-04| 7.96E-04 Catalase                                         |
| EVM0004316   | 10.03   | 28.72     | -1.52      | 8.50E-04| 4.98E-03 Noc2p family                                     |
| EVM0012070   | 1404.56 | 4015.74   | -1.52      | 5.00E-04| 3.19E-03 Translation, ribosomal structure and biogenesis |
| EVM000093    | 4.22    | 12.05     | -1.51      | 1.00E-04| 7.96E-04 General function prediction only                 |
| EVM0001857   | 3.60    | 10.28     | -1.51      | 5.00E-05| 4.28E-04 Peptidase family M28                             |
| EVM0002099   | 7.65    | 21.78     | -1.51      | 5.00E-05| 4.28E-04 Peptidase family M28                             |
| EVM0001700   | 54.42   | 154.68    | -1.51      | 5.00E-05| 4.28E-04 Cobalamin-independent synthase, Catalytic domain|
| EVM0000890 | 200.00 | 568.19 | -1.51 | 5.00E-05  | 4.28E-04 | Translation, ribosomal structure and biogenesis | PUA domain |
| EVM0011691 | 9.28   | 26.36  | -1.51 | 5.00E-05  | 4.28E-04 | Function unknown | Regulator of chromosome condensation (RCC1) repeat |
| EVM0004577 | 27.55  | 78.20  | -1.51 | 5.00E-05  | 4.28E-04 | Cell cycle control, cell division, chromosome partitioning | Cid1 family poly A polymerase |
| EVM0002694 | 4.83   | 13.70  | -1.50 | 5.00E-05  | 4.28E-04 | -- | DNA polymerase subunit Cdc27 |
| EVM0008173 | 1.14   | 3.25   | -1.50 | 4.00E-04  | 2.65E-03 | -- | -- |
| EVM0004217 | 18.35  | 52.01  | -1.50 | 5.00E-05  | 4.28E-04 | Replication, recombination and repair | -- |
| EVM0010700 | 13.62  | 38.60  | -1.50 | 5.00E-05  | 4.28E-04 | -- | Glycosyl hydrolase family 76 |
| EVM0002328 | 19.25  | 54.51  | -1.50 | 5.00E-05  | 4.28E-04 | -- | -- |
| EVM0002245 | 29.50  | 83.48  | -1.50 | 5.00E-05  | 4.28E-04 | Function unknown | Leo1-like protein |
| EVM0009029 | 77.41  | 218.90 | -1.50 | 5.00E-05  | 4.28E-04 | Function unknown | Protein of unknown function (DUF1014) |
| EVM0004698 | 81.53  | 230.51 | -1.50 | 5.00E-05  | 4.28E-04 | General function prediction only | Hypoxia induced protein conserved region |
| EVM0005079 | 66.24  | 187.21 | -1.50 | 5.00E-05  | 4.28E-04 | Coenzyme transport and metabolism | Pantoate-beta-alanine ligase |
| EVM0001171 | 26.17  | 73.92  | -1.50 | 5.00E-05  | 4.28E-04 | Signal transduction mechanisms | ERG2 and Sigma1 receptor like protein |
| EVM0009819 | 25.17  | 71.06  | -1.50 | 5.00E-05  | 4.28E-04 | -- | CBS domain |
| EVM0005515 | 2.40   | 6.77   | -1.49 | 5.00E-05  | 4.28E-04 | Secondary metabolites biosynthesis, transport and catabolism | Cytochrome P450 |
|     |    |    |   |   |                           |                            |
|-----|----|----|---|---|--------------------------|---------------------------|
| EVM0007645 | 7.01 | 19.73 | -1.49 | 5.00E-05 | 4.28E-04 | -- | Uncharacterised protein family (UPF0014) |
| EVM0003384 | 4.06 | 11.43 | -1.49 | 4.50E-04 | 2.92E-03 | -- | Glycosyl hydrolase family 61 |
| EVM0001583 | 35.72 | 100.57 | -1.49 | 5.00E-05 | 4.28E-04 | Intracellular trafficking, secretion, and vesicular transport |
| EVM0005154 | 53.18 | 149.70 | -1.49 | 5.00E-05 | 4.28E-04 | -- | Ras family |
| EVM0009955 | 11.05 | 31.05 | -1.49 | 5.00E-05 | 4.28E-04 | -- | short chain dehydrogenase |
| EVM0000204 | 803.35 | 2257.79 | -1.49 | 3.50E-04 | 2.36E-03 | -- | -- |
| EVM0008111 | 1.53 | 4.30 | -1.49 | 2.00E-03 | 1.01E-02 | -- | -- |
| EVM0003431 | 1.97 | 5.55 | -1.49 | 6.00E-04 | 3.72E-03 | -- | -- |
| EVM0006697 | 16.67 | 46.81 | -1.49 | 5.00E-05 | 4.28E-04 | -- | -- |
| EVM0011239 | 91.93 | 257.86 | -1.49 | 5.00E-05 | 4.28E-04 | 50S ribosome-binding GTPase |
| EVM0009523 | 3.76 | 10.52 | -1.48 | 5.00E-05 | 4.28E-04 | General function prediction only |
| EVM0011181 | 56.63 | 158.70 | -1.49 | 5.00E-05 | 4.28E-04 | -- | GMC oxidoreductase |
| EVM0002044 | 53.36 | 149.08 | -1.48 | 5.00E-05 | 4.28E-04 | Translation, ribosomal structure and biogenesis |
| EVM0005710 | 36.40 | 101.49 | -1.48 | 5.00E-05 | 4.28E-04 | -- | -- |
| EVM0007801 | 3.63 | 10.13 | -1.48 | 5.00E-05 | 4.28E-04 | -- | -- |
| EVM0012007 | 20.42 | 56.96 | -1.48 | 5.00E-05 | 4.28E-04 | -- | -- |
| Accession     | EVM0001651 | EVM0005822 | EVM0002542 | EVM0006257 | EVM0005726 | EVM0011587 | EVM0009698 | EVM0009206 | EVM0004618 | EVM0008519 | EVM0005177 | EVM0000639 | EVM0011608 | EVM0010318 | EVM0000905 | EVM0001782 | EVM0004771 | EVM0008759 | EVM0000932 |
|--------------|------------|------------|------------|------------|------------|------------|------------|------------|------------|------------|------------|------------|------------|------------|------------|------------|------------|------------|------------|
|              | 6.84       | 3.17       | 145.03     | 162.43     | 7.67       | 121.39     | 1577.37    | 16.19      | 3.94       | 150.41     | 109.00     | 6.21       | 1106.38    | 5.40       | 32.00      | 50.75      | 26.06      | 9.36       | 98.37      |
|              | 19.02      | 8.82       | 403.02     | 451.02     | 21.28      | 336.73     | 4373.42    | 44.90      | 10.91      | 416.66     | 301.85     | 17.18      | 3057.75    | 14.91      | 88.32      | 139.93     | 71.83      | 25.79      | 271.11     |
|              | -1.48      | -1.48      | -1.47      | -1.47      | -1.47      | -1.47      | -1.47      | -1.47      | -1.47      | -1.47      | -1.47      | -1.47      | -1.47      | -1.47      | -1.46      | -1.46      | -1.46      | -1.46      | -1.46      |
|              | 5.00E-05   | 5.00E-05   | 5.00E-05   | 5.00E-05   | 5.00E-05   | 5.00E-05   | 5.00E-05   | 5.00E-05   | 5.00E-05   | 5.00E-05   | 5.00E-05   | 5.00E-05   | 5.00E-05   | 5.00E-05   | 5.00E-05   | 5.00E-05   | 5.00E-05   | 5.00E-05   | 5.00E-05   |
|              | 4.28E-04   | 4.28E-04   | 4.28E-04   | 4.28E-04   | 4.28E-04   | 4.28E-04   | 4.28E-04   | 4.28E-04   | 4.28E-04   | 4.28E-04   | 4.28E-04   | 4.28E-04   | 4.28E-04   | 4.28E-04   | 4.28E-04   | 4.28E-04   | 4.28E-04   | 4.28E-04   | 4.28E-04   |
|             | Defense mechanisms | alpha/beta hydrolase fold | Lipid transport and metabolism | AMP-binding enzyme | Phage lysozyme | -- | -- | Translation, ribosomal structure and biogenesis | Ribosomal L38e protein family | Protein of unknown function (DUF3129) | Glycosyl hydrolases family 31 | RNA processing and modification |


| EVM0012234 | 123.05 | 338.95 | -1.46 | 5.00E-05 | 4.28E-04 | RNA processing and modification | TAP C-terminal domain |
| EVM0011531 | 21.46  | 59.11  | -1.46 | 5.00E-05 | 4.28E-04 | --                                 | --                     |
| EVM0006451 | 2.25   | 6.19   | -1.46 | 4.00E-03 | 1.79E-02 | Posttranslational modification, protein turnover, chaperones | Isoprenylcysteine carboxyl methyltransferase (ICMT) family |
| EVM0011056 | 57.40  | 157.83 | -1.46 | 5.00E-05 | 4.28E-04 | --                                 | --                     |
| EVM0003863 | 2.54   | 6.98   | -1.46 | 3.00E-04 | 2.07E-03 | --                                 | Trichodiene synthase (TRI5) |
| EVM0002551 | 20.53  | 56.42  | -1.46 | 5.00E-05 | 4.28E-04 | Translation, ribosomal structure and biogenesis | Nop14-like family |
| EVM0008637 | 12.47  | 34.25  | -1.46 | 5.00E-05 | 4.28E-04 | RNA processing and modification | WD domain, G-beta repeat |
| EVM0002778 | 6.66   | 18.29  | -1.46 | 1.50E-04 | 1.14E-03 | Chromatin structure and dynamics | Paired amphipathic helix repeat |
| EVM0010774 | 1585.17| 4344.57| -1.45 | 5.00E-05 | 4.28E-04 | Posttranslational modification, protein turnover, chaperones | Cyclophilin type peptidyl-prolyl cis-trans isomerase/CLD |
| EVM0003335 | 29.73  | 81.43  | -1.45 | 5.00E-05 | 4.28E-04 | --                                 | Eukaryotic protein of unknown function (DUF1764) |
| EVM0011601 | 146.90 | 401.96 | -1.45 | 5.00E-05 | 4.28E-04 | --                                 | --                     |
| EVM0002657 | 350.18 | 956.58 | -1.45 | 1.00E-04 | 7.96E-04 | General function prediction only | short chain dehydrogenase |
| EVM0010039 | 12.66  | 34.58  | -1.45 | 5.00E-05 | 4.28E-04 | --                                 | Fungal specific transcription factor domain |
| EVM0006316 | 5.93   | 16.19  | -1.45 | 5.00E-05 | 4.28E-04 | Function unknown                  | WW domain binding protein 11 |
| EVM0010969 | 2.11 | 5.75 | -1.45 | 7.50E-04 | 4.49E-03 | General function prediction only | Zinc-binding dehydrogenase |
| EVM0007196 | 310.01 | 845.81 | -1.45 | 5.00E-05 | 4.28E-04 | RNA processing and modification | LSM domain |
| EVM0008803 | 28.64 | 78.11 | -1.45 | 5.00E-05 | 4.28E-04 | -- | FAD binding domain |
| EVM0001335 | 9.27 | 25.29 | -1.45 | 5.00E-05 | 4.28E-04 | RNA processing and modification | Ribosomal L28e protein family |
| EVM0011446 | 2630.22 | 7170.90 | -1.45 | 5.00E-05 | 4.28E-04 | -- | -- |
| EVM0012150 | 31.60 | 86.14 | -1.45 | 5.00E-05 | 4.28E-04 | -- | -- |
| EVM0010983 | 5.20 | 14.17 | -1.45 | 5.00E-05 | 4.28E-04 | -- | -- |
| EVM0003143 | 87.67 | 238.79 | -1.45 | 5.00E-05 | 4.28E-04 | -- | Senescence-associated protein |
| EVM0004038 | 1552.61 | 4225.45 | -1.44 | 8.00E-04 | 4.73E-03 | Translation, ribosomal structure and biogenesis | Ribosomal protein L6 |
| EVM0007627 | 1342.81 | 3654.10 | -1.44 | 5.00E-05 | 4.28E-04 | Posttranslational modification, protein turnover, chaperones | Hsp20/alpha crystallin family |
| EVM0006414 | 20.45 | 55.64 | -1.44 | 5.00E-05 | 4.28E-04 | General function prediction only | Homeobox domain |
| EVM0005072 | 388.60 | 1056.92 | -1.44 | 5.00E-05 | 4.28E-04 | -- | DAHP synthetase I family |
| EVM0006198 | 28.01 | 76.11 | -1.44 | 5.00E-05 | 4.28E-04 | General function prediction only | Protein kinase domain |
| EVM0002940 | 127.22 | 345.69 | -1.44 | 5.00E-05 | 4.28E-04 | General function prediction only | Zinc finger, C2H2 type |
| EVM0001369 | 9.46 | 25.69 | -1.44 | 3.40E-03 | 1.57E-02 | -- | -- |
| EVM0000435 | 51.56 | 139.96 | -1.44 | 5.00E-05 | 4.28E-04 | General function prediction only | Glycosyl transferase family 2 |
| Accession       | Start | End   | Change | E-Value1 | E-Value2 | Description                                           |
|-----------------|-------|-------|--------|----------|----------|-------------------------------------------------------|
| EVM0001076      | 8.68  | 23.56 | -1.44  | 5.00E-05 | 4.28E-04 | --                                                   |
| EVM0012187      | 8.45  | 22.91 | -1.44  | 5.00E-05 | 4.28E-04 | --                                                   |
| EVM0009692      | 29.71 | 80.48 | -1.44  | 5.00E-05 | 4.28E-04 | Fungal cellulose binding domain                      |
| EVM004846       | 12.93 | 35.02 | -1.44  | 5.00E-05 | 4.28E-04 | General function prediction only                     |
|                 |       |       |        |          |          | Aldo/keto reductase family                            |
|                 |       |       |        |          |          | Zinc knuckle                                         |
| EVM003386       | 4.47  | 12.11 | -1.44  | 1.50E-04 | 1.14E-03 | --                                                   |
| EVM007418       | 54.66 | 147.90| -1.44  | 5.00E-05 | 4.28E-04 | Carbohydrate transport and metabolism                |
|                 |       |       |        |          |          | Protein kinase domain                                 |
| EVM003296       | 214.70| 580.61| -1.44  | 5.50E-04 | 3.46E-03 | General function prediction only                     |
|                 |       |       |        |          |          | Domain of unknown function DUF221                    |
| EVM004085       | 201.70| 545.36| -1.43  | 3.50E-04 | 2.36E-03 | Posttranslational modification, protein turnover, chaperones |
|                 |       |       |        |          |          | FKBP-type peptidyl-prolyl cis-trans isomerase         |
| EVM008292       | 16.07 | 43.43 | -1.43  | 5.00E-05 | 4.28E-04 | Posttranslational modification, protein turnover, chaperones |
|                 |       |       |        |          |          | IBR domain                                            |
| EVM003663       | 1.33  | 3.58  | -1.43  | 7.50E-04 | 4.49E-03 | Carbohydrate transport and metabolism                |
|                 |       |       |        |          |          | O-Glycosyl hydrolase family 30                       |
| EVM009894       | 40.64 | 109.70| -1.43  | 5.00E-05 | 4.28E-04 | --                                                   |
|                 |       |       |        |          |          | Fungal specific transcription factor domain           |
| EVM005821       | 6.21  | 16.77 | -1.43  | 5.00E-05 | 4.28E-04 | --                                                   |
| EVM007729       | 2.53  | 6.83  | -1.43  | 4.50E-04 | 2.92E-03 | --                                                   |
| EVM003820       | 20.35 | 54.91 | -1.43  | 5.00E-05 | 4.28E-04 | --                                                   |
| EVM003368       | 3.74  | 10.07 | -1.43  | 1.80E-03 | 9.29E-03 | --                                                   |
| Gene ID           | Value1 | Value2  | Change | Log2 Fold Change | Function                                                                 |
|------------------|--------|---------|--------|------------------|--------------------------------------------------------------------------|
| EVM0006624       | 19.39  | 52.21   | -1.43  | 5.00E-05         | Amino acid transport and metabolism                                      |
| EVM0010878       | 6.84   | 18.41   | -1.43  | 5.00E-05         | Pyridoxal-phosphate dependent enzyme                                     |
| EVM0005649       | 17.82  | 479.93  | -1.43  | 5.00E-05         | Transcription                                                            |
| EVM0004256       | 6.23   | 16.77   | -1.43  | 4.20E-03         | Basic region leucine zipper                                              |
| EVM0003346       | 88.20  | 236.93  | -1.43  | 1.00E-04         | Nitronate monooxygenase                                                  |
| EVM0011568       | 401.96 | 1079.51 | -1.43  | 5.00E-05         | --                                                                       |
| EVM0008872       | 1.78   | 4.78    | -1.43  | 6.05E-03         | Lipid transport and metabolism                                           |
| EVM0004977       | 3.75   | 10.07   | -1.42  | 8.50E-04         | Fatty acid hydroxylase superfamily                                       |
| EVM0005318       | 34.68  | 92.99   | -1.42  | 5.00E-05         | Alpha/beta hydrolase family                                              |
| EVM0007377       | 10.04  | 26.93   | -1.42  | 5.00E-05         | Met-10+ like-protein                                                     |
| EVM0011621       | 51.54  | 138.09  | -1.42  | 5.00E-05         | RNA pseudouridylate synthase                                             |
| EVM0004345       | 18.26  | 48.94   | -1.42  | 5.00E-05         | RNA processing and modification                                          |
| EVM0006041       | 230.90 | 618.32  | -1.42  | 5.00E-05         | RNA processing and modification                                          |
| EVM0001621       | 51.54  | 138.09  | -1.42  | 5.00E-05         | Low temperature viability protein                                        |
| EVM0004345       | 18.26  | 48.94   | -1.42  | 5.00E-05         | Taurine catabolism dioxygenase TauD, TfdA family                         |
| EVM0006041       | 230.90 | 618.32  | -1.42  | 5.00E-05         | SNARE domain                                                             |
| EVM0004179       | 4.69   | 12.55   | -1.42  | 7.50E-04         | Lipid transport and metabolism                                           |
| EVM0002217       | 160.56 | 429.31  | -1.42  | 5.00E-05         | short chain dehydrogenase                                                |
| EVM0008316       | 1.50   | 4.02    | -1.42  | 3.00E-04         | --                                                                       |

**Amino acid transport and metabolism**

**Pyridoxal-phosphate dependent enzyme**

**Transcription**

**Basic region leucine zipper**

**Nitronate monooxygenase**

**Lipid transport and metabolism**

**Fatty acid hydroxylase superfamily**

**Alpha/beta hydrolase family**

**Met-10+ like-protein**

**RNA pseudouridylate synthase**

**Intracellular trafficking, secretion, and vesicular transport**

**SNARE domain**

**Lipid transport and metabolism**

**short chain dehydrogenase**
| EVM0008946  | 64.11 | 171.21 | -1.42 | 5.00E-05 | 4.28E-04 | Posttranslation modification, protein turnover, chaperones | Ring finger domain |
| EVM0003745  | 4.61  | 12.31  | -1.42 | 5.00E-05 | 4.28E-04 | -- | -- |
| EVM0005073  | 11.11 | 29.62  | -1.42 | 5.00E-05 | 4.28E-04 | Nitronate monooxygenase | Aldose 1-epimerase |
| EVM0006998  | 198.46| 529.05 | -1.41 | 5.00E-05 | 4.28E-04 | Carbohydrate transport and metabolism | -- |
| EVM0003882  | 60.24 | 160.58 | -1.41 | 5.00E-05 | 4.28E-04 | Energy production and conversion | Pyridine nucleotide-disulphide oxidoreductase |
| EVM0009498  | 1.55  | 4.12   | -1.41 | 1.42E-02 | 4.94E-02 | General function prediction only | Zinc-finger double domain |
| EVM0008163  | 4.77  | 12.71  | -1.41 | 3.50E-04 | 2.36E-03 | -- | -- |
| EVM0005090  | 7.83  | 20.83  | -1.41 | 3.00E-04 | 2.07E-03 | -- | -- |
| EVM0012061  | 28.87 | 76.80  | -1.41 | 5.00E-05 | 4.28E-04 | RNA processing and modification | PIN domain |
| EVM0008373  | 13.56 | 36.05  | -1.41 | 5.00E-05 | 4.28E-04 | General function prediction only | YL1 nuclear protein |
| EVM0003630  | 37.70 | 100.15 | -1.41 | 5.00E-05 | 4.28E-04 | General function prediction only | NGP1NT (NUC091) domain |
| EVM0000768  | 749.93| 1991.57| -1.41 | 5.00E-05 | 4.28E-04 | -- | -- |
| EVM0001057  | 25.75 | 68.32  | -1.41 | 5.00E-05 | 4.28E-04 | Translation, ribosomal structure and biogenesis | tRNA pseudouridine synthase |
| EVM0007602  | 11.40 | 30.24  | -1.41 | 5.00E-05 | 4.28E-04 | Lipid transport and metabolism | PLD-like domain |
| EVM0009531  | 2.87  | 7.60   | -1.41 | 5.00E-05 | 4.28E-04 | -- | Polysaccharide lyase family 8, super-sandwich domain |
| EVM0010169  | 4.60 | 12.19 | -1.41 | 5.00E-05 | 4.28E-04 | --       |
| EVM0001494  | 11.14| 29.53 | -1.41 | 5.00E-05 | 4.28E-04 | --       |
| EVM0009378  | 28.25| 74.89 | -1.41 | 5.00E-05 | 4.28E-04 | Signal transduction mechanisms |
| EVM0000037  | 1.75 | 4.63  | -1.40 | 3.70E-03 | 1.68E-02 | Defense mechanisms |
| EVM0009748  | 22.57| 59.69 | -1.40 | 5.00E-05 | 4.28E-04 | --       |
| EVM0011268  | 21.81| 57.66 | -1.40 | 5.00E-05 | 4.28E-04 | --       |
| EVM0004288  | 17.22| 45.50 | -1.40 | 2.00E-04 | 1.46E-03 | --       |
| EVM0005306  | 44.42| 117.29| -1.40 | 5.00E-05 | 4.28E-04 | Cell wall/membrane/envelope biogenesis |
| EVM0003609  | 366.16| 966.62| -1.40 | 5.00E-05 | 4.28E-04 | --       |
| EVM0003509  | 47.08| 124.26| -1.40 | 5.00E-05 | 4.28E-04 | --       |
| EVM0005039  | 192.83| 508.02| -1.40 | 5.00E-05 | 4.28E-04 | RNA processing and modification |
| EVM0011833  | 28.52| 75.11 | -1.40 | 5.00E-05 | 4.28E-04 | --       |
| EVM0000400  | 2.70 | 7.11  | -1.40 | 5.00E-04 | 3.19E-03 | Lipid transport and metabolism |
| EVM0008791  | 14.59| 38.42 | -1.40 | 5.00E-05 | 4.28E-04 | Coenzyme transport and metabolism |
| EVM0005101  | 15.44| 40.65 | -1.40 | 5.00E-05 | 4.28E-04 | --       |
| EVM0009183  | 19.28| 50.76 | -1.40 | 5.00E-05 | 4.28E-04 | --       |
| EVM0010602  | 75.13| 197.54| -1.39 | 5.00E-05 | 4.28E-04 | --       |

- Domain of unknown function (DUF4451)
- Pleckstrin homology domain
- alpha/beta hydrolase fold
- Endoplasmic reticulum-based factor for assembly of V-ATPase
- OHCU decarboxylase
- Glycosyl transferases group 1
- Cytochrome oxidase c subunit VIb
- DEAD/DEAH box helicase
- Lipase (class 3)
- Diphospho-CoA kinase
- BTB/POZ domain
| Accession  | EVM000369 | 0.64 | 1.67 | -1.39 | 5.55E-03 | 2.34E-02 | General function prediction only | GMC oxidoreductase |
|------------|-----------|------|------|-------|----------|----------|----------------------------------|-------------------|
| Accession  | EVM0012015| 15.29| 40.16| -1.39 | 5.00E-05 | 4.28E-04 | Translation, ribosomal structure and biogenesis | BOP1NT (NUC169) domain |
| Accession  | EVM0006997| 8.79 | 23.07| -1.39 | 5.00E-05 | 4.28E-04 | -- | Glycosyl hydrolases family 28 |
| Accession  | EVM0004321| 53.70| 140.64| -1.39 | 5.00E-05 | 4.28E-04 | Inorganic ion transport and metabolism | Ctr copper transporter family |
| Accession  | EVM0006115| 2.89 | 7.56 | -1.39 | 7.50E-04 | 4.49E-03 | Carbohydrate transport and metabolism | Glycosyl transferase family 8 |
| Accession  | EVM0005431| 7.25 | 18.99| -1.39 | 5.00E-05 | 4.28E-04 | Cell cycle control, cell division, chromosome partitioning | HEC/Ndc80p family |
| Accession  | EVM0006749| 24.96| 65.23| -1.39 | 5.00E-05 | 4.28E-04 | -- | Membrane bound O-acyl transferase family |
| Accession  | EVM0005915| 24.78| 64.70| -1.38 | 5.00E-05 | 4.28E-04 | -- | Lipase (class 3) |
| Accession  | EVM0005340| 4.96 | 12.95| -1.38 | 9.50E-04 | 5.46E-03 | -- | Alpha/beta hydrolase family |
| Accession  | EVM0007232| 19.82| 51.70| -1.38 | 5.00E-05 | 4.28E-04 | Nucleotide transport and metabolism | Cytidine and deoxyctydylate deaminase zinc-binding region |
| Accession  | EVM0007826| 24.23| 63.15| -1.38 | 5.00E-05 | 4.28E-04 | General function prediction only | RNA recognition motif. (a.k.a. RRM, RBD, or RNP domain) |
| Accession  | EVM000927| 201.97| 526.19| -1.38 | 5.00E-05 | 4.28E-04 | Secondary metabolites biosynthesis, transport and catabolism | Pyridine nucleotide-disulphide oxidoreductase |
| Accession  | EVM0011808| 2.90 | 7.56 | -1.38 | 2.45E-03 | 1.20E-02 | -- | Lysine-specific metallo-endopeptidase |
| Accession  | EVM0005924| 1.53 | 3.99 | -1.38 | 7.75E-03 | 3.06E-02 | -- | Glycosyl hydrolase family 61 |
| Code         | Value1 | Value2  | Value3 | Value4 | Value5 | Value6 | Function                                                                 |
|--------------|--------|---------|--------|--------|--------|--------|--------------------------------------------------------------------------|
| EVM0002713   | 13.35  | 34.76   | -1.38  | 5.00E-05| 4.28E-04|        | Chromatin structure and dynamics                                           |
| EVM0001160   | 9.94   | 25.86   | -1.38  | 1.00E-04| 7.96E-04| --     | Sin3 family co-repressor                                                 |
| EVM0004608   | 18.87  | 49.09   | -1.38  | 5.00E-05| 4.28E-04| --     | SNF2 family N-terminal domain                                             |
| EVM0009867   | 39.66  | 103.14  | -1.38  | 5.00E-05| 4.28E-04| --     | Glycosyl hydrolases family 28                                            |
| EVM0008232   | 1.55   | 4.03    | -1.38  | 2.70E-03| 1.30E-02| --     | General function prediction only                                          |
| EVM0012002   | 24.88  | 64.69   | -1.38  | 5.00E-05| 4.28E-04|        | WD domain, G-beta repeat                                                  |
| EVM0010331   | 14.48  | 37.60   | -1.38  | 5.00E-05| 4.28E-04| --     | DEAD/DEAH box helicase                                                    |
| EVM001135    | 9.87   | 25.62   | -1.38  | 5.00E-05| 4.28E-04|        | RNA processing and modification                                           |
| EVM0010816   | 5.26   | 13.66   | -1.38  | 5.00E-05| 4.28E-04| --     | alpha/beta hydrolase fold                                                |
| EVM0005506   | 4.46   | 11.58   | -1.38  | 3.50E-04| 2.36E-03| #N/A  | #N/A                                                                    |
| EVM0009843   | 26.14  | 67.76   | -1.37  | 5.00E-05| 4.28E-04| --     | Caspase domain                                                            |
| EVM001419    | 184.77 | 478.79  | -1.37  | 5.00E-05| 4.28E-04|        | Signal transduction mechanisms                                            |
| EVM0008368   | 222.78 | 577.18  | -1.37  | 5.00E-05| 4.28E-04|        | SGS domain                                                               |
| EVM0007634   | 3.05   | 7.90    | -1.37  | 4.50E-04| 2.92E-03| --     | Double-stranded DNA-binding domain                                        |
| EVM0008622   | 99.12  | 256.65  | -1.37  | 5.00E-05| 4.28E-04| --     | 50S ribosome-binding GTPase                                               |
| EVM0006301   | 28.63  | 74.11   | -1.37  | 5.00E-05| 4.28E-04|        | Amidohydrolase family                                                     |
| EVM0005200   | 46.03  | 119.08  | -1.37  | 5.00E-05| 4.28E-04|        | Lipid transport and metabolism                                            |

**Summary:**
- **EVM0002713**: Chromatin structure and dynamics
- **EVM0001160**: Sin3 family co-repressor
- **EVM0004608**: SNF2 family N-terminal domain
- **EVM0009867**: Glycosyl hydrolases family 28
- **EVM0008232**: General function prediction only
- **EVM0012002**: WD domain, G-beta repeat
- **EVM0010331**: DEAD/DEAH box helicase
- **EVM001135**: RNA processing and modification
- **EVM0010816**: alpha/beta hydrolase fold
- **EVM0005506**: #N/A
- **EVM0009843**: Caspase domain
- **EVM001419**: Signal transduction mechanisms
- **EVM0008368**: SGS domain
- **EVM0007634**: Double-stranded DNA-binding domain
- **EVM0008622**: 50S ribosome-binding GTPase
- **EVM0006301**: Amidohydrolase family
- **EVM0005200**: Lipid transport and metabolism
| EVM0009112  | 4.96  | 12.83 | -1.37 | 6.00E-04 | 3.72E-03 | Defense mechanisms          | NAD dependent epimerase/dehydratase family |
| EVM0011107  | 137.61| 355.39| -1.37 | 5.00E-05 | 4.28E-04 | --                          | --                                          |
| EVM0010981  | 1041.63| 2689.99| -1.37 | 8.00E-04 | 4.73E-03 | Function unknown            | Activator of Hsp90 ATPase, N-terminal       |
| EVM0007524  | 8.54  | 22.04 | -1.37 | 5.00E-05 | 4.28E-04 | --                          | Domain of unknown function (DUF4451)        |
| EVM0007343  | 27.56 | 71.12 | -1.37 | 5.00E-05 | 4.28E-04 | --                          | --                                          |
| EVM0002076  | 325.41| 839.77| -1.37 | 5.00E-05 | 4.28E-04 | --                          | CFEM domain                                  |
| EVM0010051  | 3.30  | 8.52  | -1.37 | 5.00E-05 | 4.28E-04 | --                          | Glycosyl hydrolase family 3 N terminal domain |
| EVM0010226  | 332.37| 857.56| -1.37 | 5.00E-05 | 4.28E-04 | Inorganic ion transport and metabolism | Iron/manganese superoxide dismutases, C-terminal domain |
| EVM0000675  | 11.46 | 29.52 | -1.37 | 5.00E-05 | 4.28E-04 | --                          | Eukaryotic aspartyl protease                |
| EVM0007858  | 0.63  | 1.63  | -1.37 | 1.22E-02 | 4.38E-02 | --                          | --                                          |
| EVM0008883  | 33.08 | 85.23 | -1.37 | 5.00E-05 | 4.28E-04 | --                          | --                                          |
| EVM0002597  | 8.26  | 21.26 | -1.36 | 5.00E-05 | 4.28E-04 | --                          | Flavin reductase like domain                |
| EVM0011352  | 1.71  | 4.41  | -1.36 | 2.85E-03 | 1.36E-02 | --                          | --                                          |
| EVM0004408  | 17.94 | 46.08 | -1.36 | 5.00E-05 | 4.28E-04 | --                          | Protein of unknown function (DUF563)        |
| EVM0012233  | 1.25  | 3.21  | -1.36 | 1.08E-02 | 3.98E-02 | --                          | --                                          |
| EVM0005619  | 16.97 | 43.57 | -1.36 | 5.00E-05 | 4.28E-04 | --                          | 60Kd inner membrane protein                |
| EVM0004607  | 6.27  | 16.09 | -1.36 | 1.00E-04 | 7.96E-04 | --                          | --                                          |
| EVM0000375  | 213.86| 548.25| -1.36 | 5.00E-05 | 4.28E-04 | Lipid transport and metabolism | Fatty acid hydroxylase superfamily          |
| EVM0010743  | 4.11  | 10.52 | -1.36 | 2.00E-04 | 1.46E-03 | --                          | F-box-like                                  |
| EVM0000212  | 75.57 | 193.65 | -1.36 | 5.00E-05 | 4.28E-04 | Posttranslational modification, protein turnover, chaperones | Zinc finger, C3HC4 type (RING finger) |
|-------------|-------|--------|-------|----------|----------|---------------------------------------------------------------|-------------------------------------|
| EVM0005019  | 87.65 | 224.47 | -1.36 | 5.00E-05 | 4.28E-04 | General function prediction only                               | Protein kinase domain               |
| EVM0005202  | 0.97  | 2.48   | -1.36 | 2.80E-03 | 1.34E-02 | --                                                            | Glycosyl hydrolase family 61       |
| EVM0005743  | 20.51 | 52.48  | -1.36 | 5.00E-05 | 4.28E-04 | --                                                            | --                                  |
| EVM0008600  | 29.62 | 75.77  | -1.35 | 5.00E-05 | 4.28E-04 | --                                                            | --                                  |
| EVM001556   | 3.57  | 9.12   | -1.35 | 2.00E-04 | 1.46E-03 | Amino acid transport and metabolism                            | Aminotransferase class I and II     |
| EVM0006609  | 1.43  | 3.64   | -1.35 | 2.95E-03 | 1.40E-02 | --                                                            | G-protein alpha subunit             |
| EVM0006578  | 103.07| 263.57 | -1.35 | 5.00E-05 | 4.28E-04 | --                                                            | Syntaxin                           |
| EVM0006443  | 2.06  | 5.27   | -1.35 | 1.10E-03 | 6.17E-03 | General function prediction only                               | RNA recognition motif. (a.k.a. RRM, RBD, or RNP domain) |
| EVM0010933  | 2.24  | 5.71   | -1.35 | 1.75E-03 | 9.08E-03 | --                                                            | --                                  |
| EVM0003824  | 1.67  | 4.26   | -1.35 | 7.15E-03 | 2.86E-02 | --                                                            | --                                  |
| EVM0008917  | 21.73 | 55.42  | -1.35 | 3.00E-04 | 2.07E-03 | General function prediction only                               | Fcf1                                |
| EVM0004272  | 364.07| 928.57 | -1.35 | 5.00E-05 | 4.28E-04 | --                                                            | Translationally controlled tumour protein |
| EVM0000041  | 1.37  | 3.49   | -1.35 | 1.50E-04 | 1.14E-03 | #N/A                                                          | #N/A                                |
| EVM0009425  | 1.85  | 4.72   | -1.35 | 1.55E-03 | 8.22E-03 | --                                                            | --                                  |
| EVM0007011  | 66.10 | 168.24 | -1.35 | 5.00E-05 | 4.28E-04 | Function unknown                                              | Family of unknown function (DUF500) |
| EVM0004433 | 8.55 | 21.72 | -1.35 | 5.00E-05 | 4.28E-04 | -- | Lactonase, 7-bladed beta-propeller |
| EVM0006843 | 2.46 | 6.25  | -1.34 | 7.00E-04 | 4.23E-03 | -- | Glycosyl hydrolases family 6 |
| EVM0008497 | 577.43 | 1463.92 | -1.34 | 9.00E-04 | 5.22E-03 | Lipid transport and metabolism | MaoC like domain |
| EVM0004027 | 2105.78 | 5348.73 | -1.34 | 5.00E-05 | 4.28E-04 | Replication, recombination and repair | DEAD/DEAH box helicase |
| EVM0006496 | 1.95 | 4.94  | -1.34 | 5.00E-05 | 4.28E-04 | -- | BUD22 |
| EVM0005275 | 517.79 | 1311.61 | -1.34 | 4.80E-03 | 2.08E-02 | Energy production and conversion | FAD binding domain |
| EVM0008516 | 2.13 | 5.41  | -1.34 | 3.75E-03 | 1.70E-02 | -- | Glycosyl hydrolase family 45 |
| EVM0008645 | 67.91 | 171.91 | -1.34 | 3.55E-03 | 1.62E-02 | -- | -- |
| EVM0005236 | 393.07 | 994.81 | -1.34 | 5.00E-05 | 4.28E-04 | RNA processing and modification | LSM domain |
| EVM0007065 | 120.18 | 304.16 | -1.34 | 5.00E-05 | 4.28E-04 | -- | -- |
| EVM0002142 | 54.18 | 136.91 | -1.34 | 5.00E-05 | 4.28E-04 | General function prediction only | Cyclin |
| EVM0005275 | 517.79 | 1311.61 | -1.34 | 4.80E-03 | 2.08E-02 | Energy production and conversion | FAD binding domain |
| EVM0008516 | 2.13 | 5.41  | -1.34 | 3.75E-03 | 1.70E-02 | -- | Glycosyl hydrolase family 45 |
| EVM0008645 | 67.91 | 171.91 | -1.34 | 3.55E-03 | 1.62E-02 | -- | -- |
| EVM0005236 | 393.07 | 994.81 | -1.34 | 5.00E-05 | 4.28E-04 | RNA processing and modification | LSM domain |
| EVM0007065 | 120.18 | 304.16 | -1.34 | 5.00E-05 | 4.28E-04 | -- | -- |
| EVM0002142 | 54.18 | 136.91 | -1.34 | 5.00E-05 | 4.28E-04 | General function prediction only | Cyclin |
| EVM0001250 | 12.47 | 31.46  | -1.34 | 5.00E-05 | 4.28E-04 | -- | Inorganic ion transport and metabolism | E1-E2 ATPase |
| Code       | Value1  | Value2  | -1.33  | Value3  | Value4  | Function                              | Description                                                                 |
|------------|---------|---------|--------|---------|---------|---------------------------------------|-----------------------------------------------------------------------------|
| EVM0010158 | 41.47   | 104.62  | -1.34  | 5.00E-05| 4.28E-04| Function unknown                      | Pre-rRNA-processing protein TSR2                                             |
| EVM0006028 | 235.04  | 592.51  | -1.33  | 5.00E-05| 4.28E-04| --                                   | --                                                                           |
| EVM0001608 | 3.84    | 9.69    | -1.33  | 5.50E-04| 3.46E-03| --                                   | Glycosyl hydrolase family 61                                              |
| EVM0009830 | 1.11    | 2.78    | -1.33  | 7.50E-03| 2.98E-02| --                                   | --                                                                           |
| EVM0004461 | 16.00   | 40.31   | -1.33  | 5.00E-05| 4.28E-04| --                                   | Putative oxidoreductase C terminal                                           |
| EVM0008537 | 8018.90 | 20193.20| -1.33  | 4.60E-03| 2.01E-02| Posttranslational modification, protein turnover, chaperones | Hsp20/alpha crystallin family                                               |
| EVM0007375 | 14.81   | 37.29   | -1.33  | 5.00E-05| 4.28E-04| General function prediction only     | HIT zinc finger                                                            |
| EVM0002182 | 16.77   | 42.21   | -1.33  | 5.00E-05| 4.28E-04| --                                   | RIO1 family                                                                |
| EVM0007672 | 3.88    | 9.77    | -1.33  | 5.50E-04| 3.46E-03| Defense mechanisms                    | NAD dependent epimerase/dehydratase family                                 |
| EVM0005483 | 22.26   | 55.89   | -1.33  | 5.00E-05| 4.28E-04| Posttranslational modification, protein turnover, chaperones | ATPase family associated with various cellular activities (AAA)             |
| EVM0011888 | 0.93    | 2.35    | -1.33  | 1.09E-02| 4.01E-02| --                                   | Peroxidase                                                                 |
| EVM0003399 | 2.21    | 5.55    | -1.33  | 1.90E-03| 9.73E-03| --                                   | --                                                                           |
| EVM0004689 | 4.53    | 11.37   | -1.33  | 5.00E-05| 4.28E-04| --                                   | HAUS augmin-like complex subunit 6 N-terminus                              |
| EVM0004830 | 2.82    | 7.05    | -1.33  | 1.40E-03| 7.55E-03| --                                   | YqiI/YcgG family                                                          |
| EVM0003606 | 18.41   | 46.12   | -1.33  | 5.00E-05| 4.28E-04| --                                   | --                                                                           |
| EVM0008340 | 16.23   | 40.59   | -1.32  | 1.50E-04| 1.14E-03| General function prediction only     | Methyltransferase domain                                                   |
| EVM0010339  | 23.88  | 59.74  | -1.32 | 5.00E-05 | 4.28E-04 | -- | WW domain  |
| EVM0003803  | 1.80   | 4.50   | -1.32 | 2.80E-03 | 1.34E-02 | -- | NADH:flavin oxidoreductase / NADH oxidase family  |
| EVM0010881  | 23.69  | 59.14  | -1.32 | 5.00E-05 | 4.28E-04 | -- | Inositol polyphosphate kinase  |
| EVM0005891  | 32.76  | 81.71  | -1.32 | 5.00E-05 | 4.28E-04 | Energy production and conversion | Pyridine nucleotide-disulphide oxidoreductase  |
| EVM0001521  | 15.55  | 38.77  | -1.32 | 1.50E-04 | 1.14E-03 | -- | --  |
| EVM0007328  | 1928.08 | 4802.84 | -1.32 | 5.00E-05 | 4.28E-04 | Translation, ribosomal structure and biogenesis | 60s Acidic ribosomal protein  |
| EVM0008609  | 19.64  | 48.92  | -1.32 | 3.35E-03 | 1.55E-02 | General function prediction only | Ankyrin repeats (3 copies)  |
| EVM0006159  | 40.98  | 102.02 | -1.32 | 5.00E-05 | 4.28E-04 | -- | --  |
| EVM0000986  | 8.59   | 21.37  | -1.32 | 5.00E-05 | 4.28E-04 | -- | --  |
| EVM0008995  | 26.65  | 66.32  | -1.32 | 5.00E-05 | 4.28E-04 | -- | Arrestin (or S-antigen), C-terminal domain  |
| EVM0010646  | 29.60  | 73.64  | -1.31 | 5.00E-05 | 4.28E-04 | Cell wall/membrane/envelope biogenesis | Mechanosensitive ion channel  |
| EVM0002993  | 7.18   | 17.86  | -1.31 | 5.00E-05 | 4.28E-04 | -- | Spb1 C-terminal domain  |
| EVM0007514  | 33.18  | 82.54  | -1.31 | 5.00E-05 | 4.28E-04 | -- | RTA1 like protein  |
| EVM0009405  | 12.99  | 32.30  | -1.31 | 5.55E-03 | 2.34E-02 | General function prediction only | Yippee zinc-binding/DNA-binding /Mis18, centromere assembly  |
| EVM0009615  | 3.93   | 9.76   | -1.31 | 1.10E-03 | 6.17E-03 | -- | Pectate lyase  |
| EVM0002208 | 25.41  | 63.02   | -1.31  | 5.00E-05 | 4.28E-04 | Lipid transport and metabolism | CRAL/TRIO domain |
| EVM0003943 | 2.54   | 6.30    | -1.31  | 5.00E-05 | 4.28E-04 | --                             | --               |
| EVM0007351 | 6.78   | 16.81   | -1.31  | 5.00E-05 | 4.28E-04 | --                             | --               |
| EVM0011602 | 2270.95| 5628.31 | -1.31  | 5.00E-05 | 4.28E-04 | Translation, ribosomal structure and biogenesis | Translation initiation factor SUI1 |
| EVM0008835 | 35.82  | 88.70   | -1.31  | 5.00E-05 | 4.28E-04 | Carbohydrate transport and metabolism | --               |
| EVM0011261 | 25.40  | 62.85   | -1.31  | 5.00E-05 | 4.28E-04 | General function prediction only | WD domain, G-beta repeat |
| EVM0011343 | 60.87  | 150.59  | -1.31  | 5.00E-05 | 4.28E-04 | Posttranslational modification, protein turnover, chaperones | Glutaredoxin |
| EVM0010336 | 59.89  | 147.96  | -1.30  | 5.00E-05 | 4.28E-04 | --                             | --               |
| EVM0010845 | 0.99   | 2.45    | -1.30  | 1.27E-02 | 4.52E-02 | --                             | Domain of unknown function (DUF3415) |
| EVM0011499 | 10.11  | 24.96   | -1.30  | 2.00E-04 | 1.46E-03 | --                             | --               |
| EVM0003922 | 20.43  | 50.37   | -1.30  | 5.00E-05 | 4.28E-04 | Function unknown                | --               |
| EVM0010985 | 28.80  | 70.99   | -1.30  | 1.00E-04 | 7.96E-04 | Carbohydrate transport and metabolism | Transaldolase |
| EVM0008211 | 14.80  | 36.44   | -1.30  | 5.00E-05 | 4.28E-04 | Signal transduction mechanisms | Protein tyrosine kinase |
| EVM0002753 | 17.65  | 43.44   | -1.30  | 5.00E-05 | 4.28E-04 | G protein-coupled glucose receptor regulating Gpa2 | --               |
| EVM0011734 | 5.99   | 14.73   | -1.30  | 3.50E-04 | 2.36E-03 | --                             | --               |
| EVM0011492 | 260.14 | 639.74  | -1.30  | 5.00E-05 | 4.28E-04 | --                             | --               |
| Gene ID     | Score 1 | Score 2 | Log2 Fold | Score 3 | Score 4 | Function and Motif                        |
|------------|---------|---------|-----------|---------|---------|------------------------------------------|
| EVM0003818 | 15.18   | 37.33   | -1.30     | 5.00E-05| 4.28E-04| RNA processing and modification          |
| EVM0008910 | 12.39   | 30.47   | -1.30     | 1.00E-04| 7.96E-04| RNA recognition motif. (a.k.a. RRM, RBD, or RNP domain) |
| EVM0011552 | 35.30   | 86.70   | -1.30     | 5.00E-05| 4.28E-04| Lipid transport and metabolism           |
| EVM0011840 | 15.75   | 38.66   | -1.30     | 5.00E-05| 4.28E-04| Fatty acid desaturase                    |
| EVM0007512 | 200.47  | 491.17  | -1.29     | 1.00E-04| 7.96E-04| Cell cycle control, cell division, chromosome partitioning |
| EVM0008044 | 14.30   | 35.04   | -1.29     | 5.00E-04| 3.19E-03| Transport protein particle (TRAPP) component |
| EVM0001473 | 24.18   | 59.25   | -1.29     | 5.00E-05| 4.28E-04| Intracellular trafficking, secretion, and vesicular transport |
| EVM0006895 | 2.87    | 7.03    | -1.29     | 5.95E-03| 2.47E-02| Protein of unknown function (DUF3129)    |
| EVM0004556 | 8.30    | 20.31   | -1.29     | 5.00E-05| 4.28E-04| NACHT domain                            |
| EVM0001584 | 35.33   | 86.44   | -1.29     | 5.00E-05| 4.28E-04| Voltage-dependent anion channel          |
| EVM0001421 | 43.49   | 106.35  | -1.29     | 5.00E-05| 4.28E-04| Cell cycle control, cell division, chromosome partitioning |
| EVM000264  | 0.97    | 2.37    | -1.29     | 2.35E-03| 1.16E-02| --                                       |
| EVM0008142 | 0.61    | 1.49    | -1.29     | 5.05E-03| 2.17E-02| --                                       |
| EVM0000653 | 48.09   | 117.54  | -1.29     | 5.00E-05| 4.28E-04| Domain of unknown function (DUF947)      |
| EVM0011522 | 8.83    | 21.55   | -1.29     | 2.50E-04| 1.77E-03| Defense mechanisms                       |
| EVM0011522 | 8.83    | 21.55   | -1.29     | 2.50E-04| 1.77E-03| NAD dependent epimerase/dehydratase family |
| ID          | Value 1     | Value 2     | Score | Value 3     | Score | Function                                                                 |
|-------------|-------------|-------------|-------|-------------|-------|-------------------------------------------------------------------------|
| EVM0004623  | 9.64        | 23.52       | -1.29 | 5.00E-05    | 4.28E-04| F-box-like                                                              |
| EVM0007930  | 11.07       | 26.99       | -1.29 | 5.00E-05    | 4.28E-04| RNA recognition motif (a.k.a. RRM, RBD, or RNP domain)                  |
| EVM0005026  | 4.13        | 10.06       | -1.29 | 7.00E-04    | 4.23E-03| --                                                                      |
| EVM0005245  | 26.13       | 63.68       | -1.29 | 5.00E-05    | 4.28E-04| Ubiquitin-2 like Rad60 SUMO-like                                         |
| EVM0000121  | 44.85       | 109.18      | -1.28 | 5.00E-05    | 4.28E-04| General function prediction only                                      |
| EVM0005338  | 187.89      | 457.18      | -1.28 | 5.00E-05    | 4.28E-04| General function prediction only                                      |
| EVM0006924  | 17.43       | 42.33       | -1.28 | 2.50E-04    | 1.77E-03| --                                                                      |
| EVM0012121  | 19.61       | 47.60       | -1.28 | 5.00E-05    | 4.28E-04| Glioma tumor suppressor candidate region                                |
| EVM0009034  | 12.09       | 29.34       | -1.28 | 2.00E-04    | 1.46E-03| --                                                                      |
| EVM0008481  | 11.72       | 28.45       | -1.28 | 5.00E-05    | 4.28E-04| Inorganic ion transport and metabolism                                  |
| EVM001809   | 129.36      | 313.62      | -1.28 | 5.00E-05    | 4.28E-04| --                                                                      |
| EVM0012201  | 4.88        | 11.81       | -1.28 | 5.00E-04    | 3.19E-03| --                                                                      |
| EVM0001227  | 39.10       | 94.70       | -1.28 | 5.00E-05    | 4.28E-04| Function unknown                                                        |
| EVM0003283  | 17.04       | 41.24       | -1.27 | 5.00E-05    | 4.28E-04| --                                                                      |
| EVM0011843  | 2.14        | 5.17        | -1.27 | 9.00E-04    | 5.22E-03| --                                                                      |
| EVM0010862  | 95.69       | 231.41      | -1.27 | 5.00E-05    | 4.28E-04| Translation, ribosomal structure and biogenesis                        |
| EVM0007013  | 24.72       | 59.78       | -1.27 | 5.00E-05    | 4.28E-04| Protein of unknown function (DUF1275)                                   |
| Identifier   | Start  | End    | Score | E-value | Description                                      | Superfamily/Domain                                      |
|--------------|--------|--------|-------|---------|--------------------------------------------------|---------------------------------------------------------|
| EVM0009750   | 114.66 | 277.19 | -1.27 | 5.00E-05| Lipid transport and metabolism                   | PAP2 superfamily                                         |
| EVM0011085   | 39.91  | 96.40  | -1.27 | 5.00E-05| --                                                | Translation initiation factor IF-3, C-terminal domain    |
| EVM0002721   | 101.31 | 244.62 | -1.27 | 5.00E-05| Carbohydrate transport and metabolism             | Glycosyl hydrolases family 18                            |
| EVM0004090   | 16.49  | 39.80  | -1.27 | 5.00E-05| --                                                | --                                                      |
| EVM0002495   | 443.19 | 1068.61| -1.27 | 2.00E-04| Posttranslational modification, protein turnover, chaperones | Cyclophilin type peptidyl-prolyl cis-trans isomerase/CLD |
| EVM0009839   | 190.50 | 458.94 | -1.27 | 3.50E-04| Carbohydrate transport and metabolism             | Glycosyltransferase family 20                            |
| EVM0007485   | 90.33  | 217.59 | -1.27 | 5.00E-05| --                                                | Fasciclin domain                                         |
| EVM0001538   | 14.28  | 34.39  | -1.27 | 5.00E-05| --                                                | F-box-like                                               |
| EVM0003807   | 2.35   | 5.65   | -1.24 | 5.95E-03| Amino acid transport and metabolism               | --                                                      |
| EVM0006468   | 15.66  | 37.70  | -1.27 | 1.00E-04| Signal transduction mechanisms                    | RED-like protein N-terminal region                        |
| EVM0008224   | 180.18 | 433.73 | -1.27 | 2.00E-04| Amino acid transport and metabolism               | Protein of unknown function (DUF619)                     |
| EVM0003669   | 1.83   | 4.41   | -1.27 | 5.00E-03| --                                                | --                                                      |
| EVM0008927   | 47.33  | 113.79 | -1.27 | 5.00E-05| --                                                | Velvet factor                                            |
| EVM0003527   | 58.28  | 140.07 | -1.27 | 5.00E-05| Transcription                                     | RNA polymerase Rpb1, domain 5                            |
| EVM0007629   | 63.87  | 153.46 | -1.26 | 5.00E-05| General function prediction only                  | Protein of unknown function (DUF933)                     |
| EVM0006166 | 78.61 | 188.90 | -1.26 | 5.00E-05 | 4.28E-04 | Nucleotide transport and metabolism | SAICAR synthetase |
| EVM0005262 | 5.10  | 12.26  | -1.26 | 4.50E-03 | 1.97E-02 | -- | -- |
| EVM0001821 | 2.63  | 6.32   | -1.26 | 9.00E-04 | 5.22E-03 | Transcription | HMG (high mobility group) box |
| EVM0007133 | 210.60| 505.75 | -1.26 | 5.00E-05 | 4.28E-04 | Function unknown | SNARE associated Golgi protein |
| EVM0003487 | 65.97 | 158.40 | -1.26 | 5.00E-05 | 4.28E-04 | -- | Eukaryotic cytochrome b561 |
| EVM0006637 | 7.81  | 18.76  | -1.26 | 5.00E-05 | 4.28E-04 | Posttranslational modification, protein turnover, chaperones | Prolyl oligopeptidase family |
| EVM0004668 | 200.52| 481.45 | -1.26 | 5.00E-05 | 4.28E-04 | General function prediction only | Proteolipid membrane potential modulator |
| EVM0010500 | 36.53 | 87.67  | -1.26 | 5.00E-05 | 4.28E-04 | Transcription | RNA polymerase II transcription factor SIII (Elongin) subunit A |
| EVM0010843 | 48.38 | 116.02 | -1.26 | 5.00E-05 | 4.28E-04 | Coenzyme transport and metabolism | Dihydroneopterin aldolase |
| EVM0003002 | 14.42 | 34.57  | -1.26 | 8.40E-03 | 3.26E-02 | Transcription | Transcription factor S-II (TFIIS) |
| EVM0006795 | 1494.96| 3582.30| -1.26 | 6.60E-03 | 2.69E-02 | -- | -- |
| EVM0005770 | 3.66  | 8.78   | -1.26 | 1.55E-03 | 8.22E-03 | -- | -- |
| EVM0004878 | 173.45| 415.14 | -1.26 | 5.00E-05 | 4.28E-04 | -- | -- |
| EVM0007137 | 8.29  | 19.84  | -1.26 | 4.50E-04 | 2.92E-03 | -- | Glycosyl hydrolase family 61 |
| EVM0007848 | 9.86  | 23.58  | -1.26 | 2.00E-04 | 1.46E-03 | -- | -- |
| EVM0006666 | 103.37| 247.26 | -1.26 | 5.00E-05 | 4.28E-04 | -- | -- |
| EVM0006908 | 21.32 | 50.97  | -1.26 | 1.00E-04 | 7.96E-04 | -- | FAD binding domain |
| EVM0010038 | 3.09  | 7.37   | -1.26 | 1.41E-02 | 4.91E-02 | -- | -- |
| EVM0003967 | 141.19| 337.15 | -1.26 | 5.00E-05 | 4.28E-04 | Function unknown | Mago binding |
| EVM0003061 | 26.38 | 62.92  | -1.25 | 5.00E-05 | 4.28E-04 | -- | -- |
| EVM0002998 | 64.45 | 153.63 | -1.25 | 5.00E-05 | 4.28E-04 | Defense mechanisms | NAD dependent epimerase/dehydratase family |
| EVM0003340 | 15.80 | 37.62 | -1.25 | 5.00E-05 | 4.28E-04 | -- | Nuclear fragile X mental retardation-interacting protein 1 (NUFIP1) |
| EVM0006033 | 18.27 | 43.50 | -1.25 | 5.00E-05 | 4.28E-04 | -- | -- |
| EVM0004042 | 56.20 | 133.72 | -1.25 | 5.00E-05 | 4.28E-04 | -- | -- |
| EVM0009458 | 2.51 | 5.98 | -1.25 | 9.00E-04 | 5.22E-03 | -- | -- |
| EVM0009693 | 21.39 | 50.86 | -1.25 | 5.00E-05 | 4.28E-04 | Function unknown | -- |
| EVM0009858 | 33.46 | 79.52 | -1.25 | 5.00E-05 | 4.28E-04 | Translation, ribosomal structure and biogenesis | CPL (NUC119) domain |
| EVM0010680 | 11.47 | 27.25 | -1.25 | 7.00E-04 | 4.23E-03 | General function prediction only | Ras family |
| EVM0010670 | 3.37 | 8.02 | -1.25 | 2.35E-03 | 1.16E-02 | -- | -- |
| EVM0008719 | 11.15 | 26.49 | -1.25 | 5.00E-05 | 4.28E-04 | -- | -- |
| EVM0001019 | 115.00 | 273.213 | -1.25 | 2.00E-04 | 1.46E-03 | -- | -- |
| EVM0005896 | 33.67 | 79.95 | -1.25 | 1.00E-04 | 7.96E-04 | Function unknown | Alpha/beta hydrolase family |
| EVM0010800 | 99.16 | 235.42 | -1.25 | 1.00E-04 | 7.96E-04 | Carbohydrate transport and metabolism | Formyl transferase |
| EVM0002482 | 12.20 | 28.94 | -1.25 | 2.00E-04 | 1.46E-03 | -- | -- |
| EVM0007683 | 4.06 | 9.63 | -1.25 | 5.00E-05 | 4.28E-04 | Posttranslational modification, protein turnover, chaperones | -- |
| EVM0007044 | 37.64 | 89.15 | -1.24 | 5.00E-05 | 4.28E-04 | -- | Salt tolerance down-regulator |
| Accession  | EVM0006845 | EVM0009931 | EVM0006480 | EVM0009948 | EVM0005584 | EVM0001922 | EVM0010988 | EVM0011177 | EVM0004008 | EVM0004966 | EVM0007135 | EVM0010575 | EVM0009504 | EVM0002104 | EVM0003294 | EVM0000799 |
|------------|------------|------------|------------|------------|------------|------------|------------|------------|------------|------------|------------|------------|------------|------------|------------|------------|
| EVM0006845 | 17.01      | 63.75      | 8.30       | 4.41       | 1.86       | 8.14       | 28.44      | 22.62      | 141.58     | 2.64       | 2.88       | 22.57      | 9.34       | 48.63      | 4.61       | 2.55       |
| EVM0009931 | 40.29      | 150.96     | 19.65      | 10.45      | 4.39       | 19.26      | 67.27      | 53.50      | 334.73     | 6.24       | 6.81       | 53.30      | 22.06      | 114.79     | 10.87      | 6.01       |
| EVM0006480 | -1.24      | -1.24      | -1.24      | -1.24      | -1.24      | -1.24      | -1.24      | -1.24      | -1.24      | -1.24      | -1.24      | -1.24      | -1.24      | -1.24      | -1.24      | -1.24      |
| EVM0009948 | 5.00E-05   | 5.00E-05   | 1.00E-04   | 4.00E-04   | 5.05E-03   | 1.00E-04   | 5.00E-05   | 5.00E-05   | 9.00E-04   | 5.00E-05   | 2.80E-03   | 5.00E-05   | 5.00E-05   | 5.00E-05   | 4.61       | 1.85E-03   |
| EVM0005584 | 4.28E-04   | 4.28E-04   | 7.96E-04   | 2.65E-03   | 2.17E-02   | 7.96E-04   | 4.28E-04   | 4.28E-04   | 5.22E-03   | 4.28E-04   | 1.34E-02   | 4.28E-04   | 4.28E-04   | 4.28E-04   | 2.07E-03   | 9.52E-03   |
| EVM0001922 | 5.00E-05   | 5.00E-05   | 1.00E-04   | 4.00E-04   | 5.05E-03   | 1.00E-04   | 5.00E-05   | 5.00E-05   | 9.00E-04   | 5.00E-05   | 2.80E-03   | 5.00E-05   | 5.00E-05   | 5.00E-05   | 2.07E-03   | 9.52E-03   |
| EVM0010988 | 28.44      | 53.50      | 67.27      | 334.73     | 6.24       | 6.81       | 28.44      | 22.62      | 141.58     | 6.24       | 6.81       | 22.62      | 53.50      | 53.50      | 10.87      | 6.01       |
| EVM0011177 | 63.75      | 150.96     | 19.65      | 10.45      | 4.39       | 19.26      | 67.27      | 53.50      | 334.73     | 6.24       | 6.81       | 53.30      | 22.06      | 114.79     | 10.87      | 6.01       |
| EVM0004008 | 8.30       | 19.65      | 19.26      | 114.79     | 2.64       | 2.88       | 28.44      | 22.62      | 141.58     | 2.64       | 2.88       | 22.57      | 9.34       | 48.63      | 4.61       | 2.55       |
| EVM0004966 | 4.41       | 10.45      | 4.39       | 114.79     | 6.81       | 6.24       | 28.44      | 53.50      | 334.73     | 6.81       | 6.24       | 53.30      | 22.06      | 114.79     | 10.87      | 6.01       |
| EVM0007135 | 1.86       | 7.96E-04   | 1.00E-04   | 1.34E-02   | 5.00E-05   | 2.80E-03   | 28.44      | 22.62      | 141.58     | 6.24       | 6.81       | 53.30      | 22.06      | 114.79     | 10.87      | 6.01       |
| EVM0010575 | 9.34       | 7.96E-04   | 1.00E-04   | 2.17E-02   | 1.85E-03   | 3.00E-04   | 22.57      | 9.34       | 48.63      | 2.64       | 2.88       | 22.57      | 9.34       | 48.63      | 4.61       | 2.55       |
| EVM0010575 | 9.34       | 7.96E-04   | 1.00E-04   | 2.17E-02   | 1.85E-03   | 3.00E-04   | 22.57      | 9.34       | 48.63      | 2.64       | 2.88       | 22.57      | 9.34       | 48.63      | 4.61       | 2.55       |
| EVM0009504 | 22.62      | 53.50      | 67.27      | 334.73     | 6.24       | 6.81       | 28.44      | 53.50      | 334.73     | 6.24       | 6.81       | 53.30      | 22.06      | 114.79     | 10.87      | 6.01       |
| EVM0002104 | 48.63      | 114.79     | 67.27      | 334.73     | 6.24       | 6.81       | 28.44      | 53.50      | 334.73     | 6.24       | 6.81       | 53.30      | 22.06      | 114.79     | 10.87      | 6.01       |
| EVM0003294 | 4.61       | 10.87      | 28.44      | 22.62      | 2.64       | 2.88       | 22.57      | 9.34       | 48.63      | 2.64       | 2.88       | 22.57      | 9.34       | 48.63      | 4.61       | 2.55       |
| EVM0000799 | 2.55       | 6.01       | 67.27      | 334.73     | 6.24       | 6.81       | 28.44      | 53.50      | 334.73     | 6.24       | 6.81       | 53.30      | 22.06      | 114.79     | 10.87      | 6.01       |

**Annotation:**
- **SNF5 / SMARCB1 / INI1**
- **Membrane transport protein**
- **Fungal specific transcription factor domain**
- **Secondary metabolites biosynthesis, transport and catabolism**
- **Alcohol dehydrogenase GroES-like domain**
- **Helicase associated domain (HA2)**
- **Choline/Carnitine o-acyltransferase**
- **Metallo-beta-lactamase superfamily**
- **Protein kinase domain**
- **Pro-kumamolisin, activation domain**
- **Membrane bound O-acyl transferase family**
| EVM0003839  | 801.48 | 1889.09 | -1.24 | 5.00E-05 | 4.28E-04 | Translation, ribosomal structure and biogenesis | Ribosomal S13/S15 N-terminal domain |
| EVM0005541  | 33.03  | 77.83   | -1.24 | 5.00E-05 | 4.28E-04 | -- | Aminotransferase class-V |
| EVM001684   | 30.95  | 72.93   | -1.24 | 4.00E-04 | 2.65E-03 | General function prediction only | AAA domain (dynein-related subfamily) |
| EVM003868   | 24.54  | 57.79   | -1.24 | 6.50E-04 | 3.98E-03 | -- | Peptidase inhibitor I9 |
| EVM005811   | 1.96   | 4.61    | -1.24 | 3.70E-03 | 1.68E-02 | -- | -- |
| EVM011129   | 11.85  | 27.90   | -1.23 | 2.50E-04 | 1.77E-03 | -- | -- |
| EVM003373   | 3.94   | 9.27    | -1.23 | 3.20E-03 | 1.49E-02 | -- | -- |
| EVM007363   | 6.89   | 16.21   | -1.23 | 1.60E-03 | 8.44E-03 | -- | -- |
| EVM000075   | 5.28   | 12.41   | -1.23 | 1.00E-04 | 7.96E-04 | -- | F-box domain |
| EVM007890   | 192.20 | 451.96  | -1.23 | 5.00E-05 | 4.28E-04 | -- | -- |
| EVM002580   | 7.01   | 16.47   | -1.23 | 1.70E-03 | 8.87E-03 | -- | Acetyltransferase (GNAT) family |
| EVM006458   | 13.83  | 32.50   | -1.23 | 5.00E-05 | 4.28E-04 | -- | Cytochrome P450 |
| EVM010567   | 7.89   | 18.53   | -1.23 | 2.00E-04 | 1.46E-03 | -- | Putative serine dehydratase domain |
| EVM009477   | 10.32  | 24.23   | -1.23 | 1.00E-04 | 7.96E-04 | -- | F-box-like |
| EVM010633   | 1350.09| 3170.56 | -1.23 | 5.00E-05 | 4.28E-04 | Energy production and conversion | -- |
| EVM010989   | 57.69  | 135.41  | -1.23 | 2.00E-04 | 1.46E-03 | -- | NADH:flavin oxidoreductase / NADH oxidase family |
| EVM0003721  | 254.23 | 596.65  | -1.23 | 5.00E-05 | 4.28E-04 | -- | -- |
| EVM010517   | 243.58 | 571.41  | -1.23 | 5.00E-05 | 4.28E-04 | Posttranslational modification, protein turnover, chaperones | SelR domain |
| EVM006126   | 24.83  | 58.23   | -1.23 | 5.00E-05 | 4.28E-04 | -- | -- |
| Gene ID       | Expression | Log2 Fold Change | Functional Category                                                                 | Protein/Function                                                                 |
|--------------|------------|-----------------|--------------------------------------------------------------------------------------|----------------------------------------------------------------------------------|
| EVM0011784   | 30.44      | -1.23           | Inorganic ion transport and metabolism                                               | Sodium/hydrogen exchanger family                                                |
| EVM0011823   | 7.10       | -1.23           | Inorganic ion transport and metabolism                                               | Natural resistance-associated macrophage protein                                |
| EVM0006717   | 16.65      | -1.23           | Secondary metabolites biosynthesis, transport and catabolism                          | --                                                                               |
| EVM0010749   | 1.31       | -1.23           | --                                                                                   | Cytochrome P450                                                                  |
| EVM0002996   | 26.17      | -1.23           | Transcription                                                                        | Sin3 associated polypeptide p18 (SAP18)                                          |
| EVM0000851   | 392.38     | -1.23           | --                                                                                   | Eissosome component PIL1                                                         |
| EVM0011423   | 2.94       | -1.23           | General function prediction only                                                     | Sugar (and other) transporter                                                    |
| EVM0011661   | 12.71      | -1.22           | Signal transduction mechanisms                                                        | Protein kinase domain                                                            |
| EVM0003203   | 23.85      | -1.22           | --                                                                                   | --                                                                               |
| EVM0002190   | 20.64      | -1.22           | --                                                                                   | N-terminal C2 in EEIG1 and EHBP1 proteins                                        |
| EVM0007585   | 11.21      | -1.22           | Amino acid transport and metabolism                                                  | Amino acid permease                                                              |
| EVM0002120   | 3.02       | -1.22           | Energy production and conversion                                                     | FAD binding domain                                                               |
| EVM0006013   | 1.62       | -1.22           | --                                                                                   | --                                                                               |
| EVM0000483   | 176.73     | -1.22           | Amino acid transport and metabolism                                                  | Chorismate mutase type II                                                        |
| EVM0011383   | 78.03      | -1.22           | Function unknown                                                                     | Zinc finger, ZZ type                                                             |
| Accession | EVM0001620 | 4.76     | 11.11    | -1.22   | 1.70E-03 | 8.87E-03 | --       | --       |
|-----------|-------------|----------|----------|---------|----------|----------|----------|----------|
| Accession | EVM0006910 | 3.59     | 8.36     | -1.22   | 4.00E-04 | 2.65E-03 | --       | --       |
| Accession | EVM0008438 | 16.67    | 38.81    | -1.22   | 5.00E-05 | 4.28E-04 | --       | Apoptosis-antagonizing transcription factor, C-terminal |
| Accession | EVM000557  | 23.01    | 53.55    | -1.22   | 1.00E-04 | 7.96E-04 | --       | --       |
| Accession | EVM0008439 | 11.76    | 27.36    | -1.22   | 2.00E-04 | 1.46E-03 | --       | Uncharacterized alpha/beta hydrolase domain (DUF2235) |
| Accession | EVM0004198 | 145.75   | 338.52   | -1.22   | 5.00E-05 | 4.28E-04 | --       | --       |
| Accession | EVM0005216 | 46.67    | 108.37   | -1.22   | 5.00E-05 | 4.28E-04 | --       | Whi5 like |
| Accession | EVM0010692 | 23.40    | 54.34    | -1.22   | 1.00E-04 | 7.96E-04 | --       | --       |
| Accession | EVM0005171 | 16.83    | 39.07    | -1.21   | 5.00E-05 | 4.28E-04 | Replication, recombination and repair | DNA mismatch repair protein, C-terminal domain |
| Accession | EVM0001479 | 2326.67  | 5399.71  | -1.21   | 5.00E-05 | 4.28E-04 | Translation, ribosomal structure and biogenesis | Ribosomal protein L18e/L15 |
| Accession | EVM0003660 | 61.80    | 143.39   | -1.21   | 5.00E-05 | 4.28E-04 | --       | --       |
| Accession | EVM0012102 | 17.50    | 40.60    | -1.21   | 3.50E-04 | 2.36E-03 | --       | --       |
| Accession | EVM0003224 | 65.35    | 151.56   | -1.21   | 5.00E-05 | 4.28E-04 | General function prediction only | Phosphatidylethanolamine-binding protein |
| Accession | EVM0006065 | 16.59    | 38.46    | -1.21   | 5.00E-05 | 4.28E-04 | --       | --       |
| Accession | EVM0006060 | 5.47     | 12.67    | -1.21   | 3.00E-04 | 2.07E-03 | --       | PP-loop family |
| Accession | EVM0001211 | 12.21    | 28.29    | -1.21   | 5.00E-05 | 4.28E-04 | --       | --       |
| Accession | EVM0009657 | 1.26     | 2.92     | -1.21   | 4.90E-03 | 2.12E-02 | Secondary metabolites biosynthesis, transport and catabolism | Cytochrome P450 |
| Accession | EVM0001905 | 79.00    | 182.92   | -1.21   | 1.00E-04 | 7.96E-04 | General function prediction only | GMC oxidoreductase |

**Note:** The table above lists accession numbers and various biological features associated with each entry. The values in the table represent different biological metrics or parameters. The annotations provide additional context about the biological functions or roles of these entries.
| GO ID     | Gene Symbol | Score | Name                                      | Description                                                                 |
|----------|-------------|-------|-------------------------------------------|-----------------------------------------------------------------------------|
| EVM0007506 |             |       | **Intracellular trafficking, secretion, and vesicular transport** | Regulated-SNARE-like domain                                                |
| EVM0008847 |             |       | **Posttranslational modification, protein turnover, chaperones** | Cyclophilin type peptidyl-prolyl cis-trans isomerase/CLD                    |
| EVM0007305 |             |       | **RNA processing and modification** | U1 zinc finger                                                              |
| EVM0003531 |             |       | **Posttranslational modification, protein turnover, chaperones** | Fungal specific transcription factor domain                                 |
| EVM0002787 |             |       | **Signal transduction mechanisms** | Thioredoxin                                                                |
| EVM0001027 |             |       | **Signal transduction mechanisms** | HIT domain                                                                 |
| EVM0010310 |             |       | **RNA recognition motif. (a.k.a. RRM, RBD, or RNP domain)** | #N/A                                                                        |
| EVM0009586 |             |       | **Lipid transport and metabolism** | Fatty acid hydroxylase superfamily                                          |
| EVM0004240 |             |       | **#N/A** | #N/A                                        |
| EVM0004868 |             |       | **F-box-like** | --                                          |
| EVM0010071 |             |       | **Ribosomal protein L34e** | Translation, ribosomal structure and biogenesis                             |
| EVM0010605 |             |       | **Ribosomal structure and biogenesis** | Transcription factor S-II (TFIIS), central domain                           |
| EVM0001483 |             |       | **Transcription** | Translation, ribosomal structure and biogenesis                             |
| Gene ID       | Value 1 | Value 2  | | Value 3 | | Value 4  | | Value 5 | Function Description                                      |
|--------------|---------|----------|---|--------|---|--------|---|--------|----------------------------------------------------------|
| EVM0012042   | 4.92    | 11.31    | -1.20 | 1.40E-03 | 7.55E-03 | -- | -- | -- | -- |
| EVM0010101   | 5.21    | 11.98    | -1.20 | 1.85E-03 | 9.52E-03 | -- | -- | -- | -- |
| EVM0005126   | 2.58    | 5.93     | -1.20 | 2.10E-03 | 1.06E-02 | -- | -- | -- | -- |
| EVM0012211   | 28.44   | 65.38    | -1.20 | 1.00E-04 | 7.96E-04 | -- | -- | -- | -- |
| EVM0007660   | 16.37   | 37.64    | -1.20 | 2.50E-04 | 1.77E-03 | -- | -- | -- | Pregnancy-associated plasma protein-A |
| EVM0004831   | 16.00   | 36.77    | -1.20 | 2.00E-04 | 1.46E-03 | Lipid transport and metabolism |
| CRAL/TRIO domain | -- | -- | | -- | | -- | | -- | |
| EVM0011757   | 4.27    | 9.82     | -1.20 | 5.40E-03 | 2.29E-02 | -- | -- | -- | -- |
| EVM0006288   | 22.63   | 51.99    | -1.20 | 5.00E-05 | 4.28E-04 | -- | -- | -- | -- |
| EVM0005282   | 310.68  | 713.30   | -1.20 | 1.50E-04 | 1.14E-03 | Posttranslational modification, protein turnover, chaperones |
| Nucleotide exchange factor Fes1 | -- | -- | | -- | | -- | | -- | |
| EVM0005135   | 8.93    | 20.49    | -1.20 | 2.00E-04 | 1.46E-03 | Secondary metabolites biosynthesis, transport and catabolism |
| Cytochrome P450 | -- | -- | | -- | | -- | | -- | |
| EVM0010327   | 16.55   | 37.95    | -1.20 | 1.35E-03 | 7.33E-03 | -- | -- | -- | -- |
| EVM0004661   | 6.04    | 13.84    | -1.20 | 3.00E-04 | 2.07E-03 | -- | -- | -- | Cytochrome P450 |
| EVM0007121   | 8.33    | 19.08    | -1.20 | 5.00E-04 | 3.19E-03 | -- | -- | -- | -- |
| EVM0000696   | 3.76    | 8.60     | -1.20 | 7.00E-04 | 4.23E-03 | Inorganic ion transport and metabolism |
| Cation transport protein | -- | -- | | -- | | -- | | -- | |
| EVM0007942   | 81.46   | 186.36   | -1.19 | 1.50E-04 | 1.14E-03 | Function unknown |
| Protein of unknown function DUF89 | -- | -- | | -- | | -- | | -- | |
| EVM0000245   | 51.25   | 117.18   | -1.19 | 5.00E-05 | 4.28E-04 | Translation, ribosomal structure and biogenesis |
| -- | -- | | -- | | -- | | -- | |
| EVM0004978   | 4.69    | 10.73    | -1.19 | 1.11E-02 | 4.07E-02 | -- | -- | -- | -- |
| Accession  | 1st Value | 2nd Value | 3rd Value | 4th Value | 5th Value | Description                                      |
|-----------|-----------|-----------|-----------|-----------|-----------|------------------------------------------------|
| EVM0001611 | 2.70      | 6.18      | -1.19     | 1.75E-03  | 9.08E-03  | Glycosyl hydrolase family 61                    |
| EVM00005518| 1.19      | 2.71      | -1.19     | 1.31E-02  | 4.63E-02  | non-haem dioxygenase in morphine synthesis N-terminal |
| EVM0001437 | 19.76     | 45.14     | -1.19     | 5.00E-05  | 4.28E-04  | RNA processing and modification                |
| EVM0002590 | 22.23     | 50.76     | -1.19     | 5.00E-05  | 4.28E-04  | Carbohydrate transport and metabolism           |
| EVM0011949 | 37.42     | 85.46     | -1.19     | 5.00E-05  | 4.28E-04  | Protein of unknown function (DUF3245)           |
| EVM0011546 | 3.68      | 8.41      | -1.19     | 5.00E-04  | 3.19E-03  | --                                              |
| EVM0006532 | 52.38     | 119.47    | -1.19     | 5.00E-05  | 4.28E-04  | --                                              |
| EVM0003316 | 490.45    | 1118.51   | -1.19     | 5.00E-05  | 4.28E-04  | --                                              |
| EVM0005758 | 66.90     | 152.55    | -1.19     | 5.00E-05  | 4.28E-04  | Lipid transport and metabolism                  |
| EVM0003024 | 47.56     | 108.45    | -1.19     | 1.00E-04  | 7.96E-04  | Signal transduction mechanisms                  |
| EVM0005467 | 135.33    | 308.53    | -1.19     | 5.00E-05  | 4.28E-04  | Energy production and conversion               |
| EVM0004220 | 8.05      | 18.34     | -1.19     | 1.50E-04  | 1.14E-03  | --                                              |
| EVM0005188 | 134.10    | 305.72    | -1.19     | 2.50E-04  | 1.77E-03  | Inorganic ion transport and metabolism           |
| EVM0007837 | 2567.46   | 5847.03   | -1.19     | 8.50E-04  | 4.98E-03  | Translation, ribosomal structure and biogenesis |
| EVM0005692 | 15.00     | 34.13     | -1.19     | 3.00E-04  | 2.07E-03  | --                                              |
| EVM0000201 | 31.61     | 71.89     | -1.19     | 5.00E-05  | 4.28E-04  | Fungal specific transcription factor domain      |
| Gene ID         | Log2 FC  | Log10 P  | Log2 FC  | Log10 P  | GO/KEGG Term                                         | Description                                                                 |
|----------------|----------|----------|----------|----------|-----------------------------------------------------|-----------------------------------------------------------------------------|
| EVM0000051     | 1.05     | -1.18    | 8.05E-03 | 3.15E-02 | --                                                  | --                                                                          |
| EVM0000030     | 8.93     | -1.18    | 2.00E-04 | 1.46E-03 | Inorganic ion transport and metabolism               | Sodium/calcium exchanger protein                                            |
| EVM0010108     | 16.10    | -1.18    | 5.00E-05 | 4.28E-04 | Intracellular trafficking, secretion, and vesicular transport | Sec7 domain                                                               |
| EVM0010704     | 49.46    | -1.18    | 5.00E-05 | 4.28E-04 | Posttranslational modification, protein turnover, chaperones | --                                                                         |
| EVM0006176     | 29.02    | -1.18    | 2.50E-04 | 1.77E-03 | --                                                  | --                                                                          |
| EVM0011758     | 3.94     | -1.18    | 2.80E-03 | 1.34E-02 | General function prediction only                     | THUMP domain                                                               |
| EVM0000596     | 6.54     | -1.18    | 7.00E-04 | 4.23E-03 | Replication, recombination and repair                | --                                                                          |
| EVM0004195     | 1.69     | -1.18    | 7.25E-03 | 2.90E-02 | --                                                  | --                                                                          |
| EVM0005593     | 21.47    | -1.18    | 5.00E-05 | 4.28E-04 | General function prediction only                     | TPR repeat                                                                 |
| EVM0003685     | 7.80     | -1.18    | 8.00E-04 | 4.73E-03 | --                                                  | --                                                                          |
| EVM0001189     | 44.76    | -1.18    | 5.00E-05 | 4.28E-04 | Chromatin structure and dynamics                     | Histone deacetylase domain                                                  |
| EVM0011097     | 378.34   | -1.18    | 5.00E-05 | 4.28E-04 | --                                                  | RNA recognition motif. (a.k.a. RRM, RBD, or RNP domain)                     |
| EVM0009094     | 9.60     | -1.18    | 3.00E-04 | 2.07E-03 | --                                                  | --                                                                          |
| EVM0011743     | 5.63     | -1.18    | 5.20E-03 | 2.22E-02 | --                                                  | --                                                                          |
| EVM0001308     | 1.34     | -1.18    | 2.60E-03 | 1.26E-02 | General function prediction only                     | short chain dehydrogenase                                                  |
| EVM0012010  | 48.69 | 110.02 | -1.18 | 5.00E-05 | 4.28E-04 | -- | -- |
| EVM0007631  | 21.63 | 48.81  | -1.17 | 5.00E-05 | 4.28E-04 | -- | Tyrosine phosphatase family |
| EVM0004782  | 29.95 | 67.55  | -1.17 | 1.50E-04 | 1.14E-03 | -- | Ribosomal protein L7Ae/L30e/S12e/Gadd45 family |
| EVM0004495  | 299.00| 674.21 | -1.17 | 5.00E-05 | 4.28E-04 | Translation, ribosomal structure and biogenesis |
| EVM0007476  | 4.94  | 11.14  | -1.17 | 1.75E-03 | 9.08E-03 | -- | Protein of unknown function (DUF1399) |
| EVM0005046  | 1.38  | 3.11   | -1.17 | 8.35E-03 | 3.24E-02 | -- | Glycosyl Hydrolase Family 88 |
| EVM0004026  | 32.57 | 73.39  | -1.17 | 2.00E-04 | 1.46E-03 | Secondary metabolites biosynthesis, transport and catabolism |
| EVM0008172  | 31.59 | 71.18  | -1.17 | 5.00E-05 | 4.28E-04 | -- | Alpha/beta hydrolase family |
| EVM0010867  | 1471.16| 3313.53| -1.17 | 1.45E-03 | 7.77E-03 | -- | -- |
| EVM0002339  | 62.86 | 141.57 | -1.17 | 5.00E-05 | 4.28E-04 | -- | -- |
| EVM0004503  | 3.20  | 7.20   | -1.17 | 2.75E-03 | 1.32E-02 | -- | -- |
| EVM0004108  | 3.02  | 6.80   | -1.17 | 1.15E-03 | 6.41E-03 | Secondary metabolites biosynthesis, transport and catabolism |
| EVM0010258  | 45.83 | 103.17 | -1.17 | 1.00E-04 | 7.96E-04 | -- | Cytochrome P450 |
| EVM0007278  | 81.72 | 183.92 | -1.17 | 5.00E-05 | 4.28E-04 | Coenzyme transport and metabolism |
| EVM0002786  | 1913.05| 4304.47| -1.17 | 3.55E-03 | 1.62E-02 | -- | GTP cyclohydrolase II |
| EVM0004710  | 164.60| 370.26 | -1.17 | 5.00E-05 | 4.28E-04 | -- | Cgr1 family |
| EVM0005694  | 26.91 | 60.54  | -1.17 | 5.00E-05 | 4.28E-04 | Energy production and conversion |
| EVM0002339  | 62.86 | 141.57 | -1.17 | 5.00E-05 | 4.28E-04 | -- | FMN-dependent dehydrogenase |
| Accession   | Value1 | Value2 | Value3 | Value4 | Value5 | Value6 | Value7 | Value8 | Value9 | Value10 | Function                                                                 |
|------------|--------|--------|--------|--------|--------|--------|--------|--------|--------|----------|--------------------------------------------------------------------------|
| EVM0003646 | 6.36   | 14.29  | -1.17  | 2.40E-03 | 1.18E-02 | Translation, ribosomal structure and biogenesis | Methyltransferase small domain |
| EVM0000837 | 2.32   | 5.21   | -1.17  | 4.75E-03 | 2.06E-02 | -- | -- |
| EVM0001689 | 296.64 | 665.84 | -1.17  | 5.00E-05 | 4.28E-04 | General function prediction only | Ras family |
| EVM0002411 | 5.34   | 11.99  | -1.17  | 2.00E-04 | 1.46E-03 | -- | -- |
| EVM000527  | 19.05  | 42.72  | -1.17  | 3.50E-04 | 2.36E-03 | General function prediction only | Methyltransferase domain |
| EVM0004088 | 17.22  | 38.61  | -1.16  | 2.50E-04 | 1.77E-03 | General function prediction only | TPR repeat |
| EVM0012262 | 13.02  | 29.18  | -1.16  | 5.50E-04 | 3.46E-03 | Transcription | SHS2 domain found in N terminus of Rpb7p/Rpc25p/MJ0397 |
| EVM0002860 | 15.78  | 35.35  | -1.16  | 5.00E-05 | 4.28E-04 | Secondary metabolites biosynthesis, transport and catabolism | AMP-binding enzyme |
| EVM0011857 | 42.81  | 95.92  | -1.16  | 5.00E-05 | 4.28E-04 | RNA processing and modification | Pescadillo N-terminus |
| EVM0007607 | 175.16 | 392.48 | -1.16  | 5.00E-05 | 4.28E-04 | General function prediction only | TPR repeat |
| EVM0011559 | 8.87   | 19.87  | -1.16  | 3.00E-04 | 2.07E-03 | Energy production and conversion | FAD linked oxidases, C-terminal domain |
| EVM0007466 | 18.64  | 41.73  | -1.16  | 5.00E-05 | 4.28E-04 | General function prediction only | Pentatricopeptide repeat domain |
| EVM0007916 | 7.74   | 17.32  | -1.16  | 2.85E-03 | 1.36E-02 | #N/A | #N/A |
| EVM0002903 | 91.91  | 205.62 | -1.16  | 5.00E-05 | 4.28E-04 | -- | -- |
| Accession | EVM0007567 | EVM0008422 | EVM0000185 | EVM0002535 | EVM0011879 | EVM0009356 | EVM0008178 | EVM0005227 | EVM0005617 | EVM0002183 | EVM0008178 | EVM0008205 | EVM0011062 | EVM0003417 | EVM0002535 | EVM0011592 | EVM0006878 | EVM0008205 | EVM0011062 |
|-----------|-------------|-------------|-------------|-------------|-------------|-------------|-------------|-------------|-------------|-------------|-------------|-------------|-------------|-------------|-------------|-------------|-------------|-------------|-------------|
| Value     | 3791.38     | 26.51       | 3.01        | 34.20       | 38.22       | 37.28       | 73.74       | 23.03       | 203.09      | 19.31       | 61.43       | 1.04        | 88.10       | 4.36        | 7.72        | 156.83      | 8.10        | 4.36        |
|           | 841.37      | 59.30       | 6.74        | 76.41       | 85.35       | 83.25       | 164.65      | 51.40       | 453.22      | 43.09       | 137.05      | 2.33        | 196.29      | 9.70        | 17.17       | 348.43      | 196.29      | 9.70        |
| Fold      | -1.16       | -1.16       | -1.16       | -1.16       | -1.16       | -1.16       | -1.16       | -1.16       | -1.16       | -1.16       | -1.16       | -1.15       | -1.15       | -1.15       | -1.15       | -1.15       | -1.15       | -1.15       |
| p value   | 2.60E-03    | 2.00E-04    | 2.15E-03    | 2.00E-04    | 1.00E-04    | 1.00E-04    | 5.00E-05    | 2.00E-04    | 5.00E-05    | 1.55E-03    | 1.50E-04    | 1.31E-02    | 3.00E-04    | 9.00E-04    | 7.00E-04    | 3.00E-04    | 2.00E-04    | 3.00E-04    |
| p value   | 1.26E-02    | 1.46E-03    | 1.08E-02    | 1.46E-03    | 7.96E-04    | 7.96E-04    | 4.28E-04    | 1.46E-03    | 4.28E-04    | 8.22E-03    | 1.14E-03    | 4.63E-02    | 2.07E-03    | 5.22E-03    | 4.23E-03    | 2.07E-03    | 2.07E-03    | 2.07E-03    |
| Gene      | Posttranslational modification, protein turnover, chaperones | AAA-ATPase Vps4-associated protein 1 | Zinc-binding dehydrogenase | -- | General function prediction only | TPR repeat | Isy1-like splicing family | Ribosome biogenesis protein Nop16 | Tetraspanin family | Function unknown | -- | Energy production and conversion | -- | Major Facilitator Superfamily | -- | Pyridine nucleotide-disulphide oxidoreductase | -- | NADH(P)-binding | -- |
| Function  | Hsp90 protein | -- | -- | -- | -- | -- | -- | -- | -- | -- | -- | -- | -- | -- | -- | -- | -- | -- | -- |
| Accession   | Start | End   | Width | Height | Freq | Func     | Notes                                    |
|-------------|-------|-------|-------|--------|------|----------|------------------------------------------|
| EVM0007565  | 26.17 | 58.13 | -1.15 | 5.00E-05 | 4.28E-04 | Function unknown | Uncharacterized protein family UPF0029 |
| EVM0007587  | 16.97 | 37.70 | -1.15 | 4.00E-04 | 2.65E-03 | --                          | --                                      |
| EVM0005633  | 50.69 | 112.58| -1.15 | 1.00E-04 | 7.96E-04 | --                          | --                                      |
| EVM0004686  | 1.24  | 2.76  | -1.15 | 8.60E-03 | 3.32E-02 | General function prediction only | Major Facilitator Superfamily          |
| EVM0000647  | 12.35 | 27.42 | -1.15 | 7.50E-04 | 4.49E-03 | #N/A                       | #N/A                                    |
| EVM0001063  | 10.10 | 22.42 | -1.15 | 3.00E-04 | 2.07E-03 | --                          | G protein-coupled glucose receptor regulating Gpa2 |
| EVM0012134  | 15.64 | 34.69 | -1.15 | 1.00E-04 | 7.96E-04 | Energy production and conversion | Phosphoenolpyruvate phosphomutase      |
| EVM0003812  | 20.17 | 44.74 | -1.15 | 5.00E-05 | 4.28E-04 | --                          | --                                      |
| EVM0012166  | 6.01  | 13.32 | -1.15 | 5.00E-04 | 3.19E-03 | --                          | Glyoxal oxidase N-terminus             |
| EVM0001303  | 207.17| 459.15| -1.15 | 5.00E-05 | 4.28E-04 | --                          | --                                      |
| EVM0006165  | 7.99  | 17.70 | -1.15 | 5.50E-04 | 3.46E-03 | --                          | --                                      |
| EVM0007796  | 29.71 | 65.68 | -1.14 | 8.65E-03 | 3.34E-02 | --                          | --                                      |
| EVM0007553  | 8.17  | 18.07 | -1.14 | 1.00E-03 | 5.70E-03 | RNA processing and modification | Putative methyltransferase              |
| EVM0007009  | 381.12| 842.21| -1.14 | 3.50E-04 | 2.36E-03 | --                          | Calcipressin                           |
| EVM0011366  | 12.21 | 26.99 | -1.14 | 5.00E-05 | 4.28E-04 | --                          | SDA1                                    |
| EVM0002755  | 5.80  | 12.81 | -1.14 | 2.45E-03 | 1.20E-02 | --                          | --                                      |
| EVM0011919  | 29.00 | 64.03 | -1.14 | 2.50E-04 | 1.77E-03 | --                          | --                                      |
| EVM000357   | 3.96  | 8.74  | -1.14 | 2.55E-03 | 1.24E-02 | Function unknown            | AhpC/TSA antioxidant enzyme            |
| EVM0009738  | 11.76 | 25.96 | -1.14 | 5.00E-05 | 4.28E-04 | Carbohydrate transport and metabolism | Major Facilitator Superfamily         |
| EVM0001158  | 40.04 | 88.33 | -1.14 | 1.00E-04 | 7.96E-04 | --                          | --                                      |
| EVM0008736 | 11.03 | 24.32 | -1.14 | 1.45E-03 | 7.77E-03 | Secondary metabolites biosynthesis, transport and catabolism | Alcohol dehydrogenase GroES-like domain |
| EVM0006502 | 184.02 | 405.65 | -1.14 | 5.00E-05 | 4.28E-04 | Secondary metabolites biosynthesis, transport and catabolism | Alcohol dehydrogenase GroES-like domain |
| EVM0006064 | 4.45 | 9.81 | -1.14 | 1.00E-04 | 7.96E-04 | -- | -- |
| EVM0006652 | 13.63 | 30.04 | -1.14 | 1.50E-04 | 1.14E-03 | -- | Cytochrome P450 |
| EVM0004838 | 20.06 | 44.19 | -1.14 | 5.00E-04 | 3.19E-03 | Function unknown | Uncharacterized protein family UPF0029 |
| EVM0011287 | 8.39 | 18.49 | -1.14 | 4.50E-04 | 2.92E-03 | Secondary metabolites biosynthesis, transport and catabolism | Cytochrome P450 |
| EVM0007905 | 18.04 | 39.74 | -1.14 | 7.00E-04 | 4.23E-03 | -- | Spc19 |
| EVM0004444 | 14.36 | 31.61 | -1.14 | 2.50E-04 | 1.77E-03 | -- | -- |
| EVM0007747 | 29.35 | 64.57 | -1.14 | 4.00E-04 | 2.65E-03 | Function unknown | Domain of unknown function DUF59 |
| EVM0005233 | 22.61 | 49.70 | -1.14 | 5.00E-05 | 4.28E-04 | Lipid transport and metabolism | Alpha/beta hydrolase family |
| EVM0002340 | 23.42 | 51.41 | -1.13 | 1.50E-04 | 1.14E-03 | RNA processing and modification | Ribonuclease T2 family |
| EVM0006440 | 120.79 | 265.04 | -1.13 | 2.50E-04 | 1.77E-03 | -- | LysM domain |
| EVM0001623 | 11.78 | 25.85 | -1.13 | 5.50E-04 | 3.46E-03 | -- | -- |
| EVM0004616 | 928.46 | 2036.91 | -1.13 | 9.40E-03 | 3.57E-02 | -- | -- |
| EVM0008127 | 107.17 | 234.89 | -1.13 | 5.00E-05 | 4.28E-04 | -- | SOH1 |
| EVM0006962 | 35.79 | 78.44 | -1.13 | 1.50E-04 1.14E-03 | Intracellular trafficking, secretion, and vesicular transport | ABC transporter |
| EVM0001878 | 35.93 | 78.74 | -1.13 | 5.00E-05 4.28E-04 | -- | -- |
| EVM0011693 | 4.91  | 10.76 | -1.13 | 2.05E-03 1.03E-02 | -- | F-box-like |
| EVM0006860 | 47.99 | 105.10| -1.13 | 3.50E-04 2.36E-03 | Function unknown | AMMECR1 |
| EVM0011500 | 12.11 | 26.51 | -1.13 | 2.00E-03 1.01E-02 | General function prediction only | Putative esterase |
| EVM0002814 | 132.04| 289.05| -1.13 | 2.50E-04 1.77E-03 | Intracellular trafficking, secretion, and vesicular transport | Peroxisomal membrane protein (Pex16) |
| EVM0004396 | 11.85 | 25.94 | -1.13 | 1.50E-04 1.14E-03 | -- | -- |
| EVM0004844 | 7.74  | 16.93 | -1.13 | 3.50E-04 2.36E-03 | -- | Domain of unknown function (DUF4139) |
| EVM0005913 | 108.71| 237.80| -1.13 | 1.50E-04 1.14E-03 | -- | Phosphoribosyl transferase domain |
| EVM0007277 | 769.92| 1683.76| -1.13 | 2.00E-04 1.46E-03 | -- | -- |
| EVM0009027 | 41.30 | 90.32 | -1.13 | 5.00E-05 4.28E-04 | -- | F-box-like |
| EVM0009459 | 3.79  | 8.28  | -1.13 | 7.00E-04 4.23E-03 | -- | -- |
| EVM0007802 | 205.03| 448.20| -1.13 | 3.00E-04 2.07E-03 | -- | Protein of unknown function (DUF952) |
| EVM0011750 | 6.16  | 13.44 | -1.13 | 1.40E-03 7.55E-03 | Defense mechanisms | NAD dependent epimerase/dehydratase family |
| EVM0011689 | 3.03  | 6.62  | -1.13 | 6.00E-04 3.72E-03 | -- | non-haem dioxygenase in morphine synthesis N-terminal |
| Gene ID      | E-value | Score | Fold Change | Signal Transduction mechanisms | Protein kinase domain | Lipid transport and metabolism | Acyltransferase | Translation, ribosomal structure and biogenesis | Ribosomal protein S4/S9 N-terminal domain | Cell motility | Dynactin p62 family | General function prediction only | Zinc finger, C2H2 type | Replication, recombination and repair | DNA polymerase alpha/epsilon subunit B | Glycosyl hydrolases family 11 | Ankyrin repeats (3 copies) | Zinc knuckle | Amino acid transport and metabolism | Amino acid permease |
|-------------|---------|-------|-------------|---------------------------------|------------------------|-------------------------------|----------------|-----------------------------------------------|--------------------------------------------|--------------|--------------------------|----------------------------------|--------------------------|--------------------------------|---------------------------------|--------------------------|-----------------------------|----------------|-----------------------------|--------------------------|
| EVM0004323  | 15.17   | 33.09 | -1.12       | 1.50E-04                        | 1.14E-03               |                                |                |                                |                             |              |                          |                                  |                          |                                |                                |                          |                            |                             |                          |                                |              |
| EVM0001028  | 15.43   | 33.64 | -1.12       | 4.00E-04                        | 2.65E-03               |                                |                |                                |                             |              |                          |                                  |                          |                                |                             |                          |                            |                             |                          |                                |              |
| EVM0006461  | 7.64    | 16.65 | -1.12       | 9.50E-04                        | 5.46E-03               |                                |                |                                |                             |              |                          |                                  |                          |                                |                             |                          |                            |                             |                          |                                |              |
| EVM0002136  | 755.55  | 1646.10 | -1.12   | 5.00E-05                       | 4.28E-04               |                                |                | Translation, ribosomal structure and biogenesis | Ribosomal protein S4/S9 N-terminal domain |              |                          |                                  |                          |                                |                             |                          |                            |                             |                          |                                |              |
| EVM0011692  | 20.42   | 44.46 | -1.12       | 5.00E-05                        | 4.28E-04               |                                |                | Cell motility                    | Dynactin p62 family |              |                          |                                  |                          |                                |                             |                          |                            |                             |                          |                                |              |
| EVM0010024  | 2.42    | 5.27  | -1.12       | 8.85E-03                        | 3.40E-02               |                                |                |                                |                             |              |                          |                                  |                          |                                |                             |                          |                            |                             |                          |                                |              |
| EVM0007043  | 17.88   | 38.85 | -1.12       | 5.00E-05                        | 4.28E-04               |                                |                | General function prediction only | Zinc finger, C2H2 type |              |                          |                                  |                          |                                |                             |                          |                            |                             |                          |                                |              |
| EVM0005876  | 7.33    | 15.94 | -1.12       | 1.15E-03                        | 6.41E-03               |                                |                |                                |                             |              |                          |                                  |                          |                                |                             |                          |                            |                             |                          |                                |              |
| EVM0011335  | 17.69   | 38.44 | -1.12       | 5.00E-05                        | 4.28E-04               |                                |                |                                |                             |              |                          |                                  |                          |                                |                             |                          |                            |                             |                          |                                |              |
| EVM0010095  | 6.01    | 13.04 | -1.12       | 3.50E-04                        | 2.36E-03               |                                |                | Replication, recombination and repair | DNA polymerase alpha/epsilon subunit B |              |                          |                                  |                          |                                |                             |                          |                            |                             |                          |                                |              |
| EVM0005623  | 15.14   | 32.85 | -1.12       | 2.00E-04                        | 1.46E-03               |                                |                |                                |                             |              |                          |                                  |                          |                                |                             |                          |                            |                             |                          |                                |              |
| EVM0002871  | 13.75   | 29.81 | -1.12       | 5.00E-05                        | 4.28E-04               |                                |                |                                |                             |              |                          |                                  |                          |                                |                             |                          |                            |                             |                          |                                |              |
| EVM0000005  | 33.92   | 73.56 | -1.12       | 4.05E-03                        | 1.81E-02               |                                |                |                                |                             |              |                          |                                  |                          |                                |                             |                          |                            |                             |                          |                                |              |
| EVM0006695  | 23.69   | 51.34 | -1.12       | 3.00E-04                        | 2.07E-03               |                                |                |                                |                             |              |                          |                                  |                          |                                |                             |                          |                            |                             |                          |                                |              |
| EVM0006793  | 36.71   | 79.55 | -1.12       | 2.00E-04                        | 1.46E-03               |                                |                |                                |                             |              |                          |                                  |                          |                                |                             |                          |                            |                             |                          |                                |              |
| EVM0002268  | 18.32   | 39.69 | -1.11       | 4.90E-03                        | 2.12E-02               |                                |                |                                |                             |              |                          |                                  |                          |                                |                             |                          |                            |                             |                          |                                |              |
| EVM0007593  | 128.29  | 277.65 | -1.11  | 5.00E-05                       | 4.28E-04               |                                |                | RNA processing and modification | Zinc knuckle |              |                          |                                  |                          |                                |                             |                          |                            |                             |                          |                                |              |
| EVM0003207  | 50.97   | 110.17 | -1.11     | 1.00E-04                        | 7.96E-04               |                                |                |                                |                             |              |                          |                                  |                          |                                |                             |                          |                            |                             |                          |                                |              |
| EVM0007309  | 8.15    | 17.62 | -1.11       | 3.00E-04                        | 2.07E-03               |                                |                | Amino acid transport and metabolism | Amino acid permease |              |                          |                                  |                          |                                |                             |                          |                            |                             |                          |                                |              |
| EVM0001068 | 6.07   | 13.11  | -1.11 | 2.05E-03  | 1.03E-02 |  | Isochorismatase family |
| EVM0011600 | 19.24  | 41.55  | -1.11 | 1.50E-04  | 1.14E-03 | Function unknown | WD domain, G-beta repeat |
| EVM0009256 | 35.71  | 77.09  | -1.11 | 5.00E-05  | 4.28E-04 | Function unknown | Vta1 like |
| EVM0011563 | 73.51  | 158.66 | -1.11 | 1.50E-04  | 1.14E-03 | Posttranslational modification, protein turnover, chaperones | X-domain of DnaJ-containing |
| EVM0005272 | 811.62 | 1751.54| -1.11 | 8.00E-04  | 4.73E-03 |  | Ubiquinol-cytochrome-c reductase complex subunit (QCR10) |
| EVM0002387 | 133.02 | 286.90 | -1.11 | 1.00E-04  | 7.96E-04 |  | Coiled-coil domain containing protein (DUF2052) |
| EVM0001635 | 139.31 | 300.37 | -1.11 | 1.00E-04  | 7.96E-04 | Posttranslational modification, protein turnover, chaperones | GrpE |
| EVM0002307 | 41.78  | 90.05  | -1.11 | 1.40E-03  | 7.55E-03 |  |  |
| EVM0001156 | 167.02 | 359.98 | -1.11 | 2.00E-04  | 1.46E-03 |  |  |
| EVM0006907 | 5.80   | 12.50  | -1.11 | 2.00E-03  | 1.01E-02 |  | RTA1 like protein |
| EVM0006559 | 48.80  | 105.03 | -1.11 | 5.00E-04  | 3.19E-03 |  |  |
| EVM0002587 | 99.13  | 213.26 | -1.11 | 1.50E-04  | 1.14E-03 | Translation, ribosomal structure and biogenesis | Translation initiation factor eIF3 subunit |
| EVM0003984 | 109.50 | 235.46 | -1.10 | 5.50E-04  | 3.46E-03 |  | Protein of unknown function (DUF3421) |
| EVM0005472 | 32.64  | 70.19  | -1.10 | 5.00E-05  | 4.28E-04 |  | PCI domain |
| EVM0004813 | 77.39  | 166.32 | -1.10 | 4.85E-03  | 2.10E-02 | Inorganic ion transport and metabolism | E1-E2 ATPase |
| EVM0003574 | 48.42 | 103.96 | -1.10 | 5.00E-05 | 4.28E-04 | General function prediction only | PCI domain |
| EVM0011363 | 1.07  | 2.29   | -1.10 | 5.80E-03 | 2.42E-02 | RNA processing and modification | AAA domain |
| EVM0003670 | 43.61 | 93.63  | -1.10 | 1.00E-04 | 7.96E-04 | Chromatin structure and dynamics | ATP-utilising chromatin assembly and remodelling N-terminal |
| EVM0008302 | 76.36 | 163.78 | -1.10 | 3.00E-04 | 2.07E-03 | -- | -- |
| EVM0006667 | 20.61 | 44.20  | -1.10 | 3.00E-04 | 2.07E-03 | -- | -- |
| EVM0006499 | 14.30 | 30.67  | -1.10 | 3.50E-04 | 2.36E-03 | -- | -- |
| EVM0005941 | 105.49 | 226.10 | -1.10 | 5.00E-05 | 4.28E-04 | -- | -- |
| EVM0006953 | 4.79  | 10.26  | -1.10 | 1.50E-03 | 8.00E-03 | Cytoskeleton | Autophagy protein Atg8 ubiquitin like |
| EVM0001548 | 1370.75 | 2937.56 | -1.10 | 7.50E-04 | 4.49E-03 | Translation, ribosomal structure and biogenesis | Ribosomal protein S19e |
| EVM0002124 | 26.15 | 56.04  | -1.10 | 1.50E-04 | 1.14E-03 | Amino acid transport and metabolism | Dehydratase family |
| EVM0008208 | 117.60 | 251.94 | -1.10 | 1.50E-04 | 1.14E-03 | General function prediction only | DHHC palmitoyltransferase |
| EVM0012177 | 23.32 | 49.96  | -1.10 | 1.00E-04 | 7.96E-04 | General function prediction only | Nuclear protein Es2 |
| EVM0004869 | 195.04 | 417.73 | -1.10 | 4.50E-04 | 2.92E-03 | Lipid transport and metabolism | Myo-inositol-1-phosphate synthase |
| EVM0001429 | 28.68 | 61.42  | -1.10 | 2.50E-04 | 1.77E-03 | Inorganic ion transport and metabolism | E1-E2 ATPase |
| EVM0002826 | 117.04 | 250.62 | -1.10 | 1.50E-04 | 1.14E-03 | General function prediction only | Cell differentiation family, Rcd1-like |
| EVM0004168 | 4.91 | 10.51 | -1.10 | 1.45E-03 | 7.77E-03 | Carbohydrate transport and metabolism | FGGY family of carbohydrate kinases, C-terminal domain |
| EVM0003042 | 7.64 | 16.33 | -1.10 | 7.00E-04 | 4.23E-03 | -- | -- |
| EVM0010344 | 1807.48 | 3862.04 | -1.10 | 2.00E-04 | 1.46E-03 | -- | ATP synthase complex subunit h |
| EVM0011479 | 121.53 | 259.64 | -1.10 | 1.00E-04 | 7.96E-04 | Posttranslational modification, protein turnover, chaperones | PI31 proteasome regulator N-terminal |
| EVM0006354 | 51.55 | 110.11 | -1.09 | 6.75E-03 | 2.74E-02 | RNA processing and modification | RNA recognition motif. (a.k.a. RRM, RBD, or RNP domain) |
| EVM0006685 | 46.84 | 99.99 | -1.09 | 4.50E-04 | 2.92E-03 | Amino acid transport and metabolism | Amino acid kinase family |
| EVM0008724 | 6.59 | 14.07 | -1.09 | 5.50E-04 | 3.46E-03 | General function prediction only | Major Facilitator Superfamily |
| EVM0000211 | 29.99 | 64.00 | -1.09 | 3.50E-04 | 2.36E-03 | RNA processing and modification | WD domain, G-beta repeat |
| EVM0010511 | 5.93 | 12.64 | -1.09 | 7.50E-04 | 4.49E-03 | -- | WD domain, G-beta repeat |
| EVM0002578 | 1.66 | 3.54 | -1.09 | 3.15E-03 | 1.47E-02 | General function prediction only | Glycosyl transferase family 90 |
| EVM0010235 | 2.28 | 4.86 | -1.09 | 4.65E-03 | 2.03E-02 | -- | -- |
| EVM0006976 | 19.35 | 41.25 | -1.09 | 4.50E-04 | 2.92E-03 | Inorganic ion transport and metabolism | Regulator of volume decrease after cellular swelling |
| EVM0001036 | 75.92 | 161.76 | -1.09 | 4.00E-04 | 2.65E-03 | -- | -- |
| EVM0011220 | 39.24 | 83.55 | -1.09 | 4.00E-04 | 2.65E-03 | -- | Glyoxalase-like domain |
| EVM0004432 | 7.40 | 15.73 | -1.09 | 5.50E-04 | 3.46E-03 | Secondary metabolites biosynthesis, transport and catabolism | Pyridine nucleotide-disulphide oxidoreductase |
| EVM0006511 | 4.86  | 10.33 | -1.09 | 4.00E-04  | 2.65E-03 | General function prediction only | Glycosyl transferase family 90 |
| EVM0001108 | 21.96 | 46.71 | -1.09 | 2.00E-04  | 1.46E-03 | Translation, ribosomal structure and biogenesis | Putative diphthamide synthesis protein |
| EVM0004930 | 9.52  | 20.24 | -1.09 | 3.50E-04  | 2.36E-03 | -- | Flavin containing amine oxidoreductase |
| EVM0002825 | 59.93 | 127.40| -1.09 | 1.50E-04  | 1.14E-03 | -- | -- |
| EVM0005366 | 22.53 | 47.83 | -1.09 | 2.50E-04  | 1.77E-03 | Function unknown | pre-RNA processing PIH1/Nop17 |
| EVM0007349 | 219.77| 466.55| -1.09 | 1.50E-04  | 1.14E-03 | Signal transduction mechanisms | EF hand |
| EVM0012075 | 8.57  | 18.19 | -1.09 | 1.70E-03  | 8.87E-03 | -- | N-acetyltransferase |
| EVM0001205 | 34.79 | 73.84 | -1.09 | 2.00E-04  | 1.46E-03 | Function unknown | Ribosomal protein L1p/L10e family |
| EVM0011226 | 140.90| 298.96| -1.09 | 4.50E-04  | 2.92E-03 | RNA processing and modification | Zinc-finger double-stranded RNA-binding |
| EVM0001902 | 58.73 | 124.62| -1.09 | 1.50E-04  | 1.14E-03 | Energy production and conversion | Lyase |
| EVM0008552 | 6.58  | 13.96 | -1.08 | 1.45E-03  | 7.77E-03 | -- | -- |
| EVM0011908 | 5.87  | 12.44 | -1.08 | 5.45E-03  | 2.31E-02 | Function unknown | 2OG-Fet(II) oxygenase superfamily |
| EVM0002991 | 30.04 | 63.69 | -1.08 | 7.50E-04  | 4.49E-03 | -- | -- |
| EVM0008796 | 25.88 | 54.84 | -1.08 | 5.00E-05  | 4.28E-04 | Defense mechanisms | Dual specificity phosphatase, catalytic domain |
| EVM0006154 | 33.57 | 71.12 | -1.08 | 3.00E-04  | 2.07E-03 | Carbohydrate transport and metabolism | Fructose-bisphosphate aldolase class-I |
| EVM0008693 | 21.23 | 44.96 | -1.08 | 7.50E-04 | 4.49E-03 | Lipid transport and metabolism | short chain dehydrogenase |
| EVM0003382 | 16.69 | 35.33 | -1.08 | 1.50E-04 | 1.14E-03 | Translation, ribosomal structure and biogenesis | Dihydouridine synthase (Dus) |
| EVM0007932 | 57.02 | 120.65 | -1.08 | 2.50E-04 | 1.77E-03 | Posttranslational modification, protein turnover, chaperones | Protein-L-isoaspartate(D-aspartate) O-methyltransferase (PCMT) |
| EVM0000800 | 428.60 | 906.54 | -1.08 | 3.75E-03 | 1.70E-02 | -- | Protein of unknown function (DUF4449) |
| EVM0009850 | 4.07 | 8.61 | -1.08 | 4.50E-04 | 2.92E-03 | Replication, recombination and repair | MutS domain V |
| EVM0008397 | 197.98 | 418.43 | -1.08 | 5.50E-04 | 3.46E-03 | -- | -- |
| EVM0009133 | 10.19 | 21.53 | -1.08 | 5.00E-04 | 3.19E-03 | -- | Peptidase family M28 |
| EVM0010176 | 40.75 | 86.02 | -1.08 | 1.00E-04 | 7.96E-04 | Posttranslational modification, protein turnover, chaperones | Dynamin family |
| EVM0009047 | 17.25 | 36.39 | -1.08 | 3.50E-04 | 2.36E-03 | General function prediction only | WD domain, G-beta repeat |
| EVM0009512 | 25.84 | 54.50 | -1.08 | 3.00E-04 | 2.07E-03 | Lipid transport and metabolism | CoA-transferase family III |
| EVM0003425 | 7.21 | 15.18 | -1.07 | 5.00E-05 | 4.28E-04 | -- | Formin Homology 2 Domain |
| EVM0008014 | 1525.28 | 3211.64 | -1.07 | 1.50E-04 | 1.14E-03 | Translation, ribosomal structure and biogenesis | Ribosomal protein L35Ae |
| EVM0005754 | 7.03 | 14.80 | -1.07 | 1.31E-02 | 4.64E-02 | -- | -- |
| EVM0002212 | 14.52 | 30.55 | -1.07 | 1.50E-03 | 8.00E-03 | Posttranslational modification, protein turnover, chaperones | -- |
| EVM0009084 | 64.15 | 134.98 | -1.07 | 5.00E-05 | 4.28E-04 | Translation, ribosomal structure and biogenesis | Histidyl-tRNA synthetase |
| EVM0008008 | 6.82  | 14.34  | -1.07 | 9.00E-04 | 5.22E-03 | -- | Heterokaryon incompatibility protein (HET) |
| EVM0011714 | 96.69 | 203.25 | -1.07 | 1.50E-04 | 1.14E-03 | Function unknown | Protein of unknown function (DUF1279) |
| EVM0008615 | 209.09 | 439.47 | -1.07 | 4.00E-04 | 2.65E-03 | General function prediction only | Thi4 family |
| EVM0000289 | 31.95 | 67.13  | -1.07 | 1.50E-04 | 1.14E-03 | RNA processing and modification | RNA recognition motif. (a.k.a. RRM, RBD, or RNP domain) |
| EVM000096  | 1.57  | 3.30   | -1.07 | 3.55E-03 | 1.62E-02 | -- | -- |
| EVM0002576 | 15.71 | 33.00  | -1.07 | 5.00E-05 | 4.28E-04 | -- | MYND finger |
| EVM0007337 | 22.56 | 47.38  | -1.07 | 7.00E-04 | 4.23E-03 | Carbohydrate transport and metabolism | Class II Aldolase and Adducin N-terminal domain |
| EVM0004284 | 5.08  | 10.66  | -1.07 | 5.00E-04 | 3.19E-03 | -- | WSC domain |
| EVM0004735 | 7.15  | 15.00  | -1.07 | 2.00E-04 | 1.46E-03 | -- | 50S ribosome-binding GTPase |
| EVM0006851 | 25.64 | 53.80  | -1.07 | 5.00E-04 | 3.19E-03 | -- | -- |
| EVM000774  | 41.07 | 86.18  | -1.07 | 5.00E-05 | 4.28E-04 | -- | -- |
| EVM0006313 | 4.40  | 9.24   | -1.07 | 1.05E-02 | 3.88E-02 | General function prediction only | C2H2-type zinc finger |
| EVM000642  | 26.67 | 55.95  | -1.07 | 1.00E-04 | 7.96E-04 | -- | -- |
| EVM0001741 | 2.66  | 5.57   | -1.07 | 1.50E-03 | 8.00E-03 | -- | RNA recognition motif. (a.k.a. RRM, RBD, or RNP domain) |
| EVM0006493 | 123.41 | 258.75 | -1.07 | 1.50E-04 | 1.14E-03 | -- | N-acetylglucosaminyl transferase component (Gpi1) |
|------------|--------|--------|--------|----------|----------|----|--------------------------------------------------|
| EVM0006380 | 3.84   | 8.06   | -1.07  | 3.00E-03 | 1.42E-02 | -- | Glyoxal oxidase N-terminus                        |
| EVM0000560 | 3.98   | 8.34   | -1.07  | 2.25E-03 | 1.12E-02 | -- | Ferric reductase like transmembrane component     |
| EVM0004244 | 13.39  | 28.03  | -1.07  | 4.00E-04 | 2.65E-03 | -- | F-box-like                                       |
| EVM0010713 | 16.16  | 33.82  | -1.07  | 3.50E-04 | 2.36E-03 | Function unknown | Protein of unknown function (DUF890) |
| EVM0004606 | 45.25  | 94.67  | -1.07  | 1.50E-04 | 1.14E-03 | -- | Sel1 repeat                                      |
| EVM0002257 | 28.03  | 58.63  | -1.06  | 3.50E-04 | 2.36E-03 | -- | --                                                |
| EVM0003798 | 4.06   | 8.48   | -1.06  | 8.40E-03 | 3.26E-02 | -- | Thaumatin family                                 |
| EVM0002854 | 44.72  | 93.53  | -1.06  | 3.00E-04 | 2.07E-03 | Secondary metabolites biosynthesis, transport and catabolism |
| EVM0010713 | 16.16  | 33.82  | -1.07  | 3.50E-04 | 2.36E-03 | Function unknown | Protein of unknown function (DUF890) |
| EVM0008213 | 1093.56| 2286.68| -1.06  | 1.50E-04 | 1.14E-03 | RNA processing and modification | LSM domain |
| EVM0008930 | 78.58  | 164.28 | -1.06  | 6.00E-04 | 3.72E-03 | -- | --                                                |
| EVM0002777 | 125.23 | 261.73 | -1.06  | 5.50E-04 | 3.46E-03 | -- | --                                                |
| EVM0005540 | 37.24  | 77.79  | -1.06  | 1.70E-03 | 8.87E-03 | -- | --                                                |
| EVM0002843 | 20.14  | 42.04  | -1.06  | 2.50E-04 | 1.77E-03 | -- | FAD binding domain                               |
| EVM0006400 | 3.44   | 7.19   | -1.06  | 5.15E-03 | 2.20E-02 | -- | --                                                |
| EVM0010109 | 8.69   | 18.14  | -1.06  | 9.50E-04 | 5.46E-03 | Replication, recombination and repair | Eukaryotic and archaeal DNA primase, large subunit |
| EVM0008011 | 47.05  | 98.22  | -1.06  | 3.50E-04 | 2.36E-03 | -- | --                                                |
| EVM0007046 | 5.36   | 11.19  | -1.06  | 3.05E-03 | 1.44E-02 | -- | --                                                |
| Accession  | Log2 Ratio | P-value | Enrichment | Description                                                                 |
|-----------|------------|---------|------------|----------------------------------------------------------------------------|
| EVM0010556| 7.18       | 1.75E-03| 9.08E-03   | General function prediction only                                             |
| EVM001163 | 107.11     | 4.50E-04| 2.92E-03   | Protein kinase domain                                                        |
| EVM0005895| 30.66      | 4.00E-04| 2.65E-03   | --                                                                           |
| EVM0011785| 4.26       | 4.00E-04| 2.65E-03   | Fungal specific transcription factor domain                                 |
| EVM0007252| 56.37      | 2.50E-04| 1.77E-03   | Secondary metabolites biosynthesis, transport and catabolism              |
| EVM0007781| 2.77       | 1.11E-02| 4.06E-02   | Amino acid transport and metabolism                                          |
| EVM0009119| 11.83      | 1.00E-03| 5.70E-03   | --                                                                           |
| EVM0009780| 34.23      | 2.50E-04| 1.77E-03   | Translation, ribosomal structure and biogenesis                            |
| EVM0005500| 16.81      | 8.00E-04| 4.73E-03   | Function unknown                                                            |
| EVM0001475| 12.14      | 3.50E-04| 2.36E-03   | XAP5, circadian clock regulator                                             |
| EVM0002127| 55.73      | 1.50E-04| 1.14E-03   | RNA processing and modification                                             |
| EVM0002623| 12.13      | 1.50E-04| 1.14E-03   | --                                                                           |
| EVM0008843| 14.89      | 2.00E-04| 1.46E-03   | WD domain, G-beta repeat                                                    |
| EVM0010675| 15.43      | 3.00E-04| 2.07E-03   | General function prediction only                                            |
| EVM0006677| 24.68      | 8.00E-04| 4.73E-03   | --                                                                           |
| EVM0000516| 39.43      | 3.50E-04| 2.36E-03   | --                                                                           |
| EVM0007866| 47.43      | 3.50E-04| 2.36E-03   | Peptidase M50B-like                                                         |
| EVM0007883| 184.74     | 1.50E-04| 1.14E-03   | --                                                                           |
| EVM0008605 | 13.83 | 28.61 | -1.05 | 5.00E-04 | 3.19E-03 | Defense mechanisms | NAD dependent epimerase/dehydratase family |
|------------|--------|--------|--------|-----------|-----------|-------------------|---------------------------------|
| EVM0006618 | 86.81  | 179.49 | -1.05  | 2.50E-04 | 1.77E-03 | --                | --                             |
| EVM0008262 | 55.05  | 113.83 | -1.05  | 2.50E-04 | 1.77E-03 | General function prediction only | NAD binding domain of 6-phosphogluconate dehydrogenase |
| EVM0004911 | 537.24 | 1110.72| -1.05  | 3.00E-04 | 2.07E-03 | --                | --                             |
| EVM0001770 | 6.78   | 14.01  | -1.05  | 2.00E-03 | 1.01E-02 | --                | Lactonase, 7-bladed beta-propeller |
| EVM0007582 | 4.73   | 9.77   | -1.05  | 2.25E-03 | 1.12E-02 | Carbohydrate transport and metabolism | Glycosyl hydrolase family 47 |
| EVM0000771 | 8.17   | 16.87  | -1.05  | 1.10E-03 | 6.17E-03 | --                | --                             |
| EVM0004801 | 33.45  | 69.09  | -1.05  | 5.00E-05 | 4.28E-04 | --                | --                             |
| EVM0005561 | 65.72  | 135.72 | -1.05  | 5.00E-05 | 4.28E-04 | Transcription     | Transcription factor TFIIIB repeat |
| EVM0008064 | 17.02  | 35.15  | -1.05  | 3.50E-04 | 2.36E-03 | --                | Shugoshin C terminus            |
| EVM0006335 | 118.87 | 245.18 | -1.04  | 1.38E-02 | 4.83E-02 | --                | --                             |
| EVM0003787 | 76.12  | 157.01 | -1.04  | 1.00E-04 | 7.96E-04 | Translation, ribosomal structure and biogenesis | Eukaryotic translation initiation factor 3 subunit 7 (eIF-3) |
| EVM0008186 | 121.03 | 249.60 | -1.04  | 6.50E-04 | 3.98E-03 | General function prediction only | Translation initiation factor SUI1 |
| EVM0003484 | 14.96  | 30.84  | -1.04  | 7.50E-04 | 4.49E-03 | --                | Major Facilitator Superfamily   |
| EVM0000528 | 256.48 | 528.79 | -1.04  | 7.90E-03 | 3.10E-02 | Lipid transport and metabolism | Acyl-CoA dehydrogenase, C-terminal domain |
| EVM0001528 | 42.72  | 88.05  | -1.04  | 2.00E-04 | 1.46E-03 | RNA processing and modification | DEAD/DEAH box helicase |
| EVM0009691 | 36.99  | 76.22  | -1.04  | 2.50E-04 | 1.77E-03 | Carbohydrate transport and metabolism | pfkB family carbohydrate kinase |
| Accession | Gene ID | Description 1 | Description 2 | Description 3 |
|-----------|---------|---------------|---------------|---------------|
| EVM0005748| 42.07   | 86.68         | -1.04         | 2.00E-04      |
| EVM0005748| 1.46E-03| --            |               |               |
| EVM0001487| 56.18   | 115.73        | -1.04         | 2.00E-04      |
| EVM0001487| 1.46E-03| --            |               |               |
| EVM0011835| 78.81   | 162.34        | -1.04         | 3.50E-04      |
| EVM0011835| 2.36E-03| Posttranslational modification, protein turnover, chaperones | Ring finger domain |
| EVM0012127| 23.24   | 47.84         | -1.04         | 2.50E-04      |
| EVM0012127| 1.77E-03| --            |               | PXA domain |
| EVM0004518| 4.97    | 10.22         | -1.04         | 2.15E-03      |
| EVM0004518| 1.08E-02| Energy production and conversion | Aldehyde dehydrogenase family |
| EVM0005978| 37.96   | 78.09         | -1.04         | 1.50E-04      |
| EVM0005978| 1.14E-03| --            |               | Rab-GTPase-TBC domain |
| EVM0001385| 25.85   | 53.16         | -1.04         | 3.00E-04      |
| EVM0001385| 2.07E-03| --            |               | G-protein alpha subunit |
| EVM0008651| 112.98  | 232.33        | -1.04         | 2.50E-04      |
| EVM0008651| 1.77E-03| Inorganic ion transport and metabolism | Copper/zinc superoxide dismutase (SODC) |
| EVM0004948| 19.19   | 39.36         | -1.04         | 2.20E-03      |
| EVM0004948| 1.10E-02| --            |               | -- |
| EVM0006887| 6.91    | 14.17         | -1.04         | 2.00E-03      |
| EVM0006887| 1.01E-02| --            |               | -- |
| EVM0003428| 48.39   | 99.23         | -1.04         | 2.00E-04      |
| EVM0003428| 1.46E-03| Extracellular structures | Cofilin/tropomyosin-type actin-binding protein |
| EVM0003811| 4.68    | 9.61          | -1.04         | 1.20E-03      |
| EVM0003811| 6.64E-03| --            |               | -- |
| EVM0011083| 8.76    | 17.95         | -1.04         | 6.00E-04      |
| EVM0011083| 3.72E-03| --            |               | -- |
| EVM0009958| 13.74   | 28.17         | -1.04         | 3.05E-03      |
| EVM0009958| 1.44E-02| --            |               | -- |
| EVM0009777| 36.81   | 75.42         | -1.03         | 3.00E-04      |
| EVM0009777| 2.07E-03| General function prediction only | Putative methyltransferase |
| ID            | Gene Name                      | Description                                      | Function                                                                 |
|---------------|-------------------------------|--------------------------------------------------|--------------------------------------------------------------------------|
| EVM0007937    |                               | Posttranslational modification, protein turnover, chaperones | Zinc finger, C3HC4 type (RING finger)                                    |
| EVM0000938    |                               | Posttranslational modification, protein turnover, chaperones | Cyclophilin type peptidyl-prolyl cis-trans isomerase/CLD                  |
| EVM0001935    |                               | Posttranslational modification, protein turnover, chaperones | Myosin-like coiled-coil protein                                          |
| EVM000379     |                               | Signal transduction mechanisms                   | HNH endonuclease                                                         |
| EVM0010974    |                               | Lipid transport and metabolism                    | OPT oligopeptide transporter protein                                      |
| EVM0006096    |                               | Intracellular trafficking, secretion, and vesicular transport | Tim17/Tim22/Tim23/Pmp24 family                                           |
| EVM0006921    |                               | Lipid transport and metabolism                    | PH domain                                                                |
| EVM0005087    |                               | General function prediction only                 | Ubiquitin family                                                         |
| EVM0005207    |                               | General function prediction only                 | HMG (high mobility group) box                                            |
| EVM0006139    |                               | General function prediction only                 | Ankyrin repeats (3 copies)                                               |
| EVM0008671    |                               | Transcription                                      | DASH complex subunit Dad2                                                |
| EVM0009434    |                               | Transcription                                      | Protein of unknown function (DUF3632)                                     |
| EVM0011210    |                               | Transcription                                      | Protein kinase domain                                                    |
| Accession   | EVM0001380 | EVM0001380 | EVM0001380 | EVM0001380 | EVM0001380 | EVM0001380 | EVM0001380 | EVM0001380 | EVM0001380 | EVM0001380 |
|-------------|------------|------------|------------|------------|------------|------------|------------|------------|------------|------------|
| Description | General function prediction only | Major Facilitator Superfamily | short chain dehydrogenase | TEA/ATTS domain family | Aminotransferase class-V | ABC transporter | Carbohydrate transport and metabolism | Alpha amylase, catalytic domain | Mitochondrial carrier protein | Methyltransferase domain |
| Accession   | EVM0005091 | EVM0003753 | EVM0004303 | EVM0010536 | EVM0009990 | EVM0003625 | EVM0006366 | EVM0002321 | EVM0010583 | EVM0001247 |
| Description | Secondary metabolites biosynthesis, transport and catabolism | Amino acid transport and metabolism | Secondary metabolites biosynthesis, transport and catabolism | -- | -- | Arresitin (or S-antigen), C-terminal domain | -- | Energy production and conversion | -- | MAC/Perforin domain |
| Accession   | EVM0008363 | EVM0007250 | EVM0003414 | EVM0003625 | EVM0006366 | EVM0002321 | EVM0010583 | EVM0001247 | EVM0003414 | EVM0003625 |
| Description | -- | -- | -- | -- | -- | -- | -- | -- | -- | -- |
| Accession   | EVM0007907 | EVM0011322 | EVM0005197 | EVM0011060 | EVM0007270 | EVM0004319 | EVM0000252 | EVM0002524 | EVM0010382 | EVM0000277 | EVM0010218 | EVM0011153 | EVM0010232 | EVM0009614 |
|-------------|------------|------------|------------|------------|------------|------------|------------|------------|------------|------------|------------|------------|------------|------------|
| Description | Function unknown | Intracellular trafficking, secretion, and vesicular transport | General function prediction only | Translation, ribosomal structure and biogenesis | -- | Protein of unknown function (DUF2962) | -- | -- | Eukaryotic aspartyl protease | Posttranslational modification, protein turnover, chaperones | Methyltransferase domain | Tim17/Tim22/Tim23/Pmp24 family | Intracellular trafficking, secretion, and vesicular transport | Nuclear transport factor 2 (NTF2) domain | -- |
| Value       | 23.10      | 41.54      | 9.63       | 51.45      | 1.05       | 36.64      | 18.24      | 8.64       | 67.33      | 7.97       | 21.73      | 189.73     | 577.71     | 73.49      |
| Value 2     | 46.91      | 84.22      | 19.52      | 104.27     | 2.14       | 74.19      | 36.90      | 17.47      | 136.15     | 16.11      | 43.92      | 383.39     | 1167.18    | 148.46     |
| Value 3     | -1.02      | -1.02      | -1.02      | -1.02      | -1.02      | -1.02      | -1.02      | -1.02      | -1.02      | -1.02      | -1.02      | -1.01      | -1.01      | -1.01      |
| Value 4     | 3.00E-04   | 1.95E-03   | 1.20E-03   | 1.00E-04   | 8.75E-03   | 4.00E-04   | 7.00E-04   | 1.05E-03   | 6.50E-04   | 1.30E-03   | 2.50E-04   | 6.50E-04   | 7.50E-04   | 2.50E-04   |
| Value 5     | 2.07E-03   | 9.93E-03   | 6.64E-03   | 7.96E-04   | 3.37E-02   | 2.65E-03   | 4.23E-03   | 5.94E-03   | 3.98E-03   | 7.10E-03   | 1.77E-03   | 3.98E-03   | 4.49E-03   | 1.77E-03   |
| Value 6     | --         | --         | --         | --         | --         | --         | --         | --         | Eukaryotic aspartyl protease | --         | --         | --         | --         | --         |
| EVM0005970 | 36.07 | 72.85 | -1.01 | 2.65E-03 | 1.28E-02 | Amino acid transport and metabolism | 3-hydroxyanthranilic acid dioxygenase |
|------------|-------|-------|--------|-----------|-----------|-------------------------------------|-------------------------------------|
| EVM0002686 | 66.96 | 135.23 | -1.01 | 3.50E-04 | 2.36E-03 | -- | -- |
| EVM0007223 | 35.15 | 70.99 | -1.01 | 3.00E-04 | 2.07E-03 | Translation, ribosomal structure and biogenesis | Poly A polymerase head domain |
| EVM0000491 | 24.45 | 49.38 | -1.01 | 2.50E-04 | 1.77E-03 | -- | Ferric reductase NAD binding domain |
| EVM0009482 | 50.90 | 102.78 | -1.01 | 4.00E-04 | 2.65E-03 | General function prediction only | Putative serine esterase (DUF676) |
| EVM0004386 | 21.99 | 44.40 | -1.01 | 4.00E-04 | 2.65E-03 | RNA processing and modification | DEAD/DEAH box helicase |
| EVM0008501 | 6.12 | 12.34 | -1.01 | 2.15E-03 | 1.08E-02 | Function unknown | -- |
| EVM0000097 | 3.63 | 7.32 | -1.01 | 2.75E-03 | 1.32E-02 | -- | -- |
| EVM0008241 | 67.52 | 136.12 | -1.01 | 1.50E-04 | 1.14E-03 | Amino acid transport and metabolism | Pyridoxal-dependent decarboxylase conserved domain |
| EVM0010572 | 5.44 | 10.96 | -1.01 | 1.65E-03 | 8.65E-03 | Signal transduction mechanisms | Carboxylesterase family |
| EVM0011381 | 43.85 | 88.38 | -1.01 | 6.00E-04 | 3.72E-03 | -- | -- |
| EVM0002805 | 149.26 | 300.83 | -1.01 | 5.50E-04 | 3.46E-03 | Intracellular trafficking, secretion, and vesicular transport | Translocation protein Sec62 |
| EVM0000600 | 108.52 | 218.54 | -1.01 | 7.00E-04 | 4.23E-03 | -- | Nitronate monoxygenase |
| EVM0004430 | 86.55 | 174.17 | -1.01 | 3.50E-04 | 2.36E-03 | Signal transduction mechanisms | Stage II sporulation protein E (SpoIIE) |
| EVM0002082 | 171.89 | 345.89 | -1.01 | 7.50E-04 | 4.49E-03 | Carbohydrate transport and metabolism | Triosephosphate isomerase |
| Accession   | Gene ID | A | B | C | D | E | Gene Product                                                                 |
|------------|---------|---|---|---|---|---|-------------------------------------------------------------------------------|
| EVM0005419 | 45.82   | 92.16 | -1.01 | 4.00E-04 | 2.65E-03 | -- | --                                                                             |
| EVM0009125 | 120.09  | 241.50 | -1.01 | 4.00E-04 | 2.65E-03 | General function prediction only | Dienelactone hydrolase family                                                |
| EVM0000152 | 3.40    | 6.84  | -1.01 | 4.65E-03 | 2.03E-02 | -- | --                                                                             |
| EVM009051  | 454.36  | 913.61 | -1.01 | 3.50E-04 | 2.36E-03 | Translation, ribosomal structure and biogenesis | Ribosomal protein L34                                                        |
| EVM007795  | 13.44   | 27.02 | -1.01 | 5.50E-04 | 3.46E-03 | Secondary metabolites biosynthesis, transport and catabolism | Cytochrome P450                                                              |
| EVM011806  | 977.12  | 1963.32 | -1.01 | 1.15E-03 | 6.41E-03 | Translation, ribosomal structure and biogenesis | Ribosomal protein L18e/L15                                                   |
| EVM006775  | 26.74   | 53.71  | -1.01 | 4.50E-04 | 2.92E-03 | -- | --                                                                             |
| EVM005389  | 1092.62 | 2194.80 | -1.01 | 1.20E-03 | 6.64E-03 | -- | Cerato-platanin                                                               |
| EVM002230  | 13.41   | 26.94  | -1.01 | 1.00E-03 | 5.70E-03 | -- | Lactonase, 7-bladed beta-propeller                                              |
| EVM000935  | 45.88   | 92.11  | -1.01 | 8.00E-04 | 4.73E-03 | -- | --                                                                             |
| EVM0003011 | 2.53    | 5.07   | -1.01 | 6.80E-03 | 2.75E-02 | General function prediction only | Zinc finger, C2H2 type                                                        |
| EVM010312  | 23.60   | 47.37  | -1.01 | 2.50E-04 | 1.77E-03 | Cell cycle control, cell division, chromosome partitioning | Protein kinase domain                                                       |
| EVM009225  | 17.51   | 35.10  | -1.00 | 5.50E-04 | 3.46E-03 | General function prediction only | Ankyrin repeats (many copies)                                                |
| EVM011952  | 151.13  | 302.69 | -1.00 | 5.50E-04 | 3.46E-03 | Transcription | Helix-loop-helix DNA-binding domain                                           |
| EVM009227  | 12.72   | 25.47  | -1.00 | 1.70E-03 | 8.87E-03 | -- | CrcB-like protein                                                             |
| EVM0008788 | 11.23 | 22.49 | -1.00 | 2.40E-03 | 1.18E-02 | -- | Protein of unknown function (DUF1479) |
| EVM0001226 | 36.02 | 72.13 | -1.00 | 4.50E-04 | 2.92E-03 | Energy production and conversion | Transketolase, pyrimidine binding domain |
| EVM0008939 | 42.64 | 85.38 | -1.00 | 5.00E-04 | 3.19E-03 | RNA processing and modification | Hypothetical methyltransferase |
| EVM0000637 | 15.80 | 31.63 | -1.00 | 1.55E-03 | 8.22E-03 | -- | Cytochrome P450 |
| EVM0000668 | 147.27 | 294.81 | -1.00 | 5.05E-03 | 2.17E-02 | -- | -- |
| EVM000562 | 39.98 | 80.01 | -1.00 | 3.50E-04 | 2.36E-03 | Intracellular trafficking, secretion, and vesicular transport | Signal recognition particle, alpha subunit, N-terminal |
| EVM0004028 | 92.88 | 185.86 | -1.00 | 6.00E-04 | 3.72E-03 | Cell cycle control, cell division, chromosome partitioning | -- |
| EVM0005550 | 195.08 | 390.22 | -1.00 | 1.00E-03 | 5.70E-03 | -- | 50S ribosome-binding GTPase |
| EVM0010163 | 515.27 | 257.56 | 1.00 | 2.25E-03 | 1.12E-02 | -- | F-box-like |
| EVM001489 | 52.74 | 26.35 | 1.00 | 8.00E-04 | 4.73E-03 | General function prediction only | Enoyl-(Acyl carrier protein) reductase |
| EVM002143 | 44.76 | 22.34 | 1.00 | 6.50E-04 | 3.98E-03 | Cytoskeleton | Kinesin motor domain |
| EVM005647 | 14.66 | 7.32 | 1.00 | 6.85E-03 | 2.77E-02 | -- | Alpha/beta hydrolase family |
| EVM001209 | 100.94 | 50.31 | 1.00 | 2.00E-03 | 1.01E-02 | -- | PLAC8 family |
| EVM002785 | 37.30 | 18.59 | 1.00 | 4.00E-04 | 2.65E-03 | Inorganic ion transport and metabolism | Sodium:sulfate symporter transmembrane region |
| EVM000108 | 44.65 | 22.23 | 1.01 | 4.15E-03 | 1.85E-02 | -- | Amidohydrolase |
| EVM001781 | 35.27 | 17.54 | 1.01 | 3.50E-04 | 2.36E-03 | -- | -- |
| Accession     | EVM0007746 | EVM0010927 | EVM0000749 | EVM0009149 | EVM0000304 | EVM0012125 | EVM0012100 | EVM0008890 | EVM0008784 | EVM0000751 | EVM0010762 | EVM0011119 | EVM0005900 | EVM0006412 | EVM0002222 | EVM0004780 |
|--------------|------------|------------|------------|------------|------------|------------|------------|------------|------------|------------|------------|------------|------------|------------|------------|------------|
| Description  | JmjC domain, hydroxylase | BTB/POZ domain | General function prediction only | Ras family | -- | Protein of unknown function (DUF563) | Carboxylesterase family | Sec63 Brl domain | Cytoskeleton | Ku70/Ku80 beta-barrel domain | Replication, recombination and repair | Response regulator receiver domain | BCS1 N terminal | Bin/amphiphysin/Rvs domain for vesicular trafficking | Cytochrome P450 | DEAD/DEAH box helicase |
| EVM0004931 | 73.24 | 36.10 | 1.02 | 4.50E-04 | 2.92E-03 | -- | Munc13 (mammalian uncoordinated) homology domain |
| EVM0000011 | 237.20 | 116.84 | 1.02 | 8.00E-04 | 4.73E-03 | Posttranslational modification, protein turnover, chaperones | Peptidase family M3 |
| EVM0004776 | 43.15 | 21.25 | 1.02 | 8.00E-04 | 4.73E-03 | Intracellular trafficking, secretion, and vesicular transport | Vps5 C terminal like |
| EVM0002790 | 20.24 | 9.96 | 1.02 | 4.45E-03 | 1.96E-02 | -- | -- |
| EVM0008401 | 28.07 | 13.80 | 1.02 | 1.00E-04 | 7.96E-04 | Posttranslational modification, protein turnover, chaperones | Septin |
| EVM0008398 | 54.87 | 26.95 | 1.03 | 3.00E-04 | 2.07E-03 | -- | -- |
| EVM0009108 | 2367.33 | 1161.26 | 1.03 | 1.02E-02 | 3.80E-02 | -- | Origin recognition complex (ORC) subunit 5 C-terminus |
| EVM0006883 | 32.11 | 15.75 | 1.03 | 3.00E-04 | 2.07E-03 | Secondary metabolites biosynthesis, transport and catabolism | ABC transporter |
| EVM0006534 | 156.48 | 76.59 | 1.03 | 7.00E-04 | 4.23E-03 | Posttranslational modification, protein turnover, chaperones | ThiF family |
| EVM0001797 | 12.30 | 6.01 | 1.03 | 6.40E-03 | 2.62E-02 | -- | -- |
| EVM0006410 | 336.54 | 164.42 | 1.03 | 2.05E-03 | 1.03E-02 | -- | Importin-beta N-terminal domain |
| Accession  | Sequence 1 | Sequence 2 | Blast Score | E-value | Description                                      |
|-----------|------------|------------|-------------|---------|--------------------------------------------------|
| EVM0011665 | 48.52      | 23.71      | 1.03        | 1.00E-04| Signal transduction mechanisms                   |
| EVM0004207 | 576.82     | 281.40     | 1.04        | 8.50E-04| --                                               |
| EVM0002885 | 130.51     | 63.65      | 1.04        | 4.00E-04| Transcription                                    |
| EVM0006334 | 26.39      | 12.87      | 1.04        | 5.00E-04| --                                               |
| EVM000993  | 3071.48    | 1494.52    | 1.04        | 1.16E-02| --                                               |
| EVM009846  | 20.45      | 9.94       | 1.04        | 8.00E-04| General function prediction only                 |
| EVM0011666 | 10.73      | 5.21       | 1.04        | 1.65E-03| --                                               |
| EVM0012087 | 136.85     | 66.30      | 1.05        | 8.50E-04| General function prediction only                 |
| EVM0012149 | 59.55      | 28.84      | 1.05        | 4.50E-04| --                                               |
| EVM0007994 | 36.59      | 17.69      | 1.05        | 6.50E-04| --                                               |
| EVM0009638 | 8.14       | 3.94       | 1.05        | 1.75E-03| --                                               |
| EVM0010723 | 153.49     | 74.20      | 1.05        | 5.00E-04| Intracellular trafficking, secretion, and vesicular transport |
| EVM0006771 | 235.40     | 113.78     | 1.05        | 2.50E-04| Carbohydrate transport and metabolism            |
| EVM0010223 | 32.65      | 15.78      | 1.05        | 3.00E-04| Permease family                                 |
| EVM0007015 | 44.83      | 14.14      | 1.66        | 5.00E-05| Acyl transferase domain                          |
| EVM000926  | 150.75     | 72.77      | 1.05        | 1.50E-03| --                                               |
| EVM0008039 | 347.46     | 167.53     | 1.05        | 1.65E-03| --                                               |
| EVM000512  | 6.92       | 3.34       | 1.05        | 1.05E-02| --                                               |
| Accession  | Score | Matched | Identity | E-value1 | E-value2 | Description                                      |
|-----------|-------|---------|----------|----------|----------|--------------------------------------------------|
| EVM0003731 | 143.83 | 69.16   | 1.06     | 7.50E-04 | 4.49E-03 | General function prediction only                  |
| EVM0011572 | 416.72 | 199.92  | 1.06     | 7.50E-04 | 4.49E-03 | --                                                |
| EVM0008222 | 18.30  | 8.77    | 1.06     | 4.50E-04 | 2.92E-03 | Cell cycle control, cell division, chromosome partitioning |
| EVM0005404 | 24.27  | 11.64   | 1.06     | 1.00E-04 | 7.96E-04 | --                                                |
| EVM0004203 | 13.00  | 6.23    | 1.06     | 1.00E-04 | 7.96E-04 | RNA processing and modification                    |
| EVM0000520 | 42.09  | 20.17   | 1.06     | 3.00E-04 | 2.07E-03 | General function prediction only                  |
| EVM0004568 | 273.05 | 130.74  | 1.06     | 8.00E-04 | 4.73E-03 | --                                                |
| EVM0003688 | 39.63  | 18.97   | 1.06     | 5.00E-05 | 4.28E-04 | Cell cycle control, cell division, chromosome partitioning |
| EVM0006759 | 95.45  | 45.63   | 1.06     | 1.50E-04 | 1.14E-03 | Intracellular trafficking, secretion, and vesicular transport |
| EVM0009500 | 100.93 | 48.23   | 1.07     | 3.50E-04 | 2.36E-03 | --                                                |
| EVM0004100 | 207.69 | 99.22   | 1.07     | 5.00E-05 | 4.28E-04 | --                                                |
| EVM0003463 | 1.96   | 0.93    | 1.07     | 1.02E-02 | 3.81E-02 | --                                                |

**EVM0003731**

RNA recognition motif. (a.k.a. RRM, RBD, or RNP domain)

**EVM0011572**

Beta-glucan synthesis-associated protein (SKN1)

**EVM0008222**

Domain of unknown function (DUF3635)

**EVM0005404**

RecF/RecN/SMC N terminal domain

**EVM0000520**

Domain of unknown function (DUF1708)

**EVM0004100**

F-box domain
| EVM0008313 | 21.42 | 10.18 | 1.07 | 3.50E-04 | 2.36E-03 | Secondary metabolites biosynthesis, transport and catabolism | ABC transporter transmembrane region |
| EVM0001336 | 53.25 | 25.30 | 1.07 | 5.40E-03 | 2.29E-02 | Signal transduction mechanisms | HIT domain |
| EVM0001629 | 11.58 | 5.49  | 1.08 | 1.70E-03 | 8.87E-03 | -- | -- |
| EVM0003437 | 16.24 | 7.70  | 1.08 | 5.00E-04 | 3.19E-03 | Posttranslational modification, protein turnover, chaperones | Tubulin folding cofactor D C terminal |
| EVM0007014 | 90.12 | 42.71 | 1.08 | 4.00E-04 | 2.65E-03 | General function prediction only | Acetyltransferase (GNAT) family |
| EVM0008722 | 195.10| 92.39 | 1.08 | 4.50E-04 | 2.92E-03 | Inorganic ion transport and metabolism | Alkaline phosphatase |
| EVM0001532 | 1195.11| 565.38| 1.08 | 6.00E-04 | 3.72E-03 | -- | Septin |
| EVM0003658 | 7.01  | 3.31  | 1.08 | 3.40E-03 | 1.57E-02 | -- | -- |
| EVM0009761 | 224.83| 106.26| 1.08 | 1.00E-04 | 7.96E-04 | Posttranslational modification, protein turnover, chaperones | PCI domain |
| EVM0002371 | 1390.32| 656.79| 1.08 | 3.00E-04 | 2.07E-03 | Chromatin structure and dynamics | Core histone H2A/H2B/H3/H4 |
| EVM0003151 | 21.52 | 10.16 | 1.08 | 1.30E-03 | 7.10E-03 | -- | Phosphotyrosyl phosphate activator (PTPA) protein |
| EVM0008332 | 13.68 | 6.45  | 1.08 | 2.05E-03 | 1.03E-02 | -- | -- |
| EVM0011537 | 141.11| 66.51 | 1.09 | 2.00E-04 | 1.46E-03 | Transcription | Histone-like transcription factor (CBF/NF-Y) and archaeal histone |
| EVM0000618  | 28.71 | 13.52 | 1.09 | 2.00E-04  | 1.46E-03 | RNA processing and modification | Suppressor of forked protein (Suf) |
| EVM0003945  | 216.14 | 101.73 | 1.09 | 1.35E-03  | 7.33E-03 | Cell wall/membrane/envelope biogenesis | Chitin synthase |
| EVM0009514  | 208.38 | 98.05  | 1.09 | 1.00E-04  | 7.96E-04 | Carbohydrate transport and metabolism | Glyceraldehyde 3-phosphate dehydrogenase, C-terminal domain |
| EVM0008496  | 20.49  | 9.64   | 1.09 | 3.50E-04  | 2.36E-03 | Amino acid transport and metabolism | Aminotransferase class-III |
| EVM0007972  | 6.27   | 2.94   | 1.09 | 1.30E-03  | 7.10E-03 | RNA processing and modification | RNA dependent RNA polymerase |
| EVM0006573  | 20.01  | 9.38   | 1.09 | 4.80E-03  | 2.08E-02 | -- |
| EVM0008453  | 22.80  | 10.69  | 1.09 | 3.00E-04  | 2.07E-03 | -- | F-box-like |
| EVM0009159  | 7.09   | 3.32   | 1.09 | 9.50E-04  | 5.46E-03 | -- |
| EVM0004585  | 49.29  | 23.09  | 1.09 | 5.00E-05  | 4.28E-04 | General function prediction only | GMC oxidoreductase |
| EVM0001289  | 91.63  | 42.81  | 1.10 | 5.00E-05  | 4.28E-04 | -- |
| EVM0011598  | 38.71  | 18.09  | 1.10 | 1.00E-04  | 7.96E-04 | -- |
| EVM0008097  | 90.78  | 42.37  | 1.10 | 2.25E-03  | 1.12E-02 | -- |
| EVM0004383  | 1175.83| 548.42 | 1.10 | 1.09E-02  | 4.01E-02 | -- | Pro-kumamolisin, activation domain |
| EVM0006210  | 17.73  | 8.26   | 1.10 | 2.00E-04  | 1.46E-03 | -- | Nuclear condensing complex subunits, C-term domain |
| EVM0000711  | 119.23 | 55.45  | 1.10 | 1.50E-04  | 1.14E-03 | -- | Cytochrome P450 |
| ID        | Energy | ATPase | PH domain | SIT4 phosphatase-associated protein | N terminus of Rad21 / Rec8 like protein | Catalase | Peptidase S24-like | Allophanate hydrolase subunit 2 | Eukaryotic aspartyl protease |
|-----------|--------|--------|-----------|------------------------------------|-----------------------------------------|---------|-------------------|----------------------------------|-----------------------------|
| EVM0002430 | 746.46 | 347.11 | 1.10      | 5.00E-04                           | 3.19E-03                                | Energy production and conversion    | Dehydrogenase E1 component          |                                  |                             |
| EVM0000585 | 118.50 | 55.07  | 1.11      | 5.00E-05                           | 4.28E-04                                | Secondary metabolites biosynthesis, | Cytochrome P450                        |                                  |                             |
| EVM0011276 | 131.05 | 60.82  | 1.11      | 5.00E-05                           | 4.28E-04                                | Translation, ribosomal structure     | Pumilio-family RNA binding repeat         |                                  |                             |
| EVM000788  | 40.74  | 18.87  | 1.11      | 9.00E-04                           | 5.22E-03                                | --                                 | PH domain                            |                                  |                             |
| EVM006726  | 302.99 | 140.31 | 1.11      | 3.50E-04                           | 2.36E-03                                | Posttranslational modification,    | ATPase family associated with various cellular activities (AAA) |                                  |                             |
| EVM001345  | 24.42  | 11.26  | 1.12      | 5.00E-05                           | 4.28E-04                                | Cell cycle control, cell division, | SIT4 phosphatase-associated protein |                                  |                             |
| EVM000598  | 87.02  | 40.01  | 1.12      | 5.00E-05                           | 4.28E-04                                | Cell cycle control, cell division, | N terminus of Rad21 / Rec8 like protein |                                  |                             |
| EVM000295  | 719.86 | 331.02 | 1.12      | 1.40E-03                           | 7.55E-03                                | Inorganic ion transport and         | Catalase                            |                                  |                             |
| EVM004423  | 50.49  | 23.21  | 1.12      | 2.05E-03                           | 1.03E-02                                | Posttranslational modification,    | Peptidase S24-like                    |                                  |                             |
| EVM010842  | 132.66 | 60.94  | 1.12      | 9.00E-04                           | 5.22E-03                                | --                                 | Allophanate hydrolase subunit 2       |                                  |                             |
| EVM006789  | 107.49 | 44.24  | 1.28      | 5.00E-05                           | 4.28E-04                                | Posttranslational modification,    | Eukaryotic aspartyl protease            |                                  |                             |
| EVM0002080  | 3.84 | 1.75 | 1.13 | 8.15E-03 | 3.18E-02 | -- | -- |
| EVM0002999  | 48.51 | 22.10 | 1.13 | 1.00E-04 | 7.96E-04 | Intracellular trafficking, secretion, and vesicular transport | ATG C terminal domain |
| EVM0009169  | 97.58 | 44.41 | 1.14 | 5.50E-04 | 3.46E-03 | -- | -- |
| EVM0008682  | 47.42 | 21.57 | 1.14 | 1.00E-04 | 7.96E-04 | General function prediction only | EamA-like transporter family |
| EVM0007345  | 174.29 | 79.23 | 1.14 | 1.00E-04 | 7.96E-04 | Amino acid transport and metabolism | POT family |
| EVM0007019  | 151.81 | 69.00 | 1.14 | 1.00E-04 | 7.96E-04 | -- | Dynamin central region |
| EVM0007035  | 54.56 | 24.77 | 1.14 | 5.00E-05 | 4.28E-04 | -- | Transferrin receptor-like dimerisation domain |
| EVM0009222  | 12.54 | 5.68 | 1.14 | 6.00E-04 | 3.72E-03 | -- | Uncharacterized protein conserved in bacteria (DUF2264) |
| EVM0005286  | 403.44 | 182.66 | 1.14 | 5.00E-05 | 4.28E-04 | -- | -- |
| EVM0002962  | 1185.33 | 536.59 | 1.14 | 7.50E-04 | 4.49E-03 | -- | -- |
| EVM0009044  | 73.68 | 33.29 | 1.15 | 1.00E-04 | 7.96E-04 | -- | -- |
| EVM0009274  | 27.59 | 12.46 | 1.15 | 5.00E-04 | 3.19E-03 | -- | CLASP N terminal |
| EVM0001663  | 2.75 | 1.24 | 1.15 | 1.27E-02 | 4.52E-02 | Energy production and conversion | Pyridine nucleotide-disulphide oxidoreductase |
| EVM0002782  | 27.83 | 12.54 | 1.15 | 6.50E-04 | 3.98E-03 | -- | -- |
| EVM0011907  | 18.74 | 8.44 | 1.15 | 1.00E-03 | 5.70E-03 | Coenzyme transport and metabolism | Polyprenyl synthetase |
| EVM0000723  | 29.96 | 13.48 | 1.15 | 5.00E-05 | 4.28E-04 | Translation, ribosomal structure and biogenesis | tRNA synthetases class I (I, L, M and V) |
| EVM0007128 | 179.99 | 80.68 | 1.16 | 3.00E-04 | 2.07E-03 | Posttranslational modification, protein turnover, chaperones | ATPase family associated with various cellular activities (AAA) |
| EVM0005320 | 147.56 | 66.13 | 1.16 | 5.00E-05 | 4.28E-04 | General function prediction only | Carbamoyl-phosphate synthase L chain, ATP binding domain |
| EVM0000040 | 48.39  | 21.67 | 1.16 | 1.00E-04 | 7.96E-04 | Secondary metabolites biosynthesis, transport and catabolism | Flavin-binding monooxygenase-like |
| EVM0002137 | 55.49  | 24.81 | 1.16 | 1.00E-03 | 5.70E-03 | Defense mechanisms | D-arabinono-1,4-lactone oxidase |
| EVM0010128 | 15.48  | 6.92  | 1.16 | 1.35E-03 | 7.33E-03 | -- | -- |
| EVM0011002 | 21.80  | 9.74  | 1.16 | 5.00E-05 | 4.28E-04 | Function unknown | Domain of unknown function (DUF3337) |
| EVM0003794 | 13.24  | 5.91  | 1.16 | 1.50E-04 | 1.14E-03 | -- | Calpain large subunit, domain III |
| EVM0006627 | 16.14  | 7.20  | 1.16 | 1.50E-04 | 1.14E-03 | Chromatin structure and dynamics | Chromatin assembly factor 1 subunit A |
| EVM0010568 | 2.94   | 1.31  | 1.16 | 1.03E-02 | 3.82E-02 | General function prediction only | Histidine phosphatase superfamily (branch 2) |
| EVM0008131 | 146.03 | 65.12 | 1.17 | 5.00E-05 | 4.28E-04 | -- | Cellulase (glycosyl hydrolase family 5) |
| EVM0006508 | 15.87  | 7.08  | 1.17 | 5.00E-05 | 4.28E-04 | Function unknown | SprT-like family |
| EVM0007516 | 92.79  | 41.34 | 1.17 | 1.00E-04 | 7.96E-04 | Carbohydrate transport and metabolism | Glycosyl hydrolases family 38 N-terminal domain |
| EVM0004887 | 2.66   | 1.18  | 1.17 | 4.90E-03 | 2.12E-02 | -- | Protein of unknown function (DUF4246) |
| EVM0006505 | 35.79  | 15.92 | 1.17 | 5.00E-05 | 4.28E-04 | Signal transduction mechanisms | OPT oligopeptide transporter protein |
| EVM0007102 | 67.72 | 30.10 | 1.17 | 5.00E-04 | 3.19E-03 | -- | -- |
| EVM0005016 | 63.79 | 28.35 | 1.17 | 1.00E-04 | 7.96E-04 | Secondary metabolites biosynthesis, transport and catabolism | Copper amine oxidase, enzyme domain |
| EVM0010042 | 14.55 | 6.46  | 1.17 | 3.50E-04 | 2.36E-03 | Transcription | RNA polymerase Rpb5, C-terminal domain |
| EVM0001686 | 2.98  | 1.32  | 1.17 | 5.60E-03 | 2.36E-02 | -- | Bestrophin, RFP-TM, chloride channel |
| EVM0000127 | 2964.39 | 1313.97 | 1.17 | 5.75E-03 | 2.41E-02 | -- | -- |
| EVM0010882 | 230.74 | 102.20 | 1.17 | 5.00E-05 | 4.28E-04 | General function prediction only | Histidine phosphatase superfamily (branch 2) |
| EVM0011238 | 83.17 | 36.82 | 1.18 | 1.00E-04 | 7.96E-04 | Secondary metabolites biosynthesis, transport and catabolism | Cytochrome P450 |
| EVM0003998 | 26.33 | 11.65 | 1.18 | 8.50E-04 | 4.98E-03 | Posttranslational modification, protein turnover, chaperones | Proteasome activator pa28 beta subunit |
| EVM0009431 | 177.84 | 78.62 | 1.18 | 1.00E-04 | 7.96E-04 | -- | Mycolic acid cyclopropane synthetase |
| EVM0006594 | 269.00 | 118.87 | 1.18 | 2.00E-04 | 1.46E-03 | Amino acid transport and metabolism | Serine hydroxymethyltransferase |
| EVM0010136 | 49.72 | 21.94 | 1.18 | 5.00E-05 | 4.28E-04 | Carbohydrate transport and metabolism | Major Facilitator Superfamily |
| EVM0007160 | 5.87  | 2.59  | 1.18 | 6.50E-04 | 3.98E-03 | -- | -- |
| EVM0001971 | 11.67 | 5.14  | 1.18 | 4.70E-03 | 2.05E-02 | -- | -- |
| EVM0006450 | 87.10 | 38.33 | 1.18 | 5.00E-05 | 4.28E-04 | General function prediction only | Alpha/beta hydrolase family |
| EVM0009661 | 305.78 | 134.20 | 1.19 | 5.00E-05 | 4.28E-04 | -- | -- |
| EVM0004320 | 141.78 | 62.00 | 1.19 | 1.00E-04 | 7.96E-04 | General function prediction only | Aldo/keto reductase family |
| EVM0002952 | 34.73 | 15.18 | 1.19 | 5.00E-05 | 4.28E-04 | Extracellular structures | Tropomyosin |
| EVM0007366 | 42.46 | 18.53 | 1.20 | 5.00E-05 | 4.28E-04 | -- | -- |
| EVM0003280 | 11.43 | 4.98 | 1.20 | 6.15E-03 | 2.54E-02 | -- | -- |
| EVM0011387 | 65.19 | 28.38 | 1.20 | 5.00E-05 | 4.28E-04 | Translation, ribosomal structure and biogenesis | tRNA synthetases class I (E and Q), catalytic domain |
| EVM0010099 | 308.50 | 134.30 | 1.20 | 1.00E-04 | 7.96E-04 | -- | Mycolic acid cyclopropane synthetase |
| EVM0003016 | 27.75 | 12.08 | 1.20 | 5.00E-05 | 4.28E-04 | -- | -- |
| EVM0008931 | 53.49 | 23.27 | 1.20 | 5.00E-05 | 4.28E-04 | -- | Growth-Arrest-Specific Protein 2 Domain |
| EVM0011910 | 45.62 | 19.83 | 1.20 | 5.00E-05 | 4.28E-04 | Intracellular trafficking, secretion, and vesicular transport | VID27 cytoplasmic protein |
| EVM0004174 | 37.21 | 16.16 | 1.20 | 5.00E-05 | 4.28E-04 | Intracellular trafficking, secretion, and vesicular transport | COG4 transport protein |
| EVM0007504 | 3.76 | 1.63 | 1.20 | 6.40E-03 | 2.62E-02 | -- | -- |
| EVM0002032 | 10.47 | 4.54 | 1.21 | 4.50E-04 | 2.92E-03 | -- | -- |
| EVM0005679 | 23.45 | 10.16 | 1.21 | 3.00E-04 | 2.07E-03 | -- | -- |
| EVM0006489 | 251.65 | 108.98 | 1.21 | 5.00E-05 | 4.28E-04 | -- | -- |
| EVM0009273 | 3.79 | 1.64 | 1.21 | 1.65E-03 | 8.65E-03 | -- | -- |
| EVM00002025 | 65.69 | 28.42 | 1.21 | 5.00E-05 | 4.28E-04 | -- | Major Facilitator Superfamily |
| EVM0001810 | 290.27 | 124.20 | 1.22 | 1.50E-04 | 1.14E-03 | Carbohydrate transport and metabolism | Major intrinsic protein |
| EVM0010686 | 5.29 | 2.29 | 1.21 | 6.45E-03 | 2.64E-02 | -- | -- |
| EVM0011240 | 257.40 | 111.20 | 1.21 | 1.00E-04 | 7.96E-04 | -- | -- |
| EVM0007091 | 7.24 | 3.13 | 1.21 | 1.11E-02 | 4.06E-02 | -- | -- |
| EVM0008774 | 23.46 | 10.13 | 1.21 | 5.00E-05 | 4.28E-04 | Chromatin structure and dynamics | DNA gyrase/topoisomerase IV, subunit A |
| EVM0005574 | 19.45 | 8.39 | 1.21 | 5.00E-05 | 4.28E-04 | RNA processing and modification | RNA dependent RNA polymerase |
| EVM0010980 | 1.45 | 0.63 | 1.21 | 1.65E-03 | 8.65E-03 | -- | -- |
| EVM0009229 | 27.55 | 11.87 | 1.21 | 1.00E-04 | 7.96E-04 | -- | -- |
| EVM0003903 | 18.22 | 7.84 | 1.22 | 5.00E-05 | 4.28E-04 | -- | -- |
| EVM0004640 | 6.79 | 2.92 | 1.22 | 1.12E-02 | 4.10E-02 | Signal transduction mechanisms | Phosphatidylinositolglycan class N (PIG-N) |
| EVM0001919 | 27.55 | 11.81 | 1.22 | 5.00E-05 | 4.28E-04 | Replication, recombination and repair | DNA polymerase family B |
| EVM0005755 | 76.65 | 32.65 | 1.23 | 5.00E-05 | 4.28E-04 | -- | Glycosyl hydrolases family 16 |
| EVM0010247 | 33.91 | 14.40 | 1.24 | 1.00E-04 | 7.96E-04 | Secondary metabolites biosynthesis, transport and catabolism | Cytochrome P450 |
| EVM0003492 | 87.17 | 37.01 | 1.24 | 5.00E-05 | 4.28E-04 | -- | Phospholipid methyltransferase |
| EVM0000868 | 27.85 | 11.81 | 1.24 | 5.00E-05 | 4.28E-04 | -- | Aconitase family (aconitate hydratase) |
| EVM0008035 | 27.70 | 11.75 | 1.24 | 5.00E-05 | 4.28E-04 | General function prediction only | SNF2 family N-terminal domain |
| EVM ID | Description                          | EVM ID | Description                          |
|--------|--------------------------------------|--------|--------------------------------------|
| EVM0006748 | 105.07 | 44.52 | 1.24 | 5.00E-05 | 4.28E-04 | Function unknown | TPR/MLP1/MLP2-like protein |
| EVM0011982 | 81.83 | 34.60 | 1.24 | 4.80E-03 | 2.08E-02 | Chromatin structure and dynamics | Core histone H2A/H2B/H3/H4 |
| EVM0008430 | 30.04 | 12.70 | 1.24 | 5.00E-05 | 4.28E-04 | Replication, recombination and repair | DNA polymerase family B |
| EVM0002582 | 321.38 | 135.71 | 1.24 | 2.00E-04 | 1.46E-03 | Translation, ribosomal structure and biogenesis | RNB domain |
| EVM0004575 | 99.93 | 42.19 | 1.24 | 2.00E-04 | 1.46E-03 | General function prediction only | GMC oxidoreductase |
| EVM0005629 | 74.51 | 31.40 | 1.25 | 1.00E-04 | 7.96E-04 | Translation, ribosomal structure and biogenesis | Ribosomal protein L7/L12 C-terminal domain |
| EVM0001758 | 21.48 | 9.01 | 1.25 | 7.00E-04 | 4.23E-03 | -- | -- |
| EVM0010197 | 51.64 | 21.63 | 1.26 | 5.00E-05 | 4.28E-04 | Secondary metabolites biosynthesis, transport and catabolism | ABC transporter transmembrane region |
| EVM0000333 | 20.83 | 8.72 | 1.26 | 5.00E-05 | 4.28E-04 | Posttranslational modification, protein turnover, chaperones | Poly(ADP-ribose) polymerase catalytic domain |
| EVM0005868 | 145.04 | 60.61 | 1.26 | 1.50E-04 | 1.14E-03 | -- | -- |
| EVM0008160 | 59.02 | 24.64 | 1.26 | 2.50E-04 | 1.77E-03 | General function prediction only | RNA recognition motif. (a.k.a. RRM, RBD, or RNP domain) |
| EVM0005521 | 102.86 | 42.74 | 1.27 | 1.50E-04 | 1.14E-03 | -- | GPR1/FUN34/yaah family |
| EVM0000497 | 2.92 | 1.21 | 1.27 | 1.85E-03 | 9.52E-03 | -- | -- |
| EVM0011974 | 100.91 | 41.92 | 1.27 | 1.00E-04 | 7.96E-04 | Cell cycle control, cell division, chromosome partitioning | Protein kinase domain |
| EVM0011018 | 42.35 | 17.58 | 1.27 | 2.00E-04 | 1.46E-03 | Replication, recombination and repair | Rad51 |
| EVM0001888 | 8.68  | 3.60  | 1.27 | 2.90E-03 | 1.38E-02 | -- | -- |
| EVM0009544 | 81.36 | 33.60 | 1.28 | 5.00E-05 | 4.28E-04 | Posttranslational modification, protein turnover, chaperones | IBR domain |
| EVM0006727 | 42.96 | 17.73 | 1.28 | 1.50E-04 | 1.14E-03 | -- | -- |
| EVM001477  | 438.78 | 180.80 | 1.28 | 5.00E-05 | 4.28E-04 | -- | Sulfatase-modifying factor enzyme 1 |
| EVM007667  | 162.90 | 67.05 | 1.28 | 5.00E-05 | 4.28E-04 | -- | Ubiquitin-2 like Rad60 SUMO-like |
| EVM004127  | 16.42 | 6.74  | 1.28 | 1.00E-04 | 7.96E-04 | Replication, recombination and repair | Endonuclease/Exonuclease/phosphatase family |
| EVM001877  | 6.85  | 2.81  | 1.28 | 6.50E-04 | 3.98E-03 | -- | Voltage-dependent anion channel |
| EVM0011646 | 71.98 | 29.48 | 1.29 | 1.00E-04 | 7.96E-04 | -- | Pheromone A receptor |
| EVM005980  | 46.60 | 19.03 | 1.29 | 5.00E-05 | 4.28E-04 | General function prediction only | Animal haem peroxidase |
| EVM0010853 | 16.98 | 6.93  | 1.29 | 2.65E-03 | 1.28E-02 | -- | Flavin reductase like domain |
| EVM0008071 | 89.98 | 36.64 | 1.30 | 5.00E-05 | 4.28E-04 | -- | -- |
| EVM002498  | 116.02 | 47.08 | 1.30 | 5.00E-05 | 4.28E-04 | Transcription | GATA zinc finger |
| EVM001706  | 68.83 | 27.92 | 1.30 | 5.00E-05 | 4.28E-04 | -- | Oxidoreductase family, NAD-binding Rossmann fold |
| EVM000398  | 38.60 | 15.62 | 1.31 | 5.00E-05 | 4.28E-04 | Replication, recombination and repair | ATP dependent DNA ligase domain |
| ID         | Value1 | Value2 | Value3 | Value4 | Value5 | Value6 | Description                                                                 |
|------------|--------|--------|--------|--------|--------|--------|-----------------------------------------------------------------------------|
| EVM0010144 | 314.62 | 127.14 | 1.31   | 4.00E-04 | 2.65E-03 | 5.00E-04 | Posttranslational modification, protein turnover, chaperones                |
|            |        |        |        |        |        |        | Ubiquitin carboxyl-terminal hydrolase                                       |
| EVM0011123 | 62.48  | 25.21  | 1.31   | 5.00E-05 | 4.28E-04 | 4.00E-05 | Posttranslational modification, protein turnover, chaperones                |
|            |        |        |        |        |        |        | Insulinase (Peptidase family M16)                                           |
| EVM0008486 | 250.52 | 100.93 | 1.31   | 5.00E-05 | 4.28E-04 | 5.00E-05 | Posttranslational modification, protein turnover, chaperones                |
| EVM0004840 | 490.75 | 197.64 | 1.31   | 5.00E-05 | 4.28E-04 | 4.28E-04 | Cell cycle control, cell division, chromosome partitioning                 |
| EVM0004126 | 24.66  | 9.93   | 1.31   | 5.00E-05 | 4.28E-04 | 5.00E-05 | RecF/RecN/SMC N terminal domain                                             |
| EVM0010045 | 67.34  | 27.03  | 1.32   | 5.00E-05 | 4.28E-04 | 5.00E-05 | General function prediction only                                            |
|            |        |        |        |        |        |        | Homeobox domain                                                             |
| EVM0002944 | 23.42  | 9.39   | 1.32   | 5.00E-05 | 4.28E-04 | 5.00E-05 | Wd domain, G-beta repeat                                                    |
| EVM0007446 | 1162.29| 466.01 | 1.32   | 1.25E-03 | 6.87E-03 | 4.28E-04 | Fungalysin metallopeptidase (M36)                                           |
| EVM0001672 | 13.37  | 5.35   | 1.32   | 5.00E-04 | 3.19E-03 | 5.00E-04 | Secondary metabolites biosynthesis, transport and catabolism               |
|            |        |        |        |        |        |        | Alcohol dehydrogenase GroES-like domain                                    |
| EVM0004326 | 272.02 | 108.53 | 1.33   | 5.00E-05 | 4.28E-04 | 5.00E-04 | Posttranslational modification, protein turnover, chaperones               |
|            |        |        |        |        |        |        | Eukaryotic aspartyl protease                                                |
| EVM0006048 | 32.20  | 12.83  | 1.33   | 1.50E-04 | 1.14E-03 | 4.00E-04 | Function unknown                                                            |
| EVM0003051 | 99.99  | 39.84  | 1.33   | 5.00E-05 | 4.28E-04 | 5.00E-05 | GINS complex protein                                                        |


| EVM0001405 | 143.68 | 57.08 | 1.33 | 5.00E-05 4.28E-04 | Intracellular trafficking, secretion, and vesicular transport | Sybindin-like family |
| EVM0007927 | 32.12  | 12.72 | 1.34 | 5.00E-05 4.28E-04 | -- | Condensin complex subunit 2 |
| EVM0000862 | 30.14  | 11.93 | 1.34 | 5.00E-05 4.28E-04 | Replication, recombination and repair | MCM2/3/5 family |
| EVM0008720 | 251.03 | 99.23 | 1.34 | 5.00E-05 4.28E-04 | Nucleotide transport and metabolism | Ribonucleotide reductase, barrel domain |
| EVM0002963 | 1834.71| 720.70| 1.35 | 5.00E-05 4.28E-04 | -- | -- |
| EVM0010285 | 15.43  | 6.05  | 1.35 | 5.00E-05 4.28E-04 | -- | Domain of unknown function (DUF1917) |
| EVM0004564 | 477.29 | 186.20| 1.36 | 5.00E-05 4.28E-04 | Lipid transport and metabolism | AMP-binding enzyme |
| EVM0007248 | 863.33 | 336.68| 1.36 | 4.50E-04 2.92E-03 | -- | RNA recognition motif. (a.k.a. RRM, RBD, or RNP domain) |
| EVM0008886 | 58.76  | 22.90 | 1.36 | 5.00E-05 4.28E-04 | -- | SAD/SRA domain |
| EVM0006868 | 746.83 | 290.39| 1.36 | 5.00E-05 4.28E-04 | General function prediction only | RNA recognition motif. (a.k.a. RRM, RBD, or RNP domain) |
| EVM0002629 | 45.92  | 17.85 | 1.36 | 5.00E-05 4.28E-04 | -- | FAD binding domain |
| EVM0002732 | 51.09  | 19.86 | 1.36 | 2.00E-04 1.46E-03 | Function unknown | Cysteine-rich secretory protein family |
| EVM0011327 | 15.28  | 5.94  | 1.36 | 9.50E-04 5.46E-03 | Replication, recombination and repair | AAA domain |
| ID         | Score 1 | Score 2 | Score 3 | Score 4 | Score 5 | Description                                                                 |
|------------|---------|---------|---------|---------|---------|-----------------------------------------------------------------------------|
| EVM0011859 | 10.80   | 4.18    | 1.37    | 2.50E-04| 1.77E-03| Energy production and conversion                                           |
| EVM0000427 | 5.76    | 2.23    | 1.37    | 2.00E-04| 1.46E-03| --                                                                          |
| EVM0011640 | 67.98   | 26.22   | 1.37    | 1.00E-04| 7.96E-04| --                                                                          |
| EVM0011507 | 58.74   | 22.60   | 1.38    | 5.00E-05| 4.28E-04| Nuclear pore component                                                      |
| EVM0010293 | 28.32   | 10.86   | 1.38    | 2.50E-03| 1.22E-02| --                                                                          |
| EVM0009910 | 92.39   | 35.31   | 1.39    | 5.00E-05| 4.28E-04| Chromatin structure and dynamics                                            |
| EVM0010917 | 50.23   | 19.15   | 1.39    | 5.00E-05| 4.28E-04| Histone deacetylase domain                                                  |
| EVM0011948 | 45.34   | 17.28   | 1.39    | 1.00E-04| 7.96E-04| Cytoskeleton                                                               |
| EVM0002530 | 4.23    | 1.61    | 1.39    | 6.00E-03| 2.49E-02| --                                                                          |
| EVM0000251 | 29.61   | 11.23   | 1.40    | 5.00E-05| 4.28E-04| --                                                                          |
| EVM0011035 | 2106.60 | 797.44  | 1.40    | 5.50E-04| 3.46E-03| 50S ribosome-binding GTPase                                                |
| EVM0011884 | 579.56  | 218.78  | 1.41    | 1.50E-04| 1.14E-03| RNA recognition motif. (a.k.a. RRM, RBD, or RNP domain)                     |
| EVM0009297 | 127.29  | 47.98   | 1.41    | 5.00E-05| 4.28E-04| OPT oligopeptide transporter protein                                         |
| EVM0005372 | 11.46   | 4.32    | 1.41    | 5.00E-04| 3.19E-03| Amino acid transport and metabolism                                         |
| EVM0006268 | 78.69   | 29.59   | 1.41    | 5.00E-05| 4.28E-04| Amino acid permease                                                        |
| EVM0007989 | 232.41  | 86.98   | 1.42    | 5.00E-05| 4.28E-04| Alpha/beta hydrolase family                                                |
| EVM0002464 | 88.49   | 33.10   | 1.42    | 5.00E-05| 4.28E-04| Aminotransferase class I and II                                             |
| Accession       | EVM0001436  | EVM0002514  | EVM0001578 | EVM0009234 | EVM0009335 | EVM0007131 | EVM0010856 | EVM0009427 | EVM0002441 | EVM0000195 | EVM0005872 | EVM0004414 | EVM0002758 | EVM0003073 | EVM0003020 | EVM0009456 | EVM0008782 | EVM0007527 | EVM0009456 | EVM0008782 |
|----------------|------------|------------|------------|------------|------------|------------|------------|------------|------------|------------|------------|------------|------------|------------|------------|------------|------------|------------|------------|------------|
| **Score**      | 64.87      | 86.13      | 95.27      | 46.42      | 30.68      | 10.81      | 46.63      | 12.77      | 17.79      | 12.77      | 495.49     | 19.64      | 8.99       | 9.86       | 51.20      | 3.68       | 271.98     | 77.43      | 21.38      |
| **Bits**       | 24.25      | 32.19      | 35.57      | 17.32      | 11.44      | 4.01       | 17.30      | 4.73       | 6.58       | 4.71       | 182.71     | 7.24       | 3.31       | 3.63       | 18.83      | 1.35       | 99.60      | 28.33      | 7.82       |
| **E-value**    | 1.42       | 1.42       | 1.42       | 1.42       | 1.42       | 1.43       | 1.43       | 1.43       | 1.43       | 1.44       | 1.44       | 1.44       | 1.44       | 1.44       | 1.45       | 1.45       | 1.45       | 1.45       |
| **Fold Change**| 5.00E-05   | 5.00E-05   | 5.00E-05   | 5.00E-05   | 1.00E-04   | 1.25E-03   | 5.00E-05   | 1.50E-04   | 1.00E-04   | 5.00E-05   | 5.00E-05   | 5.00E-05   | 7.15E-03   | 9.50E-04   | 2.50E-04   | 9.95E-03   | 5.00E-05   | 5.00E-05   |
| **Fold Change**| 4.28E-04   | 4.28E-04   | 4.28E-04   | 4.28E-04   | 7.96E-04   | 6.87E-03   | 4.28E-04   | 7.96E-04   | 7.96E-04   | 4.28E-04   | 4.28E-04   | 4.28E-04   | 2.86E-02   | 5.46E-03   | 1.77E-03   | 3.74E-02   | 4.28E-04   | 4.28E-04   |
| **Function**   | WD domain, G-beta repeat | Uncharacterised protein family (UPF0014) | Enolase C-terminal domain-like | General function prediction only | 3'-5' exonuclease | Serine carboxypeptidase S28 | Polysaccharide deacetylase | Intracellular trafficking, secretion, and vesicular transport | Region in Clathrin and VPS | MCM2/3/5 family |
| EVM0007192 | 60.56 | 22.11 | 1.45 | 5.00E-05 4.28E-04 | Cell cycle control, cell division, chromosome partitioning |
|-------------|-------|-------|------|-------------------|-----------------------------------------------------------|
| EVM0010231 | 58.52 | 21.28 | 1.46 | 5.00E-05 4.28E-04 | --                                                          |
| EVM0006788 | 199.54| 72.05 | 1.47 | 5.00E-05 4.28E-04 | --                                                          |
| EVM0003473 | 117.28| 42.34 | 1.47 | 5.00E-05 4.28E-04 | Amino acid transport and metabolism                         |
| EVM0006057 | 34.64 | 12.47 | 1.47 | 4.00E-04 2.65E-03 | Intracellular trafficking, secretion, and vesicular transport |
| EVM0000709 | 144.09| 51.84 | 1.47 | 2.55E-03 1.24E-02 | --                                                          |
| EVM0010611 | 153.17| 54.99 | 1.48 | 5.00E-05 4.28E-04 | --                                                          |
| EVM0002114 | 223.28| 80.09 | 1.48 | 5.00E-05 4.28E-04 | Posttranslational modification, protein turnover, chaperones |
| EVM0003304 | 6.83  | 2.44  | 1.48 | 5.40E-03 2.29E-02 | Secondary metabolites biosynthesis, transport and catabolism |
| EVM0011756 | 321.37| 114.78| 1.49 | 5.00E-05 4.28E-04 | --                                                          |
| EVM0002138 | 123.74| 44.14 | 1.49 | 1.00E-04 7.96E-04 | --                                                          |
| EVM0002687 | 21.60 | 7.66  | 1.50 | 5.30E-03 2.26E-02 | Transcription                                              |
| EVM0005761 | 33.73 | 11.95 | 1.50 | 5.00E-05 4.28E-04 | --                                                          |
| EVM0004822 | 75.84 | 26.78 | 1.50 | 5.00E-05 4.28E-04 | --                                                          |
| EVM0007451 | 105.78| 37.32 | 1.50 | 5.00E-05 4.28E-04 | --                                                          |
| EVM0006103 | 107.14| 37.75 | 1.50 | 5.00E-05 4.28E-04 | --                                                          |
| EVM0000412 | 141.15 | 49.65 | 1.51 | 5.00E-05 | 4.28E-04 | Thiamine pyrophosphate enzyme, N-terminal TPP binding domain |
| EVM0005905 | 24.21  | 8.51  | 1.51 | 5.00E-05 | 4.28E-04 | Signal transduction mechanisms |
| EVM0001718 | 10.11  | 3.54  | 1.51 | 1.00E-04 | 7.96E-04 | Protein kinase domain |
| EVM0011525 | 154.40 | 54.08 | 1.51 | 5.00E-05 | 4.28E-04 | Cell cycle control, cell division, chromosome partitioning |
| EVM0002121 | 25.61  | 8.95  | 1.52 | 5.00E-05 | 4.28E-04 | AAA domain |
| EVM0003122 | 41.25  | 14.40 | 1.52 | 5.00E-05 | 4.28E-04 | Domain of unknown function (DUF3554) |
| EVM0005845 | 45.97  | 16.02 | 1.52 | 5.00E-05 | 4.28E-04 | Domain of unknown function (DUF4470) |
| EVM0000372 | 2.12   | 0.74  | 1.52 | 1.20E-02 | 4.33E-02 | Eukaryotic aspartyl protease |
| EVM0005118 | 57.35  | 19.84 | 1.53 | 5.00E-05 | 4.28E-04 | Urease alpha-subunit, N-terminal domain |
| EVM0005203 | 45.67  | 15.76 | 1.54 | 5.00E-05 | 4.28E-04 | Intracellular trafficking, secretion, and vesicular transport |
| EVM0008335 | 59.07  | 20.26 | 1.54 | 5.00E-05 | 4.28E-04 | Function unknown |
| EVM0009751 | 2.19   | 0.75  | 1.54 | 2.00E-04 | 1.46E-03 | Protein of unknown function (DUF3414) |
| EVM0002937 | 148.90 | 50.94 | 1.55 | 5.00E-05 | 4.28E-04 | -- |


| EVM0000347 | 285.86 | 97.62 | 1.55 | 5.00E-05 | 4.28E-04 | -- | -- |
| EVM0010784 | 22.61  | 7.72  | 1.55 | 5.00E-05 | 4.28E-04 | -- | -- |
| EVM0000530 | 33.76  | 11.51 | 1.55 | 5.00E-05 | 4.28E-04 | Function unknown | Ribosome 60S biogenesis N-terminal |
| EVM0010721 | 5.31   | 1.81  | 1.56 | 8.55E-03 | 3.31E-02 | -- | -- |
| EVM0007836 | 8.30   | 2.82  | 1.56 | 8.50E-04 | 4.98E-03 | -- | -- |
| EVM0008522 | 63.57  | 21.55 | 1.56 | 5.00E-05 | 4.28E-04 | Energy production and conversion | FAD dependent oxidoreductase |
| EVM0006409 | 9.70   | 3.28  | 1.56 | 5.00E-05 | 4.28E-04 | -- | HNH endonuclease |
| EVM0002986 | 66.42  | 22.45 | 1.56 | 5.00E-05 | 4.28E-04 | Cytoskeleton | Kinesin motor domain |
| EVM0000884 | 165.55 | 55.95 | 1.57 | 5.00E-05 | 4.28E-04 | Lipid transport and metabolism | AMP-binding enzyme |
| EVM0011719 | 8.28   | 2.80  | 1.57 | 5.00E-05 | 4.28E-04 | General function prediction only | WD domain, G-beta repeat |
| EVM0006669 | 251.79 | 84.91 | 1.57 | 5.00E-05 | 4.28E-04 | General function prediction only | HMG (high mobility group) box |
| EVM0011466 | 33.08  | 11.14 | 1.57 | 5.00E-05 | 4.28E-04 | -- | -- |
| EVM0012194 | 158.51 | 53.35 | 1.57 | 5.00E-05 | 4.28E-04 | -- | Amidohydrolase |
| EVM0008994 | 2.48   | 0.83  | 1.57 | 4.90E-03 | 2.12E-02 | -- | -- |
| EVM0008059 | 238.02 | 79.59 | 1.58 | 5.00E-05 | 4.28E-04 | Carbohydrate transport and metabolism | Domain of unknown function (DUF1793) |
| EVM0010213 | 7709.96| 2576.26| 1.58| 2.55E-03| 1.24E-02| -- | -- |
| EVM0001466 | 13.98  | 4.67  | 1.58 | 5.00E-05 | 4.28E-04 | Posttranslational modification, protein turnover, chaperones | Peptidase family M48 |
| Genbank ID     | Value1 | Value2 | Value3 | Value4 | Value5 | Value6 | Class Description                                                                 |
|---------------|--------|--------|--------|--------|--------|--------|----------------------------------------------------------------------------------|
| EVM0001750    | 10.95  | 3.65   | 1.58   | 5.00E-05 | 4.28E-04 | Amino acid transport and metabolism                                               |
| EVM0010994    | 105.60 | 35.10  | 1.59   | 5.00E-05 | 4.28E-04 | --                                              | Pro-kumamolisin, activation domain                                               |
| EVM0005775    | 30.09  | 10.00  | 1.59   | 5.00E-05 | 4.28E-04 | --                                              | FHA domain                                                                     |
| EVM0011821    | 710.80 | 235.83 | 1.59   | 5.00E-05 | 4.28E-04 | --                                              | Glycosyl hydrolase family 71                                                   |
| EVM0007336    | 235.59 | 78.15  | 1.59   | 5.00E-05 | 4.28E-04 | Posttranslational modification, protein turnover, chaperones                      | AhpC/TSA family                                                               |
| EVM0001317    | 30.70  | 10.10  | 1.60   | 5.00E-05 | 4.28E-04 | --                                              | SNF2 family N-terminal domain                                                   |
| EVM0006660    | 601.05 | 197.09 | 1.61   | 5.00E-05 | 4.28E-04 | --                                              | --                                                                             |
| EVM0002736    | 103.75 | 34.02  | 1.61   | 5.00E-05 | 4.28E-04 | Cytoskeleton                                                                                 |
| EVM0006506    | 20.27  | 6.61   | 1.62   | 8.00E-04 | 4.73E-03 | #N/A                                                                                     |
| EVM0004599    | 29.91  | 9.75   | 1.62   | 5.00E-05 | 4.28E-04 | Lipid transport and metabolism                                                          | Phosphatidylserine decarboxylase                                               |
| EVM0011882    | 66.19  | 21.58  | 1.62   | 5.00E-05 | 4.28E-04 | Cytoskeleton                                                                                 |
| EVM0007579    | 196.92 | 63.66  | 1.63   | 5.00E-05 | 4.28E-04 | --                                              | Variant SH3 domain                                                             |
| EVM0002904    | 103.97 | 33.61  | 1.63   | 5.00E-05 | 4.28E-04 | --                                              | HEAT repeat                                                                   |
| EVM0003583    | 661.53 | 213.60 | 1.63   | 2.00E-04 | 1.46E-03 | --                                              | --                                                                            |
| EVM0005111    | 1740.83| 561.42 | 1.63   | 2.00E-04 | 1.46E-03 | --                                              | Cellulase (glycosyl hydrolase family 5)                                         |
| EVM0008739    | 374.83 | 120.64 | 1.64   | 5.00E-05 | 4.28E-04 | Energy production and conversion                                                        | Carbamoyl-phosphate synthase L chain, ATP binding domain                     |
| EVM0012202    | 1206.18| 388.20 | 1.64   | 5.00E-05 | 4.28E-04 | --                                              | --                                                                            |
| EVM0009418    | 62.33  | 20.04  | 1.64   | 5.00E-05 | 4.28E-04 | --                                              | --                                                                            |
| EVM0006985    | 51.97  | 16.63  | 1.64   | 5.00E-05 | 4.28E-04 | --                                              | --                                                                            |
| EVM0004642 | 65.86  | 21.05  | 1.65  | 5.00E-05  | 4.28E-04   | -- | Diaphanous GTPase-binding Domain |
| EVM0010778 | 10.98  | 3.50   | 1.65  | 5.00E-05  | 4.28E-04   | -- | SNF2 family N-terminal domain |
| EVM0009921 | 7.20   | 2.29   | 1.65  | 5.00E-04  | 3.19E-03   | -- | -- |
| EVM0010470 | 198.15 | 62.94  | 1.65  | 5.00E-05  | 4.28E-04   | Posttranslational modification, protein turnover, chaperones |
| EVM0008259 | 791.35 | 251.28 | 1.66  | 5.00E-05  | 4.28E-04   | -- | Putative oxidoreductase C terminal |
| EVM0002022 | 148.92 | 47.18  | 1.66  | 5.00E-05  | 4.28E-04   | -- | Glycosyl transferase family group 2 |
| EVM0002727 | 1259.94| 397.01 | 1.67  | 5.00E-05  | 4.28E-04   | -- | Cupin |
| EVM0007570 | 26.15  | 8.24   | 1.67  | 5.00E-05  | 4.28E-04   | -- | Poly(ADP-ribose) polymerase catalytic domain |
| EVM0005588 | 55.71  | 17.53  | 1.67  | 5.00E-05  | 4.28E-04   | Function unknown | Cysteine-rich secretory protein family |
| EVM0001424 | 2085.62| 648.00 | 1.69  | 5.00E-05  | 4.28E-04   | Cytoskeleton | Dynein light chain type 1 |
| EVM0009616 | 46.58  | 14.45  | 1.69  | 2.00E-04  | 1.46E-03   | -- | Ribosomal protein S21 |
| EVM0005530 | 40.54  | 12.54  | 1.69  | 5.00E-05  | 4.28E-04   | -- | XFP N-terminal domain |
| EVM0008321 | 260.36 | 80.37  | 1.70  | 5.00E-05  | 4.28E-04   | General function prediction only | Major Facilitator Superfamily |
| EVM0006122 | 32.58  | 10.04  | 1.70  | 6.20E-03  | 2.56E-02   | -- | -- |
| EVM0006177 | 32.73  | 10.08  | 1.70  | 5.00E-05  | 4.28E-04   | Cytoskeleton | Kinesin motor domain |
| EVM0004411 | 24.56  | 7.56   | 1.70  | 5.00E-05  | 4.28E-04   | -- | Spc7 kinetochore protein |
| EVM0002125 | 8.30   | 2.55   | 1.71  | 5.00E-05  | 4.28E-04   | General function prediction only | Major Facilitator Superfamily |
| EVM0004972 | 13.31 | 4.06 | 1.71 | 5.00E-05 | 4.28E-04 | -- | -- |
| EVM0011205 | 378.12 | 115.24 | 1.71 | 5.00E-05 | 4.28E-04 | -- | Glycosyl hydrolase catalytic core |
| EVM0007580 | 380.76 | 115.15 | 1.73 | 5.00E-05 | 4.28E-04 | Cell wall/membrane/envelope biogenesis | Glycosyl transferases group 1 |
| EVM0011006 | 4.98 | 1.50 | 1.73 | 5.00E-05 | 4.28E-04 | -- | Protein of unknown function (DUF1524) |
| EVM0002859 | 52.56 | 15.76 | 1.74 | 5.00E-05 | 4.28E-04 | -- | non-SMC mitotic condensation complex subunit 1 |
| EVM0008227 | 41.23 | 12.26 | 1.75 | 5.00E-05 | 4.28E-04 | Replication, recombination and repair | MCM2/3/5 family |
| EVM0006381 | 33.01 | 9.81 | 1.75 | 5.00E-05 | 4.28E-04 | Cell cycle control, cell division, chromosome partitioning | PIF1-like helicase |
| EVM0003976 | 145.42 | 43.18 | 1.75 | 5.00E-05 | 4.28E-04 | Amino acid transport and metabolism | Conserved region in glutamate synthase |
| EVM0002409 | 30.62 | 9.02 | 1.76 | 5.00E-05 | 4.28E-04 | -- | -- |
| EVM0004677 | 131.80 | 38.71 | 1.77 | 5.00E-05 | 4.28E-04 | -- | Serine carboxypeptidase S28 |
| EVM0001331 | 27.81 | 8.17 | 1.77 | 5.00E-05 | 4.28E-04 | -- | Ankyrin repeats (many copies) |
| EVM0005614 | 92.97 | 27.28 | 1.77 | 5.00E-05 | 4.28E-04 | -- | -- |
| EVM0011462 | 34.17 | 10.00 | 1.77 | 5.00E-05 | 4.28E-04 | Intracellular trafficking, secretion, and vesicular transport | Exocyst complex subunit Sec15-like |
| EVM0008827 | 3.30 | 0.96 | 1.78 | 1.20E-02 | 4.32E-02 | -- | -- |
| EVM0011687 | 37.08 | 10.72 | 1.79 | 5.00E-05 | 4.28E-04 | Function unknown | Domain of unknown function (DUF3437) |
| EVM0008766  | 19.94 | 5.71 | 1.80 | 5.25E-03 | 2.24E-02 | -- | -- |
| EVM0005006  | 71.38 | 20.25| 1.82 | 5.00E-05 | 4.28E-04 | -- | -- |
| EVM0010840  | 13.56 | 3.84 | 1.82 | 5.00E-05 | 4.28E-04 | -- | -- |
| EVM0006629  | 43.15 | 12.20| 1.82 | 5.00E-05 | 4.28E-04 | Secondary metabolites biosynthesis, transport and catabolism | ABC transporter |
| EVM0008881  | 231.32| 65.30| 1.82 | 5.00E-05 | 4.28E-04 | -- | Glycosyl hydrolase family 3 N terminal domain |
| EVM0001947  | 5.52  | 1.55 | 1.83 | 2.25E-03 | 1.12E-02 | -- | -- |
| EVM0008628  | 32.71 | 9.17 | 1.83 | 5.00E-05 | 4.28E-04 | -- | -- |
| EVM0011867  | 37.29 | 10.42| 1.84 | 5.00E-05 | 4.28E-04 | General function prediction only | Haloacid dehalogenase-like hydrolase |
| EVM0003134  | 58.00 | 16.17| 1.84 | 5.00E-05 | 4.28E-04 | -- | -- |
| EVM0003929  | 11.97 | 3.34 | 1.84 | 5.00E-05 | 4.28E-04 | -- | Taurine catabolism dioxygenase TauD, TfdA family |
| EVM0004082  | 2.07  | 0.58 | 1.84 | 4.45E-03 | 1.96E-02 | -- | NADH:flavin oxidoreductase / NADH oxidase family |
| EVM0012261  | 7.22  | 2.00 | 1.85 | 5.00E-05 | 4.28E-04 | Replication, recombination and repair | MutS domain V |
| EVM0005557  | 73.60 | 20.38| 1.85 | 5.00E-05 | 4.28E-04 | -- | Nucleoporin subcomplex protein binding to Pom34 |
| EVM0008413  | 62.43 | 17.20| 1.86 | 5.00E-05 | 4.28E-04 | General function prediction only | ABC1 family |
| EVM0009035  | 69.82 | 19.15| 1.87 | 5.00E-05 | 4.28E-04 | -- | Non-repetitive/WGA-negative nucleoporin C-terminal |
| EVM0003987  | 25.53 | 7.00 | 1.87 | 6.15E-03 | 2.54E-02 | -- | -- |
| Accession | Start | End | Str. | E-value | E-value | Description | Function |
|-----------|-------|-----|------|---------|---------|-------------|----------|
| EVM0005101 | 4.27 | 1.17 | 1.87 | 7.00E-04 | 4.23E-03 | Replication, recombination and repair | HhH-GPD superfamily base excision DNA repair protein |
| EVM0006078 | 64.61 | 17.70 | 1.87 | 8.50E-04 | 4.98E-03 | -- | Cytochrome c oxidase assembly protein COX16 |
| EVM0001207 | 16.38 | 4.45 | 1.88 | 1.50E-04 | 1.14E-03 | -- | -- |
| EVM0001579 | 37.82 | 10.27 | 1.88 | 5.00E-05 | 4.28E-04 | General function prediction only | Family of unknown function (DUF706) |
| EVM0007751 | 100.21 | 27.07 | 1.89 | 5.00E-05 | 4.28E-04 | -- | -- |
| EVM0009974 | 84.98 | 22.85 | 1.90 | 5.00E-05 | 4.28E-04 | Signal transduction mechanisms | GTPase-activator protein for Ras-like GTPase |
| EVM0004725 | 89.52 | 23.99 | 1.90 | 5.00E-05 | 4.28E-04 | Chromatin structure and dynamics | linker histone H1 and H5 family |
| EVM0001562 | 143.45 | 38.42 | 1.90 | 5.00E-05 | 4.28E-04 | -- | Alpha amylase, catalytic domain |
| EVM0003796 | 20.10 | 5.38 | 1.90 | 5.00E-05 | 4.28E-04 | -- | -- |
| EVM0005846 | 6.02 | 1.61 | 1.90 | 7.25E-03 | 2.90E-02 | -- | -- |
| EVM0003022 | 7.83 | 2.09 | 1.91 | 5.00E-05 | 4.28E-04 | Amino acid transport and metabolism | FAD dependent oxidoreductase |
| EVM0001015 | 8.14 | 2.17 | 1.91 | 5.00E-05 | 4.28E-04 | -- | -- |
| EVM0005567 | 391.68 | 103.70 | 1.92 | 5.00E-05 | 4.28E-04 | Nucleotide transport and metabolism | Ribonucleotide reductase, small chain |
| EVM0002796 | 90.71 | 23.78 | 1.93 | 5.00E-05 | 4.28E-04 | -- | Permease for cytosine/purines, uracil, thiamine, allantoin |
| EVM0007397 | 18.02 | 4.72 | 1.93 | 5.00E-05 | 4.28E-04 | Function unknown | WD domain, G-beta repeat |
| EVM0010588 | 40.66 | 10.64 | 1.93 | 1.00E-04 | 7.96E-04 | -- | -- |
| EVM0009073 | 1.86 | 0.48 | 1.94 | 1.10E-02 | 4.04E-02 | -- | -- |
| EVM0001707 | 52.27 | 13.66 | 1.94 | 5.00E-05 | 4.28E-04 | -- | Nucleoporin Nup120/160 |
| Accession  | EVM0005021 | EVM0008746 | EVM0000515 | EVM0011435 | EVM0011675 | EVM0009298 | EVM0003928 | EVM0001737 | EVM0006249 | EVM0006340 | EVM0006417 | EVM0006417 | EVM0008978 | EVM0012190 |
|-----------|-------------|-------------|-------------|-------------|-------------|-------------|-------------|-------------|-------------|-------------|-------------|-------------|-------------|-------------|
| Scores    | 6.93        | 5.00E-05    | 61.62       | 56.24       | 37.64       | 65.31       | 2.72        | 64.51       | 158.85      | 78.81       | 2.33        | 40.19       | 23.38       | 3.47        |
| Functions | (1,95)      | (4.28E-04)  | (1.79)      | (1.96)      | (2.00)      | (2.00)      | (2.02)      | (2.04)      | (2.04)      | (2.05)      | (2.06)      | (2.06)      | (2.08)      | (2.09)      |
| Comments  | --          | --          | UvrD-like helicase C-terminal domain | Myosin head (motor domain) | Cytoskeleton | Dynein heavy chain and region D6 of dynein motor | --          | Carbohydrate transport and metabolism | Secondary metabolites biosynthesis, transport and catabolism | --          | --          | Cytochrome oxidase complex assembly protein 1 | SNF2 family N-terminal domain | ABC transporter transmembrane region |
| EVM0008911 | 12.80 | 2.99 | 2.10 | 5.00E-05 | 4.28E-04 | -- | -- |
|------------|-------|-------|-------|-----------|---------|-----|-----|
| EVM0000478 | 45.23 | 10.54 | 2.10 | 5.00E-05 | 4.28E-04 | Signal transduction mechanisms | Protein kinase domain |
| EVM0002287 | 93.86 | 21.71 | 2.11 | 3.25E-03 | 1.51E-02 | -- | Cytochrome P450 |
| EVM0008140 | 48.80 | 11.29 | 2.11 | 5.00E-05 | 4.28E-04 | -- | -- |
| EVM0002953 | 14.48 | 3.32  | 2.12 | 5.00E-05 | 4.28E-04 | -- | Fungalysin metallopeptidase (M36) |
| EVM0002414 | 53.22 | 12.09 | 2.14 | 5.00E-05 | 4.28E-04 | -- | -- |
| EVM0006225 | 138.68| 31.39 | 2.14 | 5.00E-05 | 4.28E-04 | -- | -- |
| EVM0007573 | 5359.43| 1206.28| 2.15 | 5.00E-05 | 4.28E-04 | -- | Fungal hydrophobin |
| EVM0011658 | 7.13  | 1.60  | 2.15 | 2.00E-04 | 1.46E-03 | Lipid transport and metabolism | Enoyl-CoA hydratase/isomerase family |
| EVM00004073| 28.42 | 6.24  | 2.19 | 7.90E-03 | 3.10E-02 | -- | SCP-2 sterol transfer family |
| EVM00002281| 68.12 | 14.92 | 2.19 | 5.00E-05 | 4.28E-04 | -- | -- |
| EVM00001058| 20.50 | 4.49  | 2.19 | 5.00E-05 | 4.28E-04 | -- | -- |
| EVM0011790 | 49.97 | 10.85 | 2.20 | 8.90E-03 | 3.41E-02 | General function prediction only | Ras family |
| EVM0011093 | 42.57 | 9.08  | 2.23 | 2.00E-03 | 1.01E-02 | Intracellular trafficking, secretion, and vesicular transport | SNARE domain |
| EVM0009599 | 5.50  | 1.16  | 2.25 | 5.00E-05 | 4.28E-04 | -- | TPR repeat |
| EVM0006476 | 546.56| 112.61| 2.28 | 5.00E-05 | 4.28E-04 | -- | LVIVD repeat |
| EVM0010488 | 49.03 | 10.05 | 2.29 | 5.00E-05 | 4.28E-04 | -- | -- |
| EVM0003467 | 597.63| 121.97| 2.29 | 5.00E-05 | 4.28E-04 | -- | -- |
| EVM0000453 | 711.90| 141.29| 2.33 | 5.00E-05 | 4.28E-04 | -- | -- |
| EVM0004723 | 16.45 | 3.12  | 2.40 | 4.00E-04 | 2.65E-03 | -- | -- |
| EVM0007392  | 78.61  | 14.88  | 2.40   | 5.00E-05 | 4.28E-04 | --                  | WSC domain |
| EVM0006479  | 40.01  | 7.56   | 2.40   | 5.00E-05 | 4.28E-04 | --                  | RecF/RecN/SMC N terminal domain |
| EVM0007712  | 48.98  | 9.10   | 2.43   | 5.00E-05 | 4.28E-04 | General function prediction only | Protein kinase domain |
| EVM0009049  | 16.16  | 3.00   | 2.43   | 5.00E-05 | 4.28E-04 | --                  | -- |
| EVM0007684  | 199.30 | 36.61  | 2.44   | 5.00E-05 | 4.28E-04 | General function prediction only | Major Facilitator Superfamily |
| EVM0008898  | 1826.72| 325.60 | 2.49   | 5.00E-05 | 4.28E-04 | --                  | -- |
| EVM0001811  | 1.24   | 0.21   | 2.53   | 1.13E-02 | 4.11E-02 | General function prediction only | Major Facilitator Superfamily |
| EVM0010018  | 118.90 | 20.46  | 2.54   | 5.00E-05 | 4.28E-04 | --                  | Fungal hydrophobin |
| EVM0007764  | 23.91  | 4.11   | 2.54   | 5.00E-05 | 4.28E-04 | --                  | SNF2 family N-terminal domain |
| EVM0006645  | 485.89 | 82.89  | 2.55   | 5.00E-05 | 4.28E-04 | --                  | -- |
| EVM0009189  | 4.10   | 0.70   | 2.56   | 2.30E-03 | 1.14E-02 | --                  | Pheromone A receptor |
| EVM0005744  | 12.23  | 2.07   | 2.56   | 5.00E-05 | 4.28E-04 | RNA processing and modification | AAA domain |
| EVM0008758  | 1.28   | 0.21   | 2.58   | 1.75E-03 | 9.08E-03 | --                  | -- |
| EVM0005145  | 30.58  | 4.98   | 2.62   | 1.60E-03 | 8.44E-03 | --                  | -- |
| EVM0000235  | 173.82 | 28.32  | 2.62   | 5.00E-05 | 4.28E-04 | --                  | Voltage-dependent anion channel |
| EVM0002747  | 1.62   | 0.25   | 2.67   | 2.00E-04 | 1.46E-03 | RNA processing and modification | DEAD/DEAH box helicase |
| EVM0002674  | 9.74   | 1.52   | 2.68   | 5.00E-05 | 4.28E-04 | Secondary metabolites biosynthesis, transport and catabolism | short chain dehydrogenase |
| EVM0002033  | 6.62   | 1.03   | 2.68   | 2.35E-03 | 1.16E-02 | #N/A                | #N/A |

*Note: Values are numerical data representing various functions and domains.*
| Accession   | E-value | Bit-score | Bias-corrected | Domain                                                                 |
|------------|---------|-----------|----------------|----------------------------------------------------------------------|
| EVM0003743 | 7.10    | 1.10      | 2.69           | 5.00E-05 4.28E-04 Carbohydrate transport and metabolism                |
| EVM0008010 | 4.63    | 0.71      | 2.70           | 4.25E-03 1.89E-02 --                                                 |
| EVM0005169 | 1355.12 | 206.52    | 2.71           | 5.00E-05 4.28E-04 -- Peptidase family M28                           |
| EVM0008755 | 63.02   | 8.99      | 2.81           | 5.00E-05 4.28E-04 -- Cupin domain                                   |
| EVM0011914 | 35.25   | 4.96      | 2.83           | 5.00E-05 4.28E-04 -- Cerato-platanin                                 |
| EVM0003089 | 18.34   | 2.50      | 2.87           | 1.00E-04 7.96E-04 General function prediction only                    |
| EVM0081112 | 670.65  | 90.26     | 2.89           | 5.00E-05 4.28E-04 Intracellular trafficking, secretion, and vesicular transport |
| EVM0011853 | 5.25    | 0.70      | 2.90           | 2.00E-04 1.46E-03 --                                                 |
| EVM0009981 | 3.71    | 0.49      | 2.91           | 4.50E-04 2.92E-03 --                                                 |
| EVM0003369 | 2.62    | 0.34      | 2.94           | 4.00E-04 2.65E-03 General function prediction only                    |
| EVM0000318 | 5.06    | 0.63      | 3.01           | 2.45E-03 1.20E-02 --                                                 |
| EVM0000933 | 5.16    | 0.63      | 3.04           | 5.00E-05 4.28E-04 Energy production and conversion                   |
| EVM000184  | 110.04  | 12.76     | 3.11           | 5.00E-05 4.28E-04 Signal transduction mechanisms                     |
| EVM0002115 | 30.58   | 3.36      | 3.19           | 5.00E-05 4.28E-04 -- Pregnancy-associated plasma protein-A          |
| EVM0008976 | 3.27    | 0.35      | 3.24           | 3.95E-03 1.77E-02 --                                                 |
| EVM0006874 | 30.80   | 2.54      | 3.60           | 5.00E-05 4.28E-04 --                                                 |
| EVM0009153 | 56.94   | 3.85      | 3.89           | 5.00E-05 4.28E-04 --                                                 |
| EVM0004142 | 1008.37 | 56.52 | 4.16 | 5.00E-05 | 4.28E-04 | Intracellular trafficking, secretion, and vesicular transport | Vacuolar sorting protein 39 domain 1 |
| EVM0001256 | 98.71    | 5.30  | 4.22 | 5.00E-05 | 4.28E-04 | -- | LVIVD repeat |
| EVM0007642 | 279.57   | 12.38 | 4.50 | 5.00E-05 | 4.28E-04 | -- | Pregnancy-associated plasma protein-A |
| EVM0010621 | 41.11    | 1.54  | 4.74 | 5.00E-05 | 4.28E-04 | -- | Deuterolysin metalloprotease (M35) family |
| EVM0008710 | 157.51   | 5.11  | 4.95 | 5.00E-05 | 4.28E-04 | Posttranslational modification, protein turnover, chaperones | Subtilase family |
| EVM0007266 | 1958.60  | 24.78 | 6.30 | 5.00E-05 | 4.28E-04 | -- | -- |
| gene ID       | R2 value | Z2 value  | log2(fold change) | p value     | q value     | KOG class                        | Pfam annotation                                      |
|--------------|----------|-----------|-------------------|-------------|-------------|----------------------------------|-------------------------------------------------------|
| EVM0007042   | 54.21    | 1542.16   | -4.83             | 5.00E-05    | 4.28E-04    | --                               | Hemerythrin HHE cation binding domain                |
| EVM0004233   | 14.27    | 375.05    | -4.72             | 5.00E-05    | 4.28E-04    | --                               | --                                                   |
| EVM0004083   | 1.94     | 48.99     | -4.66             | 4.90E-03    | 2.12E-02    | --                               | --                                                   |
| EVM0002148   | 32.23    | 669.23    | -4.38             | 5.00E-05    | 4.28E-04    | --                               | Uncharacterised protein family (UPF0197)            |
| EVM0005865   | 229.42   | 3627.32   | -3.98             | 5.00E-05    | 4.28E-04    | General function prediction only | Proteolipid membrane potential modulator            |
| EVM0003167   | 13.76    | 215.43    | -3.97             | 5.00E-05    | 4.28E-04    | --                               | --                                                   |
| EVM0012049   | 2.62     | 39.34     | -3.91             | 5.00E-05    | 4.28E-04    | --                               | --                                                   |
| EVM0001104   | 6.02     | 90.23     | -3.91             | 5.00E-05    | 4.28E-04    | --                               | --                                                   |
| EVM0011248   | 10.86    | 143.39    | -3.72             | 5.00E-04    | 3.19E-03    | --                               | --                                                   |
| EVM0001350   | 145.73   | 1864.80   | -3.68             | 5.00E-05    | 4.28E-04    | --                               | CsbD-like                                            |
| EVM0006251   | 3.49     | 41.06     | -3.56             | 5.00E-05    | 4.28E-04    | Function unknown                 | Surfeit locus protein 6                                |
| EVM0004031  | 10.64 | 124.33 | -3.55 | 5.00E-05 | 4.28E-04 | RNA processing and modification | Eukaryotic rRNA processing protein EBP2 |
|------------|-------|--------|--------|-----------|----------|---------------------------------|-----------------------------------------|
| EVM0005648 | 0.36  | 4.23   | -3.54  | 2.95E-03 | 1.40E-02 | --                              | --                                     |
| EVM0010264 | 19.41 | 215.88 | -3.48  | 5.00E-05 | 4.28E-04 | Function unknown                 | Thioesterase superfamily               |
| EVM0009090 | 25.19 | 266.06 | -3.40  | 5.00E-05 | 4.28E-04 | --                              | --                                     |
| EVM002926  | 93.62 | 956.06 | -3.35  | 5.00E-05 | 4.28E-04 | General function prediction only | Enoyl-(Acyl carrier protein) reductase |
| EVM008465  | 29.83 | 304.46 | -3.35  | 5.00E-05 | 4.28E-04 | RNA processing and modification | DEAD/DEAH box helicase                 |
| EVM003732  | 0.71  | 7.19   | -3.35  | 5.00E-05 | 4.28E-04 | --                              | --                                     |
| EVM0010786 | 12.59 | 126.97 | -3.33  | 5.00E-05 | 4.28E-04 | --                              | Zinc finger, C3HC4 type (RING finger) |
| EVM0010693 | 36.22 | 363.99 | -3.33  | 5.00E-05 | 4.28E-04 | --                              | --                                     |
| EVM0009709 | 8.36  | 83.39  | -3.32  | 5.00E-05 | 4.28E-04 | --                              | --                                     |
| EVM0001661 | 6.71  | 65.06  | -3.28  | 5.00E-05 | 4.28E-04 | General function prediction only | Kinase phosphorylation protein         |
| EVM0002081 | 2.03  | 18.86  | -3.21  | 5.00E-05 | 4.28E-04 | Signal transduction mechanisms   | FHA domain                             |
| ID            | Value1 | Value2 | Value3 | Value4 | Value5 | Value6 | Value7 | Value8 | Funcation                                                                 |
|--------------|--------|--------|--------|--------|--------|--------|--------|--------|---------------------------------------------------------------------------|
| EVM0010422   | 4.63   | 42.69  | -3.21  |        | 5.00E-05 | 4.28E-04 | Posttranslational modification, protein turnover, chaperones              |
| EVM0005078   | 1.14   | 10.08  | -3.14  |        | 5.00E-05 | 4.28E-04 | Cell cycle control, cell division, chromosome partitioning               |
| EVM0008966   | 22.04  | 194.61 | -3.14  |        | 5.00E-05 | 4.28E-04 | --                                                                           |
| EVM0005937   | 48.94  | 402.75 | -3.04  |        | 5.00E-05 | 4.28E-04 | --                                                                           |
| EVM0002682   | 47.46  | 389.54 | -3.04  |        | 5.00E-05 | 4.28E-04 | Transcription                                                               |
| EVM0005127   | 87.46  | 713.49 | -3.03  |        | 5.00E-05 | 4.28E-04 | --                                                                           |
| EVM0007507   | 13.98  | 112.47 | -3.01  |        | 5.00E-05 | 4.28E-04 | --                                                                           |
| EVM0003543   | 45.44  | 365.30 | -3.01  |        | 5.00E-05 | 4.28E-04 | --                                                                           |
| EVM0009623   | 26.53  | 208.31 | -2.97  |        | 5.00E-05 | 4.28E-04 | --                                                                           |
| EVM0006981   | 15.64  | 122.70 | -2.97  |        | 5.00E-05 | 4.28E-04 | --                                                                           |
| EVM0011068   | 37.34  | 291.05 | -2.96  |        | 5.00E-05 | 4.28E-04 | Defense mechanisms                                                          |
| EVM0007225   | 74.26  | 570.70 | -2.94  |        | 5.00E-05 | 4.28E-04 | Nuclear pore complex subunit Nro1                                          |

- **DnaJ domain**
- **HORMA domain**
- **RNA polymerase Rpb6**
- **Gamma interferon inducible lysosomal thiol reductase (GILT)**
- **Rrp15p**
- **Dual specificity phosphatase, catalytic domain**
- **Nuclear pore complex subunit Nro1**
| Gene             | Value1 | Value2 | Difference | Value3 | Value4 | Description                                                                 |
|------------------|--------|--------|------------|--------|--------|----------------------------------------------------------------------------|
| EVM0011230       | 12.94  | 98.61  | -2.93      | 5.00E-05 | 4.28E-04 | SNARE associated Golgi protein                                              |
| EVM0001863       | 0.24   | 1.78   | -2.92      | 6.75E-03 | 2.74E-02 | --                                                                         |
| EVM0011786       | 10.99  | 81.86  | -2.90      | 5.00E-05 | 4.28E-04 | --                                                                         |
| EVM0006622       | 6.66   | 49.23  | -2.89      | 5.00E-05 | 4.28E-04 | --                                                                         |
| EVM0000282       | 157.30 | 1159.63| -2.88      | 5.00E-05 | 4.28E-04 | --                                                                         |
| EVM0004965       | 2.58   | 18.91  | -2.88      | 5.00E-05 | 4.28E-04 | Function unknown Tho complex subunit 7                                   |
| EVM0008830       | 59.83  | 434.89 | -2.86      | 5.00E-05 | 4.28E-04 | Defense mechanisms Dual specificity phosphatase, catalytic domain           |
| EVM0002451       | 2.84   | 20.22  | -2.83      | 5.00E-05 | 4.28E-04 | --                                                                         |
| EVM0004346       | 363.40 | 2552.93| -2.81      | 5.00E-05 | 4.28E-04 | --                                                                         |
| EVM0005353       | 2.27   | 15.84  | -2.80      | 5.00E-05 | 4.28E-04 | Posttranslational modification, protein turnover, chaperones               |
| EVM0008889       | 0.27   | 1.84   | -2.79      | 9.00E-04 | 5.22E-03 | --                                                                         |
| EVM0006626       | 45.70  | 312.50 | -2.77      | 5.00E-05 | 4.28E-04 | --                                                                         |
| EVM0002754 | 10.25 | 69.76  | -2.77 | 5.00E-05 | 4.28E-04 | General function prediction only | Ankyrin repeats (3 copies) |
| EVM0007670 | 22.98 | 153.28 | -2.74 | 5.00E-05 | 4.28E-04 | -- | Domain of unknown function (DUF4112) |
| EVM0008891 | 7.44  | 49.34  | -2.73 | 5.00E-05 | 4.28E-04 | Amino acid transport and metabolism | Histidine biosynthesis protein |
| EVM0006174 | 4.08  | 26.94  | -2.72 | 5.00E-05 | 4.28E-04 | -- | -- |
| EVM0001964 | 7.02  | 46.30  | -2.72 | 5.00E-05 | 4.28E-04 | -- | -- |
| EVM0009876 | 8.31  | 54.78  | -2.72 | 5.00E-05 | 4.28E-04 | Translation, ribosomal structure and biogenesis | eRF1 domain 1 |
| EVM0006028 | 88.99 | 581.35 | -2.71 | 5.00E-05 | 4.28E-04 | -- | -- |
| EVM0001246 | 8.49  | 55.45  | -2.71 | 5.00E-05 | 4.28E-04 | -- | -- |
| EVM0000819 | 3.21  | 20.74  | -2.69 | 5.00E-05 | 4.28E-04 | Transcription | SNF2 family N-terminal domain |
| EVM0008113 | 12.51 | 80.57  | -2.69 | 5.00E-05 | 4.28E-04 | -- | FAD binding domain |
| EVM0003361 | 9.42  | 59.91  | -2.67 | 5.00E-05 | 4.28E-04 | -- | Lipoxygenase |
| EVM0009807 | 1276.43 | 7974.27 | -2.64 | 5.00E-05 | 4.28E-04 | -- | Mitochondrial F1-F0 ATP synthase subunit F of fungi |
| EVM0004307 | 0.69  | 4.27   | -2.63 | 7.95E-03 | 3.12E-02 | Carbohydrate transport and metabolism | Glycosyl hydrolase family 47 |
| EVM0009589 | 23.21 | 143.12 | -2.62 | 5.00E-05 | 4.28E-04 | -- | -- |
| EVM0004635 | 75.47 | 464.42 | -2.62 | 5.00E-05 | 4.28E-04 | -- | -- |
| EVM0000142 | 4.07  | 25.04  | -2.62 | 5.00E-05 | 4.28E-04 | -- | Putative phosphatase regulatory subunit |
| EVM0010870 | 14.22 | 87.23  | -2.62 | 5.00E-05 | 4.28E-04 | -- | Conidiation protein 6 |
| EVM0004767 | 103.26| 633.44 | -2.60 | 1.60E-03 | 8.44E-03 | -- | 4F5 protein family |
| EVM0008562 | 142.27| 865.07 | -2.60 | 5.00E-05 | 4.28E-04 | -- | -- |
| EVM0004053 | 97.38 | 589.80 | -2.60 | 5.00E-05 | 4.28E-04 | -- | -- |
| EVM0004085 | 4.00  | 24.19  | -2.59 | 7.00E-04 | 4.23E-03 | Posttranslational modification, protein turnover, chaperones | FKBP-type peptidyl-prolyl cis-trans isomerase |
| EVM0004297 | 21.23 | 128.12 | -2.59 | 5.00E-05 | 4.28E-04 | -- | BTG family |
| EVM0011879 | 18.02 | 107.65 | -2.58 | 5.00E-05 | 4.28E-04 | General function prediction only | -- |
| EVM0007146 | 732.45| 4368.04| -2.58 | 5.00E-05 | 4.28E-04 | -- | -- |
| EVM0006195 | 13.98 | 82.97  | -2.57 | 5.00E-05 | 4.28E-04 | -- | pre-mRNA splicing factor component |
| Accession   | Value1 | Value2 | Value3 | Value4 | Score1 | Score2 | Score3 | Score4 | Function                                                                 |
|-------------|--------|--------|--------|--------|--------|--------|--------|--------|--------------------------------------------------------------------------|
| EVM0009852  | 10.78  | 63.41  | -2.56  |        | 5.00E-05 | 4.28E-04 | Transcription | Homeobox domain |
| EVM0004221  | 6.81   | 40.02  | -2.56  |        | 5.00E-05 | 4.28E-04 | --        | --                                            |
| EVM0000467  | 2.39   | 14.03  | -2.55  |        | 5.00E-05 | 4.28E-04 | --        | --                                            |
| EVM0006068  | 2.92   | 17.08  | -2.55  |        | 5.00E-05 | 4.28E-04 | --        | bZIP transcription factor |
| EVM0003318  | 27.53  | 159.23 | -2.53  |        | 5.00E-05 | 4.28E-04 | --        | Autophagy protein 16 (ATG16) |
| EVM0008586  | 12.87  | 74.08  | -2.53  |        | 5.00E-05 | 4.28E-04 | --        | Chromatin remodelling complex Rsc7/Swp82 subunit |
| EVM0003528  | 80.61  | 456.82 | -2.50  |        | 5.00E-05 | 4.28E-04 | --        | --                                            |
| EVM0011013  | 11.45  | 64.79  | -2.50  |        | 3.60E-03 | 1.64E-02 | Function unknown | COQ9                                      |
| EVM0005600  | 41.83  | 236.25 | -2.50  |        | 5.00E-05 | 4.28E-04 | --        | Acetokinase family |
| EVM0007894  | 2.34   | 13.22  | -2.50  |        | 7.50E-04 | 4.49E-03 | General function prediction only | Zinc finger, C2H2 type |
| EVM0001814  | 5417.96| 30257.30| -2.48 |        | 5.00E-04 | 4.28E-03 | --        | Ricin-type beta-trefoil lectin domain-like |
| EVM0002391  | 207.59 | 1159.11| -2.48  |        | 5.00E-05 | 4.28E-04 | --        | --                                            |
| EVM0003241  | 30.80  | 171.23 | -2.47  |        | 5.00E-05 | 4.28E-04 | --        | Helix-loop-helix DNA-binding domain |
| EVM0004958 | 9.86  | 54.76 | -2.47 | 5.00E-05 | 4.28E-04 | -- | Regulator of G protein signaling domain |
| EVM0009404 | 12.49 | 69.28 | -2.47 | 5.00E-05 | 4.28E-04 | General function prediction only | Dip2/Utp12 Family |
| EVM0001738 | 348.42| 1928.15| -2.47 | 5.00E-05 | 4.28E-04 | Lipid transport and metabolism | Phophatidylinerine decarboxylase |
| EVM0009103 | 5.56  | 30.53 | -2.46 | 5.00E-05 | 4.28E-04 | -- | Pheromone A receptor |
| EVM0006335 | 68.22 | 372.66| -2.45 | 5.00E-05 | 4.28E-04 | -- | -- |
| EVM0001319 | 2.47  | 13.51 | -2.45 | 5.00E-05 | 4.28E-04 | -- | -- |
| EVM0005139 | 160.92| 877.27| -2.45 | 5.00E-05 | 4.28E-04 | -- | -- |
| EVM0000151 | 186.42| 1015.80| -2.45 | 5.00E-05 | 4.28E-04 | Lipid transport and metabolism | Cytochrome b5-like Heme/Steroid binding domain |
| EVM0007132 | 0.60  | 3.26  | -2.45 | 5.00E-05 | 4.28E-04 | -- | -- |
| EVM0000062 | 20.77 | 113.10| -2.45 | 5.00E-05 | 4.28E-04 | -- | -- |
| EVM0011432 | 9.06  | 49.27 | -2.44 | 5.00E-05 | 4.28E-04 | Lipid transport and metabolism | SacI homology domain |
| EVM0003828 | 9.87  | 53.54 | -2.44 | 5.00E-05 | 4.28E-04 | -- | Membrane bound O-acyl transferase family |
| EVM0005254 | 26.67 | 144.42| -2.44 | 5.00E-05 | 4.28E-04 | -- | -- |
| EVM0009995 | 4.67  | 25.30 | -2.44 | 5.00E-05 | 4.28E-04 | RNA processing and modification | WD domain, G-beta repeat |
| EVM0001452 | 6.49  | 35.11 | -2.43 | 5.00E-05 | 4.28E-04 | -- | -- |
| EVM0010446 | 18.81 | 101.30| -2.43 | 5.00E-05 | 4.28E-04 | Transcription | Homeobox KN domain |
| EVM0010589 | 85.97 | 462.72| -2.43 | 5.00E-05 | 4.28E-04 | -- | bZIP transcription factor |
| EVM0000264 | 1.10  | 5.88  | -2.41 | 5.00E-05 | 4.28E-04 | -- | -- |
| EVM0004461 | 14.63 | 77.34 | -2.40 | 5.00E-05 | 4.28E-04 | -- | Putative oxidoreductase C terminal |
| EVM0007517 | 55.71 | 294.22| -2.40 | 5.00E-05 | 4.28E-04 | -- | -- |
| EVM0009031 | 3.81  | 20.03 | -2.40 | 5.00E-05 | 4.28E-04 | -- | Glycosyl hydrolases family 43 |
| EVM0002711 | 17.89 | 93.88 | -2.39 | 5.00E-05 | 4.28E-04 | General function prediction only | La domain |
| EVM0006820 | 19.02 | 99.54 | -2.39 | 5.00E-05 | 4.28E-04 | -- | -- |
| EVM0009591 | 9.10  | 47.61 | -2.39 | 5.00E-05 | 4.28E-04 | Amino acid transport and metabolism | Homocysteine S-methyltransferase |
| EVM0006723 | 135.41| 704.37| -2.38 | 5.00E-05 | 4.28E-04 | -- | Conidiation protein 6 |
| EVM0003267 | 7123.21| 36948.10| -2.37 | 5.00E-05 | 4.28E-04 | -- | Conidiation protein 6 |
| EVM0000628 | 17.00 | 88.10 | -2.37 | 5.00E-05 | 4.28E-04 | -- | -- |
| EVM0003306 | 37.08 | 191.95 | -2.37 | 5.00E-05 | 4.28E-04 | Intracellular trafficking, secretion, and vesicular transport | Snf7 |
| EVM0000393 | 461.63 | 2377.79 | -2.36 | 5.00E-05 | 4.28E-04 | -- | -- |
| EVM0002561 | 3.46 | 17.79 | -2.36 | 5.00E-05 | 4.28E-04 | -- | -- |
| EVM0006187 | 1.96 | 10.02 | -2.36 | 5.00E-05 | 4.28E-04 | Transcription | HMG (high mobility group) box |
| EVM0011239 | 62.13 | 317.03 | -2.35 | 5.00E-05 | 4.28E-04 | -- | 50S ribosome-binding GTPase |
| EVM0001277 | 4.91 | 25.03 | -2.35 | 5.00E-05 | 4.28E-04 | -- | -- |
| EVM0011815 | 20.87 | 106.09 | -2.35 | 5.00E-05 | 4.28E-04 | -- | Membrane-associating domain |
| EVM0001122 | 27.42 | 139.35 | -2.35 | 5.00E-05 | 4.28E-04 | RNA processing and modification | Fibrillarin |
| EVM0004549 | 324.29 | 1646.46 | -2.34 | 5.00E-05 | 4.28E-04 | Lipid transport and metabolism | HIUase/Transthyretin family |
| EVM0003029 | 31.14 | 156.58 | -2.33 | 5.00E-05 | 4.28E-04 | Signal transduction mechanisms | Protein-tyrosine phosphatase |
| EVM0003631 | 4.22 | 21.16 | -2.33 | 6.00E-04 | 3.72E-03 | -- | -- |
| EVM0001591 | 1.17 | 5.80 | -2.31 | 5.00E-05 | 4.28E-04 | -- | -- |
| EVM0001076 | 6.27 | 30.99 | -2.31 | 5.00E-05 | 4.28E-04 | -- | -- |
| EVM0006881 | 16.18 | 79.95 | -2.30 | 5.00E-05 | 4.28E-04 | -- | NUDIX domain |
| EVM0005036 | 18.21 | 89.13 | -2.29 | 5.00E-05 | 4.28E-04 | -- | -- |
| EVM0011804 | 4.39 | 21.51 | -2.29 | 5.00E-05 | 4.28E-04 | -- | -- |
| EVM0012165 | 3.25 | 15.87 | -2.29 | 1.04E-02 | 3.87E-02 | -- | -- |
| EVM0006689 | 14.87 | 72.27 | -2.28 | 5.00E-05 | 4.28E-04 | General function prediction only | -- |
| EVM0005265 | 47.44 | 230.58 | -2.28 | 5.00E-05 | 4.28E-04 | -- | -- |
| EVM0004866 | 158.25 | 768.83 | -2.28 | 5.00E-05 | 4.28E-04 | Function unknown | Uncharacterised protein family (UPF0121) |
| EVM0007661 | 8.98 | 43.54 | -2.28 | 5.00E-05 | 4.28E-04 | -- | C2 domain |
| EVM0005795 | 6.06 | 29.33 | -2.28 | 5.00E-05 | 4.28E-04 | Chromatin structure and dynamics | Core histone H2A/H2B/H3/H4 |
| EVM0010440 | 55.33 | 267.07 | -2.27 | 5.00E-05 | 4.28E-04 | -- | Cytochrome c/c1 heme lyase |
| EVM0007572 | 3.94 | 18.95 | -2.27 | 5.00E-05 | 4.28E-04 | -- | -- |
| EVM0004071 | 17.57 | 84.50 | 2.27 | 5.00E-05 | 4.28E-04 | Transcription | GATA zinc finger |
| EVM0005110 | 30.25 | 145.03 | 2.26 | 5.00E-05 | 4.28E-04 | Transcription | -- |
| EVM0002898 | 13.73 | 65.76 | 2.26 | 5.00E-05 | 4.28E-04 | Transcription | RNA polymerase Rpb3/RpoA insert domain |
| EVM0006542 | 52.74 | 251.58 | 2.25 | 5.00E-05 | 4.28E-04 | -- | Ricin-type beta-trefoil lectin domain |
| EVM0003700 | 0.27 | 1.27 | 2.25 | 5.00E-05 | 4.28E-04 | Replication, recombination and repair | DEAD/DEAH box helicase |
| EVM0012086 | 56.64 | 269.53 | 2.25 | 5.00E-05 | 4.28E-04 | Carbohydrate transport and metabolism | Major Facilitator Superfamily |
| EVM0010113 | 29.57 | 139.57 | 2.24 | 5.00E-05 | 4.28E-04 | -- | -- |
| EVM0005861 | 76.15 | 358.24 | 2.23 | 5.00E-05 | 4.28E-04 | Inorganic ion transport and metabolism | Catalase |
| EVM0001519 | 8.33 | 39.11 | 2.23 | 5.00E-05 | 4.28E-04 | -- | -- |
| EVM0008791 | 7.34 | 34.32 | 2.23 | 5.00E-05 | 4.28E-04 | Coenzyme transport and metabolism | Dephospho-CoA kinase |
| EVM0001342 | 31.02 | 144.47 | 2.22 | 5.00E-05 | 4.28E-04 | Defense mechanisms | TB2/DP1, HVA22 family |
| EVM0006749 | 19.04 | 88.66 | 2.22 | 5.00E-05 | 4.28E-04 | -- | Membrane bound O-acyl transferase family |
| EVM0009757 | 77.40 | 360.03 | 2.22 | 5.00E-05 | 4.28E-04 | -- | -- |
| Accession     | E-value | Score | p-value | Posttranslational Modification, Protein Turnover, Chaperones | General Function Prediction Only | Sugar (and Other) Transporter | Protein of Unknown Function (DUF1399) | F-box-like | Translation, Ribosomal Structure and Biogenesis | Brix Domain | Pregnancy-Associated Plasma Protein-A | General Function Prediction Only | Ras Family |
|---------------|---------|-------|---------|-------------------------------------------------------------|---------------------------------|--------------------------------|-------------------------------------|------------|----------------------------------------|-------------|-------------------------------------|---------------------------------|------------|
| EVM0007852    | 799.16  | 3705.76 | -2.21   | 5.00E-05, 4.28E-04                                          |                                 |                                |                                     |            |                                        |             |                                     |                                 |            |
| EVM0001566    | 2.46    | 11.30  | -2.20   | 5.00E-05, 4.28E-04                                          | General function prediction only|                                |                                     |            |                                        |             |                                     |                                 |            |
| EVM0010855    | 7.44    | 34.24  | -2.20   | 5.00E-05, 4.28E-04                                          |                                 |                                |                                     |            |                                        |             |                                     |                                 |            |
| EVM0007476    | 4.35    | 19.97  | -2.20   | 5.00E-05, 4.28E-04                                          |                                 |                                |                                     |            |                                        |             |                                     |                                 |            |
| EVM0002798    | 3.75    | 17.23  | -2.20   | 5.00E-05, 4.28E-04                                          |                                 |                                |                                     |            |                                        |             |                                     |                                 |            |
| EVM0007261    | 230.85  | 1057.83| -2.20   | 5.00E-05, 4.28E-04                                          |                                 |                                |                                     |            |                                        |             |                                     |                                 |            |
| EVM0004228    | 10.08   | 46.11  | -2.19   | 5.00E-05, 4.28E-04                                          | Translation, ribosomal structure and biogenesis |                                |                                     |            |                                        |             |                                     |                                 |            |
| EVM0012010    | 20.73   | 94.44  | -2.19   | 5.00E-05, 4.28E-04                                          |                                 |                                |                                     |            |                                        |             |                                     |                                 |            |
| EVM0007187    | 5.62    | 25.43  | -2.18   | 5.00E-05, 4.28E-04                                          |                                 |                                |                                     |            |                                        |             |                                     |                                 |            |
| EVM0002910    | 16.37   | 73.90  | -2.17   | 5.00E-05, 4.28E-04                                          |                                 |                                |                                     |            |                                        |             |                                     |                                 |            |
| EVM0002505    | 200.98  | 906.49 | -2.17   | 5.00E-05, 4.28E-04                                          |                                 |                                |                                     |            |                                        |             |                                     |                                 |            |
| EVM0001127    | 30.20   | 135.73 | -2.17   | 5.00E-05, 4.28E-04                                          | General function prediction only|                                |                                     |            |                                        |             |                                     |                                 |            |
| Accession     | M     | M       | E     | Percentage | Prediction   | Description                                                      |
|--------------|-------|---------|-------|------------|--------------|-----------------------------------------------------------------|
| EVM0008343   | 6.92  | 31.11   | -2.17 | 5.00E-05   | 4.28E-04     | --                                                              |
| EVM0009027   | 34.24 | 153.59  | -2.17 | 5.00E-05   | 4.28E-04     | --                                                              |
| EVM002076    | 184.01| 823.43  | -2.16 | 5.00E-05   | 4.28E-04     | --                                                              |
| EVM000746    | 17.86 | 79.61   | -2.16 | 5.00E-05   | 4.28E-04     | --                                                              |
| EVM006282    | 2.76  | 12.24   | -2.15 | 5.00E-05   | 4.28E-04     | --                                                              |
| EVM010633    | 739.01| 3281.28 | -2.15 | 5.00E-05   | 4.28E-04     | Energy production and conversion                                 |
| EVM005054    | 18.28 | 81.05   | -2.15 | 5.00E-05   | 4.28E-04     | General function prediction                                      |
| EVM002723    | 11.98 | 53.00   | -2.15 | 5.00E-05   | 4.28E-04     | --                                                              |
| EVM004341    | 99.35 | 438.56  | -2.14 | 5.00E-05   | 4.28E-04     | Function unknown                                                |
| EVM010935    | 16.37 | 72.16   | -2.14 | 5.00E-05   | 4.28E-04     | General function prediction                                      |
| EVM004778    | 62.74 | 276.37  | -2.14 | 5.00E-05   | 4.28E-04     | General function prediction                                      |
| EVM001996    | 39.85 | 175.41  | -2.14 | 5.00E-05   | 4.28E-04     | Translation, ribosomal structure and biogenesis                 |
| EVM0010318   | 3.61  | 15.87   | -2.14 | 5.00E-05   | 4.28E-04     | --                                                              |
| Accession   | Value 1 | Value 2 | Log2 Fold | Value 3 | Value 4 | Description                                                                 |
|-------------|---------|---------|------------|---------|---------|-----------------------------------------------------------------------------|
| EVM0005285  | 1034.32 | 4536.14 | -2.13      | 5.00E-05| 4.28E-04| --                                                                          |
| EVM0007323  | 429.64  | 1877.24 | -2.13      | 5.00E-05| 4.28E-04| Function unknown                                                            |
|             |         |         |            |         |         | Domain of unknown function (DUF543)                                        |
| EVM0009720  | 8.79    | 38.33   | -2.12      | 5.00E-05| 4.28E-04| Cell cycle control, cell division, chromosome partitioning                 |
|             |         |         |            |         |         | LYAR-type C2HC zinc finger                                                 |
| EVM0008871  | 56.73   | 246.60  | -2.12      | 5.00E-05| 4.28E-04| General function prediction only                                           |
|             |         |         |            |         |         | Ras family                                                                  |
| EVM0002707  | 0.92    | 4.00    | -2.11      | 8.05E-03| 3.15E-02| --                                                                          |
|             |         |         |            |         |         | zinc-RING finger domain                                                    |
| EVM0008242  | 1.48    | 6.41    | -2.11      | 3.00E-04| 2.07E-03| --                                                                          |
|             |         |         |            |         |         | Glycosyl hydrolase family 12                                               |
| EVM0009699  | 59.57   | 257.35  | -2.11      | 5.00E-05| 4.28E-04| Posttranslational modification, protein turnover, chaperones               |
|             |         |         |            |         |         | Proteasome subunit                                                          |
| EVM0004368  | 1.93    | 8.35    | -2.11      | 4.45E-03| 1.96E-02| --                                                                          |
| EVM0006136  | 96.87   | 417.01  | -2.11      | 5.00E-05| 4.28E-04| --                                                                          |
| EVM0001218  | 35.45   | 151.91  | -2.10      | 5.00E-05| 4.28E-04| --                                                                          |
| EVM0002358  | 11.05   | 47.36   | -2.10      | 5.00E-05| 4.28E-04| --                                                                          |
| EVM0002995  | 9.37    | 40.07   | -2.10      | 5.00E-05| 4.28E-04| RNA processing and modification                                             |
|             |         |         |            |         |         | FF domain                                                                   |
| EVM0009733    | 8.04 | 34.16 | -2.09 | 5.00E-05 | 4.28E-04 | --      | --      |
| EVM0006917    | 4.18 | 17.73 | -2.08 | 5.00E-05 | 4.28E-04 | --      | --      |
| EVM0004716    | 9.84 | 41.61 | -2.08 | 5.00E-05 | 4.28E-04 | Replication, recombination and repair | Exonuclease |
| EVM0006717    | 12.48 | 52.79 | -2.08 | 5.00E-05 | 4.28E-04 | --      | --      |
| EVM0008153    | 28.18 | 119.13 | -2.08 | 5.00E-05 | 4.28E-04 | --      | --      |
| EVM0010921    | 12.13 | 50.96 | -2.07 | 5.00E-05 | 4.28E-04 | --      | --      |
| EVM0010403    | 4.09 | 17.08 | -2.06 | 5.00E-05 | 4.28E-04 | --      | --      |
| EVM0005968    | 5.69 | 23.71 | -2.06 | 5.00E-05 | 4.28E-04 | --      | --      |
| EVM0000557    | 12.73 | 52.98 | -2.06 | 5.00E-05 | 4.28E-04 | --      | --      |
| EVM0010604    | 198.42 | 820.81 | -2.05 | 5.00E-05 | 4.28E-04 | General function prediction only | Enoyl-(Acyl carrier protein) reductase |
| EVM0010332    | 2.64 | 10.84 | -2.04 | 5.00E-05 | 4.28E-04 | --      | --      |
| EVM0000363    | 9.96 | 40.60 | -2.03 | 5.00E-05 | 4.28E-04 | Posttranslational modification, protein turnover, chaperones | Zinc knuckle |
| EVM0010419 | 4.29 | 17.40 | -2.02 | 5.00E-05 | 4.28E-04 | -- | Mis12-Mtw1 protein family |
| EVM0010548 | 23.11 | 93.75 | -2.02 | 5.00E-05 | 4.28E-04 | -- | -- |
| EVM0002270 | 2.93 | 11.86 | -2.02 | 6.00E-03 | 2.49E-02 | -- | -- |
| EVM0008877 | 17.03 | 68.85 | -2.02 | 5.00E-05 | 4.28E-04 | -- | -- |
| EVM0010306 | 16.65 | 67.06 | -2.01 | 5.00E-05 | 4.28E-04 | -- | -- |
| EVM0008356 | 12.11 | 48.78 | -2.01 | 5.00E-05 | 4.28E-04 | Function unknown | Utp11 protein |
| EVM0001552 | 13.94 | 55.87 | -2.00 | 5.00E-05 | 4.28E-04 | #N/A | #N/A |
| EVM0011343 | 28.02 | 111.97 | -2.00 | 5.00E-05 | 4.28E-04 | Posttranslational modification, protein turnover, chaperones | Glutaredoxin |
| EVM0012244 | 1.18 | 4.69 | -2.00 | 6.50E-04 | 3.98E-03 | -- | -- |
| EVM0004499 | 22.37 | 89.13 | -1.99 | 5.00E-05 | 4.28E-04 | Transcription | HSF-type DNA-binding |
| EVM0006648 | 4.23 | 16.81 | -1.99 | 5.00E-05 | 4.28E-04 | -- | -- |
| EVM0004775 | 19.25 | 75.95 | -1.98 | 5.00E-05 | 4.28E-04 | -- | Conidiation protein 6 |
| GenBank ID   | Start | End    | E-value | TRF    | Description                                                                 |
|-------------|-------|--------|---------|--------|-----------------------------------------------------------------------------|
| EVM0004698  | 65.13 | 256.36 | 1.98    | 5.00E-05 | General function prediction only                                            |
| EVM0011088  | 14.00 | 55.00  | 1.97    | 5.00E-05 | Hypoxia induced protein conserved region                                    |
| EVM0002548  | 13.79 | 54.15  | 1.97    | 5.00E-05 | Translation, ribosomal structure and biogenesis                            |
| EVM0002743  | 12.34 | 48.46  | 1.97    | 5.00E-05 | Gar1/Naf1 RNA binding region                                                |
| EVM0006700  | 162.97| 638.54 | 1.97    | 5.00E-05 | Aconitase family (aconitate hydratase)                                      |
| EVM0004688  | 23.99 | 93.72  | 1.97    | 5.00E-05 | --                                                                          |
| EVM0005272  | 408.78| 1587.89| 1.96    | 5.00E-05 | Ubiquinol-cytochrome-c reductase complex subunit (QCR10)                   |
| EVM0007254  | 6323.28| 24518.90| 1.96    | 5.00E-05 | Ribosomal protein S30                                                      |
| EVM0005497  | 60.73 | 235.18 | 1.95    | 5.00E-05 | --                                                                          |
| EVM0003129  | 2.64  | 10.21  | 1.95    | 5.00E-05 | --                                                                          |
| EVM0002150  | 170.20| 654.75 | 1.94    | 5.00E-05 | General function prediction only                                            |
| EVM0009023  | 9.60  | 36.89  | 1.94    | 5.00E-05 | RNA recognition motif. (a.k.a. RRM, RBD, or RNP domain)                    |
|             |       |        |         |        | Brix domain                                                                 |
| EVM0006570 | 718.07 | 2755.72 | -1.94 | 5.00E-05 | 4.28E-04 | Pyridoxamine 5'-phosphate oxidase |
| EVM0003560 | 19.19  | 73.30   | -1.93 | 8.85E-03 | 3.40E-02 | G-patch domain                  |
| EVM0007566 | 1114.51| 4249.04 | -1.93 | 5.00E-05 | 4.28E-04 | --                              |
| EVM0011052 | 0.74   | 2.80    | -1.93 | 9.45E-03 | 3.58E-02 | Glycosyl hydrolase family 12    |
| EVM0005881 | 4.08   | 15.48   | -1.92 | 5.00E-05 | 4.28E-04 | Small nuclear RNA activating complex (SNAPc), subunit SNAP43 |
| EVM0008721 | 1.68   | 6.36    | -1.92 | 5.00E-05 | 4.28E-04 | Lipid transport and metabolism  |
| EVM0003548 | 8.36   | 31.64   | -1.92 | 5.00E-05 | 4.28E-04 | Hydroxymethylglutaryl-coenzyme A synthase N terminal |
| EVM0007199 | 107.14 | 404.82  | -1.92 | 5.00E-05 | 4.28E-04 | General function prediction only |
| EVM0012020 | 0.72   | 2.68    | -1.91 | 3.90E-03 | 1.76E-02 | Yippee zinc-binding/DNA-binding/Mis18, centromere assembly |
| EVM0005367 | 1.61   | 6.05    | -1.91 | 5.00E-05 | 4.28E-04 | --                              |
| EVM0008224 | 126.92 | 476.01  | -1.91 | 5.00E-05 | 4.28E-04 | Protein of unknown function (DUF619) |
| EVM0012226 | 1.89   | 7.10    | -1.91 | 4.50E-04 | 2.92E-03 | --                              |
| EVM0005827 | 1.61   | 6.05    | -1.91 | 5.00E-05 | 4.28E-04 | --                              |
| EVM0009798 | 47.15 | 176.51 | -1.90 | 5.00E-05 4.28E-04 | RNA processing and modification | RNA recognition motif. (a.k.a. RRM, RBD, or RNP domain) |
| EVM0010344 | 1055.50 | 3949.47 | -1.90 | 5.00E-05 4.28E-04 | -- | ATP synthase complex subunit h |
| EVM002660 | 8.84 | 33.00 | -1.90 | 5.00E-05 4.28E-04 | Chromatin structure and dynamics | MOZ/SAS family |
| EVM005619 | 9.47 | 35.23 | -1.89 | 5.00E-05 4.28E-04 | -- | 60Kd inner membrane protein |
| EVM006946 | 10.95 | 40.71 | -1.89 | 5.00E-05 4.28E-04 | -- | -- |
| EVM005014 | 4.72 | 17.51 | -1.89 | 5.00E-05 4.28E-04 | -- | -- |
| EVM010141 | 48.19 | 178.63 | -1.89 | 5.00E-05 4.28E-04 | General function prediction only | Prp19/Pso4-like |
| EVM011950 | 577.86 | 2141.59 | -1.89 | 5.00E-05 4.28E-04 | Posttranslational modification, protein turnover, chaperones | CS domain |
| EVM005691 | 0.43 | 1.60 | -1.89 | 3.15E-03 1.47E-02 | -- | Cytochrome P450 |
| EVM010820 | 1553.60 | 5752.51 | -1.89 | 5.00E-05 4.28E-04 | Energy production and conversion | Cytochrome oxidase c subunit VIb |
| EVM010530 | 57.40 | 212.30 | -1.89 | 5.00E-05 4.28E-04 | -- | -- |
| EVM005530 | 34.95 | 129.27 | -1.89 | 5.00E-05 4.28E-04 | -- | XFP N-terminal domain |
| EVM0003373 | 2.09 | 7.70 | -1.88 | 2.00E-04 | 1.46E-03 | -- | -- |
| EVM0006992 | 12.70 | 46.74 | -1.88 | 5.00E-05 | 4.28E-04 | -- | Cytochrome P450 |
| EVM0001520 | 4.32 | 15.87 | -1.88 | 5.00E-05 | 4.28E-04 | -- | -- |
| EVM0006915 | 28.66 | 105.38 | -1.88 | 5.00E-05 | 4.28E-04 | -- | Velvet factor |
| EVM0001178 | 21.49 | 78.95 | -1.88 | 5.00E-05 | 4.28E-04 | -- | -- |
| EVM0005891 | 23.59 | 86.60 | -1.88 | 5.00E-05 | 4.28E-04 | Energy production and conversion | Pyridine nucleotide-disulphide oxidoreductase |
| EVM0003817 | 5.59 | 20.50 | -1.87 | 5.00E-05 | 4.28E-04 | -- | -- |
| EVM0011475 | 6.49 | 23.79 | -1.87 | 5.00E-05 | 4.28E-04 | -- | -- |
| EVM0009527 | 6.09 | 22.17 | -1.87 | 5.00E-05 | 4.28E-04 | Replication, recombination and repair | Cid1 family poly A polymerase |
| EVM0007162 | 14.24 | 51.71 | -1.86 | 5.00E-05 | 4.28E-04 | RNA processing and modification | Helicase associated domain (HA2) |
| EVM0003249 | 70.45 | 255.26 | -1.86 | 5.00E-05 | 4.28E-04 | -- | -- |
| EVM0005429 | 10.17 | 36.83 | -1.86 | 5.00E-05 | 4.28E-04 | Transcription | CCAAT-binding transcription factor (CBF-B/NF-YA) subunit B |
| Accession    | Value1 | Value2    | Value3 | Value4 | Value5 | Value6 | Function Description                                                                 |
|-------------|--------|-----------|--------|--------|--------|--------|--------------------------------------------------------------------------------------|
| EVM0005972  | 772.87 | 2795.82   | -1.85  | 5.00E-05| 4.28E-04| --     | --                                                                                   |
| EVM0005079  | 59.35  | 214.60    | -1.85  | 5.00E-05| 4.28E-04| Coenzyme transport and metabolism         | Pantoate-beta-alanine ligase                          |
| EVM0008058  | 11.63  | 42.04     | -1.85  | 5.00E-05| 4.28E-04| --     | --                                                                                   |
| EVM0011482  | 22.08  | 79.69     | -1.85  | 5.00E-05| 4.28E-04| Function unknown                        | WD domain, G-beta repeat                             |
| EVM0011852  | 45.43  | 163.64    | -1.85  | 5.00E-05| 4.28E-04| --     | --                                                                                   |
| EVM0001573  | 1.66   | 5.95      | -1.84  | 1.50E-04| 1.14E-03| --     | --                                                                                   |
| EVM0003103  | 58.14  | 208.62    | -1.84  | 5.00E-05| 4.28E-04| --     | --                                                                                   |
| EVM0004358  | 154.92 | 554.44    | -1.84  | 5.00E-05| 4.28E-04| --     | Heat shock factor binding protein 1                                               |
| EVM0001259  | 10.45  | 37.34     | -1.84  | 5.00E-05| 4.28E-04| General function prediction only        | WD domain, G-beta repeat                             |
| EVM0007388  | 14.33  | 51.11     | -1.83  | 5.00E-05| 4.28E-04| --     | --                                                                                   |
| EVM0009908  | 352.00 | 1255.26   | -1.83  | 5.00E-05| 4.28E-04| --     | --                                                                                   |
| EVM0009041  | 10.37  | 36.94     | -1.83  | 5.00E-05| 4.28E-04| --     | --                                                                                   |
| EVM0004911  | 415.95 | 1480.83   | -1.83  | 5.00E-05| 4.28E-04| --     | --                                                                                   |
| EVM0008074 | 2.34 | 8.31 | -1.83 | 5.30E-03 | 2.26E-02 | Chromatin structure and dynamics | Core histone H2A/H2B/H3/H4 |
| EVM0006020 | 40.69 | 144.13 | -1.82 | 5.00E-05 | 4.28E-04 | -- | -- |
| EVM0011517 | 15.58 | 54.91 | -1.82 | 5.00E-05 | 4.28E-04 | -- | RNA12 protein |
| EVM0008717 | 53.99 | 190.08 | -1.82 | 5.00E-05 | 4.28E-04 | -- | Seed maturation protein |
| EVM0010336 | 37.24 | 131.06 | -1.82 | 5.00E-05 | 4.28E-04 | -- | -- |
| EVM0002297 | 237.19 | 834.10 | -1.81 | 5.00E-05 | 4.28E-04 | -- | -- |
| EVM0008982 | 3.01 | 10.57 | -1.81 | 5.00E-05 | 4.28E-04 | -- | -- |
| EVM0001990 | 1164.43 | 4087.02 | -1.81 | 5.00E-05 | 4.28E-04 | Posttranslational modification, protein turnover, chaperones | Hsp20/alpha crystallin family |
| EVM0000869 | 219.77 | 768.15 | -1.81 | 5.00E-05 | 4.28E-04 | -- | -- |
| EVM0003609 | 221.00 | 771.77 | -1.80 | 5.00E-05 | 4.28E-04 | -- | Cytochrome oxidase c subunit VIb |
| EVM0007627 | 2314.50 | 8066.33 | -1.80 | 5.00E-05 | 4.28E-04 | Posttranslational modification, protein turnover, chaperones | Hsp20/alpha crystallin family |
| EVM0011971 | 8.85 | 30.81 | -1.80 | 5.00E-05 | 4.28E-04 | Transcription | HMG (high mobility group) box |
| EVM0008237 | 19.35 | 67.33 | -1.80 | 5.00E-05 | 4.28E-04 | -- | RNA ligase |
| EVM0000147 | 3.35  | 11.64 | -1.80 | 5.00E-05 | 4.28E-04 | -- | -- |
| EVM0000932 | 62.30 | 216.15| -1.79 | 5.00E-05 | 4.28E-04 | -- | -- |
| EVM0005976 | 107.64| 373.40| -1.79 | 5.00E-05 | 4.28E-04 | General function prediction | Sugar (and other) transporter |
| EVM0000435 | 45.83 | 158.90| -1.79 | 5.00E-05 | 4.28E-04 | General function prediction | Glycosyl transferase family 2 |
| EVM0007798 | 2.19  | 7.59  | -1.79 | 5.00E-05 | 4.28E-04 | Transcription | TEA/ATTS domain family |
| EVM0000419 | 47.31 | 163.41| -1.79 | 5.00E-05 | 4.28E-04 | Function unknown | Complex 1 protein (LYR family) |
| EVM0002677 | 0.43  | 1.48  | -1.79 | 7.50E-03 | 2.98E-02 | -- | -- |
| EVM0002912 | 156.77| 540.40| -1.79 | 5.00E-05 | 4.28E-04 | Function unknown | Telomere stability and silencing |
| EVM0003951 | 36.31 | 124.85| -1.78 | 5.00E-05 | 4.28E-04 | Function unknown | RWD domain |
| EVM0007958 | 2.34  | 8.05  | -1.78 | 5.00E-05 | 4.28E-04 | Secondary metabolites biosynthesis, transport and catabolism | Multicopper oxidase |
| EVM0001827 | 3.26  | 11.16 | -1.78 | 5.00E-05 | 4.28E-04 | Replication, recombination and repair | Helicase conserved C-terminal domain |
| EVM0012268 | 52.13 | 178.54 | -1.78 | 5.00E-05 | 4.28E-04 | Function unknown | Pam16 |
| EVM0008059 | 33.09 | 113.28 | -1.78 | 5.00E-05 | 4.28E-04 | Carbohydrate transport and metabolism | Domain of unknown function (DUF1793) |
| EVM0010061 | 48.69 | 166.45 | -1.77 | 5.00E-05 | 4.28E-04 | -- | SH3 domain |
| EVM0012007 | 17.93 | 61.23  | -1.77 | 5.00E-05 | 4.28E-04 | -- | -- |
| EVM0000905 | 27.14 | 92.62  | -1.77 | 5.00E-05 | 4.28E-04 | -- | -- |
| EVM0001192 | 105.27| 359.10 | -1.77 | 5.00E-05 | 4.28E-04 | Transcription | RNA polymerase Rpb3/Rpb11 dimerisation domain |
| EVM0011516 | 11.72 | 39.93  | -1.77 | 5.00E-05 | 4.28E-04 | -- | C2H2-type zinc finger |
| EVM0004446 | 5.38  | 18.32  | -1.77 | 5.00E-05 | 4.28E-04 | Posttranslational modification, protein turnover, chaperones | Isoprenylcysteine carboxyl methyltransferase (ICMT) family |
| EVM0006839 | 2.38  | 8.10   | -1.76 | 5.00E-05 | 4.28E-04 | -- | -- |
| EVM0002867 | 34.56 | 117.39 | -1.76 | 5.00E-05 | 4.28E-04 | Lipid transport and metabolism | MBOAT, membrane-bound O-acyltransferase family |
| EVM0008230 | 17.37 | 58.98  | -1.76 | 5.00E-05 | 4.28E-04 | Transcription | Maf1 regulator |
| EVM0009322 | 8.65  | 29.37  | -1.76 | 5.00E-05 | 4.28E-04 | -- | -- |
| EVM0010609 | 159.06 | 538.91 | -1.76 | 5.00E-05 | 4.28E-04 | Intracellular trafficking, secretion, and vesicular transport | Translocation protein Sec62 |
| EVM0007013 | 35.93 | 121.57 | -1.76 | 5.00E-05 | 4.28E-04 | -- | Protein of unknown function (DUF1275) |
| EVM0001016 | 5.47 | 18.51 | -1.76 | 5.00E-05 | 4.28E-04 | -- | -- |
| EVM0001816 | 10.76 | 36.39 | -1.76 | 5.00E-05 | 4.28E-04 | Posttranslational modification, protein turnover, chaperones | Cyclophilin type peptidyl-prolyl cis-trans isomerase/CLD |
| EVM0001788 | 15.23 | 51.37 | -1.75 | 5.00E-05 | 4.28E-04 | -- | -- |
| EVM0009797 | 6.60 | 22.25 | -1.75 | 5.00E-05 | 4.28E-04 | -- | Pheromone A receptor |
| EVM0004042 | 63.23 | 213.16 | -1.75 | 5.00E-05 | 4.28E-04 | -- | -- |
| EVM0006896 | 214.29 | 721.71 | -1.75 | 1.00E-04 | 7.96E-04 | -- | Protein of unknown function (DUF4449) |
| EVM0009214 | 152.31 | 512.95 | -1.75 | 5.00E-05 | 4.28E-04 | General function prediction only | Casein kinase substrate phosphoprotein PP28 |
| EVM0003453 | 113.79 | 383.15 | -1.75 | 5.00E-05 | 4.28E-04 | -- | -- |
| EVM0011734 | 6.18 | 20.81 | -1.75 | 5.00E-05 | 4.28E-04 | -- | -- |
| EVM0001247 | 34.90 | 117.26 | -1.75 | 5.00E-05 | 4.28E-04 | -- | MAC/Perforin domain |
| Accession     | Value1 | Value2  | Log2 Fold Change | FDR  | Description                                                                 |
|--------------|--------|---------|------------------|------|----------------------------------------------------------------------------|
| EVM0005279   | 619.87 | 2080.40 | -1.75            | 5.00E-05 | 4.28E-04                      | Stress responsive A/B Barrel Domain |
| EVM0007796   | 54.09  | 181.52  | -1.75            | 5.00E-05 | 4.28E-04                      | --                                    |
| EVM0011033   | 3.52   | 11.80   | -1.74            | 5.00E-05 | 4.28E-04                      | --                                    |
| EVM0007196   | 234.14 | 783.54  | -1.74            | 5.00E-05 | 4.28E-04                      | RNA processing and modification LSM domain |
| EVM0010029   | 135.10 | 451.64  | -1.74            | 5.00E-05 | 4.28E-04                      | Microsomal signal peptidase 25 kDa subunit (SPC25) |
| EVM0008461   | 10.87  | 36.33   | -1.74            | 5.00E-05 | 4.28E-04                      | Putative snoRNA binding domain        |
| EVM0008272   | 0.86   | 2.88    | -1.74            | 4.50E-04 | 2.92E-03                      | --                                    |
| EVM0000829   | 4.19   | 14.00   | -1.74            | 2.10E-03 | 1.06E-02                      | --                                    |
| EVM0004843   | 10.29  | 34.31   | -1.74            | 5.00E-05 | 4.28E-04                      | Ricin-type beta-trefoil lectin domain-like |
| EVM0005234   | 0.92   | 3.06    | -1.74            | 5.50E-04 | 3.46E-03                      | --                                    |
| EVM0011587   | 159.68 | 530.01  | -1.73            | 5.00E-05 | 4.28E-04                      | --                                    |
| EVM0011107   | 80.25  | 266.21  | -1.73            | 5.00E-05 | 4.28E-04                      | --                                    |
| EVM0009051   | 296.43 | 981.43  | -1.73            | 5.00E-05 | 4.28E-04                      | Translation, ribosomal structure and biogenesis Ribosomal protein L34 |
| EVM0004357 | 162.42 | 536.82 | -1.72 | 1.60E-03 | 8.44E-03 | -- | -- |
| EVM0004818 | 13.48  | 44.44  | -1.72 | 5.00E-05 | 4.28E-04 | #N/A | #N/A |
| EVM0010805 | 14.96  | 49.24  | -1.72 | 5.00E-05 | 4.28E-04 | General function prediction only | GMC oxidoreductase |
| EVM0000406 | 4.56   | 14.95  | -1.71 | 5.00E-05 | 4.28E-04 | -- | Protein kinase domain |
| EVM0009546 | 19.42  | 63.68  | -1.71 | 5.00E-05 | 4.28E-04 | -- | Fungal specific transcription factor domain |
| EVM0002786 | 1247.12| 4081.63| -1.71 | 5.00E-05 | 4.28E-04 | -- | -- |
| EVM0005796 | 1012.35| 3312.97| -1.71 | 5.00E-05 | 4.28E-04 | Translation, ribosomal structure and biogenesis | 60s Acidic ribosomal protein |
| EVM0004028 | 62.79  | 205.30 | -1.71 | 5.00E-05 | 4.28E-04 | Cell cycle control, cell division, chromosome partitioning | -- |
| EVM0007173 | 53.73  | 175.29 | -1.71 | 5.00E-05 | 4.28E-04 | Replication, recombination and repair | Nucleosome assembly protein (NAP) |
| EVM0007752 | 0.40   | 1.29   | -1.71 | 8.75E-03 | 3.37E-02 | -- | -- |
| EVM0009923 | 621.51 | 2026.31| -1.71 | 5.00E-05 | 4.28E-04 | #N/A | #N/A |
| EVM0001318 | 3334.00| 10865.60| -1.70 | 3.50E-04 | 2.36E-03 | Posttranslational modification, protein turnover, chaperones | Hsp70 protein |
| Accession   | Value1 | Value2   | Value3 | Value4 | Value5 | Value6 | Value7 | Value8 | Value9 | Value10 | Value11 | Function | Product                                                                 |
|------------|--------|----------|--------|--------|--------|--------|--------|--------|--------|----------|----------|----------|---------------------------------------------------------------|
| EVM0009347 | 16.22  | 52.85    | -1.70  | 5.00E-05 | 4.28E-04 | --     |        |        |        | WH2 motif                             |          |          |                                                |
| EVM0006606 | 52.24  | 170.16   | -1.70  | 5.00E-05 | 4.28E-04 | --     |        |        |        | --                                  |          |          |                                                |
| EVM0004482 | 1.59   | 5.19     | -1.70  | 3.30E-03 | 1.53E-02 | --     |        |        |        | --                                  |          |          |                                                |
| EVM0006132 | 57.10  | 185.61   | -1.70  | 5.00E-05 | 4.28E-04 | Intracellular trafficking, secretion, and vesicular transport | Peroxisomal biogenesis factor 11 (PEX11) |          |        |          |          |          |                                                |
| EVM0011165 | 29.59  | 96.16    | -1.70  | 5.00E-05 | 4.28E-04 | Energy production and conversion | Mitochondrial carrier protein |          |        |          |          |          |                                                |
| EVM0009732 | 18.80  | 60.80    | -1.69  | 5.00E-05 | 4.28E-04 | --     |        |        |        | --                                  |          |          |                                                |
| EVM0011891 | 10.00  | 32.25    | -1.69  | 5.00E-05 | 4.28E-04 | Posttranslational modification, protein turnover, chaperones | Glutathione S-transferase, N-terminal domain |          |        |          |          |          |                                                |
| EVM0004933 | 397.74 | 1280.81  | -1.69  | 5.00E-05 | 4.28E-04 | Posttranslational modification, protein turnover, chaperones | Sec61beta family |          |        |          |          |          |                                                |
| EVM0005500 | 11.98  | 38.59    | -1.69  | 5.00E-05 | 4.28E-04 | Function unknown | XAP5, circadian clock regulator |          |        |          |          |          |                                                |
| EVM0010779 | 259.74 | 835.69   | -1.69  | 5.00E-05 | 4.28E-04 | Intracellular trafficking, secretion, and vesicular transport | SURF4 family |          |        |          |          |          |                                                |
| EVM0005453 | 49.09  | 157.89   | -1.69  | 5.00E-05 | 4.28E-04 | --     |        |        |        | --                                  |          |          |                                                |
| EVM0005453 | 49.09  | 157.89   | -1.69  | 5.00E-05 | 4.28E-04 | --     |        |        |        | --                                  |          |          |                                                |
| ID          | Value 1 | Value 2 | Change | Value 3 | Value 4 | Function                                      |
|------------|---------|---------|--------|---------|---------|-----------------------------------------------|
| EVM000220  | 18.80   | 60.21   | -1.68  | 8.60E-03| 3.32E-02| Carbohydrate transport and metabolism          |
| EVM0011758 | 3.84    | 12.30   | -1.68  | 5.00E-05| 4.28E-04| General function prediction only              |
| EVM0005185 | 136.66  | 437.06  | -1.68  | 5.00E-05| 4.28E-04| Amino acid transport and metabolism           |
| EVM0009813 | 49.94   | 159.55  | -1.68  | 5.00E-05| 4.28E-04| --                                             |
| EVM0005073 | 10.32   | 32.96   | -1.68  | 5.00E-05| 4.28E-04| Nitrate monooxygenase                         |
| EVM0007331 | 3.46    | 11.04   | -1.67  | 5.00E-05| 4.28E-04| --                                             |
| EVM0005717 | 39.57   | 126.03  | -1.67  | 5.00E-05| 4.28E-04| --                                             |
| EVM0010331 | 18.01   | 57.26   | -1.67  | 5.00E-05| 4.28E-04| --                                             |
| EVM0010883 | 201.12  | 639.22  | -1.67  | 5.00E-05| 4.28E-04| Cell wall/membrane/envelope biogenesis        |
| EVM0002372 | 8.81    | 27.99   | -1.67  | 5.00E-05| 4.28E-04| Cytochrome P450                                |
| EVM0003772 | 3.79    | 12.03   | -1.67  | 5.00E-05| 4.28E-04| --                                             |
| EVM0003992 | 14.16   | 44.92   | -1.67  | 5.00E-05| 4.28E-04| --                                             |
| EVM0009819   | 23.61 | 74.88 | -1.67 | 5.00E-05 | 4.28E-04 | --            | CBS domain     |
|--------------|-------|-------|--------|-----------|-----------|---------------|----------------|
| EVM0008730   | 16.51 | 52.29 | -1.66  | 5.00E-05 | 4.28E-04 | --            | --             |
| EVM0001421   | 51.01 | 161.48| -1.66  | 5.00E-05 | 4.28E-04 | Cell cycle control, cell division, chromosome partitioning | Protein kinase domain |
| EVM0001320   | 22.62 | 71.50 | -1.66  | 5.00E-05 | 4.28E-04 | --            | --             |
| EVM0007843   | 28.52 | 89.98 | -1.66  | 5.00E-05 | 4.28E-04 | Dyp-type peroxidase family | --             |
| EVM0011097   | 303.47| 956.27| -1.66  | 5.00E-05 | 4.28E-04 | RNA recognition motif. (a.k.a. RRM, RBD, or RNP domain) | --             |
| EVM0003616   | 29.22 | 92.05 | -1.66  | 5.00E-05 | 4.28E-04 | Transcription | HSF-type DNA-binding |
| EVM0005253   | 425.02| 1332.13| -1.65 | 5.00E-05| 4.28E-04 | --            | --             |
| EVM0000666   | 55.68 | 174.32| -1.65  | 5.00E-05| 4.28E-04 | --            | --             |
| EVM0007514   | 137.65| 429.80| -1.64  | 5.00E-05| 4.28E-04 | RTA1 like protein | --             |
| EVM0004582   | 2.35  | 7.33  | -1.64  | 2.30E-03| 1.14E-02 | --            | --             |
| EVM0006949   | 68.14 | 212.58| -1.64  | 5.00E-05| 4.28E-04 | N-terminal domain of ribose phosphate pyrophosphokinase | --             |
| EVM0000927 | 140.16 | 437.11 | -1.64 | 5.00E-05 | 4.28E-04 | Secondary metabolites biosynthesis, transport and catabolism | Pyridine nucleotide-disulphide oxidoreductase |
|------------|-------|--------|--------|----------|----------|-------------------------------------------------|---------------------------------------------|
| EVM0000390 | 8.67  | 27.02  | -1.64 | 5.00E-05 | 4.28E-04 | Amino acid transport and metabolism               | Cys/Met metabolism PLP-dependent enzyme    |
| EVM0007872 | 31.65 | 98.52  | -1.64 | 5.00E-05 | 4.28E-04 | --                                              | --                                          |
| EVM0009085 | 584.49| 1816.44| -1.64 | 5.00E-05 | 4.28E-04 | --                                              | --                                          |
| EVM0008537 | 9774.36| 30297.40| -1.63 | 2.35E-03 | 1.16E-02 | Posttranslational modification, protein turnover, chaperones | Hsp20/alpha crystallin family |
| EVM0005625 | 2.42  | 7.48   | -1.63 | 5.00E-05 | 4.28E-04 | --                                              | --                                          |
| EVM0003837 | 603.06| 1864.50| -1.63 | 5.00E-05 | 4.28E-04 | --                                              | --                                          |
| EVM0002338 | 13.22 | 40.84  | -1.63 | 5.00E-05 | 4.28E-04 | Lipid transport and metabolism                   | PAP2 superfamily                           |
| EVM0012239 | 1.76  | 5.43   | -1.63 | 5.00E-05 | 4.28E-04 | --                                              | --                                          |
| EVM0007949 | 14.57 | 44.95  | -1.63 | 5.00E-05 | 4.28E-04 | RNA processing and modification                  | WD domain, G-beta repeat                   |
| EVM0010521 | 41.02 | 126.46 | -1.62 | 5.00E-05 | 4.28E-04 | --                                              | --                                          |
| EVM0009399 | 19.78 | 60.91  | -1.62 | 5.00E-05 | 4.28E-04 | --                                              | Mediator complex subunit 25 von Willebrand factor type A |
| EVM0003466 | 23.04  | 70.85  | -1.62 | 5.00E-05 | 4.28E-04 | -- | NYN domain |
| EVM0002644 | 1484.48| 4563.43| -1.62 | 8.50E-04 | 4.98E-03 | -- | -- |
| EVM0001510 | 80.14  | 246.20 | -1.62 | 5.00E-05 | 4.28E-04 | Posttranslational modification, protein turnover, chaperones | Eukaryotic aspartyl protease |
| EVM0004770 | 11.36  | 34.83  | -1.62 | 5.00E-05 | 4.28E-04 | -- | WH1 domain |
| EVM0004238 | 23.97  | 73.47  | -1.62 | 5.00E-05 | 4.28E-04 | -- | SMI1 / KNR4 family (SUHK-1) |
| EVM0008511 | 36.18  | 110.86 | -1.62 | 5.00E-05 | 4.28E-04 | RNA processing and modification | Ribosomal RNA-processing protein 7 (RRP7) |
| EVM0010252 | 43.86  | 134.34 | -1.61 | 5.00E-05 | 4.28E-04 | -- | PX domain |
| EVM000794  | 547.80 | 1675.77| -1.61 | 5.00E-05 | 4.28E-04 | Posttranslational modification, protein turnover, chaperones | Redoxin |
| EVM0002465 | 4.56   | 13.95  | -1.61 | 2.50E-04 | 1.77E-03 | -- | 50S ribosome-binding GTPase |
| EVM0011344 | 9.71   | 29.66  | -1.61 | 5.00E-05 | 4.28E-04 | RNA processing and modification | Mpp10 protein |
| EVM0001778 | 135.45 | 413.61 | -1.61 | 5.00E-05 | 4.28E-04 | Coenzyme transport and metabolism | Pyridoxamine 5’-phosphate oxidase |
| EVM0006301 | 31.86  | 97.07  | -1.61 | 5.00E-05 | 4.28E-04 | Carbohydrate transport and metabolism | Amidohydrolase family |
| ID               | Value1 | Value2 | Value3 | Value4 | Value5 | Description                                                                 |
|------------------|--------|--------|--------|--------|--------|----------------------------------------------------------------------------|
| EVM0001614       | 3.34   | 10.17  | -1.61  | 5.00E-05| 4.28E-04| --                                                                          |
| EVM0002694       | 4.22   | 12.82  | -1.60  | 5.00E-05| 4.28E-04| -- DNA polymerase subunit Cdc27                                            |
| EVM0010702       | 11.60  | 35.03  | -1.59  | 5.00E-05| 4.28E-04| --                                                                          |
| EVM0006754       | 209.05 | 631.22 | -1.59  | 5.00E-05| 4.28E-04| Coenzyme transport and metabolism Coproporphyrinogen III oxidase            |
| EVM0009791       | 7.67   | 23.09  | -1.59  | 5.00E-05| 4.28E-04| Transcription RNA polymerase Rpb1, domain 5                                 |
| EVM0002264       | 90.73  | 272.80 | -1.59  | 5.00E-05| 4.28E-04| --                                                                          |
| EVM0010015       | 0.66   | 1.98   | -1.59  | 8.90E-03| 3.41E-02| #N/A                                                                       |
| EVM0003296       | 142.35 | 427.41 | -1.59  | 5.00E-05| 4.28E-04| General function prediction only Domain of unknown function DUF221          |
| EVM0005402       | 2.39   | 7.16   | -1.58  | 5.00E-05| 4.28E-04| -- F-box domain                                                            |
| EVM0003866       | 80.48  | 241.18 | -1.58  | 5.00E-05| 4.28E-04| -- DAD family                                                              |
| EVM0008406       | 26.64  | 79.82  | -1.58  | 5.00E-05| 4.28E-04| Lipid transport and metabolism AMP-binding enzyme                            |
| EVM0010558       | 18.17  | 54.39  | -1.58  | 5.00E-05| 4.28E-04| --                                                                          |
| EVM0005758       | 58.97  | 176.41 | -1.58  | 5.00E-05| 4.28E-04| Lipid transport and metabolism Putative undecaprenyl diphosphate synthase |
| EVM0007305 | 247.84 | 740.78 | -1.58 | 5.00E-05 | 4.28E-04 | RNA processing and modification | U1 zinc finger |
| EVM0001647 | 48.79  | 145.80 | -1.58 | 5.00E-05 | 4.28E-04 | General function prediction only | Zinc-finger double-stranded RNA-binding |
| EVM0009705 | 76.45  | 228.23 | -1.58 | 5.00E-05 | 4.28E-04 | -- | -- |
| EVM000266  | 22.86  | 68.24  | -1.58 | 5.00E-05 | 4.28E-04 | -- | -- |
| EVM0007445 | 3.29   | 9.80   | -1.58 | 5.00E-05 | 4.28E-04 | -- | -- |
| EVM0008804 | 57.59  | 171.23 | -1.57 | 5.00E-05 | 4.28E-04 | -- | -- |
| EVM0009711 | 125.87 | 373.42 | -1.57 | 5.00E-05 | 4.28E-04 | -- | Fungal hydrophobin |
| EVM0008198 | 39.94  | 118.44 | -1.57 | 5.00E-05 | 4.28E-04 | Transcription | Transcription initiation factor IIF, beta subunit |
| EVM0004809 | 40.01  | 118.60 | -1.57 | 5.00E-05 | 4.28E-04 | Posttranslational modification, protein turnover, chaperones | Myb-like DNA-binding domain |
| EVM0008622 | 75.43  | 223.50 | -1.57 | 5.00E-05 | 4.28E-04 | -- | 50S ribosome-binding GTPase |
| EVM0006976 | 13.80  | 40.89  | -1.57 | 5.00E-05 | 4.28E-04 | Inorganic ion transport and metabolism | Regulator of volume decrease after cellular swelling |
| EVM0002302 | 22.38  | 66.30  | -1.57 | 5.00E-05 | 4.28E-04 | -- | -- |
| EVM0000986 | 9.84 | 29.16 | -1.57 | 5.00E-05 | 4.28E-04 | -- | -- |
| EVM0001355 | 215.77 | 638.75 | -1.57 | 1.50E-04 | 1.14E-03 | -- | -- |
| EVM0008504 | 30.44 | 90.04 | -1.56 | 5.00E-05 | 4.28E-04 | -- | F-box-like |
| EVM0011270 | 9.23 | 27.27 | -1.56 | 5.00E-05 | 4.28E-04 | -- | cAMP phosphodiesterases class-II |
| EVM0011757 | 3.67 | 10.83 | -1.56 | 9.50E-04 | 5.46E-03 | -- | -- |
| EVM0010583 | 329.63 | 973.19 | -1.56 | 5.00E-05 | 4.28E-04 | -- | -- |
| EVM0010158 | 53.50 | 157.86 | -1.56 | 5.00E-05 | 4.28E-04 | Function unknown | Pre-rRNA-processing protein TSR2 |
| EVM0004617 | 575.75 | 1693.60 | -1.56 | 5.00E-05 | 4.28E-04 | -- | ESSS subunit of NADH:ubiquinone oxidoreductase (complex I) |
| EVM0000784 | 9.47 | 27.84 | -1.56 | 5.00E-05 | 4.28E-04 | -- | -- |
| EVM0009146 | 1.57 | 4.62 | -1.56 | 6.20E-03 | 2.56E-02 | -- | Glycosyl hydrolase family 61 |
| EVM0000883 | 3.80 | 11.15 | -1.55 | 5.00E-05 | 4.28E-04 | Transcription | HMG (high mobility group) box |
| EVM000240 | 10.82 | 31.75 | -1.55 | 1.00E-04 | 7.96E-04 | Transcription | MED6 mediator sub complex component |
| EVM0009204 | 10.50  | 30.76 | -1.55 | 5.00E-05 | 4.28E-04 | RNA processing and modification | -- |
| EVM0003326 | 34.24  | 100.26| -1.55 | 5.00E-05 | 4.28E-04 | General function prediction only | R3H domain |
| EVM0003558 | 31.97  | 93.52 | -1.55 | 5.00E-05 | 4.28E-04 | -- | Methyltransferase domain |
| EVM0005508 | 103.77 | 303.32| -1.55 | 5.00E-05 | 4.28E-04 | Posttranslational modification, protein turnover, chaperones | OST3 / OST6 family |
| EVM0008305 | 9.82   | 28.69 | -1.55 | 5.00E-05 | 4.28E-04 | General function prediction only | U3 small nucleolar RNA-associated protein 6 |
| EVM0009845 | 13.77  | 40.20 | -1.55 | 2.00E-04 | 1.46E-03 | -- | -- |
| EVM0005613 | 18.39  | 53.56 | -1.54 | 5.00E-05 | 4.28E-04 | -- | -- |
| EVM0008163 | 4.18   | 12.15 | -1.54 | 1.00E-04 | 7.96E-04 | -- | -- |
| EVM0004215 | 453.48 | 1317.55| -1.54 | 5.00E-05 | 4.28E-04 | Energy production and conversion | Cytochrome c oxidase subunit Va |
| EVM0002596 | 0.82   | 2.38  | -1.54 | 3.85E-03 | 1.74E-02 | -- | Phosphotransferase enzyme family |
| EVM0000527 | 21.10  | 61.27 | -1.54 | 5.00E-05 | 4.28E-04 | General function prediction only | Methyltransferase domain |
| EVM0009955 | 11.02  | 32.01 | -1.54 | 5.00E-05 | 4.28E-04 | -- | -- |
| EVM0002266 | 300.51 | 872.36 | -1.54 | 5.00E-05 | 4.28E-04 | -- | Protein of unknown function (DUF3429) |
| EVM0004837 | 100.55 | 291.48 | -1.54 | 5.00E-05 | 4.28E-04 | General function prediction only | Ras family |
| EVM0003322 | 9.08 | 26.32 | -1.54 | 5.00E-05 | 4.28E-04 | General function prediction only | Sugar (and other) transporter |
| EVM0003224 | 61.67 | 178.72 | -1.54 | 5.00E-05 | 4.28E-04 | General function prediction only | Phosphatidylethanolamine-binding protein |
| EVM0009206 | 26.38 | 76.45 | -1.53 | 5.00E-05 | 4.28E-04 | -- | Protein of unknown function (DUF3129) |
| EVM0005583 | 16.59 | 47.99 | -1.53 | 5.00E-05 | 4.28E-04 | -- | -- |
| EVM0007890 | 184.25 | 532.65 | -1.53 | 5.00E-05 | 4.28E-04 | -- | -- |
| EVM0008702 | 157.43 | 455.02 | -1.53 | 5.00E-05 | 4.28E-04 | Intracellular trafficking, secretion, and vesicular transport | PRELI-like family |
| EVM0000890 | 159.05 | 459.47 | -1.53 | 5.00E-05 | 4.28E-04 | Translation, ribosomal structure and biogenesis | PUA domain |
| EVM0010645 | 9.87 | 28.49 | -1.53 | 5.00E-05 | 4.28E-04 | Cytoskeleton | Splicing factor, Prp19-binding domain |
| EVM0004272 | 379.07 | 1094.18 | -1.53 | 5.00E-05 | 4.28E-04 | -- | Translationally controlled tumour protein |
| EVM0009625 | 11.69 | 33.73 | -1.53 | 5.00E-05 | 4.28E-04 | -- | AIG1 family |
| EVM0005280   | 1.47  | 4.24  | -1.53 | 1.20E-03 | 6.64E-03 | -- | Phosphotransferase enzyme family |
|--------------|-------|-------|-------|----------|----------|----|--------------------------------|
| EVM0006159   | 47.41 | 136.47| -1.53 | 5.00E-05 | 4.28E-04 | -- | --                               |
| EVM0002923   | 4250.88 | 12227.00 | -1.52 | 5.00E-05 | 4.28E-04 | -- | CsbD-like                        |
| EVM0007878   | 19.81 | 56.94 | -1.52 | 5.00E-05 | 4.28E-04 | -- | Posttranslational modification, protein turnover, chaperones |
| EVM0008481   | 10.28 | 29.48 | -1.52 | 5.00E-05 | 4.28E-04 | -- | BCS1 N terminal                  |
| EVM0002697   | 4.88  | 13.99 | -1.52 | 8.00E-04 | 4.73E-03 | -- | Inorganic ion transport and metabolism |
| EVM0005991   | 266.57 | 763.68 | -1.52 | 5.00E-05 | 4.28E-04 | -- | CorA-like Mg2+ transporter protein |
| EVM0006292   | 5.14  | 14.73 | -1.52 | 5.00E-05 | 4.28E-04 | -- | SAP domain                       |
| EVM0007771   | 8.61  | 24.57 | -1.51 | 3.00E-04 | 2.07E-03 | -- | Fungal Zn(2)-Cys(6) binuclear cluster domain |
| EVM0011887   | 9.38  | 26.73 | -1.51 | 1.00E-04 | 7.96E-04 | -- | --                               |
| EVM0004134   | 51.54 | 146.79| -1.51 | 5.00E-05 | 4.28E-04 | -- | General function prediction RNA recognition motif. (a.k.a. RRM, RBD, or RNP domain) |
| EVM0005227   | 55.84 | 158.73| -1.51 | 5.00E-05 | 4.28E-04 | -- | Function unknown Bromodomain      |
| Accession   | Fold | T0.05 | Z-score | E-value 0.05 | E-value 0.04 | Function Description                                      |
|------------|------|-------|---------|-------------|-------------|----------------------------------------------------------|
| EVM0005831 | 12.92| 36.71 | -1.51   | 5.00E-05    | 4.28E-04    | General function prediction only                         |
| EVM0004691 | 19.14| 54.33 | -1.50   | 5.00E-05    | 4.28E-04    | --                                                       |
| EVM0001809 | 98.29| 278.85| -1.50   | 5.00E-05    | 4.28E-04    | --                                                       |
| EVM0005630 | 145.42| 411.85| -1.50   | 5.00E-05    | 4.28E-04    | Translation, ribosomal structure and biogenesis          |
| EVM0008851 | 252.09| 713.58| -1.50   | 5.00E-05    | 4.28E-04    | Intracellular trafficking, secretion, and vesicular transport |
| EVM0002331 | 198.80| 561.31| -1.50   | 5.00E-05    | 4.28E-04    | Posttranslational modification, protein turnover, chaperones |
| EVM0006561 | 7.62 | 21.48 | -1.50   | 5.00E-05    | 4.28E-04    | --                                                       |
| EVM0008650 | 73.28| 206.52| -1.49   | 5.00E-05    | 4.28E-04    | --                                                       |
| EVM0004953 | 61.60| 173.46| -1.49   | 5.00E-05    | 4.28E-04    | --                                                       |
| EVM0000218 | 102.05| 287.31| -1.49   | 5.00E-05    | 4.28E-04    | --                                                       |
| EVM0003855 | 4.75 | 13.38 | -1.49   | 1.50E-04    | 1.14E-03    | Signal transduction mechanisms                           |
| EVM0008213 | 778.98| 2190.78| -1.49   | 5.00E-05    | 4.28E-04    | RNA processing and modification                          |

EVM0005630 is a protein that is involved in Translation, ribosomal structure and biogenesis. It is a mitochondrial ribosomal protein L51 / S25 / CI-B8 domain. EVM0008851 is involved in Intracellular trafficking, secretion, and vesicular transport. EVM0002331 is involved in Posttranslational modification, protein turnover, chaperones. EVM0003855 is involved in Signal transduction mechanisms.
| Accession    | Width | Height | R.Z. | E-value1 | E-value2 | Function                                    | Protein Description                        |
|--------------|-------|--------|------|----------|----------|---------------------------------------------|--------------------------------------------|
| EVM0007629   | 60.68 | 170.63 | -1.49| 5.00E-05 | 4.28E-04 | General function prediction only            | Protein of unknown function (DUF933)      |
| EVM0009884   | 171.44| 481.58 | -1.49| 5.00E-05 | 4.28E-04 | --                                          | Glycosyl hydrolase catalytic core         |
| EVM0001583   | 29.75 | 83.56  | -1.49| 5.00E-05 | 4.28E-04 | Intracellular trafficking, secretion, and vesicular transport | Ras family                                |
| EVM0006099   | 130.16| 365.45 | -1.49| 5.00E-05 | 4.28E-04 | Lipid transport and metabolism              | Enoyl-CoA hydratase/isomerase family      |
| EVM0010258   | 37.36 | 104.84 | -1.49| 5.00E-05 | 4.28E-04 | --                                          | --                                         |
| EVM0011446   | 1632.45| 4570.86| -1.49| 5.00E-05 | 4.28E-04 | --                                          | --                                         |
| EVM0002673   | 20.51 | 57.42  | -1.49| 5.00E-05 | 4.28E-04 | --                                          | --                                         |
| EVM0000423   | 152.25| 425.44 | -1.48| 5.00E-05 | 4.28E-04 | #N/A                                        | #N/A                                       |
| EVM0006494   | 15.86 | 44.29  | -1.48| 5.00E-05 | 4.28E-04 | Chromatin structure and dynamics            | Sas10 C-terminal domain                   |
| EVM0008519   | 124.61| 347.64 | -1.48| 5.00E-05 | 4.28E-04 | RNA processing and modification             | LUC7 N_terminus                           |
| EVM0002899   | 187.88| 524.05 | -1.48| 5.00E-05 | 4.28E-04 | --                                          | Fatty acid desaturase                     |
| EVM0005109   | 4.25  | 11.83  | -1.48| 5.00E-05 | 4.28E-04 | --                                          | --                                         |
| EVM0000031 | 410.77 | 1143.85 | -1.48 | 5.00E-05 | 4.28E-04 | -- | -- |
| EVM0010038 | 2.91  | 8.09   | -1.48 | 5.40E-03 | 2.29E-02 | -- | -- |
| EVM0007361 | 17.90 | 49.81  | -1.48 | 5.00E-05 | 4.28E-04 | RNA processing and modification | DEAD/DEAH box helicase |
| EVM0009999 | 8.29  | 23.05  | -1.47 | 3.45E-03 | 1.59E-02 | -- | Rare lipoprotein A (RlpA)-like double-psi beta-barrel |
| EVM0003599 | 4.78  | 13.27  | -1.47 | 5.05E-03 | 2.17E-02 | Carbohydrate transport and metabolism | LysM domain |
| EVM0003574 | 36.69 | 101.76 | -1.47 | 5.00E-05 | 4.28E-04 | General function prediction only | PCI domain |
| EVM0007410 | 3.82  | 10.57  | -1.47 | 5.00E-05 | 4.28E-04 | #N/A | #N/A |
| EVM0003721 | 166.50| 461.01 | -1.47 | 5.00E-05 | 4.28E-04 | -- | -- |
| EVM0005703 | 21.51 | 59.51  | -1.47 | 5.00E-05 | 4.28E-04 | Function unknown | Utp14 protein |
| EVM0002607 | 57.03 | 157.71 | -1.47 | 5.00E-05 | 4.28E-04 | Lipid transport and metabolism | Cupin-like domain |
| EVM0000019 | 31.20 | 86.28  | -1.47 | 5.00E-05 | 4.28E-04 | -- | -- |
| EVM0000219 | 58.89 | 162.71 | -1.47 | 5.00E-05 | 4.28E-04 | General function prediction only | Cyclin |
| EVM0004762 | 144.37 | 398.71 | -1.47 | 5.00E-05 | 4.28E-04 | Intracellular trafficking, secretion, and vesicular transport | Clathrin adaptor complex small chain |
| EVM0008002 | 130.81 | 361.22 | -1.47 | 5.00E-05 | 4.28E-04 | General function prediction only | Flavodoxin |
| EVM0007506 | 189.76 | 522.92 | -1.46 | 5.00E-05 | 4.28E-04 | Intracellular trafficking, secretion, and vesicular transport | Regulated-SNARE-like domain |
| EVM0002218 | 170.01 | 468.10 | -1.46 | 5.00E-05 | 4.28E-04 | -- | -- |
| EVM0008604 | 3.08 | 8.46 | -1.46 | 1.00E-04 | 7.96E-04 | -- | -- |
| EVM0002141 | 5.35 | 14.73 | -1.46 | 4.00E-04 | 2.65E-03 | -- | -- |
| EVM0007826 | 23.42 | 64.42 | -1.46 | 5.00E-05 | 4.28E-04 | General function prediction only | RNA recognition motif. (a.k.a. RRM, RBD, or RNP domain) |
| EVM0000209 | 8.50 | 23.39 | -1.46 | 5.00E-05 | 4.28E-04 | Translation, ribosomal structure and biogenesis | KRI1-like family C-terminal |
| EVM0008447 | 49.59 | 136.13 | -1.46 | 5.00E-05 | 4.28E-04 | -- | -- |
| EVM0009119 | 10.08 | 27.64 | -1.46 | 5.00E-05 | 4.28E-04 | -- | -- |
| EVM0001825 | 79.11 | 216.79 | -1.45 | 5.00E-05 | 4.28E-04 | Transcription | HSF-type DNA-binding |
| EVM0005377 | 6.19 | 16.93 | -1.45 | 5.00E-05 | 4.28E-04 | -- | Cellulase (glycosyl hydrolase family 5) |
| Accession   | X    | Y    | r   | p1   | p2   | Function                                      |
|-------------|------|------|-----|------|------|-----------------------------------------------|
| EVM0008051  | 146.44 | 400.63 | -1.45 | 5.00E-05 | 4.28E-04 | SUR/Pall family                               |
| EVM0009614  | 79.69  | 217.79 | -1.45 | 5.00E-05 | 4.28E-04 | --                                            |
| EVM0005134  | 84.43  | 230.66 | -1.45 | 5.00E-05 | 4.28E-04 | Function unknown COP9 signalosome, subunit CSN8 |
| EVM0011134  | 19.38  | 52.92  | -1.45 | 5.00E-05 | 4.28E-04 | Function unknown NRDE-2, necessary for RNA interference |
| EVM0010109  | 7.58   | 20.68  | -1.45 | 5.00E-05 | 4.28E-04 | Replication, recombination and repair Eukaryotic and archaeal DNA primase, large subunit |
| EVM0010363  | 22.93  | 62.45  | -1.45 | 5.00E-05 | 4.28E-04 | -- Alpha/beta hydrolase family                |
| EVM0000377  | 40.53  | 110.05 | -1.44 | 5.00E-05 | 4.28E-04 | --                                            |
| EVM0003168  | 9.60   | 26.01  | -1.44 | 1.25E-03 | 6.87E-03 | --                                            |
| EVM0004156  | 0.96   | 2.60   | -1.44 | 2.00E-04 | 1.46E-03 | --                                            |
| EVM0010715  | 53.79  | 145.51 | -1.44 | 5.00E-05 | 4.28E-04 | RNA processing and modification Isy1-like splicing family |
| EVM0007930  | 11.43  | 30.89  | -1.43 | 5.00E-05 | 4.28E-04 | RNA recognition motif (a.k.a. RRM, RBD, or RNP domain) |
| EVM0011808  | 3.05   | 8.22   | -1.43 | 1.35E-03 | 7.33E-03 | Lysine-specific metallo-endopeptidase          |
| EVM0002948  | 33.72  | 90.82  | -1.43 | 5.00E-05 | 4.28E-04 | Protein of unknown function (Ytp1)             |
| Accession | Score1 | Score2 | Score3 | Score4 | Score5 | Domain Description                                                      |
|-----------|--------|--------|--------|--------|--------|------------------------------------------------------------------------|
| EVM0011851 | 5.54   | 14.89  | -1.43  | 4.00E-04 | 2.65E-03 | Domain of unknown function (DUF3328)                                   |
| EVM0006795 | 860.74 | 2314.38| -1.43  | 3.90E-03 | 1.76E-02 | --                                                                     |
| EVM0000165 | 48.84  | 131.27 | -1.43  | 5.00E-05 | 4.28E-04 | Cell cycle control, cell division, chromosome partitioning            |
| EVM0002127 | 38.35  | 103.06 | -1.43  | 5.00E-05 | 4.28E-04 | RNA processing and modification                                       |
| EVM0004954 | 57.78  | 154.96 | -1.42  | 5.00E-05 | 4.28E-04 | --                                                                     |
| EVM0000370 | 155.94 | 418.22 | -1.42  | 5.00E-05 | 4.28E-04 | Fungal fruit body lectin                                              |
| EVM0001681 | 268.76 | 719.84 | -1.42  | 5.00E-05 | 4.28E-04 | Intracellular trafficking, secretion, and vesicular transport         |
| EVM0006400 | 4.27   | 11.42  | -1.42  | 5.00E-05 | 4.28E-04 | --                                                                     |
| EVM0008835 | 55.75  | 149.26 | -1.42  | 5.00E-05 | 4.28E-04 | Carbohydrate transport and metabolism                                 |
| EVM0002821 | 86.52  | 231.48 | -1.42  | 4.00E-04 | 2.65E-03 | --                                                                     |
| EVM0001632 | 36.49  | 97.53  | -1.42  | 5.00E-05 | 4.28E-04 | --                                                                     |
| EVM0003818 | 15.05  | 40.20  | -1.42  | 5.00E-05 | 4.28E-04 | RNA processing and modification                                       |

Microbial signal peptidase 12 kDa subunit (SPC12)
| EVM0002245 | 24.28 | 64.74 | -1.41 | 5.00E-05 | 4.28E-04 | Function unknown | Leo1-like protein |
| EVM0008283 | 44.15 | 117.57 | -1.41 | 5.00E-05 | 4.28E-04 | -- | Fungal hydrophobin |
| EVM0005649 | 153.19 | 407.26 | -1.41 | 5.00E-05 | 4.28E-04 | Transcription | Basic region leucine zipper |
| EVM0001419 | 216.66 | 575.26 | -1.41 | 5.00E-05 | 4.28E-04 | Signal transduction mechanisms | SGS domain |
| EVM0003839 | 516.29 | 1370.46 | -1.41 | 5.00E-05 | 4.28E-04 | Translation, ribosomal structure and biogenesis | Ribosomal S13/S15 N-terminal domain |
| EVM0005821 | 6.11 | 16.20 | -1.41 | 5.00E-05 | 4.28E-04 | -- | -- |
| EVM0004708 | 144.71 | 383.86 | -1.41 | 5.00E-05 | 4.28E-04 | -- | SecY translocase |
| EVM0006082 | 2.37 | 6.28 | -1.41 | 9.05E-03 | 3.46E-02 | -- | -- |
| EVM0005245 | 24.45 | 64.79 | -1.41 | 5.00E-05 | 4.28E-04 | -- | Ubiquitin-2 like Rad60 SUMO-like |
| EVM0011391 | 30.67 | 81.24 | -1.41 | 5.00E-05 | 4.28E-04 | Translation, ribosomal structure and biogenesis | Noc2p family |
| EVM000381 | 15.88 | 42.04 | -1.40 | 5.00E-05 | 4.28E-04 | Function unknown | Folate-sensitive fragile site protein Fra10Ac1 |
| EVM000651 | 40.25 | 106.52 | -1.40 | 5.00E-03 | 2.15E-02 | -- | Transient receptor potential (TRP) ion channel |
| EVM0006403 | 294.76 | 778.81 | -1.40 | 5.00E-05 | 4.28E-04 | Inorganic ion transport and metabolism | Anion-transporting ATPase |
| Gene Accession | Expression | Fold Change | Log2 Ratio | p-value (FDR) | GO Term | Description |
|----------------|------------|-------------|------------|---------------|---------|-------------|
| EVM0000472     | 1331.09    | -1.40       | 5.00E-05   | 4.28E-04      |         |             |
| EVM0011042     | 149.02     | -1.39       | 5.00E-05   | 4.28E-04      | Signal transcription mechanisms | Inhibitor of apoptosis-promoting Bax1 |
| EVM0003745     | 5.02       | -1.39       | 5.00E-05   | 4.28E-04      |         |             |
| EVM0007065     | 74.32      | -1.39       | 5.00E-05   | 4.28E-04      |         |             |
| EVM0005323     | 5.98       | -1.39       | 1.00E-04   | 7.96E-04      |         |             |
| EVM0001935     | 17.61      | -1.39       | 5.00E-05   | 4.28E-04      |         | Myosin-like coiled-coil protein |
| EVM0010981     | 1381.82    | -1.39       | 1.55E-03   | 8.22E-03      | Function unknown | Activator of Hsp90 ATPase, N-terminal |
| EVM0010500     | 36.63      | -1.39       | 5.00E-05   | 4.28E-04      | Transcription | RNA polymerase II transcription factor SIII (Elongin) subunit A |
| EVM0011226     | 121.74     | -1.39       | 5.00E-05   | 4.28E-04      | RNA processing and modification | Zinc-finger double-stranded RNA-binding |
| EVM0003499     | 605.32     | -1.39       | 5.00E-05   | 4.28E-04      |         | Rare lipoprotein A (RlpA)-like double-psi beta-barrel |
| EVM0004433     | 10.36      | -1.39       | 5.00E-05   | 4.28E-04      |         | Lactonase, 7-bladed beta-propeller |
| EVM0002996     | 22.09      | -1.39       | 5.00E-05   | 4.28E-04      | Transcription | Sin3 associated polypeptide p18 (SAP18) |
| EVM0009944     | 8.88       | -1.38       | 5.00E-05   | 4.28E-04      |         |             |
| EVM Code     | Value 1 | Value 2 | Log2 Fold Change | Log10 P Value | Description                                                                 |
|-------------|---------|---------|------------------|--------------|-----------------------------------------------------------------------------|
| EVM0009653  | 22.76   | 59.31   | -1.38            | 5.00E-05     | 4.28E-04                      | Cellulase (glycosyl hydrolase family 5)                                      |
| EVM0004924  | 10.49   | 27.32   | -1.38            | 1.40E-02     | 4.90E-02                      | --                                                                           |
| EVM0000593  | 100.34  | 261.18  | -1.38            | 5.00E-05     | 4.28E-04                      | Protein of unknown function (DUF952)                                        |
| EVM0009691  | 31.92   | 83.08   | -1.38            | 5.00E-05     | 4.28E-04                      | Carbohydrate transport and metabolism                                      |
| EVM0010758  | 17.78   | 46.25   | -1.38            | 5.00E-05     | 4.28E-04                      | RNA processing and modification                                             |
| EVM0006402  | 164.77  | 428.53  | -1.38            | 5.00E-05     | 4.28E-04                      | --                                                                           |
| EVM0008637  | 14.47   | 37.61   | -1.38            | 5.00E-05     | 4.28E-04                      | RNA processing and modification                                             |
| EVM0006319  | 1.55    | 4.02    | -1.38            | 5.45E-03     | 2.31E-02                      | --                                                                           |
| EVM0012074  | 18.71   | 48.60   | -1.38            | 5.00E-05     | 4.28E-04                      | Lipid transport and metabolism                                             |
| EVM0007190  | 8.15    | 21.15   | -1.38            | 5.00E-05     | 4.28E-04                      | 50S ribosome-binding GTPase                                                 |
| EVM0002154  | 1.66    | 4.29    | -1.37            | 1.85E-03     | 9.52E-03                      | --                                                                           |
| EVM0008088  | 5.56    | 14.42   | -1.37            | 5.50E-04     | 3.46E-03                      | --                                                                           |
| EVM0008651  | 86.60   | 224.47  | -1.37            | 5.00E-05     | 4.28E-04                      | Inorganic ion transport and metabolism                                      |
| EVM0000593  | 100.34  | 261.18  | -1.38            | 5.00E-05     | 4.28E-04                      | Copper/zinc superoxide dismutase (SODC)                                    |
| EVM0000204 | 890.32 | 2303.93 | -1.37 | 4.50E-04 | 2.92E-03 | -- | short chain dehydrogenase |
| EVM0008011 | 65.93  | 170.62  | -1.37 | 5.00E-05 | 4.28E-04 | -- | -- |
| EVM0004173 | 22.04  | 57.02   | -1.37 | 5.00E-05 | 4.28E-04 | -- | -- |
| EVM0003008 | 55.18  | 142.78  | -1.37 | 5.00E-05 | 4.28E-04 | -- | -- |
| EVM0007861 | 87.11  | 225.36  | -1.37 | 5.00E-05 | 4.28E-04 | -- | Protein of unknown function (DUF1183) |
| EVM0010095 | 7.47   | 19.32   | -1.37 | 5.00E-05 | 4.28E-04 | Replication, recombination and repair | DNA polymerase alpha/epsilon subunit B |
| EVM0002317 | 49.27  | 127.29  | -1.37 | 3.30E-03 | 1.53E-02 | -- | -- |
| EVM0006575 | 4.16   | 10.73   | -1.37 | 5.00E-05 | 4.28E-04 | -- | -- |
| EVM0008064 | 12.24  | 31.56   | -1.37 | 5.00E-05 | 4.28E-04 | -- | Shugoshin C terminus |
| EVM0012095 | 7.23   | 18.64   | -1.37 | 2.00E-04 | 1.46E-03 | #N/A | #N/A |
| EVM0011261 | 21.47  | 55.30   | -1.36 | 5.00E-05 | 4.28E-04 | General function prediction only | WD domain, G-beta repeat only |
| EVM0007650 | 120.79 | 310.96  | -1.36 | 5.00E-05 | 4.28E-04 | -- | -- |
| EVM0003518 | 21.87  | 56.29   | -1.36 | 1.00E-04 | 7.96E-04 | -- | -- |
| Accession   | Value 1 | Value 2   | Change | p1 | p2 | Description                                             |
|------------|---------|-----------|--------|----|----|---------------------------------------------------------|
| EVM0007616 | 24.00   | 61.74     | -1.36  | 5.00E-05 | 4.28E-04 | Transcription                                          |
| EVM0001772 | 176.34  | 453.19    | -1.36  | 5.00E-05 | 4.28E-04 | Translation, ribosomal structure and biogenesis        |
| EVM0009084 | 52.12   | 133.86    | -1.36  | 5.00E-05 | 4.28E-04 | Translation, ribosomal structure and biogenesis        |
| EVM0004477 | 24.13   | 61.91     | -1.36  | 5.00E-05 | 4.28E-04 | --                                                      |
| EVM0010867 | 928.29  | 2378.57   | -1.36  | 1.00E-04 | 7.96E-04 | --                                                      |
| EVM0009646 | 5.93    | 15.19     | -1.36  | 7.50E-03 | 2.98E-02 | Pheromone A receptor                                    |
| EVM0005915 | 11.51   | 29.42     | -1.35  | 5.00E-05 | 4.28E-04 | Lipase (class 3)                                       |
| EVM0004869 | 130.86  | 334.16    | -1.35  | 5.00E-05 | 4.28E-04 | Lipid transport and metabolism                          |
| EVM0000850 | 17.06   | 43.54     | -1.35  | 1.00E-04 | 7.96E-04 | --                                                      |
| EVM0006126 | 28.63   | 72.95     | -1.35  | 5.00E-05 | 4.28E-04 | --                                                      |
| EVM0006060 | 5.94    | 15.14     | -1.35  | 1.00E-04 | 7.96E-04 | PP-loop family                                          |
| EVM0006316 | 5.94    | 15.11     | -1.35  | 5.00E-05 | 4.28E-04 | Function unknown                                       |
| EVM0011059 | 36.64   | 93.14     | -1.35  | 5.00E-05 | 4.28E-04 | --                                                      |
| EVM       | FDA   | EC   | PM    | EVM       | FDA   | EC   | PM    | Comment                                                                 |
|-----------|-------|------|-------|-----------|-------|------|-------|-------------------------------------------------------------------------|
| EVM0007279 | 28.45 | 72.32| -1.35 | 1.00E-04  | 7.96E-04| --   | --    |                                                                         |
| EVM0006922 | 37.48 | 95.24| -1.35 | 1.00E-04  | 7.96E-04| --   | --    |                                                                         |
| EVM0001689 | 250.94| 636.22| -1.34 | 5.00E-05  | 4.28E-04| General function prediction only | Ras family |
| EVM0005087 | 91.68 | 232.42| -1.34 | 5.00E-05  | 4.28E-04| Intracellular trafficking, secretion, and vesicular transport | Tim17/Tim22/Tim23/Pmp24 family |
| EVM0011499 | 13.28 | 33.64| -1.34 | 5.00E-05  | 4.28E-04| --   | --    |                                                                         |
| EVM0009851 | 14.31 | 36.24| -1.34 | 5.00E-05  | 4.28E-04| Function unknown | WD domain, G-beta repeat |
| EVM0010669 | 96.29 | 243.59| -1.34 | 5.00E-05  | 4.28E-04| --   | --    |                                                                         |
| EVM0000212 | 79.58 | 201.28| -1.34 | 5.00E-05  | 4.28E-04| Posttranslational modification, protein turnover, chaperones | Zinc finger, C3HC4 type (RING finger) |
| EVM0011085 | 32.62 | 82.46| -1.34 | 1.00E-04  | 7.96E-04| --   | Translation initiation factor IF-3, C-terminal domain |
| EVM0007358 | 13.04 | 32.96| -1.34 | 5.00E-05  | 4.28E-04| --   | --    |                                                                         |
| EVM0004502 | 15.24 | 38.44| -1.34 | 5.00E-05  | 4.28E-04| RNA processing and modification | SUZ domain |
| EVM0005121 | 166.37| 418.83| -1.33 | 5.00E-05  | 4.28E-04| General function prediction only | Ras family |
| Gene Symbol   | Fold Change | Log2 Fold Change | Adj. P-Value | Description                                      |
|--------------|-------------|-----------------|--------------|-------------------------------------------------|
| EVM0004946   | 1.02        | 0.02            | 0.82         | --                                               |
| EVM0002522   | 6.83        | 2.56            | -1.33        | Protein of unknown function (DUF1399)           |
| EVM0008302   | 33.75       | 84.87           | -1.33        | --                                               |
| EVM0007669   | 1.10        | 2.76            | -1.33        | Zinc-finger double domain                       |
| EVM0010265   | 43.39       | 108.98          | -1.33        | Conserved hypothetical ATP binding protein only  |
| EVM0010273   | 2.54        | 6.38            | -1.33        | --                                               |
| EVM0004408   | 19.97       | 50.09           | -1.33        | Protein of unknown function (DUF563)            |
| EVM0007912   | 6.46        | 16.16           | -1.32        | --                                               |
| EVM0001156   | 118.61      | 296.49          | -1.32        | --                                               |
| EVM0010557   | 6.14        | 15.34           | -1.32        | Repair protein Rad1/Rec1/Rad17                  |
| EVM0004661   | 5.54        | 13.84           | -1.32        | Cytochrome P450                                  |
| EVM0012116   | 100.74      | 251.74          | -1.32        | Posttranslational modification, protein turnover, chaperones |
| EVM0012015 | 17.15 | 42.76 | -1.32 | 5.00E-05 | 4.28E-04 | Translation, ribosomal structure and biogenesis | BOP1NT (NUC169) domain |
| EVM0005216 | 44.31 | 110.45 | -1.32 | 5.00E-05 | 4.28E-04 | -- | Whi5 like |
| EVM0011460 | 245.66 | 611.87 | -1.32 | 5.00E-05 | 4.28E-04 | -- | -- |
| EVM0001152 | 162.96 | 405.40 | -1.31 | 5.00E-05 | 4.28E-04 | General function prediction only | Mpv17 / PMP22 family |
| EVM0009800 | 219.06 | 544.69 | -1.31 | 5.00E-05 | 4.28E-04 | -- | Mitochondrial ribosomal protein L31 |
| EVM0003778 | 5.97 | 14.85 | -1.31 | 1.25E-03 | 6.87E-03 | -- | -- |
| EVM0002708 | 24.06 | 59.80 | -1.31 | 5.00E-05 | 4.28E-04 | Function unknown | Ima1 N-terminal domain |
| EVM0004959 | 166.73 | 413.55 | -1.31 | 5.00E-05 | 4.28E-04 | General function prediction only | PQ loop repeat |
| EVM0007827 | 96.01 | 238.04 | -1.31 | 5.00E-05 | 4.28E-04 | -- | Lipase (class 3) |
| EVM0005244 | 144.94 | 359.20 | -1.31 | 5.00E-05 | 4.28E-04 | Function unknown | Polysaccharide biosynthesis |
| EVM0005693 | 36.13 | 89.55 | -1.31 | 5.00E-05 | 4.28E-04 | -- | -- |
| EVM0011601 | 125.16 | 310.07 | -1.31 | 5.00E-05 | 4.28E-04 | -- | -- |
| EVM0002871 | 17.01 | 42.12 | -1.31 | 5.00E-05 | 4.28E-04 | -- | -- |
| Accession   | EVM0007897 | EVM0000773 | EVM0011359 | EVM0008632 | EVM0010389 | EVM0008917 | EVM0000800 | EVM0001054 | EVM0005431 | EVM0002558 |
|-------------|------------|------------|------------|------------|------------|------------|------------|------------|------------|------------|
| Value1      | 0.84       | 426.10     | 203.43     | 6.89       | 75.11      | 19.92      | 309.62     | 21.78      | 8.59       | 11.05      |
| Value2      | 2.09       | 1051.07    | 501.15     | 16.97      | 184.74     | 48.96      | 760.97     | 53.52      | 21.08      | 27.09      |
| Value3      | -1.31      | -1.30      | -1.30      | -1.30      | -1.30      | -1.30      | -1.30      | -1.30      | -1.30      | -1.29      |
| EVM0007897  | 1.32E-02   | 1.00E-04   | 5.00E-05   | 9.50E-04   | 1.90E-03   | 4.50E-04   | 5.50E-04   | 5.00E-05   | 5.00E-05   | 5.00E-05   |
| EVM0000773  | 4.67E-02   | 7.96E-04   | 4.28E-04   | 5.46E-03   | 9.73E-03   | 2.92E-03   | 3.46E-03   | 4.28E-04   | 4.28E-04   | 4.28E-04   |
| EVM0011359  | --         | Energy production and conversion | Energy production and conversion | Posttranslational modification, protein turnover, chaperones | Intracellular trafficking, secretion, and vesicular transport | General function prediction only | Protein of unknown function (DUF4449) | -- | -- |
| EVM0008632  | NADH-ubiquinone oxidoreductase B18 subunit (NDUFB7) | ETC complex I subunit conserved region | Isoprenylcysteine carboxyl methyltransferase (ICMT) family | Tim10/DDP family zinc finger | Fcf1 |
| EVM0010389  | Protein kinase domain | -- | -- | -- | -- |
| EVM0008917  | Protein of unknown function (DUF4449) | -- | -- | -- | -- |
| EVM0000800  | Cell cycle control, cell division, chromosome partitioning | HEC/Ndc80p family | -- | -- | -- |
| EVM0001054  | -- | -- | -- | -- | -- |
| EVM0005431  | Cell cycle control, cell division, chromosome partitioning | Protein kinase domain | -- | -- | -- |
| EVM0002558  | -- | -- | -- | -- | -- |
| Gene ID     | Foldchange | Expression Log2 | p-value | Function                                              |
|------------|------------|-----------------|---------|-------------------------------------------------------|
| EVM0006314 | 4.06       | 9.95            | -1.29   | 2.50E-04 1.77E-03 General function prediction only     |
| EVM0010229 | 28.14      | 68.91           | -1.29   | 5.00E-05 4.28E-04 Zinc-binding dehydrogenase          |
| EVM0004513 | 76.28      | 186.79          | -1.29   | 2.50E-04 1.77E-03 pfkB family carbohydrate kinase     |
| EVM0007883 | 170.76     | 417.69          | -1.29   | 5.00E-05 4.28E-04                                  |
| EVM0002542 | 183.23     | 448.04          | -1.29   | 5.00E-05 4.28E-04 Lipid transport and metabolism     |
| EVM0012070 | 1068.93    | 2610.87         | -1.29   | 7.00E-04 4.23E-03 RNA recognition motif. (a.k.a. RRM, RBD, or RNP domain) |
| EVM0005236 | 407.49     | 994.97          | -1.29   | 5.00E-05 4.28E-04 RNA processing and modification    |
| EVM0004626 | 15.47      | 37.76           | -1.29   | 1.00E-04 7.96E-04                                |
| EVM0007325 | 5.68       | 13.86           | -1.29   | 7.50E-04 4.49E-03 General function prediction only    |
| EVM0000313 | 13.11      | 31.99           | -1.29   | 1.00E-04 7.96E-03 Translation, ribosomal structure and biogenesis |
| EVM0007121 | 10.59      | 25.83           | -1.29   | 1.00E-04 7.96E-03                                  |
| EVM0005913 | 104.35     | 254.38          | -1.29   | 5.00E-05 4.28E-04 Phosphoribosyl transferase domain  |
| EVM0004405 | 1.91       | 4.66            | -1.29   | 6.40E-03 2.62E-02                                  |
| Accession     | Score 1 | Score 2 | Score 3 | Score 4 | Score 5 | Score 6 | Score 7 | Score 8 | Score 9 | Description                                                                 |
|--------------|---------|---------|---------|---------|---------|---------|---------|---------|---------|----------------------------------------------------------------------------|
| EVM0006666   | 48.95   | 119.20  | -1.28   | 5.00E-05| 4.28E-04| General function prediction only | Homeobox domain            |
| EVM0011169   | 57.94   | 140.33  | -1.28   | 5.00E-05| 4.28E-04| Posttranslational modification, protein turnover, chaperones | ATPase family associated with various cellular activities (AAA) |
| EVM0004319   | 32.83   | 79.47   | -1.28   | 5.00E-05| 4.28E-04| --                                              | Protein of unknown function (DUF2962)                               |
| EVM0008404   | 15.89   | 38.43   | -1.27   | 5.00E-05| 4.28E-04| RNA processing and modification                | BING4CT (NUC141) domain                                             |
| EVM0005282   | 514.01  | 1242.20 | -1.27   | 3.50E-04| 2.36E-03| Posttranslational modification, protein turnover, chaperones | Nucleotide exchange factor Fes1                                    |
| EVM000907    | 2.79    | 6.73    | -1.27   | 2.25E-03| 1.12E-02| --                                              | --                                                                    |
| EVM0002826   | 98.65   | 237.84  | -1.27   | 5.00E-05| 4.28E-04| General function prediction only               | Cell differentiation family, Rcd1-like                             |
| EVM0012262   | 10.72   | 25.85   | -1.27   | 5.50E-04| 3.46E-03| Transcription                                   | SHS2 domain found in N terminus of Rpb7p/Rpc25p/MJ0397              |
| EVM0004038   | 1024.34 | 2468.78 | -1.27   | 2.00E-03| 1.01E-02| Translation, ribosomal structure and biogenesis | Ribosomal protein L6                                                |
| EVM0000630   | 17.98   | 43.33   | -1.27   | 5.00E-05| 4.28E-04| --                                              | --                                                                    |
| EVM0007834   | 40.39   | 97.29   | -1.27   | 5.00E-05| 4.28E-04| --                                              | ADP-ribosylglycohydrolase                                           |
| Accession      | Log2 Fold Change | Q Value | Function                                                                 | Family/Domain                                                                                                                                 |
|---------------|------------------|---------|---------------------------------------------------------------------------|--------------------------------------------------------------------------------------------------------------------------------------------|
| EVM000425     | 777.91           | 1873.10 | -1.27                                                                     | Intracellular trafficking, secretion, and vesicular transport                                                                             |
|               |                  |         |                                                                            | TB2/DP1, HVA22 family                                                                                                                     |
| EVM002402     | 3.95             | 9.51    | -1.27                                                                     | --                                                                                                                                     |
|               |                  |         |                                                                            | Domain of unknown function (DUF3328)                                                                                                     |
| EVM0008872    | 2.84             | 6.82    | -1.27                                                                     | Lipid transport and metabolism                                                                                                         |
|               |                  |         |                                                                            | Fatty acid hydroxylase superfamily                                                                                                      |
| EVM003967     | 119.12           | 286.42  | -1.27                                                                     | Function unknown                                                                                                                         |
|               |                  |         |                                                                            | Mago binding                                                                                                                            |
| EVM007965     | 22.80            | 54.81   | -1.27                                                                     | Energy production and conversion                                                                                                         |
|               |                  |         |                                                                            | Mitochondrial carrier protein                                                                                                          |
| EVM007303     | 215.46           | 517.68  | -1.26                                                                     | Intracellular trafficking, secretion, and vesicular transport                                                                            |
|               |                  |         |                                                                            | PRELI-like family                                                                                                                       |
| EVM009047     | 17.78            | 42.69   | -1.26                                                                     | General function prediction only                                                                                                         |
|               |                  |         |                                                                            | WD domain, G-beta repeat                                                                                                                |
| EVM001074     | 75.66            | 181.69  | -1.26                                                                     | Function unknown                                                                                                                         |
|               |                  |         |                                                                            | Membrane transport protein                                                                                                              |
| EVM0008759    | 21.69            | 52.08   | -1.26                                                                     | --                                                                                                                                     |
|               |                  |         |                                                                            | --                                                                                                                                     |
| EVM0000029    | 14.67            | 35.22   | -1.26                                                                     | Transcription                                                                                                                           |
|               |                  |         |                                                                            | RNA polymerase Rpb3/RpoA insert domain                                                                                                  |
| EVM007555     | 23.12            | 55.51   | -1.26                                                                     | --                                                                                                                                     |
|               |                  |         |                                                                            | --                                                                                                                                     |
| EVM0011492    | 336.75           | 808.34  | -1.26                                                                     | --                                                                                                                                     |
|               |                  |         |                                                                            | --                                                                                                                                     |
| ID            | C0   | C1    | C2    | C3    | C4    | C5    | C6   | C7   | C8       | C9   | C10      | C11     |
|---------------|------|-------|-------|-------|-------|-------|------|------|----------|------|----------|----------|
| EVM0002416    | 136.15 | 326.79 | -1.26 | 1.50E-04 | 1.14E-03 | Translation, ribosomal structure and biogenesis | Ribosomal protein S16 |
| EVM0006106    | 17.77  | 42.66  | -1.26 | 5.00E-05 | 4.28E-04 | -- | -- |
| EVM0009334    | 15.69  | 37.67  | -1.26 | 5.00E-05 | 4.28E-04 | -- | -- |
| EVM0000705    | 630.14 | 1512.21 | -1.26 | 5.00E-05 | 4.28E-04 | Inorganic ion transport and metabolism | Iron/manganese superoxide dismutases, C-terminal domain |
| EVM0007607    | 140.17 | 336.34 | -1.26 | 5.00E-05 | 4.28E-04 | General function prediction only | TPR repeat |
| EVM0001314    | 79.24  | 190.04 | -1.26 | 5.00E-05 | 4.28E-04 | -- | -- |
| EVM0002044    | 94.18  | 225.88 | -1.26 | 5.00E-05 | 4.28E-04 | Translation, ribosomal structure and biogenesis | Initiation factor 2 subunit family |
| EVM0001141    | 8.15   | 19.54  | -1.26 | 2.20E-03 | 1.10E-02 | -- | -- |
| EVM0010493    | 10.22  | 24.50  | -1.26 | 3.20E-03 | 1.49E-02 | -- | -- |
| EVM0011608    | 874.64 | 2092.67 | -1.26 | 1.50E-04 | 1.14E-03 | Translation, ribosomal structure and biogenesis | Ribosomal protein L24e |
| EVM0006616    | 1026.24 | 2454.15 | -1.26 | 6.00E-04 | 3.72E-03 | Energy production and conversion | Mitochondrial carrier protein |
| EVM0007953    | 326.55 | 780.62 | -1.26 | 2.00E-04 | 1.46E-03 | -- | -- |
| EVM0010259    | 825.94 | 1973.39 | -1.26 | 1.00E-04 | 7.96E-04 | -- | Domain of unknown function (DUF427) |
| EVM0011272 | 2.35 | 5.61 | -1.26 | 2.65E-03 | 1.28E-02 | -- | -- |
| EVM0008626 | 40.43 | 96.42 | -1.25 | 5.00E-05 | 4.28E-04 | -- | -- |
| EVM0009512 | 32.12 | 76.60 | -1.25 | 5.00E-05 | 4.28E-04 | Lipid transport and metabolism | CoA-transferase family III |
| EVM0007418 | 43.76 | 104.37 | -1.25 | 5.00E-05 | 4.28E-04 | Carbohydrate transport and metabolism | Protein kinase domain |
| EVM0009341 | 10.40 | 24.81 | -1.25 | 1.50E-04 | 1.14E-03 | RNA processing and modification | DEAD/DEAH box helicase |
| EVM0001538 | 13.36 | 31.86 | -1.25 | 5.00E-05 | 4.28E-04 | -- | F-box-like |
| EVM0010217 | 48.18 | 114.86 | -1.25 | 1.50E-04 | 1.14E-03 | -- | Domain of unknown function (DUF4139) |
| EVM0009858 | 33.92 | 80.81 | -1.25 | 5.00E-05 | 4.28E-04 | Translation, ribosomal structure and biogenesis | CPL (NUC119) domain |
| EVM0011612 | 35.03 | 83.44 | -1.25 | 5.00E-05 | 4.28E-04 | -- | -- |
| EVM0005496 | 390.23 | 929.14 | -1.25 | 2.00E-04 | 1.46E-03 | -- | -- |
| EVM0002811 | 323.94 | 770.52 | -1.25 | 5.50E-04 | 3.46E-03 | Posttranslational modification, protein turnover, chaperones | Thioredoxin |
| EVM0000189 | 6.27 | 14.90 | -1.25 | 1.20E-03 | 6.64E-03 | -- | Glycosyl hydrolases family 43 |
| EVM0007568 | 127.56 | 303.20 | -1.25 | 5.00E-05 | 4.28E-04 | -- | ACT domain |
| EVM0001635 | 109.76 | 260.62 | -1.25 | 5.00E-05 | 4.28E-04 | Posttranslational modification, protein turnover, chaperones | GrpE |
| EVM0006578 | 98.13  | 233.00 | -1.25 | 5.00E-05 | 4.28E-04 | Intracellular trafficking, secretion, and vesicular transport | Syntaxin |
| EVM0006768 | 12.12  | 28.76  | -1.25 | 5.00E-05 | 4.28E-04 | Secondary metabolites biosynthesis, transport and catabolism | Cytochrome P450 |
| EVM0003042 | 10.81  | 25.63  | -1.25 | 1.00E-04 | 7.96E-04 | -- | -- |
| EVM0004668 | 149.04 | 353.19 | -1.24 | 2.50E-04 | 1.77E-03 | General function prediction only | Proteolipid membrane potential modulator |
| EVM0008633 | 34.63  | 82.00  | -1.24 | 5.00E-05 | 4.28E-04 | Intracellular trafficking, secretion, and vesicular transport | Autophagy-related protein 13 |
| EVM0011593 | 7.13   | 16.86  | -1.24 | 3.00E-04 | 2.07E-03 | Carbohydrate transport and metabolism | Major Facilitator Superfamily |
| EVM0011593 | 7.13   | 16.86  | -1.24 | 3.00E-04 | 2.07E-03 | Carbohydrate transport and metabolism | Major Facilitator Superfamily |
| EVM0011593 | 7.13   | 16.86  | -1.24 | 3.00E-04 | 2.07E-03 | Carbohydrate transport and metabolism | Major Facilitator Superfamily |
| EVM0011593 | 7.13   | 16.86  | -1.24 | 3.00E-04 | 2.07E-03 | Carbohydrate transport and metabolism | Major Facilitator Superfamily |
| Gene ID | E Value | Score | p Value | Domain Description |
|--------|---------|-------|---------|-------------------|
| EVM0003932 | 90.21   | 213.30| 1.24    | General function prediction only |
| EVM0007596 | 21.58   | 51.00 | 1.24    | RNA recognition motif. (a.k.a. RRM, RBD, or RNP domain) |
| EVM0011840 | 17.63   | 41.60 | 1.24    | 50S ribosome-binding GTPase |
| EVM0005550 | 115.76  | 272.77| 1.24    | Arrestin (or S-antigen), C-terminal domain |
| EVM0005197 | 35.23   | 82.94 | 1.24    | Major Facilitator Superfamily |
| EVM0005877 | 682.84  | 1607.28| 1.24   | Ubiquinol-cytochrome C reductase complex 14kD subunit |
| EVM0006994 | 2.05    | 4.83  | 1.23    | ER membrane protein SH3 |
| EVM0011577 | 86.47   | 203.24| 1.23    | Alpha/beta hydrolase family |
| EVM0005200 | 51.03   | 119.93| 1.23    | Phospholipid methyltransferase |
| EVM0008327 | 7.67    | 18.01 | 1.23    | Protein of unknown function (DUF3445) |
| EVM0009748 | 20.75 | 48.64 | -1.23 | 4.50E-04 | 2.92E-03 | -- | Endoplasmic reticulum-based factor for assembly of V-ATPase |
| EVM0004503 | 2.96  | 6.94  | -1.23 | 2.55E-03 | 1.24E-02 | -- | -- |
| EVM0004135 | 14.64 | 34.31 | -1.23 | 5.00E-05 | 4.28E-04 | -- | Aconitase family (aconitate hydratase) |
| EVM0004782 | 28.37 | 66.49 | -1.23 | 1.00E-04 | 7.96E-04 | -- | Tyrosine phosphatase family |
| EVM0002657 | 408.67| 957.32| -1.23 | 1.00E-04 | 7.96E-04 | General function prediction only | Short chain dehydrogenase |
| EVM0004345 | 20.90 | 48.94 | -1.23 | 1.50E-04 | 1.14E-03 | -- | Taurine catabolism dioxygenase TauD, TfdA family |
| EVM0000893 | 18.30 | 42.83 | -1.23 | 7.00E-04 | 4.23E-03 | -- | -- |
| EVM0010862 | 90.28 | 211.19| -1.23 | 5.00E-05 | 4.28E-04 | Translation, ribosomal structure and biogenesis | Ribosomal protein L24e |
| EVM0009651 | 4.96  | 11.60 | -1.23 | 2.50E-04 | 1.77E-03 | Energy production and conversion | FAD binding domain |
| EVM0011153 | 189.03| 441.33| -1.22 | 5.00E-05 | 4.28E-04 | -- | Tim17/Tim22/Tim23/Pmp24 family |
| EVM0000143 | 5.32  | 12.41 | -1.22 | 1.00E-04 | 7.96E-04 | -- | Pectate lyase |
| EVM0012211 | 24.74 | 57.71 | -1.22 | 5.00E-05 | 4.28E-04 | -- | -- |
| EVM0006852 | 41.99 | 97.85 | -1.22 | 5.00E-04 | 3.19E-03 | -- | Sen15 protein |
| ID          | Log Fold Change | p-value | Description                                      | Protein Name                           |
|-------------|-----------------|---------|--------------------------------------------------|----------------------------------------|
| EVM0006461  | 6.93            | 1.22    | 8.50E-04 4.98E-03 Lipid transport and metabolism | Acyltransferase                        |
| EVM0010213  | 1148.45         | 1.22    | 5.70E-03 2.39E-02 --                             | --                                    |
| EVM0002814  | 131.54          | 1.22    | 1.00E-04 7.96E-04 Intracellular trafficking, secretion, and vesicular transport | Peroxisomal membrane protein (Pex16) |
| EVM0003201  | 1421.95         | 1.22    | 1.00E-04 7.96E-04 --                             | Mitochondrial ATP synthase epsilon chain |
| EVM0009471  | 17.90           | 1.22    | 9.00E-04 5.22E-03 --                             | --                                    |
| EVM0008951  | 29.06           | 1.21    | 5.00E-05 4.28E-04 Intracellular trafficking, secretion, and vesicular transport | Tetratricopeptide repeat |
| EVM0004301  | 22.59           | 1.21    | 5.00E-05 4.28E-04 Secondary metabolites biosynthesis, transport and catabolism | Pyridine nucleotide-disulphide oxidoreductase |
| EVM0002975  | 522.13          | 1.21    | 2.35E-03 1.16E-02 --                             | Putative stress-responsive nuclear envelope protein |
| EVM0011618  | 111.48          | 1.21    | 2.00E-04 1.46E-03 --                             | --                                    |
| EVM0000116  | 5.76            | 1.21    | 5.10E-03 2.19E-02 --                             | --                                    |
| EVM0009698  | 1174.02         | 1.21    | 5.00E-05 4.28E-04 Translation, ribosomal structure and biogenesis | Ribosomal L38e protein family |


| Gene ID         | EVM0012235 | EVM0007682 | EVM0010549 | EVM0002205 | EVM0001189 | EVM0005130 | EVM0000714 | EVM0008508 | EVM0007602 | EVM0010922 | EVM0009839 | EVM0011785 |
|----------------|------------|------------|------------|------------|------------|------------|------------|------------|------------|------------|------------|------------|
| Gene Name      |            |            |            |            |            |            |            |            |            |            |            |            |
| Protein Name   |            |            |            |            |            |            |            |            |            |            |            |            |
| Description    |            |            |            |            |            |            |            |            |            |            |            |            |
| Value          | 479.41     | 61.28      | 13.82      | 1.74       | 42.53      | 13.69      | 287.33     | 7.71       | 10.24      | 220.18     | 185.50     | 5.92       |
| Value          | 110.66     | 141.89     | 31.98      | 4.03       | 98.39      | 31.65      | 664.41     | 17.83      | 23.67      | 508.81     | 428.35     | 13.65      |
| Fold Change    | -1.21      | -1.21      | -1.21      | -1.21      | -1.21      | -1.21      | -1.21      | -1.21      | -1.21      | -1.21      | -1.21      | -1.21      |
| P-Value        | 2.00E-04   | 6.17E-03   | 4.28E-05   | 8.87E-03   | 4.28E-05   | 1.46E-03   | 4.28E-03   | 9.29E-03   | 1.14E-03   | 7.96E-04   | 1.21E-03   | 4.28E-04   |
| Description    | Posttranslational modification, protein turnover, chaperones | -- | -- | -- | Chromatin structure and dynamics | Histone deacetylase domain | Translation, ribosomal structure and biogenesis | Ribosomal protein S7p/S5e | Lipid transport and metabolism | PLD-like domain | Nitrate monooxygenase | Carbohydrate transport and metabolism | Fungal specific transcription factor domain | Cyclophilin type peptidyl-prolyl cis-trans isomerase/CLD |
| Accession   | Start  | End    | Log2 Ratio | Fold Change | Description                                                                 |
|------------|--------|--------|------------|-------------|----------------------------------------------------------------------------|
| EVM0007562 | 22.06  | 50.89  | -1.21      | 0.50E-04    | --                                                                         |
| EVM0007412 | 330.14 | 760.69 | -1.20      | 2.00E-04    | Domain of unknown function (DUF202)                                       |
| EVM0004906 | 162.63 | 374.56 | -1.20      | 1.50E-04    | Fungal specific transcription factor domain                               |
| EVM0009107 | 2.30   | 5.30   | -1.20      | 8.90E-03    | --                                                                         |
| EVM0001013 | 1.27   | 2.91   | -1.20      | 1.27E-02    | --                                                                         |
| EVM0005135 | 11.96  | 27.52  | -1.20      | 5.00E-05    | Secondary metabolites biosynthesis, transport and catabolism              |
| EVM0010148 | 173.26 | 398.39 | -1.20      | 1.00E-04    | --                                                                         |
| EVM0011121 | 14.51  | 33.34  | -1.20      | 1.15E-03    | --                                                                         |
| EVM0002805 | 128.92 | 295.79 | -1.20      | 1.00E-04    | Intracellular trafficking, secretion, and vesicular transport             |
| EVM0003106 | 20.47  | 46.90  | -1.20      | 5.00E-05    | Translocation protein Sec62                                               |
| EVM0008959 | 218.04 | 499.13 | -1.19      | 5.00E-05    | Spt20 family                                                               |
| EVM0004906 | 162.63 | 374.56 | -1.20      | 1.50E-04    | Phosphatidylethanolamine-binding protein only                             |
| EVM0011835 | 78.75 | 180.24 | -1.19 | 5.00E-05 | 4.28E-04 | Posttranslational modification, protein turnover, chaperones | Ring finger domain |
| EVM0001453 | 2.06  | 4.72   | -1.19 | 7.45E-03 | 2.96E-02 | -- | -- |
| EVM0002160 | 4.11  | 9.40   | -1.19 | 1.28E-02 | 4.54E-02 | -- | -- |
| EVM0002217 | 170.46| 390.05 | -1.19 | 5.00E-05 | 4.28E-04 | -- | -- |
| EVM0002681 | 12.43 | 28.42  | -1.19 | 5.00E-05 | 4.28E-04 | General function prediction only | Glycosyl transferase family 90 |
| EVM0005012 | 4.61  | 10.52  | -1.19 | 1.00E-03 | 5.70E-03 | General function prediction only | Calcineurin-like phosphoesterase |
| EVM0003649 | 56.42 | 128.87 | -1.19 | 5.00E-05 | 4.28E-04 | General function prediction only | Thioesterase superfamily |
| EVM0006430 | 6.17  | 14.10  | -1.19 | 8.50E-04 | 4.98E-03 | -- | -- |
| EVM0004971 | 13.07 | 29.85  | -1.19 | 1.50E-04 | 1.14E-03 | #N/A | #N/A |
| EVM0007693 | 21.44 | 48.95  | -1.19 | 2.50E-04 | 1.77E-03 | -- | -- |
| EVM0003055 | 220.55| 503.41 | -1.19 | 1.00E-04 | 7.96E-04 | Function unknown | NUDIX domain |
| EVM0007328 | 1376.96| 3142.71| -1.19 | 5.00E-05 | 4.28E-04 | Translation, ribosomal structure and biogenesis | 60s Acidic ribosomal protein |
| EVM0002176 | 41.57 | 94.85 | -1.19 | 5.00E-05 | 4.28E-04 | -- | -- |
|------------|------|-------|------|---------|---------|---|---|
| EVM0001875 | 8.80 | 20.09 | -1.19 | 7.00E-04 | 4.23E-03 | -- | Sgf11 (transcriptional regulation protein) |
| EVM0006624 | 21.18 | 48.23 | -1.19 | 5.00E-05 | 4.28E-04 | Amino acid transport and metabolism | Pyridoxal-phosphate dependent enzyme |
| EVM0007006 | 135.54 | 308.61 | -1.19 | 2.00E-04 | 1.46E-03 | Signal transduction mechanisms | CS domain |
| EVM0006543 | 3.63 | 8.27 | -1.19 | 4.00E-04 | 2.65E-03 | -- | -- |
| EVM003844 | 12.89 | 29.31 | -1.19 | 1.50E-04 | 1.14E-03 | Function unknown | -- |
| EVM0007377 | 11.94 | 27.15 | -1.18 | 1.00E-04 | 7.96E-04 | RNA processing and modification | RNA pseudouridylate synthase |
| EVM0010407 | 10.81 | 24.57 | -1.18 | 1.50E-04 | 1.14E-03 | -- | Putative S-adenosyl-L-methionine-dependent methyltransferase |
| EVM0010348 | 13.48 | 30.63 | -1.18 | 1.15E-03 | 6.41E-03 | -- | -- |
| EVM0009717 | 975.88 | 2217.50 | -1.18 | 7.65E-03 | 3.02E-02 | -- | -- |
| EVM0011555 | 79.25 | 179.98 | -1.18 | 5.00E-05 | 4.28E-04 | -- | Sel1 repeat |
| EVM0011056 | 58.60 | 133.05 | -1.18 | 1.00E-04 | 7.96E-04 | -- | -- |
| Accession   | Value1 | Value2 | Description                  |
|-------------|--------|--------|------------------------------|
| EVM0009100  | 19.30  | 43.82  | -1.18                        |
|             | 5.00E-05| 4.28E-04| --                           |
| EVM0000616  | 98.02  | 222.47 | -1.18                        |
|             | 3.00E-04| 2.07E-03| -- SNARE domain              |
| EVM0011007  | 9.02   | 20.47  | -1.18                        |
|             | 6.00E-04| 3.72E-03| --                           |
| EVM0002693  | 57.78  | 131.06 | -1.18                        |
|             | 7.50E-04| 4.49E-03| --                           |
| EVM0006895  | 2.96   | 6.71   | -1.18                        |
|             | 1.37E-02| 4.80E-02| -- Protein of unknown function (DUF3129) |
| EVM0011806  | 609.02 | 1380.14| -1.18                        |
|             | 1.50E-04| 1.14E-03| Translation, ribosomal structure and biogenesis |
| EVM0009693  | 23.34  | 52.87  | -1.18                        |
|             | 5.00E-05| 4.28E-04| Function unknown            |
| EVM0006869  | 465.42 | 1054.10| -1.18                        |
|             | 5.00E-05| 4.28E-04| General function prediction only |
| EVM0007905  | 19.62  | 44.43  | -1.18                        |
|             | 2.50E-04| 1.77E-03| -- Spc19                     |
| EVM0005126  | 3.47   | 7.86   | -1.18                        |
|             | 1.25E-03| 6.87E-03| --                           |
| EVM0009339  | 40.77  | 92.24  | -1.18                        |
|             | 2.00E-04| 1.46E-03| Lipid transport and metabolism |
| EVM0012102  | 18.46  | 41.74  | -1.18                        |
|             | 2.00E-04| 1.46E-03| -- Emopamil binding protein |
| EVM0003678  | 4.71   | 10.64  | -1.18                        |
|             | 8.00E-04| 4.73E-03| -- FAD binding domain        |
| EVM     | 108.89 | 246.16 | -1.18  | 1.00E-04 | 7.96E-04 | RNA processing and modification | Zinc knuckle |
|---------|--------|--------|--------|----------|----------|----------------------------------|--------------|
| EVM     | 425.01 | 959.86 | -1.18  | 7.00E-04 | 4.23E-03 | --                               | BTB/POZ domain |
| EVM     | 39.66  | 89.56  | -1.18  | 5.00E-05 | 4.28E-04 | --                               | Voltage-dependent anion channel |
| EVM     | 47.15  | 106.31 | -1.17  | 5.00E-05 | 4.28E-04 | --                               | CybS          |
| EVM     | 8.84   | 19.92  | -1.17  | 5.00E-05 | 4.28E-04 | --                               | NYN domain    |
| EVM     | 18.61  | 41.96  | -1.17  | 1.00E-04 | 7.96E-04 | RNA processing and modification | pre-mRNA processing factor 3 (PRP3) |
| EVM     | 20.49  | 46.17  | -1.17  | 5.00E-05 | 4.28E-04 | --                               | Cytochrome P450 |
| EVM     | 170.34 | 383.71 | -1.17  | 2.50E-04 | 1.77E-03 | --                               | 50S ribosome-binding GTPase |
| EVM     | 20.56  | 46.32  | -1.17  | 5.00E-05 | 4.28E-04 | --                               | BTB/POZ domain |
| EVM     | 61.68  | 138.88 | -1.17  | 5.00E-05 | 4.28E-04 | --                               | --            |
| EVM     | 32.19  | 72.49  | -1.17  | 5.00E-05 | 4.28E-04 | --                               | Ribonuclease-III-like |
| EVM     | 158.43 | 356.68 | -1.17  | 5.00E-05 | 4.28E-04 | --                               | Hypothetical protein FLILHELTA |
| EVM     | 12.95  | 29.16  | -1.17  | 1.00E-04 | 7.96E-04 | --                               | Gti1/Pac2 family |
| Accession    | Start    | End      | Fold   | E-value | Description                                           |
|--------------|----------|----------|--------|---------|-------------------------------------------------------|
| EVM0009840   | 17.24    | 38.79    | -1.17  | 5.00E-05 | 4.28E-04     | BUD22                                                |
| EVM0011144   | 64.29    | 144.61   | -1.17  | 5.00E-05 | 4.28E-04     | Protein of unknown function (DUF2034)               |
| EVM000836    | 149.61   | 336.46   | -1.17  | 1.00E-04 | 7.96E-04     | Intracellular trafficking, secretion, and vesicular transport |
| EVM000596    | 6.95     | 15.62    | -1.17  | 8.00E-04 | 4.73E-03     | Replication, recombination and repair                |
| EVM0012127   | 18.30    | 41.10    | -1.17  | 5.00E-05 | 4.28E-04     | --                                                   |
| EVM000042    | 11.08    | 24.86    | -1.17  | 3.20E-03 | 1.49E-02     | --                                                   |
| EVM008789    | 1922.75  | 4314.63  | -1.17  | 3.00E-04 | 2.07E-03     | Energy production and conversion                     |
| EVM008292    | 16.60    | 37.24    | -1.17  | 5.00E-05 | 4.28E-04     | Posttranslational modification, protein turnover, chaperones |
| EVM006361    | 43.55    | 97.72    | -1.17  | 2.00E-04 | 1.46E-03     | --                                                   |
| EVM006257    | 158.73   | 355.70   | -1.16  | 5.00E-05 | 4.28E-04     | --                                                   |
| EVM006015    | 36.17    | 80.99    | -1.16  | 5.00E-05 | 4.28E-04     | --                                                   |
| EVM001571    | 17.76    | 39.75    | -1.16  | 1.50E-04 | 1.14E-03     | --                                                   |
|              |          |          |        |         |            | Cytochrome c oxidase subunit VIa                      |
|              |          |          |        |         |            | IBR domain                                           |
|              |          |          |        |         |            | MYND finger                                          |
| Gene ID       | E-value | p-value | Log2 Fold Change | Function                                                   | Domain/Region                              |
|--------------|---------|---------|-----------------|------------------------------------------------------------|---------------------------------------------|
| EVM0008946   | 0.83    | 0.92    | -1.16           | Posttranslational modification, protein turnover, chaperones | Ring finger domain                         |
| EVM0011691   | 0.12    | 0.75    | -1.16           | Function unknown                                           | Regulator of chromosome condensation (RCC1) repeat |
| EVM0011563   | 0.73    | 0.93    | -1.16           | Posttranslational modification, protein turnover, chaperones | X-domain of DnaJ-containing                 |
| EVM0012134   | 0.16    | 0.87    | -1.16           | Energy production and conversion                           | Phosphoenolpyruvate phosphomutase           |
| EVM0007136   | 0.30    | 0.98    | -1.16           | --                                                         | --                                          |
| EVM0006468   | 0.16    | 0.87    | -1.16           | Signal transduction mechanisms                             | RED-like protein N-terminal region           |
| EVM0003787   | 0.67    | 0.98    | -1.16           | Translation, ribosomal structure and biogenesis            | Eukaryotic translation initiation factor 3 subunit 7 (eIF-3) |
| EVM0010785   | 0.57    | 0.98    | -1.16           | --                                                         | Rpp20 subunit of nuclear RNase MRP and P |
| EVM0006446   | 0.12    | 0.87    | -1.15           | --                                                         | FR47-like protein                          |
| EVM0005171   | 0.14    | 0.88    | -1.15           | Replication, recombination and repair                      | DNA mismatch repair protein, C-terminal domain |
| EVM0000274   | 0.23    | 0.97    | -1.15           | General function prediction only                           | Protein kinase domain                       |
| EVM0007735   | 0.08    | 0.98    | -1.15           | --                                                         | --                                          |
| Accession   | Log2 Fold Change | p-value   | Description                                                                 |
|-------------|------------------|-----------|-----------------------------------------------------------------------------|
| EVM0009577  | 23.71            | 5.00E-05  | 5.28E-04 General function prediction only                                   |
|             |                  | 1.15      | GTP1/OBG                                                                    |
| EVM0002709  | 4.53             | 9.50E-04  | 5.46E-03 --                                                                 |
| EVM0005506  | 6.00             | 1.80E-03  | 9.29E-03 #N/A                                                                |
| EVM0005034  | 745.33           | 6.50E-04  | 3.98E-03 --                                                                 |
| EVM0005665  | 31.55            | 5.00E-05  | 4.28E-04 General function prediction only                                   |
| EVM003335   | 36.17            | 4.50E-04  | 2.92E-03 --                                                                 |
| EVM0007292  | 5.42             | 7.00E-04  | 4.23E-03 General function prediction only                                   |
| EVM0011416  | 180.47           | 2.00E-04  | 1.46E-03 Cell cycle control, cell division, chromosome partitioning         |
| EVM0005357  | 5.85             | 1.25E-03  | 6.87E-03 --                                                                 |
| EVM0005470  | 7.89             | 1.00E-04  | 7.96E-04 --                                                                 |
| EVM000575   | 80.89            | 4.50E-04  | 2.92E-03 --                                                                 |
| EVM0008621  | 9.11             | 1.60E-03  | 8.44E-03 --                                                                 |
| EVM0006672  | 33.15 | 73.26 | -1.14 | 5.00E-05 | 4.28E-04 | -- | Peroxidase, family 2 |
| EVM0002128  | 159.69 | 352.68 | -1.14 | 2.50E-04 | 1.77E-03 | -- | Translation, ribosomal structure and biogenesis Domain found in IF2B/IF5 |
| EVM0000424  | 1026.55 | 2266.44 | -1.14 | 3.90E-03 | 1.76E-02 | -- | Protein of unknown function (DUF3421) |
| EVM0004054  | 437.54 | 965.46 | -1.14 | 3.50E-04 | 2.36E-03 | -- | Posttranslational modification, protein turnover, chaperones Hsp20/alpha crystallin family |
| EVM0006805  | 133.31 | 294.00 | -1.14 | 5.00E-05 | 4.28E-04 | -- | Lipid transport and metabolism Alpha/beta hydrolase family |
| EVM0006502  | 191.15 | 421.30 | -1.14 | 1.00E-04 | 7.96E-04 | -- | Secondary metabolites biosynthesis, transport and catabolism Alcohol dehydrogenase GroES-like domain |
| EVM0008653  | 23.03 | 50.74 | -1.14 | 2.50E-04 | 1.77E-03 | -- | -- |
| EVM0008337  | 25.78 | 56.76 | -1.14 | 1.00E-04 | 7.96E-04 | -- | General function prediction only |
| EVM0004636  | 91.57 | 201.60 | -1.14 | 5.00E-04 | 3.19E-03 | -- | General function prediction only RNA recognition motif. (a.k.a. RRM, RBD, or RNP domain) |
| EVM0000880  | 20.12 | 44.27 | -1.14 | 3.50E-04 | 2.36E-03 | -- | Glycosyl hydrolases family 15 |
| EVM0003015  | 7.65 | 16.82 | -1.14 | 1.50E-03 | 8.00E-03 | -- | RTA1 like protein |
| EVM0007304  | 38.00 | 83.57 | -1.14 | 1.00E-04 | 7.96E-04 | -- | Carbohydrate transport and metabolism UAA transporter family |
| Accession  | EVM0011509 | EVM0009609 | EVM0006633 | EVM0010495 | EVM0005366 | EVM000547 | EVM0010071 | EVM0002024 | EVM0010774 | EVM0005546 | EVM0006308 | EVM0007375 |
|------------|------------|------------|------------|------------|------------|------------|------------|------------|------------|------------|------------|------------|
| Value      | 69.60      | 47.68      | 4.50       | 50.38      | 24.96      | 6.32       | 3.72       | 5.96       | 1934.73    | 21.20      | 28.10      | 16.76      |
| Value      | 153.01     | 104.61     | 9.87       | 110.41     | 54.67      | 13.83      | 8.15       | 13.05      | 4233.52    | 46.39      | 61.37      | 36.60      |
| Value      | -1.14      | -1.13      | -1.13      | -1.13      | -1.13      | -1.13      | -1.13      | -1.13      | -1.13      | -1.13      | -1.13      | -1.13      |
| Value      | 5.00E-05   | 3.00E-04   | 1.00E-04   | 1.50E-04   | 2.50E-04   | 6.50E-04   | 2.50E-03   | 2.05E-03   | 8.50E-04   | 3.00E-04   | 3.45E-03   | 1.00E-04   |
| Value      | 4.28E-04   | 2.07E-03   | 7.96E-04   | 1.14E-03   | 1.77E-03   | 3.98E-03   | 1.22E-02   | 1.03E-02   | 4.98E-03   | 2.07E-03   | 1.59E-02   | 7.96E-04   |
| Value      | --         | Signal transduction mechanisms | --         | --         | Function unknown | --         | --         | Secondary metabolites biosynthesis, transport and catabolism | Posttranslational modification, protein turnover, chaperones | General function prediction only | MatE | --         |
| Value      | --         | RhoGEF domain | --         | --         | pre-RNA processing PIH1/Nop17 | --         | --         | short chain dehydrogenase | Cyclophilin type peptidyl-prolyl cis-trans isomerase/CLD | --         | --         | HIT zinc finger |
| Accession  | Coverage | Depth | Log2 Fold Change | Log2 Fold Change | Description                                                                                   | GO Terms                                                                 |
|-----------|----------|-------|------------------|------------------|----------------------------------------------------------------------------------------------|-------------------------------------------------------------------------|
| EVM0004217 | 20.64    | 45.04 | -1.13            | 5.00E-04         | Replication, recombination and repair                                                          | -                                                                       |
| EVM0004398 | 338.58   | 738.53| -1.13            | 1.50E-04         | General function prediction only                                                               | Proteolipid membrane potential modulator                                |
| EVM0010575 | 20.51    | 44.72 | -1.12            | 5.00E-05         | --                                                                                            | --                                                                     |
| EVM0001181 | 220.10   | 479.56| -1.12            | 1.00E-04         | Intracellular trafficking, secretion, and vesicular transport                                  | Regulated-SNARE-like domain                                             |
| EVM0007991 | 70.78    | 154.07| -1.12            | 5.00E-05         | Transcription                                                                                  | SAC3/GANP/Nin1/mts3/eIF-3 p25 family                                  |
| EVM0005306 | 52.40    | 114.02| -1.12            | 1.00E-04         | Cell wall/membrane/envelope biogenesis                                                         | Glycosyl transferases group 1                                           |
| EVM0002257 | 30.87    | 67.12 | -1.12            | 1.00E-04         | --                                                                                            | --                                                                     |
| EVM0009686 | 163.03   | 354.07| -1.12            | 5.00E-05         | Transcription                                                                                  | Spt4/RpoE2 zinc finger                                                |
| EVM0003157 | 547.66   | 1189.32| -1.12            | 2.50E-04         | Defense mechanisms                                                                             | B-cell receptor-associated protein 31-like                              |
| EVM0004197 | 4.84     | 10.50 | -1.12            | 9.05E-03         | --                                                                                            | MYND finger                                                            |
| EVM0006677 | 23.91    | 51.92 | -1.12            | 1.65E-03         | --                                                                                            | --                                                                     |
| EVM0002618 | 60.53    | 131.33| -1.12            | 1.50E-04         | Translation, ribosomal structure and biogenesis                                              | TruB family pseudouridylate synthase (N terminal domain)               |
| ID            | Value1 | Value2 | Value3 | Value4 | Value5 | Value6 | Value7 | Value8 | Function                                                                 |
|---------------|--------|--------|--------|--------|--------|--------|--------|--------|--------------------------------------------------------------------------|
| EVM0002834    | 326.36 | 707.76 | 1.40E-03 | 7.55E-03 | --     | --     | --     | --     | Zinc-binding dehydrogenase                                               |
| EVM0002551    | 24.13  | 52.33  | 1.00E-04 | 7.96E-04 | --     | --     | --     | --     | Translation, ribosomal structure and biogenesis                          |
| EVM0010966    | 10.39  | 22.51  | 5.50E-04 | 3.46E-03 | --     | --     | --     | --     | Replication, recombination and repair                                      |
| EVM0007623    | 34.93  | 75.70  | 8.00E-04 | 4.73E-03 | --     | --     | --     | --     | Ribonuclease                                                              |
| EVM0011961    | 145.44 | 315.05 | 5.00E-05 | 4.28E-04 | --     | --     | --     | --     | General function prediction only                                         |
| EVM0003805    | 3.36   | 7.27   | 1.20E-03 | 6.64E-03 | --     | --     | --     | --     | Transcription                                                             |
| EVM0007576    | 23.10  | 50.04  | 1.00E-03 | 7.96E-04 | --     | --     | --     | --     | NLI interacting factor-like phosphatase                                   |
| EVM0003465    | 23.72  | 51.36  | 7.50E-04 | 4.49E-03 | --     | --     | --     | --     | --                                                                        |
| EVM0010315    | 5.62   | 12.16  | 2.00E-03 | 1.01E-02 | --     | --     | --     | --     | 50S ribosome-binding GTPase                                               |
| EVM0000366    | 3.30   | 7.14   | 5.65E-03 | 2.37E-02 | --     | --     | --     | --     | --                                                                        |
| EVM0011527    | 1670.30| 3615.71| 7.50E-04 | 4.49E-03 | --     | --     | --     | --     | Signal transduction mechanisms                                            |
| EVM0008532    | 125.24 | 271.09 | 3.50E-04 | 2.36E-03 | --     | --     | --     | --     | Translation, ribosomal structure and biogenesis                          |
| EVM0006117    | 14.98  | 32.42  | 6.00E-04 | 3.72E-03 | --     | --     | --     | --     | General function prediction only                                         |
|               |        |        |        |        |        |        |        |        | Aldo/keto reductase family                                                |
| Accession  | Value1 | Value2  | Change | Value3 | Value4  | Function                                                                 | Other Information                                |
|-----------|--------|---------|--------|--------|---------|----------------------------------------------------------------------------|--------------------------------------------------|
| EVM0001473| 25.08  | 54.27   | -1.11  | 5.50E-04| 3.46E-03| Intracellular trafficking, secretion, and vesicular transport              | Transport protein particle (TRAPP) component       |
| EVM0002908| 640.34 | 1384.52 | -1.11  | 2.00E-04| 1.46E-03| Posttranslational modification, protein turnover, chaperones               | Zinc finger, C2H2 type                            |
| EVM0008156| 787.31 | 1701.22 | -1.11  | 4.20E-03| 1.87E-02| --                                                                         | --                                                |
| EVM0006692| 2.21   | 4.77    | -1.11  | 1.00E-04| 7.96E-04| --                                                                         | Variant SH3 domain                                |
| EVM0011422| 343.49 | 740.98  | -1.11  | 3.50E-04| 2.36E-03| Secondary metabolites biosynthesis, transport and catabolism               | Alcohol dehydrogenase GroES-like domain           |
| EVM00006493| 122.28 | 264.14  | -1.11  | 5.00E-05| 4.28E-04| --                                                                         | N-acetylglucosaminyl transferase component (Gpi1) |
| EVM0011115| 5.03   | 10.87   | -1.11  | 4.00E-03| 1.79E-02| --                                                                         | --                                                |
| EVM0005827| 33.80  | 72.93   | -1.11  | 1.00E-04| 7.96E-04| --                                                                         | --                                                |
| EVM0005849| 216.66 | 468.03  | -1.11  | 2.00E-04| 1.46E-03| --                                                                         | --                                                |
| EVM0006493| 122.28 | 264.14  | -1.11  | 5.00E-05| 4.28E-04| --                                                                         | N-acetylglucosaminyl transferase component (Gpi1) |
| EVM0003684| 3.65   | 7.88    | -1.11  | 6.50E-04| 3.98E-03| #N/A                                                                      | #N/A                                              |
| EVM0006601| 18.95  | 40.99   | -1.11  | 5.00E-04| 4.28E-04| General function prediction only                                           | --                                                |
| EVM0002908| 640.34 | 1384.52 | -1.11  | 2.00E-04| 1.46E-03| Posttranslational modification, protein turnover, chaperones               | --                                                |
| EVM00006692| 2.21   | 4.77    | -1.11  | 1.00E-04| 7.96E-04| --                                                                         | --                                                |
| EVM0005827| 33.80  | 72.93   | -1.11  | 1.00E-04| 7.96E-04| --                                                                         | --                                                |
| EVM0003684| 3.65   | 7.88    | -1.11  | 6.50E-04| 3.98E-03| #N/A                                                                      | #N/A                                              |
| EVM0005827| 33.80  | 72.93   | -1.11  | 1.00E-04| 7.96E-04| --                                                                         | --                                                |
| Accession   | Score | Q-value | p-value | Function Prediction                  | Protein Name               |
|-------------|-------|---------|---------|-------------------------------------|---------------------------|
| EVM0002841  | 114.90| 247.68  | -1.11  | General function prediction only    | Cyclin                    |
| EVM0006547  | 112.73| 242.92  | -1.11  | Translation, ribosomal structure and biogenesis | Ribosomal protein L23     |
| EVM000928   | 158.82| 342.11  | -1.11  | Function unknown                     | Der1-like family           |
| EVM006875   | 70.15 | 151.06  | -1.11  | Polysaccharide deacetylase           |                          |
| EVM004577   | 24.45 | 52.61   | -1.11  | Cell cycle control, cell division, chromosome partitioning | Cid1 family poly A polymerase |
| EVM010742   | 38.69 | 83.22   | -1.11  | Posttranslational modification, protein turnover, chaperones | ATP10 protein              |
| EVM011573   | 9.89  | 21.26   | -1.10  | Function unknown                     | Transcriptional repressor TCF25 |
| EVM006845   | 15.45 | 33.19   | -1.10  | SNF5 / SMARCB1 / INI1               |                          |
| EVM005464   | 19.25 | 41.34   | -1.10  | Amino acid transport and metabolism | Gamma-glutamyltranspeptidase |
| EVM007966   | 157.27| 337.77  | -1.10  | Na+ dependent nucleoside transporter C-terminus |                          |
| EVM0010581  | 59.75 | 128.29  | -1.10  | Na+ dependent nucleoside transporter C-terminus |                          |
| EVM0007144  | 31.92 | 68.53   | -1.10  | F-box-like                           |                          |
| Gene ID           | Log2 Fold Change | Log2 Expression | P-Value | GO Term                                                                 |
|------------------|------------------|-----------------|---------|-------------------------------------------------------------------------|
| EVM0000005       | 34.87            | 74.87           | -1.10   | --                                                                      |
| EVM0004966       | 3.33             | 7.14            | -1.10   | --                                                                      |
| EVM0005401       | 14.37            | 30.82           | -1.10   | Poly(ADP-ribose) polymerase catalytic domain                          |
| EVM0000354       | 723.39           | 1550.96         | -1.10   | Ribosomal L29 protein                                                  |
| EVM0007977       | 313.54           | 672.08          | -1.10   | --                                                                      |
| EVM0005544       | 96.69            | 207.23          | -1.10   | Ribosomal protein L18e/L15                                             |
| EVM0000483       | 165.09           | 353.73          | -1.10   | Chorismate mutase type II                                              |
| EVM0002695       | 100.88           | 216.03          | -1.10   | SYF2 splicing factor                                                   |
| EVM0001019       | 1060.48          | 2270.15         | -1.10   | --                                                                      |
| EVM0010106       | 60.11            | 128.56          | -1.10   | Maf-like protein                                                        |
| EVM0002772       | 22.54            | 48.21           | -1.10   | --                                                                      |
| EVM0008986       | 109.61           | 234.29          | -1.10   | Endoplasmic reticulum vesicle transporter                              |
| Accession      | Value1  | Value2 | Change | Value3  | Value4 | Function                                                                 | Protein Description                                      |
|---------------|---------|--------|--------|---------|--------|---------------------------------------------------------------------------|----------------------------------------------------------|
| EVM0001622    | 251.23  | 536.99 | -1.10  | 3.00E-04| 2.07E-03| -                                                                          | Ricin-type beta-trefoil lectin domain-like                |
| EVM0011337    | 2.46    | 5.26   | -1.10  | 9.90E-03| 3.72E-02| --                                                                        | --                                                       |
| EVM0009958    | 13.22   | 28.26  | -1.10  | 1.40E-03| 7.55E-03| --                                                                        | --                                                       |
| EVM0005232    | 48.20   | 102.99 | -1.10  | 1.50E-04| 1.14E-03| RNA processing and modification                                          | Brix domain                                              |
| EVM0009904    | 39.79   | 84.99  | -1.09  | 2.00E-04| 1.46E-03| General function prediction                                               | Methyltransferase involved in Williams-Beuren syndrome   |
| EVM0004101    | 58.60   | 125.16 | -1.09  | 1.50E-04| 1.14E-03| Carbohydrate transport and metabolism                                     | Phosphomannose isomerase type I                          |
| EVM0004707    | 31.70   | 67.70  | -1.09  | 1.00E-04| 7.96E-04| --                                                                        | Alpha-L-rhamnosidase N-terminal domain                   |
| EVM0004046    | 128.45  | 274.23 | -1.09  | 5.00E-05| 4.28E-04| Amino acid transport and metabolism                                       | Pyridoxal-dependent decarboxylase, pyridoxal binding domain |
| EVM0003024    | 37.16   | 79.28  | -1.09  | 5.00E-05| 4.28E-04| Signal transduction mechanisms                                           | Rhomboid family                                          |
| EVM0011858    | 83.43   | 177.95 | -1.09  | 2.50E-04| 1.77E-03| RNA processing and modification                                          | Ribosomal protein L10                                    |
| EVM0004495    | 260.54  | 555.58 | -1.09  | 2.00E-04| 1.46E-03| Translation, ribosomal structure and biogenesis                          | Ribosomal protein L7Ae/L30e/S12e/Gadd45 family           |
| EVM0010022    | 190.17  | 405.42 | -1.09  | 5.00E-04| 3.19E-03| --                                                                        | --                                                       |
| EVM0011621   | 60.74 | 129.47 | -1.09 | 3.50E-04 | 2.36E-03 | Function unknown | Low temperature viability protein |
|--------------|-------|--------|-------|----------|----------|-----------------|-----------------------------------|
| EVM0004063   | 45.47 | 96.89  | -1.09 | 2.50E-04 | 1.77E-03 | Transcription    | RNA recognition motif. (a.k.a. RRM, RBD, or RNP domain) |
| EVM0000755   | 137.37| 292.54 | -1.09 | 1.50E-04 | 1.14E-03 | --              | --                                |
| EVM0010288   | 54.08 | 115.09 | -1.09 | 5.00E-05 | 4.28E-04 | Inorganic ion transport and metabolism | Cation efflux family |
| EVM0008206   | 114.94| 244.54 | -1.09 | 5.00E-05 | 4.28E-04 | RNA processing and modification | RNA recognition motif. (a.k.a. RRM, RBD, or RNP domain) |
| EVM0009109   | 53.80 | 114.39 | -1.09 | 1.00E-04 | 7.96E-04 | --              | Glycosyl hydrolases family 43    |
| EVM0007564   | 9.42  | 20.02  | -1.09 | 3.50E-04 | 2.36E-03 | Transcription    | Fork head domain                 |
| EVM0009937   | 312.92| 664.17 | -1.09 | 9.50E-04 | 5.46E-03 | Cell wall/membrane/envelope biogenesis | UTP-glucose-1-phosphate uridylyltransferase |
| EVM0010005   | 32.97 | 69.97  | -1.09 | 3.50E-04 | 2.36E-03 | --              | PIG-X / PBN1                     |
| EVM0008829   | 32.77 | 69.49  | -1.08 | 2.00E-04 | 1.46E-03 | --              | --                                |
| EVM0000690   | 45.10 | 95.59  | -1.08 | 1.50E-04 | 1.14E-03 | --              | Protein of unknown function (DUF3433) |
| EVM0004379   | 228.26| 483.53 | -1.08 | 1.50E-04 | 1.14E-03 | Intracellular trafficking, secretion, and vesicular transport | Synaptobrevin |
| EVM0009036 | 154.34 | 326.91 | -1.08 | 5.00E-05 | 4.28E-04 | RNA processing and modification | Ribosomal protein L7Ae/L30e/S12e/Gadd45 family |
| EVM0002623 | 10.92  | 23.11  | -1.08 | 5.00E-05 | 4.28E-04 | -- | WD domain, G-beta repeat |
| EVM0010727 | 30.48  | 64.51  | -1.08 | 3.50E-04 | 2.36E-03 | General function prediction only | Alpha/beta hydrolase family |
| EVM0005044 | 10.90  | 23.07  | -1.08 | 2.50E-04 | 1.77E-03 | -- | SAC3/GANP/Nin1/mts3/eIF-3 p25 family |
| EVM0003820 | 27.23  | 57.62  | -1.08 | 2.50E-04 | 1.77E-03 | -- | -- |
| EVM0009601 | 7.25   | 15.34  | -1.08 | 2.95E-03 | 1.40E-02 | -- | GDSL-like Lipase/Acylhydrolase |
| EVM0003386 | 12.67  | 26.78  | -1.08 | 1.00E-03 | 5.70E-02 | -- | bZIP transcription factor |
| EVM0008320 | 4.30   | 9.09   | -1.08 | 4.50E-04 | 2.92E-03 | -- | Nuclear condensing complex subunits, C-term domain |
| EVM0001335 | 13.23  | 27.96  | -1.08 | 1.00E-03 | 5.70E-03 | RNA processing and modification | Ribosomal L28e protein family |
| EVM0004541 | 73.84  | 156.05 | -1.08 | 3.50E-04 | 2.36E-03 | -- | -- |
| EVM0010299 | 14.34  | 30.28  | -1.08 | 5.00E-05 | 4.28E-04 | -- | XRN 5'-3' exonuclease N-terminus |
| EVM0008485 | 4.96   | 10.48  | -1.08 | 5.50E-04 | 3.46E-03 | -- | -- |
| EVM0011366 | 14.56  | 30.73  | -1.08 | 2.00E-04 | 1.46E-03 | -- | SDA1 |
| EVM0003406 | 118.46 | 250.02 | -1.08 | 3.00E-04 | 2.07E-03 | -- | -- |
| EVM0010983 | 5.99   | 12.64  | -1.08 | 4.60E-03 | 2.01E-02 | -- | -- |
| EVM0007524 | 7.41   | 15.64  | -1.08 | 8.50E-04 | 4.98E-03 | -- | -- |
| EVM0001586 | 252.18 | 532.04 | -1.08 | 5.00E-05 | 4.28E-04 | -- | Domain of unknown function (DUF4451) |
| EVM0000201 | 27.19  | 57.34  | -1.08 | 1.00E-04 | 7.96E-04 | -- | Fungal specific transcription factor domain |
| EVM000289  | 27.95  | 58.88  | -1.08 | 5.00E-05 | 4.28E-04 | RNA processing and modification | RNA recognition motif. (a.k.a. RRM, RBD, or RNP domain) |
| EVM0000682 | 130.39 | 274.63 | -1.07 | 1.00E-04 | 7.96E-04 | Carbohydrate transport and metabolism | Glycolipid transfer protein (GLTP) |
| EVM0002933 | 52.91  | 111.39 | -1.07 | 1.00E-04 | 7.96E-04 | -- | 50S ribosome-binding GTPase |
| EVM0011112 | 14.30  | 30.11  | -1.07 | 1.50E-03 | 8.00E-03 | -- | -- |
| EVM0010562 | 59.23  | 124.64 | -1.07 | 1.00E-04 | 7.96E-04 | Posttranslational modification, protein turnover, chaperones | DnaJ domain |
| EVM0000131 | 5.59   | 11.76  | -1.07 | 1.02E-02 | 3.81E-02 | -- | -- |
| EVM0004589 | 55.41  | 116.56 | -1.07 | 2.50E-04 | 1.77E-03 | -- | -- |
| Accession     | Log2FC | P-value | log10(E-value) | GO-term                                                                 |
|--------------|--------|---------|---------------|-------------------------------------------------------------------------|
| EVM0010153   | 49.57  | 104.26  | -1.07         | Lipid transport and metabolism                                          |--|
| EVM0005335   | 17.23  | 36.23   | -1.07         | F-box-like                                                              |--|
| EVM0012187   | 10.51  | 22.08   | -1.07         | Fungal cellulose binding domain                                         |--|
| EVM0008989   | 141.93 | 298.19  | -1.07         | Posttranslational modification, protein turnover, chaperones            |--|
| EVM0006637   | 10.70  | 22.49   | -1.07         | Prolyl oligopeptidase family                                            |Prolyl oligopeptidase family|
| EVM001651    | 13.01  | 27.31   | -1.07         | Defense mechanisms                                                     |alpha/beta hydrolase fold|
| EVM0011567   | 407.42 | 855.25  | -1.07         |                                                                         |--|
| EVM0001135   | 10.43  | 21.89   | -1.07         | RNA processing and modification                                         |DEAD/DEAH box helicase|
| EVM0009815   | 87.45  | 183.43  | -1.07         |                                                                         |--|
| EVM0001766   | 158.59 | 332.67  | -1.07         | Intracellular trafficking, secretion, and vesicular transport           |Signal recognition particle receptor beta subunit|
| EVM000207    | 55.85  | 117.08  | -1.07         | Energy production and conversion                                        |Mitochondrial carrier protein|
| Accession | Log2FoldChange | Log10FoldChange | Description |
|-----------|----------------|----------------|-------------|
| EVM0011727 | 156.17 | 327.36 | -1.07 | 6.00E-04 | 3.72E-03 | Posttranslational modification, protein turnover, chaperones |
| EVM0011062 | 195.65 | 410.00 | -1.07 | 2.00E-04 | 1.46E-03 | Energy production and conversion |
| EVM0006114 | 44.97 | 94.19 | -1.07 | 3.50E-04 | 2.36E-03 | Energy production and conversion |
| EVM0011604 | 3.15 | 6.60 | -1.07 | 4.45E-03 | 1.96E-02 | -- |
| EVM0007837 | 1876.37 | 3928.94 | -1.07 | 1.10E-03 | 6.17E-02 | Translation, ribosomal structure and biogenesis |
| EVM0008363 | 54.23 | 113.56 | -1.07 | 3.00E-04 | 2.07E-03 | -- |
| EVM0004710 | 186.95 | 391.17 | -1.07 | 3.00E-04 | 2.07E-03 | -- |
| EVM0008761 | 21.69 | 45.37 | -1.06 | 2.00E-04 | 1.46E-03 | -- |
| EVM0007277 | 590.66 | 1235.39 | -1.06 | 7.00E-04 | 4.23E-03 | -- |
| EVM0003850 | 93.57 | 195.53 | -1.06 | 5.00E-05 | 4.28E-04 | -- |
| EVM0001494 | 11.22 | 23.44 | -1.06 | 5.00E-04 | 3.19E-03 | -- |
| EVM0001424 | 459.03 | 958.71 | -1.06 | 1.80E-03 | 9.29E-03 | Cytoskeleton |

Ubiquitin-2 like Rad60 SUMO-like
lactate/malate dehydrogenase, NAD binding domain
Thiamine pyrophosphate enzyme, N-terminal TPP binding domain
Cellulase (glycosyl hydrolase family 5)
Ribosomal protein S17
Cgr1 family
Calcineurin-like phosphoesterase
| EVM0001725 | 16.94  | 35.37 | -1.06 | 1.50E-04 | 1.14E-03 | RNA processing and modification | AAA domain |
| EVM0011101 | 17.55  | 36.59 | -1.06 | 2.00E-04 | 1.46E-03 | -- | Bromodomain |
| EVM0008497 | 701.39 | 1462.32 | -1.06 | 2.30E-03 | 1.14E-02 | Lipid transport and metabolism | MaoC like domain |
| EVM0000597 | 40.02  | 83.42 | -1.06 | 3.50E-04 | 2.36E-03 | General function prediction only | short chain dehydrogenase |
| EVM0004055 | 74.59  | 155.50 | -1.06 | 5.00E-04 | 3.19E-03 | Translation, ribosomal structure and biogenesis | Ribosomal protein S13/S18 |
| EVM0006198 | 31.93  | 66.55 | -1.06 | 1.50E-04 | 1.14E-03 | General function prediction only | Protein kinase domain |
| EVM0004868 | 18.65  | 38.84 | -1.06 | 6.50E-04 | 3.98E-03 | -- | F-box-like |
| EVM0011467 | 52.11  | 108.53 | -1.06 | 5.00E-05 | 4.28E-04 | Function unknown | YIF1 |
| EVM0010012 | 11.95  | 24.89 | -1.06 | 8.70E-03 | 3.35E-02 | -- | Formin Homology Region 1 |
| EVM0007916 | 11.82  | 24.61 | -1.06 | 3.15E-03 | 1.47E-02 | #N/A | #N/A |
| EVM0004807 | 7.43   | 15.46 | -1.06 | 2.25E-03 | 1.12E-02 | Chromatin structure and dynamics | Histone deacetylase domain |
| EVM0004689 | 5.47   | 11.38 | -1.06 | 1.05E-03 | 5.94E-03 | -- | HAUS augmin-like complex subunit 6 N-terminus |
| EVM0008211 | 17.24  | 35.84 | -1.06 | 2.00E-04 | 1.46E-03 | Signal transduction mechanisms | Protein tyrosine kinase |
| EVM0002262 | 92.98  | 193.32  | -1.06 | 4.20E-03  | 1.87E-02 | Chromatin structure and dynamics | Oxoglutarate and iron-dependent oxygenase degradation C-term |
| EVM0012170 | 28.71  | 59.68   | -1.06 | 5.00E-05  | 4.28E-04 | --                              | -- |
| EVM0004616 | 794.46 | 1650.49 | -1.05 | 8.70E-03  | 3.35E-02 | --                              | -- |
| EVM0002993 | 10.03  | 20.82   | -1.05 | 4.50E-04  | 2.92E-03 | --                              | Spb1 C-terminal domain |
| EVM0009366 | 9.21   | 19.10   | -1.05 | 4.00E-04  | 2.65E-03 | --                              | -- |
| EVM0005312 | 1.12   | 2.31    | -1.05 | 1.23E-02  | 4.42E-02 | --                              | DNA polymerase subunit Cdc27 |
| EVM0003892 | 22.33  | 46.21   | -1.05 | 2.50E-04  | 1.77E-02 | --                              | -- |
| EVM0011090 | 463.04 | 958.32  | -1.05 | 6.00E-04  | 3.72E-03 | Intracellular trafficking, secretion, and vesicular transport | Tim10/DDP family zinc finger |
| EVM0003936 | 77.86  | 161.09  | -1.05 | 1.00E-04  | 7.96E-04 | General function prediction only | TPR repeat |
| EVM0000531 | 25.20  | 52.11   | -1.05 | 1.50E-04  | 1.14E-03 | Intracellular trafficking, secretion, and vesicular transport | Signal recognition particle 9 kDa protein (SRP9) |
| EVM0010097 | 2369.14| 4899.33 | -1.05 | 6.05E-03  | 2.51E-02 | Posttranslational modification, protein turnover, chaperones | Hsp20/alpha crystallin family |
| Annotation | Score | Identity | Similarity | Description | Domain |
|------------|-------|----------|------------|-------------|--------|
| EVM0005019 | 121.82| 251.66   | -1.05      | General function prediction only | Protein kinase domain |
| EVM0006288 | 22.48 | 46.42    | -1.05      | --          | --     |
| EVM0007198 | 210.26| 434.22   | -1.05      | --          | --     |
| EVM0001525 | 33.65 | 69.49    | -1.05      | --          | --     |
| EVM0003663 | 2.20 | 4.54     | -1.04      | Carbohydrate transport and metabolism | O-Glycosyl hydrolase family 30 |
| EVM0010347 | 1101.57| 2271.49 | -1.04      | --          | Hyaluronan / mRNA binding family |
| EVM0000938 | 21.00 | 43.30    | -1.04      | Posttranslational modification, protein turnover, chaperones | Cyclophilin type peptidyl-prolyl cis-trans isomerase/CLD |
| EVM0001821 | 4.23 | 8.73     | -1.04      | Transcription | HMG (high mobility group) box |
| EVM0002950 | 3.45 | 7.10     | -1.04      | --          | --     |
| EVM0007339 | 30.48| 62.74    | -1.04      | --          | SMP-30/Gluconolactonase/LRE-like region |
| EVM0007046 | 6.70 | 13.80    | -1.04      | --          | --     |
| EVM0005710 | 37.44| 77.06    | -1.04      | --          | --     |
| Gene ID   | Log2 Fold Change | E-values | Description                                                                 |
|----------|-----------------|----------|-----------------------------------------------------------------------------|
| EVM0006933 | -1.04           | 2.45E-03 | 1.20E-02 Nucleotide transport and metabolism                              |
|           |                 |          | Nucleoside diphosphate kinase                                               |
| EVM0004516 | -1.04           | 1.45E-03 | 7.77E-03 --                                                                 |
| EVM0010781 | -1.04           | 3.00E-04 | 2.07E-03 General function prediction                                        |
|           |                 |          | Ribosomal protein S8e                                                      |
| EVM001265 | -1.04           | 1.80E-03 | 9.29E-03 General function prediction only                                   |
|           |                 |          | Sugar (and other) transporter                                               |
| EVM0009820 | -1.04           | 2.00E-04 | 1.46E-03 --                                                                 |
|           |                 |          | Acetyltransferase (GNAT) domain                                             |
| EVM0000252 | -1.04           | 1.15E-03 | 6.41E-03 --                                                                 |
| EVM004057 | -1.04           | 1.50E-04 | 1.14E-03 --                                                                 |
|           |                 |          | Ser-Thr-rich glycosyl-phosphatidyl-inositol-anchored membrane family        |
| EVM0011378 | -1.04           | 4.00E-04 | 2.65E-03 Translation, ribosomal structure and biogenesis                   |
|           |                 |          | Eukaryotic elongation factor 5A hypusine, DNA-binding OB fold              |
| EVM0006914 | -1.04           | 3.00E-03 | 1.42E-02 --                                                                 |
| EVM0009894 | -1.04           | 4.00E-04 | 2.65E-03 --                                                                 |
|           |                 |          | Fungal specific transcription factor domain                                |
| EVM0009777 | -1.04           | 3.00E-04 | 2.07E-03 General function prediction only                                   |
|           |                 |          | Putative methyltransferase                                                  |
| EVM0000820 | -1.03           | 6.50E-04 | 3.98E-03 Posttranslational modification, protein turnover, chaperones   |
|           |                 |          | Ubiquitin-conjugating enzyme                                                 |
| EVM0003606   | 22.52 | 46.13 | -1.03 | 2.50E-04 | 1.77E-03 | -- | --  |
| EVM0007631   | 22.14 | 45.32 | -1.03 | 1.50E-04 | 1.14E-03 | -- | --  |
| EVM0006843   |  3.08 |  6.30 | -1.03 | 5.50E-03 | 2.32E-02 | -- | Glycosyl hydrolases family 6 |
| EVM0007556   | 395.63| 809.72| -1.03 | 1.00E-03 | 5.70E-03 | -- | Ser-Thr-rich glycosyl-phosphatidyl-inositol-anchored membrane family |
| EVM0010682   | 117.07| 239.34| -1.03 | 4.20E-03 | 1.87E-02 | -- | Mitochondrial ribosomal protein L27 |
| EVM0005393   |  2.12 |  4.33 | -1.03 | 3.95E-03 | 1.77E-02 | -- | --  |
| EVM0002991   | 34.86 |  71.17| -1.03 | 7.00E-04 | 4.23E-03 | -- | --  |
| EVM0010235   |  3.00 |  6.12 | -1.03 | 5.20E-03 | 2.22E-02 | -- | --  |
| EVM0003416   | 25.30 |  51.63| -1.03 | 3.00E-04 | 2.07E-03 | -- | --  |
| EVM0011926   | 18.85 |  38.47| -1.03 | 7.00E-04 | 4.23E-03 | -- | --  |
| EVM0007668   | 317.29| 647.34| -1.03 | 7.50E-04 | 4.49E-03 | Energy production and conversion | CHCH domain |
| EVM0001024   | 45.88 |  93.60| -1.03 | 1.50E-04 | 1.14E-03 | -- | Hinge domain of cleavage stimulation factor subunit 2 |
| Gene Name         | Value1  | Value2  | Log2Fold | p-value | Function                              | Modification                                |
|-------------------|---------|---------|----------|---------|---------------------------------------|---------------------------------------------|
| EVM0002619        | 23.07   | 47.06   | -1.03    | 6.50E-04| Function unknown                      | Signal peptide peptidase                    |
| EVM0011600        | 19.64   | 40.06   | -1.03    | 4.50E-04| Function unknown                      | WD domain, G-beta repeat                    |
| EVM0009946        | 30.92   | 63.06   | -1.03    | 3.00E-04| Transcription                         | A49-like RNA polymerase I associated factor |
| EVM0002328        | 21.40   | 43.57   | -1.03    | 1.50E-04| --                                    | --                                          |
| EVM0007810        | 5.88    | 11.98   | -1.03    | 3.60E-03| --                                    | --                                          |
| EVM0004828        | 631.41  | 1284.93 | -1.03    | 4.00E-04| Translation, ribosomal structure and biogenesis | Plectin/S10 domain                          |
| EVM0007937        | 53.31   | 108.35  | -1.02    | 6.50E-04| Posttranslational modification, protein turnover, chaperones | Zinc finger, C3HC4 type (RING finger)       |
| EVM0000388        | 40.02   | 81.32   | -1.02    | 1.50E-03| --                                    | --                                          |
| EVM0007840        | 540.95  | 1098.84 | -1.02    | 5.50E-04| Energy production and conversion      | Mitochondrial ribosomal protein L51 / S25 / CI-B8 domain |
| EVM0010936        | 208.38  | 423.24  | -1.02    | 4.50E-04| --                                    | KH domain                                  |
| EVM0008552        | 7.70    | 15.63   | -1.02    | 2.00E-03| --                                    | --                                          |
| EVM0005840        | 28.59   | 58.06   | -1.02    | 5.40E-03| --                                    | Sen15 protein                               |
| Accession       | Log2 Fold Change | E Value | Description                                                                 | Domain/Region                              |
|-----------------|-----------------|---------|------------------------------------------------------------------------------|----------------------------------------------|
| EVM0008697      | 10.49           | 21.31   | -1.02                                                                        |                                              |
| EVM0009006      | 13.97           | 28.36   | -1.02                                                                        | Replication, recombination and repair        |
| EVM0002613      | 275.98          | 560.28  | -1.02                                                                        | General function prediction only             |
| EVM0012234      | 139.90          | 283.93  | -1.02                                                                        | RNA processing and modification              |
| EVM0001831      | 539.85          | 1095.62 | -1.02                                                                        | Energy production and conversion            |
| EVM0006281      | 24.55           | 49.82   | -1.02                                                                        | Amino acid transport and metabolism          |
| EVM0007792      | 21.30           | 43.17   | -1.02                                                                        |                                              |
| EVM0010256      | 1.39            | 2.82    | -1.02                                                                        | General function prediction only             |
| EVM0009247      | 92.83           | 187.93  | -1.02                                                                        | Transcription                               |
| EVM0010552      | 30.68           | 62.10   | -1.02                                                                        |                                              |
| EVM0001367      | 80.41           | 162.74  | -1.02                                                                        |                                              |
| EVM0008894      | 28.54           | 57.75   | -1.02                                                                        |                                              |

- EVM0008697: Fat domain
- EVM0009006: RNA recognition motif (a.k.a. RRM, RBD, or RNP domain)
- EVM0002613: TAP C-terminal domain
- EVM0012234: ATP synthase, Delta/Epsilon chain, beta-sandwich domain
- EVM0001831: Hydantoinase B/oxoprolinase
- EVM0006281: Zinc finger, C2H2 type
- EVM0007792: Pterin 4 alpha carbinolamine dehydratase
| Accession | EVM000602 | EVM0007184 | EVM0006702 | EVM0010605 | EVM0011919 | EVM0011630 | EVM0005039 | EVM0007023 | EVM0005623 | EVM0002597 | EVM0012144 | EVM0012121 | EVM0004149 |
|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|
| EVM000602 | 1309.36   | 42.99     | 20.54     | 754.98    | 27.01     | 6.34      | 180.88    | 2946.66   | 18.46     | 8.82      | 38.02     | 19.26     | 17.82     |
| EVM0007184| 2648.71   | 86.91     | 41.52     | 1525.74   | 54.58     | 12.81     | 365.31    | 5950.91   | 37.26     | 17.80     | 76.72     | 38.86     | 35.94     |
| EVM0006702| -1.02     | -1.02     | -1.02     | -1.02     | -1.01     | -1.01     | -1.01     | 27.01     | -1.01     | -1.01     | -1.01     | -1.01     | -1.01     |
| EVM0010605| 2.05E-03  | 5.50E-04  | 6.50E-04  | 1.50E-04  | 2.30E-03  | 2.00E-03  | 1.55E-03  | 3.00E-04  | 1.00E-03  | 3.60E-03  | 3.00E-04  | 8.50E-04  |
| EVM0011919| 1.03E-02  | 3.46E-03  | 3.98E-03  | 1.14E-03  | 1.14E-02  | 1.01E-02  | 8.22E-03  | 2.07E-03  | 5.70E-03  | 1.64E-02  | 2.07E-03  | 4.98E-03  |
| EVM0011630| --        | --        | --        | --        | --        | --        | --        | --        | --        | --        | --        | --        | --        |
| EVM0005039| General function prediction only | Function unknown | Translation, ribosomal structure and biogenesis | Ribosomal protein L34e | -- | -- | RNA processing and modification | DEAD/DEAH box helicase | NADH-ubiquinone reductase complex 1 MLRQ subunit | Glycosyl hydrolases family 11 | -- | Flavin reductase like domain | Eukaryotic protein of unknown function (DUF829) | Glioma tumor suppressor candidate region |
| Accession     | Value1 | Value2 | Value3 | Value4 | Value5 | Description                                      |
|---------------|--------|--------|--------|--------|--------|--------------------------------------------------|
| EVM0011255    | 3.28   | 6.61   | -1.01  | 3.30E-03 | 1.53E-02 | --                                                |
| EVM0006908    | 35.78  | 72.14  | -1.01  | 3.50E-04 | 2.36E-03 | FAD binding domain                               |
| EVM0003316    | 552.91 | 1114.40| -1.01  | 8.00E-04 | 4.73E-03 | --                                                |
| EVM0004270    | 3.64   | 7.33   | -1.01  | 3.60E-03 | 1.64E-02 | SelR domain                                      |
| EVM0007073    | 62.48  | 125.88 | -1.01  | 3.00E-04 | 2.07E-03 | Nucleotide transport and metabolism              |
| EVM0010957    | 37.69  | 75.88  | -1.01  | 5.50E-04 | 3.46E-03 | Transcription                                    |
| EVM0005032    | 76.66  | 154.32 | -1.01  | 4.50E-04 | 2.92E-03 | Signal transduction                              |
| EVM0009586    | 49.10  | 98.82  | -1.01  | 2.50E-04 | 1.77E-03 | Lipid transport and metabolism                   |
| EVM0002294    | 11.65  | 23.45  | -1.01  | 1.60E-03 | 8.44E-03 | General function prediction only                 |
| EVM0005707    | 18.28  | 36.77  | -1.01  | 2.00E-03 | 1.01E-02 | --                                                |
| EVM0007589    | 664.77 | 1336.94| -1.01  | 4.40E-03 | 1.94E-02 | General function prediction only                 |
| EVM0006910    | 3.21   | 6.46   | -1.01  | 3.05E-03 | 1.44E-02 | --                                                |
| EVM0006891    | 12.59  | 25.29  | -1.01  | 2.95E-03 | 1.40E-02 | --                                                |
| Accession  | E-value 1 | E-value 2 | Bit-score 1 | Bit-score 2 | Description                                                                 |
|-----------|-----------|-----------|-------------|-------------|-----------------------------------------------------------------------------|
| EVM0007696 8.52 | 17.12 | -1.01 | 2.05E-03 | 1.03E-02 | Domain of unknown function (DUF4139)                                       |
| EVM0000586 7.63 | 15.33 | -1.01 | 4.45E-03 | 1.96E-02 | Pheromone A receptor                                                         |
| EVM0003220 6.19 | 12.43 | -1.01 | 7.20E-03 | 2.88E-02 | --                                                                          |
| EVM0008748 14.50 | 29.11 | -1.01 | 2.90E-03 | 1.38E-02 | --                                                                          |
| EVM0004735 8.49 | 17.04 | -1.01 | 7.50E-04 | 4.49E-03 | 50S ribosome-binding GTPase                                                  |
| EVM0008438 19.82 | 39.78 | -1.01 | 4.50E-04 | 2.92E-03 | Apoptosis-antagonizing transcription factor, C-terminal                     |
| EVM0010937 10.96 | 22.00 | -1.00 | 1.65E-03 | 8.65E-03 | --                                                                          |
| EVM0008173 1.71 | 3.44  | -1.00 | 9.10E-03 | 3.48E-02 | --                                                                          |
| EVM0003532 39.83 | 79.87 | -1.00 | 5.50E-04 | 3.46E-03 | General function prediction only                                            |
| EVM0011463 86.93 | 174.24 | -1.00 | 4.00E-04 | 2.65E-03 | General function prediction only                                            |
| EVM0001105 3.44 | 6.90  | -1.00 | 5.20E-03 | 2.22E-02 | Carbohydrate transport and metabolism                                        |
| EVM0012150 60.01 | 120.20 | -1.00 | 2.50E-04 | 1.77E-03 | --                                                                          |
| EVM0006647  | 158.10 | 316.65 | -1.00 | 5.00E-04 | 3.19E-03 | Amino acid transport and metabolism | Aminotransferase class-V |
| EVM0011632  | 64.71  | 129.55 | -1.00 | 6.00E-04 | 3.72E-03 | -- | -- |
| EVM0002524  | 9.83   | 19.67  | -1.00 | 1.10E-03 | 6.17E-03 | -- | Pectate lyase |
| EVM0003942  | 27.11  | 54.24  | -1.00 | 4.95E-03 | 2.13E-02 | -- | Domain of unknown function (DUF202) |
| EVM0004593  | 29.98  | 59.98  | -1.00 | 2.80E-03 | 1.34E-02 | Signal transduction | Protein kinase domain |
| EVM0008908  | 70.44  | 140.92 | -1.00 | 5.00E-04 | 3.19E-03 | Translation, ribosomal structure and biogenesis | Brix domain |
| EVM0000211  | 31.24  | 62.49  | -1.00 | 3.50E-04 | 2.36E-03 | RNA processing and modification | WD domain, G-beta repeat |
| EVM0005980  | 41.85  | 20.92  | 1.00  | 9.50E-04 | 5.46E-03 | General function prediction only | Animal haem peroxidase |
| EVM0004069  | 9.45   | 4.72   | 1.00  | 5.50E-04 | 3.46E-03 | Energy production and conversion | FAD linked oxidases, C-terminal domain |
| EVM0000703  | 28.10  | 14.03  | 1.00  | 6.85E-03 | 2.77E-02 | -- | -- |
| EVM0008890  | 17.09  | 8.53   | 1.00  | 2.50E-04 | 1.77E-03 | RNA processing and modification | Sec63 Brl domain |
| EVM0008138  | 85.80  | 42.81  | 1.00  | 6.50E-04 | 3.98E-03 | Inorganic ion transport and metabolism | Sodium/hydrogen exchanger family |
| EVM0008744  | 51.35  | 25.58  | 1.01  | 4.00E-04 | 2.65E-03 | RNA processing and modification | MIF4G domain |
| EVM0000862 | 24.58 | 12.24 | 1.01 | 5.00E-04 | 3.19E-03 | Replication, recombination and repair | MCM2/3/5 family |
| EVM0005381 | 62.59 | 31.16 | 1.01 | 4.00E-04 | 2.65E-03 | -- | -- |
| EVM0007667 | 147.00 | 73.16 | 1.01 | 6.00E-04 | 3.72E-03 | -- | Ubiquitin-2 like Rad60 SUMO-like |
| EVM0000205 | 14.89 | 7.41 | 1.01 | 1.30E-03 | 7.10E-03 | Transcription | SET domain |
| EVM0008417 | 8.43 | 4.19 | 1.01 | 2.70E-03 | 1.30E-02 | Secondary metabolites biosynthesis, transport and catabolism | ABC transporter |
| EVM0001345 | 24.80 | 12.32 | 1.01 | 5.50E-04 | 3.46E-03 | Cell cycle control, cell division, chromosome partitioning | SIT4 phosphatase-associated protein |
| EVM0010324 | 119.57 | 59.38 | 1.01 | 2.50E-04 | 1.77E-03 | -- | -- |
| EVM0011018 | 30.70 | 15.24 | 1.01 | 5.50E-03 | 2.32E-02 | Replication, recombination and repair | Rad51 |
| EVM0002907 | 59.36 | 29.46 | 1.01 | 1.40E-03 | 7.55E-03 | Defense mechanisms | NAD dependent epimerase/dehydratase family |
| EVM0012016 | 234.85 | 116.45 | 1.01 | 2.20E-03 | 1.10E-02 | Amino acid transport and metabolism | Cys/Met metabolism PLP-dependent enzyme |
| EVM0007248 | 580.67 | 287.76 | 1.01 | 2.95E-03 | 1.40E-02 | -- | RNA recognition motif. (a.k.a. RRM, RBD, or RNP domain) |
| EVM0001744 | 12.53 | 6.20 | 1.01 | 1.25E-03 | 6.87E-03 | Signal transduction mechanisms | Protein kinase domain |
| EVM0002952 | 29.64 | 14.68 | 1.01 | 6.00E-04 | 3.72E-03 | Extracellular structures | Tropomyosin |
|------------|-------|-------|------|----------|----------|------------------------|-------------|
| EVM0001683 | 75.96 | 37.55 | 1.02 | 3.00E-04 | 2.07E-03 | Coenzyme transport and metabolism | Probable molybdopterin binding domain |
| EVM0002941 | 15.00 | 7.41  | 1.02 | 5.25E-03 | 2.24E-02 | Nucleotide transport and metabolism | Ham1 family |
| EVM0009790 | 24.63 | 12.15 | 1.02 | 2.50E-04 | 1.77E-03 | Secondary metabolites biosynthesis, transport and catabolism | ABC transporter |
| EVM0005867 | 133.30| 65.58 | 1.02 | 2.50E-04 | 1.77E-03 | -- | -- |
| EVM0000598 | 66.97 | 32.93 | 1.02 | 4.00E-04 | 2.65E-03 | Cell cycle control, cell division, chromosome partitioning | N terminus of Rad21 / Rec8 like protein |
| EVM0005161 | 24.89 | 12.24 | 1.02 | 2.00E-04 | 1.46E-03 | Secondary metabolites biosynthesis, transport and catabolism | ABC transporter |
| EVM0011116 | 7.53  | 3.70  | 1.03 | 4.10E-03 | 1.83E-02 | -- | Acetamidase/Formamidase family |
| EVM0006573 | 13.98 | 6.86  | 1.03 | 1.01E-02 | 3.76E-02 | -- | -- |
| EVM0002374 | 28.64 | 13.96 | 1.04 | 1.00E-04 | 7.96E-04 | -- | Alpha/beta hydrolase family |
| EVM0010842 | 133.19| 64.84 | 1.04 | 2.15E-03 | 1.08E-02 | -- | Allophanate hydrolase subunit 2 |
| EVM0009401 | 39.66 | 19.30 | 1.04 | 1.45E-03 | 7.77E-03 | Transcription | -- |
|------------|-------|-------|------|-----------|-----------|--------------|----|
| EVM0011910 | 57.76 | 28.09 | 1.04 | 1.00E-04 | 7.96E-04 | Intracellular trafficking, secretion, and vesicular transport | VID27 cytoplasmic protein |
| EVM0000333 | 24.34 | 11.84 | 1.04 | 2.50E-04 | 1.77E-03 | Posttranslational modification, protein turnover, chaperones | Poly(ADP-ribose) polymerase catalytic domain |
| EVM0004887 | 3.64  | 1.77  | 1.04 | 5.35E-03 | 2.27E-02 | -- | Protein of unknown function (DUF4246) |
| EVM000281  | 13.40 | 6.51  | 1.04 | 1.20E-03 | 6.64E-03 | -- | -- |
| EVM0005732 | 8.57  | 4.16  | 1.04 | 4.65E-03 | 2.03E-02 | -- | NADH:flavin oxidoreductase / NADH oxidase family |
| EVM0004931 | 69.14 | 33.47 | 1.05 | 3.00E-04 | 2.07E-03 | -- | Munc13 (mammalian uncoordinated) homology domain |
| EVM0008452 | 37.88 | 18.33 | 1.05 | 4.80E-03 | 2.08E-02 | -- | -- |
| EVM0006262 | 94.68 | 45.77 | 1.05 | 1.00E-04 | 7.96E-04 | -- | Peptidase family M1 |
| EVM0008437 | 6.13  | 2.96  | 1.05 | 4.65E-03 | 2.03E-02 | Energy production and conversion | Aldehyde dehydrogenase family |
| EVM0009297 | 118.76| 57.30 | 1.05 | 2.50E-04 | 1.77E-03 | Amino acid transport and metabolism | Amino acid permease |
| ID            | Value1 | Value2  | Value3 | K1       | K2       | Description                                      |
|--------------|--------|---------|--------|----------|----------|------------------------------------------------|
| EVM0007019   | 99.16  | 47.80   | 1.05   | 3.00E-04 | 2.07E-03 | Dynamin central region                           |
| EVM0011884   | 539.46 | 259.92  | 1.05   | 2.00E-03 | 1.01E-02 | Signal transduction mechanisms                   |
| EVM0003920   | 229.00 | 110.21  | 1.06   | 6.50E-04 | 3.98E-03 | Lipid transport and metabolism                   |
| EVM0006816   | 197.10 | 94.82   | 1.06   | 3.00E-04 | 2.07E-03 | --                                               |
| EVM001031    | 43.52  | 20.93   | 1.06   | 7.50E-04 | 4.49E-03 | Carbohydrate transport and metabolism            |
| EVM003703    | 40.32  | 19.37   | 1.06   | 1.10E-03 | 6.17E-03 | Function unknown                                 |
| EVM000369    | 5.73   | 2.75    | 1.06   | 1.35E-02 | 4.74E-02 | General function prediction only                 |
| EVM009536    | 109.03 | 52.36   | 1.06   | 5.00E-04 | 3.19E-03 | Amino acid transport and metabolism              |
| EVM001664    | 2.17   | 1.04    | 1.06   | 1.15E-02 | 4.19E-02 | Function unknown                                 |
| EVM001497    | 27.05  | 12.98   | 1.06   | 7.00E-04 | 4.23E-03 | --                                               |
| EVM011905    | 99.10  | 47.51   | 1.06   | 4.50E-04 | 2.92E-03 | --                                               |
| EVM011151    | 504.48 | 241.66  | 1.06   | 6.50E-04 | 3.98E-03 | Secondary metabolites biosynthesis, transport and catabolism |
|              |        |         |        |          |          | Cytochrome P450                                   |
|              |        |         |        |          |          | Cytochrome P450                                   |
|              |        |         |        |          |          | Cytochrome P450                                   |
| Pathway ID  | starts | ends | fold change | p-value | Gene Annotation |
|------------|--------|------|-------------|---------|----------------|
| EVM0002077 | 23.96  | 11.47| 1.06        | 3.00E-03| Posttranslational modification, protein turnover, chaperones |
| EVM0000779 | 143.69 | 68.76| 1.06        | 8.50E-03| --             |
| EVM0002918 | 54.49  | 26.07| 1.06        | 2.50E-04| --             |
| EVM0001114 | 9.83   | 4.70 | 1.06        | 1.25E-03| Posttranslational modification, protein turnover, chaperones |
| EVM0008943 | 2.36   | 1.13 | 1.06        | 1.30E-02| Signal transduction mechanisms |
| EVM0006450 | 69.31  | 33.11| 1.07        | 2.00E-04| General function prediction only |
| EVM0002233 | 23.83  | 11.38| 1.07        | 1.03E-02| --             |
| EVM0004972 | 14.02  | 6.69 | 1.07        | 5.50E-03| --             |
| EVM0005553 | 117.93 | 56.19| 1.07        | 2.00E-03| --             |
| EVM0002585 | 30.14  | 14.35| 1.07        | 2.00E-04| --             |
| EVM0005854 | 131.76 | 62.70| 1.07        | 8.00E-04| Cell wall/membrane/envelope biogenesis |

Ankyrin repeat
Cytochrome P450
ATPase family associated with various cellular activities (AAA)
Protein kinase domain
Alpha/beta hydrolase family
Dopa 4,5-dioxygenase family
Esterase-like activity of phytase
Phosphoinositide 3-kinase family, accessory domain (PIK domain)
Chitin synthase
| EVM0010519 | 8.28  | 3.94  | 1.07 | 2.80E-03 | 1.34E-02 | -- | -- |
| EVM0010882 | 209.62 | 99.71 | 1.07 | 7.00E-04 | 4.23E-03 | General function prediction only | Histidine phosphatase superfamily (branch 2) |
| EVM0003014 | 115.44 | 54.87 | 1.07 | 2.00E-03 | 1.01E-02 | Amino acid transport and metabolism | Methylene-tetrahydrofolate reductase |
| EVM0006386 | 44.83  | 21.26 | 1.08 | 2.50E-03 | 1.22E-02 | -- | -- |
| EVM0000996 | 109.13 | 51.58 | 1.08 | 8.00E-04 | 4.73E-03 | Lipid transport and metabolism | Short chain dehydrogenase |
| EVM0007160 | 5.77   | 2.73  | 1.08 | 2.15E-03 | 1.08E-02 | -- | -- |
| EVM0009035 | 45.72  | 21.58 | 1.08 | 1.00E-04 | 7.96E-04 | -- | Non-repetitive/WGA-negative nucleoporin C-terminal |
| EVM0000439 | 70.92  | 33.47 | 1.08 | 1.50E-04 | 1.14E-03 | -- | Kelch motif |
| EVM0009335 | 21.15  | 9.97  | 1.08 | 2.70E-03 | 1.30E-02 | -- | -- |
| EVM0010160 | 101.30 | 47.75 | 1.09 | 1.00E-04 | 7.96E-04 | Carbohydrate transport and metabolism | Major Facilitator Superfamily |
| EVM0007366 | 59.74  | 28.14 | 1.09 | 1.50E-04 | 1.14E-03 | -- | -- |
| EVM0002944 | 23.88  | 11.24 | 1.09 | 1.40E-03 | 7.55E-03 | -- | WD domain, G-beta repeat |
| EVM0011507 | 42.35  | 19.90 | 1.09 | 2.00E-04 | 1.46E-03 | -- | Nuclear pore component |
| EVM0004480 | 16.69 | 7.83 | 1.09 | 6.50E-04 | 3.98E-03 | -- | Glycosyl hydrolases family 15 |
|------------|-------|------|------|----------|----------|----|-------------------------------|
| EVM0005478 | 8.54  | 3.99 | 1.10 | 2.20E-03 | 1.10E-02 | -- | General function prediction   |
|            |       |      |      |          |          |    | WD domain, G-beta repeat only |
| EVM0006229 | 421.19| 196.42| 1.10 | 6.00E-04 | 3.72E-03 | -- | Inorganic ion transport         |
|            |       |      |      |          |          |    | and metabolism                 |
| EVM0006013 | 4.64  | 2.16 | 1.10 | 4.25E-03 | 1.89E-02 | -- | --                            |
| EVM0001008 | 7.99  | 3.72 | 1.10 | 4.30E-03 | 1.90E-02 | -- | --                            |
| EVM0012125 | 20.80 | 9.65 | 1.11 | 2.00E-04 | 1.46E-03 | -- | Protein of unknown function    |
|            |       |      |      |          |          |    | (DUF563)                      |
| EVM0010840 | 7.40  | 3.43 | 1.11 | 5.00E-04 | 3.19E-03 | -- | --                            |
| EVM0005773 | 100.26| 46.45| 1.11 | 5.00E-05 | 4.28E-04 | -- | Secondary metabolites biosynthesis, transport and catabolism |
| EVM0004652 | 10.85 | 5.01 | 1.11 | 9.50E-04 | 5.46E-03 | -- | Heterokaryon incompatibility protein (HET) |
| EVM0009121 | 20.66 | 9.54 | 1.11 | 1.00E-04 | 7.96E-04 | -- | C-5 cytosine-specific DNA methylase |
| EVM0008160 | 41.36 | 19.10| 1.11 | 9.50E-04 | 5.46E-03 | -- | General function prediction    |
|            |       |      |      |          |          |    | RNA recognition motif. (a.k.a. RRM, RBD, or RNP domain) |
| EVM0005603 | 3.50  | 1.61 | 1.12 | 6.30E-03 | 2.59E-02 | -- | PhoD-like phosphatase          |
| Accession     | Score | E-value | Fold Change |
|--------------|-------|---------|-------------|
| EVM0006055   | 11.26 | 3.04E-02 | 1.12        |
| EVM0002221   | 24.68 | 4.49E-03 | 1.13        |
| EVM0001336   | 37.80 | 2.37E-02 | 1.13        |
| EVM0004123   | 3.63  | 9.93E-03 | 1.13        |
| EVM0001841   | 43.56 | 1.77E-03 | 1.13        |
| EVM0001119   | 43.58 | 4.28E-04 | 1.13        |
| EVM0000108   | 60.50 | 3.46E-03 | 1.13        |
| EVM0000347   | 249.76 | 4.28E-04 | 1.13        |
| EVM0004356   | 6.16  | 4.81E-02 | 1.14        |
| EVM0003763   | 5.03  | 3.19E-03 | 1.14        |
| EVM0011389   | 125.73| 1.46E-03 | 1.14        |
| EVM0004067   | 50.64 | 7.96E-04 | 1.14        |

**General function prediction only**: short chain dehydrogenase
Amino acid transport and metabolism
Signal transduction mechanisms
Telomerase ribonucleoprotein complex - RNA binding domain
Major Facilitator Superfamily
Response regulator receiver domain
Amidohydrolase
Dienelactone hydrolase family
Protein kinase domain
FAD binding domain
HMG (high mobility group) box
| EVM0000119 | 26.76 | 12.14 | 1.14 | 2.50E-04 | 1.77E-03 | -- | 3-beta hydroxysteroid dehydrogenase/isomerase family |
| EVM0003946 | 472.85 | 214.26 | 1.14 | 1.25E-03 | 6.87E-03 | -- | -- |
| EVM0006381 | 22.21 | 10.04 | 1.15 | 1.50E-04 | 1.14E-03 | Cell cycle control, cell division, chromosome partitioning | PIF1-like helicase |
| EVM0002487 | 14.15 | 6.39 | 1.15 | 6.00E-04 | 3.72E-03 | Signal transduction mechanisms | OPT oligopeptide transporter protein |
| EVM0005868 | 131.16 | 59.21 | 1.15 | 8.50E-04 | 4.98E-03 | -- | -- |
| EVM0006071 | 52.11 | 23.52 | 1.15 | 1.00E-04 | 7.96E-04 | Translation, ribosomal structure and biogenesis | tRNA synthetases class II (D, K and N) |
| EVM0008628 | 20.34 | 9.18 | 1.15 | 2.00E-04 | 1.46E-03 | -- | -- |
| EVM0010014 | 183.69 | 82.89 | 1.15 | 2.50E-04 | 1.77E-03 | General function prediction only | Calcineurin-like phosphoesterase |
| EVM0002909 | 20.45 | 9.21 | 1.15 | 2.50E-04 | 1.77E-03 | -- | NAD(P)-binding Rossmann-like domain |
| EVM0001213 | 71.20 | 32.06 | 1.15 | 3.85E-03 | 1.74E-02 | General function prediction only | Thioesterase superfamily |
| EVM0001011 | 77.08 | 34.69 | 1.15 | 1.50E-04 | 1.14E-03 | -- | Cytochrome P450 |
| EVM0011663 | 117.26 | 52.62 | 1.16 | 2.50E-04 | 1.77E-03 | Posttranslational modification, protein turnover, chaperones | Prefoldin subunit |
| EVM0000530 | 32.20 | 14.44 | 1.16 | 5.00E-05 | 4.28E-04 | Function unknown | Ribosome 60S biogenesis N-terminal |
| EVM0010598 | 4.70  | 2.11  | 1.16 | 7.75E-03 | 3.06E-02 | --              | F-box-like                       |
| EVM0004840 | 299.94 | 134.47 | 1.16 | 1.50E-04 | 1.14E-03 | --              | --                              |
| EVM0007450 | 55.67 | 24.92 | 1.16 | 2.50E-04 | 1.77E-03 | Amino acid transport and metabolism | Beta-eliminating lyase          |
| EVM0007477 | 41.72 | 18.66 | 1.16 | 2.00E-04 | 1.46E-03 | General function prediction only | Metallo-beta-lactamase superfamily |
| EVM0004619 | 45.90 | 20.52 | 1.16 | 1.00E-04 | 7.96E-04 | Nucleotide transport and metabolism | Amidohydrolase                  |
| EVM0004153 | 229.27 | 102.30 | 1.16 | 3.00E-04 | 2.07E-03 | --              | --                              |
| EVM0008035 | 24.86 | 11.08 | 1.17 | 5.00E-05 | 4.28E-04 | General function prediction only | SNF2 family N-terminal domain   |
| EVM0008257 | 56.78 | 25.30 | 1.17 | 1.30E-03 | 7.10E-03 | --              | --                              |
| EVM0002937 | 118.24 | 52.67 | 1.17 | 5.00E-05 | 4.28E-04 | --              | --                              |
| EVM0001562 | 135.12 | 60.05 | 1.17 | 4.50E-04 | 2.92E-03 | --              | Alpha amylase, catalytic domain  |
| EVM0003369 | 1.82  | 0.81  | 1.17 | 1.34E-02 | 4.73E-02 | General function prediction only | GMC oxidoreductase              |
| EVM0002999 | 53.51 | 23.77 | 1.17 | 1.00E-04 | 7.96E-04 | Intracellular trafficking, secretion, and vesicular transport | ATG C terminal domain |
| EVM0005203 | 38.75 | 17.21 | 1.17 | 1.50E-04 | 1.14E-03 | Intracellular trafficking, secretion, and vesicular transport | Pep3/Vps18/deep orange family |
| EVM0010728 | 53.05 | 23.55 | 1.17 | 5.00E-05 | 4.28E-04 | -- | -- |
| EVM0001015 | 6.89  | 3.06  | 1.17 | 3.90E-03 | 1.76E-02 | -- | -- |
| EVM0007942 | 113.13| 50.15 | 1.17 | 1.50E-03 | 1.14E-02 | Function unknown | Protein of unknown function DUF89 |
| EVM0007734 | 104.81| 46.42 | 1.18 | 5.00E-05 | 4.28E-04 | Secondary metabolites biosynthesis, transport and catabolism | Pyridine nucleotide-disulphide oxidoreductase |
| EVM0007527 | 227.68| 100.76| 1.18 | 9.00E-04 | 5.22E-03 | Intracellular trafficking, secretion, and vesicular transport | Region in Clathrin and VPS |
| EVM0008911 | 8.40  | 3.71  | 1.18 | 3.00E-04 | 2.07E-03 | -- | -- |
| EVM0003020 | 49.81 | 21.99 | 1.18 | 1.15E-03 | 6.41E-03 | -- | -- |
| EVM0011948 | 47.96 | 21.16 | 1.18 | 5.50E-04 | 3.46E-03 | Posttranslational modification, protein turnover, chaperones | Zinc knuckle |
| EVM0000617  | 24.09 | 10.61 | 1.18 | 1.00E-04 | 7.96E-04 | Cytoskeleton | Kinesin motor domain |
|-------------|-------|-------|------|-----------|-----------|--------------|---------------------|
| EVM0000645  | 775.42| 340.85| 1.19 | 1.35E-02 | 4.74E-02 | --           | Hemopexin           |
| EVM0003003  | 89.85 | 39.47 | 1.19 | 5.00E-05 | 4.28E-04 | Coenzyme transport and metabolism | Glutamate-cysteine ligase |
| EVM0005845  | 32.84 | 14.43 | 1.19 | 5.00E-05 | 4.28E-04 | --           | Domain of unknown function (DUF4470) |
| EVM000265   | 181.11| 79.43 | 1.19 | 9.50E-04 | 5.46E-03 | Cell wall/membrane/envelope biogenesis | Chitin synthase |
| EVM0004112  | 187.54| 82.22 | 1.19 | 5.00E-05 | 4.28E-04 | --           | --                 |
| EVM0010927  | 52.09 | 22.84 | 1.19 | 3.50E-04 | 2.36E-03 | --           | BTB/POZ domain     |
| EVM0009544  | 58.48 | 25.57 | 1.19 | 1.00E-04 | 7.96E-04 | Posttranslational modification, protein turnover, chaperones | IBR domain |
| EVM0001822  | 4.39  | 1.92  | 1.19 | 5.10E-03 | 2.19E-02 | --           | --                 |
| EVM0010994  | 82.75 | 36.16 | 1.19 | 5.00E-05 | 4.28E-04 | --           | Pro-kumamolisin, activation domain |
| EVM0008720  | 239.89| 104.78| 1.19 | 1.50E-04 | 1.14E-03 | Nucleotide transport and metabolism | Ribonucleotide reductase, barrel domain |
| EVM0002114 | 154.53 | 67.49 | 1.20 | 1.50E-04 | 1.14E-03 | Posttranslational modification, protein turnover, chaperones | Proteasome/cyclosome repeat |
| EVM0004023 | 91.45  | 39.91 | 1.20 | 5.00E-05 | 4.28E-04 | Secondary metabolites biosynthesis, transport and catabolism | Pyridine nucleotide-disulphide oxidoreductase |
| EVM0011704 | 26.06  | 11.37 | 1.20 | 8.50E-04 | 4.98E-03 | Inorganic ion transport and metabolism | ZIP Zinc transporter |
| EVM0008192 | 232.76 | 101.56| 1.20 | 3.50E-04 | 2.36E-03 | Posttranslational modification, protein turnover, chaperones | ThiF family |
| EVM0011483 | 145.00 | 63.26 | 1.20 | 3.00E-04 | 2.07E-03 | -- | -- |
| EVM0005159 | 86.07  | 37.55 | 1.20 | 1.00E-04 | 7.96E-04 | -- | NADH:flavin oxidoreductase / NADH oxidase family |
| EVM0010477 | 7.66   | 3.34  | 1.20 | 6.00E-04 | 3.72E-03 | Posttranslational modification, protein turnover, chaperones | Prolyl oligopeptidase family |
| EVM0000473 | 57.49  | 25.04 | 1.20 | 6.00E-04 | 3.72E-03 | -- | -- |
| EVM0005286 | 425.68 | 184.96| 1.20 | 5.00E-05 | 4.28E-04 | -- | -- |
| EVM0009688 | 13.16  | 5.71  | 1.20 | 1.30E-03 | 7.10E-03 | -- | Zinc-binding dehydrogenase |
| EVM0003473 | 161.61 | 70.13 | 1.20 | 5.00E-05 | 4.28E-04 | Amino acid transport and metabolism | POT family |
| Enzyme ID   | Expression | E-value | Bit-score | Functional Category                                      | Domain/Function                                                                 |
|------------|------------|---------|-----------|--------------------------------------------------------|--------------------------------------------------------------------------------|
| EVM0005738 | 710.86     | 2.00E-04| 1.46E-03  | RNA processing and modification                       | LSM domain                                                                     |
| EVM0012111 | 24.57      | 1.26E-02| 4.49E-02  | --                                                     | --                                                                              |
| EVM0011560 | 18.36      | 6.50E-04| 3.98E-03  | --                                                     | Membrane bound O-acyl transferase family                                     |
| EVM0007397 | 15.13      | 2.50E-04| 1.77E-03  | Function unknown                                       | WD domain, G-beta repeat                                                       |
| EVM0008335 | 49.06      | 5.00E-05| 4.28E-04  | Function unknown                                       | Protein of unknown function (DUF3414)                                          |
| EVM0005679 | 18.98      | 5.00E-04| 3.19E-03  | --                                                     | --                                                                              |
| EVM002528  | 69.71      | 5.00E-05| 4.28E-04  | Cytoskeleton                                           | WD domain, G-beta repeat                                                       |
| EVM0003132 | 166.24     | 5.00E-05| 4.28E-04  | --                                                     | Histidine-specific methyltransferase, SAM-dependent                           |
| EVM0004177 | 93.81      | 6.50E-04| 3.98E-03  | Inorganic ion transport and metabolism                | Nitrite and sulphite reductase 4Fe-4S domain                                  |
| EVM0011713 | 9.22       | 7.50E-04| 4.49E-03  | Secondary metabolites biosynthesis, transport and catabolism | Cytochrome P450                                                                  |
| EVM0006793 | 325.86     | 7.85E-03| 3.09E-02  | --                                                     | --                                                                              |
| EVM0005557 | 49.62      | 5.00E-05| 4.28E-04  | --                                                     | Nucleoporin subcomplex protein binding to Pom34                               |
| Accession   | MRC | LC   | PI  | EValue | Fold   | Description                                                                 |
|-------------|-----|------|-----|--------|--------|-----------------------------------------------------------------------------|
| EVM0000098  | 11.76 | 5.02 | 1.23 | 3.50E-04 | 2.36E-03 | Glycosyl hydrolase family 3 N terminal domain                               |
| EVM0006748  | 96.81 | 41.16 | 1.23 | 1.50E-04 | 1.14E-03 | Function unknown                                                            |
| EVM0005178  | 7.52  | 3.19 | 1.23 | 4.95E-03 | 2.13E-02 | --                                                                          |
| EVM0005776  | 238.64 | 101.39 | 1.23 | 5.00E-05 | 4.28E-04 | Posttranslational modification, protein turnover, chaperones               |
| EVM0007924  | 261.54 | 110.85 | 1.24 | 5.00E-05 | 4.28E-04 | Carbohydrate transport and metabolism                                      |
| EVM0001663  | 2.80  | 1.18 | 1.24 | 9.05E-03 | 3.46E-02 | Energy production and conversion                                            |
| EVM0008259  | 1280.14 | 541.81 | 1.24 | 7.00E-04 | 4.23E-03 | --                                                                          |
| EVM0006449  | 152.41 | 64.48 | 1.24 | 5.00E-05 | 4.28E-04 | --                                                                          |
| EVM0009922  | 116.75 | 49.39 | 1.24 | 5.00E-05 | 4.28E-04 | Protein kinase domain                                                       |
| EVM0006696  | 36.96  | 15.63 | 1.24 | 6.25E-03 | 2.57E-02 | --                                                                          |
| EVM0010847  | 296.83 | 125.53 | 1.24 | 5.00E-05 | 4.28E-04 | --                                                                          |
| EVM0007960  | 3.19  | 1.35 | 1.25 | 1.90E-03 | 9.73E-03 | Heterokaryon incompatibility protein (HET)                                  |
| Gene ID     | E-value | Percent ID | Identity | Posttranslational modification, protein turnover, chaperones | Domain of unknown function (DUF1708) | Amino acid transport and metabolism | General function prediction only | GMC oxidoreductase | Eukaryotic aspartyl protease | Piwi domain |
|------------|---------|------------|----------|---------------------------------------------------------------|--------------------------------------|----------------------------------|--------------------------------|-----------------|--------------------------------|------------|
| EVM0003998 | 28.42   | 11.97      | 1.25     | Proteasome activator pa28 beta subunit                       | --                                  |                                  |                                |                 |                                |            |
| EVM0009500 | 121.52  | 51.03      | 1.25     | --                                                            | Domain of unknown function (DUF1708) |                                  |                                |                 |                                |            |
| EVM0007131 | 10.37   | 4.35       | 1.25     | --                                                            | --                                  |                                  |                                |                 |                                |            |
| EVM0006718 | 47.56   | 19.94      | 1.25     | Amino acid transport and metabolism                           | FAD dependent oxidoreductase        |                                  |                                |                 |                                |            |
| EVM0005326 | 5.03    | 2.11       | 1.25     | General function prediction only                              | GMC oxidoreductase                  |                                  |                                |                 |                                |            |
| EVM0002000 | 42.12   | 17.63      | 1.26     | Posttranslational modification, protein turnover, chaperones | Prolyl oligopeptidase, N-terminal beta-propeller domain |                                  |                                |                 |                                |            |
| EVM0007222 | 4.11    | 1.72       | 1.26     | --                                                            | Protein of unknown function (DUF4246) |                                  |                                |                 |                                |            |
| EVM0006789 | 83.87   | 35.06      | 1.26     | Posttranslational modification, protein turnover, chaperones | Eukaryotic aspartyl protease        |                                  |                                |                 |                                |            |
| EVM0004481 | 7.50    | 3.13       | 1.26     | --                                                            | --                                  |                                  |                                |                 |                                |            |
| EVM0004594 | 108.53  | 45.20      | 1.26     | Amino acid transport and metabolism                           | Amino acid permease                 |                                  |                                |                 |                                |            |
| EVM0000790 | 13.69   | 5.70       | 1.27     | Translation, ribosomal structure and biogenesis               | Piwi domain                         |                                  |                                |                 |                                |            |
| Accession   | Score 1 | Score 2 | Score 3 | Score 4 | Score 5 | Feature Description                                      | Annotation                                      |
|-------------|---------|---------|---------|---------|---------|---------------------------------------------------------|-----------------------------------------------|
| EVM0003945  | 205.26  | 85.30   | 1.27    | 4.50E-04| 2.92E-03| Cell wall/membrane/envelope biogenesis                 | Chitin synthase                                |
| EVM0000466  | 51.44   | 21.36   | 1.27    | 5.00E-05| 4.28E-04| General function prediction only                       | Peptidase family M49                          |
| EVM0008931  | 52.62   | 21.83   | 1.27    | 5.00E-05| 4.28E-04| --                                                     | Growth-Arrest-Specific Protein 2 Domain        |
| EVM0012149  | 61.11   | 25.29   | 1.27    | 5.00E-05| 4.28E-04| --                                                     | Beta-lactamase superfamily domain             |
| EVM0010488  | 29.72   | 12.30   | 1.27    | 1.20E-03| 6.64E-03| --                                                     | --                                            |
| EVM0008962  | 28.57   | 11.78   | 1.28    | 3.50E-04| 2.36E-03| General function prediction only                       | MOSC domain                                   |
| EVM0008061  | 87.73   | 36.14   | 1.28    | 5.00E-05| 4.28E-04| General function prediction only                       | GMC oxidoreductase                            |
| EVM0009152  | 5.95    | 2.45    | 1.28    | 2.50E-04| 1.77E-03| --                                                     | Bacterial alpha-L-rhamnosidase                |
| EVM0011225  | 36.71   | 15.08   | 1.28    | 1.00E-04| 7.96E-04| RNA processing and modification                       | Ribonuclease III domain                       |
| EVM0004082  | 2.45    | 1.01    | 1.28    | 1.43E-02| 4.97E-02| --                                                     | NADH:flavin oxidoreductase / NADH oxidase family |
| EVM0000724  | 49.48   | 20.27   | 1.29    | 5.00E-05| 4.28E-04| Translation, ribosomal structure and biogenesis       | Piwi domain                                   |
| EVM0000838  | 216.34  | 88.48   | 1.29    | 5.00E-05| 4.28E-04| --                                                     | Glycosyl Hydrolase Family 88                  |
| Accession   | Number 1 | Number 2 | Number 3 | Number 4 | Number 5 | Number 6 | Description                                                                 |
|-------------|----------|----------|----------|----------|----------|----------|----------------------------------------------------------------------------|
| EVM0001687  | 16.11    | 6.58     | 1.29     | 5.00E-05 | 4.28E-04 | ---      | RecF/RecN/SMC N terminal domain                                              |
| EVM0001466  | 14.05    | 5.73     | 1.29     | 1.50E-04 | 1.14E-03 | ---      | Peptidase family M48                                                        |
| EVM0003437  | 22.07    | 8.98     | 1.30     | 5.00E-05 | 4.28E-04 | ---      | Posttranslational modification, protein turnover, chaperones                |
| EVM0003467  | 483.21   | 196.61   | 1.30     | 5.00E-05 | 4.28E-04 | ---      | Tubulin folding cofactor D C terminal                                       |
| EVM0003467  | 5.00E-05 | 4.28E-04 | ---      |          |          |          |                                                                             |
| EVM0006877  | 21.93    | 8.90     | 1.30     | 4.50E-04 | 2.92E-03 | ---      | Membrane bound O-acyl transferase family                                   |
| EVM0004984  | 129.22   | 52.46    | 1.30     | 5.00E-05 | 4.28E-03 | ---      |                                                                             |
| EVM0004984  | 129.22   | 52.46    | 1.30     | 5.00E-05 | 4.28E-03 | ---      |                                                                             |
| EVM0004984  | 129.22   | 52.46    | 1.30     | 5.00E-05 | 4.28E-03 | ---      |                                                                             |
| EVM0004984  | 129.22   | 52.46    | 1.30     | 5.00E-05 | 4.28E-03 | ---      |                                                                             |
| EVM0004984  | 129.22   | 52.46    | 1.30     | 5.00E-05 | 4.28E-03 | ---      |                                                                             |
| EVM0006959  | 20.84    | 8.45     | 1.30     | 3.00E-03 | 1.42E-02 | ---      | Cytochrome oxidase complex assembly protein 1                               |
| EVM0008057  | 3.42     | 1.38     | 1.30     | 4.25E-03 | 1.89E-02 | ---      | Energy production and conversion Aldehyde dehydrogenase family             |
| EVM0002760  | 39.53    | 15.99    | 1.31     | 7.00E-04 | 4.23E-03 | ---      |                                                                             |
| EVM0007194  | 50.62    | 20.46    | 1.31     | 5.00E-05 | 4.28E-04 | ---      | Major Facilitator Superfamily                                               |
| EVM0007451  | 84.78    | 34.11    | 1.31     | 5.00E-05 | 4.28E-04 | ---      | Beta-glucan synthesis-associated protein (SKN1)                             |
| EVM0010231  | 76.04    | 30.59    | 1.31     | 5.00E-05 | 4.28E-04 | ---      | NPL4 family                                                                |
| EVM0007272    | 43.04 | 17.31 | 1.31 | 5.00E-05 | 4.28E-04 | Pro-kumamolisin, activation domain |
| EVM0012119    | 6.10  | 2.45  | 1.32 | 4.00E-04 | 2.65E-03 | Ankyrin repeats (3 copies) |
| EVM0002146    | 6.66  | 2.67  | 1.32 | 9.00E-04 | 5.22E-03 | Pectinesterase |
| EVM0005137    | 6.31  | 2.53  | 1.32 | 1.03E-02 | 3.84E-02 | #N/A |
| EVM0010942    | 29.63 | 11.87 | 1.32 | 5.00E-05 | 4.28E-04 | -- |
| EVM0007516    | 88.32 | 35.37 | 1.32 | 5.00E-05 | 4.28E-04 | Carbohydrate transport and metabolism |
| EVM0009062    | 3.11  | 1.25  | 1.32 | 2.70E-03 | 1.30E-02 | Domain of unknown function (DUF4139) |
| EVM0008666    | 33.70 | 13.49 | 1.32 | 5.00E-05 | 4.28E-04 | Dioxygenase |
| EVM0000179    | 3.22  | 1.29  | 1.32 | 3.45E-03 | 1.59E-02 | Secondary metabolites biosynthesis, transport and catabolism |
| EVM0004320    | 149.65| 59.82 | 1.32 | 5.00E-05 | 4.28E-04 | General function prediction only |
| EVM0006268    | 77.30 | 30.87 | 1.32 | 5.00E-05 | 4.28E-04 | -- |
| EVM0007570    | 19.30 | 7.70  | 1.33 | 5.00E-05 | 4.28E-04 | Poly(ADP-ribose) polymerase catalytic domain |
| Accession   | Counts | Folds | Fold Change | p-Value | Description                                                                 |
|------------|--------|-------|-------------|---------|----------------------------------------------------------------------------|
| EVM0009974 | 82.68  | 32.89 | 1.33        | 5.00E-05 | Signal transduction mechanisms                                              |
| EVM0005979 | 5.28   | 2.10  | 1.33        | 3.50E-03 | --                                                                          |
| EVM0008616 | 72.25  | 28.70 | 1.33        | 5.00E-05 | Carbohydrate transport and metabolism                                       |
| EVM0005231 | 18.27  | 7.24  | 1.33        | 1.00E-04 | Amino acid transport and metabolism                                         |
| EVM0006160 | 23.11  | 9.12  | 1.34        | 5.00E-05 | Function unknown                                                             |
| EVM0007751 | 78.58  | 30.98 | 1.34        | 5.00E-05 | --                                                                          |
| EVM0009444 | 9517.76| 3750.32| 1.34        | 9.00E-05| Fungal hydrophobin                                                          |
| EVM0001877 | 4.63   | 1.82  | 1.35        | 1.95E-03 | Voltage-dependent anion channel                                             |
| EVM0011240 | 225.96 | 88.62 | 1.35        | 5.00E-05 | --                                                                          |
| EVM0010629 | 69.29  | 27.10 | 1.35        | 2.45E-03 | Glycosyl hydrolase family 92                                               |
| EVM0001405 | 143.94 | 56.30 | 1.35        | 5.00E-05 | Intracellular trafficking, secretion, and vesicular transport              |
| EVM0003929 | 17.66  | 6.90  | 1.36        | 1.50E-04 | --                                                                          |

- **EVM0009974**: Signal transduction mechanisms
- **EVM0005979**: --
- **EVM0008616**: Carbohydrate transport and metabolism
- **EVM0005231**: Amino acid transport and metabolism
- **EVM0006160**: Function unknown
- **EVM0007751**: --
- **EVM0009444**: Fungal hydrophobin
- **EVM0001877**: Voltage-dependent anion channel
- **EVM0011240**: --
- **EVM0010629**: Glycosyl hydrolase family 92
- **EVM0001405**: Intracellular trafficking, secretion, and vesicular transport
- **EVM0003929**: --
| Accession | EVM0006295 | EVM0003122 | EVM0008150 | EVM0011231 | EVM0009509 | EVM0011805 | EVM0002563 | EVM0002782 | EVM0011882 | EVM0009019 | EVM0006352 | EVM0010470 |
|-----------|------------|------------|------------|------------|------------|------------|------------|------------|------------|------------|------------|------------|
| Score     | 48.19      | 43.47      | 41.66      | 3.25       | 35.80      | 2.41       | 9.23       | 25.36      | 43.81      | 3.42       | 148.47     | 134.22     |
| E-value   | 18.80      | 16.92      | 16.20      | 1.26       | 13.88      | 0.93       | 3.57       | 9.81       | 16.90      | 1.32       | 57.25      | 51.70      |
| Exponent  | 0.136      | 0.136      | 0.136      | 0.136      | 0.136      | 0.136      | 0.136      | 0.136      | 0.136      | 0.136      | 0.136      | 0.136      |
| General function prediction only | Dienelactone hydrolase family | Translation, ribosomal structure and biogenesis | Energy production and conversion | Serine carboxypeptidase | General function prediction only | Tht1-like nuclear fusion protein | Protein of unknown function (DUF1399) | Cytoskeleton | Variant SH3 domain | Survival protein SurE | General function prediction only | Proteasome/cyclosome repeat |
| Accession  | E-value 1 | E-value 2 | Domain                   |
|-----------|-----------|-----------|--------------------------|
| EVM0007276| 4.44      | 1.71      | 1.38                     | 2.05E-03 1.03E-02 -- Acetyltransferase (GNAT) domain |
| EVM0009736| 31.16     | 11.99     | 1.38                     | 5.00E-05 4.28E-04 -- PhoD-like phosphatase |
| EVM0008271| 13.32     | 5.12      | 1.38                     | 1.65E-03 8.65E-03 -- |
| EVM0000536| 8.79      | 3.38      | 1.38                     | 4.35E-03 1.92E-02 -- |
| EVM0003743| 6.24      | 2.40      | 1.38                     | 1.00E-03 5.70E-03 Carbohydrate transport and metabolism Major Facilitator Superfamily |
| EVM0005149| 20.09     | 7.70      | 1.38                     | 5.00E-05 4.28E-04 -- |
| EVM0005153| 17.94     | 6.87      | 1.38                     | 1.00E-04 7.96E-04 General function prediction only Major Facilitator Superfamily |
| EVM0001489| 73.96     | 28.26     | 1.39                     | 5.00E-05 4.28E-04 General function prediction only Enoyl-(Acyl carrier protein) reductase |
| EVM0001362| 11.71     | 4.47      | 1.39                     | 1.00E-04 7.96E-04 -- Protein of unknown function (DUF1212) |
| EVM0002085| 260.21    | 99.33     | 1.39                     | 1.75E-03 9.08E-03 -- Major Facilitator Superfamily |
| EVM0011278| 744.06    | 283.63    | 1.39                     | 5.00E-05 4.28E-04 -- |
| EVM0005755| 56.14     | 21.40     | 1.39                     | 5.00E-05 4.28E-04 Glycosyl hydrolases family 16 |
| EVM0005145| 31.58     | 12.04     | 1.39                     | 6.65E-03 2.70E-02 -- |
| EVM0008313 | 24.55 | 9.35 | 1.39 | 5.00E-05 | 4.28E-04 | Secondary metabolites biosynthesis, transport and catabolism | ABC transporter transmembrane region |
|------------|-------|------|------|-----------|-----------|---------------------------------------------------------------|----------------------------------------|
| EVM0007446 | 1034.64 | 393.16 | 1.40 | 6.50E-04 | 3.98E-03 | -- | Fungalysin metallopeptidase (M36) |
| EVM0009632 | 159.39 | 60.52 | 1.40 | 1.00E-04 | 7.96E-04 | Secondary metabolites biosynthesis, transport and catabolism | Copper amine oxidase, enzyme domain |
| EVM0008081 | 409.36 | 155.28 | 1.40 | 5.00E-05 | 4.28E-04 | Translation, ribosomal structure and biogenesis | Ribosomal protein S19 |
| EVM0000747 | 20.03 | 7.58 | 1.40 | 5.00E-04 | 3.19E-03 | General function prediction only | Scavenger mRNA decapping enzyme C-term binding |
| EVM0006635 | 12.66 | 4.79 | 1.40 | 5.00E-05 | 4.28E-04 | -- | Glutaredoxin-like domain (DUF836) |
| EVM0006660 | 559.24 | 211.01 | 1.41 | 5.00E-05 | 4.28E-04 | -- | -- |
| EVM0009298 | 38.01 | 14.33 | 1.41 | 5.00E-05 | 4.28E-04 | -- | -- |
| EVM0002859 | 49.39 | 18.57 | 1.41 | 5.00E-05 | 4.28E-04 | -- | non-SMC mitotic condensation complex subunit 1 |
| EVM0002582 | 320.26 | 120.20 | 1.41 | 5.00E-05 | 4.28E-04 | Translation, ribosomal structure and biogenesis | RNB domain |
| EVM0002222 | 8.41 | 3.16 | 1.41 | 3.50E-04 | 2.36E-03 | -- | Cytochrome P450 |
| EVM0000680 | 14.42 | 5.40 | 1.42 | 2.00E-04 | 1.46E-03 | Secondary metabolites biosynthesis, transport and catabolism | Cytochrome P450 |
|-------------|-------|------|------|----------|----------|-------------------------------------------------------------|-----------------|
| EVM0011859 | 8.71  | 3.26 | 1.42 | 4.00E-04 | 2.65E-03 | Energy production and conversion                            | Phosphoenolpyruvate phosphomutase |
| EVM0000187 | 7.49  | 2.80 | 1.42 | 2.75E-03 | 1.32E-02 | --                                                          | --              |
| EVM0005170 | 9.53  | 3.55 | 1.42 | 7.50E-04 | 4.49E-03 | Secondary metabolites biosynthesis, transport and catabolism | Cytochrome P450 |
| EVM0008923 | 8.05  | 3.00 | 1.42 | 6.00E-04 | 3.72E-03 | --                                                          | --              |
| EVM0007579 | 204.50| 76.15| 1.43 | 5.00E-05 | 4.28E-04 | --                                                          | HEAT repeat     |
| EVM0009131 | 99.84 | 37.13| 1.43 | 5.00E-05 | 4.28E-04 | Lipid transport and metabolism                              | AMP-binding enzyme |
| EVM005521  | 98.68 | 36.68| 1.43 | 5.00E-05 | 4.28E-04 | --                                                          | GPR1/FUN34/yaA family |
| EVM009273  | 5.93  | 2.20 | 1.43 | 1.50E-04 | 1.14E-03 | --                                                          | --              |
| EVM011375  | 3.54  | 1.31 | 1.43 | 4.20E-03 | 1.87E-02 | --                                                          | --              |
| EVM003471  | 5.07  | 1.88 | 1.43 | 4.50E-04 | 2.92E-03 | General function prediction only                            | GMC oxidoreductase |
| EVM0005515 | 9.55 | 3.54 | 1.43 | 4.00E-04 | 2.65E-03 | Secondary metabolites biosynthesis, transport and catabolism | Cytochrome P450 |
| EVM0000884 | 30.51 | 11.28 | 1.44 | 5.00E-05 | 4.28E-04 | Lipid transport and metabolism | AMP-binding enzyme |
| EVM0008039 | 641.59 | 237.16 | 1.44 | 1.50E-04 | 1.14E-03 | -- | -- |
| EVM0001300 | 4.44 | 1.64 | 1.44 | 4.30E-03 | 1.90E-02 | -- | -- |
| EVM0010856 | 41.65 | 15.35 | 1.44 | 5.00E-03 | 4.28E-02 | -- | -- |
| EVM0004107 | 5.43 | 2.00 | 1.44 | 3.00E-03 | 1.42E-02 | -- | -- |
| EVM0012135 | 16.50 | 6.05 | 1.45 | 2.00E-03 | 1.46E-02 | -- | -- |
| EVM0002960 | 3.64 | 1.33 | 1.45 | 6.80E-03 | 2.75E-02 | -- | -- |
| EVM0004000 | 53.62 | 19.64 | 1.45 | 5.00E-05 | 4.28E-04 | Carbohydrate transport and metabolism | Glucose-6-phosphate dehydrogenase, C-terminal domain |
| EVM0006771 | 207.54 | 75.95 | 1.45 | 5.00E-05 | 4.28E-04 | Carbohydrate transport and metabolism | Alpha amylase, catalytic domain |
| EVM0006519 | 51.21 | 18.71 | 1.45 | 5.00E-05 | 4.28E-04 | -- | Putative amidotransferase |
| EVM0008140 | 28.50 | 10.38 | 1.46 | 5.00E-05 | 4.28E-04 | -- | -- |
| Gene ID     | E-value1 | E-value2 | E-value3 | Description                                                                 |
|------------|----------|----------|----------|-----------------------------------------------------------------------------|
| EVM0010535 | 7.55E-03 | 2.99E-02 |          | NmrA-like family                                                            |
| EVM0011462 | 5.00E-05 | 4.28E-04 |          | Intracellular trafficking, secretion, and vesicular transport                |
| EVM0008739 | 5.00E-05 | 4.28E-04 |          | Exocyst complex subunit Sec15-like                                           |
| EVM0008782 | 5.00E-05 | 4.28E-04 |          | Energy production and conversion                                            |
| EVM00111123| 5.00E-05 | 4.28E-04 |          | Carboxamyl-phosphate synthase L chain, ATP binding domain                   |
| EVM0004211 | 5.00E-05 | 4.28E-04 |          | Posttranslational modification, protein turnover, chaperones                |
| EVM0011159 | 6.50E-04 | 3.98E-03 |          | Insulinase (Peptidase family M16)                                           |
| EVM0004211 | 5.00E-05 | 4.28E-04 |          | ATPase family associated with various cellular activities (AAA)           |
| EVM0011159 | 6.50E-04 | 3.98E-03 |          | L-lysine 6-monoxygenase (NADPH-requiring)                                   |
| EVM0006087 | 5.00E-05 | 4.28E-04 |          | Inorganic ion transport and metabolism                                      |
| EVM0006340 | 5.00E-05 | 4.28E-04 |          | Ammonium Transporter Family                                                |
| EVM000810  | 1.44E-02 | 4.99E-02 |          | Nup53/35/40-type RNA recognition motif                                      |
| EVM0008782 | 5.00E-05 | 4.28E-04 |          | General function prediction only                                            |
| EVM0000512 | 5.00E-05 | 4.28E-04 |          | WD domain, G-beta repeat                                                    |
| EVM0000512 | 5.00E-05 | 4.28E-04 |          | MCM2/3/5 family                                                            |
| EVM ID       | Score 1 | Score 2 | E-values | Description                                                                                           |
|-------------|---------|---------|----------|-------------------------------------------------------------------------------------------------------|
| EVM0003237  | 125.74  | 45.31   | 1.47     | 5.00E-05, 4.28E-04 Amino acid transport and metabolism Glutamate/Leucine/Phenylalanine/Valine dehydrogenase |
| EVM0006267  | 327.34  | 117.24  | 1.48     | 5.00E-05, 4.28E-04 Energy production and conversion Aldo/keto reductase family                         |
| EVM0006868  | 824.81  | 295.30  | 1.48     | 5.00E-05, 4.28E-04 General function prediction only RNA recognition motif. (a.k.a. RRM, RBD, or RNP domain) |
| EVM0004436  | 3.55    | 1.27    | 1.48     | 1.03E-02, 3.82E-02 -- Acetamidase/Formamidase family                                                  |
| EVM0011188  | 13.95   | 4.98    | 1.49     | 5.00E-05, 4.28E-04 Carbohydrate transport and metabolism Major Facilitator Superfamily                |
| EVM0003971  | 22.83   | 8.15    | 1.49     | 1.00E-04, 7.96E-04 Coenzyme transport and metabolism Dihydroneopterin aldolase                        |
| EVM0006629  | 44.42   | 15.84   | 1.49     | 5.00E-05, 4.28E-04 Secondary metabolites biosynthesis, transport and catabolism ABC transporter          |
| EVM0002696  | 5.68    | 2.02    | 1.49     | 2.50E-04, 1.77E-03 Signal transduction mechanisms OPT oligopeptide transporter protein                |
| EVM0008679  | 8.03    | 2.85    | 1.50     | 5.00E-05, 4.28E-04 Signal transduction mechanisms RhoGEF domain                                       |
| EVM0004575  | 139.05  | 49.21   | 1.50     | 1.00E-04, 7.96E-04 General function prediction only GMC oxidoreductase                                |
| EVM0009784  | 7.99    | 2.83    | 1.50     | 5.50E-04, 3.46E-03 Energy production and conversion D-isomer specific 2-hydroxyacid dehydrogenase, NAD binding domain |
| EVM0010467   | 1.22 | 0.43 | 1.50 | 1.20E-02 | 4.33E-02 | Secondary metabolites biosynthesis, transport and catabolism | Cytochrome P450 |
|--------------|------|------|------|----------|----------|-------------------------------------------------------------|------------------|
| EVM0009044   | 79.78| 28.18| 1.50 | 5.00E-05 | 4.28E-04 | --                                                          | --               |
| EVM0008864   | 173.27| 61.12| 1.50 | 5.00E-05 | 4.28E-04 | Energy production and conversion                            | Acetyl-CoA hydrolase/transferase N-terminal domain |
| EVM0003583   | 822.18| 289.96| 1.50 | 3.50E-04 | 2.36E-03 | --                                                          | --               |
| EVM0009751   | 2.30 | 0.81 | 1.50 | 1.00E-04 | 7.96E-04 | --                                                          | --               |
| EVM0005610   | 92.60| 32.60| 1.51 | 5.00E-05 | 4.28E-04 | --                                                          | Acetamidase/Formamidase family |
| EVM0006727   | 43.81| 15.40| 1.51 | 5.00E-05 | 4.28E-04 | --                                                          | --               |
| EVM0011299   | 171.44| 60.19| 1.51 | 5.00E-05 | 4.28E-04 | General function prediction only                            | Sugar (and other) transporter |
| EVM0004388   | 2.41 | 0.84 | 1.51 | 5.00E-05 | 4.28E-04 | --                                                          | --               |
| EVM0010473   | 46.57| 16.33| 1.51 | 5.00E-05 | 4.28E-04 | Secondary metabolites biosynthesis, transport and catabolism | Multicopper oxidase |
| EVM0011675   | 31.01| 10.86| 1.51 | 5.00E-05 | 4.28E-04 | Cytoskeleton                                                | Dynein heavy chain and region D6 of dynein motor |
| Accession   | Value 1 | Value 2 | Coefficient | E-value | Domain                                                                 | Function                                                                 |
|-------------|---------|---------|-------------|---------|------------------------------------------------------------------------|-------------------------------------------------------------------------|
| EVM0002736  | 88.78   | 31.00   | 1.52        | 5.00E-05| Cytoskeleton                                                          | Myosin head (motor domain)                                              |
| EVM0001358  | 6.31    | 2.20    | 1.52        | 1.00E-04| General function prediction                                           | GMC oxidoreductase                                                     |
| EVM0007746  | 28.10   | 9.75    | 1.53        | 5.00E-05| --                                                                    | JmjC domain, hydroxylase                                               |
| EVM0008413  | 43.83   | 15.19   | 1.53        | 5.00E-05| General function prediction                                           | ABC1 family                                                            |
| EVM0001128  | 10.95   | 3.79    | 1.53        | 5.00E-05| --                                                                    | Cytochrome P450                                                        |
| EVM0011387  | 77.10   | 26.65   | 1.53        | 5.00E-05| Translation, ribosomal structure and biogenesis                      | tRNA synthetases class I (E and Q), catalytic domain                   |
| EVM003698   | 127.33  | 44.00   | 1.53        | 5.00E-05| --                                                                    | Alginate lyase                                                         |
| EVM0010784  | 22.55   | 7.79    | 1.53        | 5.00E-05| --                                                                    | --                                                                     |
| EVM0012202  | 1409.84 | 485.96  | 1.54        | 2.00E-04| --                                                                    | --                                                                     |
| EVM0008462  | 5.65    | 1.94    | 1.54        | 4.50E-03| --                                                                    | NADH:flavin oxidoreductase / NADH oxidase family                      |
| EVM0007192  | 40.32   | 13.86   | 1.54        | 5.00E-05| Cell cycle control, cell division, chromosome partitioning          | Protein kinase domain                                                  |
| EVM0004677  | 170.33  | 58.57   | 1.54        | 5.00E-05| --                                                                    | Serine carboxypeptidase S28                                            |
| EVM0006788 | 204.59 | 70.28 | 1.54 | 5.00E-05 | 4.28E-04 | -- | -- |
| EVM0011825 | 5.86   | 2.01  | 1.54 | 5.00E-05 | 4.28E-04 | Carbohydrate transport and metabolism | Glycosyl hydrolases family 35 |
| EVM0009138 | 8.14   | 2.78  | 1.55 | 1.00E-04 | 7.96E-04 | -- | -- |
| EVM0001810 | 190.23 | 64.65 | 1.56 | 5.00E-05 | 4.28E-04 | Carbohydrate transport and metabolism | Major intrinsic protein |
| EVM0004285 | 33.40  | 11.28 | 1.57 | 5.00E-05 | 4.28E-04 | Secondary metabolites biosynthesis, transport and catabolism | Multicopper oxidase |
| EVM0011488 | 12.84  | 4.33  | 1.57 | 5.00E-05 | 4.28E-04 | -- | -- |
| EVM0007035 | 68.03  | 22.81 | 1.58 | 5.00E-05 | 4.28E-04 | -- | Transferrin receptor-like dimerisation domain |
| EVM0010980 | 1.75   | 0.58  | 1.58 | 2.50E-04 | 1.77E-03 | -- | -- |
| EVM0007317 | 3.26   | 1.08  | 1.59 | 8.00E-04 | 4.73E-03 | -- | Protein of unknown function (DUF1399) |
| EVM0003788 | 1.97   | 0.65  | 1.59 | 4.65E-03 | 2.03E-02 | -- | -- |
| EVM0006864 | 90.08  | 29.83 | 1.59 | 4.50E-04 | 2.92E-03 | -- | Glyoxal oxidase N-terminus |
| EVM0002121 | 22.65  | 7.49  | 1.60 | 5.00E-05 | 4.28E-04 | Replication, recombination and repair | AAA domain |
| ID            | Values   | Log | Pathway                                                                 | Annotation                                              |
|--------------|----------|-----|------------------------------------------------------------------------|---------------------------------------------------------|
| EVM0003469   | 2.31     | 0.76| 1.60                                                                   | Carbohydrate transport and metabolism                   |
|              |          |     |                                                                        | Glycosyl-transferase for dystroglycan                   |
| EVM0010991   | 17.57    | 5.78| 1.60                                                                   | Carbohydrate transport and metabolism                   |
|              |          |     |                                                                        | Histidine phosphatase superfamily (branch 1)            |
| EVM0010340   | 10.47    | 3.44| 1.61                                                                   | Energy production and conversion                        |
|              |          |     |                                                                        | Pyridine nucleotide-disulphide oxidoreductase           |
| EVM0008227   | 34.98    | 11.47| 1.61                                                                   | Replication, recombination and repair                   |
|              |          |     |                                                                        | MCM2/3/5 family                                         |
| EVM0006552   | 11.35    | 3.72| 1.61                                                                   | Secondary metabolites biosynthesis, transport and catabolism |
|              |          |     |                                                                        | Male sterility protein                                  |
| EVM0003051   | 150.00   | 49.02| 1.61                                                                   | --                                                      |
|              |          |     |                                                                        | --                                                      |
| EVM0000912   | 6.36     | 2.07| 1.62                                                                   | #N/A                                                    |
|              |          |     |                                                                        | #N/A                                                    |
| EVM0006965   | 38.85    | 12.64| 1.62                                                                   | Inorganic ion transport and metabolism                  |
|              |          |     |                                                                        | Phosphate transporter family                            |
| EVM0006675   | 19.93    | 6.48 | 1.62                                                                   | --                                                      |
|              |          |     |                                                                        | --                                                      |
| EVM0002787   | 1001.29  | 323.55| 1.63                                                                  | Posttranslational modification, protein turnover, chaperones |
|              |          |     |                                                                        | Thioredoxin                                             |
| EVM0004830   | 30.62    | 9.88 | 1.63                                                                   | --                                                      |
|              |          |     |                                                                        | YqcI/YcgG family                                        |
| EVM0006225   | 85.30    | 27.53| 1.63                                                                   | --                                                      |
|              |          |     |                                                                        | --                                                      |
| Accession  | Value | Error | Coverage | Count | Description                                                      |
|-----------|-------|-------|----------|-------|-----------------------------------------------------------------|
| EVM0011867| 24.90 | 8.04  | 1.63     | 5.00E-05 | General function prediction only                                |
|           |       |       |          |       | Haloacid dehalogenase-like hydrolase                           |
| EVM0002414| 33.58 | 10.83 | 1.63     | 5.00E-05 | --                                                              |
|           |       |       |          |       | --                                                              |
| EVM0012100| 495.34| 159.46| 1.64     | 5.00E-05 | General function prediction only                                |
|           |       |       |          |       | Carboxylesterase family                                        |
| EVM0005595| 3.16  | 1.02  | 1.64     | 5.50E-04 | --                                                              |
|           |       |       |          |       | Serine carboxypeptidase                                        |
| EVM0009488| 6.57  | 2.11  | 1.64     | 2.20E-03 | --                                                              |
|           |       |       |          |       | --                                                              |
| EVM0000706| 84.78 | 27.16 | 1.64     | 5.00E-05 | --                                                              |
|           |       |       |          |       | Alginate lyase                                                 |
| EVM0011907| 51.08 | 16.32 | 1.65     | 5.00E-05 | Coenzyme transport and metabolism                             |
|           |       |       |          |       | Polyprenyl synthetase                                         |
| EVM0010778| 8.19  | 2.62  | 1.65     | 5.00E-05 | --                                                              |
|           |       |       |          |       | SNF2 family N-terminal domain                                  |
| EVM0011846| 177.26| 56.11 | 1.66     | 5.00E-05 | Posttranslational modification, protein turnover, chaperones   |
|           |       |       |          |       | Glutathione S-transferase, N-terminal domain                   |
| EVM0001971| 15.63 | 4.94  | 1.66     | 5.00E-04 | --                                                              |
|           |       |       |          |       | --                                                              |
| EVM0002115| 16.32 | 5.15  | 1.66     | 5.00E-05 | --                                                              |
|           |       |       |          |       | Pregnancy-associated plasma protein-A                         |
| EVM0000101| 23.98 | 7.56  | 1.67     | 2.00E-04 | #N/A                                                            |
|           |       |       |          |       | #N/A                                                            |
| Accession   | Name                                               | Score 1 | Score 2 | Score 3 | Score 4 | Function                                                                 |
|------------|----------------------------------------------------|---------|---------|---------|---------|--------------------------------------------------------------------------|
| EVM0011327 | AAA domain                                         | 18.95   | 5.97    | 1.67    | 1.00E-04| Replication, recombination and repair                                    |
| EVM0001061 | Posttranslational modification, protein turnover, chaperones | 1.30    | 0.41    | 1.67    | 1.75E-03| BCS1 N terminal                                                          |
| EVM0002963 | Secondary metabolites biosynthesis, transport and catabolism | 100.39  | 31.23   | 1.68    | 5.00E-05| Alcohol dehydrogenase GroES-like domain                                  |
| EVM0001672 | --                                                 | 17.06   | 5.30    | 1.69    | 5.00E-05| NmrA-like family                                                         |
| EVM0000594 | NmrA-like family                                    | 15.52   | 4.82    | 1.69    | 5.00E-05| Sulfate transporter family                                               |
| EVM0011428 | Inorganic ion transport and metabolism             | 24.49   | 7.60    | 1.69    | 5.00E-05| Glycosyl hydrolase family 3 N terminal domain                             |
| EVM0008766 | --                                                 | 25.03   | 7.76    | 1.69    | 2.30E-03| Ankyrin repeats (many copies)                                            |
| EVM0002253 | --                                                 | 2.69    | 0.83    | 1.69    | 1.65E-03| SH3-binding, glutamic acid-rich protein                                  |
| EVM0008881 | --                                                 | 197.99  | 60.98   | 1.70    | 5.00E-05| --                                                                       |
| EVM0001331 | Glycosyl hydrolase family 3 N terminal domain      | 36.49   | 11.22   | 1.70    | 5.00E-05| --                                                                       |
| EVM0011451 | SH3-binding, glutamic acid-rich protein             | 3.47    | 1.07    | 1.71    | 1.21E-02| --                                                                       |
| EVM0000646 | --                                                 | 7.84    | 2.38    | 1.72    | 8.40E-03| --                                                                       |
| EVM0008978 | 19.12 | 5.81 | 1.72 | 5.00E-05 | 4.28E-04 | Transcription | SNF2 family N-terminal domain |
| EVM0010171 | 25.83 | 7.83 | 1.72 | 5.00E-05 | 4.28E-04 | Energy production and conversion | Aldo/keto reductase family |
| EVM0001895 | 12.48 | 3.78 | 1.72 | 1.50E-04 | 1.14E-03 | -- | -- |
| EVM0001305 | 1.59  | 0.48 | 1.72 | 1.34E-02 | 4.72E-02 | -- | Domain of unknown function (DUF3328) |
| EVM0010291 | 32.34 | 9.78 | 1.72 | 2.00E-04 | 1.46E-03 | -- | MAPEG family |
| EVM0012190 | 3.58  | 1.08 | 1.73 | 2.50E-04 | 1.77E-03 | Secondary metabolites biosynthesis, transport and catabolism | ABC transporter transmembrane region |
| EVM0003849 | 66.96 | 20.19| 1.73 | 5.00E-05 | 4.28E-04 | -- | -- |
| EVM0010242 | 6.79  | 2.05 | 1.73 | 1.50E-04 | 1.14E-03 | Function unknown | WD domain, G-beta repeat |
| EVM0005614 | 93.07 | 27.97| 1.73 | 5.00E-05 | 4.28E-04 | -- | -- |
| EVM0003633 | 23.87 | 7.10 | 1.75 | 5.00E-05 | 4.28E-04 | -- | Pectate lyase superfamily protein |
| EVM0005680 | 12.19 | 3.61 | 1.76 | 5.00E-05 | 4.28E-04 | Carbohydrate transport and metabolism | Major Facilitator Superfamily |
| EVM0002173 | 1.74  | 0.51 | 1.76 | 1.35E-02 | 4.76E-02 | -- | Rad51 |
| EVM0009020 | 13.30 | 3.88 | 1.78 | 5.00E-05 | 4.28E-04 | -- | -- |
| EVM0011477 | 29.16 | 8.49 | 1.78 | 5.00E-05 | 4.28E-04 | Posttranslational modification, protein turnover, chaperones | Glutathione S-transferase, N-terminal domain |
| EVM0009637 | 38.46 | 11.18 | 1.78 | 5.00E-05 | 4.28E-04 | General function prediction only | Epoxide hydrolase N terminus |
| EVM0005805 | 4.67 | 1.35 | 1.79 | 1.00E-03 | 5.70E-03 | -- | -- |
| EVM0010323 | 71.21 | 20.60 | 1.79 | 5.00E-05 | 4.28E-04 | Inorganic ion transport and metabolism | ATP-sulfurylase |
| EVM0010721 | 6.47 | 1.87 | 1.79 | 2.25E-03 | 1.12E-02 | -- | -- |
| EVM0005713 | 1.33 | 0.38 | 1.80 | 1.43E-02 | 4.97E-02 | -- | Serine carboxypeptidase |
| EVM0008970 | 56.30 | 16.17 | 1.80 | 5.00E-05 | 4.28E-04 | -- | Cytochrome P450 |
| EVM0003089 | 11.28 | 3.23 | 1.80 | 1.80E-03 | 9.29E-03 | General function prediction only | Uncharacterised protein family (UPF0172) |
| EVM0003976 | 195.19 | 55.88 | 1.80 | 5.00E-05 | 4.28E-04 | Amino acid transport and metabolism | Conserved region in glutamate synthase |
| EVM0010136 | 97.45 | 27.89 | 1.80 | 5.00E-05 | 4.28E-04 | Carbohydrate transport and metabolism | Major Facilitator Superfamily |
| EVM0005194 | 2.02 | 0.58 | 1.81 | 5.90E-03 | 2.46E-02 | -- | Glycosyl hydrolases family 28 |
| EVM                | 35.85 | 10.17 | 1.82 | 5.00E-05  | 4.28E-04 | Posttranslational modification, protein turnover, chaperones | ATPase family associated with various cellular activities (AAA) |
|--------------------|-------|-------|------|-----------|----------|------------------------------------------------------------|----------------------------------------------------------|
| EVM0007544         | 5.55  | 1.57  | 1.82 | 5.00E-05  | 4.28E-04 | Posttranslational modification, protein turnover, chaperones | Eukaryotic aspartyl protease                              |
| EVM0011213         | 15.31 | 4.32  | 1.83 | 4.95E-03  | 2.13E-02 | --                                                         | --                                                      |
| EVM0001872         | 6.38  | 1.80  | 1.83 | 4.00E-03  | 1.79E-02 | --                                                         | --                                                      |
| EVM0005724         | 89.82 | 25.30 | 1.83 | 5.00E-05  | 4.28E-04 | --                                                         | Protein of unknown function (Ytp1)                       |
| EVM0002854         | 96.47 | 27.12 | 1.83 | 5.00E-05  | 4.28E-04 | Secondary metabolites biosynthesis, transport and catabolism | Multicopper oxidase                                     |
| EVM0007881         | 2.86  | 0.80  | 1.83 | 4.60E-03  | 2.01E-02 | --                                                         | Ubiquitin 3 binding protein But2 C-terminal domain       |
| EVM0008303         | 3.71  | 1.04  | 1.83 | 4.45E-03  | 1.96E-02 | Lipid transport and metabolism                            | Short chain dehydrogenase                               |
| EVM0009346         | 2.46  | 0.69  | 1.84 | 7.35E-03  | 2.93E-02 | --                                                         | Alpha/beta hydrolase family                             |
| EVM0003956         | 1.40  | 0.39  | 1.84 | 8.15E-03  | 3.18E-02 | --                                                         | Glycosyl hydrolase family                                |
| EVM0005925         | 37.48 | 10.37 | 1.85 | 5.00E-05  | 4.28E-04 | --                                                         | Cytochrome P450                                          |
| Gene ID         | Start | End   | Score | E-value | Function                                                                 |
|----------------|-------|-------|-------|---------|-------------------------------------------------------------------------|
| EVM0006594     | 421.38| 115.37| 1.87  | 5.00E-05| Amino acid transport and metabolism                                     |
| EVM0012269     | 442.14| 120.91| 1.87  | 5.00E-05| Cell wall/membrane/envelope biogenesis                                  |
| EVM0001482     | 3.51  | 0.95  | 1.88  | 3.20E-03| Lipid transport and metabolism                                         |
| EVM0006030     | 41.62 | 11.29 | 1.88  | 5.00E-05| --                                                                       |
| EVM0002050     | 159.91| 43.37 | 1.88  | 1.26E-02| --                                                                       |
| EVM0006479     | 34.65 | 9.23  | 1.91  | 5.00E-05| RecF/RecN/SMC N terminal domain                                         |
| EVM0009154     | 62.07 | 16.51 | 1.91  | 5.00E-05| --                                                                       |
| EVM0004904     | 16.97 | 4.49  | 1.92  | 5.00E-05| FAD binding domain                                                      |
| EVM0007712     | 37.77 | 9.99  | 1.92  | 5.00E-05| General function prediction only                                        |
| EVM0002674     | 8.85  | 2.34  | 1.92  | 5.00E-05| Secondary metabolites biosynthesis, transport and catabolism            |
| EVM0005310     | 577.96| 152.52| 1.92  | 5.00E-05| General function prediction only                                        |
| EVM0011435     | 55.96 | 14.72 | 1.93  | 5.00E-05| Cytoskeleton                                                            |

**Function**
- Serine hydroxymethyltransferase
- SIS domain
- short chain dehydrogenase
- Lipid transport and metabolism
- --
- RecF/RecN/SMC N terminal domain
- --
- --
- FAD binding domain
- Protein kinase domain
- short chain dehydrogenase
- General function prediction only
- Enoyl-(Acyl carrier protein) reductase
- Myosin head (motor domain)
| EVM0004571 | 1.17 | 0.31 | 1.93 | 4.45E-03 | 1.96E-02 | -- | Pectate lyase |
| EVM0002793 | 33.32 | 8.68 | 1.94 | 4.00E-04 | 2.65E-03 | -- | Cerato-platanin |
| EVM000933  | 3.88  | 1.01 | 1.94 | 1.00E-04 | 7.96E-03 | -- | Energy production and conversion |
| EVM0009846 | 22.15 | 5.72 | 1.95 | 5.00E-05 | 4.28E-04 | -- | General function prediction only |
| EVM0006476 | 593.32 | 152.82 | 1.96 | 5.00E-05 | 4.28E-04 | -- | LVIVD repeat |
| EVM0009616 | 43.31 | 11.11 | 1.96 | 5.00E-05 | 4.28E-04 | -- | Ribosomal protein S21 |
| EVM0005846 | 9.38  | 2.40 | 1.97 | 1.85E-03 | 9.52E-03 | -- | -- |
| EVM0001888 | 15.78 | 4.04 | 1.97 | 5.00E-05 | 4.28E-04 | -- | -- |
| EVM0012233 | 12.95 | 3.31 | 1.97 | 5.00E-05 | 4.28E-04 | -- | -- |
| EVM0008308 | 2.22  | 0.57 | 1.97 | 1.85E-03 | 9.52E-03 | -- | -- |
| EVM0008614 | 19.15 | 4.87 | 1.98 | 5.00E-05 | 4.28E-04 | -- | -- |
| EVM0006744 | 7.97  | 2.02 | 1.98 | 5.00E-05 | 4.28E-04 | -- | General function prediction only |
| EVM0006489 | 267.22 | 67.64 | 1.98 | 5.00E-05 | 4.28E-04 | -- | -- |
| EVM0003996  | 109.01 | 27.53 | 1.99 | 5.00E-05 | 4.28E-04 | -- | -- |
|--------------|--------|-------|------|-----------|-----------|----|----|
| EVM0000637   | 86.49  | 21.67 | 2.00 | 5.00E-05 | 4.28E-04 | -- | Cytochrome P450 |
| EVM0002953   | 38.71  | 9.67  | 2.00 | 5.00E-05 | 4.28E-04 | -- | Fungalysin metallopeptidase (M36) |
| EVM0005188   | 166.95 | 41.40 | 2.01 | 5.00E-05 | 4.28E-04 | -- | Inorganic ion transport and metabolism |
|              |        |       |      |           |           |    | Carbonic anhydrase |
| EVM0008197   | 49.64  | 12.24 | 2.02 | 5.00E-05 | 4.28E-04 | -- | Amino acid transport and metabolism |
|              |        |       |      |           |           |    | Carbon-nitrogen hydrolase |
| EVM0000202   | 149.45 | 36.66 | 2.03 | 5.00E-05 | 4.28E-04 | -- | Glycosyl transferase family group 2 |
| EVM0010083   | 2.22   | 0.54  | 2.03 | 9.10E-03 | 3.48E-02 | -- | Domain of unknown function (DUF3328) |
| EVM0004219   | 256.53 | 62.65 | 2.03 | 5.00E-05 | 4.28E-04 | -- | NADH:flavin oxidoreductase / NADH oxidase family |
| EVM0001750   | 15.06  | 3.66  | 2.04 | 5.00E-05 | 4.28E-04 | -- | Amino acid transport and metabolism |
|              |        |       |      |           |           |    | Amino acid permease |
| EVM0007684   | 137.09 | 33.25 | 2.04 | 5.00E-05 | 4.28E-04 | -- | General function prediction only |
|              |        |       |      |           |           |    | Major Facilitator Superfamily |
| EVM0008827   | 3.91   | 0.95  | 2.05 | 4.05E-03 | 1.81E-02 | -- | -- |
| EVM0005744   | 9.94   | 2.37  | 2.07 | 5.00E-05 | 4.28E-04 | -- | RNA processing and modification |
|              |        |       |      |           |           |    | AAA domain |
| EVM0009981   | 3.40   | 0.81  | 2.07 | 6.50E-04 | 3.98E-03 | -- | -- |
| Accession  | Value1 | Value2 | Value3 | Value4          | Value5          | Value6          | Description                                           |
|------------|--------|--------|--------|-----------------|-----------------|-----------------|-------------------------------------------------------|
| EVM0002420 | 19.64  | 4.64   | 2.08   | 1.07E-02        | 3.94E-02        | --              | --                                                   |
| EVM0006122 | 39.58  | 9.33   | 2.09   | 1.40E-03        | 7.55E-03        | --              | --                                                   |
| EVM0007573 | 3633.65| 847.04 | 2.10   | 5.00E-05        | 4.28E-04        | --              | Fungal hydrophobin                                    |
| EVM0001569 | 11.74  | 2.73   | 2.10   | 5.00E-05        | 4.28E-04        | General function prediction only | Major Facilitator Superfamily |
| EVM0003690 | 10.87  | 2.50   | 2.12   | 5.00E-05        | 4.28E-04        | --              | Caspase domain                                       |
| EVM0009599 | 5.52   | 1.27   | 2.12   | 5.00E-05        | 4.28E-04        | --              | TPR repeat                                            |
| EVM0007764 | 19.32  | 4.41   | 2.13   | 5.00E-05        | 4.28E-04        | --              | SNF2 family N-terminal domain                         |
| EVM0002710 | 47.07  | 10.71  | 2.14   | 5.00E-05        | 4.28E-04        | --              | Aldo/keto reductase family                            |
| EVM0011356 | 5.26   | 1.19   | 2.15   | 5.00E-05        | 4.28E-04        | --              | Glyoxal oxidase N-terminus                            |
| EVM0011562 | 151.91 | 34.28  | 2.15   | 5.00E-05        | 4.28E-04        | --              | --                                                   |
| EVM0010117 | 8.23   | 1.85   | 2.16   | 5.00E-05        | 4.28E-04        | --              | --                                                   |
| EVM0009436 | 3.79   | 0.85   | 2.16   | 5.45E-03        | 2.31E-02        | --              | NADH:flavin oxidoreductase / NADH oxidase family      |
| EVM0002747 | 1.73   | 0.38   | 2.18   | 4.00E-04        | 2.65E-03        | RNA processing and modification | DEAD/DEAH box helicase                                |
| EVM0009153 | 26.15 | 5.75 | 2.18 | 5.00E-05 | 4.28E-04 | -- | -- |
|------------|-------|------|------|----------|----------|----|-----|
| EVM0008746 | 59.21 | 12.92| 2.20 | 5.00E-05 | 4.28E-04 | -- | UvrD-like helicase C-terminal domain |
| EVM0005372 | 22.57 | 4.92 | 2.20 | 5.00E-05 | 4.28E-04 | -- | Alpha/beta hydrolase family |
| EVM0007492 | 233.52| 50.77| 2.20 | 3.50E-04 | 2.36E-03 | -- | Amino acid transport and metabolism |
| EVM0003142 | 1.86  | 0.40 | 2.23 | 2.65E-03 | 1.28E-02 | -- | Carbohydrate transport and metabolism |
| EVM0011658 | 8.49  | 1.80 | 2.24 | 1.50E-04 | 1.14E-03 | -- | Lipid transport and metabolism |
| EVM0002737 | 7.89  | 1.67 | 2.24 | 2.00E-04 | 1.46E-03 | -- | -- |
| EVM0001737 | 97.00 | 20.42| 2.25 | 5.00E-05 | 4.28E-04 | -- | Secondary metabolites biosynthesis, transport and catabolism |
| EVM0011790 | 13.12 | 2.76 | 2.25 | 4.00E-04 | 2.65E-03 | -- | General function prediction only |
| EVM0000478 | 56.73 | 11.75| 2.27 | 5.00E-05 | 4.28E-04 | -- | Signal transduction mechanisms |
| EVM0011687 | 46.34 | 9.58 | 2.27 | 5.00E-05 | 4.28E-04 | -- | Function unknown |
| EVM0007836 | 10.03 | 2.05 | 2.29 | 1.50E-04 | 1.14E-03 | -- | -- |
| Accession   | EVM0008735 | EVM0007392 | EVM0010471 | EVM0009169 | EVM0009561 | EVM0008408 | EVM0001579 | EVM0007578 | EVM0008758 | EVM0011853 | EVM0003903 | EVM0010699 | EVM0008722 |
|------------|------------|------------|------------|------------|------------|------------|------------|------------|------------|------------|------------|------------|------------|
| E-value    | 635.35     | 73.79      | 10.43      | 589.43     | 5.91       | 7.88       | 175.78     | 3.30       | 1.13       | 2.13       | 39.03      | 3005.31    | 340.50     |
| FDR        | 129.24     | 14.80      | 2.05       | 115.82     | 1.16       | 1.54       | 33.77      | 0.63       | 0.21       | 0.40       | 7.38       | 563.67     | 62.89      |
| Max Score  | 2.30       | 2.32       | 2.35       | 2.35       | 2.35       | 2.36       | 2.38       | 2.38       | 2.40       | 2.40       | 2.40       | 2.41       | 2.44       |
| S.D.       | 5.00E-05   | 5.00E-05   | 5.00E-05   | 5.00E-05   | 1.02E-02   | 3.45E-03   | 5.00E-05   | 2.50E-04   | 2.40E-03   | 7.55E-03   | 5.00E-05   | 2.45E-03   | 5.00E-05   |
| Fold Change| 4.28E-04   | 4.28E-04   | 4.28E-04   | 4.28E-04   | 3.80E-02   | 1.59E-02   | 4.28E-04   | 1.77E-04   | 1.18E-03   | 2.99E-02   | 4.28E-04   | 1.20E-02   | 4.28E-04   |
| Description| NmrA-like family | WSC domain | Cytochrome P450 | -- | -- | -- | General function prediction only | Family of unknown function (DUF706) | General function prediction only | GMC oxidoreductase | -- | -- | Aldo/keto reductase family | Inorganic ion transport and metabolism | Alkaline phosphatase |
| Accession  | Value1 | Value2 | Value3 | Value4 | Value5 | Value6 | Value7 | Value8 | Function                                      |
|------------|--------|--------|--------|--------|--------|--------|--------|--------|-----------------------------------------------|
| EVM0008249 | 29.07  | 5.31   | 2.45   | 5.00E-05 | 4.28E-04 | --     | --     | --     |                                               |
| EVM0000318 | 3.51   | 0.64   | 2.46   | 4.10E-03 | 1.83E-02 | --     | --     | --     |                                               |
| EVM0002732 | 68.12  | 12.32  | 2.47   | 5.00E-05 | 4.28E-04 | Function unknown | Cysteine-rich secretory protein family |
| EVM0009073 | 2.04   | 0.36   | 2.49   | 8.85E-03 | 3.40E-02 | --     | --     | --     |                                               |
| EVM0008569 | 15.71  | 2.79   | 2.49   | 3.55E-03 | 1.62E-02 | --     | --     | --     |                                               |
| EVM0000446 | 38.04  | 6.70   | 2.51   | 5.00E-05 | 4.28E-04 | Signal transduction mechanisms | Carboxylesterase family |
| EVM0009588 | 51.43  | 9.03   | 2.51   | 5.00E-05 | 4.28E-04 | Secondary metabolites biosynthesis, transport and catabolism | Cytochrome P450 |
| EVM0008919 | 3.08   | 0.54   | 2.52   | 6.00E-04 | 3.72E-03 | --     | --     | --     |                                               |
| EVM0008117 | 18.49  | 3.19   | 2.54   | 5.00E-05 | 4.28E-04 | --     | --     | --     |                                               |
| EVM0005069 | 6.01   | 1.00   | 2.58   | 5.00E-05 | 4.28E-04 | Energy production and conversion | FAD binding domain |
| EVM0009217 | 24.61  | 4.11   | 2.58   | 5.00E-05 | 4.28E-04 | Secondary metabolites biosynthesis, transport and catabolism | Cytochrome P450 |
| EVM0004536 | 18.84  | 3.09   | 2.61   | 1.00E-04 | 7.96E-04 | --     | --     | Hydrophobic surface binding protein A          |
| Accession   | Score 1 | Score 2 | E-value | Lipid transport and metabolism | Carbohydrate transport and metabolism | Major intrinsic protein | Cerato-platanin | General function prediction only | Zinc-binding dehydrogenase | Fungal hydrophobin | Serine carboxypeptidase S28 | Peptidase family M28 | SMP-30/Gluconolacase/LRE-like region | Major Facilitator Superfamily |
|------------|---------|---------|---------|---------------------------------|---------------------------------------|------------------------|---------------|----------------------------------|-----------------------------|-------------------|-------------------------------|-------------------|-------------------------------------------------|-----------------------------|
| EVM0002733 | 34.79   | 5.51    | 2.66    | 5.00E-05 4.28E-04               |                                       |                        |               |                                  |                             |                   |                               |                   |                                                 |                             |
| EVM0007992 | 4.70    | 0.74    | 2.66    | 1.16E-02 4.20E-02               |                                       |                        |               |                                  |                             |                   |                               |                   |                                                 |                             |
| EVM0008898 | 1620.69 | 255.57  | 2.66    | 5.00E-05 4.28E-04               |                                       |                        |               |                                  |                             |                   |                               |                   |                                                 |                             |
| EVM0006645 | 372.93  | 58.00   | 2.68    | 5.00E-05 4.28E-04               |                                       |                        |               |                                  |                             |                   |                               |                   |                                                 |                             |
| EVM0011914 | 105.82  | 16.29   | 2.70    | 5.00E-05 4.28E-04               |                                       |                        |               |                                  |                             |                   |                               |                   |                                                 | Cerato-platanin |
| EVM0003422 | 67.28   | 10.35   | 2.70    | 5.00E-05 4.28E-04               | General function prediction only      |                        |               |                                  |                             |                   |                               |                   |                                                 | Zinc-binding dehydrogenase |
| EVM0010018 | 86.16   | 13.21   | 2.71    | 5.00E-05 4.28E-04               |                                       |                        |               |                                  |                             |                   |                               |                   |                                                 | Fungal hydrophobin |
| EVM0000195 | 46.72   | 7.06    | 2.73    | 5.00E-05 4.28E-04               |                                       |                        |               |                                  |                             |                   |                               |                   |                                                 | Serine carboxypeptidase S28 |
| EVM0002281 | 47.04   | 7.08    | 2.73    | 5.00E-05 4.28E-04               |                                       |                        |               |                                  |                             |                   |                               |                   |                                                 | -- |
| EVM0009326 | 3.23    | 0.48    | 2.74    | 3.00E-04 2.07E-03               |                                       |                        |               |                                  |                             |                   |                               |                   |                                                 | SMP-30/Gluconolacase/LRE-like region |
| EVM0005169 | 1103.72 | 164.25  | 2.75    | 5.00E-05 4.28E-04               |                                       |                        |               |                                  |                             |                   |                               |                   |                                                 | Peptidase family M28 |
| EVM0004978 | 23.68   | 3.48    | 2.77    | 5.00E-05 4.28E-04               |                                       |                        |               |                                  |                             |                   |                               |                   |                                                 | -- |
| EVM0002125 | 20.91   | 3.05    | 2.78    | 5.00E-05 4.28E-04               | General function prediction only      |                        |               |                                  |                             |                   |                               |                   |                                                 | Major Facilitator Superfamily |
| Protein ID   | EVM0001981 | EVM0007990 | EVM0002401 | EVM0003134 | EVM0009189 | EVM0008755 | EVM0011006 | EVM0002399 | EVM0009049 | EVM0002629 | EVM0004350 | EVM0005375 |
|-------------|------------|------------|------------|------------|------------|------------|------------|------------|------------|------------|------------|------------|
| Value       | 72.41      | 30.74      | 21.10      | 60.76      | 2.59       | 71.14      | 18.23      | 134.22     | 11.25      | 803.85     | 2640.24    | 15.40      |
| Standard    | 10.40      | 4.40       | 2.96       | 8.07       | 0.34       | 9.38       | 2.40       | 16.43      | 1.37       | 96.36      | 313.04     | 1.76       |
| Confidence  | 2.80       | 2.80       | 2.83       | 2.91       | 2.92       | 2.92       | 2.93       | 3.03       | 3.04       | 3.06       | 3.08       | 3.13       |
| Score       | 5.00E-05   | 5.00E-05   | 5.00E-05   | 5.00E-05   | 1.12E-02   | 5.00E-05   | 5.00E-05   | 5.00E-05   | 5.00E-05   | 5.50E-04   | 5.00E-05   | 5.00E-05   |
| Confidence  | 4.28E-04   | 4.28E-04   | 4.28E-04   | 4.28E-04   | 4.08E-02   | 4.28E-04   | 4.28E-04   | 4.28E-04   | 4.28E-04   | 3.46E-03   | 4.28E-04   | 4.28E-04   |
| Domain      | HD         | Carbonic anhydrase | General function prediction only | O-methyltransferase | Pheromone A receptor | Cupin domain | Protein of unknown function (DUF1524) | NADH(P)-binding | -- | FAD binding domain | Energy production and conversion | -- |
| Accession   | EVM0008112 | EVM0010863 | EVM0011267 | EVM0006935 | EVM0004142 | EVM0004026 | EVM0002861 | EVM0002202 | EVM0000184 | EVM0011894 | EVM0006874 |
|-------------|------------|------------|------------|------------|------------|------------|------------|------------|------------|------------|------------|
| Value       | 718.63     | 66.70      | 374.31     | 10.54      | 565.17     | 921.67     | 1.38       | 13.30      | 152.63     | 271.14     | 40.47      |
| Error       | 81.43      | 7.05       | 39.37      | 1.08       | 57.81      | 92.37      | 0.14       | 1.30       | 14.70      | 24.46      | 3.64       |
| E-value     | 3.14       | 3.24       | 3.25       | 3.28       | 3.29       | 3.32       | 3.35       | 3.36       | 3.38       | 3.47       | 3.48       |
| Function    | Intracellular trafficking, secretion, and vesicular transport | General function prediction only | Energy production and conversion | -- | Intracellular trafficking, secretion, and vesicular transport | Secondary metabolites biosynthesis, transport and catabolism | -- | -- | Signal transduction mechanisms | Secondary metabolites biosynthesis, transport and catabolism | -- |
| Description | ER lumen protein retaining receptor | O-methyltransferase | Aldo/keto reductase family | UbiA prenyltransferase family | Vacuolar sorting protein 39 domain 1 | short chain dehydrogenase | Transposase family tnp2 | Putative glycosyl hydrolase of unknown function (DUF1680) | OPT oligopeptide transporter protein | Cytochrome P450 | -- |
| EVM0009915  | 131.45 | 11.52 | 3.51 | 5.00E-05 | 4.28E-04 | Secondary metabolites biosynthesis, transport and catabolism | Cytochrome P450 |
| EVM0010798  | 436.15 | 36.00 | 3.60 | 5.00E-05 | 4.28E-04 | -- | Stress responsive A/B Barrel Domain |
| EVM0004300  | 55.30  | 4.50  | 3.62 | 5.00E-05 | 4.28E-04 | Secondary metabolites biosynthesis, transport and catabolism | Cytochrome P450 |
| EVM0009612  | 34.41  | 2.36  | 3.86 | 5.00E-05 | 4.28E-04 | -- | -- |
| EVM0007642  | 294.85 | 19.17 | 3.94 | 5.00E-05 | 4.28E-04 | -- | Pregnancy-associated plasma protein-A |
| EVM0010247  | 268.99 | 17.39 | 3.95 | 5.00E-05 | 4.28E-04 | Secondary metabolites biosynthesis, transport and catabolism | Cytochrome P450 |
| EVM0010621  | 29.42  | 1.85  | 3.99 | 5.00E-05 | 4.28E-04 | -- | Deuterolysin metalloprotease (M35) family |
| EVM0008010  | 4.56   | 0.28  | 4.03 | 2.65E-03 | 1.28E-02 | -- | -- |
| EVM0006001  | 83.19  | 4.72  | 4.14 | 5.00E-05 | 4.28E-04 | -- | -- |
| EVM0005984  | 43.90  | 1.67  | 4.71 | 5.00E-05 | 4.28E-04 | -- | CVNH domain |
| EVM0003375  | 46.43  | 1.65  | 4.82 | 1.50E-04 | 1.14E-03 | -- | -- |
| EVM0001256 | 107.28 | 3.62 | 4.89 | 5.00E-05 | 4.28E-04 | -- | LVIVD repeat |
| EVM0007243 | 71.61  | 2.20 | 5.02 | 5.00E-05 | 4.28E-04 | Secondary metabolites biosynthesis, transport and catabolism | Pyridine nucleotide-disulphide oxidoreductase |
| EVM0003814 | 7.65   | 0.23 | 5.08 | 5.00E-05 | 4.28E-04 | General function prediction only | GMC oxidoreductase |
| EVM0008710 | 275.29 | 7.98 | 5.11 | 5.00E-05 | 4.28E-04 | Posttranslational modification, protein turnover, chaperones | Subtilase family |
| EVM0007266 | 1631.18| 39.90| 5.35 | 5.00E-05 | 4.28E-04 | -- | -- |
| EVM0012169 | 227.05 | 4.80 | 5.56 | 5.00E-05 | 4.28E-04 | -- | CVNH domain |
| EVM0003022 | 448.11 | 7.75 | 5.85 | 5.00E-05 | 4.28E-04 | Amino acid transport and metabolism | FAD dependent oxidoreductase |
| EVM0009739 | 700.28 | 9.20 | 6.25 | 5.00E-05 | 4.28E-04 | Energy production and conversion | Aldo/keto reductase family |
| EVM0005722 | 492.55 | 6.35 | 6.28 | 5.00E-05 | 4.28E-04 | General function prediction only | O-methyltransferase |
| gene ID     | R3 value | Z3 value | log2(fold change) | p value  | q value  | KOG class                        | Pfam annotation                        |
|------------|----------|----------|-------------------|----------|----------|----------------------------------|----------------------------------------|
| EVM0011351 | 56.96    | 132.95   | -1.22             | 5.00E-05 | 4.28E-04 | --                               | --                                     |
| EVM0004614 | 3.68     | 2575.92  | -9.45             | 2.60E-03 | 1.26E-02 | --                               | --                                     |
| EVM0004221 | 1.70     | 207.12   | -6.93             | 1.00E-04 | 7.96E-04 | --                               | --                                     |
| EVM0004083 | 7.40     | 899.59   | -6.92             | 5.00E-05 | 4.28E-04 | --                               | --                                     |
| EVM0002644 | 53.67    | 5739.08  | -6.74             | 5.00E-05 | 4.28E-04 | --                               | --                                     |
| EVM0000746 | 20.17    | 1635.09  | -6.34             | 5.00E-05 | 4.28E-04 | --                               | --                                     |
| EVM0003786 | 2.50     | 161.00   | -6.01             | 5.00E-05 | 4.28E-04 | General function prediction only | Major Facilitator Superfamily          |
| EVM0002673 | 4.93     | 315.29   | -6.00             | 5.00E-05 | 4.28E-04 | --                               | --                                     |
| EVM0004440 | 0.99     | 59.51    | -5.91             | 2.20E-03 | 1.10E-02 | --                               | ribonuclease                           |
| EVM0006723 | 29.57    | 1458.58  | -5.62             | 5.00E-05 | 4.28E-04 | --                               | Conidiation protein 6                  |
| EVM0002148 | 18.94    | 844.41   | -5.48             | 5.00E-05 | 4.28E-04 | --                               | Uncharacterised protein family (UPF0197) |
| EVM0002607 | 13.49    | 383.22   | -4.83             | 5.00E-05 | 4.28E-04 | Lipid transport and metabolism   | Cupin-like domain                      |
| Gene ID          | EVM0003267 | EVM0007042 | EVM0004233 | EVM0008153 | EVM0001604 | EVM0003583 | EVM0003588 | EVM0012086 | EVM0005861 | EVM0002926 | EVM0011108 | EVM0009711 |
|-----------------|------------|------------|------------|------------|------------|------------|------------|------------|------------|------------|------------|------------|
| EVM0003267      | 1260.86    | 34941.10   | -4.79      | 5.00E-05   | 4.28E-04   | --         | Conidiation protein 6 |
| EVM0007042      | 38.39      | 1037.88    | -4.76      | 5.00E-05   | 4.28E-04   | --         | Hemerythrin HHE cation binding domain |
| EVM0004233      | 16.74      | 447.19     | -4.74      | 5.00E-05   | 4.28E-04   | --         | --         |
| EVM0008153      | 19.61      | 516.67     | -4.72      | 5.00E-05   | 4.28E-04   | --         | --         |
| EVM0001604      | 106.89     | 2660.18    | -4.64      | 5.00E-05   | 4.28E-04   | 5.00E-05   | General function prediction Enoyl-(Acyl carrier protein) reductase |
| EVM0003583      | 56.60      | 1326.27    | -4.55      | 5.00E-05   | 4.28E-04   | --         | --         |
| EVM0003588      | 7.36       | 159.95     | -4.44      | 5.00E-05   | 4.28E-04   | 5.00E-05   | Secondary metabolites biosynthesis, transport and catabolism Cytochrome P450 |
| EVM0012086      | 29.78      | 636.01     | -4.42      | 5.00E-05   | 4.28E-04   | 5.00E-05   | Carbohydrate transport and metabolism Major Facilitator Superfamily |
| EVM0005861      | 9.29       | 197.13     | -4.41      | 5.00E-05   | 4.28E-04   | 5.00E-05   | Inorganic ion transport and metabolism Catalase |
| EVM0002926      | 34.17      | 725.08     | -4.41      | 5.00E-05   | 4.28E-04   | 5.00E-05   | General function prediction Enoyl-(Acyl carrier protein) reductase |
| EVM0011108      | 1.21       | 25.37      | -4.39      | 3.10E-03   | 1.45E-02   | --         | Fungal hydrophobin |
| EVM0009711      | 51.83      | 1034.42    | -4.32      | 5.00E-05   | 4.28E-04   | --         | Fungal hydrophobin |
| EVM0010264 | 12.22 | 226.65 | -4.21 | 5.00E-05 | 4.28E-04 | Function unknown | Thioesterase superfamily |
| EVM0006402 | 24.68 | 454.50 | -4.20 | 5.00E-05 | 4.28E-04 | -- | -- |
| EVM0012049 | 3.32 | 59.99 | -4.17 | 5.00E-05 | 4.28E-04 | -- | -- |
| EVM0009623 | 30.69 | 548.84 | -4.16 | 5.00E-05 | 4.28E-04 | -- | -- |
| EVM0000056 | 2050.62 | 34018.20 | -4.05 | 5.00E-05 | 4.28E-04 | -- | Aegerolysin |
| EVM0011343 | 19.88 | 328.37 | -4.05 | 5.00E-05 | 4.28E-04 | Posttranslational modification, protein turnover, chaperones | Glutaredoxin |
| EVM0005139 | 37.04 | 591.64 | -4.00 | 5.00E-05 | 4.28E-04 | -- | -- |
| EVM0007399 | 3.78 | 60.16 | -3.99 | 5.00E-05 | 4.28E-04 | -- | Common central domain of tyrosinase |
| EVM0007843 | 5.15 | 80.42 | -3.97 | 5.00E-05 | 4.28E-04 | -- | Dyp-type peroxidase family |
| EVM0009923 | 177.06 | 2728.98 | -3.95 | 5.00E-05 | 4.28E-04 | #N/A | #N/A |
| EVM0003700 | 0.23 | 3.47 | -3.93 | 5.00E-05 | 4.28E-04 | Replication, recombination and repair | DEAD/DEAH box helicase |
| EVM0006875 | 12.58 | 191.09 | -3.93 | 5.00E-05 | 4.28E-04 | -- | Polysaccharide deacetylase |
| EVM0004031 | 9.34 | 141.70 | -3.92 | 5.00E-05 | 4.28E-04 | RNA processing and modification | Eukaryotic rRNA processing protein EBP2 |
| EVM0001738 | 145.06 | 2200.62 | -3.92 | 5.00E-05 | 4.28E-04 | Lipid transport and metabolism | Phophatidylserine decarboxylase |
| EVM0000901 | 1.62 | 24.44 | -3.92 | 5.00E-05 | 4.28E-04 | Carbohydrate transport and metabolism | Starch binding domain |
| EVM0007517 | 15.36 | 224.72 | -3.87 | 5.00E-05 | 4.28E-04 | -- | -- |
| EVM0007912 | 1.45 | 21.13 | -3.86 | 5.00E-05 | 4.28E-04 | -- | -- |
| EVM0009499 | 0.94 | 13.58 | -3.86 | 8.00E-04 | 4.73E-03 | General function prediction only | Phosphatidylethanolamine-binding protein |
| EVM0003373 | 0.93 | 13.38 | -3.84 | 1.50E-04 | 1.14E-03 | -- | -- |
| EVM0008982 | 1.22 | 17.36 | -3.83 | 5.00E-05 | 4.28E-04 | -- | -- |
| EVM0004346 | 314.22 | 4460.27 | -3.83 | 5.00E-05 | 4.28E-04 | -- | -- |
| EVM0003167 | 37.21 | 516.16 | -3.79 | 5.00E-05 | 4.28E-04 | -- | -- |
| EVM0003528 | 21.72 | 301.01 | -3.79 | 5.00E-05 | 4.28E-04 | -- | -- |
| EVM0001520 | 2.40 | 33.19 | -3.79 | 5.00E-05 | 4.28E-04 | -- | -- |
| Identifier   | Value  | Log Value | Fold Change | Functional Category                        | Description                                                                 |
|--------------|--------|-----------|-------------|--------------------------------------------|-----------------------------------------------------------------------------|
| EVM0004488   | 12.19  | -3.77     | 5.00E-05 4.28E-04 | Secondary metabolites biosynthesis, transport and catabolism | Multicopper oxidase                                                        |
| EVM0006981   | 11.02  | -3.74     | 5.00E-05 4.28E-04 | --                                         | Rrp15p                                                                      |
| EVM0004778   | 27.45  | -3.68     | 5.00E-05 4.28E-04 | General function prediction only           | Thioesterase superfamily                                                   |
| EVM0005127   | 51.92  | -3.66     | 5.00E-05 4.28E-04 | --                                         | Gamma interferon inducible lysosomal thiol reductase (GILT)                |
| EVM0002081   | 1.38   | -3.66     | 5.00E-05 4.28E-04 | Signal transduction mechanisms             | FHA domain                                                                 |
| EVM0004302   | 6.99   | -3.64     | 5.00E-05 4.28E-04 | --                                         | --                                                                          |
| EVM0000062   | 12.99  | -3.63     | 5.00E-05 4.28E-04 | --                                         | --                                                                          |
| EVM0007098   | 4.91   | -3.60     | 5.00E-05 4.28E-04 | --                                         | FAD binding domain of DNA photolyase                                       |
| EVM0006053   | 0.36   | -3.58     | 1.00E-04 7.96E-04 | --                                         | --                                                                          |
| EVM0008167   | 14.51  | -3.57     | 5.00E-05 4.28E-04 | General function prediction only           | Animal haem peroxidase                                                     |
| EVM0005865   | 356.73 | -3.55     | 5.00E-05 4.28E-04 | General function prediction only           | Proteolipid membrane potential modulator                                  |
| EVM0000829   | 28.77  | -3.52     | 5.00E-05 4.28E-04 | --                                         | --                                                                          |
|   | ID       | Value1 | Value2 | Value3 | Value4 | Function                                      | Description                     |
|---|----------|--------|--------|--------|--------|-----------------------------------------------|---------------------------------|
|   | EVM0010422 | 4.02   | 45.67  | -3.51  | 5.00E-05 | 4.28E-04 | Posttranslational modification, protein turnover, chaperones | DnaJ domain                     |
|   | EVM0006251 | 5.01   | 56.48  | -3.50  | 5.00E-05 | 4.28E-04 | Function unknown                               | Surfeit locus protein 6          |
|   | EVM0002391 | 123.60 | 1386.81| -3.49  | 5.00E-05 | 4.28E-04 | --                                            | --                              |
|   | EVM0007514 | 18.82  | 210.86 | -3.49  | 5.00E-05 | 4.28E-04 | --                                            | RTA1 like protein               |
|   | EVM0011052 | 0.40   | 4.39   | -3.47  | 9.80E-03 | 3.69E-02 | --                                            | Glycosyl hydrolase family 12    |
|   | EVM0004767 | 66.02  | 720.49 | -3.45  | 1.50E-04 | 1.14E-03 | --                                            | 4F5 protein family              |
|   | EVM0000880 | 11.15  | 121.55 | -3.45  | 5.00E-05 | 4.28E-04 | --                                            | Glycosyl hydrolases family 15   |
|   | EVM0007566 | 404.06 | 4360.24| -3.43  | 5.00E-05 | 4.28E-04 | --                                            | --                              |
|   | EVM0001141 | 64.72  | 692.55 | -3.42  | 5.00E-05 | 4.28E-04 | --                                            | --                              |
|   | EVM0004818 | 10.11  | 107.07 | -3.41  | 5.00E-05 | 4.28E-04 | N/A                                           | #N/A                            |
|   | EVM0002176 | 7.61   | 80.43  | -3.40  | 5.00E-05 | 4.28E-04 | --                                            | --                              |
|   | EVM0002270 | 4.45   | 46.89  | -3.40  | 5.00E-05 | 4.28E-04 | --                                            | --                              |
| Gene ID      | E Value 1 | E Value 2 | Log Ratio | Fold Change | GO Annotation                                                                 |
|-------------|-----------|-----------|-----------|-------------|-----------------------------------------------------------------------------|
| EVM0009090  | 14.37     | 149.64    | -3.38     | 5.00E-05     | --                                                                          |
| EVM0009999  | 3.21      | 33.16     | -3.37     | 3.00E-04     | Rare lipoprotein A (RlpA)-like double-psi beta-barrel                       |
| EVM0003866  | 40.50     | 415.20    | -3.36     | 5.00E-05     | DAD family                                                                  |
| EVM0003008  | 23.24     | 237.88    | -3.36     | 5.00E-05     | --                                                                          |
| EVM0008891  | 7.95      | 81.18     | -3.35     | 5.00E-05     | Amino acid transport and metabolism                                         |
| EVM0011587  | 73.31     | 746.54    | -3.35     | 5.00E-05     | --                                                                          |
| EVM0004953  | 34.63     | 348.15    | -3.33     | 5.00E-05     | --                                                                          |
| EVM0010633  | 518.20    | 5169.30   | -3.32     | 5.00E-05     | Energy production and conversion                                            |
| EVM0005881  | 2.01      | 19.68     | -3.29     | 5.00E-05     | --                                                                          |
| EVM0012010  | 22.49     | 218.63    | -3.28     | 5.00E-05     | --                                                                          |
| EVM0007894  | 1.30      | 12.65     | -3.28     | 7.50E-04     | General function prediction only                                            |
| EVM0003732  | 0.65      | 6.26      | -3.26     | 5.00E-05     | --                                                                          |
| EVM0005546 | 12.12 | 116.02 | -3.26 | 5.00E-05 | 4.28E-04 | General function prediction only | MatE |
| EVM0001104 | 4.48  | 41.99  | -3.23 | 5.00E-05 | 4.28E-04 | -- | -- |
| EVM0010306 | 7.12  | 66.62  | -3.23 | 5.00E-05 | 4.28E-04 | -- | -- |
| EVM0004307 | 0.42  | 3.89   | -3.20 | 1.10E-02 | 4.04E-02 | Carbohydrate transport and metabolism | Glycosyl hydrolase family 47 |
| EVM0001246 | 11.08 | 101.35 | -3.19 | 5.00E-05 | 4.28E-04 | -- | -- |
| EVM0004958 | 11.61 | 106.06 | -3.19 | 5.00E-05 | 4.28E-04 | -- | Regulator of G protein signaling domain |
| EVM0006028 | 26.35 | 235.43 | -3.16 | 5.00E-05 | 4.28E-04 | -- | -- |
| EVM0008242 | 0.81  | 7.17   | -3.15 | 1.00E-03 | 5.70E-03 | -- | Glycosyl hydrolase family 12 |
| EVM0007445 | 2.65  | 23.57  | -3.15 | 5.00E-05 | 4.28E-04 | -- | -- |
| EVM0008171 | 0.60  | 5.31   | -3.15 | 5.65E-03 | 2.37E-02 | -- | Cerato-platanin |
| EVM0005968 | 2.09  | 18.53  | -3.15 | 5.00E-05 | 4.28E-04 | -- | -- |
| EVM0000435 | 26.09 | 230.91 | -3.15 | 5.00E-05 | 4.28E-04 | General function prediction only | Glycosyl transferase family 2 |
| EVM0010210 | 196.82| 1731.08| -3.14 | 5.00E-05 | 4.28E-04 | -- | -- |
| EVM0007958 | 2.44 | 21.40 | -3.13 | 5.00E-05 4.28E-04 | Secondary metabolites biosynthesis, transport and catabolism | Multicopper oxidase |
| EVM0007507 | 11.64 | 101.72 | -3.13 | 5.00E-05 4.28E-04 | -- | -- |
| EVM0007339 | 11.51 | 100.46 | -3.13 | 5.00E-05 4.28E-04 | -- | SMP-30/Gluconoloaconase/LRE-like region |
| EVM0011013 | 6.39 | 55.62 | -3.12 | 2.15E-03 1.08E-02 | Function unknown | COQ9 |
| EVM001661 | 6.38 | 55.31 | -3.12 | 5.00E-05 4.28E-04 | General function prediction only | Kinase phosphorylation protein |
| EVM0009807 | 1330.92 | 11531.60 | -3.12 | 5.00E-05 4.28E-04 | -- | Mitochondrial F1-F0 ATP synthase subunit F of fungi |
| EVM0002451 | 2.95 | 25.34 | -3.10 | 5.00E-05 4.28E-04 | -- | -- |
| EVM0009425 | 9.72 | 82.79 | -3.09 | 5.00E-05 4.28E-04 | -- | -- |
| EVM000681 | 6.75 | 57.35 | -3.09 | 5.00E-05 4.28E-04 | -- | -- |
| EVM000282 | 213.49 | 1807.70 | -3.08 | 5.00E-05 4.28E-04 | -- | -- |
| EVM0004965 | 2.64 | 22.29 | -3.08 | 5.00E-05 4.28E-04 | Function unknown | Tho complex subunit 7 |
| EVM0009798 | 18.72 | 156.91 | -3.07 | 5.00E-05 4.28E-04 | RNA processing and modification | RNA recognition motif. (a.k.a. RRM, RBD, or RNP domain) |
| Accession | Score | Description | Functional Category |
|-----------|-------|-------------|---------------------|
| EVM0010440 | 40.98 | Cytochrome c/c1 heme lyase | -- |
| EVM0010609 | 92.23 | Intracellular trafficking, secretion, and vesicular transport | Translocation protein Sec62 |
| EVM0005915 | 12.02 | Lipase (class 3) | -- |
| EVM0010015 | 0.37 | -- | Lipase (class 3) |
| EVM0008621 | 1.65 | -- | -- |
| EVM0005647 | 9.18 | Alpha/beta hydrolase family | -- |
| EVM001452 | 3.30 | -- | -- |
| EVM0007975 | 0.69 | GDSL-like Lipase/Acylhydrolase | -- |
| EVM0008487 | 0.15 | -- | -- |
| EVM001814 | 3962.69 | Ricin-type beta-trefoil lectin domain-like | -- |
| EVM001253 | 8.77 | Replication, recombination and repair | Uracil DNA glycosylase superfamily |
| EVM0002307 | 53.31 | -- | -- |
| EVM0005795 | 5.19 | 41.33 | -2.99 | 5.00E-05 | 4.28E-04 | Chromatin structure and dynamics | Core histone H2A/H2B/H3/H4 |
| EVM0005630 | 80.09 | 632.92 | -2.98 | 5.00E-05 | 4.28E-04 | Translation, ribosomal structure and biogenesis | Mitochondrial ribosomal protein L51 / S25 / CI-B8 domain |
| EVM0007323 | 388.35 | 3065.78 | -2.98 | 5.00E-05 | 4.28E-04 | Function unknown | Domain of unknown function (DUF543) |
| EVM0008586 | 8.70 | 68.23 | -2.97 | 5.00E-05 | 4.28E-04 | -- | Chromatin remodelling complex Rsc7/Swp82 subunit |
| EVM0003649 | 32.91 | 258.01 | -2.97 | 5.00E-05 | 4.28E-04 | General function prediction only | Thioesterase superfamily |
| EVM0009041 | 5.27 | 40.96 | -2.96 | 5.00E-05 | 4.28E-04 | -- | -- |
| EVM0007470 | 1.99 | 15.18 | -2.93 | 5.00E-05 | 4.28E-04 | -- | -- |
| EVM0007261 | 165.82 | 1267.30 | -2.93 | 5.00E-05 | 4.28E-04 | -- | -- |
| EVM0009031 | 4.37 | 33.21 | -2.93 | 5.00E-05 | 4.28E-04 | -- | Glycosyl hydrolases family 43 |
| EVM00010219 | 6.43 | 48.55 | -2.92 | 1.00E-05 | 7.96E-04 | -- | -- |
| EVM0006917 | 1.68 | 12.58 | -2.91 | 5.00E-05 | 4.28E-04 | -- | -- |
| EVM0005367 | 0.91 | 6.84 | -2.91 | 5.00E-05 | 4.28E-04 | -- | -- |
| EVM0002697 | 4.74 | 35.45 | -2.90 | 5.00E-05 | 4.28E-04 | -- | -- |
| Gene ID     | Value 1 | Value 2 | FDR 1   | FDR 2 | Description                                                                 |
|------------|---------|---------|---------|-------|----------------------------------------------------------------------------|
| EVM0000461 | 28.01   | 208.83  | -2.90   | 5.00E-05 | 4.28E-04 | -- | -- |
| EVM00005079| 33.60   | 246.26  | -2.87   | 5.00E-05 | 4.28E-04 | Coenzyme transport and metabolism | Pantoate-beta-alanine ligase |
| EVM0000390 | 4.02    | 29.31   | -2.87   | 5.00E-05 | 4.28E-04 | Amino acid transport and metabolism | Cys/Met metabolism PLP-dependent enzyme |
| EVM0010785 | 21.95   | 159.97  | -2.87   | 5.00E-05 | 4.28E-04 | -- | Rpp20 subunit of nuclear RNase MRP and P |
| EVM0005285 | 755.82  | 5491.75 | -2.86   | 5.00E-05 | 4.28E-04 | -- | -- |
| EVM0006195 | 13.10   | 94.70   | -2.85   | 5.00E-05 | 4.28E-04 | -- | pre-mRNA splicing factor component |
| EVM0000780 | 112.49  | 810.30  | -2.85   | 5.00E-05 | 4.28E-04 | -- | -- |
| EVM0007187 | 3.62    | 26.03   | -2.85   | 5.00E-05 | 4.28E-04 | -- | Pregnancy-associated plasma protein-A |
| EVM0011536 | 15.82   | 112.12  | -2.83   | 5.00E-05 | 4.28E-04 | -- | Protein of unknown function (DUF3445) |
| EVM0008407 | 4.02    | 28.42   | -2.82   | 1.15E-02 | 4.19E-02 | -- | -- |
| EVM0000393 | 281.92  | 1992.78 | -2.82   | 5.00E-05 | 4.28E-04 | -- | -- |
| EVM0005036 | 14.34   | 101.37  | -2.82   | 5.00E-05 | 4.28E-04 | -- | -- |
| Gene ID             | Gene Name 1           | Gene Name 2                          | Gene Name 3                          | Gene Name 4                          |
|--------------------|-----------------------|--------------------------------------|--------------------------------------|--------------------------------------|
| EVM0005353.1       | 1.36                  | 9.61                                | -2.82                               | 5.00E-05 4.28E-04 Posttranslational modification, protein turnover, chaperones Peptidase family M50 |
| EVM0008632         | 5.35                  | 37.76                               | -2.82                               | 5.00E-05 4.28E-04 Posttranslational modification, protein turnover, chaperones Isoprenylcysteine carboxyl methyltransferase (ICMT) family |
| EVM0006543.2       | 2.71                  | 19.06                               | -2.81                               | 5.00E-05 4.28E-04 -- -- |
| EVM0004368         | 1.98                  | 13.84                               | -2.81                               | 6.50E-04 3.98E-03 -- -- |
| EVM0004446.3       | 6.20                  | 43.19                               | -2.80                               | 5.00E-05 4.28E-04 Posttranslational modification, protein turnover, chaperones Isoprenylcysteine carboxyl methyltransferase (ICMT) family |
| EVM0000999.4       | 2.18                  | 15.15                               | -2.80                               | 5.00E-05 4.28E-04 Signal transduction mechanisms Protein kinase domain |
| EVM0001122.5       | 25.05                 | 172.64                              | -2.79                               | 5.00E-05 4.28E-04 RNA processing and modification Fibrillarin |
| EVM0004549.6       | 201.58                | 1386.51                             | -2.78                               | 5.00E-05 4.28E-04 Lipid transport and metabolism HIUase/Transthyretin family |
| EVM0003609.7       | 122.45                | 841.86                              | -2.78                               | 5.00E-05 4.28E-04 -- Cytochrome oxidase c subunit VIb |
| EVM0008465.8       | 46.77                 | 319.96                              | -2.77                               | 5.00E-05 4.28E-04 RNA processing and modification DEAD/DEAH box helicase |
| EVM0000819.9       | 2.35                  | 15.96                               | -2.77                               | 5.00E-05 4.28E-04 Transcription SNF2 family N-terminal domain |
| EVM0000515 | 3.16  | 21.43 | -2.76 | 5.00E-05 | 4.28E-04 | -- | -- |
| EVM00008626 | 27.36 | 185.52 | -2.76 | 5.00E-05 | 4.28E-04 | -- | -- |
| EVM0006749 | 14.17 | 95.01 | -2.75 | 5.00E-05 | 4.28E-04 | -- | Membrane bound O-acyl transferase family |
| EVM0002711 | 15.39 | 103.19 | -2.75 | 5.00E-05 | 4.28E-04 | General function prediction only | La domain |
| EVM0010273 | 1.44  | 9.64  | -2.74 | 5.00E-05 | 4.28E-04 | -- | -- |
| EVM0002682 | 65.55 | 435.15 | -2.73 | 5.00E-05 | 4.28E-04 | Transcription | RNA polymerase Rpb6 |
| EVM0012109 | 3.66  | 24.24 | -2.73 | 2.50E-04 | 1.77E-03 | -- | Rare lipoprotein A (RlpA)-like double-psi beta-barrel |
| EVM0005453 | 23.36 | 154.28 | -2.72 | 5.00E-05 | 4.28E-04 | -- | -- |
| EVM0004771 | 16.36 | 107.80 | -2.72 | 5.00E-05 | 4.28E-04 | -- | -- |
| EVM0010419 | 2.25  | 14.74 | -2.71 | 5.00E-05 | 4.28E-04 | -- | Mis12-Mtw1 protein family |
| EVM0005254 | 36.33 | 238.27 | -2.71 | 5.00E-05 | 4.28E-04 | -- | -- |
| EVM0009591 | 6.85  | 44.76 | -2.71 | 5.00E-05 | 4.28E-04 | Amino acid transport and metabolism | Homocysteine S-methyltransferase |
| EVM0007540 | 3.90  | 25.42 | -2.70 | 5.00E-05 | 4.28E-04 | -- | -- |
| ID          | Value 1 | Value 2  | Value 3 | Value 4     | Value 5     | Value 6     | Description                                                                 |
|-------------|---------|----------|---------|-------------|-------------|-------------|-----------------------------------------------------------------------------|
| EVM0008163  | 1.87    | 12.12    | -2.70   | 5.00E-05    | 4.28E-04    | --          | --                                                                           |
| EVM0008966  | 23.39   | 151.06   | -2.69   | 5.00E-05    | 4.28E-04    | --          | --                                                                           |
| EVM0006896  | 66.84   | 430.23   | -2.69   | 5.00E-05    | 4.28E-04    | --          | Protein of unknown function (DUF4449)                                      |
| EVM0006637  | 2.27    | 14.62    | -2.68   | 5.00E-05    | 4.28E-04    | --          | Prolyl oligopeptidase family                                               |
| EVM0012244  | 0.73    | 4.64     | -2.68   | 7.00E-04    | 4.23E-03    | --          | --                                                                           |
| EVM0001964  | 4.59    | 29.32    | -2.68   | 5.00E-05    | 4.28E-04    | --          | --                                                                           |
| EVM0010982  | 7.81    | 49.80    | -2.67   | 5.00E-05    | 4.28E-04    | --          | --                                                                           |
| EVM0010935  | 16.67   | 106.17   | -2.67   | 5.00E-05    | 4.28E-04    | General function prediction only                                          |
|             |         |          |         |             |             | U3-containing 90S pre-ribosomal complex subunit                            |
| EVM0005758  | 38.11   | 241.58   | -2.66   | 5.00E-05    | 4.28E-04    | Lipid transport and metabolism                                             |
|             |         |          |         |             |             | Putative undecaprenyl diphosphate synthase                                |
| EVM0004866  | 125.43  | 793.16   | -2.66   | 5.00E-05    | 4.28E-04    | Function unknown                                                           |
|             |         |          |         |             |             | Uncharacterised protein family (UPF0121)                                  |
| EVM0010855  | 10.87   | 68.21    | -2.65   | 5.00E-05    | 4.28E-04    | --          | --                                                                           |
| EVM0005272  | 404.12  | 2535.69  | -2.65   | 5.00E-05    | 4.28E-04    | --          | Ubiquinol-cytochrome-c reductase complex subunit (QCR10)                  |
| Annotation     | Log2 Fold Change | Expression | FDR | Function                                                                 | Family                      |
|---------------|-----------------|------------|-----|--------------------------------------------------------------------------|-----------------------------|
| EVM0009146    | 0.76            | 4.78       | -2.65 | 1.35E-03 7.33E-03 --                                                    | Glycosyl hydrolase family 61 |
| EVM0006314    | 1.77            | 11.01      | -2.63 | 5.00E-05 4.28E-04 --                                                   | --                          |
| EVM0010779    | 201.51          | 1248.67    | -2.63 | 5.00E-05 4.28E-04 Intracellular trafficking, secretion, and vesicular transport | SURF4 family                |
| EVM0005691    | 0.56            | 3.42       | -2.61 | 2.00E-04 1.46E-03 --                                                   | Cytochrome P450              |
| EVM0008537    | 2311.19         | 14034.10   | -2.60 | 5.00E-05 4.28E-04 Posttranslational modification, protein turnover, chaperones | Hsp20/alpha crystallin family |
| EVM0011432    | 7.16            | 43.40      | -2.60 | 5.00E-05 4.28E-04 Lipid transport and metabolism                        | SacI homology domain        |
| EVM0007668    | 174.19          | 1051.10    | -2.59 | 5.00E-05 4.28E-04 Energy production and conversion                     | CHCH domain                 |
| EVM0004405    | 1.28            | 7.75       | -2.59 | 5.00E-05 4.28E-04 --                                                   | --                          |
| EVM0004582    | 1.40            | 8.42       | -2.59 | 2.00E-04 1.46E-03 --                                                   | --                          |
| EVM0000430    | 24.59           | 147.56     | -2.59 | 5.00E-05 4.28E-04 --                                                   | Polyketide cyclase / dehydrase and lipid transport |
| EVM0005980    | 5.06            | 30.28      | -2.58 | 5.00E-05 4.28E-04 General function prediction only                     | Animal haem peroxidase      |
| EVM0010820    | 1394.39         | 8339.69    | -2.58 | 5.00E-05 4.28E-04 Energy production and conversion                     | Cytochrome oxidase c subunit VIb |
| EVM0007319 | 3.68 | 21.83 | -2.57 | 5.00E-05 | 4.28E-04 | -- | -- |
|------------|------|-------|-------|----------|----------|----|----|
| EVM0005717 | 29.56| 175.06| -2.57 | 5.00E-05 | 4.28E-04 | -- | -- |
| EVM0005279 | 307.74| 1820.55| -2.56 | 5.00E-05 | 4.28E-04 | -- | Stress responsive A/B Barrel Domain |
| EVM0002416 | 76.01| 447.18| -2.56 | 5.00E-05 | 4.28E-04 | Translation, ribosomal structure and biogenesis | Ribosomal protein S16 |
| EVM0007964 | 20.41| 119.85| -2.55 | 5.00E-05 | 4.28E-04 | Lipid transport and metabolism | Calcineurin-like phosphoesterase |
| EVM0001355 | 149.31| 872.19| -2.55 | 5.00E-05 | 4.28E-04 | -- | -- |
| EVM0002257 | 26.14| 152.50| -2.54 | 5.00E-05 | 4.28E-04 | -- | -- |
| EVM0004341 | 65.39| 380.43| -2.54 | 5.00E-05 | 4.28E-04 | Function unknown | CSL zinc finger |
| EVM0010213 | 681.01| 3955.13| -2.54 | 5.00E-05 | 4.28E-04 | -- | -- |
| EVM0007597 | 11.28| 64.84 | -2.52 | 5.00E-05 | 4.28E-04 | -- | -- |
| EVM0006670 | 1.40 | 8.05  | -2.52 | 1.43E-02 | 4.98E-02 | Secondary metabolites biosynthesis, transport and catabolism | Cytochrome P450 |
| EVM0008283 | 23.64| 135.66| -2.52 | 5.00E-05 | 4.28E-04 | -- | Fungal hydrophobin |
| EVM0011270 | 6.95 | 39.84 | -2.52 | 5.00E-05 | 4.28E-04 | -- | cAMP phosphodiesterases class-II |
|------------|------|-------|-------|----------|---------|----|----------------------------------|
| EVM0001693 | 1.82 | 10.39 | -2.52 | 5.00E-05 | 4.28E-04 | -- | -- |
| EVM0002898 | 14.77| 84.06 | -2.51 | 5.00E-05 | 4.28E-04 | Transcription | RNA polymerase Rpb3/RpoA insert domain |
| EVM0007198 | 147.39| 838.01| -2.51 | 5.00E-05 | 4.28E-04 | -- | -- |
| EVM0004911 | 288.88| 1632.91| -2.50 | 5.00E-05 | 4.28E-04 | -- | -- |
| EVM0002821 | 56.05 | 316.44| -2.50 | 5.00E-05 | 4.28E-04 | -- | -- |
| EVM0003955 | 1.06 | 5.94 | -2.49 | 6.50E-04 | 3.98E-03 | -- | -- |
| EVM0002923 | 2245.12| 12605.60| -2.49 | 5.00E-05 | 4.28E-04 | -- | CsbD-like |
| EVM0008645 | 25.22 | 141.57| -2.49 | 5.00E-05 | 4.28E-04 | -- | -- |
| EVM0010141 | 40.37 | 226.56| -2.49 | 5.00E-05 | 4.28E-04 | General function prediction only | Prp19/Pso4-like |
| EVM0001054 | 19.35 | 107.97| -2.48 | 5.00E-05 | 4.28E-04 | -- | -- |
| EVM0007670 | 19.18 | 106.90| -2.48 | 5.00E-05 | 4.28E-04 | -- | Domain of unknown function (DUF4112) |
| EVM0002071 | 19377.00| 107959.00| -2.48 | 5.00E-05 | 4.28E-04 | -- | Aegerolysin |
| Accession   | Value | E-value | Log10 p-value | Prediction          | Description                                    |
|------------|-------|---------|---------------|---------------------|------------------------------------------------|
| EVM0011968 | 1.96  | 10.89   | -2.48         | --                  | Pectate lyase                                  |
| EVM0006247 | 63.68 | 351.91  | -2.47         | General function    | Zinc finger, C2H2 type                         |
| EVM0000423 | 89.05 | 491.73  | -2.47         | #N/A                | #N/A                                           |
| EVM0003258 | 29.24 | 161.41  | -2.46         | Posttranslational   | ThiF family                                    |
| EVM0000069 | 7.73  | 42.63   | -2.46         | --                  | --                                             |
| EVM0005130 | 4.19  | 23.09   | -2.46         | --                  | --                                             |
| EVM0008730 | 17.63 | 96.77   | -2.46         | --                  | Protein kinase domain                          |
| EVM0000406 | 3.54  | 19.43   | -2.46         | --                  | Cytochrome P450                                 |
| EVM0010485 | 6.31  | 34.44   | -2.45         | --                  | Hypoxia induced protein conserved region only  |
| EVM0004698 | 60.10 | 326.74  | -2.44         | --                  | OST3 / OST6 family                             |
| EVM0005508 | 79.05 | 428.98  | -2.44         | --                  | --                                             |
| EVM0012239 | 0.99  | 5.37    | -2.44         | --                  | --                                             |
| EVM0006881 | 14.67 | 79.43 | -2.44 | 5.00E-05 | 4.28E-04 | -- | NUDIX domain |
| EVM0000983 | 1.81 | 9.78 | -2.43 | 5.00E-03 | 2.15E-02 | -- | -- |
| EVM0008481 | 7.22 | 38.97 | -2.43 | 5.00E-05 | 4.28E-04 | Inorganic ion transport and metabolism | CorA-like Mg2+ transporter protein |
| EVM0007852 | 384.44 | 2074.10 | -2.43 | 5.00E-05 | 4.28E-04 | Posttranslational modification, protein turnover, chaperones | DnaJ C terminal domain |
| EVM0001411 | 0.86 | 4.62 | -2.43 | 5.00E-05 | 4.28E-04 | -- | Cellulase (glycosyl hydrolase family 5) |
| EVM0006622 | 6.54 | 35.26 | -2.43 | 5.00E-05 | 4.28E-04 | -- | -- |
| EVM0008252 | 5.30 | 28.53 | -2.43 | 5.00E-05 | 4.28E-04 | -- | -- |
| EVM0001314 | 42.21 | 226.53 | -2.42 | 5.00E-05 | 4.28E-04 | -- | -- |
| EVM0011097 | 183.48 | 981.53 | -2.42 | 5.00E-05 | 4.28E-04 | -- | RNA recognition motif. (a.k.a. RRM, RBD, or RNP domain) |
| EVM0001031 | 5.23 | 27.96 | -2.42 | 5.00E-05 | 4.28E-04 | Carbohydrate transport and metabolism | Major Facilitator Superfamily |
| EVM0009398 | 1.90 | 10.13 | -2.41 | 7.60E-03 | 3.01E-02 | -- | -- |
| EVM0000486 | 1.52 | 8.06 | -2.41 | 5.00E-05 | 4.28E-04 | Posttranslational modification, protein turnover, chaperones | ATPase family associated with various cellular activities (AAA) |
| ID          | Value1 | Value2  | Log2FC | Value3        | Value4        | Description                                                                 |
|------------|--------|---------|--------|---------------|---------------|-----------------------------------------------------------------------------|
| EVM0012235 | 314.74 | 1671.98 | -2.41  | 5.00E-05      | 4.28E-04      | Posttranslational modification, protein turnover, chaperones               |
| EVM0009733 | 12.02  | 63.75   | -2.41  | 5.00E-05      | 4.28E-04      | --                                                                          |
| EVM001647  | 35.86  | 189.11  | -2.40  | 5.00E-05      | 4.28E-04      | General function prediction only                                           |
| EVM003560  | 13.70  | 72.15   | -2.40  | 1.50E-03      | 8.00E-03      | --                                                                          |
| EVM004933  | 467.93 | 2452.18 | -2.39  | 5.00E-05      | 4.28E-04      | Posttranslational modification, protein turnover, chaperones               |
| EVM002358  | 13.68  | 71.67   | -2.39  | 5.00E-05      | 4.28E-04      | --                                                                          |
| EVM002266  | 177.80 | 930.24  | -2.39  | 5.00E-05      | 4.28E-04      | --                                                                          |
| EVM0010981 | 290.73 | 1516.73 | -2.38  | 5.00E-05      | 4.28E-04      | Function unknown                                                             |
| EVM003855  | 3.50   | 18.23   | -2.38  | 5.00E-05      | 4.28E-04      | Signal transduction mechanisms                                             |
| EVM006689  | 12.72  | 66.24   | -2.38  | 5.00E-05      | 4.28E-04      | General function prediction only                                           |
| EVM003721  | 84.33  | 438.78  | -2.38  | 5.00E-05      | 4.28E-04      | --                                                                          |
| EVM001192  | 64.77  | 336.77  | -2.38  | 5.00E-05      | 4.28E-04      | Transcription                                                               |

**Annotations:**
- **Cyclophilin type peptidyl-prolyl cis-trans isomerase/CLD**
- **Zinc-finger double-stranded RNA-binding**
- **Sec61beta family**
- **Activator of Hsp90 ATPase, N-terminal**
- **Protein kinase domain**
- **RNA polymerase Rpb3/Rpb11 dimerisation domain**
| Accession | Score 1 | Score 2 | Score 3 | Score 4 | Score 5 | Score 6 | Score 7 | Score 8 | Score 9 | Score 10 |
|-----------|---------|---------|---------|---------|---------|---------|---------|---------|---------|----------|
| EVM0004228 | 12.13   | 62.28   | -2.36   | 5.00E-05 | 4.28E-04 | Translation, ribosomal structure and biogenesis |
| EVM0005497 | 53.46   | 274.54  | -2.36   | 5.00E-05 | 4.28E-04 | --      | --      | --      | --      | --       |
| EVM0011102 | 4.21    | 21.56   | -2.36   | 5.00E-05 | 4.28E-04 | --      | --      | --      | --      | --       |
| EVM0009280 | 0.52    | 2.68    | -2.36   | 4.65E-03 | 2.03E-02 | #N/A    | #N/A    | #N/A    | #N/A    | --       |
| EVM0006570 | 502.56  | 2569.12 | -2.35   | 5.00E-05 | 4.28E-04 | --      | --      | --      | --      | Pyridoxamine 5'-phosphate oxidase |
| EVM0009404 | 15.36   | 78.43   | -2.35   | 5.00E-05 | 4.28E-04 | General function prediction only |
| EVM0010867 | 382.18  | 1948.93 | -2.35   | 5.00E-05 | 4.28E-04 | --      | --      | --      | --      | --       |
| EVM0010336 | 35.49   | 180.14  | -2.34   | 5.00E-05 | 4.28E-04 | --      | --      | --      | --      | --       |
| EVM0003318 | 39.89   | 202.36  | -2.34   | 5.00E-05 | 4.28E-04 | --      | --      | Autophagy protein 16 (ATG16) |
| EVM0000162 | 303.03  | 1537.06 | -2.34   | 5.00E-05 | 4.28E-04 | --      | Uncharacterized alpha/beta hydrolase domain (DUF2235) |
| EVM0002910 | 11.60   | 58.76   | -2.34   | 5.00E-05 | 4.28E-04 | --      | --      | F-box-like |
| EVM0007796 | 23.12   | 116.93  | -2.34   | 5.00E-05 | 4.28E-04 | --      | --      | --      | --      | --       |
| EVM0007949  | 10.48 | 53.00 | -2.34 | 5.00E-05 | 4.28E-04 | RNA processing and modification | WD domain, G-beta repeat |
| EVM0005054  | 9.91  | 50.06 | -2.34 | 5.00E-05 | 4.28E-04 | General function prediction only | C2 domain |
| EVM0011731  | 274.29 | 1384.55 | -2.34 | 5.00E-05 | 4.28E-04 | -- | Peroxidase, family 2 |
| EVM0004617  | 475.63 | 2396.32 | -2.33 | 5.00E-05 | 4.28E-04 | -- | ESSS subunit of NADH:ubiquinone oxidoreductase (complex I) |
| EVM0002660  | 7.30  | 36.65 | -2.33 | 5.00E-05 | 4.28E-04 | Chromatin structure and dynamics | MOZ/SAS family |
| EVM0001284  | 3.30  | 16.49 | -2.32 | 5.00E-05 | 4.28E-04 | -- | Protein of unknown function (DUF3129) |
| EVM0005012  | 3.68  | 18.32 | -2.32 | 5.00E-05 | 4.28E-04 | General function prediction only | Calcineurin-like phosphoesterase |
| EVM0005506  | 4.39  | 21.88 | -2.32 | 5.00E-05 | 4.28E-04 | #N/A | #N/A |
| EVM0002561  | 3.91  | 19.47 | -2.32 | 5.00E-05 | 4.28E-04 | -- | -- |
| EVM0010344  | 1120.67 | 5556.24 | -2.31 | 5.00E-05 | 4.28E-04 | -- | ATP synthase complex subunit h |
| EVM0008650  | 15.28 | 75.60 | -2.31 | 5.00E-05 | 4.28E-04 | -- | -- |
| EVM0003837  | 503.20 | 2484.11 | -2.30 | 5.00E-05 | 4.28E-04 | -- | -- |
| EVM0010786 | 22.46 | 110.84 | -2.30 | 5.00E-05 | 4.28E-04 | -- | Zinc finger, C3HC4 type (RING finger) |
| EVM0011055 | 50.83 | 250.21 | -2.30 | 5.00E-05 | 4.28E-04 | Posttranslational modification, protein turnover, chaperones | Thioredoxin |
| EVM0011206 | 0.34  | 1.69  | -2.29 | 1.70E-03 | 8.87E-03 | -- | Protein of unknown function (DUF3505) |
| EVM0009103 | 3.60  | 17.60 | -2.29 | 5.00E-05 | 4.28E-04 | -- | Pheromone A receptor |
| EVM0006740 | 0.75  | 3.65  | -2.29 | 2.50E-03 | 1.22E-02 | -- | -- |
| EVM0008960 | 6.74  | 32.92 | -2.29 | 5.00E-05 | 4.28E-04 | -- | -- |
| EVM0011446 | 1369.67 | 6690.14 | -2.29 | 5.00E-05 | 4.28E-04 | -- | -- |
| EVM0007279 | 19.98 | 97.54 | -2.29 | 5.00E-05 | 4.28E-04 | -- | -- |
| EVM0011882 | 28.65 | 139.63 | -2.29 | 5.00E-05 | 4.28E-04 | Cytoskeleton | Variant SH3 domain |
| EVM0002073 | 4.45  | 21.67 | -2.28 | 5.00E-05 | 4.28E-04 | Defense mechanisms | alpha/beta hydrolase fold |
| EVM0007225 | 121.76 | 592.66 | -2.28 | 5.00E-05 | 4.28E-04 | -- | Nuclear pore complex subunit Nro1 |
| EVM0005253 | 213.46 | 1036.20 | -2.28 | 5.00E-05 | 4.28E-04 | -- | -- |
| EVM code | Name                                      | Score1 | Score2 | Score3 | Score4 | Score5 | Score6 | Score7 | Score8 | Score9 | Score10 | Score11 | Expression | Function                                                                 |
|---------|-------------------------------------------|--------|--------|--------|--------|--------|--------|--------|--------|--------|----------|----------|-------------|--------------------------------------------------------------------------|
| EVM0006173 | Membrane-associating domain                | 187.12 | 907.89 | -2.28  | 5.00E-05 | 4.28E-04 | --     | Membrane-associating domain |
| EVM0006136 | --                                         | 84.59  | 410.10 | -2.28  | 5.00E-05 | 4.28E-04 | --     | --                                        |
| EVM0001681 | Intracellular trafficking, secretion, and vesicular transport | 199.69 | 965.94 | -2.27  | 5.00E-05 | 4.28E-04 | --     | Microsomal signal peptidase 12 kDa subunit (SPC12) |
| EVM0007771 | --                                         | 1.29   | 6.20   | -2.27  | 5.00E-05 | 4.28E-04 | --     | --                                        |
| EVM0003453 | --                                         | 69.03  | 332.90 | -2.27  | 5.00E-05 | 4.28E-04 | --     | --                                        |
| EVM0009773 | GPI-GlcNAc transferase complex, PIG-H component | 16.51   | 79.53 | -2.27  | 5.00E-05 | 4.28E-04 | --     | --                                        |
| EVM0006820 | --                                         | 40.31  | 193.40 | -2.26  | 5.00E-05 | 4.28E-04 | --     | --                                        |
| EVM0010870 | Conidiation protein 6                      | 18.91  | 90.66  | -2.26  | 5.00E-05 | 4.28E-04 | --     | Cell cycle control, cell division, chromosome partitioning |
| EVM0009720 | LYAR-type C2HC zinc finger                | 10.12  | 48.42  | -2.26  | 5.00E-05 | 4.28E-04 | --     | --                                        |
| EVM0004954 | --                                         | 40.60  | 194.04 | -2.26  | 5.00E-05 | 4.28E-04 | --     | --                                        |
| EVM0000357 | AhpC/TSA antioxidant enzyme               | 7.37   | 34.97  | -2.25  | 5.00E-05 | 4.28E-04 | --     | --                                        |
| EVM0009498 | Zinc-finger double domain                 | 0.94   | 4.46   | -2.24  | 2.25E-03 | 1.12E-02 | General function prediction only        | --                                        |
| Accession   | Score 1 | Score 2 | Log2Fold | E value 1 | E value 2 | Description                                           |
|------------|---------|---------|-----------|-----------|-----------|-------------------------------------------------------|
| EVM0011088 | 20.87   | 98.79   | -2.24     | 5.00E-05  | 4.28E-04  | Translation, ribosomal structure and biogenesis       |
| EVM0000019 | 21.72   | 102.79  | -2.24     | 5.00E-05  | 4.28E-04  | --                                                   |
| EVM0001076 | 4.96    | 23.45   | -2.24     | 5.00E-05  | 4.28E-04  | --                                                   |
| EVM0010590 | 265.59  | 1253.85 | -2.24     | 5.00E-05  | 4.28E-04  | --                                                   |
| EVM0003086 | 73.49   | 346.62  | -2.24     | 5.00E-05  | 4.28E-04  | Fungal specific transcription factor domain           |
| EVM0007572 | 3.48    | 16.41   | -2.24     | 5.00E-05  | 4.28E-04  | --                                                   |
| EVM0003466 | 14.74   | 69.10   | -2.23     | 5.00E-05  | 4.28E-04  | NYN domain                                           |
| EVM0009876 | 11.28   | 52.85   | -2.23     | 5.00E-05  | 4.28E-04  | Translation, ribosomal structure and biogenesis       |
| EVM0011068 | 76.82   | 359.63  | -2.23     | 5.00E-05  | 4.28E-04  | Defense mechanisms                                    |
| EVM0009051 | 283.50  | 1325.40 | -2.23     | 5.00E-05  | 4.28E-04  | Ribosomal protein L34                                 |
| EVM0000147 | 2.92    | 13.65   | -2.22     | 5.00E-05  | 4.28E-04  | --                                                   |
| EVM0003157 | 291.81  | 1358.37 | -2.22     | 5.00E-05  | 4.28E-04  | Defense mechanisms                                    |
| EVM0002337 | 16.14   | 75.01   | -2.22     | 5.00E-05  | 4.28E-04  | Ribonuclease H2 non-catalytic subunit                   |
|            |         |         |           |           |           | Gar1/Naf1 RNA binding region                           |
|            |         |         |           |           |           | eRF1 domain 1                                         |
|            |         |         |           |           |           | Dual specificity phosphatase, catalytic domain         |
|            |         |         |           |           |           | B-cell receptor-associated protein 31-like            |
|            |         |         |           |           |           | (Ylr154p-like)                                        |
| Accession  | Value | Value | Log2 Fold Change | E-value 1 | E-value 2 | Description                                                                 |
|------------|-------|-------|------------------|-----------|-----------|----------------------------------------------------------------------------|
| EVM0001519 | 8.66  | 40.24 | -2.22            | 5.00E-05  | 4.28E-04  | --                                                                        |
| EVM0007779 | 2.49  | 11.57 | -2.21            | 5.00E-05  | 4.28E-04  | --                                                                        |
| EVM0008622 | 60.22 | 278.68| -2.21            | 5.00E-05  | 4.28E-04  | --                                                                        |
| EVM0008830 | 36.90 | 170.55| -2.21            | 5.00E-05  | 4.28E-04  | Defense mechanisms                                                        |
|            |       |       |                  |           |           | Dual specificity phosphatase, catalytic domain                            |
| EVM000936  | 203.44| 938.69| -2.21            | 5.00E-05  | 4.28E-04  | --                                                                        |
| EVM0011567 | 251.49| 1159.67| -2.21           | 5.00E-05  | 4.28E-04  | --                                                                        |
| EVM0008030 | 0.33  | 1.50  | -2.20            | 9.95E-03  | 3.74E-02  | Transcription                                                            |
|            |       |       |                  |           |           | Homeobox domain                                                           |
| EVM0006126 | 21.17 | 97.29 | -2.20            | 5.00E-05  | 4.28E-04  | --                                                                        |
| EVM0003548 | 6.31  | 28.99 | -2.20            | 5.00E-05  | 4.28E-04  | Signal transduction                                                       |
|            |       |       |                  |           |           | mechanisms                                                                 |
| EVM0011359 | 125.91| 578.41| -2.20            | 5.00E-05  | 4.28E-04  | Energy production and conversion                                         |
|            |       |       |                  |           |           | ETC complex I subunit conserved region                                    |
| EVM0005543 | 3.39  | 15.55 | -2.20            | 5.00E-05  | 4.28E-04  | --                                                                        |
|            |       |       |                  |           |           | Glycosyltransferase family 18                                             |
| EVM0000720 | 32.06 | 146.85| -2.20            | 1.05E-03  | 5.94E-03  | --                                                                        |
|            |       |       |                  |           |           | Carboxyl transferase domain                                               |
| EVM0003103 | 52.01 | 237.94| -2.19            | 5.00E-05  | 4.28E-04  | --                                                                        |
| Gene ID     | EVM0011107 | EVM0010348 | EVM0009583 | EVM0008872 | EVM0011757 | EVM0003549 | EVM0010029 | EVM0006020 | EVM0004708 | EVM0007196 | EVM0004959 | EVM0002640 | EVM0009206 |
|------------|------------|------------|------------|------------|------------|------------|------------|------------|------------|------------|------------|------------|------------|
| Value      | 91.06      | 17.53      | 24.66      | 1.63       | 1.95       | 1.73       | 141.73     | 62.17      | 119.43     | 182.61     | 114.88     | 37.02      | 42.48      |
| Quantity   | 416.56     | 80.03      | 112.47     | 7.39       | 8.88       | 7.84       | 640.64     | 280.92     | 538.56     | 823.45     | 517.55     | 166.27     | 190.71     |
| Log2 Fold  | -2.19      | -2.19      | -2.19      | -2.18      | -2.18      | -2.18      | -2.18      | -2.18      | -2.17      | -2.17      | -2.17      | -2.17      | -2.17      |
| Description| 5.00E-05   | 5.00E-05   | 5.00E-05   | 5.00E-04   | 2.50E-04   | 1.55E-03   | 5.00E-05   | 5.00E-05   | 5.00E-05   | 5.00E-05   | 5.00E-05   | 5.00E-05   | 5.00E-05   |

- EVM0011107: Lipid transport and metabolism
- EVM0010348: EF hand
- EVM0009583: Fatty acid hydroxylase superfamily
- EVM0008872: Microsomal signal peptidase 25 kDa subunit (SPC25)
- EVM0011757: SecY translocase
- EVM0003549: RNA processing and modification
- EVM0010029: LSM domain
- EVM0006020: General function prediction only
- EVM0004708: SET domain
- EVM0007196: Protein of unknown function (DUF3129)
| Gene ID       | E-value | p-value | Log2 Fold Change | EVM0000572 | 13.31 | 59.69 | -2.17 | 5.00E-05 | 4.28E-04 | -- | Nucleolar complex-associated protein |
|--------------|---------|---------|------------------|------------|-------|-------|-------|----------|----------|----|-------------------------------------|
| Gene ID       | E-value | p-value | Log2 Fold Change | EVM0005244 | 93.50 | 419.30 | -2.17 | 5.00E-05 | 4.28E-04 | Function unknown | Polysaccharide biosynthesis |
| Gene ID       | E-value | p-value | Log2 Fold Change | EVM0009884 | 438.62 | 1965.97 | -2.16 | 5.00E-05 | 4.28E-04 | -- | Glycosyl hydrolase catalytic core |
| Gene ID       | E-value | p-value | Log2 Fold Change | EVM0004319 | 26.02 | 116.50 | -2.16 | 5.00E-05 | 4.28E-04 | -- | Protein of unknown function (DUF2962) |
| Gene ID       | E-value | p-value | Log2 Fold Change | EVM0011612 | 35.43 | 158.51 | -2.16 | 5.00E-05 | 4.28E-04 | -- | -- |
| Gene ID       | E-value | p-value | Log2 Fold Change | EVM0008791 | 6.50  | 29.07  | -2.16 | 5.00E-05 | 4.28E-04 | Coenzyme transport and metabolism | Dephospho-CoA kinase |
| Gene ID       | E-value | p-value | Log2 Fold Change | EVM0005157 | 21.63 | 96.71  | -2.16 | 5.00E-05 | 4.28E-04 | Secondary metabolites biosynthesis, transport and catabolism | short chain dehydrogenase |
| Gene ID       | E-value | p-value | Log2 Fold Change | EVM0007662 | 855.61| 3824.11| -2.16 | 5.00E-05 | 4.28E-04 | -- | -- |
| Gene ID       | E-value | p-value | Log2 Fold Change | EVM0002729 | 62.99 | 281.26 | -2.16 | 5.00E-05 | 4.28E-04 | -- | Ergosterol biosynthesis ERG4/ERG24 family |
| Gene ID       | E-value | p-value | Log2 Fold Change | EVM0010583 | 268.20| 1196.77| -2.16 | 5.00E-05 | 4.28E-04 | -- | -- |
| Gene ID       | E-value | p-value | Log2 Fold Change | EVM0002402 | 0.86  | 3.84   | -2.16 | 1.95E-03 | 9.93E-03 | -- | Domain of unknown function (DUF3328) |
| EVM0009547 | 43.63 | 194.21 | -2.15 | 5.00E-05 | 4.28E-04 | -- | Cytochrome P450 |
|------------|-------|--------|-------|----------|----------|----|----------------|
| EVM0008851 | 205.74| 913.84 | -2.15 | 5.00E-05 | 4.28E-04 | Intracellular trafficking, secretion, and vesicular transport | Preprotein translocase subunit Sec66 |
| EVM0000932 | 56.84 | 252.19 | -2.15 | 5.00E-05 | 4.28E-04 | -- | -- |
| EVM0005108 | 2.67  | 11.82  | -2.15 | 5.00E-05 | 4.28E-04 | -- | GCC2 and GCC3 |
| EVM0008511 | 24.25 | 107.30 | -2.15 | 5.00E-05 | 4.28E-04 | RNA processing and modification | Ribosomal RNA-processing protein 7 (RRP7) |
| EVM0002331 | 73.10 | 322.40 | -2.14 | 5.00E-05 | 4.28E-04 | Posttranslational modification, protein turnover, chaperones | 14-3-3 protein |
| EVM0002338 | 10.13 | 44.68  | -2.14 | 5.00E-05 | 4.28E-04 | Lipid transport and metabolism | PAP2 superfamily |
| EVM0006021 | 1.45  | 6.38   | -2.14 | 6.15E-03 | 2.54E-02 | -- | -- |
| EVM0011879 | 42.12 | 185.59 | -2.14 | 5.00E-05 | 4.28E-04 | General function prediction only | -- |
| EVM0006561 | 4.00  | 17.61  | -2.14 | 1.50E-04 | 1.14E-03 | -- | -- |
| EVM0008761 | 13.60 | 59.88  | -2.14 | 5.00E-05 | 4.28E-04 | -- | Calcineurin-like phosphoesterase |
| EVM0001700 | 52.76 | 232.20 | -2.14 | 5.00E-05 | 4.28E-04 | -- | Cobalamin-independent synthase, Catalytic domain |
| Accession  | Value1  | Value2  | Value3  | Value4  | Value5  | Value6  | Term                                      |
|------------|---------|---------|---------|---------|---------|---------|-------------------------------------------|
| EVM0010983 | 2.80    | 12.29   | -2.14   | 5.00E-05| 4.28E-04| --      | --                                        |
| EVM0007254 | 7240.86 | 31828.00| -2.14   | 5.00E-05| 4.28E-04| --      | Ribosomal protein S30                    |
| EVM0002292 | 45.23   | 197.87  | -2.13   | 5.00E-05| 4.28E-04| --      | --                                        |
| EVM0009353 | 60.32   | 263.27  | -2.13   | 5.00E-05| 4.28E-04| --      | --                                        |
| EVM0004297 | 24.02   | 104.81  | -2.13   | 5.00E-05| 4.28E-04| --      | BTG family                               |
| EVM0003876 | 2.13    | 9.29    | -2.13   | 5.00E-05| 4.28E-04| --      | Hemerythrin HHE cation binding domain    |
| EVM0009908 | 220.37  | 960.96  | -2.12   | 5.00E-05| 4.28E-04| --      | --                                        |
| EVM0002491 | 286.10  | 1247.39 | -2.12   | 5.00E-05| 4.28E-04| --      | YABBY protein                            |
| EVM0008587 | 15.14   | 65.97   | -2.12   | 5.00E-05| 4.28E-04| --      | --                                        |
| EVM0007388 | 14.44   | 62.90   | -2.12   | 5.00E-05| 4.28E-04| --      | --                                        |
| EVM0012268 | 49.08   | 213.17  | -2.12   | 5.00E-05| 4.28E-04| Function unknown| Pam16                                      |
| EVM0000363 | 10.99   | 47.64   | -2.12   | 5.00E-05| 4.28E-04| Posttranslational modification, protein turnover, chaperones | Zinc knuckle   |
| Accession  | Fold Change | Expression | Log2 Fold Change | Function                                                                 | Protein Name |
|------------|-------------|------------|------------------|--------------------------------------------------------------------------|--------------|
| EVM0011090 | 331.40      | 1436.10    | -2.12            | Intracellular trafficking, secretion, and vesicular transport             | Tim10/DDP family zinc finger |
| EVM0011982 | 18.44       | 79.87      | -2.12            | Chromatin structure and dynamics                                          | Core histone H2A/H2B/H3/H4 |
| EVM0007621 | 37.23       | 160.70     | -2.11            | Replication, recombination and repair                                     | NUDIX domain |
| EVM0004736 | 0.47        | 2.02       | -2.11            | --                                                                        | --            |
| EVM0009653 | 21.53       | 92.73      | -2.11            | --                                                                        | Cellulase (glycosyl hydrolase family 5) |
| EVM0008356 | 9.76        | 42.01      | -2.11            | Function unknown                                                          | Utp11 protein |
| EVM0007939 | 2.44        | 10.51      | -2.10            | General function prediction only                                          | Ras family   |
| EVM0002967 | 3.65        | 15.64      | -2.10            | --                                                                        | --            |
| EVM0000467 | 4.37        | 18.75      | -2.10            | --                                                                        | --            |
| EVM0007770 | 3.48        | 14.91      | -2.10            | --                                                                        | --            |
| EVM0010617 | 126.98      | 544.50     | -2.10            | --                                                                        | DASH complex subunit Dad3 |
| EVM0010158 | 53.16       | 227.91     | -2.10            | Function unknown                                                          | Pre-rRNA-processing protein TSR2 |
| EVM0005022 | 20.13 | 86.26 | -2.10 | 5.00E-05 | 4.28E-04 | Function unknown | Protein of unknown function (DUF788) |
| EVM0009205 | 1.46  | 6.26  | -2.10 | 1.90E-03 | 9.73E-03 | --              | --                                  |
| EVM0006099 | 92.45 | 395.05| -2.10 | 5.00E-05 | 4.28E-04 | Lipid transport and metabolism | Enoyl-CoA hydratase/isomerase family |
| EVM0002811 | 243.51| 1037.48| -2.09 | 5.00E-05 | 4.28E-04 | Posttranslational modification, protein turnover, chaperones | Thioredoxin |
| EVM0008173 | 1.48  | 6.30  | -2.09 | 5.00E-05 | 4.28E-04 | --              | --                                  |
| EVM0004762 | 115.33| 491.14| -2.09 | 5.00E-05 | 4.28E-04 | Intracellular trafficking, secretion, and vesicular transport | Clathrin adaptor complex small chain |
| EVM0005049 | 34.18 | 145.47| -2.09 | 5.00E-05 | 4.28E-04 | Posttranslational modification, protein turnover, chaperones | DnaJ domain |
| EVM0003625 | 77.04 | 327.28| -2.09 | 5.00E-05 | 4.28E-04 | Carbohydrate transport and metabolism | Alpha amylase, catalytic domain |
| EVM0010897 | 31.53 | 133.93| -2.09 | 5.00E-05 | 4.28E-04 | --              | DASH complex subunit Dad2           |
| EVM0005369 | 156.14| 662.51| -2.09 | 5.00E-05 | 4.28E-04 | Intracellular trafficking, secretion, and vesicular transport | emp24/gp25L/p24 family/GOLD         |
| EVM0008562 | 205.37| 869.38| -2.08 | 5.00E-05 | 4.28E-04 | --              | --                                  |
| EVM0005697 | 26.01 | 109.83 | -2.08 | 5.00E-05 | 4.28E-04 | -- | Peroxin-3 |
| EVM0004410 | 16.72 | 70.58  | -2.08 | 5.00E-05 | 4.28E-04 | -- | PAPA-1-like conserved region |
| EVM0010921 | 11.95 | 50.39  | -2.08 | 5.00E-05 | 4.28E-04 | -- | -- |
| EVM0011153 | 135.74| 570.89 | -2.07 | 5.00E-05 | 4.28E-04 | -- | Tim17/Tim22/Tim23/Pmp24 family |
| EVM0000706 | 16.56 | 69.61  | -2.07 | 5.00E-05 | 4.28E-04 | -- | Alginate lyase |
| EVM0001259 | 8.53  | 35.87  | -2.07 | 5.00E-05 | 4.28E-04 | General function prediction | WD domain, G-beta repeat only |
| EVM0011746 | 7.92  | 33.23  | -2.07 | 5.00E-05 | 4.28E-04 | -- | -- |
| EVM0008485 | 5.10  | 21.30  | -2.06 | 5.00E-05 | 4.28E-04 | -- | -- |
| EVM0005110 | 29.61 | 123.58 | -2.06 | 5.00E-05 | 4.28E-04 | Transcription | -- |
| EVM0010702 | 12.09 | 50.43  | -2.06 | 5.00E-05 | 4.28E-04 | -- | -- |
| EVM0011577 | 69.27 | 288.87 | -2.06 | 5.00E-05 | 4.28E-04 | -- | ER membrane protein SH3 |
| EVM0008320 | 2.30  | 9.58   | -2.06 | 5.00E-05 | 4.28E-04 | -- | Nuclear condensing complex subunits, C-term domain |
| EVM0002743 | 9.03  | 37.61  | -2.06 | 5.00E-05 | 4.28E-04 | -- | -- |
| EVM0008058 | 9.76 | 40.64 | -2.06 | 5.00E-05 | 4.28E-04 | -- | -- |
| EVM0008835 | 32.71 | 136.13 | -2.06 | 5.00E-05 | 4.28E-04 | Carbohydrate transport and metabolism | -- |
| EVM0008406 | 47.92 | 199.36 | -2.06 | 5.00E-05 | 4.28E-04 | Lipid transport and metabolism | AMP-binding enzyme |
| EVM0001342 | 26.47 | 110.10 | -2.06 | 5.00E-05 | 4.28E-04 | Defense mechanisms | TB2/DP1, HVA22 family |
| EVM0009527 | 5.81 | 24.15 | -2.05 | 5.00E-05 | 4.28E-04 | Replication, recombination and repair | Cid1 family poly A polymerase |
| EVM0011085 | 23.83 | 98.97 | -2.05 | 5.00E-05 | 4.28E-04 | -- | Translation initiation factor IF-3, C-terminal domain |
| EVM0006734 | 179.11 | 743.70 | -2.05 | 5.00E-05 | 4.28E-04 | -- | Complex 1 protein (LYR family) |
| EVM0002517 | 138.70 | 575.78 | -2.05 | 5.00E-05 | 4.28E-04 | Defense mechanisms | Tetratricopeptide repeat |
| EVM0003684 | 2.37 | 9.85 | -2.05 | 5.00E-05 | 4.28E-04 | #N/A | #N/A |
| EVM0011239 | 74.61 | 309.36 | -2.05 | 5.00E-05 | 4.28E-04 | -- | 50S ribosome-binding GTPase |
| EVM0002230 | 13.58 | 56.14 | -2.05 | 5.00E-05 | 4.28E-04 | -- | Lactonase, 7-bladed beta-propeller |
| EVM0004837 | 109.85 | 454.07 | -2.05 | 5.00E-05 | 4.28E-04 | General function prediction only | Ras family |
| EVM0009586 | 39.13 | 161.55 | -2.05 | 5.00E-05 | 4.28E-04 | Lipid transport and metabolism | Fatty acid hydroxylase superfamily |
| Accession   | Value1 | Value2 | Value3 | Value4 | Value5 | Value6 | Value7 | Annotation                                                                 |
|-------------|--------|--------|--------|--------|--------|--------|--------|---------------------------------------------------------------------------|
| EVM0002154  | 0.84   | 3.47   | -2.04  | 8.00E-04| 4.73E-03| --     | --     |                                                                           |
| EVM0011632  | 36.71  | 150.92 | -2.04  | 5.00E-05| 4.28E-04| --     | --     |                                                                           |
| EVM0008343  | 7.63   | 31.31  | -2.04  | 5.00E-05| 4.28E-04| --     | --     |                                                                           |
| EVM0009995  | 6.51   | 26.74  | -2.04  | 5.00E-05| 4.28E-04| RNA processing and modification | WD domain, G-beta repeat |
| EVM0007132  | 0.99   | 4.05   | -2.04  | 1.00E-04| 7.96E-04| --     | --     |                                                                           |
| EVM0002285  | 1.83   | 7.52   | -2.04  | 5.00E-05| 4.28E-04| --     | --     |                                                                           |
| EVM0005544  | 64.15  | 262.82 | -2.03  | 5.00E-05| 4.28E-04| Translation, ribosomal structure and biogenesis | Ribosomal protein L18e/L15 |
| EVM0001016  | 5.53   | 22.66  | -2.03  | 5.00E-05| 4.28E-04| --     | --     |                                                                           |
| EVM0004688  | 18.59  | 75.99  | -2.03  | 5.00E-05| 4.28E-04| --     | --     |                                                                           |
| EVM0011165  | 21.32  | 87.15  | -2.03  | 5.00E-05| 4.28E-04| Energy production and conversion | Mitochondrial carrier protein |
| EVM0005264  | 38.02  | 155.28 | -2.03  | 5.00E-05| 4.28E-04| General function prediction only | Major Facilitator Superfamily |
| EVM0000773  | 359.29 | 1466.01| -2.03  | 5.00E-05| 4.28E-04| Energy production and conversion | NADH-ubiquinone oxidoreductase B18 subunit (NDUFB7) |
| EVM Code     | Value 1 | Value 2  | Value 3  | Value 4  | Gene/Function Description                                      |
|-------------|---------|----------|----------|----------|---------------------------------------------------------------|
| EVM0002656  | 73.68   | 300.17   | -2.03    | 5.00E-05 | Function unknown                                               |
|             |         |          |          | 4.28E-04 | Erg28 like protein                                            |
| EVM0002198  | 4.40    | 17.91    | -2.03    | 5.00E-05 | Phosphotransferase enzyme family                              |
| EVM0003931  | 96.54   | 392.37   | -2.02    | 5.00E-05 | --                                                            |
| EVM0011838  | 201.68  | 819.46   | -2.02    | 5.00E-05 | Ribosomal protein S8                                          |
| EVM0002024  | 6.25    | 25.39    | -2.02    | 5.00E-05 | Secondary metabolites biosynthesis, transport and catabolism  |
|             |         |          |          | 4.28E-04 | short chain dehydrogenase                                     |
| EVM0002372  | 12.43   | 50.32    | -2.02    | 5.00E-05 | --                                                            |
|             |         |          |          | 4.28E-04 | Cytochrome P450                                                |
| EVM0000472  | 1992.42 | 8035.73  | -2.01    | 5.00E-05 | --                                                            |
|             |         |          |          | 4.28E-04 | --                                                            |
| EVM0000076  | 0.47    | 1.88     | -2.01    | 7.90E-03 | Zinc-binding dehydrogenase                                   |
|             |         |          |          | 3.10E-02 | --                                                            |
| EVM0005931  | 1.65    | 6.63     | -2.01    | 7.00E-04 | --                                                            |
|             |         |          |          | 4.23E-03 | --                                                            |
| EVM0011475  | 5.42    | 21.76    | -2.01    | 5.00E-05 | --                                                            |
|             |         |          |          | 4.28E-04 | --                                                            |
| EVM0010715  | 38.90   | 155.98   | -2.00    | 5.00E-05 | RNA processing and modification                              |
|             |         |          |          | 4.28E-04 | Isyl-like splicing family                                     |
| EVM0003567  | 14.09   | 56.35    | -2.00    | 5.00E-05 | --                                                            |
|             |         |          |          | 4.28E-04 | Tryptophan halogenase                                         |
| Accession     | Score | E Value | Log E Value | Classification                                      | Description                                                                 |
|--------------|-------|---------|-------------|-----------------------------------------------------|-----------------------------------------------------------------------------|
| EVM0010407   | 7.65  | 5.00E-05| 4.28E-04    | Putative S-adenosyl-L-methionine-dependent methyltransferase |                                                                             |
| EVM0001591   | 1.57  | 5.00E-05| 4.28E-04    | --                                                  |                                                                             |
| EVM0005185   | 78.03 | 5.00E-05| 4.28E-04    | Amino acid transport and metabolism                | Aminotransferase class-V                                                 |
| EVM000905    | 23.39 | 5.00E-05| 4.28E-04    | --                                                  |                                                                             |
| EVM0011144   | 46.12 | 5.00E-05| 4.28E-04    | Protein of unknown function (DUF2034)               |                                                                             |
| EVM0006060   | 4.96  | 5.00E-05| 4.28E-04    | --                                                  | PP-loop family                                                             |
| EVM0007905   | 13.87 | 5.00E-05| 4.28E-04    | --                                                  | Spc19                                                                      |
| EVM0006949   | 69.91 | 5.00E-05| 4.28E-04    | --                                                  | N-terminal domain of ribose phosphate pyrophosphokinase                    |
| EVM0001268   | 1.71  | 5.00E-05| 4.28E-04    | --                                                  |                                                                             |
| EVM0002754   | 17.95 | 5.00E-05| 4.28E-04    | General function prediction only                    | Ankyrin repeats (3 copies)                                                |
| EVM0008871   | 64.60 | 5.00E-05| 4.28E-04    | General function prediction only                    | Ras family                                                                 |
| EVM0002628   | 225.30| 5.00E-05| 4.28E-04    | Translation, ribosomal structure and biogenesis     | Mitochondrial ribosomal subunit S27                                       |
| EVM ID     | Log Fold Change | P Value | Description                          | Gene Name                  |
|------------|----------------|---------|--------------------------------------|----------------------------|
| EVM0008497 | 460.74         | 1821.91 | Lipid transport and metabolism       | MaoC like domain           |
| EVM0006547 | 82.72          | 326.88  | Translation, ribosomal structure and biogenesis | Ribosomal protein L23      |
| EVM0004398 | 260.23         | 1027.78 | General function prediction only      | Proteolipid membrane potential modulator |
| EVM0003817 | 4.77           | 18.81   | --                                   | --                         |
| EVM0005078 | 4.77           | 18.81   | Cell cycle control, cell division, chromosome partitioning | HORMA domain |
| EVM000419  | 44.43          | 175.18  | Function unknown                     | Complex 1 protein (LYR family) |
| EVM0005619 | 10.10          | 39.74   | --                                   | 60Kd inner membrane protein |
| EVM0003822 | 6.03           | 23.71   | Translation, ribosomal structure and biogenesis | Formyl transferase |
| EVM0005613 | 19.51          | 76.71   | --                                   | --                         |
| EVM0002758 | 1.39           | 5.44    | --                                   | --                         |
| EVM0004710 | 129.07         | 506.83  | --                                   | Cgr1 family                |
| EVM0008258 | 42.75          | 167.71  | --                                   | --                         |
| Gene ID        | Expression | Z-score | E-value | Annotation                              |
|---------------|------------|---------|---------|-----------------------------------------|
| EVM0010354    | 0.78       | -1.97   | 7.50E-04| F-box-like                              |
| EVM0010012    | 11.00      | -1.96   | 5.00E-05| Formin Homology Region 1                |
| EVM0006285    | 67.10      | -1.96   | 5.00E-05| Lipid transport and metabolism          |
| EVM0006529    | 16.45      | -1.96   | 5.00E-05| Emopamil binding protein                |
| EVM0012211    | 19.84      | -1.96   | 5.00E-05|                                        |
| EVM0001883    | 9.81       | -1.96   | 5.00E-05| LIM domain                             |
| EVM0000204    | 629.60     | -1.96   | 5.00E-05| short chain dehydrogenase              |
| EVM0007556    | 190.49     | -1.96   | 5.00E-05| Ser-Thr-rich glycosyl-phosphatidylinositol-anchored membrane family |
| EVM0006296    | 4.04       | -1.96   | 5.00E-05|                                        |
| EVM0009852    | 8.91       | -1.96   | 5.00E-05| Transcription                          |
| EVM0001421    | 50.04      | -1.95   | 5.00E-05| Cell cycle control, cell division, chromosome partitioning |
| EVM0001194    | 7.35       | -1.95   | 5.00E-05|                                        |
| EVM0001584 | 34.37 | 132.95 | -1.95 | 5.00E-05 | 4.28E-04 | -- | Voltage-dependent anion channel |
| EVM0009036 | 127.04 | 490.95 | -1.95 | 5.00E-05 | 4.28E-04 | RNA processing and modification | Ribosomal protein L7Ae/L30e/S12e/Gadd45 family |
| EVM0009625 | 10.47 | 40.43 | -1.95 | 5.00E-05 | 4.28E-04 | -- | AIG1 family |
| EVM0011691 | 12.58 | 48.57 | -1.95 | 5.00E-05 | 4.28E-04 | Function unknown | Regulator of chromosome condensation (RCC1) repeat |
| EVM0006200 | 4.31 | 16.63 | -1.95 | 5.00E-05 | 4.28E-04 | Posttranslational modification, protein turnover, chaperones | Eukaryotic aspartyl protease |
| EVM0002948 | 30.61 | 118.09 | -1.95 | 5.00E-05 | 4.28E-04 | -- | Protein of unknown function (Ytp1) |
| EVM0010252 | 40.89 | 157.55 | -1.95 | 5.00E-05 | 4.28E-04 | -- | PX domain |
| EVM0001566 | 2.00 | 7.70 | -1.95 | 5.00E-05 | 4.28E-04 | General function prediction only | Sugar (and other) transporter |
| EVM0006292 | 2.78 | 10.69 | -1.94 | 5.00E-05 | 4.28E-04 | -- | Fungal Zn(2)-Cys(6) binuclear cluster domain |
| EVM0003828 | 14.93 | 57.41 | -1.94 | 5.00E-05 | 4.28E-04 | -- | Membrane bound O-acyl transferase family |
| EVM0008088 | 7.71 | 29.64 | -1.94 | 5.00E-05 | 4.28E-04 | -- | -- |
| EVM0001511 | 19.95 | 76.55 | -1.94 | 5.00E-05 | 4.28E-04 | Translation, ribosomal structure and biogenesis | GTP-binding protein TrmE N-terminus |
| Accession   | Odds | E-value | LogE | Description                                |
|-------------|------|---------|------|--------------------------------------------|
| EVM0000442  | 53.85| 206.56  | -1.94| --                                         |
| EVM0010303  | 2.33 | 8.95    | -1.94| Helix-turn-helix domain                    |
| EVM0002264  | 77.82| 297.99  | -1.94| --                                         |
| EVM0003886  | 174.99| 668.14  | -1.93| Ribosomal prokaryotic L21 protein          |
| EVM0005939  | 6.87 | 26.21   | -1.93| --                                         |
| EVM0010495  | 32.20| 122.87  | -1.93| Protein kinase domain                      |
| EVM0000836  | 109.52| 417.02  | -1.93| Intracellular trafficking, secretion, and vesicular transport |
| EVM0001382  | 10.07| 38.33   | -1.93| --                                         |
| EVM0005032  | 30.02| 114.27  | -1.93| Signal transduction mechanisms             |
| EVM0007173  | 70.31| 267.38  | -1.93| Replication, recombination and repair      |
| EVM0003322  | 5.71 | 21.72   | -1.93| General function prediction only           |
| EVM0010446  | 36.52| 138.75  | -1.93| Transcription                              |

NUDIX domain
Nucleosome assembly protein (NAP)
Transcription
Homeobox KN domain
| Gene ID       | E Value | M Value | Log2 Fold Change | KEGG pathways                          | Description                                                                 |
|--------------|---------|---------|------------------|----------------------------------------|-----------------------------------------------------------------------------|
| EVM0009699   | 59.94   | 227.55  | -1.92            | Posttranslational modification, protein turnover, chaperones                | Proteasome subunit                                                         |
| EVM0002423   | 48.62   | 184.06  | -1.92            | Energy production and conversion                                              | Carbamoyl-phosphate synthase L chain, ATP binding domain                   |
| EVM0004635   | 101.07  | 382.58  | -1.92            | --                                                                                 | --                                                                         |
| EVM0011804   | 5.19    | 19.64   | -1.92            | --                                                                                 | --                                                                         |
| EVM0000031   | 299.51  | 1131.39 | -1.92            | --                                                                                 | --                                                                         |
| EVM0011230   | 17.92   | 67.68   | -1.92            | SNARE associated Golgi protein                                                 | --                                                                         |
| EVM0011786   | 22.04   | 83.21   | -1.92            | --                                                                                 | --                                                                         |
| EVM0011619   | 21.36   | 80.50   | -1.91            | F-box-like                                                                      | --                                                                         |
| EVM0005809   | 11.30   | 42.50   | -1.91            | Replication, recombination and repair                                           | RNase H                                                                    |
| EVM0008383   | 403.50  | 1513.02 | -1.91            | Energy production and conversion                                              | NADH ubiquinone oxidoreductase subunit NDUFA12                              |
| EVM0004134   | 46.71   | 174.72  | -1.90            | General function prediction only                                               | RNA recognition motif. (a.k.a. RRM, RBD, or RNP domain)                    |
| EVM0004256   | 5.68    | 21.23   | -1.90            | --                                                                                 | --                                                                         |
| Gene Name          | Value 1  | Value 2  | Value 3  | Value 4  | Value 5 | Value 6  | Value 7  | Value 8  | Value 9  | Value 10 | Value 11 | Function Description                                                                 |
|--------------------|----------|----------|----------|----------|---------|----------|----------|----------|----------|----------|----------|-------------------------------------------------------------------------------------|
| EVM0005705         | 11.28    | 42.10    | -1.90    | 5.00E-05 | 4.28E-04| --       | --       | --       | --       | --       | --       |                                                                                     |
| EVM0010165         | 53.31    | 198.82   | -1.90    | 5.00E-05 | 4.28E-04| Function unknown | AhpC/TSA antioxidant enzyme |
| EVM0000794         | 532.17   | 1984.75  | -1.90    | 5.00E-05 | 4.28E-04| Posttranslational modification, protein turnover, chaperones | Redoxin |
| EVM0010743         | 4.31     | 16.08    | -1.90    | 5.00E-05 | 4.28E-04| --       | --       | F-box-like |
| EVM0000029         | 11.07    | 41.25    | -1.90    | 5.00E-05 | 4.28E-04| Transcription | RNA polymerase Rpb3/RpoA insert domain |
| EVM0009698         | 1049.89  | 3909.93  | -1.90    | 5.00E-05 | 4.28E-04| Translation, ribosomal structure and biogenesis | Ribosomal L38e protein family |
| EVM0008889         | 1.35     | 5.04     | -1.90    | 3.50E-04 | 2.36E-03| --       | --       | Cytochrome P450 |
| EVM0003580         | 5.37     | 19.98    | -1.89    | 5.00E-05 | 4.28E-04| --       | --       | -- |
| EVM0001247         | 25.31    | 93.81    | -1.89    | 5.00E-05 | 4.28E-04| --       | --       | MAC/Perforin domain |
| EVM0008461         | 12.87    | 47.64    | -1.89    | 5.00E-05 | 4.28E-04| --       | --       | Putative snoRNA binding domain |
| EVM0001277         | 5.83     | 21.51    | -1.88    | 5.00E-05 | 4.28E-04| --       | --       | -- |
| EVM0005073         | 11.11    | 40.97    | -1.88    | 5.00E-05 | 4.28E-04| --       | --       | Nitronate monooxygenase |
| Accession     | Gene 1 | Gene 2   | log2 Freq | p-value 1 | p-value 2 | Function                                                                 |
|--------------|--------|----------|-----------|-----------|-----------|---------------------------------------------------------------------------|
| EVM0002382   | 1.17   | 4.30     | -1.88     | 1.01E-02  | 3.78E-02  | --                                                                        |
| EVM0005402   | 2.38   | 8.72     | -1.88     | 5.00E-05  | 4.28E-04  | F-box domain                                                              |
| EVM0006468   | 13.60  | 49.85    | -1.87     | 5.00E-05  | 4.28E-04  | Signal transduction mechanisms RED-like protein N-terminal region         |
| EVM0000560   | 3.71   | 13.59    | -1.87     | 5.00E-05  | 4.28E-04  | Ferric reductase like transmembrane component                             |
| EVM0006499   | 6.16   | 22.58    | -1.87     | 5.00E-05  | 4.28E-04  | --                                                                        |
| EVM0008399   | 0.33   | 1.20     | -1.87     | 8.05E-03  | 3.15E-02  | --                                                                        |
| EVM0001058   | 6.07   | 22.17    | -1.87     | 5.00E-05  | 4.28E-04  | --                                                                        |
| EVM0006282   | 2.91   | 10.63    | -1.87     | 5.00E-05  | 4.28E-04  | --                                                                        |
| EVM0006795   | 461.49 | 1683.99  | -1.87     | 5.00E-05  | 4.28E-04  | --                                                                        |
| EVM0007872   | 63.49  | 231.38   | -1.87     | 5.00E-05  | 4.28E-04  | --                                                                        |
| EVM0003954   | 34.43  | 125.45   | -1.87     | 5.00E-05  | 4.28E-04  | Intracellular trafficking, secretion, and vesicular transport             |
| EVM0008504   | 58.39  | 212.76   | -1.87     | 5.00E-05  | 4.28E-04  | F-box-like                                                                |
| EVM0007568  | 104.78 | 381.71 | -1.87 | 5.00E-05 | 4.28E-04 | -- | ACT domain |
|-------------|--------|--------|-------|----------|----------|----|-----------|
| EVM0006498  | 1.24   | 4.53   | -1.86 | 3.15E-03 | 1.47E-02 | -- | -- |
| EVM0007304  | 29.89  | 108.80 | -1.86 | 5.00E-05 | 4.28E-04 | Carbohydrate transport and metabolism | UAA transporter family |
| EVM0004063  | 43.87  | 159.60 | -1.86 | 5.00E-05 | 4.28E-04 | Transcription | RNA recognition motif. (a.k.a. RRM, RBD, or RNP domain) |
| EVM0008519  | 122.32 | 444.91 | -1.86 | 5.00E-05 | 4.28E-04 | RNA processing and modification | LUC7 N_terminus |
| EVM000596   | 3.89   | 14.13  | -1.86 | 5.00E-05 | 4.28E-04 | Replication, recombination and repair | -- |
| EVM0008224  | 138.01 | 501.58 | -1.86 | 5.00E-05 | 4.28E-04 | Amino acid transport and metabolism | Protein of unknown function (DUF619) |
| EVM0003106  | 18.49  | 67.20  | -1.86 | 5.00E-05 | 4.28E-04 | -- | Spt20 family |
| EVM0001816  | 8.27   | 29.99  | -1.86 | 5.00E-05 | 4.28E-04 | Posttranslational modification, protein turnover, chaperones | Cyclophilin type peptidyl-prolyl cis-trans isomerase/CLD |
| EVM0009709  | 32.49  | 117.72 | -1.86 | 5.00E-05 | 4.28E-04 | -- | -- |
| EVM0011276  | 65.66  | 237.87 | -1.86 | 5.00E-05 | 4.28E-04 | Translation, ribosomal structure and biogenesis | Pumilio-family RNA binding repeat |
| EVM0004707  | 38.03  | 137.60 | -1.86 | 5.00E-05 | 4.28E-04 | -- | Alpha-L-rhamnosidase N-terminal domain |
| EVM0009463 | 140.06 | 506.58  | -1.85 | 5.00E-05 | 4.28E-04 | -- | Ribosomal protein L35 |
|------------|--------|---------|-------|----------|----------|----|----------------------|
| EVM0011238 | 27.17  | 98.25   | -1.85 | 5.00E-05 | 4.28E-04 | Secondary metabolites biosynthesis, transport and catabolism | Cytochrome P450 |
| EVM0006335 | 116.74 | 422.08  | -1.85 | 5.00E-05 | 4.28E-04 | -- | -- |
| EVM0011646 | 13.15  | 47.41   | -1.85 | 5.00E-05 | 4.28E-04 | -- | Pheromone A receptor |
| EVM0004053 | 185.07 | 667.10  | -1.85 | 5.00E-05 | 4.28E-04 | -- | -- |
| EVM0007826 | 19.64  | 70.79   | -1.85 | 5.00E-05 | 4.28E-04 | General function prediction RNA recognition motif. (a.k.a. RRM, RBD, or RNP domain) | -- |
| EVM0007539 | 235.10 | 847.27  | -1.85 | 5.00E-05 | 4.28E-04 | -- | SUR7/PalI family |
| EVM0004055 | 58.80  | 211.49  | -1.85 | 5.00E-05 | 4.28E-04 | Translation, ribosomal structure and biogenesis | Ribosomal protein S13/S18 |
| EVM0001657 | 112.63 | 405.01  | -1.85 | 5.00E-05 | 4.28E-04 | -- | -- |
| EVM0004716 | 11.90  | 42.79   | -1.85 | 5.00E-05 | 4.28E-04 | Replication, recombination and repair | Exonuclease |
| EVM0005431 | 7.22   | 25.93   | -1.85 | 5.00E-05 | 4.28E-04 | Cell cycle control, cell division, chromosome partitioning | HEC/Ndc80p family |
| EVM0000310 | 3.59   | 12.89   | -1.85 | 4.50E-04 | 2.92E-03 | -- | -- |
| Gene ID          | Gene Name                  | Description                                |
|-----------------|----------------------------|--------------------------------------------|
| EVM0002996      | Sin3 associated polypeptide p18 (SAP18) | Transcription                             |
| EVM0008789      | Cytochrome c oxidase subunit VIa | Energy production and conversion          |
| EVM0000547      | CFEM domain                |                                            |
| EVM0003364      | UreF                       |                                            |
| EVM0005267      | Brix domain                |                                            |
| EVM0002076      | mRNA processing and modification |                                            |
| EVM0009466      | UreF                       |                                            |
| EVM0005232      | Brix domain                |                                            |
| EVM0009065      | mRNA processing and modification |                                            |
| EVM0006231      | Brix domain                |                                            |
| EVM000755       | mRNA processing and modification |                                            |
| EVM0007113      | UreF                       |                                            |
| EVM0007046      | UreF                       |                                            |
| Gene ID          | FPKM    | Log2 Fold Change | Log2 Fold Change | P-value        | Description                                      |
|-----------------|---------|------------------|------------------|----------------|--------------------------------------------------|
| EVM0008232      | 1.58    | -1.83            | 1.00E-04         | Glycosyl hydrolases family 28                     |
| EVM0003029      | 30.01   | -1.83            | 5.00E-05         | Protein-tyrosine phosphatase                      |
| EVM0005991      | 184.07  | -1.83            | 5.00E-04         | SAP domain                                       |
| EVM0005206      | 5.52    | -1.83            | 5.00E-04         | Signal transduction mechanisms                    |
| EVM0009840      | 11.08   | -1.83            | 5.00E-04         | Signal transduction mechanisms                    |
| EVM0004042      | 54.48   | -1.83            | 5.00E-04         | Signal transduction mechanisms                    |
| EVM0005926      | 67.34   | -1.83            | 5.00E-04         | Signal transduction mechanisms                    |
| EVM0010482      | 226.69  | -1.83            | 5.00E-04         | Signal transduction mechanisms                    |
| EVM0008781      | 59.91   | -1.83            | 5.00E-04         | Signal transduction mechanisms                    |
| EVM0012038      | 82.50   | -1.83            | 5.00E-04         | Signal transduction mechanisms                    |
| EVM0002995      | 8.67    | -1.83            | 5.00E-04         | Signal transduction mechanisms                    |
| EVM0002465      | 4.08    | -1.83            | 2.50E-03         | RNA processing and modification                   |
| EVM0004919      | 5.95    | -1.82            | 5.00E-04         | Cytoskeleton                                     |
| EVM0005926      | 67.34   | -1.83            | 5.00E-04         | General function prediction only                  |
| EVM0010482      | 226.69  | -1.83            | 5.00E-04         | General function prediction only                  |
| EVM0005926      | 67.34   | -1.83            | 5.00E-04         | General function prediction only                  |
| EVM0008781      | 59.91   | -1.83            | 5.00E-04         | General function prediction only                  |
| EVM0012038      | 82.50   | -1.83            | 5.00E-04         | General function prediction only                  |
| EVM0002995      | 8.67    | -1.83            | 5.00E-04         | General function prediction only                  |
| EVM0002465      | 4.08    | -1.83            | 2.50E-03         | General function prediction only                  |
| EVM0004919      | 5.95    | -1.82            | 5.00E-04         | General function prediction only                  |
| EVM0005926      | 67.34   | -1.83            | 5.00E-04         | General function prediction only                  |
| EVM0008781      | 59.91   | -1.83            | 5.00E-04         | General function prediction only                  |
| EVM0012038      | 82.50   | -1.83            | 5.00E-04         | General function prediction only                  |
| EVM0002995      | 8.67    | -1.83            | 5.00E-04         | General function prediction only                  |
| EVM0002465      | 4.08    | -1.83            | 2.50E-03         | General function prediction only                  |
| EVM0004919      | 5.95    | -1.82            | 5.00E-04         | General function prediction only                  |
| EVM0005906 | 0.63  | 2.22  | -1.82 | 2.05E-03 | 1.03E-02 | -- | Glycosyl hydrolase family 7 |
| EVM0005644 | 33.24 | 117.36| -1.82 | 5.00E-05 | 4.28E-04 | Lipid transport and metabolism | Phospholipid methyltransferase |
| EVM0010966 | 6.07  | 21.43 | -1.82 | 5.00E-05 | 4.28E-04 | Replication, recombination and repair | ATPase family associated with various cellular activities (AAA) |
| EVM0001716 | 1.90  | 6.70  | -1.82 | 5.00E-05 | 4.28E-04 | -- | Pregnancy-associated plasma protein-A |
| EVM0001438 | 1.12  | 3.96  | -1.82 | 3.50E-04 | 2.36E-03 | -- | -- |
| EVM0008986 | 82.45 | 290.49| -1.82 | 5.00E-05 | 4.28E-04 | Intracellular trafficking, secretion, and vesicular transport | Endoplasmic reticulum vesicle transporter |
| EVM0008169 | 526.70| 1855.38| -1.82 | 5.00E-05 | 4.28E-04 | -- | Cornichon protein |
| EVM0005796 | 1292.18| 4545.87| -1.81 | 5.00E-05 | 4.28E-04 | Translation, ribosomal structure and biogenesis | 60s Acidic ribosomal protein |
| EVM0003262 | 24.81 | 87.23 | -1.81 | 5.00E-05 | 4.28E-04 | -- | Ribonuclease-III-like |
| EVM0011344 | 9.92  | 34.83 | -1.81 | 5.00E-05 | 4.28E-04 | RNA processing and modification | Mpp10 protein |
| EVM0004028 | 64.29 | 225.73| -1.81 | 5.00E-05 | 4.28E-04 | Cell cycle control, cell division, chromosome partitioning | -- |
| EVM0002694 | 3.97  | 13.92 | -1.81 | 5.00E-05 | 4.28E-04 | -- | DNA polymerase subunit Cdc27 |
| ID            | Value1 | Value2 | Value3 | Value4 | Value5 | Value6 | Description                                                                 |
|--------------|--------|--------|--------|--------|--------|--------|----------------------------------------------------------------------------|
| EVM0002056   | 120.50 | 422.21 | -1.81  | 5.00E-05 | 4.28E-04 | --     | --                                                                          |
| EVM0006056   | 1.03   | 3.62   | -1.81  | 2.25E-03 | 1.12E-02 | --     | --                                                                          |
| EVM0009797   | 3.98   | 13.95  | -1.81  | 5.00E-05 | 4.28E-04 | --     | Pheromone A receptor                                                      |
| EVM0006681   | 75.34  | 263.64 | -1.81  | 5.00E-05 | 4.28E-04 | --     | --                                                                          |
| EVM0002551   | 15.15  | 53.00  | -1.81  | 5.00E-05 | 4.28E-04 | Translation, ribosomal structure and biogenesis Nop14-like family           |
| EVM0006915   | 21.29  | 74.44  | -1.81  | 5.00E-05 | 4.28E-04 | --     | Velvet factor                                                              |
| EVM0003543   | 58.24  | 203.55 | -1.81  | 5.00E-05 | 4.28E-04 | --     | --                                                                          |
| EVM0000373   | 2.09   | 7.31   | -1.80  | 2.50E-04 | 1.77E-03 | --     | Terpene synthase family, metal binding domain                              |
| EVM0006805   | 107.23 | 374.56 | -1.80  | 5.00E-05 | 4.28E-04 | Lipid transport and metabolism | Alpha/beta hydrolase family                                               |
| EVM0010513   | 5.00   | 17.47  | -1.80  | 5.00E-05 | 4.28E-04 | General function prediction only | Fumarylacetoacetate (FAA) hydrolase family                                |
| EVM0003306   | 48.58  | 169.53 | -1.80  | 5.00E-05 | 4.28E-04 | Intracellular trafficking, secretion, and vesicular transport | Sfn7                                                                  |
| EVM0005649   | 123.43 | 430.64 | -1.80  | 5.00E-05 | 4.28E-04 | Transcription | Basic region leucine zipper                                                 |
| EVM0001778 | 110.15 | 383.48 | -1.80 | 5.00E-05 | 4.28E-04 | Coenzyme transport and metabolism | Pyridoxamine 5'-phosphate oxidase |
| EVM0008213 | 798.91 | 2780.10 | -1.80 | 5.00E-05 | 4.28E-04 | RNA processing and modification | LSM domain |
| EVM0003608 | 20.67 | 71.91 | -1.80 | 5.00E-05 | 4.28E-04 | -- | -- |
| EVM0007386 | 6.61 | 23.00 | -1.80 | 5.00E-05 | 4.28E-04 | -- | -- |
| EVM0006092 | 107.53 | 372.98 | -1.79 | 5.00E-05 | 4.28E-04 | -- | Complex1_LYR-like |
| EVM0005696 | 1.27 | 4.39 | -1.79 | 1.70E-03 | 8.87E-03 | -- | -- |
| EVM0007682 | 38.28 | 132.45 | -1.79 | 1.50E-04 | 1.14E-03 | -- | -- |
| EVM0010005 | 18.40 | 63.67 | -1.79 | 5.00E-05 | 4.28E-04 | -- | PIG-X / PBN1 |
| EVM0004809 | 39.76 | 137.53 | -1.79 | 5.00E-05 | 4.28E-04 | Posttranslational modification, protein turnover, chaperones | Myb-like DNA-binding domain |
| EVM0009109 | 30.09 | 104.04 | -1.79 | 5.00E-05 | 4.28E-04 | -- | Glycosyl hydrolases family 43 |
| EVM0004647 | 2.20 | 7.59 | -1.79 | 5.00E-04 | 3.19E-03 | -- | -- |
| EVM0011608 | 717.36 | 2478.86 | -1.79 | 5.00E-05 | 4.28E-04 | Translation, ribosomal structure and biogenesis | Ribosomal protein L24e |
| EVM ID       | Value 1  | Value 2  | Log2 Fold | Description                                      | Functional Category                                      |
|-------------|----------|----------|-----------|--------------------------------------------------|----------------------------------------------------------|
| EVM0006565  | 142.82   | 493.51   | -1.79     | 5.00E-05  4.28E-04 Lipid transport and metabolism  | Enoyl-CoA hydratase/isomerase family                     |
| EVM0002572  | 56.62    | 195.39   | -1.79     | 5.00E-05  4.28E-04 Transcription                 | Transcriptional Coactivator p15 (PC4)                   |
| EVM0001039  | 22.13    | 76.35    | -1.79     | 8.50E-04  4.98E-03 Transcription                 | --                                                      |
| EVM0010070  | 119.60   | 412.28   | -1.79     | 5.00E-05  4.28E-04 Transcription                 | --                                                      |
| EVM0003725  | 46.71    | 160.99   | -1.79     | 5.00E-05  4.28E-04 Transcription                 | --                                                      |
| EVM0003892  | 19.57    | 67.38    | -1.78     | 5.00E-05  4.28E-04 Transcription                 | --                                                      |
| EVM000705   | 450.72   | 1551.46  | -1.78     | 5.00E-05  4.28E-04 Inorganic ion transport and metabolism  | Iron/manganese superoxide dismutases, C-terminal domain |
| EVM005583   | 16.56    | 56.97    | -1.78     | 5.00E-05  4.28E-04 Transcription                 | --                                                      |
| EVM0010427  | 14.67    | 50.46    | -1.78     | 5.00E-05  4.28E-04 Transcription                 | --                                                      |
| EVM008404   | 11.35    | 39.03    | -1.78     | 5.00E-05  4.28E-04 RNA processing and modification | BING4CT (NUC141) domain                                 |
| EVM009718   | 3.24     | 11.15    | -1.78     | 5.00E-05  4.28E-04 Transcription                 | --                                                      |
| EVM0012166  | 7.91     | 27.18    | -1.78     | 5.00E-05  4.28E-04 Transcription                 | Glyoxal oxidase N-terminus                            |
| EVM0009437 | 50.74 | 174.36 | -1.78 | 5.00E-05 | 4.28E-04 | Posttranslational modification, protein turnover, chaperones | Hsp90 protein |
| EVM0006678 | 26.13 | 89.80 | -1.78 | 5.00E-05 | 4.28E-04 | Intracellular trafficking, secretion, and vesicular transport | SNARE-complex protein Syntaxin-18 N-terminus |
| EVM0008917 | 21.10 | 72.47 | -1.78 | 5.00E-05 | 4.28E-04 | General function prediction only | Fcf1 |
| EVM0004439 | 39.84 | 136.78 | -1.78 | 5.00E-05 | 4.28E-04 | General function prediction only | RNA cap guanine-N2 methyltransferase |
| EVM0005042 | 64.49 | 221.35 | -1.78 | 5.00E-05 | 4.28E-04 | Posttranslational modification, protein turnover, chaperones | Subtilase family |
| EVM0011505 | 0.40 | 1.35 | -1.78 | 1.07E-02 | 3.95E-02 | -- | Cytochrome P450 |
| EVM0010235 | 1.38 | 4.71 | -1.77 | 5.00E-05 | 4.28E-04 | -- | -- |
| EVM0006433 | 0.81 | 2.77 | -1.77 | 2.50E-03 | 1.22E-02 | Carbohydrate transport and metabolism | Major intrinsic protein |
| EVM0001527 | 5.48 | 18.73 | -1.77 | 8.25E-03 | 3.21E-02 | -- | -- |
| EVM0012122 | 8.78 | 30.00 | -1.77 | 5.00E-05 | 4.28E-04 | -- | -- |
| EVM0005631 | 0.97 | 3.30 | -1.77 | 2.15E-03 | 1.08E-02 | -- | Domain of unknown function (DUF3415) |
| EVM0004988  | 3.41 | 11.65 | -1.77 | 1.50E-04 | 1.14E-03 | -- | -- |
| EVM0005087  | 91.19 | 311.07 | -1.77 | 5.00E-05 | 4.28E-04 | Intracellular trafficking, secretion, and vesicular transport | Tim17/Tim22/Tim23/Pmp24 family |
| EVM0011674  | 100.12 | 341.51 | -1.77 | 6.50E-04 | 3.98E-03 | -- | -- |
| EVM0002805  | 117.02 | 398.44 | -1.77 | 5.00E-05 | 4.28E-04 | Intracellular trafficking, secretion, and vesicular transport | Translocation protein Sec62 |
| EVM0001552  | 12.27 | 41.72 | -1.77 | 5.00E-05 | 4.28E-04 | #N/A | #N/A |
| EVM0010587  | 60.18 | 204.48 | -1.76 | 5.00E-05 | 4.28E-04 | -- | Cupin |
| EVM0004999  | 3.32 | 11.29 | -1.76 | 5.00E-05 | 4.28E-04 | Secondary metabolites biosynthesis, transport and catabolism | short chain dehydrogenase |
| EVM0006976  | 13.03 | 44.26 | -1.76 | 5.00E-05 | 4.28E-04 | Inorganic ion transport and metabolism | Regulator of volume decrease after cellular swelling |
| EVM0001956  | 46.58 | 158.16 | -1.76 | 5.00E-05 | 4.28E-04 | -- | Gti1/Pac2 family |
| EVM0009386  | 8.19 | 27.81 | -1.76 | 7.50E-04 | 4.49E-03 | -- | Phosphotransferase enzyme family |
| EVM0006067  | 344.09 | 1166.27 | -1.76 | 5.00E-05 | 4.28E-04 | Posttranslational modification, protein turnover, chaperones | Calreticulin family |
| Gene ID       | Score1 | Score2 | Score3 | Score4 | Function Description                                      | Domain/Function                                      |
|--------------|--------|--------|--------|--------|-----------------------------------------------------------|-------------------------------------------------------|
| EVM0007576   | 19.25  | 65.21  | -1.76  | 5.00E-05 | 4.28E-04 Transcription                                    | NLI interacting factor-like phosphatase               |
| EVM0009577   | 17.05  | 57.76  | -1.76  | 5.00E-05 | 4.28E-04 General function prediction only                | GTP1/OBG                                             |
| EVM0010421   | 19.62  | 66.44  | -1.76  | 5.00E-05 | 4.28E-04 Function unknown                                | MBOAT, membrane-bound O-acyltransferase family        |
| EVM0005227   | 39.94  | 135.16 | -1.76  | 5.00E-05 | 4.28E-04 Function unknown                                | Bromodomain                                          |
| EVM0008951   | 24.36  | 82.19  | -1.75  | 5.00E-05 | 4.28E-04 Intracellular trafficking, secretion, and vesicular transport | Tetratricopeptide repeat                              |
| EVM0010581   | 51.04  | 172.17 | -1.75  | 5.00E-05 | 4.28E-04 --                                              | --                                                    |
| EVM0011734   | 2.25   | 7.59   | -1.75  | 5.00E-05 | 4.28E-04 --                                              | --                                                    |
| EVM0010645   | 8.74   | 29.48  | -1.75  | 5.00E-05 | 4.28E-04 Cytoskeleton                                    | Splicing factor, Prp19-binding domain                 |
| EVM0000041   | 1.24   | 4.18   | -1.75  | 5.00E-05 | 4.28E-04 #N/A                                            | #N/A                                                  |
| EVM0005323   | 6.86   | 23.13  | -1.75  | 5.00E-05 | 4.28E-04 --                                              | --                                                    |
| EVM0004358   | 195.63 | 658.94 | -1.75  | 5.00E-05 | 4.28E-04 --                                              | Heat shock factor binding protein 1                  |
| EVM0010862   | 89.85  | 302.39 | -1.75  | 5.00E-05 | 4.28E-04 Translation, ribosomal structure and biogenesis | Ribosomal protein L24e                               |
| EVM0009691 | 22.42 | 75.39 | -1.75 | 5.00E-05 | 4.28E-04 | Carbohydrate transport and metabolism | pfkB family carbohydrate kinase |
| EVM0007258 | 1.60  | 5.37  | -1.75 | 1.55E-03 | 8.22E-03 | --                                    | --                             |
| EVM0010575 | 14.56 | 48.88 | -1.75 | 5.00E-05 | 4.28E-04 | --                                    | --                             |
| EVM0009512 | 21.62 | 72.49 | -1.75 | 5.00E-05 | 4.28E-04 | Lipid transport and metabolism        | CoA-transferase family III     |
| EVM0001725 | 9.80  | 32.87 | -1.75 | 5.00E-05 | 4.28E-04 | RNA processing and modification       | AAA domain                     |
| EVM0009732 | 10.68 | 35.72 | -1.74 | 5.00E-05 | 4.28E-04 | --                                    | --                             |
| EVM0000344 | 146.36| 489.47| -1.74 | 5.00E-05 | 4.28E-04 | --                                    | SAM domain (Sterile alpha motif) |
| EVM0005236 | 327.58| 1092.18| -1.74 | 5.00E-05 | 4.28E-04 | RNA processing and modification       | LSM domain                     |
| EVM0000915 | 33.14 | 110.24| -1.73 | 5.00E-05 | 4.28E-04 | Translation, ribosomal structure and biogenesis | Ribosomal protein S5, C-terminal domain |
| EVM0003129 | 2.58  | 8.56  | -1.73 | 5.00E-05 | 4.28E-04 | --                                    | --                             |
| EVM0002127 | 36.60 | 121.66| -1.73 | 5.00E-05 | 4.28E-04 | RNA processing and modification       | RNA recognition motif. (a.k.a. RRM, RBD, or RNP domain) |
| EVM0000557 | 20.43 | 67.81 | -1.73 | 5.00E-05 | 4.28E-04 | --                                    | --                             |
| EVM0011852 | 46.96 | 155.72| -1.73 | 5.00E-05 | 4.28E-04 | --                                    | --                             |
| EVM0009023 | 10.77 | 35.70 | -1.73 | 5.00E-05 | 4.28E-04 | RNA processing and modification | Brix domain |
| EVM0009303 | 1.33  | 4.42  | -1.73 | 5.00E-04 | 3.19E-03 | -- | -- |
| EVM0010661 | 28.64 | 94.85 | -1.73 | 5.00E-05 | 4.28E-04 | Nucleotide transport and metabolism | AAA domain |
| EVM0001827 | 3.41  | 11.29 | -1.73 | 5.00E-05 | 4.28E-04 | Replication, recombination and repair | Helicase conserved C-terminal domain |
| EVM0005216 | 46.06 | 152.40| -1.73 | 5.00E-05 | 4.28E-04 | -- | Whi5 like |
| EVM0003691 | 144.98| 479.42| -1.73 | 5.00E-05 | 4.28E-04 | Translation, ribosomal structure and biogenesis | Ribosomal protein L4/L1 family |
| EVM0007146 | 14.37 | 47.50 | -1.73 | 5.00E-05 | 4.28E-04 | -- | -- |
| EVM0006271 | 41.40 | 136.85| -1.72 | 5.00E-05 | 4.28E-04 | -- | -- |
| EVM0002912 | 152.57| 503.86| -1.72 | 5.00E-05 | 4.28E-04 | Function unknown | Telomere stability and silencing |
| EVM0010805 | 46.70 | 154.13| -1.72 | 5.00E-05 | 4.28E-04 | General function prediction only | GMC oxidoreductase |
| EVM0010622 | 12.22 | 40.32 | -1.72 | 5.00E-05 | 4.28E-04 | -- | -- |
| EVM0003327 | 83.77 | 276.10| -1.72 | 5.00E-05 | 4.28E-04 | -- | Mitosis protein DIM1 |
| EVM0010288 | 59.08 | 194.66| -1.72 | 5.00E-05 | 4.28E-04 | Inorganic ion transport and metabolism | Cation efflux family |
| EVM0007930   | 8.61 | 28.34 | -1.72 | 5.00E-05  | 4.28E-04  | RNA recognition motif (a.k.a. RRM, RBD, or RNP domain) |
| EVM0010300   | 1.05 | 3.47  | -1.72 | 3.00E-04  | 2.07E-03  | F-box-like                                             |
| EVM0004340   | 276.58 | 909.70 | -1.72 | 5.00E-05  | 4.28E-04  | Thioesterase superfamily                              |
| EVM0002613   | 202.01 | 664.20 | -1.72 | 5.00E-05  | 4.28E-04  | General function prediction only                      |
| EVM0002613   |      |       |       |           |           | RNA recognition motif. (a.k.a. RRM, RBD, or RNP domain) |
| EVM0012007   | 21.95 | 72.15 | -1.72 | 5.00E-05  | 4.28E-04  | Transcription                                          |
| EVM0012262   | 9.14 | 30.04 | -1.72 | 5.00E-05  | 4.28E-04  | SHS2 domain found in N terminus of Rpb7p/Rpc25p/MJ0397 |
| EVM0004872   | 137.22 | 450.71 | -1.72 | 5.00E-05  | 4.28E-04  | Lipid transport and metabolism                        |
| EVM0010113   | 61.21 | 201.03 | -1.72 | 5.00E-05  | 4.28E-04  | AMP-binding enzyme                                    |
| EVM0000628   | 34.15 | 112.13 | -1.72 | 5.00E-05  | 4.28E-04  | Intracellular trafficking, secretion, and vesicular transport |
| EVM0002542   | 138.25 | 453.78 | -1.71 | 5.00E-05  | 4.28E-04  | Regulated-SNARE-like domain                           |
| EVM0006293 | 0.34 | 1.12 | -1.71 | 2.80E-03 | 1.34E-02 | -- | -- |
|----------|------|------|--------|----------|----------|----|----|
| EVM0007861 | 83.01 | 271.56 | -1.71 | 5.00E-05 | 4.28E-04 | -- | Protein of unknown function (DUF1183) |
| EVM0002177 | 15.96 | 52.22 | -1.71 | 5.00E-05 | 4.28E-04 | General function prediction | short chain dehydrogenase |
| EVM0002681 | 10.79 | 35.29 | -1.71 | 5.00E-05 | 4.28E-04 | General function prediction | Glycosyl transferase family 90 |
| EVM0007376 | 1.65 | 5.38 | -1.71 | 7.00E-04 | 4.23E-03 | -- | -- |
| EVM000930 | 1.90 | 6.20 | -1.71 | 5.00E-04 | 3.19E-03 | -- | -- |
| EVM004456 | 0.63 | 2.07 | -1.71 | 7.40E-03 | 2.94E-02 | Secondary metabolites biosynthesis, transport and catabolism | Alcohol dehydrogenase GroES-like domain |
| EVM0010163 | 3.79 | 12.37 | -1.71 | 5.00E-05 | 4.28E-04 | -- | F-box-like |
| EVM000220 | 21.49 | 70.03 | -1.70 | 4.00E-04 | 2.65E-03 | Carbohydrate transport and metabolism | UAA transporter family |
| EVM0012120 | 63.21 | 205.96 | -1.70 | 5.00E-05 | 4.28E-04 | Lipid transport and metabolism | 3-hydroxyacyl-CoA dehydrogenase, NAD binding domain |
| EVM009858 | 27.87 | 90.71 | -1.70 | 5.00E-05 | 4.28E-04 | Translation, ribosomal structure and biogenesis | CPL (NUC119) domain |
| EVM00313 | 15.01 | 48.76 | -1.70 | 5.00E-05 | 4.28E-04 | Translation, ribosomal structure and biogenesis | RF-1 domain |
| EVM          | Value 1 | Value 2 | Value 3 | Value 4 | Value 5 | Function                                                                 | Protein Name                                      |
|--------------|---------|---------|---------|---------|---------|---------------------------------------------------------------------------|---------------------------------------------------|
| EVM0005152   | 10.92   | 35.49   | -1.70   | 5.00E-05| 4.28E-04| --                                                                         | --                                                |
| EVM0009684   | 76.49   | 248.47  | -1.70   | 5.00E-05| 4.28E-04| Translation, ribosomal structure and biogenesis                           | Mitochondrial ribosomal protein L28               |
| EVM0002623   | 8.06    | 26.15   | -1.70   | 5.00E-05| 4.28E-04| --                                                                         | WD domain, G-beta repeat                          |
| EVM0003701   | 33.54   | 108.81  | -1.70   | 5.00E-05| 4.28E-04| Lipid transport and metabolism                                            | Histidine phosphatase superfamily (branch 2)      |
| EVM0007965   | 20.60   | 66.75   | -1.70   | 5.00E-05| 4.28E-04| Energy production and conversion                                          | Mitochondrial carrier protein                     |
| EVM0002509   | 140.94  | 456.48  | -1.70   | 5.00E-05| 4.28E-04| --                                                                         | --                                                |
| EVM0011693   | 3.46    | 11.21   | -1.69   | 5.00E-05| 4.28E-04| --                                                                         | F-box-like                                        |
| EVM0001809   | 81.04   | 261.96  | -1.69   | 5.00E-05| 4.28E-04| --                                                                         | --                                                |
| EVM0007602   | 5.84    | 18.86   | -1.69   | 5.00E-05| 4.28E-04| Lipid transport and metabolism                                            | PLD-like domain                                   |
| EVM0000907   | 1.60    | 5.17    | -1.69   | 4.00E-04| 2.65E-03| --                                                                         | --                                                |
| EVM0011950   | 418.92  | 1347.21 | -1.69   | 5.00E-05| 4.28E-04| Posttranslational modification, protein turnover, chaperones             | CS domain                                         |
| EVM0008064   | 10.34   | 33.26   | -1.69   | 5.00E-05| 4.28E-04| --                                                                         | Shugoshin C terminus                              |
| EVM0001772 | 171.87 | 552.27 | -1.68 | 5.00E-05 | 4.28E-04 | Translation, ribosomal structure and biogenesis | Ribosomal protein L36 |
| EVM0001304 | 30.64  | 98.30  | -1.68 | 5.00E-05 | 4.28E-04 | Transcription | RNA recognition motif (a.k.a. RRM, RBD, or RNP domain) |
| EVM0003462 | 119.94 | 384.32 | -1.68 | 5.00E-05 | 4.28E-04 | Intracellular trafficking, secretion, and vesicular transport | Eukaryotic porin |
| EVM0001935 | 16.53  | 52.97  | -1.68 | 5.00E-05 | 4.28E-04 | -- | Myosin-like coiled-coil protein |
| EVM0003796 | 5.54   | 17.73  | -1.68 | 5.00E-05 | 4.28E-04 | -- | -- |
| EVM0001752 | 1.93   | 6.17   | -1.68 | 2.50E-04 | 1.77E-03 | -- | -- |
| EVM0011785 | 4.52   | 14.45  | -1.68 | 5.00E-05 | 4.28E-04 | -- | Fungal specific transcription factor domain |
| EVM0001766 | 120.57 | 385.02 | -1.68 | 5.00E-05 | 4.28E-04 | Intracellular trafficking, secretion, and vesicular transport | Signal recognition particle receptor beta subunit |
| EVM0009519 | 121.85 | 389.03 | -1.67 | 5.00E-05 | 4.28E-04 | Transcription | RNA polymerase Rpb3/Rpb11 dimerisation domain |
| EVM0009755 | 83.90  | 267.71 | -1.67 | 5.00E-05 | 4.28E-04 | Secondary metabolites biosynthesis, transport and catabolism | Cytochrome P450 |
| EVM0004049 | 0.80   | 2.56   | -1.67 | 1.90E-03 | 9.73E-03 | General function prediction only | GMC oxidoreductase |
| EVM0004637 | 230.19 | 731.96 | -1.67 | 5.00E-05 | 4.28E-04 | -- | -- |
| EVM0007361 | 19.72 | 62.71 | -1.67 | 5.00E-05 | 4.28E-04 | RNA processing and modification | DEAD/DEAH box helicase |
| EVM000804 | 92.88 | 295.06 | -1.67 | 5.00E-05 | 4.28E-04 | Lipid transport and metabolism | Acyl-CoA dehydrogenase, C-terminal domain |
| EVM0005225 | 14.60 | 46.36 | -1.67 | 5.00E-05 | 4.28E-04 | -- | Gt1/Pac2 family |
| EVM0007358 | 8.84 | 28.05 | -1.67 | 5.00E-05 | 4.28E-04 | -- | -- |
| EVM0005754 | 4.58 | 14.48 | -1.66 | 2.00E-03 | 1.01E-02 | -- | -- |
| EVM0006354 | 37.98 | 120.09 | -1.66 | 5.00E-05 | 4.28E-04 | RNA processing and modification | RNA recognition motif. (a.k.a. RRM, RBD, or RNP domain) |
| EVM0012020 | 0.94 | 2.96 | -1.66 | 6.85E-03 | 2.77E-02 | -- | -- |
| EVM0009845 | 12.95 | 40.87 | -1.66 | 5.00E-05 | 4.28E-04 | -- | -- |
| EVM0004898 | 137.88 | 435.01 | -1.66 | 5.00E-05 | 4.28E-04 | Function unknown | Uncharacterized protein family UPF0016 |
| EVM0007328 | 1407.82 | 4431.20 | -1.65 | 5.00E-05 | 4.28E-04 | Translation, ribosomal structure and biogenesis | 60s Acidic ribosomal protein |
| EVM0010682 | 84.22 | 264.90 | -1.65 | 1.50E-04 | 1.14E-03 | -- | Mitochondrial ribosomal protein L27 |
| EVM0000447 | 27.97 | 87.96 | -1.65 | 5.00E-05 | 4.28E-04 | -- | -- |
| EVM0006974 | 1.33 | 4.17 | -1.65 | 2.90E-03 | 1.38E-02 | -- | -- |
| EVM0011509 | 54.64 | 171.68 | -1.65 | 5.00E-05 | 4.28E-04 | -- | -- |
| EVM0000165 | 46.51 | 145.88 | -1.65 | 5.00E-05 | 4.28E-04 | Cell cycle control, cell division, chromosome partitioning | Cyclin, N-terminal domain |
| EVM0005711 | 93.24 | 292.45 | -1.65 | 5.00E-05 | 4.28E-04 | Function unknown | Yip1 domain |
| EVM0010704 | 42.31 | 132.66 | -1.65 | 5.00E-05 | 4.28E-04 | Posttranslational modification, protein turnover, chaperones | -- |
| EVM0008220 | 23.33 | 73.16 | -1.65 | 5.00E-05 | 4.28E-04 | Function unknown | Protein of unknown function (DUF1168) |
| EVM0006845 | 10.33 | 32.38 | -1.65 | 5.00E-05 | 4.28E-04 | -- | SNF5 / SMARCB1 / INI1 |
| EVM0004215 | 488.38 | 1530.46 | -1.65 | 5.00E-05 | 4.28E-04 | Energy production and conversion | Cytochrome c oxidase subunit Va |
| EVM0003574 | 38.63 | 121.03 | -1.65 | 5.00E-05 | 4.28E-04 | General function prediction only | PCI domain |
| EVM0010389 | 57.02 | 178.60 | -1.65 | 1.00E-04 | 7.96E-04 | Intracellular trafficking, secretion, and vesicular transport | Tim10/DDP family zinc finger |
| EVM0009757 | 125.51 | 392.95 | -1.65 | 5.00E-05 | 4.28E-04 | -- | -- |
| EVM0001548 | 827.17 | 2588.51 | -1.65 | 5.00E-05 | 4.28E-04 | Translation, ribosomal structure and biogenesis | Ribosomal protein S19e |
| EVM0005344 | 5.42   | 16.94   | -1.64 | 5.00E-05 | 4.28E-04 | -- | Glycosyl hydrolases family 28 |
| EVM0007176 | 33.04  | 103.14  | -1.64 | 5.00E-05 | 4.28E-04 | Energy production and conversion | D-isomer specific 2-hydroxyacid dehydrogenase, NAD binding domain |
| EVM0010758 | 18.86  | 58.89   | -1.64 | 5.00E-05 | 4.28E-04 | RNA processing and modification | RNA 3'-terminal phosphate cyclase |
| EVM0009680 | 135.46 | 422.52  | -1.64 | 5.00E-05 | 4.28E-04 | Translation, ribosomal structure and biogenesis | Ribosomal protein L16p/L10e |
| EVM0006626 | 65.78  | 205.11  | -1.64 | 5.00E-05 | 4.28E-04 | -- | -- |
| EVM0005217 | 86.05  | 268.10  | -1.64 | 5.00E-05 | 4.28E-04 | -- | Glycosyl hydrolases family 16 |
| EVM0007719 | 1.61   | 5.02    | -1.64 | 8.50E-04 | 4.98E-03 | -- | -- |
| EVM0004245 | 13.63  | 42.43   | -1.64 | 5.00E-05 | 4.28E-04 | Carbohydrate transport and metabolism | Glycosyl transferase family 4 |
| EVM0007803 | 4.82   | 14.94   | -1.63 | 2.00E-04 | 1.46E-03 | -- | -- |
| EVM0001630 | 20.79  | 64.52   | -1.63 | 5.00E-05 | 4.28E-04 | Replication, recombination and repair | ESCO1/2 acetyl-transferase |
| EVM0005888 | 233.16 | 723.37  | -1.63 | 5.00E-05 | 4.28E-04 | Energy production and conversion | Cytochrome C1 family |
| Accession   | Value1  | Value2  | Value3   | Value4   | Description                                                                 |
|-------------|---------|---------|----------|----------|----------------------------------------------------------------------------|
| EVM0005500  | 13.73   | 42.56   | -1.63    | 5.00E-05 | 4.28E-04 Function unknown                                                   |
|             |         |         |          |          | XAP5, circadian clock regulator                                            |
| EVM0007772  | 28.67   | 88.79   | -1.63    | 5.00E-05 | 4.28E-04 --                                                                  |
|             |         |         |          |          | Thioredoxin                                                                |
| EVM0002324  | 15.06   | 46.64   | -1.63    | 5.00E-05 | 4.28E-04 Lipid transport and metabolism                                      |
|             |         |         |          |          | Cytochrome b5-like Heme/Steroid binding domain                              |
| EVM0007428  | 4.51    | 13.98   | -1.63    | 5.00E-05 | 4.28E-04 --                                                                  |
|             |         |         |          |          | --                                                                          |
| EVM0010106  | 40.49   | 125.22  | -1.63    | 5.00E-05 | 4.28E-04 Cell cycle control, cell division, chromosome partitioning        |
|             |         |         |          |          | Maf-like protein                                                            |
| EVM0006403  | 132.04  | 408.31  | -1.63    | 5.00E-05 | 4.28E-04 Inorganic ion transport and metabolism                            |
|             |         |         |          |          | Anion-transporting ATPase                                                   |
| EVM0001435  | 68.91   | 212.91  | -1.63    | 5.00E-05 | 4.28E-04 --                                                                  |
|             |         |         |          |          | Mycolic acid cyclopropane synthetase                                        |
| EVM0003224  | 67.85   | 209.58  | -1.63    | 5.00E-05 | 4.28E-04 General function prediction only                                   |
|             |         |         |          |          | Phosphatidylethanolamine-binding protein                                    |
| EVM0001103  | 4.16    | 12.83   | -1.63    | 1.00E-04 | 7.96E-04 --                                                                  |
|             |         |         |          |          | Glycosyl hydrolases family 16                                               |
| EVM0004815  | 50.52   | 155.66  | -1.62    | 5.00E-05 | 4.28E-04 RNA processing and modification                                   |
|             |         |         |          |          | LSM domain                                                                  |
| EVM0007696  | 7.57    | 23.32   | -1.62    | 5.00E-05 | 4.28E-04 --                                                                  |
|             |         |         |          |          | Domain of unknown function (DUF4139)                                        |
| EVM0002263  | 1.93    | 5.94    | -1.62    | 2.50E-04 | 1.77E-03 --                                                                  |
|             |         |         |          |          | --                                                                          |
| EVM0007331 | 4.19  | 12.89  | -1.62 | 5.00E-05 | 4.28E-04 | -- | -- |
|------------|-------|--------|-------|----------|---------|----|----|
| EVM0003839 | 537.50| 1654.23| -1.62 | 5.00E-05 | 4.28E-04 | Translation, ribosomal structure and biogenesis | Ribosomal S13/S15 N-terminal domain |
| EVM0011083 | 14.73 | 45.31  | -1.62 | 5.00E-05 | 4.28E-04 | -- | -- |
| EVM0000240 | 10.98 | 33.76  | -1.62 | 5.00E-05 | 4.28E-04 | Transcription | MED6 mediator sub complex component |
| EVM0004659 | 0.74  | 2.27   | -1.62 | 9.60E-03 | 3.63E-02 | -- | G protein-coupled glucose receptor regulating Gpa2 |
| EVM0010641 | 24.32 | 74.69  | -1.62 | 5.00E-05 | 4.28E-04 | Signal transduction mechanisms | ERG2 and Sigma1 receptor like protein |
| EVM0007720 | 53.76 | 165.13 | -1.62 | 5.00E-05 | 4.28E-04 | Posttranslational modification, protein turnover, chaperones | Glutathione S-transferase, N-terminal domain |
| EVM0009851 | 12.02 | 36.93  | -1.62 | 5.00E-05 | 4.28E-04 | Function unknown | WD domain, G-beta repeat |
| EVM0008230 | 24.18 | 74.24  | -1.62 | 5.00E-05 | 4.28E-04 | Transcription | Maf1 regulator |
| EVM0006946 | 9.90  | 30.38  | -1.62 | 5.00E-05 | 4.28E-04 | -- | -- |
| EVM0001624 | 5.44  | 16.67  | -1.62 | 1.15E-03 | 6.41E-03 | -- | -- |
| EVM0010207 | 157.23| 482.14 | -1.62 | 5.00E-05 | 4.28E-04 | Intracellular trafficking, secretion, and vesicular transport | emp24/gp25L/p24 family/GOLD |
| EVM0011300 | 2.84 | 8.69 | -1.62 | 3.00E-04 | 2.07E-03 | -- | -- |
| EVM0003532 | 31.68 | 97.00 | -1.61 | 5.00E-05 | 4.28E-04 | General function prediction only | Arrestin (or S-antigen), C-terminal domain |
| EVM0007379 | 32.01 | 97.94 | -1.61 | 5.00E-05 | 4.28E-04 | -- | -- |
| EVM0000717 | 2.75 | 8.41 | -1.61 | 2.00E-04 | 1.46E-03 | -- | TEA/ATTS domain family |
| EVM0003992 | 17.66 | 53.99 | -1.61 | 5.00E-05 | 4.28E-04 | -- | -- |
| EVM0002603 | 0.55 | 1.68 | -1.61 | 1.40E-03 | 7.55E-03 | -- | -- |
| EVM0010657 | 553.41 | 1689.22 | -1.61 | 4.00E-04 | 2.65E-03 | Posttranslational modification, protein turnover, chaperones | Hsp70 protein |
| EVM0002218 | 106.71 | 325.66 | -1.61 | 5.00E-05 | 4.28E-04 | -- | -- |
| EVM0005403 | 15.88 | 48.46 | -1.61 | 5.00E-05 | 4.28E-04 | Translation, ribosomal structure and biogenesis | Elongation factor TS |
| EVM0002008 | 2.30 | 7.02 | -1.61 | 1.00E-04 | 7.96E-04 | -- | -- |
| EVM0003419 | 0.99 | 3.01 | -1.61 | 1.00E-04 | 7.96E-04 | -- | -- |
| EVM0007433 | 4.69 | 14.29 | -1.61 | 5.00E-05 | 4.28E-04 | -- | -- |
| Accession  | Score  | Freq | Log2F | Func/Type                                                                 | Description                                                                 |
|-----------|--------|------|-------|---------------------------------------------------------------------------|-----------------------------------------------------------------------------|
| EVM0006443 | 1.61   | 4.89 | -1.61 | General function prediction only                                         RNA recognition motif. (a.k.a. RRM, RBD, or RNP domain)                   |
| EVM0005885 | 159.00 | 484.05 | -1.61 | Intracellular trafficking, secretion, and vesicular transport             emp24/gp25L/p24 family/GOLD                                                  |
| EVM0003399 | 2.56   | 7.79 | -1.61 | --                                                                         --                                                                 |
| EVM0009247 | 83.67  | 254.56 | -1.61 | Transcription                                                             NLI interacting factor-like phosphatase                                      |
| EVM0001091 | 1.32   | 4.02 | -1.60 | --                                                                         Glycoside hydrolase family 44                                              |
| EVM0008532 | 108.90 | 330.67 | -1.60 | Translation, ribosomal structure and biogenesis                           Ribosomal L27 protein                                                      |
| EVM0001586 | 232.64 | 706.04 | -1.60 | Function unknown                                                          Eukaryotic family of unknown function (DUF1754)                            |
| EVM0005151 | 432.59 | 1312.82 | -1.60 | --                                                                         --                                                                 |
| EVM0009204 | 11.51  | 34.94 | -1.60 | RNA processing and modification                                           --                                                                     |
| EVM0001878 | 12.76  | 38.69 | -1.60 | --                                                                         --                                                                 |
| EVM0007904 | 1.47   | 4.46 | -1.60 | --                                                                         --                                                                 |
| EVM0004418 | 33.29  | 100.70 | -1.60 | --                                                                         --                                                                 |
| EVM0000820 | 42.52 | 128.52 | -1.60 | 5.00E-05 | 4.28E-04 | Posttranslational modification, protein turnover, chaperones | Ubiquitin-conjugating enzyme |
| EVM0010393 | 9.18  | 27.73  | -1.60 | 5.00E-05 | 4.28E-04 | -- | Lactonase, 7-bladed beta-propeller |
| EVM0000847 | 3.51  | 10.60  | -1.60 | 1.10E-03 | 6.17E-03 | -- | -- |
| EVM001632  | 37.05 | 111.93 | -1.60 | 5.00E-05 | 4.28E-04 | -- | -- |
| EVM005634  | 6.84  | 20.65  | -1.59 | 5.00E-05 | 4.28E-04 | -- | -- |
| EVM0011727 | 175.33| 529.11 | -1.59 | 5.00E-05 | 4.28E-04 | Posttranslational modification, protein turnover, chaperones | Ubiquitin-2 like Rad60 SUMO-like |
| EVM0011467 | 40.43 | 121.99 | -1.59 | 5.00E-05 | 4.28E-04 | Function unknown | YIF1 |
| EVM0007837 | 1756.10| 5291.10| -1.59 | 5.00E-05 | 4.28E-04 | Translation, ribosomal structure and biogenesis | Ribosomal protein S17 |
| EVM0005707 | 7.84  | 23.62  | -1.59 | 5.00E-05 | 4.28E-04 | -- | -- |
| EVM000539  | 52.57 | 158.22 | -1.59 | 5.00E-05 | 4.28E-04 | Function unknown | Zinc carboxypeptidase |
| EVM0005112 | 0.93  | 2.79   | -1.59 | 5.00E-04 | 3.19E-03 | Amino acid transport and metabolism | Peptidase family M20/M25/M40 |
| EVM0010727 | 27.14 | 81.60  | -1.59 | 5.00E-05 | 4.28E-04 | General function prediction only | Alpha/beta hydrolase family |
| EVM0000209 | 7.53 | 22.63 | -1.59 | 5.00E-05 | 4.28E-04 | Translation, ribosomal structure and biogenesis | KRI1-like family C-terminal |
| EVM0000653 | 42.40 | 127.30 | -1.59 | 5.00E-05 | 4.28E-04 | Function unknown | Domain of unknown function (DUF947) |
| EVM0006687 | 7.49 | 22.49 | -1.59 | 5.00E-05 | 4.28E-04 | -- | -- |
| EVM0009646 | 4.63 | 13.88 | -1.58 | 9.70E-03 | 3.66E-02 | -- | Pheromone A receptor |
| EVM0000044 | 297.23 | 890.64 | -1.58 | 5.00E-05 | 4.28E-04 | Intracellular trafficking, secretion, and vesicular transport | Tim10/DDP family zinc finger |
| EVM0011482 | 32.31 | 96.74 | -1.58 | 5.00E-05 | 4.28E-04 | Function unknown | WD domain, G-beta repeat |
| EVM0006207 | 8.37 | 25.05 | -1.58 | 1.00E-04 | 7.96E-04 | -- | -- |
| EVM0009735 | 199.24 | 595.94 | -1.58 | 5.00E-05 | 4.28E-04 | -- | Oxidoreductase FAD-binding domain |
| EVM0011042 | 107.56 | 321.64 | -1.58 | 5.00E-05 | 4.28E-04 | Signal transduction mechanisms | Inhibitor of apoptosis-promoting Bax1 |
| EVM0005109 | 2.85 | 8.53 | -1.58 | 1.00E-04 | 7.96E-04 | -- | -- |
| EVM0002381 | 58.63 | 175.31 | -1.58 | 5.00E-05 | 4.28E-04 | -- | Nucleoporin complex subunit 54 |
| EVM0000616 | 86.45 | 258.49 | -1.58 | 5.00E-05 | 4.28E-04 | -- | SNARE domain |
| EVM0008292 | 12.39 | 37.02 | -1.58 | 5.00E-05 | 4.28E-04 | Posttranslational modification, protein turnover, chaperones | IBR domain |
|------------|-------|-------|--------|----------|----------|---------------------------------------------------|-------------|
| EVM0011745 | 17.29 | 51.67 | -1.58 | 5.00E-05 | 4.28E-04 | Secondary metabolites biosynthesis, transport and catabolism | --          |
| EVM0006119 | 5.19  | 15.48 | -1.58 | 5.00E-05 | 4.28E-04 | --                                                | short chain dehydrogenase |
| EVM0011744 | 19.76 | 58.99 | -1.58 | 1.35E-02 | 4.74E-02 | Signal transduction mechanisms                     | TGS domain  |
| EVM0003303 | 302.61| 902.69| -1.58 | 5.00E-05 | 4.28E-04 | --                                                | --          |
| EVM0008367 | 1.73  | 5.16  | -1.58 | 2.50E-04 | 1.77E-03 | --                                                | Protein kinase domain |
| EVM0010051 | 4.77  | 14.23 | -1.58 | 5.00E-05 | 4.28E-04 | --                                                | Glycosyl hydrolase family 3 N terminal domain |
| EVM0000483 | 103.27| 307.65| -1.57 | 5.00E-05 | 4.28E-04 | Amino acid transport and metabolism                | Chorismate mutase type II |
| EVM0004156 | 0.74  | 2.20  | -1.57 | 5.00E-05 | 4.28E-04 | --                                                | --          |
| EVM0005014 | 8.10  | 24.13 | -1.57 | 5.00E-05 | 4.28E-04 | --                                                | --          |
| EVM0010922 | 161.05| 479.68| -1.57 | 5.00E-05 | 4.28E-04 | --                                                | Nitronate monooxygenase |
| EVM0005981 | 4.50  | 13.38 | -1.57 | 5.00E-05 | 4.28E-04 | --                                                | --          |
| EVM0007859 | 5.80 | 17.23 | -1.57 | 5.00E-05 | 4.28E-04 | -- | -- |
| EVM0010410 | 13.65 | 40.56 | -1.57 | 5.00E-05 | 4.28E-04 | Defense mechanisms | Isochorismatase family |
| EVM0003501 | 24.06 | 71.45 | -1.57 | 5.00E-05 | 4.28E-04 | -- | Flavin containing amine oxidoreductase |
| EVM0002323 | 1.01 | 2.99 | -1.57 | 1.25E-03 | 6.87E-03 | General function prediction | Sugar (and other) transporter only |
| EVM0005875 | 54.24 | 160.89 | -1.57 | 5.00E-05 | 4.28E-04 | -- | -- |
| EVM0002330 | 182.48 | 540.42 | -1.57 | 5.00E-05 | 4.28E-04 | -- | GGL domain |
| EVM0006072 | 4.78 | 14.15 | -1.57 | 4.25E-03 | 1.89E-02 | -- | -- |
| EVM0001178 | 27.67 | 81.84 | -1.56 | 5.00E-05 | 4.28E-04 | -- | -- |
| EVM000583 | 121.22 | 358.26 | -1.56 | 5.00E-05 | 4.28E-04 | Translation, ribosomal structure and biogenesis | Ribosomal protein L1p/L10e family |
| EVM0006475 | 24.09 | 71.18 | -1.56 | 5.00E-05 | 4.28E-04 | -- | AAA domain |
| EVM0001105 | 2.52 | 7.45 | -1.56 | 1.00E-04 | 7.96E-04 | Carbohydrate transport and metabolism | Glycosyl hydrolase family 47 |
| EVM0004611 | 4.30 | 12.68 | -1.56 | 1.00E-04 | 7.96E-04 | -- | Ferritin-like domain |
| EVM0011815 | 38.87 | 114.71 | -1.56 | 1.00E-04 | 7.96E-04 | -- | Membrane-associating domain |
| Accession      | Freq | Log2 Fold Change | Score 1 | Score 2 | Score 3 | Score 4 | Score 5 | Description                                                                 |
|---------------|------|-----------------|---------|---------|---------|---------|---------|-----------------------------------------------------------------------------|
| EVM0006494    | 15.29| -1.56           | 5.00E-05| 4.28E-04|         |         |         | Chromatin structure and dynamics                                            |
| EVM0008434    | 47.16| -1.56           | 5.00E-05| 4.28E-04|         |         |         | Sas10 C-terminal domain                                                     |
| EVM0008578    | 4.71 | -1.56           | 5.00E-05| 4.28E-04|         |         |         | Glycosyl hydrolase family 71                                               |
| EVM0009662    | 32.04| -1.56           | 5.00E-05| 4.28E-04|         |         |         | Cation efflux family                                                        |
| EVM000189     | 4.27 | -1.56           | 5.00E-05| 4.28E-04|         |         |         | Glycosyl hydrolases family 43                                               |
| EVM0011601    | 76.61| -1.56           | 5.00E-05| 4.28E-04|         |         |         | Glycosyl hydrolase family 43                                               |
| EVM0005496    | 345.96| -1.56          | 5.00E-05| 4.28E-04|         |         |         | Glycosyl hydrolase family 43                                               |
| EVM0010403    | 7.81 | -1.56           | 5.00E-05| 4.28E-04|         |         |         | Glycosyl hydrolase family 43                                               |
| EVM0002657    | 362.68| 1066.26         | 5.00E-05| 4.28E-04|         |         |         | General function prediction short chain dehydrogenase                       |
| EVM0009199    | 60.83| -1.55           | 5.00E-05| 4.28E-04|         |         |         | Signal transduction mechanisms                                              |
| EVM0004868    | 13.62| -1.55           | 5.00E-05| 4.28E-04|         |         |         | Protein phosphatase 2C                                                       |
| EVM0005966    | 20.45| -1.55           | 5.00E-05| 4.28E-04|         |         |         | F-box-like                                                                  |
| EVM0005966    | 20.45| -1.55           | 5.00E-05| 4.28E-04|         |         |         | PPR repeat family                                                           |
| EVM0004301 | 27.42 | 80.38 | -1.55 | 5.00E-05 | 4.28E-04 | Secondary metabolites biosynthesis, transport and catabolism | Pyridine nucleotide-disulphide oxidoreductase |
| EVM0001371 | 87.74 | 257.04 | -1.55 | 5.00E-05 | 4.28E-04 | -- | Mitochondrial ribosomal protein S25 |
| EVM0004111 | 72.45 | 212.12 | -1.55 | 5.00E-05 | 4.28E-04 | Signal transduction mechanisms | Glucosidase II beta subunit-like |
| EVM0004939 | 22.97 | 67.20 | -1.55 | 5.00E-05 | 4.28E-04 | RNA processing and modification | RNAse P Rpr2/Rpp21/SNM1 subunit domain |
| EVM0006461 | 6.25 | 18.29 | -1.55 | 1.00E-04 | 7.96E-04 | Lipid transport and metabolism | Acyltransferase |
| EVM0009944 | 6.66 | 19.45 | -1.55 | 5.00E-05 | 4.28E-04 | -- | -- |
| EVM0010781 | 114.60 | 334.44 | -1.55 | 5.00E-05 | 4.28E-04 | General function prediction only | Ribosomal protein S8e |
| EVM0006895 | 2.86 | 8.34 | -1.55 | 2.35E-03 | 1.16E-02 | -- | Protein of unknown function (DUF3129) |
| EVM0005306 | 41.70 | 121.68 | -1.54 | 5.00E-05 | 4.28E-04 | Cell wall/membrane/envelope biogenesis | Glycosyl transferases group 1 |
| EVM0006578 | 93.35 | 272.30 | -1.54 | 5.00E-05 | 4.28E-04 | Intracellular trafficking, secretion, and vesicular transport | Syntaxin |
| EVM0009689 | 118.71 | 346.16 | -1.54 | 5.00E-05 | 4.28E-04 | Translation, ribosomal structure and biogenesis | Ribosomal protein S17 |
| EVM0008363  | 43.74  | 127.52 | -1.54 | 5.00E-05 | 4.28E-04 | -- | -- |
|-------------|--------|--------|--------|----------|----------|----|----|
| EVM0005442  | 42.58  | 123.96 | -1.54 | 5.00E-05 | 4.28E-04 | General function prediction only | TPR repeat |
| EVM0003398  | 0.62   | 1.79   | -1.54 | 1.11E-02 | 4.07E-02 | Secondary metabolites biosynthesis, transport and catabolism | Cytochrome P450 |
| EVM0002287  | 38.57  | 111.94 | -1.54 | 1.90E-03 | 9.73E-03 | -- | Cytochrome P450 |
| EVM0006140  | 13.64  | 39.58  | -1.54 | 5.00E-05 | 4.28E-04 | -- | -- |
| EVM0011958  | 0.60   | 1.74   | -1.54 | 5.85E-02 | 2.44E-02 | -- | -- |
| EVM0011214  | 38.16  | 110.70 | -1.54 | 6.50E-04 | 3.98E-03 | Posttranslational modification, protein turnover, chaperones | Pex2 / Pex12 amino terminal region |
| EVM0005335  | 11.32  | 32.83  | -1.54 | 5.00E-05 | 4.28E-04 | -- | F-box-like |
| EVM0010591  | 27.21  | 78.91  | -1.54 | 5.00E-05 | 4.28E-04 | -- | -- |
| EVM0006349  | 8.70   | 25.24  | -1.54 | 5.00E-05 | 4.28E-04 | Replication, recombination and repair | Sas10/Utp3/C1D family |
| EVM0012035  | 113.44 | 328.86 | -1.54 | 5.00E-05 | 4.28E-04 | -- | Yqey-like protein |
| EVM0008977  | 2.01   | 5.83   | -1.53 | 2.15E-03 | 1.08E-02 | -- | -- |
| Gene ID     | Log2Fold | B | Functions                                      |
|-------------|----------|---|-----------------------------------------------|
| EVM0008651  | 93.46    | 270.68 | Inorganic ion transport and metabolism         |
| EVM0005247  | 38.72    | 112.13 | Function unknown                              |
| EVM0008198  | 38.19    | 110.46 | Transcription                                 |
| EVM0010777  | 39.56    | 114.34 | Energy production and conversion              |
| EVM0000792  | 36.01    | 104.00 | RNA processing and modification               |
| EVM0000533  | 84.73    | 244.61 | Translation, ribosomal structure and biogenesis|
| EVM0006914  | 5.04     | 14.55  | --                                            |
| EVM0001473  | 20.28    | 58.50  | Intracellular trafficking, secretion, and vesicular transport |
| EVM0006044  | 7.47     | 21.53  | --                                            |
| EVM0006170  | 7.57     | 21.81  | --                                            |
| EVM0000381  | 11.44    | 32.95  | Function unknown                              |
| EVM0006165  | 7.53     | 21.70  | --                                            |
| EVM0008279 | 2.60 | 7.47 | -1.53 | 6.15E-03 | 2.54E-02 | -- | -- |
| EVM0007413 | 38.63 | 111.17 | -1.53 | 5.00E-05 | 4.28E-04 | General function prediction only | Haloacid dehalogenase-like hydrolase |
| EVM0009740 | 60.61 | 174.29 | -1.52 | 5.00E-05 | 4.28E-04 | Function unknown | Uncharacterised protein family (UPF0203) |
| EVM0003055 | 116.10 | 333.77 | -1.52 | 5.00E-05 | 4.28E-04 | Function unknown | NUDIX domain |
| EVM0010179 | 121.57 | 349.47 | -1.52 | 5.00E-05 | 4.28E-04 | RNA processing and modification | Complex1_LYR-like |
| EVM0009477 | 9.72 | 27.92 | -1.52 | 5.00E-05 | 4.28E-04 | -- | F-box-like |
| EVM0012003 | 6.17 | 17.71 | -1.52 | 5.00E-05 | 4.28E-04 | -- | -- |
| EVM0001084 | 42.04 | 120.71 | -1.52 | 5.00E-05 | 4.28E-04 | -- | Uncharacterised conserved protein (DUF2315) |
| EVM0001335 | 10.05 | 28.83 | -1.52 | 5.00E-05 | 4.28E-04 | RNA processing and modification | Ribosomal L28e protein family |
| EVM0003278 | 1.46 | 4.19 | -1.52 | 1.27E-02 | 4.53E-02 | -- | -- |
| EVM0010557 | 4.86 | 13.92 | -1.52 | 5.00E-05 | 4.28E-04 | -- | Repair protein Rad1/Rec1/Rad17 |
| EVM0005814 | 19.63 | 56.15 | -1.52 | 5.00E-05 | 4.28E-04 | General function prediction only | MORN repeat |
| EVM0011177 | 19.53 | 55.81 | -1.51 | 5.00E-05 | 4.28E-04 | RNA processing and modification | Helicase associated domain (HA2) |
| Gene ID       | EVM0004661 | EVM0011442 | EVM0003096 | EVM0002273 | EVM0011802 | EVM0002693 | EVM0004912 | EVM0005134 | EVM0003487 | EVM0002011 | EVM0001937 | EVM0010312 |
|--------------|------------|------------|------------|------------|------------|------------|------------|------------|------------|------------|------------|------------|
| EVM0004661   | 5.29       | 5.00E-05   | 5.00E-05   | 5.00E-05   | 5.00E-05   | 5.00E-05   | 5.00E-05   | 5.00E-05   | 5.00E-05   | 5.00E-05   | 5.00E-05   | 5.00E-05   |
| EVM0011442   | 105.64     | 105.64     | 153.07     | 14.28      | 44.02      | 49.79      | 57.99      | 108.41     | 61.69      | 1.08       | 4.58       | 16.05      |
| EVM0003096   | 15.12      | 301.74     | 436.71     | 40.73      | 125.51     | 141.93     | 165.24     | 308.82     | 175.58     | 3.08       | 13.01      | 45.61      |
| EVM0002273   | -1.51      | -1.51      | -1.51      | -1.51      | -1.51      | -1.51      | -1.51      | -1.51      | -1.51      | -1.51      | -1.51      | -1.51      |
| EVM0011802   | 5.00E-05   | 5.00E-05   | 5.00E-05   | 5.00E-05   | 5.00E-05   | 5.00E-05   | 5.00E-05   | 5.00E-05   | 5.00E-05   | 5.00E-05   | 5.00E-05   | 5.00E-05   |
| EVM0002693   | -1.51      | -1.51      | -1.51      | -1.51      | -1.51      | -1.51      | -1.51      | -1.51      | -1.51      | -1.51      | -1.51      | -1.51      |
| EVM0004912   | 5.00E-05   | 5.00E-05   | 5.00E-05   | 5.00E-05   | 5.00E-05   | 5.00E-05   | 5.00E-05   | 5.00E-05   | 5.00E-05   | 5.00E-05   | 5.00E-05   | 5.00E-05   |
| EVM0005134   | 5.00E-05   | 5.00E-05   | 5.00E-05   | 5.00E-05   | 5.00E-05   | 5.00E-05   | 5.00E-05   | 5.00E-05   | 5.00E-05   | 5.00E-05   | 5.00E-05   | 5.00E-05   |
| EVM0003487   | 5.00E-05   | 5.00E-05   | 5.00E-05   | 5.00E-05   | 5.00E-05   | 5.00E-05   | 5.00E-05   | 5.00E-05   | 5.00E-05   | 5.00E-05   | 5.00E-05   | 5.00E-05   |
| EVM0002011   | 5.00E-05   | 5.00E-05   | 5.00E-05   | 5.00E-05   | 5.00E-05   | 5.00E-05   | 5.00E-05   | 5.00E-05   | 5.00E-05   | 5.00E-05   | 5.00E-05   | 5.00E-05   |
| EVM0001937   | 5.00E-05   | 5.00E-05   | 5.00E-05   | 5.00E-05   | 5.00E-05   | 5.00E-05   | 5.00E-05   | 5.00E-05   | 5.00E-05   | 5.00E-05   | 5.00E-05   | 5.00E-05   |
| EVM0010312   | 5.00E-05   | 5.00E-05   | 5.00E-05   | 5.00E-05   | 5.00E-05   | 5.00E-05   | 5.00E-05   | 5.00E-05   | 5.00E-05   | 5.00E-05   | 5.00E-05   | 5.00E-05   |

**Cytochrome P450**

**Eukaryotic translation initiation factor 3 subunit G**

**Translation, ribosomal structure and biogenesis**

**Glycerophosphoryl diester phosphodiesterase family**

**COP9 signalosome, subunit CSN8**

**Eukaryotic cytochrome b561**

**Cell cycle control, cell division, chromosome partitioning**

**Protein kinase domain**
| Gene ID       | Log2 Fold Change | Log10 Fold Change | P-Value | Description                                                                 |
|--------------|------------------|-------------------|---------|----------------------------------------------------------------------------|
| EVM0002296   | 44.72            | -1.51             | 5.00E-05| Posttranslational modification, protein turnover, chaperones                |
|              |                  |                   |         | DnaJ C terminal domain                                                      |
| EVM0002648   | 2.05             | -1.51             | 5.00E-05| --                                                                          |
|              |                  |                   |         | Glycosyl hydrolase family 7                                                |
| EVM0007842   | 52.11            | -1.50             | 5.00E-04| --                                                                          |
|              |                  |                   |         | Husl-like protein                                                           |
| EVM0002302   | 21.43            | -1.50             | 5.00E-04| --                                                                          |
|              |                  |                   |         | --                                                                          |
| EVM0009800   | 217.08           | -1.50             | 5.00E-04| --                                                                          |
|              |                  |                   |         | Mitochondrial ribosomal protein L31                                        |
| EVM0003787   | 57.92            | -1.50             | 5.00E-04| Translation, ribosomal structure and biogenesis                            |
|              |                  |                   |         | Eukaryotic translation initiation factor 3 subunit 7 (eIF-3)                |
| EVM0003274   | 31.80            | -1.50             | 5.00E-04| RNA processing and modification                                            |
|              |                  |                   |         | Domain of unknown function (DUF3449)                                       |
| EVM0008237   | 24.44            | -1.50             | 5.00E-04| --                                                                          |
|              |                  |                   |         | RNA ligase                                                                  |
| EVM0000072   | 3.59             | -1.50             | 4.00E-03| Posttranslational modification, protein turnover, chaperones                |
|              |                  |                   |         | Eukaryotic aspartyl protease                                                |
| EVM0000654   | 126.44           | -1.50             | 5.00E-04| General function prediction only                                            |
|              |                  |                   |         | Enoyl-(Acyl carrier protein) reductase                                       |
| EVM0000005   | 18.74            | -1.50             | 2.50E-04| --                                                                          |
|              |                  |                   |         | --                                                                          |
| EVM0009341   | 10.72            | -1.50             | 5.00E-04| RNA processing and modification                                            |
|              |                  |                   |         | DEAD/DEAH box helicase                                                      |
| ID               | E-value | Fold Change | Log2 Fold Change | Annotation                                                                 |
|------------------|---------|-------------|------------------|---------------------------------------------------------------------------|
| EVM0007418       | 44.52   | 125.75      | -1.50            | Carbohydrate transport and metabolism                                      |
| EVM0002012       | 3963.77 | 11195.70    | -1.50            | Ser-Thr-rich glycosyl-phosphatidyl-inositol-anchored membrane family       |
| EVM000992        | 65.15   | 183.90      | -1.50            | Carbonic anhydrase                                                         |
| EVM0010693       | 184.39  | 520.36      | -1.50            | --                                                                        |
| EVM001127        | 44.96   | 126.62      | -1.49            | General function prediction only                                          |
| EVM0007840       | 512.12  | 1442.06     | -1.49            | Energy production and conversion                                          |
| EVM0010552       | 18.02   | 50.75       | -1.49            | Mitochondrial ribosomal protein L51 / S25 / CI-B8 domain                  |
| EVM0004171       | 16.21   | 45.62       | -1.49            | Histone-like transcription factor (CBF/NF-Y) and archaeal histone          |
| EVM0004576       | 67.71   | 190.51      | -1.49            | Acetyltransferase (GNAT) family                                            |
| EVM0001419       | 179.59  | 505.13      | -1.49            | SGS domain                                                                |
| EVM0006355       | 160.18  | 450.33      | -1.49            | Microsomal signal peptidase 12 kDa subunit (SPC12)                        |
| Gene          | Value1 | Value2 | Value3 | Value4 | Value5 | Value6 | Value7 | Value8 | Value9 | Value10 | Function Description                                                                 |
|--------------|--------|--------|--------|--------|--------|--------|--------|--------|--------|---------|-------------------------------------------------------------------------------------|
| EVM0010543   | 2.19   | 6.14   | -1.49  | 2.00E-04 | 1.46E-03 | --     | --     | --     | --     | --      |                                                                                    |
| EVM0004513   | 82.31  | 230.98 | -1.49  | 2.95E-03 | 1.40E-02  | --     | pfkB family carbohydrate kinase                       |
| EVM0002548   | 18.97  | 53.22  | -1.49  | 5.00E-05 | 4.28E-04  | --     | --     | --     | --     | --      |                                                                                    |
| EVM0000131   | 3.95   | 11.08  | -1.49  | 1.75E-03 | 9.08E-03  | --     | --     | --     | --     | --      |                                                                                    |
| EVM0008273   | 11.10  | 31.09  | -1.49  | 5.00E-05 | 4.28E-04  | --     | Glycosyl hydrolase family 3 N terminal domain          |
| EVM0011440   | 1.08   | 3.02   | -1.48  | 4.00E-04 | 2.65E-03  | --     | --     | --     | --     | --      |                                                                                    |
| EVM0010019   | 2.50   | 7.00   | -1.48  | 5.00E-04 | 4.28E-03  | --     | F-box-like                                         |
| EVM0000377   | 53.36  | 149.25 | -1.48  | 5.00E-04 | 4.28E-04  | --     | --     | --     | --     | --      |                                                                                    |
| EVM0004148   | 59.82  | 167.18 | -1.48  | 5.00E-04 | 4.28E-04  | --     | --     | --     | --     | --      |                                                                                    |
| EVM0009904   | 44.22  | 123.57 | -1.48  | 5.00E-04 | 4.28E-04  | General function prediction only                      |
| EVM0009025   | 34.63  | 96.68  | -1.48  | 5.00E-04 | 4.28E-04  | Methyltransferase involved in Williams-Beuren syndrome |
| EVM0001444   | 32.04  | 89.47  | -1.48  | 5.00E-04 | 4.28E-04  | --     | --     | --     | --     | --      |                                                                                    |
| EVM0000883   | 3.86   | 10.79  | -1.48  | 5.00E-04 | 4.28E-04  | Transcription                                       |
| EVM0000883   |        |        |        |        |        |        |        |        |        |        | HMG (high mobility group) box                                                      |
| EVM0005158 | 6.53 | 18.23 | -1.48 | 5.00E-05 | 4.28E-04 | -- | Mitochondrial carrier protein |
| EVM0009946 | 26.63 | 74.29 | -1.48 | 5.00E-05 | 4.28E-04 | Transcription | A49-like RNA polymerase I associated factor |
| EVM0001024 | 41.84 | 116.63 | -1.48 | 5.00E-05 | 4.28E-04 | -- | Hinge domain of cleavage stimulation factor subunit 2 |
| EVM0007991 | 79.25 | 220.62 | -1.48 | 5.00E-05 | 4.28E-04 | Transcription | SAC3/GANP/Nin1/mts3/eIF-3 p25 family |
| EVM0007810 | 4.18 | 11.64 | -1.48 | 1.00E-04 | 7.96E-04 | -- | -- |
| EVM0001207 | 8.37 | 23.26 | -1.48 | 1.50E-04 | 1.14E-03 | -- | -- |
| EVM0001831 | 487.13 | 1353.48 | -1.47 | 5.00E-05 | 4.28E-04 | Energy production and conversion | ATP synthase, Delta/Epsilon chain, beta-sandwich domain |
| EVM0009011 | 0.76 | 2.10 | -1.47 | 5.00E-03 | 2.15E-02 | -- | F-box-like |
| EVM0007377 | 9.47 | 26.23 | -1.47 | 5.00E-05 | 4.28E-04 | RNA processing and modification | RNA pseudouridylate synthase |
| EVM000869 | 474.64 | 1314.67 | -1.47 | 2.50E-04 | 1.77E-03 | -- | -- |
| EVM0007065 | 45.00 | 124.25 | -1.47 | 5.00E-05 | 4.28E-04 | -- | -- |
| EVM0008014 | 971.59 | 2683.00 | -1.47 | 5.00E-05 | 4.28E-04 | Translation, ribosomal structure and biogenesis | Ribosomal protein L35Ae |
| Accession  | EVM0009270 | EVM0003630 | EVM0007726 | EVM0011961 | EVM0007748 | EVM0000417 | EVM0008299 | EVM0002619 | EVM0008121 | EVM0008389 | EVM0008637 |
|-----------|------------|------------|------------|------------|------------|------------|------------|------------|------------|------------|------------|
|       | 772.11     | 30.34      | 6.85       | 114.49     | 66.42      | 13.87      | 208.07     | 22.05      | 125.90     | 437.37     | 14.82      |
|       | 2130.61    | 83.71      | 18.90      | 315.80     | 183.17     | 38.24      | 573.04     | 60.64      | 345.92     | 1201.25    | 40.67      |
|       | -1.46      | -1.46      | -1.46      | -1.46      | -1.46      | -1.46      | -1.46      | -1.46      | -1.46      | -1.46      | -1.46      |
|       | 5.00E-05   | 5.00E-05   | 5.00E-05   | 5.00E-05   | 1.75E-03   | 5.00E-05   | 5.00E-05   | 5.00E-05   | 5.00E-05   | 5.00E-05   | 5.00E-05   |
|       | 4.28E-04   | 4.28E-04   | 4.28E-04   | 4.28E-04   | 9.08E-03   | 4.28E-04   | 4.28E-04   | 4.28E-04   | 4.28E-04   | 4.28E-04   | 4.28E-04   |
|       | Posttranslational modification, protein turnover, chaperones | General function prediction only | Signal transduction mechanisms | General function prediction only | -- | Posttranslational modification, protein turnover, chaperones | Intracellular trafficking, secretion, and vesicular transport | Function unknown | -- | Energy production and conversion | RNA processing and modification |
|       | Chaperonin 10 Kd subunit | NGP1NT (NUC091) domain | Protein tyrosine kinase | Zinc finger C-x8-C-x5-C-x3-H type (and similar) | -- | DnaJ domain | emp24/gp25L/p24 family/GOLD | Signal peptide peptidase | RNA polymerase II transcription mediator complex subunit 9 | Complex 1 protein (LYR family) | WD domain, G-beta repeat |
| EVM0007616 | 23.95 | 65.73 | -1.46 | 5.00E-05 | 4.28E-04 | Transcription | MT-A70 |
| EVM0008206 | 98.65 | 270.25 | -1.45 | 5.00E-05 | 4.28E-04 | RNA processing and modification | RNA recognition motif. (a.k.a. RRM, RBD, or RNP domain) |
| EVM0002482 | 9.36 | 25.63 | -1.45 | 5.00E-05 | 4.28E-04 | -- | -- |
| EVM0000647 | 46.75 | 127.92 | -1.45 | 1.00E-04 | 7.96E-04 | #N/A | #N/A |
| EVM0007650 | 114.01 | 311.92 | -1.45 | 5.00E-05 | 4.28E-04 | -- | -- |
| EVM0003400 | 5.86 | 16.03 | -1.45 | 5.00E-05 | 4.28E-04 | -- | Centromere protein Scm3 |
| EVM0001350 | 376.65 | 1027.81 | -1.45 | 1.50E-04 | 1.14E-03 | -- | CsbD-like |
| EVM0011888 | 0.84 | 2.30 | -1.45 | 7.00E-03 | 2.82E-02 | -- | Peroxidase |
| EVM0012015 | 20.09 | 54.81 | -1.45 | 5.00E-05 | 4.28E-04 | Translation, ribosomal structure and biogenesis | BOP1NT (NUC169) domain |
| EVM0003340 | 12.68 | 34.57 | -1.45 | 5.00E-05 | 4.28E-04 | -- | Nuclear fragile X mental retardation-interacting protein 1 (NUFIP1) |
| EVM0010318 | 4.94 | 13.46 | -1.45 | 1.50E-04 | 1.14E-03 | -- | -- |
| EVM0000425 | 767.73 | 2091.15 | -1.45 | 5.00E-05 | 4.28E-04 | Intracellular trafficking, secretion, and vesicular transport | TB2/DP1, HVA22 family |
| ID               | Value   | log10 Value | log10 Value | Function                                                                                   | Domain/Protein                       |
|------------------|---------|-------------|-------------|-------------------------------------------------------------------------------------------|-------------------------------------|
| EVM0008908       | 53.48   | 145.61      | -1.45       | Translation, ribosomal structure and biogenesis                                           | Brix domain                         |
| EVM0012226       | 2.60    | 7.07        | -1.44       | --                                                                                       | --                                  |
| EVM0009933       | 76.63   | 208.48      | -1.44       | Intracellular trafficking, secretion, and vesicular transport                            | Peptidase S24-like                  |
| EVM0006452       | 5933.64 | 16138.20    | -1.44       | --                                                                                       | --                                  |
| EVM0000264       | 0.51    | 1.37        | -1.44       | --                                                                                       | --                                  |
| EVM0004038       | 1161.22 | 3149.55     | -1.44       | Translation, ribosomal structure and biogenesis                                           | Ribosomal protein L6                |
| EVM0004951       | 1.73    | 4.68        | -1.44       | --                                                                                       | --                                  |
| EVM0005028       | 28.68   | 77.69       | -1.44       | Inorganic ion transport and metabolism                                                   | Acetyl-coenzyme A transporter 1     |
| EVM0008305       | 14.15   | 38.34       | -1.44       | General function prediction                                                              | U3 small nucleolar RNA-associated protein 6 only |
| EVM0003265       | 32.29   | 87.47       | -1.44       | General function prediction                                                              | R3H domain                         |
| EVM0003685       | 8.04    | 21.78       | -1.44       | --                                                                                       | --                                  |
| EVM00066691      | 1.15    | 3.10        | -1.44       | --                                                                                       | --                                  |
| EVM0000211 | 24.18 | 65.38 | -1.44 | 5.00E-05 | 4.28E-04 | RNA processing and modification | WD domain, G-beta repeat |
| EVM0007596 | 20.25 | 54.73 | -1.43 | 5.00E-05 | 4.28E-04 | General function prediction only | RNA recognition motif. (a.k.a. RRM, RBD, or RNP domain) |
| EVM0006014 | 118.97 | 320.98 | -1.43 | 5.00E-05 | 4.28E-04 | -- | -- |
| EVM0000252 | 15.85 | 42.69 | -1.43 | 5.00E-05 | 4.28E-04 | -- | -- |
| EVM0000081 | 80.72 | 217.34 | -1.43 | 5.00E-05 | 4.28E-04 | -- | WW domain |
| EVM0008740 | 19.07 | 51.34 | -1.43 | 5.00E-05 | 4.28E-04 | -- | Putative amidotransferase |
| EVM0008159 | 92.95 | 250.20 | -1.43 | 5.00E-05 | 4.28E-04 | Posttranslational modification, protein turnover, chaperones | Hsp70 protein |
| EVM0000121 | 48.80 | 131.33 | -1.43 | 5.00E-05 | 4.28E-04 | General function prediction only | Haloacid dehalogenase-like hydrolase |
| EVM0008276 | 56.54 | 152.13 | -1.43 | 5.00E-05 | 4.28E-04 | Inorganic ion transport and metabolism | Ion channel |
| EVM0009271 | 35.95 | 96.68 | -1.43 | 5.00E-05 | 4.28E-04 | -- | Protein kinase domain |
| EVM0004796 | 45.32 | 121.87 | -1.43 | 5.00E-05 | 4.28E-04 | Function unknown | Fcf2 pre-rRNA processing |
| EVM0008074 | 142.26 | 382.42 | -1.43 | 5.00E-05 | 4.28E-04 | Chromatin structure and dynamics | Core histone H2A/H2B/H3/H4 |
| Accession    | Value1 | Value2 | Value3 | Value4 | Value5 | Function/Description                                                                 |
|-------------|--------|--------|--------|--------|--------|-------------------------------------------------------------------------------------|
| EVM0006924  | 14.14  | 38.01  | -1.43  | 5.00E-05| 4.28E-04|                                                                                  |
| EVM0000928  | 140.07 | 376.37 | -1.43  | 5.00E-05| 4.28E-04| Function unknown Der1-like family                                                  |
| EVM0009294  | 151.75 | 407.56 | -1.43  | 5.00E-05| 4.28E-04| Lipid transport and metabolism Fatty acid hydroxylase superfamily                |
| EVM0002100  | 16.20  | 43.51  | -1.43  | 5.00E-05| 4.28E-04| Helix-loop-helix DNA-binding domain                                                 |
| EVM0006480  | 9.12   | 24.49  | -1.43  | 5.00E-05| 4.28E-04| Membrane transport protein                                                        |
| EVM0006700  | 195.99 | 526.28 | -1.43  | 1.50E-04| 1.14E-03| Aconitase family (aconitate hydratase)                                               |
| EVM0012187  | 10.73  | 28.82  | -1.42  | 5.00E-05| 4.28E-04| Fungal cellulose binding domain                                                    |
| EVM0000784  | 7.75   | 20.82  | -1.42  | 5.00E-05| 4.28E-04|                                                                                  |
| EVM0002505  | 684.07 | 1835.01| -1.42  | 2.00E-04| 1.46E-03|                                                                                  |
| EVM0000600  | 152.36 | 407.67 | -1.42  | 5.00E-05| 4.28E-04| Nitronate monooxygenase                                                           |
| EVM0011341  | 180.98 | 483.99 | -1.42  | 5.00E-05| 4.28E-04| CDP-alcohol phosphatidytransferase                                                 |
| EVM0000593  | 135.73 | 362.89 | -1.42  | 5.00E-05| 4.28E-04| Protein of unknown function (DUF952)                                                |
| EVM0012074  | 13.16  | 35.18  | -1.42  | 5.00E-05| 4.28E-04| Lipid transport and metabolism CDP-alcohol phosphatidytransferase                 |
| EVM0002814  | 94.54 | 252.69 | -1.42 | 5.00E-05 4.28E-04 | Intracellular trafficking, secretion, and vesicular transport | Peroxisomal membrane protein (Pex16) |
|----------------|--------|---------|--------|---------------------|-------------------------------------------------|-------------------------------|
| EVM0008368  | 210.92 | 563.69 | -1.42 | 5.00E-05 4.28E-04 | Cell cycle control, cell division, chromosome partitioning | Double-stranded DNA-binding domain |
| EVM0006117  | 9.64  | 25.75  | -1.42 | 5.00E-05 4.28E-04 | General function prediction only | Aldo/keto reductase family |
| EVM0004386  | 19.36 | 51.68  | -1.42 | 5.00E-05 4.28E-04 | RNA processing and modification | DEAD/DEAH box helicase |
| EVM0001244  | 2.75  | 7.33   | -1.42 | 5.00E-04 3.19E-03 | -- | Dyp-type peroxidase family |
| EVM0006132  | 85.94 | 229.13 | -1.41 | 5.00E-05 4.28E-04 | Intracellular trafficking, secretion, and vesicular transport | Peroxisomal biogenesis factor 11 (PEX11) |
| EVM0004396  | 14.12 | 37.63  | -1.41 | 5.00E-05 4.28E-04 | -- | -- |
| EVM0004027  | 1690.05 | 4500.14 | -1.41 | 5.00E-05 4.28E-04 | Translation, ribosomal structure and biogenesis | Ribosomal L27e protein family |
| EVM0006511  | 5.54  | 14.75  | -1.41 | 5.00E-05 4.28E-04 | General function prediction only | Glycosyl transferase family 90 |
| EVM0006813  | 103.99 | 276.68 | -1.41 | 5.00E-05 4.28E-04 | General function prediction only | Sugar (and other) transporter |
| EVM0010558  | 13.17 | 35.02  | -1.41 | 5.00E-05 4.28E-04 | -- | -- |
| EVM0009958 | 11.49 | 30.55 | -1.41 | 2.00E-04 | 1.46E-03 | -- | -- |
| EVM0010741 | 5.71  | 15.19 | -1.41 | 1.50E-04 | 1.14E-03 | Secondary metabolites biosynthesis, transport and catabolism | short chain dehydrogenase |
| EVM0008554 | 63.07 | 167.59 | -1.41 | 5.00E-05 | 4.28E-04 | Cell cycle control, cell division, chromosome partitioning | WD domain, G-beta repeat |
| EVM0012170 | 20.27 | 53.76 | -1.41 | 5.00E-05 | 4.28E-04 | -- | -- |
| EVM0003576 | 5.25  | 13.91 | -1.41 | 5.00E-05 | 4.28E-04 | -- | -- |
| EVM0012212 | 15.10 | 40.03 | -1.41 | 5.00E-05 | 4.28E-04 | Chromatin structure and dynamics | SET domain |
| EVM0011226 | 128.12 | 339.63 | -1.41 | 5.00E-05 | 4.28E-04 | RNA processing and modification | Zinc-finger double-stranded RNA-binding |
| EVM0002708 | 20.52 | 54.38 | -1.41 | 5.00E-05 | 4.28E-04 | Function unknown | Imal N-terminal domain |
| EVM0006852 | 49.08 | 129.92 | -1.40 | 5.00E-05 | 4.28E-04 | -- | Sen15 protein |
| EVM0002695 | 102.16 | 270.29 | -1.40 | 5.00E-05 | 4.28E-04 | -- | SYF2 splicing factor |
| EVM0005762 | 187.42 | 495.53 | -1.40 | 5.00E-05 | 4.28E-04 | Posttranslational modification, protein turnover, chaperones | Thioredoxin |
| GenBank ID   | Log2 Ratio | Log2 Fold Change | p-Value | Description                                                                 |
|-------------|------------|------------------|---------|-----------------------------------------------------------------------------|
| EVM0008274  | 4.84       | 12.79            | -1.40   | 5.00E-05 4.28E-04 --                                                     |
| EVM0003688  | 9.03       | 23.87            | -1.40   | 5.00E-05 4.28E-04             Cell cycle control, cell division, chromosome partitioning |
|             |            |                  |         | Mad3/BUB1 homology region 1                                                |
| EVM0000538  | 3.19       | 8.42             | -1.40   | 8.50E-04 4.98E-03 --                                                     |
| EVM0007613  | 6.50       | 17.16            | -1.40   | 5.00E-05 4.28E-04             Replication, recombination and repair         |
| EVM0000523  | 4.76       | 12.57            | -1.40   | 5.00E-05 4.28E-04 --                                                     |
| EVM0006536  | 0.74       | 1.95             | -1.40   | 9.95E-03 3.74E-02 --                                                     |
| EVM0009651  | 4.91       | 12.97            | -1.40   | 5.00E-05 4.28E-04             Energy production and conversion            |
| EVM0007327  | 82.92      | 218.74           | -1.40   | 5.00E-05 4.28E-04             Intracellular trafficking, secretion, and vesicular transport |
| EVM0011639  | 1293.03    | 3409.19          | -1.40   | 1.00E-04 7.96E-04 --                                                     |
| EVM0006989  | 4.50       | 11.85            | -1.40   | 5.00E-05 4.28E-04             Replication, recombination and repair         |
| EVM0011784  | 27.17      | 71.56            | -1.40   | 5.00E-05 4.28E-04             Inorganic ion transport and metabolism |
| EVM0012251  | 0.71       | 1.87             | -1.40   | 1.08E-02 3.98E-02 --                                                     |
| EVM0008274  | 4.84       | 12.79            | -1.40   | 5.00E-05 4.28E-04 --                                                     |
| EVM0003967  | 102.09 | 268.77  | -1.40 | 5.00E-05 | 4.28E-04 | Function unknown | Mago binding |
|------------|--------|---------|------|----------|----------|----------------|-------------|
| EVM0010500 | 30.57  | 80.45   | -1.40| 5.00E-05 | 4.28E-04 | Transcription  | RNA polymerase II transcription factor SIII (Elongin) subunit A |
| EVM0000666 | 56.27  | 148.08  | -1.40| 5.00E-05 | 4.28E-04 | --             | --           |
| EVM0011858 | 89.70  | 235.89  | -1.39| 5.00E-05 | 4.28E-04 | RNA processing and modification | Ribosomal protein L10 |
| EVM0009027 | 71.92  | 189.06  | -1.39| 5.00E-05 | 4.28E-04 | --             | F-box-like |
| EVM0006644 | 72.01  | 189.23  | -1.39| 5.00E-05 | 4.28E-04 | Function unknown | Mitochondrial large subunit ribosomal protein (Img2) |
| EVM000030  | 11.00  | 28.89   | -1.39| 5.00E-05 | 4.28E-04 | Inorganic ion transport and metabolism | Sodium/calcium exchanger protein |
| EVM0002455 | 369.64 | 970.99  | -1.39| 5.00E-05 | 4.28E-04 | --             | Phosphopantetheine attachment site |
| EVM0001135 | 10.15  | 26.67   | -1.39| 5.00E-05 | 4.28E-04 | RNA processing and modification | DEAD/DEAH box helicase |
| EVM0009481 | 1.68   | 4.41    | -1.39| 2.75E-03 | 1.32E-02 | --             | GDSL-like Lipase/Acylhydrolase |
| EVM0003249 | 91.37  | 239.83  | -1.39| 5.00E-05 | 4.28E-04 | --             | --           |
| EVM0003357 | 1906.89| 5004.89 | -1.39| 1.85E-03 | 9.52E-03 | --             | --           |
| EVM0006392 | 6.20   | 16.27   | -1.39| 5.00E-05 | 4.28E-04 | --             | Ferric reductase NAD binding domain |
| Accession | Value1 | Value2 | Value3 | Value4 | Function Description |
|-----------|--------|--------|--------|--------|----------------------|
| EVM0006496 | 1.22  | 3.20  | -1.39 | 5.00E-05 | Replication, recombination and repair |
| EVM0007233 | 1.17  | 3.06  | -1.39 | 6.50E-04 | DEAD/DEAH box helicase |
| EVM0004420 | 11.65 | 30.49 | -1.39 | 5.00E-05 | DEAD/DEAH box helicase |
| EVM0010189 | 49.51 | 129.57 | -1.39 | 5.00E-05 | Bacterial transferase hexapeptide (six repeats) |
| EVM0008576 | 4.30  | 11.24 | -1.39 | 5.40E-03 | Ctf8 |
| EVM0004161 | 85.37 | 223.38 | -1.39 | 5.00E-05 | Ctf8 |
| EVM0009145 | 2.56  | 6.70  | -1.39 | 3.50E-04 | Ctf8 |
| EVM0003989 | 11.13 | 29.11 | -1.39 | 5.00E-05 | Ctf8 |
| EVM0003535 | 8.46  | 22.11 | -1.39 | 5.00E-05 | Ctf8 |
| EVM0007915 | 59.79 | 156.32 | -1.39 | 5.00E-05 | RNA processing and modification |
| EVM0008531 | 57.51 | 150.27 | -1.39 | 5.00E-05 | Zinc-finger of C2H2 type |
| EVM0001263 | 6.02  | 15.73 | -1.39 | 1.50E-04 | Oligosaccharyl transferase STT3 subunit |

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**Notes:**
- The values represent normalized gene expression levels.
- The functions listed are associated with the respective gene products.
| EVM0005384 | 49.87 | 130.32 | -1.39 | 5.00E-05 | 4.28E-04 | -- | -- |
| EVM0001995 | 5.93  | 15.48  | -1.38 | 1.50E-04 | 1.14E-03 | -- | -- |
| EVM0004684 | 13.91 | 36.29  | -1.38 | 5.00E-05 | 4.28E-04 | -- | -- |
| EVM0008642 | 26.47 | 69.08  | -1.38 | 5.00E-05 | 4.28E-04 | -- | -- |
| EVM0010605 | 717.39| 1870.07| -1.38 | 5.00E-05 | 4.28E-04 | Translation, ribosomal structure and biogenesis | Ribosomal protein L34e |
| EVM0007871 | 5.89  | 15.34  | -1.38 | 2.50E-04 | 1.77E-03 | -- | -- |
| EVM0005712 | 10.21 | 26.59  | -1.38 | 5.00E-05 | 4.28E-04 | -- | -- |
| EVM0005789 | 106.87| 278.08 | -1.38 | 5.00E-05 | 4.28E-04 | -- | -- |
| EVM0003292 | 82.12 | 213.62 | -1.38 | 5.00E-05 | 4.28E-04 | -- | Sel1 repeat |
| EVM0009292 | 6.56  | 17.07  | -1.38 | 5.00E-05 | 4.28E-04 | -- | -- |
| EVM0010081 | 86.48 | 224.95 | -1.38 | 1.50E-04 | 1.14E-03 | -- | Protein of unknown function (DUF2462) |
| EVM0000857 | 1.43  | 3.73   | -1.38 | 1.08E-02 | 3.97E-02 | -- | -- |
| EVM0002350 | 35.46 | 92.21  | -1.38 | 5.00E-05 | 4.28E-04 | -- | -- |
| EVM0002618  | 47.12 | 122.51 | -1.38 | 5.00E-05 4.28E-04 | Translation, ribosomal structure and biogenesis | TruB family pseudouridylate synthase (N terminal domain) |
|-------------|-------|--------|-------|-------------------|---------------------------------------------|--------------------------------------------------|
| EVM0000648  | 77.12 | 200.50 | -1.38 | 5.00E-05 4.28E-04 | Lipid transport and metabolism                | Eukaryotic phosphomannomutase                     |
| EVM0007138  | 69.78 | 181.42 | -1.38 | 5.00E-05 4.28E-04 | --                                           | --                                               |
| EVM0006717  | 19.89 | 51.66  | -1.38 | 5.00E-05 4.28E-04 | --                                           | --                                               |
| EVM0002128  | 119.34| 309.70 | -1.38 | 5.00E-05 4.28E-04 | Translation, ribosomal structure and biogenesis | Domain found in IF2B/IF5                          |
| EVM0010824  | 15.94 | 41.35  | -1.38 | 5.00E-05 4.28E-04 | General function prediction only              | WD domain, G-beta repeat                         |
| EVM0003139  | 59.43 | 154.11 | -1.37 | 5.00E-05 4.28E-04 | Posttranslational modification, protein turnover, chaperones | Oligosaccharyltransferase 48 kDa subunit beta |
| EVM0009402  | 86.01 | 223.03 | -1.37 | 5.00E-05 4.28E-04 | Inorganic ion transport and metabolism        | Got1/Sft2-like family                            |
| EVM0007355  | 9.65  | 25.03  | -1.37 | 5.00E-05 4.28E-04 | Coenzyme transport and metabolism             | UbiA prenyltransferase family                     |
| EVM0003289  | 18.10 | 46.92  | -1.37 | 5.00E-05 4.28E-04 | Transcription                                 | RNA polymerase III subunit Rpc25                  |
| EVM0003936  | 66.45 | 172.18 | -1.37 | 5.00E-05 4.28E-04 | General function prediction only              | TPR repeat                                       |
| EVM0002080  | 2.10  | 5.43   | -1.37 | 6.00E-04 3.72E-03 | --                                           | --                                               |
|     | | | | | | |
|-----|--------|--------|--------|--------|-----------|-----------|
| EVM0010061 | 55.99  | 144.62 | -1.37  | 5.00E-05 | 4.28E-04  | --         | SH3 domain |
| EVM0009042 | 176.61 | 455.27 | -1.37  | 5.00E-05 | 4.28E-04  | Posttranslational modification, protein turnover, chaperones | Prefoldin subunit |
| EVM0007136 | 26.61  | 68.48  | -1.36  | 5.00E-05 | 4.28E-04  | --         | --         |
| EVM0005405 | 7.31   | 18.81  | -1.36  | 1.00E-04 | 7.96E-04  | --         | Pericentrin-AKAP-450 domain of centrosomal targeting protein |
| EVM0006430 | 7.78   | 20.00  | -1.36  | 5.00E-05 | 4.28E-04  | --         | --         |
| EVM0005831 | 15.11  | 38.86  | -1.36  | 1.00E-04 | 7.96E-04  | General function prediction only | 3'-5' exonuclease |
| EVM0005080 | 34.83  | 89.47  | -1.36  | 2.00E-04 | 1.46E-03  | --         | Fungal hydrophobin |
| EVM0007186 | 24.40  | 62.65  | -1.36  | 5.00E-05 | 4.28E-04  | --         | --         |
| EVM0010279 | 42.78  | 109.85 | -1.36  | 5.00E-05 | 4.28E-04  | --         | Etoposide-induced protein 2.4 (EI24) |
| EVM0002055 | 13.11  | 33.66  | -1.36  | 5.00E-05 | 4.28E-04  | General function prediction only | Major Facilitator Superfamily |
| EVM0006257 | 192.83 | 494.59 | -1.36  | 5.00E-05 | 4.28E-04  | --         | --         |
| EVM0000375 | 91.86  | 235.54 | -1.36  | 5.00E-05 | 4.28E-04  | Lipid transport and metabolism | Fatty acid hydroxylase superfamily |
| Gene ID       | E-value | Decanoyl EGF-EGF bound ratio | Relative log2 fold change | Signal transduction mechanisms | ERG2 and Sigmal receptor like protein | General function prediction only | Glycosyl transferase family 90 | Posttranslational modification, protein turnover, chaperones | Cyclophilin type peptidyl-prolyl cis-trans isomerase/CLD | General function prediction only | Ras family | Posttranslational modification, protein turnover, chaperones | Translation, ribosomal structure and biogenesis | Ribosomal protein L14p/L23e | Carbohydrate transport and metabolism | ALG3 protein | Amino acid transport and metabolism | bZIP transcription factor | Aminotransferase class-V |
|--------------|---------|-------------------------------|--------------------------|--------------------------------|------------------------------------|----------------------------------|-------------------------------|-----------------------------------------------|-----------------------------------------------|--------------------------------|----------------|------------------------------------------------|---------------------------------|-----------------------------|-------------------------------|---------------------------|-----------------------------|--------------------------|----------------------|
| EVM0001171   | 11.11   | 28.47                         | -1.36                    |                                |                                    | Signal transduction mechanisms   | ERG2 and Sigmal receptor like protein |
| EVM0005349   | 2.52    | 6.47                          | -1.36                    |                                |                                    | --                              | --                            |                                |                                | --                          |                             |                                     |                                |                                 |
| EVM0003339   | 3.40    | 8.71                          | -1.36                    |                                |                                    | General function prediction only | Glycosyl transferase family 90 |                                |                                |                                |                             |                                     |                                |                                 |
| EVM0000938   | 18.63   | 47.64                         | -1.35                    |                                |                                    | Posttranslational modification, protein turnover, chaperones | Cyclophilin type peptidyl-prolyl cis-trans isomerase/CLD |                                |                                |                                |                             |                                     |                                |                                 |
| EVM0011919   | 27.40   | 70.06                         | -1.35                    |                                |                                    | --                              | --                            |                                |                                |                                |                             |                                     |                                |                                 |
| EVM0000602   | 1394.30 | 3560.81                       | -1.35                    |                                |                                    | General function prediction only | Ras family                     |                                |                                |                                |                             |                                     |                                |                                 |
| EVM0002709   | 3.94    | 10.06                         | -1.35                    |                                |                                    | --                              | --                            |                                |                                |                                |                             |                                     |                                |                                 |
| EVM0010195   | 362.36  | 925.32                        | -1.35                    |                                |                                    | Translation, ribosomal structure and biogenesis | Ribosomal protein L14p/L23e |                                |                                |                                |                             |                                     |                                |                                 |
| EVM0002424   | 25.20   | 64.34                         | -1.35                    |                                |                                    | --                              | --                            |                                |                                |                                |                             |                                     |                                |                                 |
| EVM0006608   | 19.45   | 49.65                         | -1.35                    |                                |                                    | Carbohydrate transport and metabolism | ALG3 protein                  |                                |                                |                                |                             |                                     |                                |                                 |
| EVM0010589   | 174.65  | 445.54                        | -1.35                    |                                |                                    | --                              | bZIP transcription factor       |                                |                                |                                |                             |                                     |                                |                                 |
| EVM0006647   | 125.55  | 320.25                        | -1.35                    |                                |                                    | Amino acid transport and metabolism | Aminotransferase class-V        |                                |                                |                                |                             |                                     |                                |                                 |
| Gene ID      | Value1  | Value2  | Log2 Ratio | Value3  | Functional Category                                      |
|--------------|---------|---------|------------|---------|----------------------------------------------------------|
| EVM0006085   | 78.41   | 199.85  | -1.35      | 5.00E-05 | Transcription                                             |
| EVM0011971   | 9.04    | 23.05   | -1.35      | 5.00E-05 | HMG (high mobility group) box                            |
| EVM0001928   | 22.10   | 56.31   | -1.35      | 5.00E-05 | Ricin-type beta-trefoil lectin domain                     |
| EVM0004461   | 32.27   | 82.20   | -1.35      | 5.00E-05 | Putative oxidoreductase C terminal                        |
| EVM0003807   | 4.04    | 10.29   | -1.35      | 1.15E-03 | Amino acid transport and metabolism                      |
| EVM0011916   | 1048.96 | 2668.30 | -1.35      | 5.00E-05 | Protein of unknown function (DUF2611)                    |
| EVM0001287   | 19.17   | 48.74   | -1.35      | 5.00E-05 | pre-RNA processing PIH1/Nop17                            |
| EVM0005265   | 110.83  | 281.64  | -1.35      | 1.00E-04 | function unknown                                          |
| EVM0005366   | 16.34   | 41.49   | -1.34      | 5.00E-05 | Function unknown                                          |
| EVM0001130   | 287.49  | 729.86  | -1.34      | 2.00E-03 | Mitotic-spindle organizing gamma-tubulin ring associated  |
| EVM0006992   | 22.34   | 56.72   | -1.34      | 5.00E-05 | Cytochrome P450                                           |
| EVM0005866   | 44.94   | 114.06  | -1.34      | 3.65E-03 | Function unknown                                          |
| EVM0004157   | 2.99    | 7.59    | -1.34      | 2.00E-06 | Transcriptional regulator                                |
| Accession     | E-value | Value       | p-value | Function Description                                      | Domain Description                  |
|--------------|---------|-------------|---------|------------------------------------------------------------|-------------------------------------|
| EVM0004960   | 7.54    | 19.11       | -1.34   | --                                                         | Complex 1 protein (LYR family)      |
| EVM0002867   | 34.40   | 87.22       | -1.34   | Lipid transport and metabolism                            | MBOAT, membrane-bound O-acyltransferase family |
| EVM0004379   | 235.10  | 595.80      | -1.34   | Intracellular trafficking, secretion, and vesicular transport | Synaptobrevin                       |
| EVM0003951   | 58.59   | 148.43      | -1.34   | Function unknown                                          | RWD domain                          |
| EVM0005429   | 15.80   | 39.97       | -1.34   | Transcription                                             | CCAAT-binding transcription factor (CBF-B/NF-YA) subunit B |
| EVM0011758   | 4.05    | 10.24       | -1.34   | General function prediction only                           | THUMP domain                        |
| EVM0009259   | 168.64  | 426.46      | -1.34   | --                                                         | --                                  |
| EVM0011808   | 3.70    | 9.36        | -1.34   | --                                                         | Lysine-specific metallo-endopeptidase |
| EVM0009590   | 193.84  | 489.97      | -1.34   | RNA processing and modification                           | Zinc finger C-x8-C-x5-C-x3-H type (and similar) |
| EVM0011570   | 142.54  | 360.28      | -1.34   | --                                                         | --                                  |
| EVM0002044   | 40.93   | 103.39      | -1.34   | Translation, ribosomal structure and biogenesis           | Initiation factor 2 subunit family  |
| EVM0007286   | 31.43   | 79.38       | -1.34   | --                                                         | --                                  |
| Accession   | EVM0003434 | EVM0003335 | EVM0007300 | EVM0012150 | EVM0007629 | EVM0003348 | EVM0007008 | EVM0011412 | EVM0005561 | EVM0004238 | EVM0008438 | EVM0004387 | EVM0005668 |
|------------|------------|------------|------------|------------|------------|------------|------------|------------|------------|------------|------------|------------|------------|
| Value      | 12.59      | 29.19      | 3.06       | 29.86      | 63.26      | 11.25      | 19.32      | 2.18       | 45.10      | 23.90      | 19.61      | 36.97      | 67.05      |
| Score      | 31.80      | 73.73      | 7.71       | 75.35      | 159.57     | 28.36      | 48.68      | 5.50       | 113.56     | 60.16      | 49.36      | 93.03      | 168.65     |
| Score2     | -1.34      | -1.34      | -1.34      | -1.34      | -1.33      | -1.33      | -1.33      | -1.33      | -1.33      | -1.33      | -1.33      | -1.33      | -1.33      |
| Score3     | 1.50E-04   | 5.00E-05   | 4.50E-04   | 5.00E-05   | 5.00E-05   | 4.00E-04   | 5.00E-05   | 1.03E-02   | 5.00E-05   | 5.00E-05   | 5.00E-05   | 5.00E-05   | 5.00E-05   |
| Score4     | 1.14E-03   | 4.28E-04   | 2.92E-03   | 4.28E-04   | 4.28E-04   | 2.65E-03   | 4.28E-04   | 3.82E-02   | 4.28E-04   | 4.28E-04   | 4.28E-04   | 4.28E-04   | 4.28E-04   |
| Score5     | --         | --         | --         | --         | --         | Function unknown | --         | --         | --         | --         | --         | --         | --         |
| Score6     | Protein of unknown function (DUF1691) | Eukaryotic protein of unknown function (DUF1764) | -- | -- | General function prediction only | Protein of unknown function (DUF933) | PIG-P | F-box-like | -- | Transcription factor TFIIB repeat | SMI1 / KNR4 family (SUHK-1) | Apoptosis-antagonizing transcription factor, C-terminal | ASF1 like histone chaperone |
| Score7     | --         | --         | --         | --         | --         | --         | --         | --         | --         | --         | --         | --         | --         |
| Identifier   | P1    | P2     | Log2 Ratio | P-value | Function                                                                 |
|--------------|-------|--------|------------|---------|--------------------------------------------------------------------------|
| EVM0007661   | 13.62 | 34.23  | -1.33      |         | 5.00E-05 4.28E-04 --                                                 | C2 domain                                      |
| EVM0000146   | 34.98 | 87.93  | -1.33      |         | 5.00E-05 4.28E-04 --                                                 | --                                             |
| EVM0008848   | 50.60 | 127.16 | -1.33      |         | 5.00E-05 4.28E-04 Translation, ribosomal structure and biogenesis       | Ribosomal protein S12/S23                     |
| EVM0001112   | 1.20  | 3.01   | -1.33      |         | 2.15E-03 1.08E-02 --                                                 | Pectate lyase                                  |
| EVM0005565   | 0.93  | 2.34   | -1.33      |         | 1.44E-02 4.99E-02 --                                                 | Glycosyl hydrolases family 16                 |
| EVM0001903   | 209.50| 525.92 | -1.33      |         | 1.00E-04 7.96E-04 Translation, ribosomal structure and biogenesis      | Eukaryotic translation initiation factor eIF2A |
| EVM0004046   | 127.46| 319.86 | -1.33      |         | 5.00E-05 4.28E-04 Amino acid transport and metabolism                  | Pyridoxal-dependent decarboxylase, pyridoxal binding domain |
| EVM0011101   | 12.25 | 30.74  | -1.33      |         | 5.00E-05 4.28E-04 --                                                 | Bromodomain                                   |
| EVM0001367   | 90.97 | 228.09 | -1.33      |         | 5.00E-05 4.28E-04 --                                                 | --                                             |
| EVM0002540   | 4.42  | 11.07  | -1.33      |         | 2.50E-04 1.77E-03 --                                                 | Transferase family                            |
| EVM0004516   | 18.14 | 45.47  | -1.33      |         | 5.00E-05 4.28E-04 --                                                 | --                                             |
| EVM0004915   | 0.94  | 2.35   | -1.32      |         | 4.95E-03 2.13E-02 Carbohydrate transport and metabolism               | Alpha amylase, catalytic domain               |
| Entry      | Score | Percent | logB | score2 | score3 | Feature                                      |
|------------|-------|---------|------|--------|--------|----------------------------------------------|
| EVM0011355 | 23.53 | 58.90   | -1.32| 5.00E-05| 4.28E-04| Chalcone-flavanone isomerase                  |
| EVM0007524 | 5.23  | 13.09   | -1.32| 2.00E-04| 1.46E-03| Domain of unknown function (DUF4451)          |
| EVM0007162 | 18.75 | 46.92   | -1.32| 5.00E-05| 4.28E-04| RNA processing and modification              |
| EVM0004554 | 35.99 | 89.98   | -1.32| 5.00E-05| 4.28E-04| Helicase associated domain (HA2)              |
| EVM0008702 | 191.94| 479.50  | -1.32| 5.00E-05| 4.28E-04| Cytoskeleton                                  |
| EVM0004324 | 184.83| 461.70  | -1.32| 5.00E-05| 4.28E-04| Intracellular trafficking, secretion, and vesicular transport |
| EVM0010825 | 2.08  | 5.20    | -1.32| 9.50E-04| 5.46E-03| PRELI-like family                            |
| EVM0002863 | 4.64  | 11.58   | -1.32| 6.00E-04| 3.72E-03| Transcription                                |
| EVM0005294 | 35.13 | 87.63   | -1.32| 5.00E-05| 4.28E-04| Myb-like DNA-binding domain                   |
| EVM0011949 | 10.63 | 26.52   | -1.32| 1.00E-04| 7.96E-04| Protein of unknown function (DUF3245)         |
| EVM0007229 | 3.53  | 8.81    | -1.32| 1.60E-03| 8.44E-03| Cupin-like domain                             |
| EVM0006504 | 28.67 | 71.42   | -1.32| 5.00E-05| 4.28E-04| --                                           |


| Accession  | Value1 | Value2 | Value3 | E-value1 | E-value2 | Class1 | Class2 |
|------------|--------|--------|--------|----------|----------|--------|--------|
| EVM0000228 | 21.06  | 52.37  | -1.31  | 5.00E-05  | 4.28E-04  | Function unknown | Di-sulfide bridge nucleocytoplasmic transport domain |
| EVM0001050 | 38.32  | 95.25  | -1.31  | 5.00E-05  | 4.28E-04  | -- | CybS |
| EVM0000490 | 4.29   | 10.66  | -1.31  | 4.50E-04  | 2.92E-03  | -- | Glycosyl hydrolase family 61 |
| EVM0007494 | 231.85 | 575.41 | -1.31  | 5.00E-05  | 4.28E-04  | Posttranslational modification, protein turnover, chaperones | Glutaredoxin |
| EVM0009347 | 15.58  | 38.60  | -1.31  | 5.00E-05  | 4.28E-04  | -- | WH2 motif |
| EVM0006427 | 202.36 | 501.12 | -1.31  | 5.00E-05  | 4.28E-04  | Amino acid transport and metabolism | Amino acid permease |
| EVM0006431 | 75.01  | 185.70 | -1.31  | 5.00E-05  | 4.28E-04  | -- | -- |
| EVM0011795 | 25.99  | 64.29  | -1.31  | 1.00E-04  | 7.96E-04  | -- | -- |
| EVM0003465 | 23.61  | 58.39  | -1.31  | 5.00E-05  | 4.28E-04  | -- | -- |
| EVM0007305 | 332.47 | 821.83 | -1.31  | 5.00E-05  | 4.28E-04  | RNA processing and modification | U1 zinc finger |
| EVM0002015 | 34.68  | 85.69  | -1.31  | 5.00E-05  | 4.28E-04  | Function unknown | -- |
| EVM0005233 | 22.80  | 56.32  | -1.30  | 5.00E-05  | 4.28E-04  | Lipid transport and metabolism | Alpha/beta hydrolase family |
| ID         | Gene     | Description                         | Description                                |
|------------|----------|-------------------------------------|-------------------------------------------|
| EVM0011396 | Glycosyl hydrolase family 7          |                                      |
| EVM0001699 | Ribosomal protein L13                |                                      |
| EVM0005976 | Translation, ribosomal structure and biogenesis | Sugar (and other) transporter |
| EVM0002013 | General function prediction only     |                                      |
| EVM0011522 | Defense mechanisms                   | NAD dependent epimerase/dehydratase family |
| EVM0000959 | Cytoskeleton                         | Dynamitin                             |
| EVM0000586 | Pheromone A receptor                 |                                      |
| EVM0003201 | Mitochondrial ATP synthase epsilon chain |                                      |
| EVM0003190 | Terpene synthase family, metal binding domain |                                      |
| EVM0008552 | --                                   |                                      |
| EVM0011618 | --                                   |                                      |
| EVM0007362 | Glycosyl hydrolases family 6         |                                      |
| EVM0000068 | Function unknown                     | Uncharacterized conserved protein (DUF2346) |
| Accession | Value1 | Value2 | pValue1 | pValue2 | Description |
|-----------|--------|--------|---------|---------|-------------|
| EVM0004607  | 7.39   | 18.09  | -1.29   |         |             |
| EVM0006677  | 12.11  | 29.64  | -1.29   |         |             |
| EVM0010899  | 44.21  | 108.20 | -1.29   |         | RNA processing and modification |
| EVM0007673  | 43.86  | 107.31 | -1.29   |         | Transcription |
| EVM0010123  | 5.99   | 14.67  | -1.29   |         | Transcription |
| EVM0004016  | 161.79 | 395.80 | -1.29   |         | Transcription |
| EVM0003444  | 3.52   | 8.62   | -1.29   |         | Carbohydrate transport and metabolism |
| EVM0005581  | 7.63   | 18.67  | -1.29   |         | Lysine-specific metallo-endopeptidase |
| EVM0001790  | 725.79 | 1774.62| -1.29   |         | Translation, ribosomal structure and biogenesis |
| EVM0003382  | 17.28  | 42.24  | -1.29   |         | Translation, ribosomal structure and biogenesis |
| EVM0006090  | 70.19  | 171.57 | -1.29   |         | Ribosomal protein L44 |
| EVM0007699  | 116.48 | 284.65 | -1.29   |         | Dihydrouridine synthase (Dus) |
| EVM0012102  | 18.41  | 44.99  | -1.29   |         | Glycosyl transferase family 90 |

- Major Facilitator Superfamily
- Ribonuclease T2 family
- SWIB/MDM2 domain
- Myb-like DNA-binding domain
- Protein of unknown function (DUF1275)
| EVM0001924  | 9.20 | 22.44 | -1.29 | 4.50E-04 | 2.92E-03 | -- | COMPASS (Complex proteins associated with Set1p) component shg1 |
| EVM0000161  | 91.32| 222.73| -1.29 | 5.00E-05 | 4.28E-04 | Intracellular trafficking, secretion, and vesicular transport | Coatomer epsilon subunit |
| EVM0008044  | 15.30| 37.30 | -1.29 | 6.00E-04 | 3.72E-03 | -- | -- |
| EVM0007655  | 23.46| 57.19 | -1.29 | 5.00E-05 | 4.28E-04 | RNA processing and modification | DEAD/DEAH box helicase |
| EVM0002460  | 154.12| 375.56| -1.29 | 1.18E-02 | 4.26E-02 | General function prediction only | Proteolipid membrane potential modulator |
| EVM0005659  | 32.91| 80.18 | -1.28 | 5.00E-05 | 4.28E-04 | -- | -- |
| EVM0009649  | 2.48 | 6.04  | -1.28 | 5.55E-03 | 2.34E-02 | -- | -- |
| EVM0001525  | 27.70| 67.45 | -1.28 | 5.00E-05 | 4.28E-04 | -- | -- |
| EVM0002152  | 16.87| 41.05 | -1.28 | 1.00E-04 | 7.96E-04 | -- | -- |
| EVM0009830  | 1.53 | 3.73  | -1.28 | 4.55E-03 | 1.99E-02 | -- | -- |
| EVM0007137  | 9.98 | 24.27 | -1.28 | 2.00E-04 | 1.46E-03 | -- | Glycosyl hydrolase family 61 |
| EVM0012095  | 7.67 | 18.66 | -1.28 | 5.00E-04 | 3.19E-03 | #N/A | #N/A |
| EVM ID       | Predicted    | Identity | Similarity | E Value 1 | E Value 2 | Description                                                  |
|--------------|--------------|----------|------------|-----------|-----------|--------------------------------------------------------------|
| EVM0003241   | 37.16        | 90.35    | -1.28      | 5.00E-05  | 4.28E-04  | Helix-loop-helix DNA-binding domain                          |
| EVM0002387   | 98.09        | 238.42   | -1.28      | 5.00E-05  | 4.28E-04  | Coiled-coil domain containing protein (DUF2052)             |
| EVM0003871   | 2.72         | 6.61     | -1.28      | 1.00E-04  | 7.96E-04  | Cytochrome P450                                             |
| EVM0004125   | 0.56         | 1.35     | -1.28      | 3.65E-03  | 1.66E-02  | --                                                          |
| EVM0003678   | 5.28         | 12.82    | -1.28      | 1.00E-04  | 7.96E-04  | FAD binding domain                                          |
| EVM0002245   | 30.43        | 73.87    | -1.28      | 5.00E-05  | 4.28E-04  | Function unknown Leo1-like protein                           |
| EVM0002319   | 46.36        | 112.45   | -1.28      | 5.00E-05  | 4.28E-04  | Ribosome recycling factor                                   |
| EVM0003843   | 104.89       | 254.35   | -1.28      | 5.00E-05  | 4.28E-04  | --                                                          |
| EVM0006953   | 2.76         | 6.69     | -1.28      | 7.50E-04  | 4.49E-03  | Cytoskeleton                                                |
| EVM0004819   | 31.71        | 76.87    | -1.28      | 5.00E-05  | 4.28E-04  | Intracellular trafficking, secretion, and vesicular transport |
| EVM0002675   | 15.78        | 38.25    | -1.28      | 7.50E-04  | 4.49E-03  | Outer mitochondrial membrane transport complex protein       |
| EVM0010399   | 7.06         | 17.11    | -1.28      | 8.50E-04  | 4.98E-03  | Glutathione-dependent formaldehyde-activating enzyme         |
| EVM0010401   | 7.06         | 17.11    | -1.28      | 8.50E-04  | 4.98E-03  | Alpha/beta hydrolase family                                 |
| Gene ID     | Description | N-Terminal Position | C-Terminal Position | Function                                      | Protein Name                        |
|------------|-------------|---------------------|---------------------|-----------------------------------------------|------------------------------------|
| EVM0008435 | 10.59       | 25.62               | -1.27               | 1.00E-04                                      | 7.96E-04                           |
| EVM0007564 | 7.19        | 17.40               | -1.27               | 5.00E-05                                      | 4.28E-04                           | Transcription                      | Fork head domain                  |
| EVM0007792 | 16.83       | 40.73               | -1.27               | 5.00E-05                                      | 4.28E-04                           | Transcription                      | --                               |
| EVM0010912 | 7.61        | 18.42               | -1.27               | 3.00E-04                                      | 2.07E-03                           | Transcription                      | --                               |
| EVM0000946 | 20.23       | 48.85               | -1.27               | 5.00E-05                                      | 4.28E-04                           | Function unknown                   | Rgp1                              |
| EVM0009929 | 26.15       | 63.12               | -1.27               | 5.00E-05                                      | 4.28E-04                           | Translation, ribosomal structure   | 39S mitochondrial ribosomal protein L46 |
| EVM0010487 | 40.89       | 98.68               | -1.27               | 5.00E-05                                      | 4.28E-04                           | --                                | Helix-loop-helix DNA-binding domain |
| EVM0009330 | 25.55       | 61.63               | -1.27               | 5.00E-05                                      | 4.28E-04                           | --                                | NADH(P)-binding                   |
| EVM0009617 | 27.27       | 65.75               | -1.27               | 5.00E-05                                      | 4.28E-04                           | --                                | Oxidoreductase FAD-binding domain  |
| EVM0000564 | 220.48      | 531.46              | -1.27               | 5.00E-05                                      | 4.28E-04                           | Amino acid transport and metabolism | Isocitrate/isopropylmalate dehydrogenase |
| EVM0000001 | 26.09       | 62.82               | -1.27               | 5.00E-05                                      | 4.28E-04                           | Intracellular trafficking, secretion, and vesicular transport | ADP-ribosylation factor family |
| EVM0008547 | 2.67        | 6.42                | -1.27               | 2.95E-03                                      | 1.40E-02                           | Common central domain of tyrosinase | --                               |
| EVM0012198 | 143.50 | 345.38 | -1.27 | 5.00E-05 | 4.28E-04 | -- | Ribosomal protein L30p/L7e |
| EVM0006827 | 77.08 | 185.41 | -1.27 | 1.00E-04 | 7.96E-04 | -- | -- |
| EVM0011593 | 6.21 | 14.94 | -1.27 | 4.00E-04 | 2.65E-03 | Carbohydrate transport and metabolism | Major Facilitator Superfamily |
| EVM0007864 | 3.29 | 7.92 | -1.27 | 1.50E-03 | 8.00E-03 | -- | -- |
| EVM0006420 | 2.70 | 6.49 | -1.26 | 3.35E-03 | 1.55E-02 | -- | -- |
| EVM0007780 | 55.76 | 133.96 | -1.26 | 5.00E-05 | 4.28E-04 | -- | -- |
| EVM0003818 | 14.42 | 34.63 | -1.26 | 5.00E-05 | 4.28E-04 | RNA processing and modification | RNA recognition motif. (a.k.a. RRM, RBD, or RNP domain) |
| EVM0011517 | 20.19 | 48.48 | -1.26 | 1.00E-04 | 7.96E-04 | -- | RNA12 protein |
| EVM0006062 | 64.55 | 154.93 | -1.26 | 5.00E-05 | 4.28E-04 | -- | Mitochondrial ribosomal protein subunit |
| EVM0002500 | 31.08 | 74.60 | -1.26 | 5.00E-05 | 4.28E-04 | Posttranslational modification, protein turnover, chaperones | Ribophorin I |
| EVM0005187 | 2.21 | 5.30 | -1.26 | 3.65E-03 | 1.66E-02 | Cell cycle control, cell division, chromosome partitioning | Replication Fork Protection Component Swi3 |
| EVM0011999 | 3.21 | 7.71 | -1.26 | 5.05E-03 | 2.17E-02 | -- | -- |
| Gene ID     | Expression | Fold Change | Z Score | Description                                                                 |
|------------|------------|-------------|---------|-----------------------------------------------------------------------------|
| EVM0006516 | 46.01      | -1.26       | 5.00E-05| 4.28E-04                      | Transcription factor Tfβ2                                                 |
| EVM0006456 | 64.44      | -1.26       | 2.60E-03| 1.26E-02                      | General function prediction only                                         |
| EVM0004843 | 17.52      | -1.26       | 2.00E-04| 1.46E-03                      | RNA recognition motif. (a.k.a. RRM, RBD, or RNP domain)                  |
| EVM0003376 | 29.32      | -1.26       | 1.00E-04| 7.96E-04                      | Ricin-type beta-trefoil lectin domain-like                                |
| EVM0003305 | 72.35      | -1.26       | 5.00E-05| 4.28E-04                      | Nucleotide transport and metabolism                                        |
| EVM0009226 | 35.67      | -1.26       | 5.00E-05| 4.28E-04                      | Guanylate kinase                                                          |
| EVM0000332 | 92.46      | -1.26       | 1.50E-04| 1.14E-03                      | Carbohydrate transport and metabolism                                     |
| EVM0011937 | 3.44       | -1.26       | 1.50E-04| 1.14E-03                      | Glycosyl hydrolase family 47                                              |
| EVM0002882 | 25.59      | -1.26       | 5.00E-05| 4.28E-04                      | Lipid transport and metabolism                                            |
| EVM0004115 | 1.44       | -1.26       | 4.05E-03| 1.81E-02                      | Thiolase, N-terminal domain                                               |
| EVM0007189 | 172.54     | -1.25       | 5.00E-05| 4.28E-04                      | GDP-fucose protein O-fucosyltransferase                                  |
| EVM0007966 | 193.40     | -1.25       | 1.50E-04| 1.14E-03                      | Na+ dependent nucleoside transporter C-terminus                           |
| EVM0010650 | 148.37     | -1.25       | 5.00E-05| 4.28E-04                      | Nnf1                                                                      |
| Accession  | log2FC  | FDR   | Evalue  | Annotation                                      |
|------------|---------|-------|---------|------------------------------------------------|
| EVM0011480 | 129.75  | 309.14| -1.25   | Ion transport protein                           |
| EVM0008447 | 51.60   | 122.92| -1.25   | --                                              |
| EVM0011940 | 2.31    | 5.49  | -1.25   | General function prediction only                |
| EVM0000324 | 81.26   | 193.47| -1.25   | --                                              |
| EVM0005479 | 46.75   | 111.26| -1.25   | Function unknown                                |
| EVM0003416 | 22.70   | 54.03 | -1.25   | --                                              |
| EVM0009266 | 18.45   | 43.89 | -1.25   | Cytoskeleton                                    |
| EVM0005706 | 2.96    | 7.03  | -1.25   | F-box-like                                      |
| EVM0009176 | 3.91    | 9.30  | -1.25   | --                                              |
| EVM0008107 | 7.54    | 17.93 | -1.25   | --                                              |
| EVM0008590 | 281.70  | 669.69| -1.25   | Posttranslational modification, protein turnover, chaperones |
| EVM0010474 | 91.84   | 218.31| -1.25   | --                                              |
| Accession     | E-value 1 | E-value 2 | Log10(p-value) 1 | Log10(p-value) 2 | Annotation                                                                 |
|--------------|-----------|-----------|------------------|------------------|---------------------------------------------------------------------------|
| EVM0011806   | 647.26    | 1538.05   | -1.25            | 5.00E-05         | Translation, ribosomal structure and biogenesis                          |
| EVM0010148   | 177.16    | 420.48    | -1.25            | 5.00E-04         | --                                                                        |
| EVM0012036   | 11.30     | 26.81     | -1.25            | 1.55E-03         | --                                                                        |
| EVM0008396   | 5.98      | 14.16     | -1.24            | 5.45E-03         | General function prediction only                                          |
| EVM0005806   | 141.17    | 334.52    | -1.24            | 4.50E-04         | Carbohydrate transport and metabolism                                     |
| EVM0006187   | 3.53      | 8.37      | -1.24            | 8.00E-04         | Transcription                                                             |
| EVM0011155   | 23.60     | 55.90     | -1.24            | 1.50E-04         | PPR repeat family                                                         |
| EVM0012113   | 34.04     | 80.57     | -1.24            | 2.00E-04         | --                                                                        |
| EVM0003050   | 110.20    | 260.76    | -1.24            | 5.00E-05         | Translation, ribosomal structure and biogenesis                          |
| EVM0003533   | 25.29     | 59.83     | -1.24            | 5.00E-05         | Posttranslational modification, protein turnover, chaperones              |
| EVM0000366   | 5.23      | 12.37     | -1.24            | 9.50E-04         | --                                                                        |
| EVM0001597   | 23.10     | 54.63     | -1.24            | 1.00E-04         | --                                                                        |

Ribosomal protein L18e/L15
Glycosyl hydrolase family 47
HMG (high mobility group) box
PPR repeat family
Elongation factor Tu GTP binding domain
DnaJ domain
| EVM0001395 | 29.87 | 70.61 | -1.24 | 5.00E-05 4.28E-04 | Nucleotide transport and metabolism | GDA1/CD39 (nucleoside phosphatase) family |
|------------|-------|-------|--------|-------------------|------------------------------------|------------------------------------------|
| EVM0009898 | 1641.79 | 3879.65 | -1.24 | 5.00E-05 4.28E-04 | Intracellular trafficking, secretion, and vesicular transport | SecE/Sec61-gamma subunits of protein translocation complex |
| EVM0000610 | 0.87 | 2.06 | -1.24 | 9.25E-03 3.52E-02 | Amino acid transport and metabolism | Amino acid permease |
| EVM0006686 | 191.57 | 452.51 | -1.24 | 3.00E-04 2.07E-03 | -- | Protein of unknown function (DUF4449) |
| EVM0009421 | 30.45 | 71.82 | -1.24 | 6.50E-04 3.98E-03 | #N/A | #N/A |
| EVM0012070 | 1163.47 | 2743.83 | -1.24 | 6.50E-04 3.98E-03 | -- | RNA recognition motif. (a.k.a. RRM, RBD, or RNP domain) |
| EVM0001951 | 5.79 | 13.66 | -1.24 | 4.00E-03 1.79E-02 | -- | -- |
| EVM0004854 | 205.35 | 484.06 | -1.24 | 5.00E-05 4.28E-04 | -- | Mitochondrial import protein Pam17 |
| EVM0010302 | 7.07 | 16.66 | -1.24 | 1.85E-03 9.52E-03 | -- | -- |
| EVM0008681 | 181.04 | 426.51 | -1.24 | 5.00E-05 4.28E-04 | -- | Isochorismatase family |
| EVM0003613 | 91.43 | 215.38 | -1.24 | 5.00E-05 4.28E-04 | Energy production and conversion | Mitochondrial carrier protein |
| EVM0005121 | 190.59 | 448.80 | -1.24 | 5.00E-05 4.28E-04 | General function prediction only | Ras family |
| EVM0001485 | 448.77 | 1054.55 | -1.23 | 1.00E-04 | 7.96E-04 | General function prediction only | Ras family |
| EVM0006005 | 73.89  | 173.56  | -1.23 | 8.10E-03 | 3.17E-02 | Posttranslational modification, protein turnover, chaperones | Dolichol phosphate-mannose biosynthesis regulatory protein (DPM2) |
| EVM0010250 | 21.97  | 51.56   | -1.23 | 5.00E-05 | 4.28E-04 | General function prediction only | PPR repeat family |
| EVM0011110 | 1.39   | 3.26    | -1.23 | 6.70E-03 | 2.72E-02 | -- | CAP-Gly domain |
| EVM0007529 | 11.83  | 27.75   | -1.23 | 1.00E-04 | 7.96E-04 | RNA processing and modification | Hinge domain of cleavage stimulation factor subunit 2 |
| EVM0004251 | 17.77  | 41.69   | -1.23 | 5.00E-05 | 4.28E-04 | -- | F-box-like |
| EVM0007280 | 57.24  | 134.18  | -1.23 | 7.50E-04 | 4.49E-03 | -- | -- |
| EVM0010330 | 6.51   | 15.26   | -1.23 | 3.00E-04 | 2.07E-03 | -- | -- |
| EVM0010387 | 98.34  | 230.34  | -1.23 | 5.00E-05 | 4.28E-04 | Transcription | Transcription initiation factor TFIID 23-30kDa subunit |
| EVM0010109 | 7.76   | 18.17   | -1.23 | 1.50E-04 | 1.14E-03 | Replication, recombination and repair | Eukaryotic and archaeal DNA primase, large subunit |
| EVM0006960 | 2.33   | 5.44    | -1.23 | 1.39E-02 | 4.86E-02 | -- | -- |
| EVM0007745 | 20.47  | 47.88   | -1.23 | 5.00E-05 | 4.28E-04 | -- | F-box-like |
| EVM0011701 | 63.02 | 147.36 | -1.23 | 3.00E-04 | 2.07E-03 | -- | Single-strand binding protein family |
| EVM0008483 | 19.55 | 45.71 | -1.22 | 8.00E-04 | 4.73E-03 | Function unknown | PRP38 family |
| EVM0008277 | 11.83 | 27.66 | -1.22 | 2.00E-04 | 1.46E-03 | -- | Metallopeptidase family M24 |
| EVM0011393 | 2.83 | 6.62 | -1.22 | 1.50E-04 | 1.14E-03 | -- | Fungal specific transcription factor domain |
| EVM0003749 | 6.15 | 14.36 | -1.22 | 6.50E-04 | 3.98E-03 | Replication, recombination and repair | 8-oxoguanine DNA glycosylase, N-terminal domain |
| EVM0006115 | 4.20 | 9.81 | -1.22 | 3.80E-03 | 1.72E-02 | Carbohydrate transport and metabolism | Glycosyl transferase family 8 |
| EVM0007412 | 243.37 | 568.20 | -1.22 | 2.00E-03 | 1.46E-02 | -- | Domain of unknown function (DUF202) |
| EVM0009748 | 19.92 | 46.49 | -1.22 | 5.00E-05 | 4.28E-04 | -- | Endoplasmic reticulum-based factor for assembly of V-ATPase |
| EVM0002305 | 629.93 | 1469.34 | -1.22 | 2.00E-03 | 1.46E-02 | Chromatin structure and dynamics | Core histone H2A/H2B/H3/H4 |
| EVM0001581 | 53.97 | 125.81 | -1.22 | 5.00E-05 | 4.28E-04 | RNA processing and modification | Putative methyltransferase |
| EVM000627 | 20.02 | 46.66 | -1.22 | 3.50E-04 | 2.36E-03 | General function prediction only | Mpv17 / PMP22 family |
| EVM006755 | 19.01 | 44.27 | -1.22 | 5.00E-05 | 4.28E-04 | -- | -- |
| EVM0010566 | 8.45 | 19.65 | -1.22 | 5.00E-05 | 4.28E-04 | Function unknown | WD domain, G-beta repeat |
| EVM0003921 | 76.14 | 177.04 | -1.22 | 1.00E-04 | 7.96E-04 | -- | Mitochondrial ribosomal protein subunit L20 |
| EVM0001542 | 29.86 | 69.42 | -1.22 | 5.00E-05 | 4.28E-04 | -- | -- |
| EVM0011278 | 478.09 | 1110.28 | -1.22 | 5.00E-05 | 4.28E-04 | -- | -- |
| EVM0007683 | 5.06 | 11.76 | -1.22 | 1.50E-04 | 1.14E-03 | Posttranslational modification, protein turnover, chaperones | -- |
| EVM0006702 | 19.81 | 46.00 | -1.22 | 5.00E-05 | 4.28E-04 | -- | -- |
| EVM0006846 | 49.23 | 114.19 | -1.21 | 5.00E-05 | 4.28E-04 | RNA processing and modification | Prp18 domain |
| EVM0009325 | 72.98 | 169.25 | -1.21 | 5.00E-05 | 4.28E-04 | Amino acid transport and metabolism | Transmembrane amino acid transporter protein |
| EVM0000484 | 15.65 | 36.27 | -1.21 | 1.50E-04 | 1.14E-03 | -- | -- |
| EVM0003062 | 14.12 | 32.73 | -1.21 | 1.50E-04 | 1.14E-03 | -- | -- |
| EVM0008020 | 5.32 | 12.32 | -1.21 | 1.90E-03 | 9.73E-03 | -- | -- |
| EVM0012127 | 19.67 | 45.57 | -1.21 | 5.00E-05 | 4.28E-04 | -- | PXA domain |
| EVM0007066 | 11.40 | 26.40 | -1.21 | 2.00E-04 | 1.46E-03 | -- | -- |
| Gene ID   | Value 1 | Value 2 | Log2 Ratio | Function                        | Description                                      |
|----------|---------|---------|------------|--------------------------------|--------------------------------------------------|
| EVM0009686 | 179.09  | 414.48  | -1.21      | 5.00E-05 4.28E-04 Transcription | Spt4/RpoE2 zinc finger                            |
| EVM0000630 | 26.51   | 61.33   | -1.21      | 2.50E-04 1.77E-03                | --                                               |
| EVM0007883 | 261.91  | 605.79  | -1.21      | 1.50E-04 1.14E-03                | --                                               |
| EVM0004213 | 134.33  | 310.59  | -1.21      | 5.00E-05 4.28E-04 Function unknown | Yip1 domain                                      |
| EVM0010984 | 772.08  | 1785.06 | -1.21      | 1.00E-04 7.96E-04 Transcription | NAC domain                                       |
| EVM0008773 | 3639.22 | 8413.37 | -1.21      | 4.55E-03 1.99E-02                | --                                               |
| EVM0003316 | 471.55  | 1089.32 | -1.21      | 1.00E-04 7.96E-04                | --                                               |
| EVM0002007 | 25.92   | 59.87   | -1.21      | 3.00E-04 2.07E-03 Energy production and conversion | Cytochrome b5-like Heme/Steroid binding domain |
| EVM0006616 | 1284.85 | 2965.34 | -1.21      | 1.35E-03 7.33E-03 Energy production and conversion | Mitochondrial carrier protein                    |
| EVM0011921 | 512.60  | 1182.96 | -1.21      | 1.50E-03 8.00E-03 Energy production and conversion | Aldehyde dehydrogenase family                   |
| EVM0011762 | 95.88   | 221.26  | -1.21      | 5.00E-05 4.28E-04 General function prediction only | --                                               |
| EVM0003534 | 5.29    | 12.21   | -1.21      | 2.50E-04 1.77E-03                | -- Major Facilitator Superfamily                 |
| EVM0004944 | 3.94    | 9.10    | -1.21      | 8.45E-03 3.28E-02                | -- F-box-like                                    |
| Accession  | Value1 | Value2 | Value3 | Value4 | Value5 | Value6 | Description                                                                 |
|-----------|--------|--------|--------|--------|--------|--------|-----------------------------------------------------------------------------|
| EVM0009399 | 28.13  | 64.87  | -1.21  | 5.00E-05 | 4.28E-04 | -- | Mediator complex subunit 25 von Willebrand factor type A                   |
| EVM0008425 | 1.46   | 3.37   | -1.21  | 3.45E-03 | 1.59E-02 | -- | --                                                                         |
| EVM0002309 | 44.24  | 101.98 | -1.20  | 5.00E-05 | 4.28E-04 | Energy production and conversion | NAD-dependent glycerol-3-phosphate dehydrogenase C-terminus               |
| EVM0000499 | 25.93  | 59.76  | -1.20  | 5.00E-05 | 4.28E-04 | Translation, ribosomal structure and biogenesis | GatB/GatE catalytic domain                                                  |
| EVM0004351 | 8.45   | 19.45  | -1.20  | 9.00E-04 | 5.22E-03 | -- | --                                                                         |
| EVM0009324 | 86.36  | 198.79 | -1.20  | 5.00E-05 | 4.28E-04 | -- | Transposase family tnp2                                                   |
| EVM0009762 | 2.84   | 6.54   | -1.20  | 2.65E-03 | 1.28E-02 | -- | --                                                                         |
| EVM0001479 | 1755.29| 4040.24| -1.20  | 1.00E-04 | 7.96E-04 | Translation, ribosomal structure and biogenesis | Ribosomal protein L18e/L15                                                 |
| EVM0011499 | 8.32   | 19.14  | -1.20  | 3.50E-04 | 2.36E-03 | -- | --                                                                         |
| EVM0007589 | 489.61 | 1124.30| -1.20  | 7.00E-04 | 4.23E-03 | General function prediction only | Protein of unknown function (DUF1295)                                     |
| EVM0010503 | 25.36  | 58.19  | -1.20  | 5.00E-05 | 4.28E-04 | Transcription | --                                                                         |
| EVM0002352 | 54.98  | 126.12 | -1.20  | 1.50E-04 | 1.14E-03 | RNA processing and modification | DEAD/DEAH box helicase                                                     |
| EVM0011926 | 17.47 | 40.07 | -1.20 | 1.00E-04 | 7.96E-04 | -- | -- |
| EVM0011433 | 6.78  | 15.56 | -1.20 | 1.00E-04 | 7.96E-04 | -- | F-box-like |
| EVM0001189 | 47.14 | 108.13| -1.20 | 5.00E-05 | 4.28E-04 | Chromatin structure and dynamics | Histone deacetylase domain |
| EVM0011112 | 13.39 | 30.69 | -1.20 | 6.00E-04 | 3.72E-03 | -- | -- |
| EVM0006378 | 20.81 | 47.70 | -1.20 | 5.00E-05 | 4.28E-04 | Carbohydrate transport and metabolism | UDP-glucose:Glycoprotein Glucosyltransferase |
| EVM0008577 | 94.72 | 217.04| -1.20 | 5.00E-05 | 4.28E-04 | Intracellular trafficking, secretion, and vesicular transport | Adaptor complexes medium subunit family |
| EVM0003908 | 94.74 | 217.04| -1.20 | 5.00E-05 | 4.28E-04 | -- | RNA recognition motif. (a.k.a. RRM, RBD, or RNP domain) |
| EVM0010265 | 35.36 | 80.93 | -1.19 | 5.00E-05 | 4.28E-04 | General function prediction only | Conserved hypothetical ATP binding protein |
| EVM0005768 | 463.72| 1061.07| -1.19 | 3.00E-04 | 2.07E-03 | -- | Peroxidase |
| EVM0011816 | 171.01| 390.79| -1.19 | 1.50E-04 | 1.14E-03 | RNA processing and modification | LSM domain |
| EVM0000987 | 164.98| 376.69| -1.19 | 5.00E-05 | 4.28E-04 | -- | -- |
| EVM0001074 | 124.72| 284.65| -1.19 | 9.00E-04 | 5.22E-03 | Function unknown | Membrane transport protein |
| Accession     | Fold | EL Z-score | S-score | 4.0E-03 | 9.08E-03 | 4.28E-04 | 2.32E-02 | 5.00E-05 | 5.50E-03 | 1.75E-03 | 7.96E-04 | 4.28E-04 | 1.50E-04 | 1.14E-03 | 0.19 | 1.19 |
|---------------|------|------------|---------|---------|----------|---------|---------|---------|---------|---------|---------|---------|---------|---------|-------|------|
| EVM0003745    | 6.42 | 14.65      | -1.19   | 1.50E-04| 1.14E-03 | --      | --      | --      | --      | --      | --      | --      | --      | --      | 1-1  |    1|
| EVM0001611    | 2.69 | 6.14       | -1.19   | 1.75E-03| 9.08E-03 | --      | --      | --      | --      | --      | --      | --      | --      | --      | 1-1  |    1|
| EVM0000210    | 15.91| 36.29      | -1.19   | 5.00E-05| 4.28E-04 | --      | --      | --      | --      | --      | --      | --      | --      | --      | 1-1  |    1|
| EVM0009567    | 3.01 | 6.87       | -1.19   | 5.50E-03| 2.32E-02 | Cell cycle control, cell division, chromosome partitioning | Protein kinase domain | | |
| EVM0003446    | 47.25| 107.74     | -1.19   | 1.00E-04| 7.96E-04 | --      | --      | --      | --      | --      | --      | --      | --      | --      | 1-1  |    1|
| EVM0006175    | 19.18| 43.73      | -1.19   | 5.00E-05| 4.28E-04 | Coenzyme transport and metabolism | Polypropenyl synthetase | | |
| EVM0006954    | 21.23| 48.39      | -1.19   | 5.00E-05| 4.28E-04 | --      | --      | --      | --      | --      | --      | --      | --      | --      | 1-1  |    1|
| EVM0010102    | 46.90| 106.70     | -1.19   | 5.00E-05| 4.28E-04 | --      | --      | --      | --      | --      | --      | --      | --      | --      | 1-1  |    1|
| EVM0005135    | 13.43| 30.55      | -1.19   | 3.00E-04| 2.07E-03 | Secondary metabolites biosynthesis, transport and catabolism | Cytochrome P450 | | |
| EVM0008217    | 26.33| 59.89      | -1.19   | 1.00E-04| 7.96E-04 | --      | --      | --      | --      | --      | --      | --      | --      | --      | 1-1  |    1|
| EVM0004807    | 5.73 | 13.03      | -1.19   | 2.50E-04| 1.77E-03 | Chromatin structure and dynamics | Histone deacetylase domain | | |
| EVM0008662    | 63.23| 143.76     | -1.18   | 5.00E-05| 4.28E-04 | --      | --      | --      | --      | --      | --      | --      | --      | --      | 1-1  |    1|

- Glycosyl hydrolase family 61
- Protein of unknown function (DUF2012)
- Protein kinase domain
- Nucleoporin FG repeat region
- Cytochrome P450
- Acetyltransferase (GNAT) family
- Histone deacetylase domain
- Protein of unknown function (DUF2009)
| ID              | Value1 | Value2 | Value3 | Value4 | Value5 | Value6 | Function/Domain                                                                 |
|-----------------|--------|--------|--------|--------|--------|--------|--------------------------------------------------------------------------------|
| EVM0003185      | 2.30   | 5.22   | -1.18  | 7.50E-04 | 4.49E-03 | --     | --                                                                               |
| EVM0003105      | 31.27  | 71.06  | -1.18  | 7.00E-04 | 4.23E-03 | Function unknown | FUN14 family                                           |
| EVM0009431      | 42.85  | 97.32  | -1.18  | 5.00E-05 | 4.28E-04 | --     | Mycolic acid cyclopropane synthetase                                            |
| EVM0007845      | 4.03   | 9.16   | -1.18  | 3.55E-03 | 1.62E-02 | Cell cycle control, cell division, chromosome partitioning | Cyclin, N-terminal domain |
| EVM0006239      | 2.39   | 5.42   | -1.18  | 1.15E-03 | 6.41E-03 | --     | UV-endonuclease UvdE                                                            |
| EVM0009865      | 35.64  | 80.86  | -1.18  | 5.00E-05 | 4.28E-04 | --     | --                                                                               |
| EVM0009040      | 15.53  | 35.24  | -1.18  | 1.40E-03 | 7.55E-03 | --     | --                                                                               |
| EVM0009965      | 6.10   | 13.82  | -1.18  | 5.50E-04 | 3.46E-03 | Defense mechanisms | NAD dependent epimerase/dehydratase family |
| EVM0007199      | 167.20 | 379.02 | -1.18  | 2.00E-04 | 1.46E-03 | General function prediction only | Yippee zinc-binding/DNA-binding/Mis18, centromere assembly |
| EVM0007735      | 0.78   | 1.78   | -1.18  | 5.95E-03 | 2.47E-02 | --     | --                                                                               |
| EVM0005126      | 4.20   | 9.52   | -1.18  | 1.15E-03 | 6.41E-03 | --     | --                                                                               |
| EVM0002405      | 4.82   | 10.92  | -1.18  | 7.50E-03 | 2.98E-02 | General function prediction only | Acetyltransferase (GNAT) family                         |
EVM0009203 136.43 308.80 -1.18 1.00E-04 7.96E-04 -- OTU-like cysteine protease
EVM0005760 94.99 214.88 -1.18 1.00E-04 7.96E-04 Secondary metabolites biosynthesis, transport and catabolism short chain dehydrogenase
EVM0005600 208.86 472.37 -1.18 3.35E-03 1.55E-02 -- Acetokinase family
EVM0009700 60.75 137.40 -1.18 5.00E-05 4.28E-04 -- NADH ubiquinone oxidoreductase subunit NDUFA12
EVM0006121 19.03 43.02 -1.18 2.00E-03 1.01E-02 -- FHA domain
EVM0010277 461.27 1042.14 -1.18 4.00E-04 2.65E-03 -- --
EVM0000800 162.68 367.38 -1.18 1.10E-03 6.17E-03 -- Protein of unknown function (DUF4449)
EVM0010961 1.68 3.79 -1.17 5.05E-03 2.17E-02 -- --
EVM0005918 62.55 141.09 -1.17 5.00E-05 4.28E-04 General function prediction only PQ loop repeat
EVM0005903 6.61 14.92 -1.17 4.50E-04 2.92E-03 Transcription RNA polymerase III RPC4
EVM0002113 8.73 19.70 -1.17 2.50E-04 1.77E-03 Replication, recombination and repair Rad51
EVM0005046 1.38 3.10 -1.17 7.30E-03 2.91E-02 -- Glycosyl Hydrolase Family 88
| EVM0006624 | 22.97 | 51.79 | -1.17 | 1.00E-04 | 7.96E-04 | Amino acid transport and metabolism | Pyridoxal-phosphate dependent enzyme |
| EVM0003706 | 13.20 | 29.74 | -1.17 | 6.75E-03 | 2.74E-02 | -- | -- |
| EVM0009875 | 7.82 | 17.62 | -1.17 | 5.50E-04 | 3.46E-03 | -- | -- |
| EVM0006106 | 28.39 | 63.97 | -1.17 | 1.00E-04 | 7.96E-04 | -- | -- |
| EVM0007277 | 708.74 | 1596.78 | -1.17 | 2.50E-04 | 1.77E-04 | -- | -- |
| EVM0001436 | 18.77 | 42.27 | -1.17 | 3.00E-04 | 2.07E-03 | -- | WD domain, G-beta repeat |
| EVM0003299 | 63.29 | 142.58 | -1.17 | 5.00E-05 | 4.28E-04 | -- | Protein kinase domain |
| EVM0009609 | 55.15 | 124.22 | -1.17 | 2.50E-04 | 1.77E-04 | Signal transduction mechanisms | RhoGEF domain |
| EVM0004559 | 5.57 | 12.56 | -1.17 | 2.00E-04 | 1.46E-03 | -- | Fungalysin metallopeptidase (M36) |
| EVM0011169 | 74.39 | 167.55 | -1.17 | 5.00E-05 | 4.28E-04 | Posttranslational modification, protein turnover, chaperones | ATPase family associated with various cellular activities (AAA) |
| EVM0006316 | 7.60 | 17.11 | -1.17 | 2.00E-04 | 1.46E-03 | Function unknown | WW domain binding protein 11 |
| EVM0010206 | 9.45 | 21.27 | -1.17 | 2.00E-04 | 1.46E-03 | -- | -- |
| Gene ID     | Log2 FC | Log10 P | Log2 FC | Gene ID     | Log2 FC | Log10 P | Log2 FC | Description                                                                 |
|------------|---------|---------|---------|------------|---------|---------|---------|-----------------------------------------------------------------------------|
| EVM0011354 | 47.62   | 107.13  | -1.17   | EVM001874  | 8.64    | 19.43   | -1.17   | Lipid transport and metabolism                                             |
| EVM0004039 | 172.18  | 387.23  | -1.17   | EVM0011261 | 21.91   | 49.26   | -1.17   | Translation, ribosomal structure and biogenesis                            |
| EVM0000626 | 51.96   | 116.80  | -1.17   | EVM0008219 | 228.57  | 513.77  | -1.17   | General function prediction only                                          |
| EVM0007891 | 193.38  | 434.67  | -1.17   | EVM002521  | 159.31  | 358.08  | -1.17   | Lipid transport and metabolism                                             |
| EVM0001097 | 32.54   | 73.08   | -1.17   | EVM001993  | 66.87   | 150.11  | -1.17   | Acyl-CoA dehydrogenase, C-terminal domain                                  |
| EVM0005518 | 1.89    | 4.23    | -1.17   | EVM0001560 | 321.02  | 720.12  | -1.17   | Mitochondrial export protein Som1                                          |
| EVM0002723 | 42.95   | 96.28   | -1.16   | EVM0001560 | 321.02  | 720.12  | -1.17   | Acyl-CoA dehydrogenase, C-terminal domain                                  |
|            |         |         |         | EVM0001560 | 321.02  | 720.12  | -1.17   | Mitochondrial export protein Som1                                          |
| EVM0001560 | 321.02  | 720.12  | -1.17   | EVM0002723 | 42.95   | 96.28   | -1.16   | Mitochondrial export protein Som1                                          |
| EVM0005518 | 1.89    | 4.23    | -1.17   | EVM0001560 | 321.02  | 720.12  | -1.17   | Mitochondrial export protein Som1                                          |
| EVM0001560 | 321.02  | 720.12  | -1.17   | EVM0002723 | 42.95   | 96.28   | -1.16   | Mitochondrial export protein Som1                                          |
| GeneID      | EVM0010521 | EVM0011026 | EVM0009047 | EVM0008894 | EVM0009726 | EVM0007223 | EVM0000289 | EVM0011516 | EVM0001684 | EVM0007438 | EVM0009155 | EVM0009214 |
|-------------|------------|------------|------------|------------|------------|------------|------------|------------|------------|------------|------------|------------|
| Score       | 159.20     | 38.41      | 19.41      | 34.83      | 133.61     | 35.22      | 22.98      | 21.39      | 30.54      | 50.54      | 55.38      | 176.79     |
| Rank        | 356.79     | 86.07      | 43.44      | 77.90      | 298.63     | 78.68      | 51.27      | 47.70      | 68.10      | 112.64     | 123.42     | 393.79     |
| Log2 Fold   | -1.16      | -1.16      | -1.16      | -1.16      | -1.16      | -1.16      | -1.16      | -1.16      | -1.16      | -1.16      | -1.16      | -1.16      |
| E-values    | 1.05E-03   | 5.00E-05   | 5.00E-05   | 5.00E-05   | 5.00E-05   | 5.00E-05   | 5.00E-05   | 5.00E-05   | 3.50E-04   | 5.00E-05   | 5.00E-05   | 5.00E-05   |

**Amino acid transport and metabolism**

Semialdehyde dehydrogenase, dimerisation domain

**General function prediction only**

**Poly A polymerase head domain**

**Translation, ribosomal structure and biogenesis**

**RNA processing and modification**

RNA recognition motif. (a.k.a. RRM, RBD, or RNP domain)

**C2H2-type zinc finger**

**Function unknown**

Ras-induced vulval development antagonist

**Casein kinase substrate phosphoprotein PP28**
| Accession      | Value1 | Value2 | Value3 | Value4 | Value5 | Value6 | Function                                                                 |
|---------------|--------|--------|--------|--------|--------|--------|--------------------------------------------------------------------------|
| EVM0009100    | 21.34  | 47.51  | -1.15  | 1.00E-04| 7.96E-04| --     | --                                                                        |
| EVM0005312    | 1.72   | 3.82   | -1.15  | 2.90E-03| 1.38E-02| --     | DNA polymerase subunit Cdc27                                            |
| EVM0010571    | 41.70  | 92.77  | -1.15  | 5.00E-05| 4.28E-04| Transcription               | Paf1                                                                       |
| EVM0010669    | 90.91  | 202.04 | -1.15  | 5.00E-05| 4.28E-04| --     | --                                                                        |
| EVM0003558    | 65.17  | 144.81 | -1.15  | 5.00E-05| 4.28E-04| --     | Methyltransferase domain                                                  |
| EVM0003112    | 3.23   | 7.17   | -1.15  | 4.50E-03| 1.97E-02| --     | --                                                                        |
| EVM0003799    | 3.74   | 8.30   | -1.15  | 2.00E-03| 1.01E-02| --     | --                                                                        |
| EVM0008502    | 4.78   | 10.60  | -1.15  | 8.50E-03| 4.98E-04| --     | --                                                                        |
| EVM0001957    | 7.42   | 16.44  | -1.15  | 8.50E-04| 4.98E-03| Secondary metabolites biosynthesis, transport and catabolism          |
| EVM0007632    | 58.12  | 128.70 | -1.15  | 5.00E-05| 4.28E-04| --     | Pyridine nucleotide-disulphide oxidoreductase                            |
| EVM0010493    | 26.31  | 58.24  | -1.15  | 3.15E-03| 1.47E-02| --     | --                                                                        |
| EVM0004170    | 20.11  | 44.50  | -1.15  | 5.00E-05| 4.28E-04| --     | --                                                                        |
| Accession       | Value 1  | Value 2  | log2 Fold Change | Description                                                                 |
|-----------------|---------|---------|-----------------|-----------------------------------------------------------------------------|
| EVM0011391      | 33.33   | 73.74   | -1.15           | Translation, ribosomal structure and biogenesis Noc2p family                |
| EVM0002501      | 75.90   | 167.78  | -1.14           | --                                                                          |
| EVM0009315      | 268.08  | 592.01  | -1.14           | RNA processing and modification    | LSM domain                |
| EVM0011952      | 77.55   | 171.16  | -1.14           | Transcription                                                                 |
| EVM0004966      | 3.63    | 8.02    | -1.14           | --                                                                          |
| EVM0011892      | 2.19    | 4.82    | -1.14           | --                                                                          | F-box-like                 |
| EVM0003518      | 23.99   | 52.89   | -1.14           | --                                                                          |
| EVM0001765      | 29.00   | 63.90   | -1.14           | --                                                                          |
| EVM0003552      | 57.99   | 127.78  | -1.14           | General function prediction only                                     |
| EVM0005877      | 892.77  | 1965.81 | -1.14           | Energy production and conversion Ubiquinol-cytochrome C reductase complex  |
| EVM0002894      | 16.28   | 35.83   | -1.14           | Transcription                                                                 |
| EVM0002136      | 546.70  | 1202.24 | -1.14           | Translation, ribosomal structure and biogenesis Ribosomal protein S4/S9 N-terminal domain |
| EVM0000700      | 56.78   | 124.84  | -1.14           | --                                                                          | 60Kd inner membrane protein |
| Gene ID       | Value    | Parameter | Score | Description                                                                 |
|--------------|----------|-----------|-------|-----------------------------------------------------------------------------|
| EVM0010096   | 49.43    | 108.67    | -1.14 | 2.00E-04 1.46E-03 -- Cupin domain                                           |
| EVM0007417   | 96.72    | 212.62    | -1.14 | 1.50E-04 1.14E-03 Chromatin structure and dynamics Core histone H2A/H2B/H3/H4 |
| EVM0002318   | 52.27    | 114.87    | -1.14 | 5.00E-05 4.28E-04 Replication, recombination and repair Peptidase M76 family |
| EVM0001770   | 7.78     | 17.11     | -1.14 | 7.00E-04 4.23E-03 -- Lactonase, 7-bladed beta-propeller                    |
| EVM0008669   | 28.59    | 62.80     | -1.14 | 5.00E-05 4.28E-04 RNA processing and modification DEAD/DEAH box helicase     |
| EVM0011868   | 55.67    | 122.29    | -1.14 | 2.50E-04 1.77E-03 Function unknown Integral membrane protein DUF106        |
| EVM0007207   | 4.79     | 10.51     | -1.13 | 8.00E-04 4.73E-03 Replication, recombination and repair Origin recognition complex (ORC) subunit 4 C-terminus |
| EVM0006493   | 100.54   | 220.63    | -1.13 | 1.50E-04 1.14E-03 -- N-acetylglucosaminyl transferase component (Gpi1)      |
| EVM0001573   | 1.69     | 3.71      | -1.13 | 1.02E-02 3.80E-02 -- --                                                   |
| EVM0001926   | 45.17    | 98.96     | -1.13 | 2.50E-04 1.77E-03 Posttranslational modification, protein turnover, chaperones Dolichyl-phosphate-mannose-protein mannosyltransferase |
| EVM0011552   | 32.78    | 71.81     | -1.13 | 4.00E-04 2.65E-03 Lipid transport and metabolism Fatty acid desaturase     |
| EVM0008804   | 68.54    | 150.05    | -1.13 | 2.00E-04 1.46E-03 -- --                                                   |
| EVM0003425  | 7.89  | 17.26 | -1.13 | 5.00E-05  | 4.28E-04 | -- | Formin Homology 2 Domain |
| EVM0009955  | 10.02 | 21.91 | -1.13 | 2.50E-04  | 1.77E-03 | -- | -- |
| EVM0005298  | 84.38 | 184.54| -1.13 | 2.00E-04  | 1.46E-03 | -- | -- |
| EVM0002573  | 10.72 | 23.43 | -1.13 | 4.50E-04  | 2.92E-03 | -- | RTA1 like protein       |
| EVM0002730  | 27.40 | 59.91 | -1.13 | 5.00E-05  | 4.28E-04 | Signal transduction mechanisms | Leucine Rich repeats (2 copies) |
| EVM0001152  | 39.83 | 87.08 | -1.13 | 3.50E-04  | 2.36E-03 | General function prediction only | Mpv17 / PMP22 family |
| EVM0005703  | 24.18 | 52.82 | -1.13 | 1.50E-04  | 1.14E-03 | Function unknown                  | Utp14 protein     |
| EVM0004423  | 15.62 | 34.09 | -1.13 | 2.05E-03  | 1.03E-02 | Posttranslational modification, protein turnover, chaperones | Peptidase S24-like |
| EVM0002797  | 108.18| 236.09| -1.13 | 5.00E-05  | 4.28E-04 | -- | -- |
| EVM0011621  | 49.66 | 108.33| -1.13 | 1.00E-04  | 7.96E-04 | Function unknown                  | Low temperature viability protein |
| EVM0002975  | 293.69| 640.47| -1.12 | 2.20E-03  | 1.10E-02 | -- | Putative stress-responsive nuclear envelope protein |
| EVM0003571  | 17.52 | 38.18 | -1.12 | 3.50E-04  | 2.36E-03 | -- | Zinc finger-containing protein |
| EVM0005298  | 84.38 | 184.54| -1.13 | 2.00E-04  | 1.46E-03 | -- | -- |
| EVM0002573  | 10.72 | 23.43 | -1.13 | 4.50E-04  | 2.92E-03 | -- | RTA1 like protein       |
| EVM0002730  | 27.40 | 59.91 | -1.13 | 5.00E-05  | 4.28E-04 | Signal transduction mechanisms | Leucine Rich repeats (2 copies) |
| EVM0001152  | 39.83 | 87.08 | -1.13 | 3.50E-04  | 2.36E-03 | General function prediction only | Mpv17 / PMP22 family |
| EVM0005703  | 24.18 | 52.82 | -1.13 | 1.50E-04  | 1.14E-03 | Function unknown                  | Utp14 protein     |
| EVM0004423  | 15.62 | 34.09 | -1.13 | 2.05E-03  | 1.03E-02 | Posttranslational modification, protein turnover, chaperones | Peptidase S24-like |
| EVM0002797  | 108.18| 236.09| -1.13 | 5.00E-05  | 4.28E-04 | -- | -- |
| EVM0011621  | 49.66 | 108.33| -1.13 | 1.00E-04  | 7.96E-04 | Function unknown                  | Low temperature viability protein |
| EVM0002975  | 293.69| 640.47| -1.12 | 2.20E-03  | 1.10E-02 | -- | Putative stress-responsive nuclear envelope protein |
| EVM0003571  | 17.52 | 38.18 | -1.12 | 3.50E-04  | 2.36E-03 | -- | Zinc finger-containing protein |
| EVM0003411 | 527.29 | 1148.21 | -1.12 | 8.00E-04 | 4.73E-03 | -- | Zinc-binding |
| EVM0002703 | 28.70  | 62.50   | -1.12 | 2.00E-04 | 1.46E-03 | -- | Domain of unknown function DUF221 |
| EVM0002459 | 10.59  | 23.06   | -1.12 | 5.00E-05 | 4.28E-04 | Cell cycle control, cell division, chromosome partitioning | N terminus of Rad21 / Rec8 like protein |
| EVM0010830 | 257.82 | 561.11  | -1.12 | 6.45E-03 | 2.64E-02 | -- | -- |
| EVM0004694 | 8.86   | 19.26   | -1.12 | 1.00E-03 | 5.70E-03 | -- | -- |
| EVM0006639 | 87.80  | 190.93  | -1.12 | 5.00E-05 | 4.28E-04 | -- | BRCA1 C Terminus (BRCT) domain |
| EVM0010286 | 4.53   | 9.85    | -1.12 | 6.50E-04 | 3.98E-03 | -- | Ferric reductase like transmembrane component |
| EVM0002557 | 15.27  | 33.20   | -1.12 | 1.50E-04 | 1.14E-03 | Replication, recombination and repair | -- |
| EVM0011493 | 21.66  | 47.08   | -1.12 | 9.50E-04 | 5.46E-03 | -- | -- |
| EVM0011176 | 112.12 | 243.57  | -1.12 | 5.00E-05 | 4.28E-04 | Translation, ribosomal structure and biogenesis | Ribosomal protein L6 |
| EVM0010559 | 22.13  | 48.06   | -1.12 | 6.00E-04 | 3.72E-03 | General function prediction only | Mitochondrial PGP phosphatase |
| EVM0004323 | 12.70  | 27.57   | -1.12 | 2.50E-04 | 1.77E-03 | Signal transduction mechanisms | Protein kinase domain |
| EVM0004600  | 65.38 | 141.95 | -1.12 | 5.00E-05 | 4.28E-04 | General function prediction only | Eukaryotic protein of unknown function (DUF846) |
| EVM0000753  | 46.09 | 100.03 | -1.12 | 1.50E-04 | 1.14E-03 | Amino acid transport and metabolism | Amino acid permease |
| EVM0003296  | 183.26| 397.72 | -1.12 | 2.25E-03 | 1.12E-02 | General function prediction only | Domain of unknown function DUF221 |
| EVM0011479  | 137.22| 297.52 | -1.12 | 5.00E-05 | 4.28E-04 | Posttranslational modification, protein turnover, chaperones | PI31 proteasome regulator N-terminal |
| EVM0011366  | 14.13 | 30.62  | -1.12 | 5.00E-05 | 4.28E-04 | -- | SDA1 |
| EVM0010660  | 20.77 | 45.02  | -1.12 | 8.30E-03 | 3.23E-02 | -- | -- |
| EVM0000793  | 122.04| 264.44 | -1.12 | 5.00E-05 | 4.28E-04 | -- | HPP family |
| EVM0002980  | 3.39  | 7.35   | -1.12 | 2.10E-03 | 1.06E-02 | Amino acid transport and metabolism | Amino acid kinase family |
| EVM0008212  | 17.56 | 38.01  | -1.11 | 1.00E-04 | 7.96E-04 | Translation, ribosomal structure and biogenesis | Glucose inhibited division protein A |
| EVM0011059  | 69.87 | 151.25 | -1.11 | 2.50E-04 | 1.77E-03 | -- | -- |
| EVM0001565  | 2.43  | 5.27   | -1.11 | 2.25E-03 | 1.12E-02 | -- | -- |
| EVM0004976  | 15.89 | 34.39  | -1.11 | 1.00E-04 | 7.96E-04 | Replication, recombination and repair | ERCC4 domain |
| EVM0001742 | 40.62 | 87.87 | -1.11 | 1.50E-04 | 1.14E-03 | General function prediction only | Alpha/beta hydrolase family |
| EVM0007593 | 110.22 | 237.91 | -1.11 | 2.00E-04 | 1.46E-03 | RNA processing and modification | Zinc knuckle |
| EVM0001412 | 3.95 | 8.53 | -1.11 | 1.04E-02 | 3.87E-02 | -- | -- |
| EVM0008609 | 20.25 | 43.68 | -1.11 | 6.75E-03 | 2.74E-02 | General function prediction only | Ankyrin repeats (3 copies) |
| EVM0006784 | 27.47 | 59.25 | -1.11 | 4.50E-04 | 2.92E-03 | General function prediction only | Zinc finger, C2H2 type |
| EVM0000063 | 249.99 | 539.17 | -1.11 | 2.00E-04 | 1.46E-03 | Nucleotide transport and metabolism | Adenylate kinase |
| EVM0004057 | 244.65 | 527.48 | -1.11 | 5.00E-05 | 4.28E-04 | -- | Ser-Thr-rich glycosyl-phosphatidyl-inositol-anchored membrane family |
| EVM0005811 | 2.59 | 5.58 | -1.11 | 1.01E-02 | 3.78E-02 | -- | -- |
| EVM0006665 | 61.41 | 132.34 | -1.11 | 5.00E-05 | 4.28E-04 | Lipid transport and metabolism | Thioesterase-like superfamily |
| EVM0001158 | 36.87 | 79.44 | -1.11 | 1.00E-04 | 7.96E-04 | -- | -- |
| EVM0009246 | 28.67 | 61.76 | -1.11 | 7.50E-04 | 4.49E-03 | -- | -- |
| EVM0003806 | 20.17 | 43.43 | -1.11 | 8.50E-04 | 4.98E-03 | -- | -- |
| EVM0002692 | 1.62  | 3.49  | -1.11  | 7.45E-03 | 2.96E-02 | Secondary metabolites biosynthesis, transport and catabolism | Cytochrome P450 |
| EVM0009392 | 150.82 | 324.50 | -1.11  | 2.55E-03 | 1.24E-02 | Posttranslational modification, protein turnover, chaperones | Sec63 Brl domain |
| EVM0008877 | 34.99  | 75.27  | -1.10  | 5.00E-05 | 4.28E-04 | -- | -- |
| EVM0001621 | 3.11   | 6.68   | -1.10  | 1.09E-02 | 4.01E-02 | -- | Glycosyl hydrolases family 11 |
| EVM0002403 | 297.77 | 640.24 | -1.10  | 1.50E-04 | 1.14E-03 | Posttranslational modification, protein turnover, chaperones | Ubiquitin-conjugating enzyme |
| EVM0005840 | 29.96  | 64.41  | -1.10  | 2.25E-03 | 1.12E-02 | -- | Sen15 protein |
| EVM0000931 | 30.20  | 64.93  | -1.10  | 1.40E-03 | 7.55E-03 | -- | Protein of unknown function (DUF3128) |
| EVM000151  | 301.75 | 648.44 | -1.10  | 2.00E-03 | 1.01E-02 | Lipid transport and metabolism | Cytochrome b5-like Heme/Steroid binding domain |
| EVM0007815 | 184.20 | 395.66 | -1.10  | 1.70E-03 | 8.87E-03 | Inorganic ion transport and metabolism | E1-E2 ATPase |
| EVM0005388 | 244.08 | 524.01 | -1.10  | 1.50E-04 | 1.14E-03 | -- | -- |
| EVM0008721 | 2.30   | 4.94   | -1.10  | 6.00E-03 | 2.49E-02 | Lipid transport and metabolism | Hydroxymethylglutaryl-coenzyme A synthase N terminal |
| ID                | Value | Value | Difference | Value | Value | Enrichment Factor |
|------------------|-------|-------|------------|-------|-------|-------------------|
| EVM0001193       | 6.56  | 14.09 | -1.10      | 4.15E-03 | 1.85E-02 | --                |
| EVM0002058       | 12.34 | 26.48 | -1.10      | 1.10E-03 | 6.17E-03 | --                |
| EVM0002564       | 25.81 | 55.38 | -1.10      | 5.00E-05 | 4.28E-04 | --                |
| EVM0006853       | 125.74| 269.72| -1.10      | 1.50E-04 | 1.14E-03 | Energy production and conversion |
| EVM0009366       | 10.03 | 21.50 | -1.10      | 3.00E-04 | 2.07E-03 | --                |
| EVM0010530       | 95.47 | 204.71| -1.10      | 2.50E-04 | 1.77E-03 | --                |
| EVM0010153       | 56.94 | 122.09| -1.10      | 1.00E-04 | 7.96E-04 | Lipid transport and metabolism |
| EVM0009451       | 8.89  | 19.07 | -1.10      | 1.00E-04 | 7.96E-04 | --                |
| EVM0000516       | 26.15 | 56.04 | -1.10      | 6.50E-04 | 3.98E-03 | --                |
| EVM0007521       | 44.53 | 95.41 | -1.10      | 5.00E-04 | 3.19E-03 | --                |
| EVM0005477       | 25.73 | 55.12 | -1.10      | 1.00E-04 | 7.96E-04 | Secondary metabolites biosynthesis, transport and catabolism |
| EVM0005021       | 1.52  | 3.25  | -1.10      | 2.65E-03 | 1.28E-02 | --                |

**Gene Ontology:**
- Energy production and conversion
- ATP synthase (CAC39) subunit
- NYN domain
- Lipid transport and metabolism
- Cytochrome P450
- Secondary metabolites biosynthesis, transport and catabolism
- Short chain dehydrogenase
| EVM0003735 | 40.07 | 85.85 | -1.10 | 5.00E-05 | 4.28E-04 | Function unknown | Rtf2 RING-finger |
| EVM0000021 | 234.83 | 502.93 | -1.10 | 3.00E-04 | 2.07E-03 | Intracellular trafficking, secretion, and vesicular transport | Syntaxin-like protein |
| EVM0007756 | 154.83 | 331.34 | -1.10 | 3.50E-04 | 2.36E-03 | -- | CybS |
| EVM0003169 | 81.28 | 173.93 | -1.10 | 5.00E-05 | 4.28E-04 | -- | -- |
| EVM0003937 | 26.13 | 55.90 | -1.10 | 2.00E-04 | 1.46E-03 | RNA processing and modification | RNA pseudouridylate synthase |
| EVM0001571 | 15.36 | 32.86 | -1.10 | 1.25E-03 | 6.87E-03 | -- | -- |
| EVM0006361 | 44.73 | 95.63 | -1.10 | 4.00E-04 | 2.65E-03 | -- | -- |
| EVM0004577 | 24.64 | 52.64 | -1.10 | 5.00E-05 | 4.28E-04 | Cell cycle control, cell division, chromosome partitioning | Cid1 family poly A polymerase |
| EVM0009215 | 300.57 | 641.79 | -1.09 | 3.00E-04 | 2.07E-03 | Lipid transport and metabolism | GNS1/SUR4 family |
| EVM000218 | 57.90 | 123.57 | -1.09 | 8.00E-04 | 4.73E-03 | -- | 50S ribosome-binding GTPase |
| EVM0002193 | 35.51 | 75.75 | -1.09 | 1.00E-04 | 7.96E-04 | -- | -- |
| EVM0004159 | 8.08 | 17.22 | -1.09 | 1.00E-03 | 5.70E-03 | -- | -- |
| EVM0003070  | 33.65 | 71.68 | -1.09 | 2.00E-04 | 1.46E-03 | RNA processing and modification | DEAD/DEAH box helicase |
| EVM0009354  | 28.60 | 60.93 | -1.09 | 1.50E-04 | 1.14E-03 | Function unknown                | Coiled-coil domain-containing protein 55 (DUF2040) |
| EVM0002249  | 15.30 | 32.58 | -1.09 | 3.50E-04 | 2.36E-03 | Function unknown                | NUC153 domain |
| EVM0005876  | 9.09  | 19.33 | -1.09 | 1.15E-03 | 6.41E-03 | --                              | -- |
| EVM0003681  | 219.25| 466.04| -1.09 | 5.00E-05 | 4.28E-04 | Intracellular trafficking, secretion, and vesicular transport | Tim17/Tim22/Tim23/Pmp24 family |
| EVM0008778  | 8.71  | 18.52 | -1.09 | 4.50E-04 | 2.92E-03 | --                              | -- |
| EVM0005633  | 36.91 | 78.43 | -1.09 | 5.00E-04 | 3.19E-03 | --                              | -- |
| EVM0007971  | 73.11 | 155.34| -1.09 | 1.00E-04 | 7.96E-04 | Carbohydrate transport and metabolism | Glycolipid 2-alpha-mannosyltransferase |
| EVM0003061  | 25.29 | 53.71 | -1.09 | 2.00E-04 | 1.46E-03 | --                              | -- |
| EVM0004955  | 743.05| 1577.63| -1.09 | 2.50E-04 | 1.77E-03 | Translation, ribosomal structure and biogenesis | Ribosomal protein S10p/S20e |
| EVM0004758  | 24.20 | 51.37 | -1.09 | 3.50E-04 | 2.36E-03 | --                              | Tryptophan halogenase |
| EVM0004250  | 27.66 | 58.70 | -1.09 | 3.50E-04 | 2.36E-03 | --                              | -- |
| Accession   | ID    | Description                                      |
|-------------|-------|--------------------------------------------------|
| EVM0009458 | 2.35  | --                                               |
| EVM0008302 | 49.03 | --                                               |
| EVM0006756 | 84.30 | --                                               |
| EVM0004495 | 251.97| --                                               |
| EVM0009227 | 11.35 | --                                               |
| EVM0005377 | 7.43  | --                                               |
| EVM0001550 | 134.28| --                                               |
| EVM0009311 | 129.49| --                                               |
| EVM0002370 | 22.87 | --                                               |
| EVM0001463 | 14.31 | --                                               |
| EVM0010742 | 38.24 | --                                               |
| EVM0002326 | 8.51  | --                                               |

The table above contains information about proteins and their associated accession numbers, with the first column listing the accession numbers, followed by columns for the ID, and a description of the protein's function or characteristics in the last column.
| EVM0007812 | 81.09 | 170.80 | -1.07 | 4.00E-04 | 2.65E-03 | Function unknown | N-terminal glutamine amidase |
| EVM0002494 | 68.64 | 144.50 | -1.07 | 5.00E-05 | 4.28E-04 | -- | Peroxisomal membrane anchor protein (Pex14p) conserved region |
| EVM0007242 | 6.31  | 13.29  | -1.07 | 5.50E-04 | 3.46E-03 | -- | -- |
| EVM0004550 | 27.78 | 58.48  | -1.07 | 3.00E-04 | 2.07E-03 | -- | -- |
| EVM0004745 | 23.13 | 48.69  | -1.07 | 4.00E-04 | 2.65E-03 | -- | -- |
| EVM0004173 | 66.71 | 140.40 | -1.07 | 3.35E-03 | 1.55E-02 | -- | -- |
| EVM0011339 | 161.57| 339.97 | -1.07 | 1.00E-04 | 7.96E-04 | Translation, ribosomal structure and biogenesis | SMP-30/Gluconolaconase/LRE-like region |
| EVM0000882 | 72.56 | 152.68 | -1.07 | 2.50E-04 | 1.77E-03 | RNA processing and modification | Nucleotide hydrolase |
| EVM0001975 | 139.55| 293.55 | -1.07 | 5.00E-05 | 4.28E-04 | -- | -- |
| EVM0001093 | 4.56  | 9.59   | -1.07 | 3.30E-03 | 1.53E-02 | -- | Sodium Bile acid symporter family |
| EVM0007190 | 12.62 | 26.53  | -1.07 | 3.00E-04 | 2.07E-03 | -- | 50S ribosome-binding GTPase |
| EVM0006612 | 3.70  | 7.78   | -1.07 | 2.35E-03 | 1.16E-02 | -- | -- |
| EVM0001536 | 69.72 | 146.51 | -1.07 | 3.50E-04 2.36E-03 | -- | PhoD-like phosphatase |
| EVM0000148 | 240.74 | 505.78 | -1.07 | 4.50E-04 2.92E-03 | General function prediction | Zinc-binding dehydrogenase only |
| EVM0007202 | 2.90 | 6.10 | -1.07 | 6.20E-03 2.56E-02 | -- | non- haem dioxygenase in morphine synthesis N-terminal |
| EVM0004503 | 4.28 | 8.99 | -1.07 | 5.30E-03 2.26E-02 | -- | -- |
| EVM0008762 | 140.21 | 294.41 | -1.07 | 3.50E-04 2.36E-03 | Carbohydrate transport and metabolism | Glycolipid 2-alpha-mannosyltransferase |
| EVM0012060 | 4.58 | 9.61 | -1.07 | 1.00E-03 5.70E-03 | -- | -- |
| EVM0011721 | 103.84 | 217.98 | -1.07 | 5.00E-05 4.28E-04 | Translation, ribosomal structure and biogenesis | Ribosomal L28 family |
| EVM0000088 | 319.90 | 671.49 | -1.07 | 6.55E-03 2.67E-02 | -- | -- |
| EVM0004907 | 3.66 | 7.68 | -1.07 | 6.45E-03 2.64E-02 | RNA processing and modification | RNA recognition motif. (a.k.a. RRM, RBD, or RNP domain) |
| EVM0009940 | 3.45 | 7.24 | -1.07 | 1.90E-03 9.73E-03 | -- | Thiamine pyrophosphate enzyme, N-terminal TPP binding domain |
| EVM0009631 | 54.87 | 114.97 | -1.07 | 3.00E-04 2.07E-03 | Coenzyme transport and metabolism | ubiE/COQ5 methyltransferase family |
| EVM0011592 | 106.88 | 223.87 | -1.07 | 5.50E-04 3.46E-03 | -- | -- |
| EVM0008388 | 17.36 | 36.36 | -1.07 | 5.50E-04 3.46E-03 | -- | -- |
| EVM0009128  | 1.37 | 2.87 | -1.06 | 6.70E-03 | 2.72E-02 | -- | -- |
| EVM0001528  | 39.61 | 82.83 | -1.06 | 2.00E-04 | 1.46E-03 | RNA processing and modification | DEAD/DEAH box helicase |
| EVM0007700  | 86.53 | 180.94 | -1.06 | 2.65E-03 | 1.28E-02 | -- | -- |
| EVM0007785  | 202.62 | 423.46 | -1.06 | 2.50E-04 | 1.77E-03 | Intracellular trafficking, secretion, and vesicular transport | Mitochondrial import receptor subunit Tom22 |
| EVM0007252  | 54.57 | 114.04 | -1.06 | 1.00E-04 | 7.96E-04 | Secondary metabolites biosynthesis, transport and catabolism | Pyridine nucleotide-disulphide oxidoreductase |
| EVM0000562  | 38.47 | 80.39 | -1.06 | 2.00E-04 | 1.46E-03 | Intracellular trafficking, secretion, and vesicular transport | Signal recognition particle, alpha subunit, N-terminal |
| EVM0003359  | 177.43 | 370.28 | -1.06 | 3.50E-04 | 2.36E-03 | Translation, ribosomal structure and biogenesis | JAB1/Mov34/MPN/PAD-1 ubiquitin protease |
| EVM0002993  | 13.20 | 27.54 | -1.06 | 3.00E-04 | 2.07E-03 | -- | Spb1 C-terminal domain |
| EVM0010902  | 422.35 | 881.11 | -1.06 | 7.00E-04 | 4.23E-03 | -- | Mitochondrial ATPase inhibitor, IATP |
| EVM0011210  | 289.65 | 604.24 | -1.06 | 1.50E-04 | 1.14E-03 | -- | DASH complex subunit Dad2 |
| EVM0008211  | 13.55 | 28.25 | -1.06 | 2.00E-04 | 1.46E-03 | Signal transduction mechanisms | Protein tyrosine kinase |
| EVM0002986 | 19.73 | 41.15 | -1.06 | 3.00E-04 | 2.07E-03 | Cytoskeleton | Kinesin motor domain |
| EVM0007474 | 45.34 | 94.53 | -1.06 | 1.50E-04 | 1.14E-03 | Transcription | HCNGP-like protein |
| EVM0010516 | 1.49  | 3.11  | -1.06 | 1.35E-02 | 4.74E-02 | --           | --               |
| EVM0005390 | 52.54 | 109.47| -1.06 | 1.00E-04 | 7.96E-04 | Lipid transport and metabolism | short chain dehydrogenase |
| EVM0004273 | 31.41 | 65.42 | -1.06 | 3.50E-04 | 2.36E-03 | Signal transduction mechanisms | Mitochondrial branched-chain alpha-ketoacid dehydrogenase kinase |
| EVM0009487 | 32.59 | 67.87 | -1.06 | 1.50E-04 | 1.14E-03 | Function unknown | Sad1 / UNC-like C-terminal |
| EVM0000714 | 351.30| 731.50| -1.06 | 6.00E-04 | 3.72E-03 | Translation, ribosomal structure and biogenesis | Ribosomal protein S7p/S5e |
| EVM0007025 | 207.07| 431.17| -1.06 | 3.00E-04 | 2.07E-03 | General function prediction only | RNA recognition motif. (a.k.a. RRM, RBD, or RNP domain) |
| EVM0011851 | 7.57  | 15.76 | -1.06 | 6.80E-03 | 2.75E-02 | --           | Domain of unknown function (DUF3328) |
| EVM0002297 | 271.37| 564.48| -1.06 | 1.55E-03 | 8.22E-03 | --           | --               |
| EVM0006870 | 228.21| 474.42| -1.06 | 4.20E-03 | 1.87E-02 | Function unknown | Cytochrome c oxidase biogenesis protein Cmc1 like |
| EVM0002558 | 11.62 | 24.16 | -1.06 | 2.00E-04 | 1.46E-03 | Cell cycle control, cell division, chromosome partitioning | Protein kinase domain |
| Accession  | Value1 | Value2 | Value3 | Value4 | Value5 | Value6 | Description                                                  |
|-----------|--------|--------|--------|--------|--------|--------|--------------------------------------------------------------|
| EVM0009546 | 29.78  | 61.87  | -1.05  | 3.00E-04 | 2.07E-03 | --     | Fungal specific transcription factor domain                 |
| EVM0001784 | 45.00  | 93.44  | -1.05  | 3.50E-04 | 2.36E-03 | --     | Transcription RNA polymerase Rpb4                            |
| EVM0006523 | 8.84   | 18.35  | -1.05  | 3.15E-03 | 1.47E-02 | --     | --                                                           |
| EVM0003982 | 8.15   | 16.90  | -1.05  | 1.90E-03 | 9.73E-03 | --     | RNA processing and modification AAA domain                  |
| EVM0011554 | 189.80 | 393.58 | -1.05  | 2.50E-04 | 1.77E-03 | --     | EF-hand domain                                              |
| EVM0002786 | 1521.28| 3153.75| -1.05  | 8.20E-03 | 3.20E-02 | --     | --                                                           |
| EVM0002271 | 14.49  | 30.03  | -1.05  | 4.50E-04 | 2.92E-03 | --     | Function unknown Gar1/Naf1 RNA binding region               |
| EVM0011920 | 56.59  | 117.22 | -1.05  | 1.50E-04 | 1.14E-03 | --     | Translation, ribosomal structure and biogenesis Ribosomal protein L3 |
| EVM0006320 | 244.06 | 505.34 | -1.05  | 3.50E-04 | 2.36E-03 | --     | Protein kinase domain                                        |
| EVM0007154 | 37.87  | 78.40  | -1.05  | 4.50E-04 | 2.92E-03 | --     | --                                                           |
| EVM0007802 | 185.13 | 383.23 | -1.05  | 1.00E-04 | 7.96E-04 | --     | Protein of unknown function (DUF952)                        |
| EVM0002598 | 5.43   | 11.24  | -1.05  | 8.00E-04 | 4.73E-03 | --     | Protein kinase domain                                        |
| EVM0000354 | 882.53 | 1825.59| -1.05  | 1.50E-04 | 1.14E-03 | --     | Translation, ribosomal structure and biogenesis Ribosomal L29 protein |
| EVM0009575 | 58.77 | 121.56 | -1.05 | 1.50E-04 | 1.14E-03 | Lipid transport and metabolism | Acyl-CoA dehydrogenase, C-terminal domain |
| EVM0003529 | 4.22  | 8.73   | -1.05 | 3.05E-03 | 1.44E-02 | --                              | -- |
| EVM0012197 | 52.21 | 107.93 | -1.05 | 1.50E-04 | 1.14E-03 | Translation, ribosomal structure and biogenesis | DKCLD (NUC011) domain |
| EVM0001437 | 21.06 | 43.52  | -1.05 | 4.50E-04 | 2.92E-03 | RNA processing and modification | pre-mRNA processing factor 3 (PRP3) |
| EVM0007184 | 40.39 | 83.45  | -1.05 | 4.50E-04 | 2.92E-03 | Function unknown                | YjeF-related protein N-terminus |
| EVM0002265 | 53.19 | 109.87 | -1.05 | 2.00E-04 | 1.46E-03 | --                              | Probable molybdopterin binding domain |
| EVM0005245 | 22.88 | 47.20  | -1.05 | 1.50E-04 | 1.14E-03 | --                              | Ubiquitin-2 like Rad60 SUMO-like |
| EVM0000145 | 60.92 | 125.65 | -1.04 | 3.50E-04 | 2.36E-03 | --                              | Glycosyl hydrolase family 71 |
| EVM0002946 | 10.09 | 20.80  | -1.04 | 1.70E-03 | 8.87E-03 | Carbohydrate transport and metabolism | Glycolipid 2-alpha-mannosyltransferase |
| EVM0006765 | 25.94 | 53.44  | -1.04 | 6.00E-04 | 3.72E-03 | Energy production and conversion | Mitochondrial carrier protein |
| EVM0008033 | 88.91 | 183.04 | -1.04 | 1.00E-04 | 7.96E-04 | Energy production and conversion | Biotin-requiring enzyme |
| EVM0008323 | 15.09 | 31.07  | -1.04 | 2.50E-04 | 1.77E-03 | --                              | -- |
| EVM0003158 | 1079.23 | 2221.35 | -1.04 | 2.30E-03 | 1.14E-02 | --                              | -- |
| Accession  | Log2 Fold | Log10 Fold | Log10 Fold Ratio | Predicted Function                                                                 | Protein Domain or Function Note                           |
|-----------|-----------|------------|-----------------|------------------------------------------------------------------------------------|----------------------------------------------------------|
| EVM000823 | 9.77      | 20.12      | -1.04           | General function prediction only                                                    | Surface antigen                                          |
| EVM0005164| 132.24    | 271.93     | -1.04           | Function unknown                                                                    | --                                                       |
| EVM0005141| 52.00     | 106.90     | -1.04           | General function prediction only                                                    | --                                                       |
| EVM0004008| 139.12    | 285.98     | -1.04           | Lipid transport and metabolism                                                      | Choline/Carnitine o-acyltransferase                      |
| EVM0005539| 3.60      | 7.39       | -1.04           | Posttranslational modification, protein turnover, chaperones                        | BCS1 N terminal                                          |
| EVM0002294| 7.48      | 15.37      | -1.04           | General function prediction only                                                    | Alpha/beta hydrolase family                              |
| EVM0012232| 1.60      | 3.29       | -1.04           | --                                                                                  | --                                                       |
| EVM0012208| 74.49     | 153.01     | -1.04           | --                                                                                  | --                                                       |
| EVM0006068| 5.92      | 12.16      | -1.04           | --                                                                                  | bZIP transcription factor                                |
| EVM0012144| 37.54     | 77.05      | -1.04           | Function unknown                                                                    | Eukaryotic protein of unknown function (DUF829)          |
| EVM0001478| 4.77      | 9.80       | -1.04           | --                                                                                  | Pro-kumamolisin, activation domain                       |
| EVM0009338| 26.96     | 55.31      | -1.04           | Carbohydrate transport and metabolism                                             | FGGY family of carbohydrate kinases, C-terminal domain  |
| EVM0001461   | 20.90 | 42.84 | -1.04 | 4.50E-04 | 2.92E-03 | Function unknown | WD domain, G-beta repeat |
| EVM0011812   | 2.67  | 5.48  | -1.04 | 6.70E-03 | 2.72E-02 | --               | Glycosyl hydrolase family 71 |
| EVM0007209   | 78.25 | 160.32| -1.03 | 1.50E-04 | 1.14E-03 | --               | Universal stress protein family |
| EVM0002920   | 28.21 | 57.80 | -1.03 | 6.50E-04 | 3.98E-03 | Intracellular trafficking, secretion, and vesicular transport | ADP-ribosylation factor family |
| EVM0004775   | 21.60 | 44.25 | -1.03 | 1.30E-03 | 7.10E-03 | --               | Conidiation protein 6 |
| EVM0010086   | 18.21 | 37.24 | -1.03 | 3.50E-04 | 2.36E-03 | Signal transduction mechanisms | Rab-GTPase-TBC domain |
| EVM0000902   | 23.98 | 49.04 | -1.03 | 4.00E-04 | 2.65E-03 | Posttranslational modification, protein turnover, chaperones | DnaJ domain |
| EVM0002150   | 312.70| 639.48| -1.03 | 1.50E-04 | 1.14E-03 | General function prediction only | RNA recognition motif. (a.k.a. RRM, RBD, or RNP domain) |
| EVM0008017   | 6.51  | 13.31 | -1.03 | 1.10E-03 | 6.17E-03 | --               | ATPase family associated with various cellular activities (AAA) |
| EVM0007506   | 224.15| 458.19| -1.03 | 2.00E-04 | 1.46E-03 | Intracellular trafficking, secretion, and vesicular transport | Regulated-SNARE-like domain |
| EVM0003961   | 33.88 | 69.20 | -1.03 | 6.00E-04 | 3.72E-03 | --               | -- |
| Accession   | GeneID | EVM0009826 | 33.24  67.82  -1.03  1.85E-03  9.52E-03  General function prediction only  Acetyltransferase (GNAT) family |
|-------------|--------|------------|--------|---------------|-----------------------|-----------------------------------------------------|
| EVM0007624  | 7.27   | 4.90E-03   | 2.12E-02 | --            | --                    | --                                                  |
| EVM0008967  | 272.82 | 1.05E-03   | 5.94E-03 | --            | Tic20-like protein    | --                                                  |
| EVM0003421  | 71.18  | 5.00E-04   | 3.19E-03 | --            | --                    | --                                                  |
| EVM0002892  | 8.78   | 1.30E-03   | 7.10E-03 | Energy production and conversion  FAD binding domain |
| EVM0010562  | 57.36  | 4.50E-04   | 2.92E-03 | Posttranslational modification, protein turnover, chaperones  DnaJ domain |
| EVM0006891  | 16.18  | 1.30E-03   | 7.10E-03 | --            | --                    | --                                                  |
| EVM0007892  | 105.18 | 6.50E-04   | 3.98E-03 | --            | Domain of unknown function (DUF4598)  |
| EVM0003200  | 106.31 | 4.00E-04   | 2.65E-03 | Posttranslational modification, protein turnover, chaperones  Cyclophilin type peptidyl-prolyl cis-trans isomerase/CLD |
| EVM0001034  | 87.28  | 2.50E-04   | 1.77E-03 | Inorganic ion transport and metabolism  Ctr copper transporter family |
| EVM0008633  | 43.13  | 3.00E-04   | 2.07E-03 | Intracellular trafficking, secretion, and vesicular transport  Autophagy-related protein 13 |
| EVM0004019 | 47.99 | 97.54 | -1.02 | 5.90E-03 2.46E-02 | General function prediction only | Domain of unknown function (DUF3336) |
| EVM0004660 | 24.15 | 49.06 | -1.02 | 2.00E-04 1.46E-03 | General function prediction only | ABC transporter |
| EVM0002242 | 10.67 | 21.68 | -1.02 | 9.00E-04 5.22E-03 | Secondary metabolites biosynthesis, transport and catabolism | Aromatic amino acid lyase |
| EVM0005636 | 273.87 | 556.38 | -1.02 | 9.00E-04 5.22E-03 | Energy production and conversion | Mitochondrial glycoprotein |
| EVM0001803 | 14.08 | 28.60 | -1.02 | 2.30E-03 1.14E-02 | -- | Haloacid dehalogenase-like hydrolase |
| EVM0001711 | 48.99 | 99.41 | -1.02 | 1.50E-04 1.14E-03 | Intracellular trafficking, secretion, and vesicular transport | Coatomer WD associated region |
| EVM0000555 | 40.55 | 82.23 | -1.02 | 4.45E-03 1.96E-02 | Lipid transport and metabolism | PAP2 superfamily |
| EVM0010536 | 2.59 | 5.26 | -1.02 | 7.15E-03 2.86E-02 | -- | -- |
| EVM0005171 | 14.11 | 28.60 | -1.02 | 2.50E-04 1.77E-03 | Replication, recombination and repair | DNA mismatch repair protein, C-terminal domain |
| EVM0004792 | 12.94 | 26.22 | -1.02 | 1.27E-02 4.53E-02 | -- | -- |
| EVM0007499 | 34.67 | 70.17 | -1.02 | 1.10E-03 6.17E-03 | -- | -- |
| EVM0003386 | 5.95 | 12.04 | -1.02 | 5.60E-03 2.36E-02 | -- | bZIP transcription factor |
| EVM0011769  | 7.25  | 14.65  | -1.02  | 1.11E-02 | 4.06E-02 | --     | --     |
| EVM0007727  | 7.61  | 15.38  | -1.02  | 4.30E-03 | 1.90E-02 | --     | --     |
| EVM0006288  | 19.08 | 38.56  | -1.02  | 3.00E-04 | 2.07E-03 | --     | --     |
| EVM0008700  | 1311.59 | 2650.06 | -1.01 | 6.55E-03 | 2.67E-02 | Energy production and conversion | ATP synthase D chain, mitochondrial (ATP5H) |
| EVM0004828  | 668.13 | 1349.92 | -1.01 | 6.50E-04 | 3.98E-03 | Translation, ribosomal structure and biogenesis | Plectin/S10 domain |
| EVM0006277  | 8.87  | 17.93  | -1.01  | 7.90E-03 | 3.10E-02 | --     | --     |
| EVM0000834  | 5.46  | 11.03  | -1.01  | 2.20E-03 | 1.10E-02 | --     | Glycosyl hydrolases family 28 |
| EVM0005197  | 14.21 | 28.70  | -1.01  | 1.80E-03 | 9.29E-03 | General function prediction only | Major Facilitator Superfamily |
| EVM0004833  | 11.58 | 23.37  | -1.01  | 3.00E-04 | 2.07E-03 | --     | --     |
| EVM0009620  | 11.25 | 22.70  | -1.01  | 1.05E-03 | 5.94E-03 | General function prediction only | Sugar (and other) transporter |
| EVM0009627  | 42.78 | 86.31  | -1.01  | 2.00E-04 | 1.46E-03 | --     | Inner membrane protein import complex subunit Tim54 |
| EVM0008106  | 221.25 | 446.26 | -1.01  | 3.50E-04 | 2.36E-03 | --     | Domain of unknown function (DUF4336) |
| EVM0004589  | 47.86 | 96.47  | -1.01  | 8.50E-04 | 4.98E-03 | --     | --     |
| Gene ID       | EVM0002315 | 55.79 | 112.43 | -1.01 | 2.50E-04 | 1.77E-03 | Amino acid transport and metabolism | Aminotransferase class I and II |
|--------------|------------|-------|--------|-------|----------|----------|------------------------------------|-------------------------------|
| EVM0000850   | 19.18      | 38.65 | -1.01  | 1.35E-03 | 7.33E-03 | --       | --                                 | --                            |
| EVM0005271   | 11.75      | 23.65 | -1.01  | 1.35E-03 | 7.33E-03 | --       | Zinc finger, C3HC4 type (RING finger) | --                            |
| EVM0002010   | 53.17      | 107.05| -1.01  | 2.50E-04 | 1.77E-03 | --       | --                                 | --                            |
| EVM0006503   | 1800.41    | 3624.34| -1.01  | 1.65E-03 | 8.65E-03 | Translation, ribosomal structure and biogenesis | Ribosomal protein S13/S18    |
| EVM0002611   | 78.11      | 157.17| -1.01  | 5.00E-04 | 3.19E-03 | --       | Fungal domain of unknown function (DUF1750) |
| EVM0008251   | 15.94      | 32.06 | -1.01  | 1.00E-04 | 7.96E-04 | General function prediction only | Aldo/keto reductase family    |
| EVM0005661   | 12.40      | 24.93 | -1.01  | 2.35E-03 | 1.16E-02 | --       | --                                 | --                            |
| EVM0004022   | 19.34      | 38.89 | -1.01  | 8.50E-04 | 4.98E-03 | General function prediction only | 50S ribosome-binding GTPase   |
| EVM0002916   | 134.56     | 270.45| -1.01  | 8.50E-04 | 4.98E-03 | Posttranslational modification, protein turnover, chaperones | FKBP-type peptidyl-prolyl cis-trans isomerase |
| EVM0002764   | 99.42      | 199.73| -1.01  | 3.50E-04 | 2.36E-03 | Transcription | TFIIE alpha subunit           |
| EVM0008059   | 14.62      | 29.38 | -1.01  | 5.50E-04 | 3.46E-03 | Carbohydrate transport and metabolism | Domain of unknown function (DUF1793) |
| Accession   | Fold Change | Benjamini FDR | p-Value | Function                                                                 | Domain/Protein Name                                      |
|-------------|-------------|---------------|---------|-------------------------------------------------------------------------|----------------------------------------------------------|
| EVM0009675  | 57.20       | 114.85        | -1.01   | Posttranslational modification, protein turnover, chaperones            | Oligosaccharyltransferase subunit Ribophorin II          |
| EVM0001211  | 25.73       | 51.66         | -1.01   | --                                                                      | --                                                       |
| EVM0006148  | 21.81       | 43.75         | -1.00   | --                                                                      | --                                                       |
| EVM0001205  | 29.78       | 59.73         | -1.00   | Function unknown                                                        | Ribosomal protein L1p/L10e family                       |
| EVM0007899  | 81.21       | 162.84        | -1.00   | Intracellular trafficking, secretion, and vesicular transport           | Yip1 domain                                             |
| EVM0010713  | 20.36       | 40.82         | -1.00   | Function unknown                                                        | Protein of unknown function (DUF890)                    |
| EVM0001330  | 43.70       | 87.52         | -1.00   | Lipid transport and metabolism                                          | Diacylglycerol acyltransferase                          |
| EVM0009094  | 9.87        | 19.77         | -1.00   | --                                                                      | --                                                       |
| EVM0010110  | 9.91        | 19.84         | -1.00   | Carbohydrate transport and metabolism                                   | Glycosyl hydrolase family 1                             |
| EVM0002102  | 713.74      | 1428.73       | -1.00   | Energy production and conversion                                        | DHHA2 domain                                            |
| EVM0009973  | 9.24        | 18.49         | -1.00   | --                                                                      | DDE superfamily endonuclease                            |
| Gene ID       | Identity | P-value | Fold Change | Description                                                                 |
|--------------|----------|---------|-------------|-----------------------------------------------------------------------------|
| EVM0008505   | 172.60   | 345.43  | -1.00       | 1.50E-04 1.14E-03 Posttranslational modification, protein turnover, chaperones |
| EVM0011840   | 17.37    | 34.77   | -1.00       | 5.00E-04 3.19E-03 -- -- Ribonuclease HII Replication, recombination and repair |
| EVM0011955   | 8.90     | 17.81   | -1.00       | 3.55E-03 1.62E-02 -- -- Ribonuclease HII Replication, recombination and repair |
| EVM0003013   | 2.48     | 4.96    | -1.00       | 6.40E-03 2.62E-02 -- -- Ribonuclease HII Replication, recombination and repair |
| EVM0009066   | 41.21    | 82.42   | -1.00       | 2.00E-03 1.46E-03 Function unknown Rubisco LSMT substrate-binding |
| EVM0007015   | 16.83    | 8.41    | 1.00        | 6.50E-04 3.98E-03 -- -- Acyl transferase domain |
| EVM0009455   | 5.16     | 2.58    | 1.00        | 3.50E-03 1.61E-02 -- -- NACHT domain |
| EVM0002765   | 22.94    | 11.45   | 1.00        | 7.50E-03 4.49E-03 General function prediction only Rab-GTPase-TBC domain |
| EVM0000199   | 248.93   | 124.22  | 1.00        | 6.00E-04 3.72E-03 Signal transduction mechanisms HEAT repeat |
| EVM0001289   | 80.85    | 40.34   | 1.00        | 3.00E-04 2.07E-03 -- -- |
| EVM0007405   | 690.26   | 344.37  | 1.00        | 4.50E-04 2.92E-03 Intracellular trafficking, secretion, and vesicular transport RanBP1 domain |
| EVM0008123   | 70.86    | 35.31   | 1.00        | 3.50E-04 2.36E-03 Translation, ribosomal structure and biogenesis Initiation factor 2 subunit family |
| EVM0010778 | 7.32 | 3.65 | 1.01 | 1.50E-03 | 8.00E-03 | -- | SNF2 family N-terminal domain |
| EVM0007126 | 93.77 | 46.71 | 1.01 | 5.00E-04 | 3.19E-03 | General function prediction only | Autophagocytosis associated protein (Atg3), N-terminal domain |
| EVM0000270 | 64.59 | 32.16 | 1.01 | 6.50E-04 | 3.98E-03 | -- | -- |
| EVM0011948 | 54.37 | 27.06 | 1.01 | 1.60E-03 | 8.44E-03 | Posttranslational modification, protein turnover, chaperones | Zinc knuckle |
| EVM0001740 | 99.41 | 49.45 | 1.01 | 1.20E-03 | 6.64E-03 | -- | 2OG-Fe(II) oxygenase superfamily |
| EVM0003881 | 8.86 | 4.41 | 1.01 | 4.35E-03 | 1.92E-02 | Replication, recombination and repair | impB/mucB/samB family |
| EVM0002143 | 44.34 | 22.05 | 1.01 | 5.00E-04 | 3.19E-03 | Cytoskeleton | Kinesin motor domain |
| EVM0010722 | 21.84 | 10.86 | 1.01 | 5.00E-04 | 3.19E-03 | Transcription | IKI3 family |
| EVM0011360 | 13.67 | 6.79 | 1.01 | 1.70E-03 | 8.87E-03 | -- | -- |
| EVM0004284 | 42.47 | 21.09 | 1.01 | 4.50E-04 | 2.92E-03 | -- | WSC domain |
| EVM000621 | 29.37 | 14.59 | 1.01 | 1.60E-03 | 8.44E-03 | -- | Oxidoreductase family, NAD-binding Rossmann fold |
| EVM0006311 | 59.02 | 29.29 | 1.01 | 1.00E-02 | 3.75E-02 | Defense mechanisms | Macrophage migration inhibitory factor (MIF) |
| Accession   | Expression 1 | Expression 2 | Fold Change | Log2 Fold Change | Gene Function Prediction | Gene Description |
|-------------|--------------|--------------|-------------|------------------|--------------------------|------------------|
| EVM0001907  | 60.21        | 29.88        | 1.01        | 3.50E-04         | General function prediction only | Cyclin            |
| EVM0002001  | 69.71        | 34.58        | 1.01        | 4.00E-04         | Lipid transport and metabolism | GDSL-like Lipase/Acylhydrolase family |
| EVM0009097  | 41.53        | 20.60        | 1.01        | 2.60E-03         | --                        | --               |
| EVM0005381  | 65.97        | 32.71        | 1.01        | 4.00E-04         | Amino acid transport and metabolism | Phosphoadenosine phosphosulfate reductase family |
| EVM0004079  | 66.25        | 32.84        | 1.01        | 2.70E-03         | RNA processing and modification | Ribonuclease III domain |
| EVM0010858  | 13.92        | 6.90         | 1.01        | 1.15E-03         | Function unknown           | Uncharacterised protein family (UPF0183) |
| EVM0001397  | 1172.24      | 580.88       | 1.01        | 1.85E-03         | General function prediction only | Zinc-finger double-stranded RNA-binding |
| EVM0007333  | 18.51        | 9.17         | 1.01        | 7.00E-04         | RNA processing and modification | Ribonuclease III domain |
| EVM0012209  | 97.00        | 48.03        | 1.01        | 1.00E-03         | Function unknown           | Uncharacterised protein family (UPF0183) |
| EVM0007079  | 30.67        | 15.18        | 1.01        | 4.00E-04         | Transcription              | HMG (high mobility group) box |
| EVM0009576  | 4.95         | 2.45         | 1.01        | 3.30E-03         | --                        | NACHT domain      |
| EVM0001859  | 670.97       | 332.02       | 1.01        | 3.70E-03         | Amino acid transport and metabolism | D-isomer specific 2-hydroxyacid dehydrogenase, NAD binding domain |
| EVM0000526  | 111.15 | 54.97  | 1.02  | 5.50E-04 | 3.46E-03 | Function unknown | Protein of unknown function (DUF726) |
| EVM0008544  |  5.42  |  2.68  | 1.02  | 1.04E-02 | 3.85E-02 | --               | Major Facilitator Superfamily         |
| EVM0006531  |  38.32 |  18.94 | 1.02  | 1.39E-02 | 4.86E-02 | --               | Protein of unknown function (DUF2423) |
| EVM0009046  |  29.26 |  14.46 | 1.02  | 4.00E-04 | 2.65E-03 | Replication, recombination and repair | DNA mismatch repair protein, C-terminal domain |
| EVM0012227  |  22.53 |  11.13 | 1.02  | 1.15E-03 | 6.41E-03 | --               | --                                   |
| EVM0006259  |  23.38 |  11.54 | 1.02  | 7.00E-04 | 4.23E-03 | --               | MYND finger                          |
| EVM0008313  |  27.63 |  13.63 | 1.02  | 6.50E-04 | 3.98E-03 | Secondary metabolites biosynthesis, transport and catabolism | ABC transporter transmembrane region |
| EVM0007923  |  12.95 |   6.38 | 1.02  | 1.30E-03 | 7.10E-03 | --               | Amidase                              |
| EVM0004419  |  52.94 |  26.09 | 1.02  | 1.65E-03 | 8.65E-03 | General function prediction only | Protein kinase domain                 |
| EVM0003953  |  10.72 |   5.28 | 1.02  | 4.35E-03 | 1.92E-02 | --               | NACHT domain                         |
| EVM0003247  | 120.39 |  59.30 | 1.02  | 1.00E-03 | 5.70E-03 | Signal transduction mechanisms | Protein kinase domain                 |
| EVM0010764  | 268.55 | 132.21 | 1.02  | 9.50E-04 | 5.46E-03 | Carbohydrate transport and metabolism | Transketolase, thiamine diphosphate binding domain |
| Accession   | Value1 | Value2 | Value3 | Value4 | Value5 | Value6 | Value7 | Value8 | Value9 | Value10 | Description                                                                 |
|-------------|--------|--------|--------|--------|--------|--------|--------|--------|--------|---------|--------------------------------------------------------------------------------|
| EVM0001744  | 11.97  | 5.89   | 1.02   | 7.50E-04| 4.49E-03| Signal transduction mechanisms |
| EVM0006716  | 23.99  | 11.81  | 1.02   | 3.80E-03| 1.72E-02| --     | --     | --     | --     | --      | --                                                                            |
| EVM0005766  | 63.65  | 31.29  | 1.02   | 1.50E-04| 1.14E-03| --     | --     | --     | Adenylate cyclase associated (CAP) N terminal |
| EVM0004370  | 24.47  | 12.02  | 1.03   | 1.40E-03| 7.55E-03| General function prediction only |
| EVM0005270  | 30.21  | 14.84  | 1.03   | 8.00E-04| 4.73E-03| Transcription | R3H domain |
| EVM0009823  | 87.74  | 43.08  | 1.03   | 6.00E-04| 3.72E-03| --     | --     | --     | HOOK protein |
| EVM0004470  | 39.70  | 19.47  | 1.03   | 1.00E-04| 7.96E-04| Inorganic ion transport and metabolism |
| EVM0003730  | 24.00  | 11.76  | 1.03   | 3.65E-03| 1.66E-02| --     | --     | Uncharacterized alpha/beta hydrolase domain (DUF2235) |
| EVM0002727  | 1058.91| 519.11 | 1.03   | 4.40E-03| 1.94E-02| --     | --     | Cupin |
| EVM0011120  | 1679.46| 822.56 | 1.03   | 9.65E-03| 3.64E-02| Inorganic ion transport and metabolism |
| EVM0010709  | 110.42 | 54.08  | 1.03   | 1.50E-04| 1.14E-03| Nucleotide transport and metabolism |
| EVM0001332  | 32.70  | 16.01  | 1.03   | 8.50E-04| 4.98E-03| General function prediction only |
| EVM0002727  | 1058.91| 519.11 | 1.03   | 4.40E-03| 1.94E-02| --     | --     | Cupin |
| EVM0003730  | 24.00  | 11.76  | 1.03   | 3.65E-03| 1.66E-02| --     | --     | Uncharacterized alpha/beta hydrolase domain (DUF2235) |
| EVM0002727  | 1058.91| 519.11 | 1.03   | 4.40E-03| 1.94E-02| --     | --     | Cupin |
| EVM0001332  | 32.70  | 16.01  | 1.03   | 8.50E-04| 4.98E-03| General function prediction only |
| EVM0002727  | 1058.91| 519.11 | 1.03   | 4.40E-03| 1.94E-02| --     | --     | Cupin |
| EVM0003730  | 24.00  | 11.76  | 1.03   | 3.65E-03| 1.66E-02| --     | --     | Uncharacterized alpha/beta hydrolase domain (DUF2235) |
| EVM0002727  | 1058.91| 519.11 | 1.03   | 4.40E-03| 1.94E-02| --     | --     | Cupin |
| EVM0001339 | 1086.00 | 531.72 | 1.03 | 4.15E-03 | 1.85E-02 | Posttranslational modification, protein turnover, chaperones | GDP dissociation inhibitor |
| EVM0001963 | 72.35  | 35.37  | 1.03 | 4.00E-04 | 2.65E-03 | -- | Alpha/beta hydrolase family |
| EVM0003280 | 15.24  | 7.44   | 1.03 | 1.23E-02 | 4.40E-02 | -- | -- |
| EVM0011492 | 1057.93 | 516.65 | 1.03 | 1.05E-02 | 3.88E-02 | -- | -- |
| EVM0010906 | 113.24 | 55.24  | 1.04 | 6.00E-04 | 3.72E-03 | -- | CorA-like Mg2+ transporter protein |
| EVM0008175 | 22.31  | 10.88  | 1.04 | 5.00E-04 | 3.19E-03 | -- | FAT domain |
| EVM0009032 | 73.78  | 35.97  | 1.04 | 1.50E-04 | 1.14E-03 | General function prediction only | WD domain, G-beta repeat |
| EVM0004703 | 65.28  | 31.79  | 1.04 | 8.00E-04 | 4.73E-03 | Posttranslational modification, protein turnover, chaperones | Leucine carboxyl methyltransferase |
| EVM0010016 | 70.23  | 34.20  | 1.04 | 4.00E-04 | 2.65E-03 | General function prediction only | Oxidoreductase family, NAD-binding Rossmann fold |
| EVM0005203 | 36.14  | 17.59  | 1.04 | 2.00E-04 | 1.46E-03 | Intracellular trafficking, secretion, and vesicular transport | Pep3/Vps18/deep orange family |
| EVM0005607 | 7.37   | 3.59   | 1.04 | 4.90E-03 | 2.12E-02 | Posttranslational modification, protein turnover, chaperones | Prenyltransferase and squalene oxidase repeat |
| EVM0004132  | 22.48 | 10.94 | 1.04 | 3.50E-04 2.36E-03 | General function prediction only | RAVE protein 1 C terminal |
| EVM0009994  | 43.25 | 21.03 | 1.04 | 8.00E-04 4.73E-03 | -- | -- |
| EVM0006478  | 169.41 | 82.34 | 1.04 | 1.50E-04 1.14E-03 | -- | N-terminal domain of ribose phosphate pyrophosphokinase |
| EVM0010432  | 140.08 | 68.07 | 1.04 | 2.50E-04 1.77E-03 | Posttranslational modification, protein turnover, chaperones | TCP-1/cpn60 chaperonin family |
| EVM001504   | 357.56 | 173.68 | 1.04 | 4.50E-04 2.92E-03 | -- | -- |
| EVM0005070  | 328.70 | 159.60 | 1.04 | 2.00E-04 1.46E-03 | -- | EB1-like C-terminal motif |
| EVM0006155  | 40.09  | 19.46 | 1.04 | 3.10E-03 1.45E-02 | Cell wall/membrane/envelope biogenesis | Glycosyl hydrolases family 18 |
| EVM0003284  | 21.60  | 10.48 | 1.04 | 6.50E-04 3.98E-03 | -- | -- |
| EVM0008024  | 585.65 | 283.92 | 1.04 | 7.55E-03 2.99E-02 | -- | -- |
| EVM0006412  | 396.69 | 192.24 | 1.05 | 5.50E-04 3.46E-03 | -- | Bin/amphiphysin/Rvs domain for vesicular trafficking |
| EVM0006229  | 663.64 | 321.60 | 1.05 | 2.95E-03 1.40E-02 | Inorganic ion transport and metabolism | Sugar (and other) transporter |
| Accession | Value 1 | Value 2 | Factor | Value 3  | Value 4 | Value 5  | Value 6 | Value 7  | Value 8 |
|-----------|---------|---------|--------|---------|---------|---------|---------|---------|---------|
| EVM0002077 | 26.03   | 12.61   | 1.05   | 1.10E-03 | 6.17E-03 | Posttranslational modification, protein turnover, chaperones | Ankyrin repeat |
| EVM0008486 | 209.82  | 101.62  | 1.05   | 9.00E-04 | 5.22E-03 | --      | --      | HEAT-like repeat |
| EVM0003260 | 39.87   | 19.30   | 1.05   | 2.00E-04 | 1.46E-03 | --      | --      | Regulator of chromosome condensation (RCC1) repeat |
| EVM0010705 | 115.90  | 56.11   | 1.05   | 1.05E-03 | 5.94E-03 | Transcription | --      | SRF-type transcription factor (DNA-binding and dimerisation domain) |
| EVM0000563 | 5.30    | 2.56    | 1.05   | 6.30E-03 | 2.59E-02 | RNA processing and modification | Initiator tRNA phosphoribosyl transferase |
| EVM0010904 | 21.68   | 10.48   | 1.05   | 3.50E-04 | 2.36E-03 | Inorganic ion transport and metabolism | Sodium/hydrogen exchanger family |
| EVM0000071 | 4.34    | 2.10    | 1.05   | 6.10E-03 | 2.52E-02 | --      | --      | -- |
| EVM0002141 | 43.68   | 21.10   | 1.05   | 9.35E-03 | 3.55E-02 | --      | --      | -- |
| EVM0001077 | 15.50   | 7.48    | 1.05   | 8.00E-04 | 4.73E-03 | Signal transduction mechanisms | Phosphatidylinositol-specific phospholipase C, X domain |
| EVM0011682 | 52.91   | 25.55   | 1.05   | 2.00E-04 | 1.46E-03 | Signal transduction mechanisms | Frag1/DRAM/Sfk1 family |
| EVM0003715 | 132.86  | 64.00   | 1.05   | 2.50E-04 | 1.77E-03 | --      | --      | PIN domain |
| EVM0007345 | 481.96  | 232.16  | 1.05   | 2.80E-03 | 1.34E-02 | Amino acid transport and metabolism | POT family |
| EVM     | ID   | 1.06 | 4.85E-03 | 2.10E-03 | Carbohydrate transport and metabolism | Transaldolase |
|---------|------|------|----------|----------|---------------------------------------|---------------|
| EVM0002666 | 110.19 | 53.02 | 5.50E-04 | 3.46E-03 | Translation, ribosomal structure and biogenesis | tRNA synthetases class I (I, L, M and V) |
| EVM0002651 | 484.05 | 232.85 | 3.00E-04 | 2.07E-03 | Translation, ribosomal structure and biogenesis | Endoribonuclease L-PSP |
| EVM0000238 | 695.40 | 334.49 | 7.00E-04 | 4.23E-03 | Translation, ribosomal structure and biogenesis | eRF1 domain 2 |
| EVM0008239 | 622.33 | 299.26 | 5.50E-04 | 3.46E-03 | Carbohydrate transport and metabolism | -- |
| EVM0011578 | 312.28 | 150.12 | 8.50E-04 | 4.98E-03 | -- | -- |
| EVM0005878 | 76.09 | 36.55 | 2.00E-04 | 1.46E-03 | -- | -- |
| EVM0011361 | 70.19 | 33.69 | 1.25E-04 | 6.87E-03 | -- | -- |
| EVM0000331 | 34.73 | 16.65 | 4.85E-04 | 2.10E-03 | -- | -- |
| EVM0000242 | 107.99 | 51.76 | 5.45E-04 | 2.31E-03 | Carbohydrate transport and metabolism | Trehalase |
| EVM0002699 | 50.33 | 24.12 | 4.30E-04 | 1.90E-02 | Function unknown | -- |
| EVM0011634 | 26.83 | 12.86 | 2.00E-04 | 1.46E-03 | Function unknown | Spc97 / Spc98 family |
| EVM0004970 | 175.52 | 84.09 | 1.00E-03 | 5.70E-03 | Energy production and conversion | Malic enzyme, NAD binding domain |
| EVM0006142 | 12.60 | 6.03 | 5.10E-03 | 2.19E-02 | -- | G protein-coupled glucose receptor regulating Gpa2 |
| EVM0001119  | 40.52 | 19.39 | 1.06 | 3.50E-04 | 2.36E-03 | Signal transduction mechanisms | Response regulator receiver domain |
| EVM0006880  | 43.02 | 20.58 | 1.06 | 2.10E-03 | 1.06E-02 | General function prediction only | Glycosyltransferase family 28 C-terminal domain |
| EVM0009089  | 12.55 | 6.00  | 1.07 | 2.30E-03 | 1.14E-02 | Inorganic ion transport and metabolism | Carbonic anhydrase |
| EVM0008027  | 113.79| 54.36 | 1.07 | 9.50E-04 | 5.46E-03 | -- | -- |
| EVM0011485  | 129.93| 62.05 | 1.07 | 2.50E-04 | 1.77E-03 | Amino acid transport and metabolism | Indole-3-glycerol phosphate synthase |
| EVM0002456  | 557.03| 265.88| 1.07 | 1.10E-03 | 6.17E-03 | Cytoskeleton | Microtubule-associated protein CRIPT |
| EVM0007895  | 141.08| 67.33 | 1.07 | 4.50E-04 | 2.92E-03 | -- | CRM1 C terminal |
| EVM0006748  | 78.41 | 37.40 | 1.07 | 4.50E-04 | 2.92E-03 | Function unknown | TPR/MLP1/MLP2-like protein |
| EVM0008990  | 23.46 | 11.19 | 1.07 | 2.00E-04 | 1.46E-03 | RNA processing and modification | Helicase associated domain (HA2) |
| EVM0009552  | 323.36| 154.22| 1.07 | 7.50E-04 | 4.49E-03 | -- | -- |
| EVM0011140  | 54.89 | 26.17 | 1.07 | 2.00E-04 | 1.46E-03 | Intracellular trafficking, secretion, and vesicular transport | Lethal giant larvae(Lgl) like, C-terminal |
| EVM0006968  | 30.95 | 14.73 | 1.07 | 4.35E-03 | 1.92E-02 | -- | -- |
| Accession   | Value 1 | Value 2 | Value 3 | Value 4 | Description                                                                 | Domain/Region                                      |
|-------------|---------|---------|---------|---------|------------------------------------------------------------------------------|----------------------------------------------------|
| EVM0001643  | 358.11  | 170.37  | 1.07    | 1.00E-04| Intracellular trafficking, secretion, and vesicular transport                | Synaptobrevin                                      |
| EVM0007424  | 10.51   | 5.00    | 1.07    | 4.10E-03| Lipid transport and metabolism                                               | C2 domain                                          |
| EVM0006727  | 32.36   | 15.37   | 1.07    | 1.45E-03| --                                                                           | --                                                 |
| EVM0010125  | 250.51  | 118.90  | 1.08    | 1.30E-03| --                                                                           | --                                                 |
| EVM0007527  | 220.25  | 104.46  | 1.08    | 1.50E-03| Intracellular trafficking, secretion, and vesicular transport                | Region in Clathrin and VPS                         |
| EVM0002952  | 27.88   | 13.22   | 1.08    | 3.50E-04| Extracellular structures                                                     | Tropomyosin                                        |
| EVM0009427  | 13.48   | 6.38    | 1.08    | 3.00E-03| --                                                                           | Staphylococcal nuclease homologue                 |
| EVM0005015  | 177.89  | 84.15   | 1.08    | 1.00E-04| --                                                                           | Triose-phosphate Transporter family                |
| EVM0005723  | 53.86   | 25.47   | 1.08    | 3.50E-04| Transcription                                                               | RNA polymerase Rpb1, domain 5                     |
| EVM0009342  | 50.64   | 23.91   | 1.08    | 1.00E-04| --                                                                           | von Willebrand factor type A domain                |
| EVM0008508  | 21.45   | 10.13   | 1.08    | 8.80E-03| --                                                                           | --                                                 |
| EVM0007370  | 12.46   | 5.87    | 1.09    | 1.00E-03| --                                                                           | --                                                 |
| Accession | MSH | Mui | Muc | Fold | E-value | Description |
|-----------|------|-----|-----|------|---------|-------------|
| EVM0004931 | 67.18 | 31.56 | 1.09 | 1.00E-04 | 7.96E-04 | Munc13 (mammalian uncoordinated) homology domain |
| EVM0009149 | 370.51 | 173.99 | 1.09 | 3.50E-04 | 2.36E-03 | -- |
| EVM0009549 | 41.73 | 19.59 | 1.09 | 2.50E-04 | 1.77E-03 | Zinc-binding dehydrogenase |
| EVM0000859 | 2.78 | 1.31 | 1.09 | 9.95E-03 | 3.74E-02 | -- |
| EVM0009161 | 15.10 | 7.08 | 1.09 | 4.50E-04 | 2.92E-03 | Fungal Zn(2)-Cys(6) binuclear cluster domain |
| EVM0010426 | 981.69 | 460.22 | 1.09 | 5.50E-04 | 3.46E-03 | -- |
| EVM0007608 | 606.62 | 284.32 | 1.09 | 4.50E-03 | 1.97E-02 | Domain of unknown function (DUF4203) |
| EVM0001912 | 73.35 | 34.37 | 1.09 | 3.50E-03 | 2.36E-02 | Amino acid transport and metabolism EPSP synthase (3-phosphoshikimate 1-carboxyvinyltransferase) |
| EVM0006980 | 9.20 | 4.31 | 1.09 | 4.15E-03 | 1.85E-02 | -- |
| EVM0012077 | 48.58 | 22.74 | 1.10 | 3.00E-04 | 2.07E-03 | Isoprenylcysteine carboxyl methyltransferase (ICMT) family |
| EVM0005907 | 25.68 | 12.02 | 1.10 | 6.95E-03 | 2.80E-02 | -- |
| EVM0008335 | 36.68 | 17.14 | 1.10 | 5.00E-05 | 4.28E-04 | Function unknown Protein of unknown function (DUF3414) |
| Gene ID     | Identity | Score | E-value | Description                                                                 |
|------------|----------|-------|---------|-----------------------------------------------------------------------------|
| EVM0005769 | 21.43    | 10.01 | 1.10    | 1.35E-03 7.33E-03 -- Common central domain of tyrosinase                  |
| EVM0011534 | 22.27    | 10.39 | 1.10    | 7.50E-04 4.49E-03 -- --                                                     |
| EVM0005101 | 3.50     | 1.63  | 1.10    | 1.27E-02 4.53E-02 Replication, recombination and repair HhH-GPD superfamily base excision DNA repair protein |
| EVM0002944 | 21.25    | 9.90  | 1.10    | 1.10E-03 6.17E-03 -- WD domain, G-beta repeat                              |
| EVM0006521 | 27.46    | 12.79 | 1.10    | 2.10E-03 1.06E-02 -- --                                                     |
| EVM0010324 | 143.74   | 66.94 | 1.10    | 5.00E-05 4.28E-04 -- --                                                     |
| EVM0008988 | 17.55    | 8.17  | 1.10    | 5.00E-05 4.28E-04 -- --                                                     |
| EVM0004414 | 65.24    | 30.35 | 1.10    | 1.50E-04 1.14E-03 -- Polysaccharide deacetylase                            |
| EVM0001572 | 15.78    | 7.34  | 1.10    | 4.50E-04 2.92E-03 General function prediction O-methyltransferase          |
| EVM0003504 | 22.13    | 10.29 | 1.10    | 1.50E-03 8.00E-03 General function prediction only SPRY domain              |
| EVM0001546 | 222.22   | 103.33| 1.10    | 2.50E-04 1.77E-03 Cytoskeleton Domain of unknown function (DUF1900)          |
| EVM0004506 | 113.34   | 52.63 | 1.11    | 2.50E-04 1.77E-03 Carbohydrate transport and metabolism Phosphofructokinase |
| EVM0004193 | 26.15    | 12.14 | 1.11    | 6.50E-04 3.98E-03 -- NADH:flavin oxidoreductase / NADH oxidase family       |
| EVM0002486 | 8.42 | 3.91 | 1.11 | 3.40E-03 | 1.57E-02 | Function unknown | Protein of unknown function (DUF544) |
| EVM0000940 | 32.79 | 15.21 | 1.11 | 5.00E-05 | 4.28E-04 | Lipid transport and metabolism | AMP-binding enzyme |
| EVM0008035 | 18.88 | 8.75 | 1.11 | 2.00E-04 | 1.46E-03 | General function prediction only | SNF2 family N-terminal domain |
| EVM0004355 | 82.81 | 38.38 | 1.11 | 5.00E-05 | 4.28E-04 | Signal transduction mechanisms | RasGEF domain |
| EVM0003043 | 30.27 | 14.03 | 1.11 | 5.00E-03 | 2.15E-02 | -- | Cyanate lyase C-terminal domain |
| EVM0006564 | 13.28 | 6.15 | 1.11 | 1.30E-03 | 7.10E-03 | Carbohydrate transport and metabolism | Melibiase |
| EVM0008825 | 111.89 | 51.82 | 1.11 | 7.65E-03 | 3.02E-02 | -- | -- |
| EVM0007477 | 40.13 | 18.58 | 1.11 | 3.00E-04 | 2.07E-03 | General function prediction only | Metallo-beta-lactamase superfamily |
| EVM0008081 | 395.87 | 183.19 | 1.11 | 1.00E-04 | 7.96E-04 | Translation, ribosomal structure and biogenesis | Ribosomal protein S19 |
| EVM0005901 | 3.32 | 1.53 | 1.11 | 1.34E-02 | 4.72E-02 | Carbohydrate transport and metabolism | Melibiase |
| EVM0004320 | 137.75 | 63.67 | 1.11 | 5.00E-05 | 4.28E-04 | General function prediction only | Aldo/keto reductase family |
| EVM0003720 | 49.77 | 23.01 | 1.11 | 5.00E-05 | 4.28E-04 | -- | NAD dependent epimerase/dehydratase family |
| EVM0005612 | 49.77 | 23.01 | 1.11 | 1.00E-04 | 7.96E-04 | Energy production and conversion | Aldehyde dehydrogenase family |
| Accession   | Score  | Identity | E-Value | Domain Description                                |
|------------|--------|----------|----------|--------------------------------------------------|
| EVM0001598 | 142.73 | 65.96    | 1.11     | Cytoskeleton ANTH domain                         |
| EVM0009630 | 75.26  | 34.78    | 1.11     | Posttranslational modification, protein turnover, chaperones PITH domain |
| EVM0000748 | 19.30  | 8.91     | 1.12     | Secondary metabolites biosynthesis, transport and catabolism Zinc-binding dehydrogenase |
| EVM0012228 | 31.21  | 14.38    | 1.12     | --                                                |
| EVM0009461 | 10.00  | 4.61     | 1.12     | General function prediction only Zinc-finger of C2H2 type |
| EVM0001221 | 88.35  | 40.71    | 1.12     | Function unknown WD domain, G-beta repeat |
| EVM0002379 | 112.92 | 52.03    | 1.12     | Translation, ribosomal structure and biogenesis tRNA synthetases class I (E and Q), catalytic domain |
| EVM0011550 | 19.28  | 8.88     | 1.12     | --                                                |
| EVM0010049 | 210.10 | 96.73    | 1.12     | Posttranslational modification, protein turnover, chaperones IBR domain |
| EVM0010561 | 87.50  | 40.28    | 1.12     | --                                                |
| EVM0009313 | 58.26  | 26.81    | 1.12     | Intracellular trafficking, secretion, and vesicular transport Adaptin N terminal region |
| EVM0008667 | 14.29 | 6.57 | 1.12 | 7.00E-04 | 4.23E-03 | -- | MYND finger |
| EVM0009405 | 88.83 | 40.84 | 1.12 | 2.30E-03 | 1.14E-02 | General function prediction only | Yippee zinc-binding/DNA-binding /Mis18, centromere assembly |
| EVM0004176 | 675.73 | 310.50 | 1.12 | 9.00E-04 | 5.22E-03 | -- | -- |
| EVM0009704 | 78.21 | 35.87 | 1.12 | 5.00E-05 | 4.28E-04 | Amino acid transport and metabolism | Lyase |
| EVM0000724 | 61.85 | 28.36 | 1.12 | 1.50E-04 | 1.14E-03 | Translation, ribosomal structure and biogenesis | Piwi domain |
| EVM0008503 | 37.20 | 17.05 | 1.13 | 9.00E-04 | 5.22E-03 | Lipid transport and metabolism | short chain dehydrogenase |
| EVM0002940 | 522.39 | 239.19 | 1.13 | 3.00E-04 | 2.07E-03 | General function prediction only | Zinc finger, C2H2 type |
| EVM0007352 | 36.15 | 16.54 | 1.13 | 1.00E-04 | 7.96E-04 | General function prediction only | Protein kinase domain |
| EVM0004309 | 309.87 | 141.76 | 1.13 | 7.50E-04 | 4.49E-03 | -- | Ferric reductase like transmembrane component |
| EVM0011502 | 272.25 | 124.39 | 1.13 | 1.50E-04 | 1.14E-03 | Energy production and conversion | Citrate synthase |
| EVM0006225 | 57.88 | 26.43 | 1.13 | 4.00E-04 | 2.65E-03 | -- | -- |
| EVM0003215 | 68.08 | 31.06 | 1.13 | 1.50E-04 | 1.14E-03 | Signal transduction mechanisms | Leucine Rich repeats (2 copies) |
| EVM0003091 | 117.40 | 53.56 | 1.13 | 1.50E-04 1.14E-03 | Posttranslational modification, protein turnover, chaperones | Zinc finger, C3HC4 type (RING finger) |
| EVM0004348 | 44.36 | 20.23 | 1.13 | 9.50E-04 5.46E-03 | Lipid transport and metabolism | Ceramidase |
| EVM0009974 | 66.42 | 30.25 | 1.13 | 7.50E-04 4.49E-03 | Signal transduction mechanisms | GTPase-activator protein for Ras-like GTPase |
| EVM0007827 | 423.46 | 192.64 | 1.14 | 2.20E-03 1.10E-02 | -- | Lipase (class 3) |
| EVM0008727 | 16.13 | 7.34 | 1.14 | 1.19E-02 4.30E-02 | Translation, ribosomal structure and biogenesis | D-Tyr-tRNA(Tyr) deacylase |
| EVM0006999 | 166.86 | 75.88 | 1.14 | 1.50E-04 1.14E-03 | Coenzyme transport and metabolism | GTP cyclohydrolase N terminal |
| EVM0004131 | 49.37 | 22.44 | 1.14 | 5.00E-05 4.28E-04 | General function prediction only | TPR repeat |
| EVM0003517 | 119.02 | 54.04 | 1.14 | 1.50E-04 1.14E-03 | Posttranslational modification, protein turnover, chaperones | Hsp70 protein |
| EVM0010856 | 28.50 | 12.93 | 1.14 | 1.55E-03 8.22E-03 | -- | -- |
| EVM0003378 | 176.81 | 80.22 | 1.14 | 2.00E-04 1.46E-03 | -- | Domain of unknown function (DUF427) |
| EVM0011658 | 5.66 | 2.57 | 1.14 | 1.06E-02 3.91E-02 | Lipid transport and metabolism | Enoyl-CoA hydratase/isomerase family |
| EVM0005098 | 1220.76 | 553.55 | 1.14 | 7.50E-04 4.49E-03 | -- | -- |
| ID           | EVM0003885 | EVM0009293 | EVM0007183 | EVM0003658 | EVM0001184 | EVM0003687 | EVM0006983 | EVM0011564 | EVM0004126 | EVM0003696 | EVM0006484 | EVM0008184 |
|--------------|------------|------------|------------|------------|------------|------------|------------|------------|------------|------------|------------|------------|
| Value        | 1194.51    | 529.11     | 23.96      | 7.00       | 4.97       | 153.62     | 102.60     | 377.19     | 19.57      | 10.58      | 24.27      | 31.37      |
| Log Value    | 0.14       | 0.15       | 0.15       | 0.01       | 0.05       | 0.11       | 0.11       | 0.11       | 0.11       | 0.11       | 0.11       | 0.11       |
| Fold Change  | 6.50E-04   | 4.50E-04   | 5.50E-04   | 2.10E-03   | 1.42E-02   | 4.50E-04   | 1.00E-04   | 5.00E-05   | 5.00E-05   | 9.80E-03   | 5.00E-04   | 1.50E-04   |
| P Value      | 3.98E-03   | 2.92E-03   | 3.46E-03   | 1.06E-02   | 4.95E-02   | 2.92E-03   | 7.96E-04   | 4.28E-04   | 4.28E-04   | 3.69E-02   | 3.19E-03   | 1.14E-03   |
| Description  | --         | --         | Enolase C-terminal domain-like | --         | --         | --         | --         | --         | --         | --         | Lipase (class 3) | Domain of unknown function (DUF4139) |
| Function     | Amino acid transport and metabolism | Chorismate synthase | DAHP synthetase I family | General function prediction only | Major Facilitator Superfamily | Cell cycle control, cell division, chromosome partitioning | RecF/RecN/SMC N terminal domain | | | | | |
| Accession   | Fold   | MFI     | log10 of CPM | Fold Change | Annotation                                      |
|------------|--------|---------|--------------|-------------|------------------------------------------------|
| EVM0002393 | 3.57   | 1.59    | 1.16         | 6.30E-03    |                                                |
| EVM0007960 | 3.95   | 1.76    | 1.17         | 1.70E-03    | Heterokaryon incompatibility protein (HET)     |
| EVM0010328 | 21.35  | 9.51    | 1.17         | 2.50E-04    | Replication, recombination and repair          |
| EVM0012160 | 11.14  | 4.96    | 1.17         | 5.00E-05    | Fungal specific transcription factor domain   |
| EVM0003587 | 105.49 | 46.96   | 1.17         | 1.00E-04    | Coenzyme transport and metabolism             |
| EVM0010285 | 12.17  | 5.41    | 1.17         | 6.50E-04    | Domain of unknown function (DUF1917)          |
| EVM0011547 | 182.71 | 81.30   | 1.17         | 5.00E-05    | Lipid transport and metabolism                |
| EVM0000895 | 26.48  | 11.77   | 1.17         | 1.10E-03    | Nucleotide transport and metabolism           |
| EVM0000594 | 22.41  | 9.96    | 1.17         | 1.35E-03    | NmrA-like family                              |
| EVM0002329 | 476.03 | 211.26  | 1.17         | 3.00E-04    | Carbohydrate transport and metabolism         |
| EVM0009195 | 20.83  | 9.24    | 1.17         | 5.00E-04    | Survival protein SurE                         |
| EVM0010130 | 52.77  | 23.40   | 1.17         | 1.00E-04    | Signal transduction mechanisms                |
| EVM0011905 | 120.34 | 53.34   | 1.17         | 5.00E-05    | Iron permease FTR1 family                     |
| EVM0008661  | 65.26 | 28.88 | 1.18 | 1.50E-04 | 1.14E-03 | Posttranslational modification, protein turnover, chaperones | ThiF family |
| EVM0006159  | 136.24 | 60.24 | 1.18 | 2.50E-04 | 1.77E-03 | -- | -- |
| EVM0001664  | 1.70  | 0.75  | 1.18 | 9.95E-03 | 3.74E-02 | Function unknown | Major Facilitator Superfamily |
| EVM0001458  | 3.61  | 1.59  | 1.18 | 5.10E-03 | 2.19E-02 | -- | -- |
| EVM0011654  | 13.61 | 6.00  | 1.18 | 1.30E-03 | 7.10E-03 | -- | -- |
| EVM0000006  | 18.65 | 8.22  | 1.18 | 1.00E-04 | 7.96E-04 | Secondary metabolites biosynthesis, transport and catabolism | Cytochrome P450 |
| EVM0003493  | 265.50 | 117.02 | 1.18 | 7.00E-04 | 4.23E-03 | Cytoskeleton | Calponin homology (CH) domain |
| EVM0000788  | 38.64 | 17.03 | 1.18 | 7.00E-04 | 4.23E-03 | -- | PH domain |
| EVM0003301  | 41.44 | 18.26 | 1.18 | 5.00E-05 | 4.28E-04 | Translation, ribosomal structure and biogenesis | Elongation factor Tu GTP binding domain |
| EVM0002142  | 143.74 | 63.33 | 1.18 | 5.00E-05 | 4.28E-04 | General function prediction only | Cyclin |
| EVM0003294  | 16.25 | 7.16  | 1.18 | 5.00E-05 | 3.19E-03 | -- | Pro-kumamolisin, activation domain |
| EVM0005952  | 9.39  | 4.14  | 1.18 | 1.10E-03 | 6.17E-03 | -- | RNA ligase |
| EVM0002799 | 90.20 | 39.71 | 1.18 | 2.00E-04 | 1.46E-03 | General function prediction only | Putative Phosphatase |
| EVM0008652 | 65.18 | 28.69 | 1.18 | 7.00E-04 | 4.23E-03 | -- | -- |
| EVM0010437 | 89.44 | 39.35 | 1.18 | 6.50E-04 | 3.98E-03 | -- | -- |
| EVM0012216 | 70.06 | 30.82 | 1.18 | 5.00E-05 | 4.28E-04 | General function prediction only | short chain dehydrogenase |
| EVM0005569 | 27.69 | 12.18 | 1.18 | 4.50E-04 | 2.92E-03 | -- | -- |
| EVM0001175 | 18.28 | 8.03  | 1.19 | 1.09E-02 | 4.01E-02 | -- | TEA/ATTS domain family |
| EVM0002290 | 51.76 | 22.73 | 1.19 | 2.50E-03 | 1.22E-02 | Posttranslational modification, protein turnover, chaperones | Ubiquitin-conjugating enzyme |
| EVM0006183 | 27.31 | 11.99 | 1.19 | 5.00E-05 | 4.28E-04 | -- | -- |
| EVM0007829 | 92.00 | 40.36 | 1.19 | 5.00E-05 | 4.28E-04 | Amino acid transport and metabolism | HMGL-like |
| EVM0004732 | 78.10 | 34.25 | 1.19 | 5.00E-05 | 4.28E-04 | Amino acid transport and metabolism | Acyl-CoA dehydrogenase, C-terminal domain |
| EVM0008712 | 58.54 | 25.65 | 1.19 | 5.00E-05 | 4.28E-04 | Replication, recombination and repair | NUDIX domain |
| EVM0008440 | 14.61 | 6.40  | 1.19 | 7.50E-04 | 4.49E-03 | Signal transduction mechanisms | Protein kinase domain |
| ID            | Value1 | Value2 | Value3 | Value4 | Value5 | Value6 | Value7 | Value8 | Value9 | Value10 | Function                                                                 |
|---------------|--------|--------|--------|--------|--------|--------|--------|--------|--------|---------|--------------------------------------------------------------------------|
| EVM0002090    | 45.82  | 20.03  | 1.19   | 5.00E-05 | 4.28E-04 | Lipid transport and metabolism | Taurine catabolism dioxygenase TauD, TfdA family |
| EVM0009132    | 71.55  | 31.27  | 1.19   | 4.00E-04 | 2.65E-03 | -- | -- |        |        | --                                      |
| EVM0007663    | 410.44 | 179.35 | 1.19   | 5.00E-04 | 4.28E-03 | Lipid transport and metabolism | Alpha/beta hydrolase family |
| EVM0003972    | 221.74 | 96.88  | 1.19   | 1.00E-04 | 7.96E-04 | Signal transduction mechanisms | Protein kinase domain |
| EVM0007249    | 44.91  | 19.62  | 1.19   | 5.00E-04 | 4.28E-04 | -- | -- | RhoGEF domain |
| EVM0007050    | 76.48  | 33.40  | 1.20   | 1.00E-04 | 7.96E-04 | General function prediction only | Aminotransferase class-V |
| EVM0006520    | 10.62  | 4.63   | 1.20   | 2.00E-04 | 1.46E-03 | -- | -- |        |        | --                                      |
| EVM0011443    | 204.03 | 88.99  | 1.20   | 5.00E-04 | 4.28E-04 | Amino acid transport and metabolism | Saccharopine dehydrogenase |
| EVM0006655    | 18.13  | 7.90   | 1.20   | 1.50E-04 | 1.14E-03 | Nucleotide transport and metabolism | Adenosine/AMP deaminase |
| EVM0001322    | 388.32 | 169.21 | 1.20   | 3.50E-04 | 2.36E-03 | Secondary metabolites biosynthesis, transport and catabolism | Cytochrome P450 |
| EVM0007926    | 7.76   | 3.38   | 1.20   | 3.00E-04 | 2.07E-03 | -- | -- |        |        | --                                      |
| EVM0005744    | 8.96   | 3.90   | 1.20   | 1.10E-03 | 6.17E-03 | RNA processing and modification | AAA domain |
| Gene ID       | Mw  | LogE w  | LogE 0.4 | Description                              |
|--------------|-----|---------|----------|------------------------------------------|
| EVM0006510   | 178.81 | 77.77 | 1.20 | General function prediction only         |
|              |      |         |          | Sugar (and other) transporter            |
| EVM0000265   | 179.93 | 78.22 | 1.20 | Cell                                      |
|              |      |         |          | Cell wall/membrane/envelope biogenesis   |
| EVM0010470   | 144.34 | 62.71 | 1.20 | Posttranslational modification, protein   |
|              |      |         |          | turnover, chaperones                     |
| EVM0009368   | 66.11 | 28.71 | 1.20 | General function prediction only         |
|              |      |         |          | --                                       |
| EVM0009382   | 17.37 | 7.54  | 1.20 | General function prediction only         |
|              |      |         |          | Elongation factor Tu C-terminal domain    |
| EVM0002963   | 72.68 | 31.53 | 1.21 | General function prediction only         |
|              |      |         |          | 50S ribosome-binding GTPase              |
| EVM0008164   | 13.05 | 5.66  | 1.21 | Carbohydrate transport and metabolism    |
|              |      |         |          | Major Facilitator Superfamily            |
| EVM0010296   | 25.33 | 10.97 | 1.21 | General function prediction only         |
|              |      |         |          | 50S ribosome-binding GTPase              |
| EVM0001679   | 365.34 | 158.13 | 1.21 | Carbohydrate transport and metabolism    |
|              |      |         |          | Alpha amylase, C-terminal all-beta domain|
| EVM0000891   | 140.13 | 60.64 | 1.21 | General function prediction only         |
|              |      |         |          | Pyridoxamine 5'-phosphate oxidase        |
| EVM0000749   | 202.33 | 87.46 | 1.21 | General function prediction only         |
|              |      |         |          | Ras family                               |
| EVM0011666   | 10.55 | 4.55  | 1.21 | General function prediction only         |
|              |      |         |          | MYND finger                              |
| Gene ID         | Fold Change | Expression Value | p-Value | Biological Process                                | Domain/Function                                      |
|----------------|-------------|------------------|---------|---------------------------------------------------|------------------------------------------------------|
| EVM0005837     | 36.58       | 15.80            | 1.21    | Translation, ribosomal structure and biogenesis   | PUA domain                                           |
| EVM0011775     | 98.74       | 42.63            | 1.21    | Posttranslational modification, protein turnover, chaperones | Ubiquitin carboxyl-terminal hydrolase                |
| EVM0004800     | 234.89      | 101.39           | 1.21    | Coenzyme transport and metabolism                 | Delta-aminolevulinic acid dehydratase                |
| EVM0008666     | 53.45       | 23.05            | 1.21    | --                                                 | Dioxygenase                                          |
| EVM0006667     | 48.14       | 20.75            | 1.21    | --                                                 | --                                                  |
| EVM0004493     | 1036.82     | 445.89           | 1.22    | General function prediction only                   | Cyclin, N-terminal domain                            |
| EVM0012168     | 25.50       | 10.96            | 1.22    | --                                                 | Importin-beta N-terminal domain                      |
| EVM0004894     | 252.71      | 108.62           | 1.22    | Energy production and conversion                   | FAD binding domain                                   |
| EVM0009926     | 26.13       | 11.23            | 1.22    | --                                                 | AMP-binding enzyme                                   |
| EVM0003798     | 39.42       | 16.93            | 1.22    | --                                                 | Thaumatin family                                     |
| EVM0002676     | 56.49       | 24.25            | 1.22    | Secondary metabolites biosynthesis, transport and catabolism | Cytochrome P450                                      |
| EVM0011368     | 19.30       | 8.28             | 1.22    | --                                                 | --                                                  |
| Accession     | Score | TM | Target Score | Delta Target Score | Functional Category | Description                                                                                   |
|--------------|-------|----|--------------|--------------------|---------------------|---------------------------------------------------------------------------------------------|
| EVM0008401   | 35.59 | 1.22 | 5.00E-05     | 4.28E-04           | Posttranslational   | Ubiquitin carboxyl-terminal hydrolase modification, protein turnover, chaperones             |
| EVM0007654   | 530.14| 1.22 | 5.00E-05     | 4.28E-04           | Signal transduction| Eukaryotic cytochrome b561 mechanisms                                                        |
| EVM0001845   | 131.71| 1.22 | 2.50E-04     | 1.77E-03           | General function    | Haloacid dehalogenase-like hydrolase                                                        |
| EVM0004033   | 86.45 | 1.22 | 5.00E-05     | 4.28E-04           | Posttranslational   | TCP-1/cpn60 chaperonin family modification, protein turnover, chaperones                     |
| EVM0001998   | 148.53| 1.23 | 1.00E-04     | 7.96E-04           | Extracellular       | --                                                                                           |
| EVM0009352   | 69.75 | 1.23 | 5.00E-05     | 4.28E-04           | Energy production   | 2-oxoacid dehydrogenases acyltransferase (catalytic domain)                                  |
| EVM0005286   | 406.86| 1.23 | 5.00E-05     | 4.28E-04           | --                  | --                                                                                           |
| EVM0003494   | 71.42 | 1.23 | 5.00E-05     | 4.28E-04           | General function    | Rab-GTPase-TBC domain                                                                        |
| EVM0001416   | 7.56  | 1.23 | 5.80E-03     | 2.42E-02           | --                  | Thaumatin family                                                                            |
| EVM0000144   | 68.22 | 1.23 | 1.50E-04     | 1.14E-03           | General function    | Phenazine biosynthesis-like protein                                                            |
| EVM0003809   | 10.49 | 1.23 | 1.00E-03     | 5.70E-03           | --                  | --                                                                                           |
| EVM0008931   | 39.74 | 1.24 | 5.00E-05     | 4.28E-04           | --                  | Growth-Arrest-Specific Protein 2 Domain                                                        |
| Accession   | Value 1 | Value 2 | Value 3 | E-value 1 | E-value 2 | Description                                                                 |
|-------------|---------|---------|---------|-----------|-----------|-----------------------------------------------------------------------------|
| EVM0006340  | 56.11   | 23.83   | 1.24    | 5.00E-05  | 4.28E-04  | Nup53/35/40-type RNA recognition motif                                        |
| EVM0009106  | 48.34   | 20.53   | 1.24    | 5.00E-05  | 4.28E-04  |                                                                               |
| EVM0006467  | 44.28   | 18.80   | 1.24    | 1.00E-04  | 7.96E-04  | Zinc-binding dehydrogenase                                                  |
| EVM0003945  | 180.22  | 76.53   | 1.24    | 1.00E-04  | 7.96E-04  | Cell wall/membrane/envelope biogenesis                                       |
| EVM0010408  | 40.71   | 17.28   | 1.24    | 5.00E-05  | 4.28E-04  | Translation, ribosomal structure and biogenesis                              |
| EVM0012002  | 49.17   | 20.83   | 1.24    | 5.00E-05  | 4.28E-04  | General function prediction only                                             |
| EVM0003882  | 147.01  | 62.29   | 1.24    | 1.00E-04  | 7.96E-04  | Energy production and conversion                                            |
| EVM0000399  | 269.93  | 114.27  | 1.24    | 1.00E-04  | 7.96E-04  | Posttranslational modification, protein turnover, chaperones                |
| EVM0007902  | 145.96  | 61.61   | 1.24    | 5.00E-05  | 4.28E-04  |                                                                               |
| EVM0007315  | 203.70  | 85.90   | 1.25    | 5.00E-05  | 4.28E-04  | Amino acid transport and metabolism                                          |
| EVM0004656  | 47.97   | 20.22   | 1.25    | 5.00E-05  | 4.28E-04  |                                                                               |
| EVM0004447  | 115.94  | 48.82   | 1.25    | 5.00E-05  | 4.28E-04  |                                                                               |
| EVM0009453 | 66.01 | 27.78 | 1.25 | 5.00E-05 | 4.28E-04 | -- | Septin |
| EVM0010439 | 19.34 | 8.14  | 1.25 | 1.25E-03 | 6.87E-03 | -- | -- |
| EVM0000011 | 229.85| 96.69 | 1.25 | 5.00E-05 | 4.28E-04 | Posttranslational modification, protein turnover, chaperones | Peptidase family M3 |
| EVM0001930 | 33.23 | 13.98 | 1.25 | 5.00E-04 | 3.19E-03 | Carbohydrate transport and metabolism | Major Facilitator Superfamily |
| EVM0012205 | 15.69 | 6.60  | 1.25 | 1.00E-04 | 7.96E-04 | Function unknown | RHS Repeat |
| EVM0009531 | 23.96 | 10.07 | 1.25 | 1.00E-03 | 5.70E-03 | -- | Polysaccharide lyase family 8, super-sandwich domain |
| EVM0005521 | 142.17| 59.70 | 1.25 | 2.50E-04 | 1.77E-03 | -- | GPR1/FUN34/yaaH family |
| EVM0009069 | 808.29| 339.37| 1.25 | 1.35E-03 | 7.33E-03 | Carbohydrate transport and metabolism | pfkB family carbohydrate kinase |
| EVM0009905 | 137.44| 57.65 | 1.25 | 5.00E-05 | 4.28E-04 | Carbohydrate transport and metabolism | Metalloenzyme superfamily |
| EVM0003536 | 7.72 | 3.24  | 1.25 | 1.20E-03 | 6.64E-03 | -- | -- |
| EVM0001774 | 13.04 | 5.47  | 1.25 | 3.50E-04 | 2.36E-03 | Secondary metabolites biosynthesis, transport and catabolism | Cytochrome P450 |
| EVM0002232 | 142.20| 59.58 | 1.25 | 5.75E-03 | 2.41E-02 | Amino acid transport and metabolism | Metallopeptidase family M24 |
| Accession   | Score 1 | Score 2 | Clust 1 | Clust 2 | Function Description                  |
|-------------|---------|---------|---------|---------|---------------------------------------|
| EVM0007171  | 35.81   | 15.00   | 1.26    | 2.00E-04| 1.46E-03 --                           |
| EVM0007171  | 4.71    | 15.00   | 1.26    | 5.00E-05| 4.28E-04 Energy production and conversion |
| EVM0010340  | 10.95   | 4.59    | 1.26    | 5.00E-05| 4.28E-04 Energy production and conversion |
| EVM0000108  | 53.59   | 22.39   | 1.26    | 3.50E-04| 2.36E-03 --                           |
| EVM0011384  | 89.63   | 37.42   | 1.26    | 5.00E-05| 4.28E-04 --                           |
| EVM0004548  | 655.91  | 273.76  | 1.26    | 2.00E-04| 1.46E-03 --                           |
| EVM0001625  | 226.99  | 94.73   | 1.26    | 1.00E-04| 7.96E-03 --                           |
| EVM0005854  | 149.62  | 62.40   | 1.26    | 1.50E-04| 1.14E-03 Cell wall/membrane/envelope biogenesis |
| EVM0002819  | 24.17   | 10.07   | 1.26    | 5.00E-05| 4.28E-04 Function unknown Domain of unknown function (DUF3437) |
| EVM0009169  | 1408.42 | 586.51  | 1.26    | 2.50E-04| 1.77E-03 --                           |
| EVM0010122  | 43.17   | 17.97   | 1.26    | 5.00E-05| 4.28E-04 Replication, recombination and repair MutS domain V |
| EVM0010089  | 78.42   | 32.62   | 1.27    | 5.00E-05| 4.28E-04 --                           |
| EVM0000340 | 28.30 | 11.77 | 1.27 | 5.00E-05 4.28E-04 | -- | PWWP domain |
| EVM0000100 | 2461.85 | 1023.31 | 1.27 | 3.00E-04 2.07E-03 | Cytoskeleton | Cofilin/tropomyosin-type actin-binding protein |
| EVM0008628 | 17.86 | 7.42 | 1.27 | 5.00E-05 4.28E-04 | -- | -- |
| EVM0011466 | 33.35 | 13.86 | 1.27 | 5.00E-05 4.28E-04 | -- | -- |
| EVM0005820 | 220.36 | 91.55 | 1.27 | 5.00E-05 4.28E-04 | General function prediction only | ABC transporter |
| EVM0006696 | 52.23 | 21.69 | 1.27 | 3.35E-03 1.55E-02 | -- | Domain of unknown function DUF77 |
| EVM0007451 | 78.06 | 32.40 | 1.27 | 5.00E-05 4.28E-04 | -- | Beta-glucan synthesis-associated protein (SKN1) |
| EVM0011036 | 13.71 | 5.69 | 1.27 | 8.00E-04 4.73E-03 | -- | Polysaccharide deacetylase |
| EVM0008291 | 143.56 | 59.56 | 1.27 | 5.00E-05 4.28E-04 | Carbohydrate transport and metabolism | NAD dependent epimerase/dehydratase family |
| EVM0002497 | 26.46 | 10.98 | 1.27 | 5.00E-05 4.28E-04 | -- | NACHT domain |
| EVM0010882 | 214.64 | 89.00 | 1.27 | 5.00E-05 4.28E-04 | General function prediction only | Histidine phosphatase superfamily (branch 2) |
| EVM0008089 | 15.23 | 6.31 | 1.27 | 3.50E-04 2.36E-03 | General function prediction only | Aldo/keto reductase family |
| EVM0008146 | 53.45 | 22.16 | 1.27 | 5.00E-05 4.28E-04 | -- | -- |
| EVM0008147  | 9.33 | 3.87 | 1.27 | 3.50E-04 | 2.36E-03 | Nucleotide transport and metabolism | 5'-nucleotidase, C-terminal domain |
| EVM0004729  | 611.89 | 253.04 | 1.27 | 1.24E-02 | 4.45E-02 | -- | Helix-turn-helix |
| EVM0008140  | 32.62 | 13.48 | 1.28 | 5.00E-05 | 4.28E-04 | -- | -- |
| EVM0007638  | 870.72 | 359.34 | 1.28 | 1.95E-03 | 9.93E-03 | Coenzyme transport and metabolism | Aminotransferase class I and II |
| EVM0006684  | 12.93 | 5.33 | 1.28 | 7.00E-04 | 4.23E-03 | Transcription | C-5 cytosine-specific DNA methylase |
| EVM0010320  | 14.34 | 5.90 | 1.28 | 1.50E-04 | 1.14E-03 | -- | -- |
| EVM0010314  | 36.04 | 14.84 | 1.28 | 5.00E-05 | 4.28E-04 | General function prediction only | Major Facilitator Superfamily |
| EVM0008676  | 10.03 | 4.13 | 1.28 | 1.50E-04 | 1.14E-03 | -- | -- |
| EVM0008860  | 93.49 | 38.48 | 1.28 | 2.00E-04 | 1.46E-03 | -- | Lipase (class 3) |
| EVM0005732  | 10.66 | 4.39 | 1.28 | 6.00E-04 | 3.72E-03 | -- | NADH:flavin oxidoreductase / NADH oxidase family |
| EVM0003987  | 26.91 | 11.07 | 1.28 | 9.60E-03 | 3.63E-02 | -- | -- |
| EVM0000613  | 15.11 | 6.21 | 1.28 | 5.00E-05 | 4.28E-04 | Defense mechanisms | AAA domain |
| EVM0003191 | 58.67 | 24.08 | 1.28 | 4.50E-04 2.92E-03 | Secondary metabolites biosynthesis, transport and catabolism | Cytochrome P450 |
| EVM0012019 | 14.39 | 5.90  | 1.29 | 4.50E-04 2.92E-03 | -- | BTB/POZ domain |
| EVM0000180 | 171.85| 70.44 | 1.29 | 2.00E-04 1.46E-03 | -- | Protein kinase domain |
| EVM0004604 | 96.58 | 39.58 | 1.29 | 2.50E-04 1.77E-03 | Signal transduction mechanisms | NUDIX domain |
| EVM0008945 | 257.59| 105.56| 1.29 | 5.00E-05 4.28E-04 | Secondary metabolites biosynthesis, transport and catabolism | Pyridine nucleotide-disulphide oxidoreductase |
| EVM0005250 | 32.98 | 13.51 | 1.29 | 5.00E-05 4.28E-04 | -- | Fungal specific transcription factor domain |
| EVM0005047 | 122.55| 50.17 | 1.29 | 5.00E-05 4.28E-04 | -- | Protein of unknown function (DUF1688) |
| EVM0002585 | 33.80 | 13.84 | 1.29 | 5.00E-05 4.28E-04 | -- | Phosphoinositide 3-kinase family, accessory domain (PIK domain) |
| EVM0009712 | 4.55  | 1.86  | 1.29 | 4.65E-03 2.03E-02 | #N/A | #N/A |
| EVM0001698 | 53.32 | 21.82 | 1.29 | 1.00E-04 7.96E-04 | -- | Fatty acid desaturase |
| EVM0005255 | 77.57 | 31.70 | 1.29 | 5.00E-05 4.28E-04 | Posttranslational modification, protein turnover, chaperones | -- |
| EVM0000743  | 21.93 | 8.95 | 1.29 | 5.00E-05 | 4.28E-04 | -- | FAD binding domain |
|-------------|-------|------|------|----------|----------|----|------------------|
| EVM0010124  | 93.16 | 37.99| 1.29 | 5.00E-05 | 4.28E-04 | -- | Fungal protein of unknown function (DUF1752) |
| EVM0004029  | 115.65| 47.02| 1.30 | 5.00E-05 | 4.28E-04 | General function prediction only | TATA-binding protein interacting (TIP20) |
| EVM0006744  | 49.64 | 20.16| 1.30 | 5.00E-05 | 4.28E-04 | General function prediction only | Carboxylesterase family |
| EVM0006690  | 55.60 | 22.58| 1.30 | 5.00E-05 | 4.28E-04 | General function prediction only | Kelch motif |
| EVM0001336  | 64.58 | 26.20| 1.30 | 4.00E-04 | 2.65E-03 | Signal transduction mechanisms | HIT domain |
| EVM0004175  | 136.81| 55.41| 1.30 | 5.00E-05 | 4.28E-04 | -- | Nitronate monooxygenase |
| EVM0001638  | 71.60 | 28.99| 1.30 | 5.00E-05 | 4.28E-04 | Amino acid transport and metabolism | Glutamine synthetase, catalytic domain |
| EVM0001547  | 6.86  | 2.77 | 1.31 | 6.00E-04 | 3.72E-03 | -- | F-box-like |
| EVM0005159  | 101.55| 41.01| 1.31 | 5.00E-05 | 4.28E-04 | -- | NADH:flavin oxidoreductase / NADH oxidase family |
| EVM0010194  | 33.25 | 13.40| 1.31 | 5.00E-05 | 4.28E-04 | -- | Protein of unknown function (DUF4246) |
| EVM0008466  | 310.04| 124.92| 1.31 | 1.00E-04 | 7.96E-04 | Energy production and conversion | ATP synthase alpha/beta family, nucleotide-binding domain |
| EVM0010598  | 4.49  | 1.81 | 1.31 | 2.15E-03 | 1.08E-02 | -- | F-box-like |
| Gene ID     | Value1 | Value2 | Value3 | Value4 | Value5 | Value6 | Value7 | Value8 | Category                          | Function                                           |
|------------|--------|--------|--------|--------|--------|--------|--------|--------|-----------------------------------|---------------------------------------------------|
| EVM0004594 | 138.25 | 55.67  | 1.31   | 5.00E-05| 4.28E-04|        |        |        | Amino acid transport and metabolism| Amino acid permease                                |
| EVM0010923 | 50.54  | 20.32  | 1.31   | 5.00E-05| 4.28E-04|        |        |        | Replication, recombination and repair| FAT domain                                        |
| EVM0004840 | 276.31 | 111.05 | 1.32   | 5.00E-05| 4.28E-04| --     |        | --     | --                                | --                                                |
| EVM0012163 | 33.80  | 13.58  | 1.32   | 5.00E-05| 4.28E-04|        |        |        | Replication, recombination and repair| DNA replication factor Dna2                        |
| EVM0005557 | 46.12  | 18.52  | 1.32   | 5.00E-05| 4.28E-04| --     |        | --     | Nucleoporin subcomplex protein binding to Pom34 |                                                    |
| EVM0009514 | 310.89 | 124.76 | 1.32   | 5.00E-05| 4.28E-04|        |        |        | Carbohydrate transport and metabolism| Glyceraldehyde 3-phosphate dehydrogenase, C-terminal domain |
| EVM0003057 | 30.01  | 12.02  | 1.32   | 3.50E-04| 2.36E-03|        |        | --     | Domain of unknown function (DUF4336)|                                                    |
| EVM000787  | 31.43  | 12.59  | 1.32   | 2.00E-04| 1.46E-03|        |        | Posttranslational modification, protein turnover, chaperones| Prenyltransferase and squalene oxidase repeat |
| EVM0010226 | 1723.10| 689.62 | 1.32   | 1.50E-04| 1.14E-03|        |        |        | Inorganic ion transport and metabolism| Iron/manganese superoxide dismutases, C-terminal domain |
| EVM001562  | 139.15 | 55.68  | 1.32   | 1.00E-04| 7.96E-04|        |        | --     | Alpha amylase, catalytic domain    |                                                    |
| EVM0004676 | 96.48  | 38.58  | 1.32   | 5.00E-05| 4.28E-04|        |        | Signal transduction mechanisms   | RhoGEF domain                                      |
| EVM0003034 | 165.29 | 66.08  | 1.32   | 3.00E-04| 2.07E-03|        |        | Coenzyme transport and metabolism| Formate--tetrahydrofolate ligase                |
| Entry       | Mass   | Charge | Accuracy | E-value1 | E-value2 | Description                                                                 |
|------------|--------|--------|----------|----------|----------|----------------------------------------------------------------------------|
| EVM0011178 | 87.12  | 1.32   | 5.00E-05 | 4.28E-04 | --       | --                                                                         |
| EVM0003271 | 2.54   | 1.32   | 4.95E-03 | 2.13E-02 | --       | Fungalysin metallopeptidase (M36)                                           |
| EVM0006280 | 29.16  | 1.32   | 5.00E-05 | 4.28E-04 | --       | Nucleotide transport and metabolism                                           |
| EVM0004085 | 36.84  | 1.33   | 1.26E-02 | 4.49E-02 | --       | 5'-nucleotidase, C-terminal domain                                            |
| EVM0010728 | 55.80  | 1.33   | 5.00E-05 | 4.28E-04 | --       | Posttranslational modification, protein turnover, chaperones                 |
| EVM0000707 | 109.33 | 1.33   | 5.00E-05 | 4.28E-04 | --       | Putative cyclase                                                             |
| EVM0000397 | 161.44 | 1.33   | 5.00E-05 | 4.28E-04 | --       | --                                                                           |
| EVM0002286 | 2.74   | 1.33   | 8.40E-03 | 3.26E-02 | --       | Cellulase (glycosyl hydrolase family 5)                                      |
| EVM0000598 | 64.58  | 1.33   | 5.00E-05 | 4.28E-04 | --       | Cell cycle control, cell division, chromosome partitioning                  |
| EVM0002966 | 213.00 | 1.33   | 5.00E-05 | 4.28E-04 | --       | N terminus of Rad21 / Rec8 like protein                                      |
| EVM0001850 | 7.00   | 1.33   | 4.10E-03 | 1.83E-02 | --       | GHMP kinases N terminal domain                                               |
| EVM0009256 | 59.87  | 1.33   | 5.00E-05 | 4.28E-04 | --       | Function unknown                                                            |
| EVM0000598 | 64.58  | 1.33   | 5.00E-05 | 4.28E-04 | --       | Vta1 like                                                                   |
| EVM0009059  | 4.28 | 1.70 | 1.33 | 5.70E-03 | 2.39E-02 | General function prediction only | short chain dehydrogenase |
| EVM0011268  | 50.07 | 19.91 | 1.33 | 1.00E-04 | 7.96E-04 | -- | -- |
| EVM0001151  | 116.37 | 46.28 | 1.33 | 5.00E-05 | 4.28E-04 | Intracellular trafficking, secretion, and vesicular transport | Exportin 1-like protein |
| EVM0001683  | 42.00 | 16.69 | 1.33 | 5.00E-05 | 4.28E-04 | Coenzyme transport and metabolism | Probable molybdopterin binding domain |
| EVM0011830  | 32.37 | 12.86 | 1.33 | 4.00E-03 | 1.79E-02 | Intracellular trafficking, secretion, and vesicular transport | Golgi CORVET complex core vacuolar protein 8 |
| EVM0002339  | 222.02 | 88.17 | 1.33 | 5.00E-05 | 4.28E-04 | -- | -- |
| EVM0002146  | 5.39 | 2.14 | 1.33 | 1.30E-03 | 7.10E-03 | -- | Pectinesterase |
| EVM0009414  | 127.37 | 50.54 | 1.33 | 5.00E-05 | 4.28E-04 | General function prediction only | Protein kinase domain |
| EVM0001824  | 62.13 | 24.65 | 1.33 | 5.00E-05 | 4.28E-04 | General function prediction only | Alpha/beta hydrolase family |
| EVM0009632  | 196.77 | 78.06 | 1.33 | 5.00E-05 | 4.28E-04 | Secondary metabolites biosynthesis, transport and catabolism | Copper amine oxidase, enzyme domain |
| EVM0010885  | 101.70 | 40.34 | 1.33 | 6.50E-04 | 3.98E-03 | Posttranslational modification, protein turnover, chaperones | BCS1 N terminal |
| Accession   | EVM0010842 | 145.53 | 57.70 | 1.33 | 5.00E-05 | 4.28E-04 | -- | Allophanate hydrolase subunit 2 |
|-------------|------------|--------|-------|------|----------|----------|----|--------------------------------|
| Accession   | EVM0004671 | 39.90  | 15.81 | 1.34 | 5.00E-05 | 4.28E-04 | Cytoskeleton | Histidine phosphatase superfamily (branch 2) |
| Accession   | EVM0002970 | 30.67  | 12.15 | 1.34 | 4.00E-04 | 2.65E-03 | -- | -- |
| Accession   | EVM0000767 | 27.72  | 10.97 | 1.34 | 5.00E-05 | 4.28E-04 | Replication, recombination and repair | MCM2/3/5 family |
| Accession   | EVM0002487 | 23.89  | 9.46  | 1.34 | 5.00E-05 | 4.28E-04 | Signal transduction mechanisms | OPT oligopeptide transporter protein |
| Accession   | EVM0004374 | 318.17 | 125.80 | 1.34 | 5.00E-05 | 4.28E-04 | -- | -- |
| Accession   | EVM0011364 | 6.37   | 2.52  | 1.34 | 8.50E-04 | 4.98E-03 | -- | Jacalin-like lectin domain |
| Accession   | EVM0007734 | 166.16 | 65.61 | 1.34 | 5.00E-05 | 4.28E-04 | Secondary metabolites biosynthesis, transport and catabolism | Pyridine nucleotide-disulphide oxidoreductase |
| Accession   | EVM0000512 | 9.27   | 3.66  | 1.34 | 1.15E-03 | 6.41E-03 | -- | -- |
| Accession   | EVM0006652 | 57.09  | 22.49 | 1.34 | 1.00E-04 | 7.96E-04 | -- | Cytochrome P450 |
| Accession   | EVM0008895 | 237.35 | 93.51 | 1.34 | 5.00E-05 | 4.28E-04 | -- | Protein kinase domain |
| Accession   | EVM0003181 | 86.97  | 34.24 | 1.34 | 5.00E-05 | 4.28E-04 | -- | -- |
| Gene ID          | Coverage | Overlap | Order | 
|------------------|----------|---------|-------|
| EVM0007738       | 299.98   | 118.07  | 1.35  | Glycosyltransferase sugar-binding region containing DXD motif |
| EVM0001400       | 39.64    | 15.59   | 1.35  | PAS fold |
| EVM0006416       | 115.73   | 45.48   | 1.35  | Secondary metabolites biosynthesis, transport and catabolism |
| EVM0008722       | 155.69   | 61.14   | 1.35  | Inorganic ion transport and metabolism |
| EVM0000439       | 83.27    | 32.69   | 1.35  | -- |
| EVM0001362       | 5.96     | 2.34    | 1.35  | Protein of unknown function (DUF1212) |
| EVM0006629       | 45.38    | 17.78   | 1.35  | Secondary metabolites biosynthesis, transport and catabolism |
| EVM0002137       | 46.93    | 18.39   | 1.35  | Defense mechanisms |
| EVM0002953       | 180.59   | 70.64   | 1.35  | D-arabinono-1,4-lactone oxidase |
| EVM0001594       | 51.23    | 20.01   | 1.36  | Secondary metabolites biosynthesis, transport and catabolism |
| EVM0010443       | 11.39    | 4.45    | 1.36  | Zinc finger C-x8-C-x5-C-x3-H type (and similar) |
| Protein ID    | EC Number | modular score | e-value | Function Description                                                                 | Domain/Function |
|--------------|-----------|---------------|---------|--------------------------------------------------------------------------------------|-----------------|
| EVM0005161   | 48.06     | 18.76         | 1.36    | Secondary metabolites biosynthesis, transport and catabolism                         | ABC transporter |
| EVM0008808   | 12.00     | 4.68          | 1.36    | General function prediction only                                                     | Haloacid dehalogenase-like hydrolase |
| EVM0005662   | 85.91     | 33.51         | 1.36    | Nucleotide transport and metabolism                                                  | AICARFT/IMPCHase bienzyme |
| EVM0000868   | 32.50     | 12.68         | 1.36    | --                                                                                    | Aconitase family (aconitate hydratase) |
| EVM0008744   | 55.28     | 21.52         | 1.36    | RNA processing and modification                                                      | MIF4G domain   |
| EVM0004686   | 6.77      | 2.63          | 1.36    | General function prediction only                                                    | Major Facilitator Superfamily |
| EVM0009644   | 25.43     | 9.90          | 1.36    | --                                                                                    | --              |
| EVM0000355   | 937.39    | 364.70        | 1.36    | --                                                                                    | --              |
| EVM0000257   | 8.31      | 3.23          | 1.36    | --                                                                                    | --              |
| EVM0007372   | 21.23     | 8.25          | 1.36    | --                                                                                    | --              |
| EVM0009793   | 5.79      | 2.25          | 1.36    | --                                                                                    | --              |
| EVM0011123   | 49.31     | 19.16         | 1.36    | Posttranslational modification, protein turnover, chaperones                         | Insulinase (Peptidase family M16) |
| Accession     | Comment 1 | Comment 2 | Comment 3 | Comment 4 | Comment 5 |
|---------------|-----------|-----------|-----------|-----------|-----------|
| EVM0005413    | 201.98    | 78.47     | 1.36      | 5.00E-05  | 4.28E-04  | Possible lysine decarboxylase |
| EVM0000054    | 8.73      | 3.39      | 1.36      | 2.00E-04  | 1.46E-03  | Secondary metabolites biosynthesis, transport and catabolism |
|               |           |           |           |           |           | Cytochrome P450 |
| EVM0004984    | 70.98     | 27.55     | 1.37      | 5.00E-05  | 4.28E-04  | -- |
|               |           |           |           |           |           | -- |
| EVM0004330    | 1700.54   | 660.07    | 1.37      | 7.20E-03  | 2.88E-02  | -- |
|               |           |           |           |           |           | -- |
| EVM0001877    | 4.08      | 1.58      | 1.37      | 2.35E-03  | 1.16E-02  | Voltage-dependent anion channel |
| EVM0009565    | 1575.72   | 610.93    | 1.37      | 2.75E-03  | 1.32E-02  | Posttranslational modification, protein turnover, chaperones |
|               |           |           |           |           |           | AAA domain (Cdc48 subfamily) |
| EVM0011313    | 7.34      | 2.84      | 1.37      | 5.00E-05  | 4.28E-04  | -- |
|               |           |           |           |           |           | -- |
| EVM0011981    | 30.89     | 11.94     | 1.37      | 5.00E-05  | 4.28E-04  | Amino acid transport and metabolism |
|               |           |           |           |           |           | Aldehyde dehydrogenase family |
| EVM0008948    | 17.26     | 6.67      | 1.37      | 1.00E-04  | 7.96E-04  | -- |
|               |           |           |           |           |           | BTB/POZ domain |
| EVM0003929    | 13.23     | 5.11      | 1.37      | 1.00E-04  | 7.96E-04  | -- |
|               |           |           |           |           |           | Taurine catabolism dioxygenase TauD, TfdA family |
| EVM000879     | 21.91     | 8.46      | 1.37      | 5.00E-05  | 4.28E-04  | Carbohydrate transport and metabolism |
|               |           |           |           |           |           | GHMP kinases C terminal |
| EVM0004924    | 59.94     | 23.14     | 1.37      | 1.29E-02  | 4.57E-02  | -- |
|               |           |           |           |           |           | -- |
| EVM0002506  | 68.64 | 26.49 | 1.37 | 1.50E-04 | 1.14E-03 | Inorganic ion transport and metabolism | Natural resistance-associated macrophage protein |
| EVM0007541  | 68.55 | 26.40 | 1.38 | 5.00E-05 | 4.28E-04 | Signal transduction mechanisms | RhoGAP domain |
| EVM0011121  | 145.48 | 56.01 | 1.38 | 1.65E-03 | 8.65E-03 | -- | -- |
| EVM0007741  | 32.26 | 12.41 | 1.38 | 5.00E-05 | 4.28E-03 | -- | SNF2 family N-terminal domain |
| EVM0011967  | 77.17 | 29.68 | 1.38 | 5.00E-05 | 4.28E-04 | -- | -- |
| EVM0009469  | 72.77 | 27.95 | 1.38 | 5.00E-05 | 4.28E-04 | -- | -- |
| EVM0008799  | 54.39 | 20.87 | 1.38 | 5.00E-05 | 4.28E-04 | -- | Right handed beta helix region |
| EVM0005856  | 620.84 | 238.21 | 1.38 | 5.00E-05 | 4.28E-04 | Translation, ribosomal structure and biogenesis | eIF-6 family |
| EVM0011151  | 643.28 | 246.79 | 1.38 | 5.00E-05 | 4.28E-04 | Secondary metabolites biosynthesis, transport and catabolism | Cytochrome P450 |
| EVM0004822  | 84.00 | 32.21 | 1.38 | 5.00E-05 | 4.28E-04 | -- | -- |
| EVM0007677  | 32.69 | 12.53 | 1.38 | 9.50E-04 | 5.46E-03 | Secondary metabolites biosynthesis, transport and catabolism | AMP-binding enzyme |
| EVM0008679  | 7.51 | 2.88 | 1.38 | 5.00E-05 | 4.28E-04 | Signal transduction mechanisms | RhoGEF domain |
| EVM0004285  | 29.82  | 11.41  | 1.39  | 5.00E-05 | 4.28E-04 | Secondary metabolites biosynthesis, transport and catabolism | Multicopper oxidase |
|-------------|--------|--------|-------|----------|----------|-------------------------------------------------------------|-------------------|
| EVM0005480  | 267.81 | 102.49 | 1.39  | 5.00E-05 | 4.28E-04 | --                                                           | --                |
| EVM0011143  | 76.16  | 29.14  | 1.39  | 5.00E-05 | 4.28E-04 | RNA processing and modification                            | DEAD/DEAH box helicase |
| EVM0007116  | 2.45   | 0.94   | 1.39  | 3.65E-03 | 1.66E-02 | Cytoskeleton                                                | Misato Segment II tubulin-like domain |
| EVM0006017  | 32.12  | 12.29  | 1.39  | 5.00E-05 | 4.28E-04 | --                                                           | Uncharacterized alpha/beta hydrolase domain (DUF2235) |
| EVM0008073  | 44.07  | 16.85  | 1.39  | 5.00E-05 | 4.28E-04 | Amino acid transport and metabolism                         | Glycosyl transferase family, a/b domain |
| EVM0000955  | 97.99  | 37.43  | 1.39  | 5.00E-05 | 4.28E-04 | General function prediction only                           | Ankyrin repeats (many copies) |
| EVM0011070  | 9.76   | 3.73   | 1.39  | 5.00E-05 | 4.28E-04 | Function unknown                                            | Domain of unknown function (DUF1741) |
| EVM0004356  | 5.31   | 2.03   | 1.39  | 7.00E-03 | 2.82E-02 | General function prediction only                           | Dienelactone hydrolase family |
| EVM0001377  | 336.39 | 128.40 | 1.39  | 3.50E-04 | 2.36E-03 | Cell wall/membrane/envelope biogenesis                      | 1,3-beta-glucan synthase component |
| EVM0008337  | 72.85  | 27.80  | 1.39  | 5.00E-05 | 4.28E-04 | General function prediction only                           | --                |
| EVM0007364  | 65.71  | 25.05  | 1.39  | 5.00E-05 | 4.28E-04 | Lipid transport and metabolism                             | alpha/beta hydrolase fold |
| Accession   | Score | Exp | Avg Exp | Seq Coverage | Domain                          |
|------------|-------|-----|---------|--------------|---------------------------------|
| EVM0008673 | 64.50 | 24.57 | 1.39    | --           | Sir2 family                     |
| EVM0005213 | 39.56 | 15.07 | 1.39    | --           | Nucleotide transport and Lyase   |
| EVM0009891 | 84.77 | 32.29 | 1.39    | --           | Fungal Zn(2)-Cys(6) binuclear   |
| EVM0006969 | 128.89| 49.07 | 1.39    | --           | --                              |
| EVM0008943 | 2.14 | 0.81  | 1.39    | 2.70E-03     | Signal transduction mechanisms   |
| EVM0011893 | 1962.61| 745.90| 1.40    | 6.65E-03     | Posttranslational modification,  |
| EVM0002766 | 427.37| 162.41| 1.40    | 5.00E-05     | Energy production and conversion|
| EVM0006221 | 19.23 | 7.27  | 1.40    | 1.50E-04     | Signal transduction mechanisms   |
| EVM0009234 | 28.85 | 10.90 | 1.40    | 5.00E-05     | Enolase C-terminal domain-like   |
| EVM0010136 | 131.96| 49.87 | 1.40    | 5.00E-05     | Carbohydrate transport and       |
| EVM0008227 | 34.62 | 13.08 | 1.40    | 5.00E-05     | Replication, recombination and   |
| EVM0005148 | 440.96| 166.50| 1.41    | 5.00E-05     | Carbohydrate transport and       |
|            |       |       |         |              | metabolism                       |
|            |       |       |         |              | 6-phosphogluconate dehydrogenase,|
|            |       |       |         |              | C-terminal domain                |
| Gene ID     | EMT       | EMT (G) | EMT (L) | EMT (M) | EMT (D) | Function Prediction                                                                 |
|------------|-----------|---------|---------|---------|---------|--------------------------------------------------------------------------------------|
| EVM0002033 | 5.91      | 2.23    | 1.41    | 9.80E-03| 3.69E-02| #N/A                                                                                 |
| EVM0004859 | 36.11     | 13.61   | 1.41    | 5.00E-05| 4.28E-04| General function prediction only short chain dehydrogenase                            |
| EVM0007330 | 189.16    | 71.27   | 1.41    | 5.00E-05| 4.28E-04| --                                                                                   |
| EVM0004424 | 38.60     | 14.53   | 1.41    | 5.00E-05| 4.28E-04| Amino acid transport and metabolism Histidinol dehydrogenase                          |
| EVM0005149 | 64.22     | 24.17   | 1.41    | 2.50E-04| 1.77E-03| --                                                                                   |
| EVM0005418 | 149.78    | 56.37   | 1.41    | 1.05E-02| 3.88E-02| Translation, ribosomal structure and biogenesis tRNA synthetases class I (I, L, M and V) |
| EVM0007721 | 42.06     | 15.82   | 1.41    | 2.50E-04| 1.77E-03| --                                                                                   |
| EVM0009501 | 137.46    | 51.67   | 1.41    | 5.00E-05| 4.28E-04| Function unknown Eukaryotic protein of unknown function (DUF914)                      |
| EVM0000536 | 6.66      | 2.50    | 1.42    | 6.10E-03| 2.52E-02| --                                                                                   |
| EVM0009861 | 155.36    | 58.22   | 1.42    | 5.00E-05| 4.28E-04| Signal transduction mechanisms Protein kinase domain                                  |
| EVM0008382 | 43.40     | 16.25   | 1.42    | 5.00E-05| 4.28E-04| General function prediction only WD domain, G-beta repeat                              |
| EVM0004947 | 16.52     | 6.18    | 1.42    | 5.00E-05| 4.28E-04| --                                                                                   |
| EVM0008890 | 18.59     | 6.96    | 1.42    | 5.00E-05| 4.28E-04| RNA processing and modification Sec63 Brl domain                                       |
| Accession     | E-value | |
|--------------|---------|----------------|
| EVM0002163   | 25.71   | 9.62           |
| EVM0003788   | 1.68    | 0.63           |
| EVM0002782   | 34.88   | 13.02          |
| EVM0007615   | 63.74   | 23.78          |
| EVM0008747   | 43.59   | 16.24          |
| EVM0005193   | 42.57   | 15.85          |
| EVM0008518   | 492.11  | 183.18         |
| EVM0007587   | 145.28  | 54.07          |
| EVM0004929   | 40.10   | 14.90          |
| EVM0010133   | 84.68   | 31.46          |
| EVM0003868   | 149.62  | 55.57          |
| EVM0008570   | 85.08   | 31.57          |
| EVM0000728   | 41.80   | 15.51          |

**Function predictions:**
- **EVM0002163:** HEAT repeat
- **EVM0003788:** --
- **EVM0002782:** --
- **EVM0007615:** Function unknown
- **EVM0008747:** General function prediction only
- **EVM0005193:** Acetyltransferase (GNAT) domain
- **EVM0008518:** Carboxymuconolactone decarboxylase family
- **EVM0007587:** --
- **EVM0004929:** General function prediction only
- **EVM0010133:** Amino acid transport and metabolism
- **EVM0003868:** --
- **EVM0008570:** --
- **EVM0000728:** 50S ribosome-binding GTPase
| EVM0004678 | 22.30 | 8.27 | 1.43 | 5.00E-05 | 4.28E-04 | -- | Cellulase (glycosyl hydrolase family 5) |
|------------|-------|------|------|---------|---------|----|-----------------------------------------|
| EVM0001405 | 169.09| 62.70| 1.43 | 5.00E-05 | 4.28E-04 | -- | Intracellular trafficking, secretion, and vesicular transport |
|            |       |      |      |         |         |    | Sybindin-like family                     |
| EVM0000233 | 26.50 | 9.81 | 1.43 | 5.00E-05 | 4.28E-04 | -- | Intracellular trafficking, secretion, and vesicular transport |
|            |       |      |      |         |         |    | Domain of unknown function in PX-proteins (DUF3818) |
| EVM0002222 | 9.31  | 3.44 | 1.44 | 5.00E-04 | 3.19E-03 | -- | Cytochrome P450                           |
| EVM0004850 | 10.43 | 3.86 | 1.44 | 5.00E-04 | 3.19E-03 | -- | Semialdehyde dehydrogenase, NAD binding domain |
| EVM0008555 | 7.10  | 2.62 | 1.44 | 5.00E-04 | 4.28E-03 | -- | SNF2 family N-terminal domain            |
| EVM0010372 | 12.25 | 4.53 | 1.44 | 5.00E-05 | 4.28E-04 | -- | Signal transduction mechanisms            |
|            |       |      |      |         |         |    | Histidine kinase-, DNA gyrase B-, and HSP90-like ATPase |
| EVM0000075 | 23.82 | 8.80 | 1.44 | 5.00E-05 | 4.28E-04 | -- | F-box domain                             |
| EVM0001004 | 96.97 | 35.80| 1.44 | 2.50E-04 | 1.77E-03 | -- | TAP-like protein                          |
| EVM0010749 | 8.23  | 3.04 | 1.44 | 4.50E-04 | 2.92E-03 | -- | Secondary metabolites biosynthesis, transport and catabolism |
|            |       |      |      |         |         |    | Cytochrome P450                           |
| EVM0008878 | 15.41 | 5.68 | 1.44 | 1.01E-02 | 3.78E-02 | -- | --                                      |
|            |       |      |      |         |         |    | --                                      |
| EVM0003012  | 120.92 | 44.56 | 1.44 | 5.00E-05 | 4.28E-04 | -- | -- |
| EVM0009659  | 179.58 | 66.17 | 1.44 | 5.00E-05 | 4.28E-04 | Posttranslational modification, protein turnover, chaperones | ICP0-binding domain of Ubiquitin-specific protease 7 |
| EVM0009401  | 42.30  | 15.57 | 1.44 | 5.00E-05 | 4.28E-04 | Transcription | -- |
| EVM0010001  | 30.49  | 11.22 | 1.44 | 3.95E-03 | 1.77E-02 | Translation, ribosomal structure and biogenesis | Endoribonuclease L-PSP |
| EVM0004812  | 213.61 | 78.61 | 1.44 | 5.00E-05 | 4.28E-04 | -- | Arrestin (or S-antigen), N-terminal domain |
| EVM0001810  | 283.77 | 104.23 | 1.45 | 5.00E-05 | 4.28E-04 | Carbohydrate transport and metabolism | Major intrinsic protein |
| EVM0001083  | 48.97  | 17.98 | 1.45 | 5.00E-05 | 4.28E-04 | Lipid transport and metabolism | short chain dehydrogenase |
| EVM0008748  | 48.27  | 17.70 | 1.45 | 5.00E-05 | 4.28E-04 | -- | -- |
| EVM0008924  | 849.90 | 311.04 | 1.45 | 3.50E-04 | 2.36E-03 | Translation, ribosomal structure and biogenesis | Elongation factor Tu GTP binding domain |
| EVM0000179  | 3.30   | 1.21  | 1.45 | 1.40E-03 | 7.55E-03 | Secondary metabolites biosynthesis, transport and catabolism | Cytochrome P450 |
| EVM0008805  | 49.99  | 18.28 | 1.45 | 5.00E-05 | 4.28E-04 | -- | -- |
| EVM0004568  | 309.51 | 113.16 | 1.45 | 5.00E-05 | 4.28E-04 | -- | Cellulase (glycosyl hydrolase family 5) |
| Gene ID     | Total Posts | Protein Posts | Average Size | Median Scaling Factor | Posttranslational modification, protein turnover, chaperones | Secondary metabolites biosynthesis, transport and catabolism | Eukaryotic aspartyl protease | ABC transporter transmembrane region | Glutathione S-transferase, N-terminal domain | Aldehyde dehydrogenase family | lactate/malate dehydrogenase, NAD binding domain | RecF/RecN/SMC N terminal domain |
|------------|-------------|---------------|--------------|----------------------|---------------------------------------------------------------|-------------------------------------------------------------|-------------------------------|-------------------------------------|------------------------------------------|--------------------------------------------|---------------------------------------------|---------------------------------------------|
| EVM0012111 | 59.25       | 21.66         | 1.45         | 5.00E-05 4.28E-04    | --                                                             | --                                                          | Eukaryotic aspartyl protease | --                                  | --                                        | --                                         | --                                          | --                                          |
| EVM0011240 | 299.49      | 109.41        | 1.45         | 5.00E-05 4.28E-04    | --                                                             | --                                                          | --                            | --                                  | --                                        | --                                         | --                                          | --                                          |
| EVM0006789 | 131.04      | 47.82         | 1.45         | 5.00E-05 4.28E-04    | Posttranslational modification, protein turnover, chaperones | Secondary metabolites biosynthesis, transport and catabolism | ABC transporter transmembrane region | Glutathione S-transferase, N-terminal domain | Aldehyde dehydrogenase family | lactate/malate dehydrogenase, NAD binding domain | Eukaryotic aspartyl protease |
| EVM00112190| 6.88        | 2.51          | 1.46         | 1.10E-03 6.17E-03    | Posttranslational modification, protein turnover, chaperones | --                                                          | --                            | --                                  | --                                        | --                                         | RecF/RecN/SMC N terminal domain |
| EVM0011846 | 159.65      | 58.16         | 1.46         | 5.00E-05 4.28E-04    | Posttranslational modification, protein turnover, chaperones | --                                                          | --                            | --                                  | --                                        | --                                         | --                                          | --                                          |
| EVM0004518 | 26.30       | 9.58          | 1.46         | 5.00E-05 4.28E-04    | Energy production and conversion                               | --                                                          | --                            | --                                  | --                                        | --                                         | --                                          | --                                          |
| EVM0000503 | 486.53      | 177.15        | 1.46         | 5.00E-05 4.28E-04    | Energy production and conversion                               | --                                                          | --                            | --                                  | --                                        | --                                         | --                                          | --                                          |
| EVM0010175 | 142.28      | 51.80         | 1.46         | 5.00E-05 4.28E-04    | Posttranslational modification, protein turnover, chaperones | --                                                          | --                            | --                                  | --                                        | --                                         | --                                          | --                                          |
| EVM0009960 | 4.17        | 1.52          | 1.46         | 9.20E-03 3.51E-02    | --                                                             | --                                                          | --                            | --                                  | --                                        | --                                         | --                                          | --                                          |
| EVM0000440 | 63.54       | 23.12         | 1.46         | 5.00E-05 4.28E-04    | --                                                             | Glutathione S-transferase, N-terminal domain                 | --                            | --                                  | --                                        | --                                         | --                                          | --                                          |
| EVM0006479 | 19.38       | 7.04          | 1.46         | 5.00E-05 4.28E-04    | --                                                             | RecF/RecN/SMC N terminal domain                              | --                            | --                                  | --                                        | --                                         | --                                          | --                                          |
| Gene ID     | Count | Percent | FDR  | Persistence | Function Description                                      |
|------------|-------|---------|------|-------------|-----------------------------------------------------------|
| EVM002184  | 1535.71 | 557.60  | 1.46 | 2.00E-04    | General function prediction only                          |
| EVM004235  | 60.80   | 22.06   | 1.46 | 5.00E-04    | Sugar (and other) transporter only                        |
| EVM006076  | 925.97  | 335.99  | 1.46 | 3.95E-03    | --                                                        |
| EVM010043  | 162.64  | 58.99   | 1.46 | 5.00E-04    | Carbohydrate transport and metabolism                     |
| EVM004098  | 137.15  | 49.69   | 1.46 | 5.00E-04    | Signal transduction mechanisms                            |
| EVM002114  | 182.00  | 65.92   | 1.47 | 5.00E-04    | Posttranslational modification, protein turnover, chaperones |
| EVM007201  | 38.52   | 13.93   | 1.47 | 5.00E-04    | --                                                        |
| EVM010942  | 43.72   | 15.79   | 1.47 | 5.00E-04    | --                                                        |
| EVM002736  | 87.69   | 31.56   | 1.47 | 5.00E-04    | Cytoskeleton                                             |
| EVM005404  | 22.41   | 8.05    | 1.48 | 5.00E-04    | Myosin head (motor domain)                               |
| EVM001842  | 83.01   | 29.81   | 1.48 | 5.00E-04    | RecF/RecN/SMC N terminal domain                           |
| EVM0010878 | 35.52   | 12.74   | 1.48 | 5.00E-04    | --                                                        |
| Accession   | Mw (kDa) | Mw (KDa) | p.I | E-value | Function                                    |
|-------------|----------|----------|-----|---------|---------------------------------------------|
| EVM0001066  | 21.88    | 7.84     | 1.48| 5.00E-05  | FAD binding domain                          |
| EVM0008834  | 120.63   | 43.20    | 1.48| 5.00E-05  | Pirin                                       |
| EVM0001225  | 23.87    | 8.55     | 1.48| 1.80E-03  | CoA binding domain                          |
| EVM0009637  | 39.19    | 14.02    | 1.48| 5.00E-05  | General function prediction only            |
| EVM0003184  | 47.21    | 16.87    | 1.48| 5.00E-05  | Intracellular trafficking, secretion, and vesicular transport |
| EVM0002464  | 98.47    | 35.18    | 1.48| 5.00E-05  | Amino acid transport and metabolism         |
| EVM0002457  | 34.01    | 12.14    | 1.49| 5.00E-05  | Coenzyme transport and metabolism           |
| EVM0002502  | 375.73   | 134.15   | 1.49| 5.00E-05  | Uncharacterized alpha/beta hydrolase domain (DUF2235) |
| EVM0006860  | 158.19   | 56.47    | 1.49| 5.00E-05  | Function unknown                            |
| EVM0005902  | 53.38    | 19.03    | 1.49| 5.00E-05  | --                                           |
| EVM0006566  | 52.76    | 18.80    | 1.49| 5.00E-05  | Protein of unknown function (DUF3533)       |
| EVM0006594  | 689.09   | 245.31   | 1.49| 5.00E-05  | Amino acid transport and metabolism         |
|             |          |          |     |         | Serine hydroxymethyltransferase            |
| EVM0008978 | 13.31 | 4.73 | 1.49 | 5.00E-05 | 4.28E-04 | Transcription | SNF2 family N-terminal domain |
| EVM0003698 | 103.03 | 36.61 | 1.49 | 5.00E-05 | 4.28E-04 | -- | Alginate lyase |
| EVM0001895 | 41.79 | 14.85 | 1.49 | 5.00E-05 | 4.28E-04 | -- | -- |
| EVM0001446 | 203.32 | 72.08 | 1.50 | 5.00E-05 | 4.28E-04 | Carbohydrate transport and metabolism | Phosphoglucone isomerase |
| EVM0006648 | 10.86 | 3.84 | 1.50 | 1.00E-04 | 7.96E-04 | -- | -- |
| EVM0006693 | 2.70 | 0.95 | 1.50 | 1.15E-03 | 6.41E-03 | -- | O-Glycosyl hydrolase family 30 |
| EVM0010152 | 24.77 | 8.75 | 1.50 | 3.00E-03 | 2.07E-03 | -- | -- |
| EVM0005752 | 102.09 | 35.99 | 1.50 | 5.00E-05 | 4.28E-04 | -- | S1/P1 Nuclease |
| EVM0011216 | 106.00 | 37.30 | 1.51 | 5.00E-05 | 4.28E-04 | -- | Oxidoreductase family, NAD-binding Rossmann fold |
| EVM0000713 | 23.54 | 8.28 | 1.51 | 5.00E-05 | 4.28E-04 | -- | ABC transporter |
| EVM0009500 | 155.93 | 54.85 | 1.51 | 5.00E-05 | 4.28E-04 | -- | Domain of unknown function (DUF1708) |
| EVM0000530 | 27.77 | 9.76 | 1.51 | 5.00E-05 | 4.28E-04 | Function unknown | Ribosome 60S biogenesis N-terminal |
| EVM0009456 | 97.87 | 34.40 | 1.51 | 5.00E-05 | 4.28E-04 | -- | -- |
| Gene ID      | E-value 1 | E-value 2 | E-value 3 | E-value 4 | E-value 5 | Function                                                                 |
|-------------|-----------|-----------|-----------|-----------|-----------|--------------------------------------------------------------------------|
| EVM0011005  | 20.73     | 7.28      | 1.51      | 5.00E-05  | 4.28E-04  | Polysaccharide deacetylase                                               |
| EVM0002522  | 17.13     | 6.02      | 1.51      | 1.00E-04  | 7.96E-04  | Protein of unknown function (DUF1399)                                    |
| EVM0003905  | 166.20    | 58.32     | 1.51      | 5.00E-05  | 4.28E-04  | Domain of unknown function (DUF4646)                                    |
| EVM0000981  | 43.74     | 15.31     | 1.51      | 9.50E-04  | 5.46E-03  | --                                                                       |
| EVM0008259  | 843.42    | 294.90    | 1.52      | 1.00E-04  | 7.96E-04  | Putative oxidoreductase C terminal                                       |
| EVM0007795  | 70.79     | 24.74     | 1.52      | 5.00E-05  | 4.28E-04  | Secondary metabolites biosynthesis, transport and catabolism             |
| EVM0004154  | 5.68      | 1.99      | 1.52      | 4.70E-03  | 2.05E-02  | --                                                                       |
| EVM0006941  | 10.17     | 3.55      | 1.52      | 5.00E-05  | 4.28E-04  | Nucleotide transport and metabolism                                      |
| EVM0005845  | 29.53     | 10.30     | 1.52      | 5.00E-05  | 4.28E-04  | Domain of unknown function (DUF4470)                                    |
| EVM0007194  | 64.63     | 22.50     | 1.52      | 5.00E-05  | 4.28E-04  | Major Facilitator Superfamily                                           |
| EVM0003437  | 25.10     | 8.74      | 1.52      | 5.00E-05  | 4.28E-04  | Posttranslational modification, protein turnover, chaperones             |
| EVM0007887  | 2305.86   | 802.44    | 1.52      | 5.00E-05  | 4.28E-04  | Cytoskeleton                                                             |

- Cytochrome P450
- Inosine-uridine preferring nucleoside hydrolase
- Tubulin folding cofactor D C terminal
| ID            | M   | E   | C   | A1  | A2  | Function                                                                 | Domain/Structure                        |
|---------------|-----|-----|-----|-----|-----|--------------------------------------------------------------------------|------------------------------------------|
| EVM0012158    | 47.59 | 16.56 | 1.52 | 5.00E-05 | 4.28E-04 | Importin-beta N-terminal domain                                          |
| EVM0005468    | 58.31 | 20.28 | 1.52 | 5.00E-05 | 4.28E-04 | Amino acid transport and metabolism                                      | Pyrroline-5-carboxylate reductase dimerisation |
| EVM001712     | 136.61 | 47.50 | 1.52 | 5.00E-05 | 4.28E-04 | Carbohydrate transport and metabolism                                   | Inositol monophosphatase family           |
| EVM000751     | 25.92 | 9.00  | 1.53 | 5.00E-05 | 4.28E-04 | Replication, recombination and repair                                   | Ku70/Ku80 beta-barrel domain              |
| EVM001822     | 3.56  | 1.23  | 1.53 | 1.60E-03  | 8.44E-03 | --                                                                        | --                                        |
| EVM0010844    | 43.61 | 15.14 | 1.53 | 5.00E-05 | 4.28E-04 | --                                                                        | Polysaccharide deacetylase               |
| EVM0011500    | 41.88 | 14.53 | 1.53 | 5.00E-05 | 4.28E-04 | General function prediction only                                        | Putative esterase                        |
| EVM0009790    | 45.44 | 15.77 | 1.53 | 5.00E-05 | 4.28E-04 | Secondary metabolites biosynthesis, transport and catabolism            | ABC transporter                          |
| EVM0006262    | 108.63 | 37.68 | 1.53 | 5.00E-05 | 4.28E-04 | --                                                                        | Peptidase family M1                     |
| EVM0006252    | 30.18 | 10.45 | 1.53 | 5.00E-05 | 4.28E-04 | --                                                                        | Protein of unknown function (DUF2454)    |
| EVM0009942    | 30.02 | 10.39 | 1.53 | 5.00E-05 | 4.28E-04 | Transcription                                                            | Domain of unknown function (DUF3535)      |
| EVM0011910    | 60.21 | 20.81 | 1.53 | 5.00E-05 | 4.28E-04 | Intracellular trafficking, secretion, and vesicular transport           | VID27 cytoplasmic protein                |
| Accession     | E   | N   | P  | Conserved Domains                                      |
|--------------|-----|-----|----|-------------------------------------------------------|
| EVM0001972   | 32.24 | 11.14 | 1.53 | --                                                     |
| EVM0004570   | 62.59 | 21.63 | 1.53 | --                                                     |
| EVM0005478   | 9.21  | 3.18  | 1.53 | --                                                     |
| EVM0007666   | 62.22 | 21.46 | 1.54 | --                                                     |
| EVM0007606   | 32.98 | 11.35 | 1.54 | --                                                     |
| EVM0007757   | 37.95 | 13.05 | 1.54 | --                                                     |
| EVM0010801   | 15.75 | 5.41  | 1.54 | --                                                     |
| EVM0009831   | 33.45 | 11.45 | 1.55 | --                                                     |
| EVM0008720   | 208.73| 71.42 | 1.55 | --                                                     |
| EVM0010648   | 58.55 | 20.01 | 1.55 | --                                                     |
| EVM0004575   | 187.92| 64.19 | 1.55 | --                                                     |
| EVM0010884   | 280.99| 95.94 | 1.55 | --                                                     |
| EVM0001064   | 1.49  | 0.51  | 1.55 | --                                                     |
| Accession     | Value1 | Value2 | Value3 | Value4 | Value5 | Value6 | Value7 | Value8 | Value9 | Value10 |
|--------------|--------|--------|--------|--------|--------|--------|--------|--------|--------|---------|
| EVM0011306   | 2.37   | 0.81   | 1.55   | 8.00E-03 | 3.13E-02 | --     | --     |        |        |         |
| EVM0002277   | 6.83   | 2.33   | 1.55   | 5.00E-05 | 4.28E-04 | --     |        |        |        | Spe97 / Spe98 family |
| EVM0007667   | 273.96 | 93.46  | 1.55   | 5.00E-05 | 4.28E-04 | --     | Ubiquitin-2 like Rad60 SUMO-like |
| EVM0010291   | 25.83  | 8.79   | 1.55   | 1.05E-03 | 5.94E-03 | --     |          |        |        | MAPEG family |
| EVM0010924   | 18.69  | 6.36   | 1.56   | 2.00E-04 | 1.46E-03 | --     | Putative amidotransferase |
| EVM0006605   | 105.69 | 35.94  | 1.56   | 5.00E-05 | 4.28E-04 | Secondary metabolites biosynthesis, transport and catabolism | Alcohol dehydrogenase GroES-like domain |
| EVM0011665   | 62.91  | 21.37  | 1.56   | 5.00E-05 | 4.28E-04 | Signal transduction mechanisms | Protein kinase domain |
| EVM0007035   | 44.51  | 15.12  | 1.56   | 5.00E-05 | 4.28E-04 | --     | Transferrin receptor-like dimerisation domain |
| EVM0007579   | 214.68 | 72.77  | 1.56   | 5.00E-05 | 4.28E-04 | --     | HEAT repeat |
| EVM0007599   | 21.07  | 7.14   | 1.56   | 1.50E-04 | 1.14E-03 | --     | --     |
| EVM0005145   | 38.58  | 13.03  | 1.57   | 2.35E-03 | 1.16E-02 | --     | --     |
| EVM0002999   | 53.99  | 18.24  | 1.57   | 5.00E-05 | 4.28E-04 | Intracellular trafficking, secretion, and vesicular transport | ATG C terminal domain |
| Accession     | ID     | E.C. | Credibility | Fold Change | Feature 1                          | Feature 2                                      |
|--------------|--------|------|-------------|-------------|------------------------------------|-----------------------------------------------|
| EVM0004740   | 49.66  | 16.77| 1.57        | 5.00E-05    | Energy production and conversion   | Iron-containing alcohol dehydrogenase        |
| EVM0002918   | 78.36  | 26.44| 1.57        | 5.00E-05    | --                                 | Cytochrome P450                               |
| EVM0004056   | 38.79  | 13.08| 1.57        | 1.50E-04    | --                                 | --                                           |
| EVM0005495   | 4.70   | 1.58 | 1.57        | 1.25E-03    | --                                 | Ketopantoate reductase PanE/A_pbA C terminal |
| EVM0009599   | 3.50   | 1.18 | 1.57        | 3.50E-03    | --                                 | TPR repeat                                    |
| EVM0005574   | 20.69  | 6.93 | 1.58        | 5.00E-05    | RNA processing and modification    | RNA dependent RNA polymerase                 |
| EVM0001966   | 44.90  | 15.03| 1.58        | 5.00E-04    | General function prediction only   | Major Facilitator Superfamily                |
| EVM0004436   | 8.61   | 2.88 | 1.58        | 4.00E-03    | --                                 | Acetamidase/Formamidase family               |
| EVM0003073   | 32.39  | 10.81| 1.58        | 5.00E-04    | --                                 | --                                           |
| EVM0006112   | 26.01  | 8.67 | 1.58        | 5.00E-04    | Carbohydrate transport and metabolism | Glycosyl hydrolases family 18                |
| EVM0009134   | 32.73  | 10.91| 1.59        | 5.00E-04    | --                                 | Domain of unknown function (DUF4139)         |
| EVM0000235   | 12.89  | 4.29 | 1.59        | 5.00E-04    | --                                 | Voltage-dependent anion channel              |
| EVM0010191   | 10.36  | 3.44 | 1.59        | 1.00E-04    | --                                 | --                                           |
| EVM0006223 | 1.57 | 0.52 | 1.59 | 9.75E-03 | 3.67E-02 | -- | -- |
| EVM0012052 | 643.55 | 213.61 | 1.59 | 5.00E-05 | 4.28E-04 | -- | Cerato-platanin |
| EVM0012202 | 2781.27 | 922.93 | 1.59 | 2.20E-03 | 1.10E-02 | -- | -- |
| EVM0003976 | 127.76 | 42.32 | 1.59 | 5.00E-05 | 4.28E-04 | -- | -- |
| EVM0003655 | 16.88 | 5.59 | 1.59 | 5.00E-05 | 4.28E-04 | -- | -- |
| EVM0002129 | 9.68 | 3.20 | 1.60 | 5.00E-05 | 4.28E-04 | -- | -- |
| EVM0011347 | 64.93 | 21.47 | 1.60 | 5.00E-05 | 4.28E-04 | -- | -- |
| EVM0007366 | 43.49 | 14.38 | 1.60 | 5.00E-05 | 4.28E-04 | -- | -- |
| EVM0004566 | 40.94 | 13.49 | 1.60 | 3.20E-03 | 1.49E-02 | -- | -- |
| EVM0000460 | 36.45 | 12.01 | 1.60 | 5.00E-05 | 4.28E-04 | -- | -- |
| EVM0006562 | 3531.04 | 1161.26 | 1.60 | 5.00E-05 | 4.28E-04 | -- | -- |
| EVM0007265 | 5.29 | 1.74 | 1.60 | 2.20E-03 | 1.10E-02 | -- | -- |

Amino acid transport and metabolism
Conserved region in glutamate synthase
Uncharacterized alpha/beta hydrolase domain (DUF2235)
Carbohydrate transport and metabolism
Major Facilitator Superfamily
Carbohydrate transport and metabolism
Alpha amylase, catalytic domain
Domain of unknown function (DUF718)
Inorganic ion transport and metabolism
Sodium/calcium exchanger protein
Posttranslational modification, protein turnover, chaperones
Glutaredoxin
| EVM0006301 | 123.07 | 40.33 | 1.61 | 5.00E-05 | 4.28E-04 | Carbohydrate transport and metabolism | Amidohydrolase family |
| EVM0006122 | 26.98 | 8.83 | 1.61 | 8.35E-03 | 3.24E-02 | -- | -- |
| EVM0006552 | 7.61 | 2.49 | 1.61 | 5.00E-05 | 4.28E-04 | Secondary metabolites biosynthesis, transport and catabolism | Male sterility protein |
| EVM0001890 | 6.00 | 1.96 | 1.61 | 1.25E-02 | 4.46E-02 | -- | -- |
| EVM0011292 | 916.28 | 298.83 | 1.62 | 5.00E-05 | 4.28E-04 | Carbohydrate transport and metabolism | Phosphoglycerate kinase |
| EVM0000747 | 12.66 | 4.13 | 1.62 | 1.00E-04 | 7.96E-04 | General function prediction only | Scavenger mRNA decapping enzyme C-term binding |
| EVM0011675 | 26.10 | 8.51 | 1.62 | 5.00E-05 | 4.28E-04 | Cytoskeleton | Dynein heavy chain and region D6 of dynein motor |
| EVM0002643 | 321.50 | 104.49 | 1.62 | 1.00E-04 | 7.96E-04 | -- | -- |
| EVM0005728 | 2.05 | 0.67 | 1.63 | 5.75E-03 | 2.41E-02 | General function prediction only | Histidine phosphatase superfamily (branch 2) |
| EVM0011309 | 1245.33 | 402.88 | 1.63 | 5.00E-05 | 4.28E-04 | -- | -- |
| EVM0008061 | 119.36 | 38.59 | 1.63 | 5.00E-05 | 4.28E-04 | General function prediction only | GMC oxidoreductase |
| EVM0003014 | 225.46 | 72.82 | 1.63 | 5.00E-05 | 4.28E-04 | Amino acid transport and metabolism | Methylenetetrahydrofolate reductase |
| EVM0007298 | 49.54 | 16.00 | 1.63 | 5.00E-05 | 4.28E-04 | General function prediction only | Major Facilitator Superfamily |
|------------|-------|-------|------|----------|----------|-----------------------------------|-----------------------------|
| EVM0003673 | 4.11  | 1.33  | 1.63 | 1.75E-03 | 9.08E-03 | --                                | Terpene synthase family, metal binding domain |
| EVM0003731 | 175.04| 56.41 | 1.63 | 5.00E-05 | 4.28E-04 | General function prediction only  | RNA recognition motif. (a.k.a. RRM, RBD, or RNP domain) |
| EVM0005975 | 128.60| 41.44 | 1.63 | 5.00E-05 | 4.28E-04 | Secondary metabolites biosynthesis, transport and catabolism | Flavin-binding monoxygenase-like |
| EVM0002084 | 159.28| 51.15 | 1.64 | 5.00E-05 | 4.28E-04 | --                                | --                          |
| EVM0002124 | 96.72 | 31.02 | 1.64 | 5.00E-05 | 4.28E-04 | Amino acid transport and metabolism | Dehydratase family           |
| EVM0006345 | 150.46| 48.23 | 1.64 | 5.00E-05 | 4.28E-04 | Signal transduction mechanisms    | HAMP domain                 |
| EVM0011448 | 71.22 | 22.81 | 1.64 | 5.00E-05 | 4.28E-04 | Carbohydrate transport and metabolism | glucanotransferase domain of human glycogen debranching enzyme |
| EVM0002201 | 90.85 | 29.05 | 1.65 | 5.00E-05 | 4.28E-04 | Energy production and conversion | Aldehyde dehydrogenase family |
| EVM0001466 | 13.74 | 4.38  | 1.65 | 5.00E-05 | 4.28E-04 | Posttranslational modification, protein turnover, chaperones | Peptidase family M48        |
| EVM0012149 | 94.14 | 30.02 | 1.65 | 5.00E-05 | 4.28E-04 | --                                | Beta-lactamase superfamily domain |
| EVM0001953  | 8.91 | 2.84 | 1.65 | 5.00E-05 | 4.28E-04 | -- | Vacuole effluxer Atg22 like |
| EVM0000709  | 69.70 | 22.17 | 1.65 | 1.75E-03 | 9.08E-03 | -- | -- |
| EVM0000418  | 196.30 | 62.40 | 1.65 | 5.00E-05 | 4.28E-04 | Posttranslational modification, protein turnover, chaperones | Isoprenylcysteine carboxyl methyltransferase (ICMT) family |
| EVM0008782  | 19.90 | 6.32 | 1.65 | 5.00E-05 | 4.28E-04 | Replication, recombination and repair | MCM2/3/5 family |
| EVM0007311  | 65.55 | 20.78 | 1.66 | 5.00E-05 | 4.28E-04 | Secondary metabolites biosynthesis, transport and catabolism | Cytochrome P450 |
| EVM0003090  | 115.35 | 36.53 | 1.66 | 5.00E-05 | 4.28E-04 | Carbohydrate transport and metabolism | Major Facilitator Superfamily |
| EVM0008798  | 7.96 | 2.52 | 1.66 | 5.00E-05 | 4.28E-04 | -- | Gt1/Pac2 family |
| EVM0010929  | 98.98 | 31.28 | 1.66 | 5.00E-05 | 4.28E-04 | -- | -- |
| EVM0010014  | 237.79 | 75.12 | 1.66 | 5.00E-05 | 4.28E-04 | General function prediction only | Calcineurin-like phosphoesterase |
| EVM0003134  | 32.98 | 10.41 | 1.66 | 5.00E-05 | 4.28E-04 | -- | -- |
| EVM0009536  | 160.50 | 50.51 | 1.67 | 5.00E-05 | 4.28E-04 | Amino acid transport and metabolism | Cys/Met metabolism PLP-dependent enzyme |
| ID          | Value | String   | String                                                                 |
|-------------|-------|----------|------------------------------------------------------------------------|
| EVM0002052  | 384.96| 121.13   | 1.67                                                                   |
| EVM0005683  | 3.94  | 1.24     | 1.67                                                                   |
| EVM0006582  | 12.30 | 3.86     | 1.67                                                                   |
| EVM0007996  | 11.95 | 3.74     | 1.68                                                                   |
| EVM0004844  | 34.34 | 10.72    | 1.68                                                                   |
| EVM0005816  | 209.67| 65.46    | 1.68                                                                   |
| EVM0001482  | 5.51  | 1.72     | 1.68                                                                   |
| EVM0002733  | 64.63 | 20.17    | 1.68                                                                   |
| EVM0007160  | 6.43  | 2.00     | 1.68                                                                   |
| EVM0010697  | 247.64| 77.11    | 1.68                                                                   |
| EVM0006577  | 211.87| 65.95    | 1.68                                                                   |

| ID          | Value | String   | String                                                                 |
|-------------|-------|----------|------------------------------------------------------------------------|
| EVM0002052  | 384.96| 121.13   | 1.67                                                                   |
| EVM0005683  | 3.94  | 1.24     | 1.67                                                                   |
| EVM0006582  | 12.30 | 3.86     | 1.67                                                                   |
| EVM0007996  | 11.95 | 3.74     | 1.68                                                                   |
| EVM0004844  | 34.34 | 10.72    | 1.68                                                                   |
| EVM0005816  | 209.67| 65.46    | 1.68                                                                   |
| EVM0001482  | 5.51  | 1.72     | 1.68                                                                   |
| EVM0002733  | 64.63 | 20.17    | 1.68                                                                   |
| EVM0007160  | 6.43  | 2.00     | 1.68                                                                   |
| EVM0010697  | 247.64| 77.11    | 1.68                                                                   |
| EVM0006577  | 211.87| 65.95    | 1.68                                                                   |

### Carbohydrate transport and metabolism
- Phosphoglucomutase/phosphomannomutase, alpha/beta/alpha domain I

### General function prediction only
- Major Facilitator Superfamily

### Signal transduction mechanisms
- Protein kinase domain

### Posttranslational modification, protein turnover, chaperones
- Isoprenylcysteine carboxyl methyltransferase (ICMT) family

### Domain of unknown function (DUF4139)

### Lipid transport and metabolism
- Short chain dehydrogenase
- Calcineurin-like phosphoesterase

### Energy production and conversion
- Aldo/keto reductase family
| Accession   | Value1 | Value2 | Value3 | Value4   | Value5   | Function               | Superfamily          |
|-------------|--------|--------|--------|----------|----------|------------------------|----------------------|
| EVM0003496  | 3.24   | 1.01   | 1.68   | 1.10E-03 | 6.17E-03 | --                     | --                   |
| EVM0005291  | 19.42  | 6.04   | 1.69   | 5.00E-05 | 4.28E-04 | --                     | --                   |
| EVM0006660  | 711.10 | 220.73 | 1.69   | 1.00E-04 | 7.96E-04 | --                     | --                   |
| EVM0005925  | 21.96  | 6.81   | 1.69   | 5.00E-05 | 4.28E-04 | --                     | Cytochrome P450      |
| EVM0006160  | 150.10 | 46.51  | 1.69   | 5.00E-05 | 4.28E-04 | Function unknown       | Major Facilitator Superfamily |
| EVM0004296  | 13.35  | 4.13   | 1.69   | 6.95E-03 | 2.80E-02 | --                     | --                   |
| EVM0004968  | 45.68  | 14.13  | 1.69   | 5.00E-05 | 4.28E-04 | Defense mechanisms     | Dual specificity phosphatase, catalytic domain |
| EVM0002674  | 4.93   | 1.53   | 1.69   | 1.20E-03 | 6.64E-03 | Secondary metabolites biosynthesis, transport and catabolism | short chain dehydrogenase |
| EVM0010839  | 116.55 | 36.04  | 1.69   | 5.00E-05 | 4.28E-04 | --                     | Heterokaryon incompatibility protein Het-C |
| EVM0007855  | 145.70 | 44.99  | 1.70   | 5.00E-05 | 4.28E-04 | --                     | C2 domain            |
| EVM0008736  | 43.29  | 13.31  | 1.70   | 5.00E-05 | 4.28E-04 | Secondary metabolites biosynthesis, transport and catabolism | Alcohol dehydrogenase GroES-like domain |
| EVM0009319 | 129.20 | 39.72 | 1.70 | 5.00E-05 | 4.28E-04 | Secondary metabolites biosynthesis, transport and catabolism | Cytochrome P450 |
| EVM0004842 | 66.07 | 20.26 | 1.71 | 5.00E-05 | 4.28E-04 | -- | Ribosomal protein L11 methyltransferase (PrmA) |
| EVM0004652 | 8.97 | 2.75 | 1.71 | 5.00E-05 | 4.28E-04 | -- | Heterokaryon incompatibility protein (HET) |
| EVM0004847 | 6.27 | 1.92 | 1.71 | 5.00E-05 | 4.28E-04 | -- | -- |
| EVM0005563 | 19.04 | 5.82 | 1.71 | 5.00E-05 | 4.28E-04 | -- | Protein of unknown function (DUF4246) |
| EVM0010821 | 1682.01 | 513.88 | 1.71 | 6.50E-04 | 3.98E-03 | -- | -- |
| EVM0001273 | 350.28 | 106.99 | 1.71 | 5.00E-05 | 4.28E-04 | Posttranslational modification, protein turnover, chaperones | Eukaryotic aspartyl protease |
| EVM0010182 | 19.82 | 6.05 | 1.71 | 5.00E-05 | 4.28E-04 | -- | Peptide N-acetyl-beta-D-glucosaminyl asparaginase amidase A |
| EVM0003410 | 100.14 | 30.58 | 1.71 | 5.00E-05 | 4.28E-04 | -- | -- |
| EVM0009049 | 7.76 | 2.37 | 1.71 | 5.00E-04 | 3.19E-03 | -- | -- |
| EVM0004076 | 124.16 | 37.80 | 1.72 | 5.00E-05 | 4.28E-04 | -- | -- |
| Accession   | EVM0010556 | 93.94 | 28.56 | 1.72 | 5.00E-05 | 4.28E-04 | General function prediction only | Major Facilitator Superfamily |
|------------|------------|-------|-------|------|---------|---------|----------------------------------|-------------------------------|
| Accession   | EVM0007712 | 28.42 | 8.63  | 1.72 | 5.00E-05 | 4.28E-04 | General function prediction only | Protein kinase domain          |
| Accession   | EVM000921  | 4.85  | 1.47  | 1.72 | 1.65E-03 | 8.65E-03 | --                               | --                            |
| Accession   | EVM003917  | 3.80  | 1.15  | 1.73 | 3.50E-04 | 2.36E-03 | Energy production and conversion | Aldehyde dehydrogenase family |
| Accession   | EVM009496  | 67.24 | 20.25 | 1.73 | 5.00E-04 | 4.28E-04 | --                               | Sir2 family                   |
| Accession   | EVM003949  | 488.94| 147.15| 1.73 | 2.00E-04 | 1.46E-03 | Energy production and conversion | Mitochondrial carrier protein |
| Accession   | EVM002121  | 19.84 | 5.97  | 1.73 | 5.00E-05 | 4.28E-04 | Replication, recombination and repair | AAA domain                   |
| Accession   | EVM001363  | 2.22  | 0.67  | 1.73 | 2.00E-04 | 1.46E-03 | RNA processing and modification | AAA domain                   |
| Accession   | EVM001287  | 35.08 | 10.54 | 1.73 | 5.00E-05 | 4.28E-04 | Secondary metabolites biosynthesis, transport and catabolism | Cytochrome P450                |
| Accession   | EVM002909  | 19.37 | 5.79  | 1.74 | 5.00E-05 | 4.28E-04 | --                               | NAD(P)-binding Rossmann-like domain |
| Accession   | EVM001244  | 16.65 | 4.97  | 1.74 | 5.00E-05 | 4.28E-04 | Carbohydrate transport and metabolism | Major Facilitator Superfamily |
| Accession   | EVM0002891 | 64.35 | 19.23 | 1.74 | 5.00E-05 | 4.28E-04 | --                               | --                            |
| Gene ID   | E Value  | P Value  | Log2 Fold | Description                                                                 |
|----------|----------|----------|-----------|----------------------------------------------------------------------------|
| EVM0003971 | 20.32    | 6.06     | 1.75      | 5.00E-05 4.28E-04 Coenzyme transport and metabolism                        |
| EVM0000698 | 78.52    | 23.39    | 1.75      | 5.00E-05 4.28E-04 --                                                      |
| EVM0003151 | 24.44    | 7.27     | 1.75      | 5.00E-05 4.28E-04 --                                                      |
| EVM0009384 | 222.15   | 65.95    | 1.75      | 5.00E-05 4.28E-04 Amino acid transport and metabolism                      |
| EVM0008394 | 87.97    | 26.10    | 1.75      | 5.00E-05 4.28E-04 General function prediction only                         |
| EVM000295  | 3685.04  | 1093.39  | 1.75      | 4.50E-04 2.92E-03 Inorganic ion transport and metabolism                  |
| EVM0007775 | 112.31   | 33.28    | 1.75      | 5.00E-05 4.28E-04 --                                                      |
| EVM0010711 | 10.34    | 3.06     | 1.76      | 5.00E-05 4.28E-04 --                                                      |
| EVM0008484 | 91.54    | 27.11    | 1.76      | 5.00E-05 4.28E-04 --                                                      |
| EVM0002233 | 134.89   | 39.94    | 1.76      | 5.00E-05 4.28E-04 --                                                      |
| EVM0003171 | 70.75    | 20.92    | 1.76      | 5.00E-05 4.28E-04 General function prediction only                         |
| EVM0010379 | 65.57    | 19.38    | 1.76      | 5.00E-05 4.28E-04 Signal transduction mechanisms                          |
| EVM0011213 | 16.88    | 4.98     | 1.76      | 4.10E-03 1.83E-02 --                                                      |
| ID               | Ref  | E   | Score | Coding | Description                                      |
|------------------|------|-----|-------|--------|------------------------------------------------|
| EVM0001110       | 61.21| 18.06| 1.76  | 5.00E-05 | 4.28E-04  | CAP-Gly domain                                 |
| EVM0009688       | 14.06| 4.14 | 1.76  | 5.00E-05 | 4.28E-04  | Zinc-binding dehydrogenase                     |
| EVM0007729       | 12.79| 3.76 | 1.77  | 5.00E-05 | 4.28E-04  | --                                              |
| EVM0000320       | 87.54| 25.73| 1.77  | 5.00E-05 | 4.28E-04  | --                                              |
| EVM0004655       | 25.29| 7.43 | 1.77  | 5.00E-05 | 4.28E-04  | Amino acid transport and metabolism             |
| EVM0008304       | 174.99| 51.41| 1.77  | 5.00E-05 | 4.28E-04  | Defense mechanisms                              |
| EVM0007222       | 4.28 | 1.26 | 1.77  | 5.00E-05 | 4.28E-04  | --                                              |
| EVM0008717       | 144.29| 42.29| 1.77  | 5.00E-05 | 4.28E-04  | --                                              |
| EVM0011790       | 15.12| 4.43 | 1.77  | 1.95E-03 | 9.93E-03  | General function prediction only                |
| EVM0007450       | 72.92| 21.29| 1.78  | 5.00E-05 | 4.28E-04  | Amino acid transport and metabolism             |
| EVM0008846       | 29.19| 8.52 | 1.78  | 5.00E-05 | 4.28E-04  | General function prediction only                |
| EVM0003774       | 30.62| 8.90 | 1.78  | 5.00E-05 | 4.28E-04  | Translation, ribosomal structure and biogenesis|
| EVM0011078       | 7.21 | 2.09 | 1.78  | 5.00E-05 | 4.28E-04  | Carbohydrate transport and metabolism           |

Methylenetetrahydrofolate reductase

Dual specificity phosphatase, catalytic domain

Protein of unknown function (DUF4246)

Seed maturation protein

Beta-eliminating lyase

Major Facilitator Superfamily

tRNA synthetases class I (R)

Glycosyl hydrolases family 18
| EVM ID          | Value 1 | Value 2 | Value 3 | Value 4 | Value 5 | Value 6 | Value 7 | Value 8 | Value 9 | Description                                                                 |
|----------------|---------|---------|---------|---------|---------|---------|---------|---------|---------|----------------------------------------------------------------------------|
| EVM0011462     | 34.50   | 9.99    | 1.79    | 5.00E-05| 4.28E-04| Intracellular trafficking, secretion, and vesicular transport | Exocyst complex subunit Sec15-like |
| EVM0002582     | 326.95  | 94.50   | 1.79    | 5.00E-05| 4.28E-04| Translation, ribosomal structure and biogenesis          | RNB domain                        |
| EVM0006955     | 70.47   | 20.36   | 1.79    | 5.00E-05| 4.28E-04| --                                                      | --                                |
| EVM0008310     | 20.15   | 5.81    | 1.79    | 5.00E-05| 4.28E-04| --                                                      | --                                |
| EVM0004128     | 93.61   | 27.00   | 1.79    | 5.00E-05| 4.28E-04| --                                                      | Peptidase family M1               |
| EVM0010040     | 113.18  | 32.57   | 1.80    | 1.00E-04| 7.96E-04| --                                                      | Polysaccharide lyase family 8, super-sandwich domain |
| EVM0006920     | 159.97  | 46.01   | 1.80    | 5.00E-05| 4.28E-04| General function prediction only                       | Leucine Rich repeat               |
| EVM0004630     | 4.64    | 1.33    | 1.80    | 8.00E-04| 4.73E-03| --                                                      | --                                |
| EVM0006268     | 101.75  | 29.19   | 1.80    | 5.00E-05| 4.28E-04| --                                                      | --                                |
| EVM0000675     | 28.95   | 8.28    | 1.81    | 5.00E-05| 4.28E-04| --                                                      | Eukaryotic aspartyl protease      |
| EVM0004012     | 1.22    | 0.35    | 1.81    | 6.30E-03| 2.59E-02| --                                                      | FAD binding domain               |
| EVM0011117     | 22.67   | 6.48    | 1.81    | 5.00E-05| 4.28E-04| Cytoskeleton                                            | Spc97 / Spc98 family             |
| Accession   | Value1 | Value2 | Value3 | Value4 | Description                                                                 | Domain/Region                                |
|-------------|--------|--------|--------|--------|------------------------------------------------------------------------------|-----------------------------------------------|
| EVM0004494  | 98.28  | 28.02  | 1.81   | 5.00E-05 4.28E-04 | Intracellular trafficking, secretion, and vesicular transport               | SacI homology domain                          |
| EVM0004035  | 87.67  | 24.94  | 1.81   | 5.00E-05 4.28E-04 | General function prediction only                                            | TPR repeat                                    |
| EVM0009262  | 370.00 | 105.06 | 1.82   | 5.00E-05 4.28E-04 | General function prediction only                                            | AN1-like Zinc finger                          |
| EVM0003363  | 124.09 | 35.23  | 1.82   | 1.00E-04 7.96E-04 | --                                                                           | --                                            |
| EVM0006432  | 31.21  | 8.86   | 1.82   | 5.00E-04 4.28E-04 | --                                                                           | Fatty acid desaturase                         |
| EVM0008930  | 175.08 | 49.61  | 1.82   | 5.00E-05 4.28E-04 | --                                                                           | --                                            |
| EVM0008780  | 2.74   | 0.78   | 1.82   | 1.13E-02 4.11E-02 | --                                                                           | Phosphotransferase enzyme family              |
| EVM0008581  | 930.61 | 262.79 | 1.82   | 5.00E-05 4.28E-04 | --                                                                           | Eisosome component PIL1                       |
| EVM0008329  | 58.45  | 16.50  | 1.83   | 2.00E-04 1.46E-03 | --                                                                           | --                                            |
| EVM0006290  | 68.26  | 19.19  | 1.83   | 5.00E-05 4.28E-04 | General function prediction only                                            | GMC oxidoreductase                            |
| EVM0009326  | 2.54   | 0.71   | 1.83   | 2.35E-03 1.16E-02 | --                                                                           | SMP-30/Gluconolaconase/LRE-like region        |
| EVM0005785  | 15.96  | 4.48   | 1.83   | 5.00E-05 4.28E-04 | --                                                                           | Variant SH3 domain                            |
| EVM0002962 | 2322.03 | 651.05 | 1.83 | 2.00E-04 | 1.46E-03 | -- | -- |
| EVM0002396 | 25.95 | 7.27 | 1.84 | 5.00E-05 | 4.28E-04 | -- | -- |
| EVM0010629 | 76.46 | 21.37 | 1.84 | 5.00E-05 | 4.28E-04 | -- | Glycosyl hydrolase family 92 |
| EVM0005615 | 5.33 | 1.49 | 1.84 | 5.00E-05 | 4.28E-04 | Function unknown | Alpha/beta hydrolase family |
| EVM0008758 | 2.54 | 0.71 | 1.84 | 3.50E-04 | 2.36E-03 | -- | -- |
| EVM0001061 | 2.44 | 0.68 | 1.84 | 5.00E-05 | 4.28E-04 | Posttranslational modification, protein turnover, chaperones | BCS1 N terminal |
| EVM0011854 | 86.88 | 24.17 | 1.85 | 5.00E-05 | 4.28E-04 | General function prediction only | Cyclic nucleotide-binding domain |
| EVM0000996 | 213.44 | 59.36 | 1.85 | 5.00E-05 | 4.28E-04 | Lipid transport and metabolism | Short chain dehydrogenase |
| EVM0000797 | 30.49 | 8.47 | 1.85 | 5.00E-05 | 4.28E-04 | Translation, ribosomal structure and biogenesis | Piwi domain |
| EVM0006965 | 44.01 | 12.21 | 1.85 | 5.00E-05 | 4.28E-04 | Inorganic ion transport and metabolism | Phosphate transporter family |
| EVM0003455 | 10.20 | 2.83 | 1.85 | 5.00E-05 | 4.28E-04 | -- | -- |
| EVM0010770 | 199.17 | 55.11 | 1.85 | 5.00E-05 | 4.28E-04 | -- | -- |
| Accession     | EVM0010991 | 14.73 | 4.08 | 1.85 | 5.00E-05 | 4.28E-04 | Carbohydrate transport and metabolism | Histidine phosphatase superfamily (branch 1) |
|--------------|------------|-------|------|------|-----------|----------|--------------------------------------|--------------------------------------------|
| Accession     | EVM0010721 | 7.09  | 1.96 | 1.85 | 1.50E-03 | 8.00E-03 | --                                   | --                                         |
| Accession     | EVM0005144 | 32.01 | 8.84 | 1.86 | 5.00E-05 | 4.28E-04 | --                                   | --                                         |
| Accession     | EVM0003003 | 137.07| 37.80| 1.86 | 5.00E-05 | 4.28E-04 | Coenzyme transport and metabolism   | Glutamate-cysteine ligase                 |
| Accession     | EVM0003622 | 2.76  | 0.76 | 1.86 | 5.50E-04 | 3.46E-03 | --                                   | Fungal Zn(2)-Cys(6) binuclear cluster domain |
| Accession     | EVM0010725 | 4.72  | 1.30 | 1.86 | 2.50E-04 | 1.77E-03 | --                                   | --                                         |
| Accession     | EVM0000790 | 18.99 | 5.23 | 1.86 | 5.00E-05 | 4.28E-04 | Translation, ribosomal structure and biogenesis | Piwi domain                                |
| Accession     | EVM0006482 | 6.08  | 1.67 | 1.86 | 5.00E-05 | 4.28E-04 | --                                   | Oxidoreductase family, NAD-binding Rossmann fold |
| Accession     | EVM0006788 | 217.88| 59.89| 1.86 | 5.00E-05 | 4.28E-04 | --                                   | --                                         |
| Accession     | EVM0005947 | 72.14 | 19.82| 1.86 | 5.00E-05 | 4.28E-04 | Signal transduction mechanisms       | Carboxylesterase family                   |
| Accession     | EVM0004530 | 69.86 | 19.19| 1.86 | 5.00E-05 | 4.28E-04 | --                                   | Methyltransferase domain                  |
| Accession     | EVM0001358 | 17.06 | 4.68 | 1.86 | 5.00E-05 | 4.28E-04 | General function prediction only     | GMC oxidoreductase only                   |
| Accession     | EVM0011158 | 410.29| 112.46| 1.87 | 5.00E-05 | 4.28E-04 | --                                   | --                                         |
| ID         | Value1 | Value2 | Log2Fold | Value3   | Value4   | Description                                                                 |
|------------|--------|--------|----------|----------|----------|----------------------------------------------------------------------------|
| EVM0007751 | 116.36 | 31.79  | 1.87     | 5.00E-05 | 4.28E-04 | --                                                                          |
| EVM0003172 | 373.90 | 102.16 | 1.87     | 5.00E-05 | 4.28E-04 | Secondary metabolites biosynthesis, transport and catabolism               |
| EVM0005288 | 2.01   | 0.55   | 1.88     | 3.10E-03 | 1.45E-02 | General function prediction only                                          |
| EVM0001047 | 238.30 | 64.77  | 1.88     | 5.00E-05 | 4.28E-04 | --                                                                         |
| EVM0007746 | 28.42  | 7.67   | 1.89     | 5.00E-05 | 4.28E-04 | JmjC domain, hydroxylase                                                  |
| EVM0005970 | 188.44 | 50.84  | 1.89     | 5.00E-05 | 4.28E-04 | Amino acid transport and metabolism                                        |
| EVM0000101 | 20.84  | 5.62   | 1.89     | 5.00E-05 | 4.28E-04 | #N/A                                                                      |
| EVM0006857 | 12.34  | 3.33   | 1.89     | 5.00E-05 | 4.28E-04 | Signal transduction mechanisms                                            |
| EVM0010734 | 48.38  | 13.02  | 1.89     | 5.00E-05 | 4.28E-04 | Energy production and conversion                                          |
| EVM0010519 | 13.40  | 3.60   | 1.90     | 5.00E-05 | 4.28E-04 | --                                                                         |
| EVM0007749 | 41.53  | 11.13  | 1.90     | 5.00E-05 | 4.28E-04 | General function prediction only                                          |
| EVM0004583 | 79.39  | 21.28  | 1.90     | 5.00E-05 | 4.28E-04 | --                                                                         |

- Animal haem peroxidase
- GMC oxidoreductase
- BTB/POZ domain
- 3-hydroxyanthranilic acid dioxygenase
- #N/A
- Protein phosphatase 2C
- Aldo/keto reductase family
- Major Facilitator Superfamily
| EVM0001702 | 15.19 | 4.07 | 1.90 | 5.00E-05 | 4.28E-04 | -- | -- |
| EVM0008190 | 107.91 | 28.89 | 1.90 | 5.00E-05 | 4.28E-04 | -- | Uncharacterized conserved protein (DUF2156) |
| EVM0005665 | 131.64 | 35.23 | 1.90 | 5.00E-05 | 4.28E-04 | General function prediction only | Zinc finger, C2H2 type |
| EVM000520 | 67.32 | 17.99 | 1.90 | 5.00E-05 | 4.28E-04 | General function prediction only | Josephin |
| EVM0010618 | 45.16 | 12.00 | 1.91 | 5.00E-05 | 4.28E-04 | -- | -- |
| EVM0008733 | 96.79 | 25.69 | 1.91 | 5.00E-05 | 4.28E-04 | Coenzyme transport and metabolism | ThiF family |
| EVM000839 | 277.42 | 73.61 | 1.91 | 5.00E-05 | 4.28E-04 | -- | -- |
| EVM0011628 | 86.64 | 22.99 | 1.91 | 5.00E-05 | 4.28E-04 | Lipid transport and metabolism | PFU (PLAA family ubiquitin binding) |
| EVM0003352 | 17.00 | 4.50 | 1.92 | 5.00E-05 | 4.28E-04 | General function prediction only | Major Facilitator Superfamily |
| EVM0008026 | 81.68 | 21.56 | 1.92 | 5.00E-05 | 4.28E-04 | -- | Reverse transcriptase (RNA-dependent DNA polymerase) |
| EVM0008742 | 41.52 | 10.98 | 1.92 | 5.00E-05 | 4.28E-04 | -- | Mycolic acid cyclopropane synthetase |

- **EVM0001702**: 15.19 | 4.07 | 1.90 | 5.00E-05 | 4.28E-04 | -- | -- |
- **EVM0008190**: 107.91 | 28.89 | 1.90 | 5.00E-05 | 4.28E-04 | -- | Uncharacterized conserved protein (DUF2156) |
- **EVM0005665**: 131.64 | 35.23 | 1.90 | 5.00E-05 | 4.28E-04 | General function prediction only | Zinc finger, C2H2 type |
- **EVM000520**: 67.32 | 17.99 | 1.90 | 5.00E-05 | 4.28E-04 | General function prediction only | Josephin |
- **EVM0010618**: 45.16 | 12.00 | 1.91 | 5.00E-05 | 4.28E-04 | -- | -- |
- **EVM0008733**: 96.79 | 25.69 | 1.91 | 5.00E-05 | 4.28E-04 | Coenzyme transport and metabolism | ThiF family |
- **EVM000839**: 277.42 | 73.61 | 1.91 | 5.00E-05 | 4.28E-04 | -- | -- |
- **EVM0011628**: 86.64 | 22.99 | 1.91 | 5.00E-05 | 4.28E-04 | Lipid transport and metabolism | PFU (PLAA family ubiquitin binding) |
- **EVM0003352**: 17.00 | 4.50 | 1.92 | 5.00E-05 | 4.28E-04 | General function prediction only | Major Facilitator Superfamily |
- **EVM0008026**: 30.26 | 8.00 | 1.92 | 5.00E-05 | 4.28E-04 | RNA processing and modification | AAA domain |
- **EVM0008742**: 41.52 | 10.98 | 1.92 | 5.00E-05 | 4.28E-04 | -- | Reverse transcriptase (RNA-dependent DNA polymerase) |
- **EVM0008759**: 30.73 | 8.12 | 1.92 | 5.00E-05 | 4.28E-04 | -- | Mycolic acid cyclopropane synthetase |
- **EVM0008353**: 81.68 | 21.56 | 1.92 | 5.00E-05 | 4.28E-04 | -- | -- |
| Accession   | M   | M2  | Acc. No. | 5.00E-05 | 4.28E-04 | -- | Protein kinase domain |
|------------|-----|-----|---------|----------|----------|----|-----------------------|
| EVM0009922 | 183.42 | 48.38 | 1.92 | 5.00E-05 | 4.28E-04 | -- | --                    |
| EVM0006559 | 79.54 | 20.97 | 1.92 | 5.00E-05 | 4.28E-04 | -- | --                    |
| EVM000963  | 35.33 | 9.30  | 1.93 | 5.00E-05 | 4.28E-04 | -- | --                    |
| EVM003132  | 208.76 | 54.75 | 1.93 | 5.00E-05 | 4.28E-04 | -- | Histidine-specific methyltransferase, SAM-dependent |
| EVM005614  | 105.86 | 27.76 | 1.93 | 5.00E-05 | 4.28E-04 | -- | --                    |
| EVM006913  | 38.72 | 10.15 | 1.93 | 5.00E-05 | 4.28E-04 | -- | --                    |
| EVM005316  | 3.63  | 0.95  | 1.93 | 9.45E-03 | 3.58E-02 | -- | Dioxygenase            |
| EVM009288  | 287.11 | 75.14 | 1.93 | 5.00E-05 | 4.28E-04 | -- | --                    |
| EVM009977  | 23.15 | 6.05  | 1.94 | 5.00E-05 | 4.28E-04 | -- | Ubiquitin 3 binding protein But2 C-terminal domain |
| EVM003531  | 43.25 | 11.28 | 1.94 | 5.00E-05 | 4.28E-04 | -- | Fungal specific transcription factor domain |
| EVM002374  | 58.22 | 15.18 | 1.94 | 5.00E-05 | 4.28E-04 | -- | Alpha/beta hydrolase family |
| EVM005199  | 18.29 | 4.76  | 1.94 | 1.20E-03 | 6.64E-03 | -- | --                    |
| Gene ID     | EVM0008199 | EVM0010065 | EVM0011687 | EVM0006071 | EVM0007085 | EVM0001556 | EVM0008739 | EVM0010940 | EVM0008582 | EVM0005538 | EVM0005867 | EVM0009164 |
|------------|------------|------------|------------|------------|------------|------------|------------|------------|------------|------------|------------|------------|
| Value 1    | 5.18       | 33.05      | 33.85      | 74.27      | 24.60      | 31.28      | 394.01     | 3.23       | 91.06      | 30.31      | 281.06     | 213.21     |
| Value 2    | 1.35       | 8.59       | 8.79       | 19.19      | 6.34       | 8.06       | 101.13     | 0.83       | 23.35      | 7.76       | 71.99      | 54.60      |
| Value 3    | 1.94       | 1.94       | 1.95       | 1.95       | 1.96       | 1.96       | 1.96       | 1.96       | 1.96       | 1.96       | 1.97       | 1.97       |
| EVM0008199 | 5.00E-05   | 5.00E-05   | 5.00E-05   | 5.00E-05   | 5.00E-05   | 5.00E-05   | 5.00E-05   | 3.00E-03   | 5.00E-05   | 5.00E-05   | 5.00E-05   | 4.60E-03   |
| EVM0010065 | 4.28E-04   | 4.28E-04   | 4.28E-04   | 4.28E-04   | 4.28E-04   | 4.28E-04   | 4.28E-04   | 1.42E-02   | 4.28E-04   | 4.28E-04   | 4.28E-04   | 2.01E-02   |
| Function 1 | Inorganic ion transport and metabolism | -- | Function unknown | Translation, ribosomal structure and biogenesis | Cytoskeleton | Amino acid transport and metabolism | Energy production and conversion | -- | General function prediction only | -- | -- | -- |
| Function 2 | E1-E2 ATPase | -- | Domain of unknown function (DUF3437) | tRNA synthetases class II (D, K and N) | Regulator of Vps4 activity in the MVB pathway | Aminotransferase class I and II | Carbamoyl-phosphate synthase L chain, ATP binding domain | -- | short chain dehydrogenase only | -- | -- | -- |
| Function 3 | -- | -- | -- | -- | -- | -- | -- | -- | -- | -- | -- | -- |

**Inorganic ion transport and metabolism**

**E1-E2 ATPase**

**Domain of unknown function (DUF3437)**

**Translation, ribosomal structure and biogenesis**

**Cytoskeleton**

**Regulator of Vps4 activity in the MVB pathway**

**Aminotransferase class I and II**

**Carbamoyl-phosphate synthase L chain, ATP binding domain**

**General function prediction only**

**short chain dehydrogenase only**

**Aldehyde dehydrogenase family**
| EVM0001672  | 22.45 | 5.74 | 1.97 | 5.00E-05 | 4.28E-04 | Secondary metabolites biosynthesis, transport and catabolism | Alcohol dehydrogenase GroES-like domain |
|-------------|-------|------|------|----------|----------|--------------------------------------------------|--------------------------------------|
| EVM0004021  | 42.66 | 10.90| 1.97 | 5.00E-05 | 4.28E-04 | --                                               | Cytochrome P450                        |
| EVM0004441  | 54.76 | 13.95| 1.97 | 5.00E-05 | 4.28E-04 | Lipid transport and metabolism                    | Squalene/phytoene synthase            |
| EVM0002115  | 25.02 | 6.37 | 1.97 | 5.00E-05 | 4.28E-04 | --                                               | Pregnancy-associated plasma protein-A |
| EVM0007759  | 91.39 | 23.26| 1.97 | 5.00E-05 | 4.28E-04 | --                                               | F-box-like                           |
| EVM0005969  | 143.32| 36.42| 1.98 | 5.00E-05 | 4.28E-04 | Function unknown                                  | Major Facilitator Superfamily         |
| EVM0006888  | 53.66 | 13.62| 1.98 | 5.00E-05 | 4.28E-04 | --                                               | Methyltransferase domain              |
| EVM0003122  | 53.18 | 13.46| 1.98 | 5.00E-05 | 4.28E-04 | Translation, ribosomal structure and biogenesis  | Domain of unknown function (DUF3554)  |
| EVM0002275  | 9.41  | 2.38 | 1.98 | 5.00E-05 | 4.28E-04 | --                                               | --                                   |
| EVM0011935  | 245.69| 61.91| 1.99 | 5.00E-05 | 4.28E-04 | Lipid transport and metabolism                    | Beta-ketoacyl synthase, N-terminal domain |
| EVM0009444  | 12118.40| 3051.67| 1.99 | 3.50E-03 | 1.61E-02 | --                                               | Fungal hydrophobin                    |
| EVM0008881  | 317.37| 79.47| 2.00 | 5.00E-05 | 4.28E-04 | --                                               | Glycosyl hydrolase family 3 N terminal domain |
| EVM0005243 | 14.65 | 3.67 | 2.00 | 5.00E-04 | 3.19E-03 | -- | -- |
| EVM0004316 | 84.39 | 21.10 | 2.00 | 5.00E-05 | 4.28E-04 | -- | -- |
| EVM0010231 | 92.02 | 23.00 | 2.00 | 5.00E-05 | 4.28E-04 | -- | NPL4 family |
| EVM0008827 | 6.39 | 1.59 | 2.01 | 1.30E-03 | 7.10E-03 | -- | -- |
| EVM0003331 | 20.11 | 5.00 | 2.01 | 5.00E-05 | 4.28E-04 | -- | Trehalose utilisation |
| EVM0006787 | 1.94 | 0.48 | 2.01 | 1.23E-02 | 4.42E-02 | -- | Membrane bound O-acyl transferase family |
| EVM0008131 | 455.01 | 112.93 | 2.01 | 5.00E-05 | 4.28E-04 | -- | Cellulase (glycosyl hydrolase family 5) |
| EVM0003669 | 16.84 | 4.18 | 2.01 | 5.00E-05 | 4.28E-04 | -- | -- |
| EVM0004619 | 33.45 | 8.28 | 2.01 | 5.00E-05 | 4.28E-04 | -- | Nucleotide transport and metabolism | Amidohydrolase |
| EVM0011824 | 10.89 | 2.69 | 2.02 | 5.00E-05 | 4.28E-04 | -- | Carbohydrate transport and metabolism | Glycosyl hydrolase family 1 |
| EVM0007351 | 55.42 | 13.69 | 2.02 | 5.00E-05 | 4.28E-04 | -- | -- |
| EVM0006868 | 762.13 | 188.25 | 2.02 | 5.00E-05 | 4.28E-04 | -- | General function prediction | RNA recognition motif. (a.k.a. RRM, RBD, or RNP domain) |
| EVM0003765 | 881.70 | 217.76 | 2.02 | 5.00E-05 | 4.28E-04 | -- | Amino acid transport and metabolism | Amino acid permease |
| EVM0004492 | 8.89 | 2.19 | 2.02 | 5.00E-05 | 4.28E-04 | -- | Ricin-type beta-trefoil lectin domain |
| EVM0009770 | 75.27 | 18.53 | 2.02 | 5.00E-05 | 4.28E-04 | Secondary metabolites biosynthesis, transport and catabolism | short chain dehydrogenase |
| EVM0004547 | 24.94 | 6.13 | 2.02 | 5.00E-05 | 4.28E-04 | -- | -- |
| EVM0006858 | 372.66 | 91.66 | 2.02 | 5.00E-05 | 4.28E-04 | Energy production and conversion | Aldehyde dehydrogenase family |
| EVM0007374 | 62.94 | 15.48 | 2.02 | 5.00E-05 | 4.28E-04 | -- | -- |
| EVM0009595 | 57.87 | 14.20 | 2.03 | 5.00E-05 | 4.28E-04 | -- | -- |
| EVM0005310 | 2602.87 | 638.49 | 2.03 | 5.00E-05 | 4.28E-04 | General function prediction only | Enoyl-(Acyl carrier protein) reductase |
| EVM0011184 | 162.54 | 39.80 | 2.03 | 5.00E-05 | 4.28E-04 | -- | NADH:flavin oxidoreductase / NADH oxidase family |
| EVM0006615 | 6.89 | 1.68 | 2.04 | 5.00E-05 | 4.28E-04 | -- | S1/P1 Nuclease |
| EVM0001389 | 177.93 | 43.33 | 2.04 | 5.00E-05 | 4.28E-04 | -- | FAD binding domain |
| EVM0009298 | 56.13 | 13.66 | 2.04 | 5.00E-05 | 4.28E-04 | -- | -- |
| EVM0011865 | 412.44 | 100.20 | 2.04 | 5.00E-05 | 4.28E-04 | Energy production and conversion | ATP synthase alpha/beta family, nucleotide-binding domain |
| EVM0009917   | 3.07 | 0.75 | 2.04     | 5.00E-05 | 4.28E-04 | --   | --   |
|--------------|------|------|----------|----------|----------|--     |
| EVM0002907   | 130.17 | 31.58 | 2.04     | 5.00E-05 | 4.28E-04 | Defense mechanisms | NAD dependent epimerase/dehydratase family |
| EVM0008764   | 103.90 | 25.18 | 2.05     | 5.00E-05 | 4.28E-04 | Amino acid transport and metabolism | Asparagine synthase |
| EVM0012016   | 688.67 | 166.76 | 2.05     | 5.00E-05 | 4.28E-04 | Amino acid transport and metabolism | Cys/Met metabolism PLP-dependent enzyme |
| EVM0011421   | 64.06 | 15.51 | 2.05     | 5.00E-05 | 4.28E-04 | #N/A | #N/A |
| EVM0002652   | 4.95 | 1.20 | 2.05     | 5.60E-03 | 2.36E-02 | --   | --   |
| EVM0007101   | 91.69 | 22.14 | 2.05     | 5.00E-03 | 4.28E-04 | --   | 50S ribosome-binding GTPase |
| EVM0000119   | 27.07 | 6.52 | 2.05     | 5.00E-05 | 4.28E-04 | --   | 3-beta hydroxysteroid dehydrogenase/isomerase family |
| EVM0010091   | 38.51 | 9.27 | 2.05     | 5.00E-05 | 4.28E-04 | --   | --   |
| EVM0009683   | 72.92 | 17.55 | 2.06     | 5.00E-05 | 4.28E-04 | --   | Cytochrome P450 |
| EVM0005295   | 33.17 | 7.97 | 2.06     | 1.00E-04 | 7.96E-04 | --   | --   |
| EVM0008439   | 48.09 | 11.52 | 2.06     | 5.00E-05 | 4.28E-04 | --   | Uncharacterized alpha/beta hydrolase domain (DUF2235) |
| EVM0000347   | 292.07 | 69.67 | 2.07     | 5.00E-05 | 4.28E-04 | --   | --   |
| Accession | E-value | Identity | Segment Size | Signal Transduction Mechanisms | Description |
|-----------|---------|----------|--------------|--------------------------------|-------------|
| EVM0011460 | 458.83  | 109.41   | 2.07         | 1.00E-04 7.96E-04              | --          |
| EVM0004481 | 35.06   | 8.35     | 2.07         | 5.00E-05 4.28E-04              | --          |
| EVM0009044 | 102.53  | 24.39    | 2.07         | 5.00E-05 4.28E-04              | --          |
| EVM0006505 | 117.78  | 27.98    | 2.07         | 5.00E-05 4.28E-04              | Signal transduction mechanisms |
| EVM0004153 | 274.66  | 65.22    | 2.07         | 5.00E-05 4.28E-04              | --          |
| EVM0004544 | 19.58   | 4.65     | 2.07         | 5.00E-05 4.28E-04              | --          |
| EVM0008715 | 44.99   | 10.63    | 2.08         | 5.00E-05 4.28E-04              | Zinc-binding dehydrogenase |
| EVM0001999 | 42.16   | 9.93     | 2.09         | 5.00E-05 4.28E-04              | --          |
| EVM0001569 | 30.77   | 7.22     | 2.09         | 5.00E-05 4.28E-04              | --          |
| EVM0012021 | 7.64    | 1.79     | 2.10         | 6.70E-03 2.72E-02              | --          |
| EVM0011011 | 13.85   | 3.23     | 2.10         | 1.50E-04 1.14E-03              | --          |
| EVM0000333 | 29.16   | 6.81     | 2.10         | 5.00E-05 4.28E-04              | Posttranslational modification, protein turnover, chaperones |

**EVM0004153**
- **Ricin-type beta-trefoil lectin domain-like**

**EVM0008715**
- **Zinc-binding dehydrogenase**

**EVM0001999**
- **Alpha/beta hydrolase family**

**EVM0001569**
- **General function prediction only**

**EVM0012021**
- **Major Facilitator Superfamily**

**EVM0011011**
- **Poly(ADP-ribose) polymerase catalytic domain**
| Accession   | E-value | Identity | Clustal W | Chromatin structure and dynamics | Paired amphipathic helix repeat |
|------------|---------|----------|-----------|----------------------------------|---------------------------------|
| EVM0002778 | 14.98   | 3.49     | 2.10      | 5.00E-05 4.28E-04                |                                 |
| EVM0003460 | 15.76   | 3.67     | 2.10      | 1.50E-04 1.14E-03                |                                 |
| EVM0002221 | 45.03   | 10.48    | 2.10      | 5.00E-04 4.28E-04                | Amino acid transport and Cys/Met metabolism |
| EVM0010242 | 6.89    | 1.60     | 2.10      | 5.00E-04 4.28E-04                | Function unknown WD domain, G-beta repeat |
| EVM0005441 | 70.03   | 16.27    | 2.11      | 5.00E-04 4.28E-04                | General function prediction Major Facilitator Superfamily |
| EVM0001497 | 39.21   | 9.10     | 2.11      | 5.00E-04 4.28E-04                | NADH(P)-binding |
| EVM0002888 | 791.05  | 183.33   | 2.11      | 5.00E-04 4.28E-04                |                                  |
| EVM0000082 | 11.75   | 2.69     | 2.12      | 2.00E-04 1.46E-03                | WSC domain |
| EVM0000559 | 3.33    | 0.76     | 2.12      | 8.25E-03 3.21E-02                | Glycosyl hydrolase family 61 |
| EVM0000944 | 1823.73 | 417.90   | 2.13      | 5.00E-04 4.28E-04                | General function prediction Aldo/keto reductase family |
| EVM0006901 | 587.01  | 134.32   | 2.13      | 5.00E-04 4.28E-04                | Acetohydroxy acid isomeroreductase, catalytic domain |
| EVM0007212 | 25.83   | 5.90     | 2.13      | 5.00E-04 4.28E-04                | Cytochrome P450 |
| EVM   | ID     | Log2 Freq | Fold | T2 Value | Log2 Fold | Description                                                                 |
|-------|--------|-----------|------|----------|-----------|-----------------------------------------------------------------------------|
| EVM001331 | 48.73  | 11.13     | 2.13 | 5.00E-05 | 4.28E-04  | Ankyrin repeats (many copies)                                              |
| EVM0008410 | 591.24 | 134.90    | 2.13 | 5.00E-05 | 4.28E-04  | Cytoskeleton                                                               |
| EVM0003064 | 8.93   | 2.03      | 2.14 | 4.10E-03 | 1.83E-02  |                                                                             |
| EVM0005776 | 353.10 | 79.92     | 2.14 | 5.00E-05 | 4.28E-04  | Posttranslational modification, protein turnover, chaperones               |
| EVM0007214 | 17.17  | 3.88      | 2.14 | 3.50E-04 | 2.36E-03  |                                                                             |
| EVM0001285 | 180.20 | 40.73     | 2.15 | 5.00E-05 | 4.28E-04  |                                                                             |
| EVM0007446 | 1647.58| 371.57    | 2.15 | 5.00E-05 | 4.28E-04  |                                                                             |
| EVM0008349 | 218.66 | 49.28     | 2.15 | 5.00E-05 | 4.28E-04  | Secondary metabolites biosynthesis, transport and catabolism               |
| EVM0011116 | 10.46  | 2.36      | 2.15 | 5.00E-05 | 4.28E-04  |                                                                             |
| EVM0010159 | 469.44 | 105.61    | 2.15 | 5.00E-05 | 4.28E-04  | Amino acid transport and metabolism                                         |
| EVM0001296 | 35.24  | 7.92      | 2.15 | 5.00E-05 | 4.28E-04  |                                                                             |
| EVM0009509 | 164.33 | 36.72     | 2.16 | 5.00E-05 | 4.28E-04  |                                                                             |

Glutathione S-transferase, N-terminal domain
Fungalysin metallopeptidase (M36)
Cytochrome P450
Acetamidase/Formamidase family
Aconitase family (aconitate hydratase)
FR47-like protein
GMC oxidoreductase
| EVM0005650 | 98.84 | 22.03 | 2.17 | 5.00E-05 | 4.28E-04 | -- | -- |
|------------|-------|-------|======|----------|----------|----|----|
| EVM0008479 | 29.16 | 6.49  | 2.17 | 5.00E-05 | 4.28E-04 | -- | Whi5 like |
| EVM0009222 | 20.99 | 4.67  | 2.17 | 5.00E-05 | 4.28E-04 | -- | Uncharacterized protein conserved in bacteria (DUF2264) |
| EVM0004179 | 14.19 | 3.15  | 2.17 | 5.00E-05 | 4.28E-04 | Lipid transport and metabolism | short chain dehydrogenase |
| EVM0004887 | 7.47  | 1.66  | 2.17 | 5.00E-05 | 4.28E-04 | -- | Protein of unknown function (DUF4246) |
| EVM0010798 | 994.61| 220.18| 2.18 | 5.00E-05 | 4.28E-04 | -- | Stress responsive A/B Barrel Domain |
| EVM0011073 | 57.72 | 12.76 | 2.18 | 5.00E-05 | 4.28E-04 | Amino acid transport and metabolism | Aminotransferase class-III |
| EVM0011946 | 4.14  | 0.91  | 2.18 | 5.15E-03 | 2.20E-02 | -- | SUR7/PalI family |
| EVM0002807 | 157.05| 34.65 | 2.18 | 5.00E-05 | 4.28E-04 | -- | -- |
| EVM0003320 | 28.79 | 6.34  | 2.18 | 5.00E-05 | 4.28E-04 | -- | -- |
| EVM0000781 | 91.72 | 20.21 | 2.18 | 5.00E-05 | 4.28E-04 | Amino acid transport and metabolism | FAD dependent oxidoreductase |
| EVM0000028 | 29.19 | 6.43  | 2.18 | 5.00E-05 | 4.28E-04 | Nucleotide transport and metabolism | AAA domain |
| ID               | M    | E    | Z    | Th1  | Th2  | Th3  | Th4  | Function                                                                 |
|------------------|------|------|------|------|------|------|------|-------------------------------------------------------------------------|
| EVM0003697       | 7.70 | 1.69 | 2.18 | 5.50E-04 | 3.46E-03 | --   | Polyketide cyclase / dehydrase and lipid transport                    |
| EVM0005515       | 17.78| 3.90 | 2.19 | 5.00E-05 | 4.28E-04 | --   | Secondary metabolites biosynthesis, transport and catabolism         |
| EVM0003226       | 345.15| 75.37| 2.20 | 5.00E-05 | 4.28E-04 | --   | Protein of unknown function (DUF3602)                                  |
| EVM0010499       | 1.90 | 0.41 | 2.21 | 1.34E-02 | 4.73E-02 | --   | Protein of unknown function (DUF4246)                                  |
| EVM0001166       | 145.86| 31.44| 2.21 | 5.00E-05 | 4.28E-04 | --   | Secondary metabolites biosynthesis, transport and catabolism         |
| EVM0012096       | 3684.23| 793.58| 2.21 | 5.00E-05 | 4.28E-04 | --   | Carbohydrate transport and metabolism                                 |
| EVM0000411       | 4.95 | 1.06 | 2.22 | 5.00E-05 | 4.28E-04 | --   | Signal transduction mechanisms                                        |
| EVM0003849       | 168.92| 36.25| 2.22 | 5.00E-05 | 4.28E-04 | --   | --                                                                      |
| EVM0006542       | 2175.70| 466.37| 2.22 | 5.00E-05 | 4.28E-04 | --   | --                                                                      |
| EVM0007990       | 21.09 | 4.52 | 2.22 | 5.00E-05 | 4.28E-04 | --   | --                                                                      |
| EVM0003801       | 52.49| 11.23| 2.23 | 5.00E-05 | 4.28E-04 | --   | --                                                                      |
| ID             | Value   | p-value | q-value | Regulation | Function                                                                 |
|---------------|---------|---------|---------|------------|--------------------------------------------------------------------------|
| EVM0005160    | 1044.83 | 2.23    | 5.00E-05| 4.28E-04   | Lipid transport and metabolism                                           |
| EVM0001737    | 43.05   | 2.23    | 5.00E-05| 4.28E-04   | Secondary metabolites biosynthesis, transport and catabolism             |
| EVM0011640    | 24.87   | 2.23    | 5.00E-05| 4.28E-04   | --                                                                       |
| EVM0011233    | 137.22  | 2.23    | 5.00E-05| 4.28E-04   | --                                                                       |
| EVM0009853    | 229.00  | 2.23    | 5.00E-05| 4.28E-04   | --                                                                       |
| EVM0001947    | 4.69    | 2.23    | 3.10E-03| 1.45E-02   | --                                                                       |
| EVM0000117    | 158.56  | 2.24    | 5.00E-05| 4.28E-04   | Peroxidase, family 2                                                     |
| EVM0006769    | 67.66   | 2.24    | 5.00E-05| 4.28E-04   | Translation, ribosomal structure and biogenesis                          |
| EVM0008687    | 55.66   | 2.25    | 5.00E-05| 4.28E-04   | Signal transduction mechanisms                                           |
| EVM0002398    | 17.31   | 2.25    | 5.00E-05| 4.28E-04   | --                                                                       |
| EVM0007713    | 17.05   | 2.25    | 1.30E-03| 7.10E-03   | --                                                                       |
| EVM0005281    | 10.26   | 2.26    | 5.00E-05| 4.28E-04   | Amino acid transport and metabolism                                      |
| EVM0005281    | 10.26   | 2.26    | 5.00E-05| 4.28E-04   | Gamma-glutamyltranspeptidase                                            |
| EVM0000117    | 158.56  | 2.24    | 5.00E-05| 4.28E-04   | Peroxidase, family 2                                                     |
| EVM0006769    | 67.66   | 2.24    | 5.00E-05| 4.28E-04   | Translation, ribosomal structure and biogenesis                          |
| EVM0008687    | 55.66   | 2.25    | 5.00E-05| 4.28E-04   | Signal transduction mechanisms                                           |
| EVM0002398    | 17.31   | 2.25    | 5.00E-05| 4.28E-04   | --                                                                       |
| EVM0007713    | 17.05   | 2.25    | 1.30E-03| 7.10E-03   | --                                                                       |
| EVM0005281    | 10.26   | 2.26    | 5.00E-05| 4.28E-04   | Amino acid transport and metabolism                                      |
| EVM0005281    | 10.26   | 2.26    | 5.00E-05| 4.28E-04   | Gamma-glutamyltranspeptidase                                            |

Phosphatidylinerse decarboxylase
Cytochrome P450
--
--
--
Peroxidase, family 2
tRNA methyltransferase complex GCD14 subunit
Low molecular weight phosphotyrosine protein phosphatase
--
PLAC8 family
| Accession  | EVM0003118 | EVM0006645 | EVM0005718 | EVM0004219 | EVM0005770 | EVM0008708 | EVM0007588 | EVM0002941 | EVM0007684 | EVM0007260 | EVM0007480 | EVM0012240 | EVM0004243 |
|-----------|------------|------------|------------|------------|------------|------------|------------|------------|------------|------------|------------|------------|------------|
| sequence  | 48.35      | 360.08     | 92.98      | 348.33     | 47.75      | 40.70      | 11.51      | 32.98      | 183.12     | 71.34      | 6.09       | 3833.40    | 2.92       |
| score      | 10.08      | 74.72      | 19.27      | 71.97      | 9.86       | 8.34       | 2.34       | 6.70       | 36.89      | 14.33      | 1.22       | 767.07     | 0.58       |
| coverage  | 2.26       | 2.27       | 2.27       | 2.28       | 2.28       | 2.29       | 2.30       | 2.30       | 2.31       | 2.32       | 2.32       | 2.32       | 2.32       |
| id        | 5.00E-05   | 5.00E-05   | 5.00E-05   | 5.00E-05   | 5.00E-05   | 5.00E-05   | 5.00E-05   | 5.00E-05   | 5.00E-05   | 5.00E-05   | 5.00E-05   | 5.00E-05   | 1.40E-03   |
| score      | 4.28E-04   | 4.28E-04   | 4.28E-04   | 4.28E-04   | 4.28E-04   | 4.28E-04   | 4.28E-04   | 4.28E-04   | 4.28E-04   | 4.28E-04   | 4.28E-04   | 4.28E-04   | 7.55E-03   |
| id         | --         | --         | General function prediction only | --         | NADH:flavin oxidoreductase / NADH oxidase family | --         | --         | Nucleotide transport and metabolism | Ham1 family | Major Facilitator Superfamily | --         | Protein of unknown function (DUF3712) | --         |
| id         | --         | --         | WD domain, G-beta repeat | --         | --         | --         | --         | --         | Domain of unknown function (DUF3328) | --         | --         | Protein tyrosine kinase | --         |
| EVM0012129 | 40.16 | 8.03 | 2.32 | 5.00E-05, 4.28E-04 | -- | -- |
| EVM0000318 | 3.10  | 0.62 | 2.33 | 4.80E-03, 2.08E-02 | -- | -- |
| EVM0010628 | 22.86 | 4.56 | 2.33 | 5.00E-05, 4.28E-04 | -- | Taurine catabolism dioxygenase TauD, TfdA family |
| EVM0001060 | 68.36 | 13.62| 2.33 | 5.00E-05, 4.28E-04 | -- | -- |
| EVM0005693 | 562.69| 112.15| 2.33 | 5.00E-05, 4.28E-04 | -- | -- |
| EVM0005948 | 4337.93| 862.63| 2.33 | 5.00E-05, 4.28E-04 | -- | -- |
| EVM0010637 | 10.79 | 2.14 | 2.34 | 5.00E-05, 4.28E-04 | -- | Enolase C-terminal domain-like |
| EVM0008011 | 979.97| 193.57| 2.34 | 1.00E-04, 7.96E-04 | -- | -- |
| EVM0006786 | 460.08| 90.57 | 2.34 | 5.00E-05, 4.28E-04 | Defense mechanisms | alpha/beta hydrolase fold |
| EVM0004529 | 1.34  | 0.26 | 2.35 | 7.95E-03, 3.12E-02 | -- | -- |
| EVM0004712 | 99.22 | 19.50| 2.35 | 5.00E-05, 4.28E-04 | Secondary metabolites biosynthesis, transport and catabolism | short chain dehydrogenase |
| EVM0000105 | 89.99 | 17.69| 2.35 | 5.00E-05, 4.28E-04 | -- | -- |
| Accession  | Value 1 | Value 2 | Value 3 | Value 4 | Value 5 | Description                                                                 |
|-----------|---------|---------|---------|---------|---------|----------------------------------------------------------------------------|
| EVM0004764 | 28.01   | 5.49    | 2.35    | 5.00E-05| 4.28E-04| -                                                                          |
| EVM0012137 | 93.51   | 18.32   | 2.35    | 5.00E-05| 4.28E-04| -                                                                          |
| EVM0007692 | 128.46  | 25.07   | 2.36    | 5.00E-05| 4.28E-04| -                                                                          |
| EVM0005324 | 26.37   | 5.13    | 2.36    | 5.00E-05| 4.28E-04| -                                                                          |
| EVM000973  | 15.49   | 3.01    | 2.36    | 5.00E-05| 4.28E-04| Energy production and conversion                                           |
| EVM0004672 | 139.39  | 27.08   | 2.36    | 5.00E-05| 4.28E-04| -                                                                          |
| EVM0004917 | 34.59   | 6.70    | 2.37    | 7.70E-03| 3.04E-02| -                                                                          |
| EVM0007307 | 151.07  | 29.17   | 2.37    | 5.00E-05| 4.28E-04| -                                                                          |
| EVM0002528 | 100.20  | 19.34   | 2.37    | 5.00E-05| 4.28E-04| Cytoskeleton                                                               |
| EVM0002737 | 27.64   | 5.33    | 2.38    | 5.00E-05| 4.28E-04| -                                                                          |
| EVM0011531 | 102.31  | 19.67   | 2.38    | 5.00E-05| 4.28E-04| -                                                                          |
| EVM0002562 | 867.94  | 166.65  | 2.38    | 5.00E-05| 4.28E-04| Posttranslational modification, protein turnover, chaperones               |
| EVM0000973 | 15.49   | 3.01    | 2.36    | 5.00E-05| 4.28E-04| FMN-dependent dehydrogenase                                               |
| EVM0004672 | 139.39  | 27.08   | 2.36    | 5.00E-05| 4.28E-04| -                                                                          |
| EVM0004917 | 34.59   | 6.70    | 2.37    | 7.70E-03| 3.04E-02| -                                                                          |
| EVM0007307 | 151.07  | 29.17   | 2.37    | 5.00E-05| 4.28E-04| -                                                                          |
| EVM0002528 | 100.20  | 19.34   | 2.37    | 5.00E-05| 4.28E-04| Cytoskeleton                                                               |
| EVM0002737 | 27.64   | 5.33    | 2.38    | 5.00E-05| 4.28E-04| -                                                                          |
| EVM0011531 | 102.31  | 19.67   | 2.38    | 5.00E-05| 4.28E-04| -                                                                          |
| EVM0002562 | 867.94  | 166.65  | 2.38    | 5.00E-05| 4.28E-04| AhpC/TSA family                                                            |
| EVM | Value 1 | Value 2 | Value 3 | Value 4 | Function Description                                    |
|-----|---------|---------|---------|---------|---------------------------------------------------------|
| EVM0003243 | 36.65   | 7.03    | 2.38    | 5.00E-05 | Secondary metabolites biosynthesis, transport and catabolism |
| EVM0008150 | 80.30   | 15.36   | 2.39    | 5.00E-05 | Energy production and conversion                        |
| EVM0011825 | 5.33    | 1.02    | 2.39    | 5.00E-05 | Carbohydrate transport and metabolism                   |
| EVM0005389 | 1978.18 | 376.35  | 2.39    | 5.00E-05 | Glycosyl hydrolases family 35                           |
| EVM0005326 | 9.75    | 1.85    | 2.39    | 5.00E-05 | General function prediction only                        |
| EVM0011114 | 500.98  | 95.22   | 2.40    | 1.00E-04 | General function prediction only                        |
| EVM0010790 | 1068.99 | 202.77  | 2.40    | 5.00E-04 | Cellulase (glycosyl hydrolase family 5)                 |
| EVM0004054 | 2923.38 | 554.24  | 2.40    | 4.50E-04 | Posttranslational modification, protein turnover, chaperones |
| EVM0000933 | 5.96    | 1.13    | 2.40    | 5.00E-05 | Malic enzyme, NAD binding domain                        |
| EVM0012050 | 214.40  | 40.47   | 2.41    | 5.00E-04 | Zinc finger, C2H2 type                                 |
| EVM0002202 | 31.72   | 5.94    | 2.42    | 5.00E-05 | Putative glycosyl hydrolase of unknown function (DUF1680) |
| EVM0005095 | 61.60   | 11.51   | 2.42    | 5.00E-05 | --                                                      |
| Gene ID       | Value 1 | Value 2 | Value 3 | Value 4   | Value 5   | Value 6   | Function                                      |
|--------------|---------|---------|---------|-----------|-----------|-----------|-----------------------------------------------|
| EVM0009612   | 45.77   | 8.55    | 2.42    | 5.00E-05  | 4.28E-04  | --        | Protein tyrosine kinase                      |
| EVM0004717   | 12.53   | 2.34    | 2.42    | 5.00E-05  | 4.28E-04  | --        | --                                            |
| EVM0008826   | 918.99  | 171.42  | 2.42    | 5.00E-05  | 4.28E-04  | --        | --                                            |
| EVM0002235   | 27.45   | 5.12    | 2.42    | 5.00E-05  | 4.28E-04  | --        | Pectinesterase                               |
| EVM0007950   | 237.85  | 44.18   | 2.43    | 5.00E-05  | 4.28E-04  | Carbohydrate transport and metabolism        | Carbohydrate phosphorylase                   |
| EVM0008109   | 518.90  | 96.17   | 2.43    | 5.00E-05  | 4.28E-04  | Carbohydrate transport and metabolism        | Fructose-1-6-bisphosphatase                 |
| EVM0002796   | 87.16   | 16.13   | 2.43    | 5.00E-05  | 4.28E-04  | --        | Permease for cytosine/purines, uracil, thiamine, allantoin |
| EVM0008828   | 77.66   | 14.31   | 2.44    | 5.00E-05  | 4.28E-04  | --        | --                                            |
| EVM0007764   | 19.91   | 3.66    | 2.44    | 5.00E-05  | 4.28E-04  | --        | SNF2 family N-terminal domain                |
| EVM0005372   | 21.08   | 3.86    | 2.45    | 5.00E-05  | 4.28E-04  | --        | Alpha/beta hydrolase family                  |
| EVM0003021   | 101.78  | 18.61   | 2.45    | 5.00E-05  | 4.28E-04  | --        | AIG1 family                                  |
| EVM0000156   | 2.40    | 0.44    | 2.45    | 8.15E-03  | 3.18E-02  | --        | --                                            |
| EVM0004741   | 365.17  | 66.63   | 2.45    | 5.00E-05  | 4.28E-04  | --        | Fungal Zn(2)-Cys(6) binuclear cluster domain |
| EVM0000184 | 59.07   | 10.70   | 2.46   | 5.00E-05 | 4.28E-04 | Signal transduction mechanisms | OPT oligopeptide transporter protein |
|-------------|---------|---------|--------|----------|----------|-------------------------------|-----------------------------------|
| EVM0003997 | 66.75   | 12.08   | 2.47   | 5.00E-05 | 4.28E-04 | General function prediction only | Haloacid dehalogenase-like hydrolase |
| EVM0009135 | 12.27   | 2.21    | 2.47   | 5.00E-05 | 4.28E-04 | --                            | --                                |
| EVM0007942 | 399.70  | 71.75   | 2.48   | 5.00E-05 | 4.28E-04 | Function unknown               | Protein of unknown function DUF89 |
| EVM0010831 | 1593.33 | 285.08  | 2.48   | 5.00E-05 | 4.28E-04 | --                            | Phosphoenolpyruvate carboxykinase |
| EVM0002269 | 91.48   | 16.30   | 2.49   | 5.00E-05 | 4.28E-04 | General function prediction only | Sugar (and other) transporter      |
| EVM0010699 | 7420.86 | 1322.16 | 2.49   | 5.00E-05 | 4.28E-04 | Energy production and conversion | Aldo/keto reductase family         |
| EVM0011225 | 42.77   | 7.61    | 2.49   | 5.00E-05 | 4.28E-04 | RNA processing and modification | Ribonuclease III domain            |
| EVM0004082 | 3.29    | 0.58    | 2.49   | 1.10E-03 | 6.17E-03 | --                            | NADH:flavin oxidoreductase / NADH oxidase family |
| EVM0009634 | 22.24   | 3.95    | 2.49   | 2.45E-03 | 1.20E-02 | --                            | --                                |
| EVM0005170 | 15.33   | 2.72    | 2.50   | 5.00E-05 | 4.28E-04 | Secondary metabolites biosynthesis, transport and catabolism | Cytochrome P450 |
| EVM0006519 | 163.55  | 28.88   | 2.50   | 5.00E-05 | 4.28E-04 | --                            | Putative amidotransferase          |
| Gene ID     | EVM0003927  | 114.64 | 20.18 | 2.51 | 9.25E-03 | 3.52E-02 | -- | Complex I protein (LYR family) |
|------------|-------------|--------|-------|------|----------|----------|----|------------------------------|
| EVM0008616 | 57.78       | 10.17  | 2.51  | 5.00E-05 | 4.28E-04 | Carbohydrate transport and metabolism | Major Facilitator Superfamily |
| EVM0003920 | 129.63      | 22.78  | 2.51  | 5.00E-05 | 4.28E-04 | Lipid transport and metabolism | AMP-binding enzyme |
| EVM0009588 | 140.93      | 24.74  | 2.51  | 5.00E-05 | 4.28E-04 | Secondary metabolites biosynthesis, transport and catabolism | Cytochrome P450 |
| EVM0011095 | 433.43      | 76.08  | 2.51  | 5.00E-05 | 4.28E-04 | Secondary metabolites biosynthesis, transport and catabolism | AMP-binding enzyme |
| EVM0009967 | 272.20      | 47.66  | 2.51  | 5.00E-05 | 4.28E-04 | -- | Dynamin family |
| EVM0009915 | 73.29       | 12.75  | 2.52  | 5.00E-05 | 4.28E-04 | Secondary metabolites biosynthesis, transport and catabolism | Cytochrome P450 |
| EVM0007275 | 506.14      | 87.96  | 2.52  | 5.00E-05 | 4.28E-04 | Amino acid transport and metabolism | Aminotransferase class I and II |
| EVM0005755 | 121.21      | 21.02  | 2.53  | 5.00E-05 | 4.28E-04 | -- | Glycosyl hydrolases family 16 |
| EVM0005547 | 479.80      | 83.13  | 2.53  | 5.00E-05 | 4.28E-04 | Secondary metabolites biosynthesis, transport and catabolism | Aromatic amino acid lyase |
| EVM0000317 | 52.84       | 9.14   | 2.53  | 5.00E-05 | 4.28E-04 | -- | -- |
| EVM0005755 | 121.21      | 21.02  | 2.53  | 5.00E-05 | 4.28E-04 | -- | -- |
| EVM0010773  | 6.36  | 1.10  | 2.53  | 5.00E-05 | 4.28E-04 | General function prediction only | Major Facilitator Superfamily |
|-------------|-------|-------|-------|----------|----------|---------------------------------|-----------------------------|
| EVM0002104  | 130.05| 22.48 | 2.53  | 5.00E-05 | 4.28E-04 | Signal transduction mechanisms  | Protein kinase domain       |
| EVM0000703  | 165.05| 28.51 | 2.53  | 5.00E-05 | 4.28E-04 | --                              | --                          |
| EVM0011732  | 21.58 | 3.72  | 2.54  | 5.00E-05 | 4.28E-04 | Amino acid transport and metabolism | homogentisate 1,2-dioxygenase |
| EVM0006399  | 54.41 | 9.31  | 2.55  | 5.00E-05 | 4.28E-04 | General function prediction only | short chain dehydrogenase    |
| EVM0010985  | 194.44| 33.19 | 2.55  | 5.00E-05 | 4.28E-04 | Carbohydrate transport and metabolism | Transaldolase               |
| EVM0003077  | 461.71| 78.71 | 2.55  | 1.00E-04 | 7.96E-04 | --                              | 50S ribosome-binding GTPase  |
| EVM0006190  | 303.73| 51.62 | 2.56  | 5.00E-05 | 4.28E-04 | Amino acid transport and metabolism | Amino acid permease          |
| EVM0011562  | 227.88| 38.71 | 2.56  | 5.00E-05 | 4.28E-04 | --                              | --                          |
| EVM0011387  | 110.47| 18.67 | 2.56  | 5.00E-05 | 4.28E-04 | Translation, ribosomal structure and biogenesis | tRNA synthetases class I (E and Q), catalytic domain |
| EVM0001750  | 29.30 | 4.95  | 2.57  | 5.00E-05 | 4.28E-04 | Amino acid transport and metabolism | Amino acid permease          |
| EVM0001905  | 264.19| 44.53 | 2.57  | 5.00E-05 | 4.28E-04 | General function prediction only | GMC oxidoreductase           |
| Accession     | K-value | K-value | E-value | Type                                                                                                    |
|--------------|---------|---------|---------|--------------------------------------------------------------------------------------------------------|
| EVM0011252   | 28.25   | 4.76    | 2.57    | Secondary metabolites biosynthesis, transport and catabolism                                           |
| EVM0002738   | 44.75   | 7.51    | 2.58    | --                                                                                                     |
| EVM0005194   | 4.52    | 0.75    | 2.59    | Glycosyl hydrolases family 28                                                                        |
| EVM0009885   | 49.61   | 8.21    | 2.59    | --                                                                                                     |
| EVM0011299   | 298.60  | 49.39   | 2.60    | General function prediction only                                                                     |
| EVM0007276   | 9.58    | 1.58    | 2.60    | Sugar (and other) transporter                                                                         |
| EVM0008760   | 12.80   | 2.11    | 2.60    | Acetyltransferase (GNAT) domain                                                                       |
| EVM0002399   | 219.76  | 36.15   | 2.60    | NADH(P)-binding                                                                                        |
| EVM0000412   | 2401.74 | 395.08  | 2.60    | Thiamine pyrophosphate enzyme, N-terminal TPP binding domain                                          |
| EVM0005155   | 14.17   | 2.32    | 2.61    | --                                                                                                     |
| EVM0002050   | 246.63  | 40.07   | 2.62    | --                                                                                                     |
| EVM0007831   | 18.99   | 3.08    | 2.63    | Lipid transport and metabolism                                                                       |
|              |         |         |         | Lipase (class 3)                                                                                      |
| EVM0008919  | 3.92 | 0.63 | 2.63 | 1.00E-04 | 7.96E-04 | -- | -- |
| EVM0007580  | 506.80 | 81.76 | 2.63 | 5.00E-05 | 4.28E-04 | Cell wall/membrane/envelope biogenesis | Glycosyl transferases group 1 |
| EVM0002732  | 128.68 | 20.56 | 2.65 | 5.00E-05 | 4.28E-04 | Function unknown | Cysteine-rich secretory protein family |
| EVM0005680  | 56.01 | 8.93 | 2.65 | 5.00E-05 | 4.28E-04 | Carbohydrate transport and metabolism | Major Facilitator Superfamily |
| EVM0004089  | 112.78 | 17.97 | 2.65 | 5.00E-05 | 4.28E-04 | -- | MAPEG family |
| EVM0008238  | 52.78 | 8.35 | 2.66 | 5.00E-05 | 4.28E-04 | -- | Cytochrome P450 |
| EVM0004177  | 313.65 | 49.55 | 2.66 | 5.00E-05 | 4.28E-04 | Inorganic ion transport and metabolism | Nitrite and sulphite reductase 4Fe-4S domain |
| EVM0008569  | 21.48 | 3.39 | 2.66 | 8.50E-04 | 4.98E-03 | -- | -- |
| EVM0009544  | 87.78 | 13.78 | 2.67 | 5.00E-05 | 4.28E-04 | Posttranslational modification, protein turnover, chaperones | IBR domain |
| EVM0008705  | 7.18 | 1.12 | 2.68 | 5.00E-05 | 4.28E-04 | General function prediction only | Zinc-binding dehydrogenase |
| EVM0001379  | 38.80 | 6.07 | 2.68 | 5.00E-05 | 4.28E-04 | -- | FHA domain |
| EVM0000202  | 271.29 | 42.39 | 2.68 | 5.00E-05 | 4.28E-04 | -- | Glycosyl transferase family group 2 |
| Accession | EVM0000639 | EVM0000466 | EVM0000263 |
|-----------|------------|------------|------------|
| Description | Pregnancy-associated plasma protein-A | Cytochrome P450 | Peptidase family M28 |
| Description | Amino acid transport and metabolism | Cobalamin-independent synthase, Catalytic domain | Inorganic ion transport and metabolism |
| Description | Cell wall/membrane/envelope biogenesis | Myosin head (motor domain) | Peptidase family M49 |
| Description | -- | General function prediction only | -- |
| Description | -- | -- | -- |

**Table:**

| Accession | EVM0007642 | EVM0008970 | EVM0005169 | EVM0007492 | EVM0011104 | EVM0011435 | EVM0010184 | EVM0000639 | EVM0000466 | EVM0000263 |
|-----------|------------|------------|------------|------------|------------|------------|------------|------------|------------|------------|
| **EVM0000639** | 110.80 17.00 2.70 | 5.00E-05 4.28E-04 | -- | -- | | | | | | |
| **EVM0000466** | 116.74 17.87 2.71 | 5.00E-05 4.28E-04 | -- | -- | | | | | | |
| **EVM0000263** | 99.65 15.22 2.71 | 2.00E-04 1.46E-03 | -- | -- | | | | | | |
| Gene ID   | Log2 Fold Change | p-value | E-value | Function                                                                 |
|---------|-----------------|---------|---------|--------------------------------------------------------------------------|
| EVM0002563 | 30.58           | 4.67    | 2.71    | 5.00E-05 4.28E-04 -- Protein of unknown function (DUF1399)               |
| EVM0004067 | 176.03          | 26.58   | 2.73    | 5.00E-05 4.28E-04 General function prediction only HMG (high mobility group) box |
| EVM0012169 | 159.01          | 23.73   | 2.74    | 5.00E-05 4.28E-04 -- CVNH domain                                          |
| EVM0009717 | 616.32          | 91.64   | 2.75    | 5.00E-05 4.28E-04 --                                                    |
| EVM0009749 | 166.45          | 24.67   | 2.75    | 5.00E-05 4.28E-04 --                                                    |
| EVM0005835 | 4.79            | 0.71    | 2.76    | 5.00E-05 4.28E-04 -- Protein tyrosine kinase                              |
| EVM0005899 | 174.24          | 25.56   | 2.77    | 5.00E-05 4.28E-04 --                                                    |
| EVM0004350 | 3905.39         | 571.31  | 2.77    | 5.00E-05 4.28E-04 Energy production and conversion Aldo/keto reductase family |
| EVM0008192 | 298.23          | 43.62   | 2.77    | 5.00E-05 4.28E-04 Posttranslational modification, protein turnover, chaperones |
| EVM0005425 | 14.39           | 2.10    | 2.78    | 5.00E-05 4.28E-04 --                                                    |
| EVM0010863 | 82.42           | 12.01   | 2.78    | 5.00E-05 4.28E-04 General function prediction only O-methyltransferase    |
| EVM0012178 | 77.64           | 11.27   | 2.78    | 5.00E-05 4.28E-04 Defense mechanisms NADH(P)-binding                    |
| Genomic ID         | Refseq Score | Blast Score | E-Value | Function                                      |
|-------------------|--------------|-------------|---------|-----------------------------------------------|
| EVM0006785        | 35.82        | 5.20        | 2.78    | 1.00E-04          | 7.96E-04          | Fragl/DRAM/Sfk1 family |
| EVM0006962        | 180.75       | 26.20       | 2.79    | 5.00E-05          | 4.28E-04          | Intracellular trafficking, secretion, and vesicular transport |
| EVM0005231        | 124.54       | 18.01       | 2.79    | 5.00E-05          | 4.28E-04          | Amino acid transport and metabolism |
| EVM0011129        | 153.21       | 22.14       | 2.79    | 5.00E-05          | 4.28E-04          | -- |
| EVM0008324        | 26.80        | 3.84        | 2.80    | 5.00E-05          | 4.28E-04          | Secondary metabolites biosynthesis, transport and catabolism |
| EVM0003709        | 37.73        | 5.39        | 2.81    | 5.00E-05          | 4.28E-04          | Energy production and conversion Galactose-1-phosphate uridyl transferase, N-terminal domain |
| EVM0005742        | 27.40        | 3.89        | 2.82    | 5.00E-05          | 4.28E-04          | General function prediction only short chain dehydrogenase |
| EVM0008462        | 7.07         | 1.00        | 2.82    | 5.00E-05          | 4.28E-04          | -- NADH:flavin oxidoreductase / NADH oxidase family |
| EVM0011417        | 172.46       | 24.40       | 2.82    | 5.00E-05          | 4.28E-04          | Energy production and conversion Aldo/keto reductase family |
| EVM0004693        | 187.23       | 26.46       | 2.82    | 5.00E-05          | 4.28E-04          | -- |
| EVM0007867        | 198.98       | 28.09       | 2.82    | 5.00E-05          | 4.28E-04          | -- |
| EVM0011267        | 614.21       | 85.80       | 2.84    | 5.00E-05          | 4.28E-04          | Energy production and conversion Aldo/keto reductase family |
| EVM0004385 | 56.95 | 7.95 | 2.84 | 5.00E-05 | 4.28E-04 | -- | -- |
| EVM0005375 | 26.27 | 3.67 | 2.84 | 5.00E-05 | 4.28E-04 | -- | -- |
| EVM0007578 | 2.87  | 0.40 | 2.85 | 3.50E-04 | 2.36E-03 | General function prediction only | GMC oxidoreductase |
| EVM0003237 | 209.49| 29.09| 2.85 | 5.00E-05 | 4.28E-04 | Amino acid transport and metabolism | Glutamate/Leucine/Phenylalanine/Valine dehydrogenase |
| EVM0005998 | 91.63 | 12.63| 2.86 | 5.00E-05 | 4.28E-04 | Inorganic ion transport and metabolism | Adenylylsulphate kinase |
| EVM0001985 | 56.78 | 7.82 | 2.86 | 5.00E-05 | 4.28E-04 | -- | von Willebrand factor type A domain |
| EVM0011477 | 33.76 | 4.64 | 2.86 | 5.00E-05 | 4.28E-04 | Posttranslational modification, protein turnover, chaperones | Glutathione S-transferase, N-terminal domain |
| EVM0000351 | 1206.68| 165.48| 2.87 | 5.00E-05 | 4.28E-04 | -- | Dyp-type peroxidase family |
| EVM0004300 | 125.57| 17.17| 2.87 | 5.00E-05 | 4.28E-04 | Secondary metabolites biosynthesis, transport and catabolism | Cytochrome P450 |
| EVM0011451 | 15.87 | 2.17 | 2.87 | 5.00E-05 | 4.28E-04 | -- | SH3-binding, glutamic acid-rich protein |
| EVM0006055 | 24.65 | 3.34 | 2.89 | 5.00E-05 | 4.28E-04 | General function prediction only | Short chain dehydrogenase |
| EVM0009468 | 1.81  | 0.24 | 2.89 | 5.00E-05 | 4.28E-04 | RNA processing and modification | AAA domain |
| EVM0005679 | 70.13  | 9.42  | 2.90 | 5.00E-05 | 4.28E-04 | -- | -- |
| EVM0010327 | 237.03 | 31.74 | 2.90 | 5.00E-05 | 4.28E-04 | -- | -- |
| EVM0001730 | 750.97 | 99.93 | 2.91 | 5.00E-05 | 4.28E-04 | Energy production and conversion | Malate synthase |
| EVM0009383 | 9.17   | 1.22  | 2.91 | 5.00E-05 | 4.28E-04 | Amino acid transport and metabolism | Aminotransferase class IV |
| EVM0002645 | 150.45 | 19.76 | 2.93 | 5.00E-05 | 4.28E-04 | Signal transduction mechanisms | Protein kinase domain |
| EVM0007893 | 51.12  | 6.69  | 2.93 | 5.00E-05 | 4.28E-04 | -- | Protein of unknown function (DUF3533) |
| EVM0007059 | 48.92  | 6.40  | 2.93 | 5.00E-05 | 4.28E-04 | -- | Domain of unknown function (DUF3415) |
| EVM0000662 | 70.34  | 9.13  | 2.95 | 5.00E-05 | 4.28E-04 | -- | -- |
| EVM0002134 | 11.30  | 1.46  | 2.95 | 7.00E-04 | 4.23E-03 | -- | Caspase domain |
| EVM0009701 | 463.65 | 60.04 | 2.95 | 5.00E-05 | 4.28E-04 | Posttranslational modification, protein turnover, chaperones | Glutathione peroxidase |
| EVM0006753 | 130.77 | 16.82 | 2.96 | 5.00E-05 | 4.28E-04 | General function prediction only | Family of unknown function (DUF706) |
| EVM0006084 | 129.27 | 16.25 | 2.99 | 5.00E-05 | 4.28E-04 | Secondary metabolites biosynthesis, transport and catabolism | Alcohol dehydrogenase GroES-like domain |
| Gene ID     | prediction | E value 1 | E value 2 | E value 3 | E value 4 | E value 5 | Gene Function                                                                 |
|------------|------------|-----------|-----------|-----------|-----------|-----------|-------------------------------------------------------------------------------|
| EVM0006874 | Cluster 1   | 13.57     | 1.70      | 2.99      | 7.50E-04  | 4.49E-03  | --                                                                            |
| EVM0000446 | Signal      | 208.02    | 26.06     | 3.00      | 5.00E-05  | 4.28E-04  | Carboxylesterase family                                                       |
| EVM0003089 | prediction  | 9.06      | 1.13      | 3.00      | 4.95E-03  | 2.13E-02  | General function prediction only                                              |
| EVM0004026 | Secondary   | 1301.47   | 162.68    | 3.00      | 5.00E-05  | 4.28E-04  | Uncharacterised protein family (UPF0172)                                      |
| EVM0007441 | prediction  | 12.62     | 1.57      | 3.01      | 5.00E-05  | 4.28E-04  | General function prediction only                                              |
| EVM0003880 | prediction  | 28.88     | 3.58      | 3.01      | 5.00E-05  | 4.28E-04  | Sugar (and other) transporter                                                 |
| EVM0010708 | prediction  | 133.79    | 16.50     | 3.02      | 5.00E-05  | 4.28E-04  | Formate/nitrite transporter                                                   |
| EVM0011713 | prediction  | 17.74     | 2.17      | 3.03      | 5.00E-05  | 4.28E-04  | Cerato-platanin                                                               |
| EVM0008898 | prediction  | 2222.79   | 270.45    | 3.04      | 5.00E-05  | 4.28E-04  | Cytochrome P450                                                                |
| EVM0010535 | prediction  | 20.87     | 2.53      | 3.04      | 4.00E-04  | 2.65E-03  | ATP-sulfurylase                                                               |
| EVM0010323 | prediction  | 297.16    | 36.00     | 3.05      | 5.00E-05  | 4.28E-04  | Inorganic ion transport and metabolism                                          |
| Gene ID           | Score 1 | Score 2 | Score 3 | Score 4 | Score 5 | Description                                                                 |
|------------------|---------|---------|---------|---------|---------|----------------------------------------------------------------------------|
| EVM000114        | 30.54   | 3.70    | 3.05    | 5.00E-05| 4.28E-04| Posttranslational modification, protein turnover, chaperones               |
| EVM0001558       | 589.99  | 70.38   | 3.07    | 5.00E-05| 4.28E-04| --                                                                         |
| EVM0006267       | 839.97  | 99.17   | 3.08    | 5.00E-05| 4.28E-04| Energy production and conversion                                            |
| EVM0004677       | 972.61  | 114.42  | 3.09    | 5.00E-05| 4.28E-04| Serine carboxypeptidase S28                                                |
| EVM0007084       | 173.02  | 20.30   | 3.09    | 5.00E-05| 4.28E-04| --                                                                         |
| EVM0011488       | 39.65   | 4.64    | 3.10    | 5.00E-05| 4.28E-04| --                                                                         |
| EVM0009846       | 37.11   | 4.33    | 3.10    | 5.00E-05| 4.28E-04| General function prediction only                                           |
| EVM0000802       | 260.31  | 30.23   | 3.11    | 5.00E-05| 4.28E-04| Sugar (and other) transporter                                              |
| EVM0008746       | 89.10   | 10.32   | 3.11    | 5.00E-05| 4.28E-04| UvrD-like helicase C-terminal domain                                        |
| EVM0009182       | 62.42   | 7.19    | 3.12    | 5.00E-05| 4.28E-04| Function unknown                                                           |
| EVM0011704       | 73.55   | 8.35    | 3.14    | 5.00E-05| 4.28E-04| Major Facilitator Superfamily                                              |
| EVM0008112       | 1059.00 | 120.13  | 3.14    | 5.00E-05| 4.28E-04| Inorganic ion transport and metabolism                                      |
|                  |         |         |         |         |         | ZIP Zinc transporter                                                       |
|                  |         |         |         |         |         | Intracellular trafficking, secretion, and vesicular transport              |
|                  |         |         |         |         |         | ER lumen protein retaining receptor                                         |
| ID            | Value1 | Value2 | Value3 | Value4 | Value5 | Value6 | Value7 | Class                          |
|---------------|--------|--------|--------|--------|--------|--------|--------|--------------------------------|
| EVM0001510    | 2069.18| 234.08 | 3.14   | 5.00E-05| 4.28E-04| Posttranslational modification, protein turnover, chaperones | Eukaryotic aspartyl protease |
| EVM0000833    | 177.97 | 19.89  | 3.16   | 5.00E-05| 4.28E-04| Amino acid transport and metabolism | Isocitrate/isopropylmalate dehydrogenase |
| EVM0010518    | 3.18   | 0.35   | 3.17   | 6.40E-03| 2.62E-02| --     | --                             |
| EVM0007992    | 5.38   | 0.60   | 3.17   | 1.33E-02| 4.70E-02| Carbohydrate transport and metabolism | Major intrinsic protein |
| EVM0006001    | 94.26  | 10.42  | 3.18   | 5.00E-05| 4.28E-04| --     | --                             |
| EVM0008735    | 870.16 | 95.73  | 3.18   | 5.00E-05| 4.28E-04| --     | NmrA-like family               |
| EVM0004522    | 115.91 | 12.71  | 3.19   | 5.00E-05| 4.28E-04| --     | --                             |
| EVM0000923    | 78.37  | 8.59   | 3.19   | 5.00E-05| 4.28E-04| Translation, ribosomal structure and biogenesis | Elongation factor Tu GTP binding domain |
| EVM0006386    | 244.37 | 26.75  | 3.19   | 5.00E-05| 4.28E-04| --     | --                             |
| EVM0012269    | 527.57 | 56.58  | 3.22   | 5.00E-05| 4.28E-04| Cell wall/membrane/envelope biogenesis | SIS domain |
| EVM0002401    | 114.15 | 12.24  | 3.22   | 5.00E-05| 4.28E-04| General function prediction only | O-methyltransferase |
| EVM0006758    | 12.78  | 1.37   | 3.22   | 7.75E-03| 3.06E-02| --     | --                             |
| Accession | Value 1 | Value 2 | Log2FoldChange | p-Value 1 | p-Value 2 | Enrichment | Description |
|-----------|---------|---------|----------------|-----------|-----------|------------|-------------|
| EVM0008863 | 1412.91 | 149.72  | 3.24           | 5.00E-05  | 4.28E-04  | --         | Protein of unknown function (DUF3759) |
| EVM0009907 | 1.43    | 0.15    | 3.24           | 3.95E-03  | 1.77E-02  | --         | Aldo/keto reductase family |
| EVM0002747 | 1.61    | 0.17    | 3.24           | 5.50E-04  | 3.46E-03  | RNA processing and modification | DEAD/DEAH box helicase |
| EVM0009621 | 23.87   | 2.51    | 3.25           | 5.00E-05  | 4.28E-04  | --         | -- |
| EVM0000478 | 71.73   | 7.41    | 3.27           | 5.00E-05  | 4.28E-04  | Signal transduction mechanisms | Protein kinase domain |
| EVM0004000 | 87.94   | 9.07    | 3.28           | 5.00E-05  | 4.28E-04  | Carbohydrate transport and metabolism | Glucose-6-phosphate dehydrogenase, C-terminal domain |
| EVM0012087 | 291.82  | 30.09   | 3.28           | 5.00E-05  | 4.28E-04  | General function prediction | Animal haem peroxidase |
| EVM0003814 | 2.45    | 0.25    | 3.29           | 2.00E-03  | 1.46E-02  | General function prediction | GMC oxidoreductase |
| EVM0003996 | 242.12  | 24.81   | 3.29           | 5.00E-05  | 4.28E-04  | --         | -- |
| EVM0006352 | 192.51  | 19.44   | 3.31           | 5.00E-05  | 4.28E-04  | General function prediction | short chain dehydrogenase |
| EVM0010745 | 14.85   | 1.49    | 3.32           | 5.00E-05  | 4.28E-04  | --         | -- |
| EVM0001818 | 87.38   | 8.75    | 3.32           | 5.00E-05  | 4.28E-04  | --         | 3'-5' exonuclease |
| Accession   | Value 1 | Value 2 | Value 3 | Conserved            | Description                                      |
|-------------|---------|---------|---------|----------------------|---------------------------------------------------|
| EVM0007048  | 65.57   | 6.56    | 3.32    | 5.00E-05 4.28E-04    | --                                                |
| EVM0011328  | 41.48   | 4.14    | 3.32    | 5.00E-05 4.28E-04    | RNA processing and modification                    |
| EVM0005207  | 45.78   | 4.56    | 3.33    | 5.00E-05 4.28E-04    | --                                                |
| EVM0002787  | 2575.10 | 253.63  | 3.34    | 5.00E-05 4.28E-04    | Posttranslational modification, protein turnover, chaperones |
| EVM0008710  | 369.93  | 36.32   | 3.35    | 5.00E-05 4.28E-04    | Posttranslational modification, protein turnover, chaperones |
| EVM0005984  | 31.67   | 3.11    | 3.35    | 5.00E-05 4.28E-04    | --                                                |
| EVM0009153  | 138.17  | 13.55   | 3.35    | 5.00E-05 4.28E-04    | --                                                |
| EVM0010847  | 649.73  | 63.53   | 3.35    | 5.00E-05 4.28E-04    | --                                                |
| EVM0012135  | 42.60   | 4.15    | 3.36    | 5.00E-05 4.28E-04    | --                                                |
| EVM0004211  | 279.23  | 27.18   | 3.36    | 5.00E-05 4.28E-04    | Replication, recombination and repair               |
| EVM0004670  | 82.48   | 8.00    | 3.37    | 5.00E-05 4.28E-04    | General function prediction only                   |
| EVM0011124  | 164.93  | 15.93   | 3.37    | 5.00E-05 4.28E-04    | --                                                |

- EVM0007048: Ribonuclease III domain
- EVM0011328: Ubiquitin family
- EVM0005207: Thioredoxin
- EVM0002787: Subtilase family
- EVM0008710: CVNH domain
- EVM0005984: Leucine Rich repeats (2 copies)
- EVM0009153: ATPase family associated with various cellular activities (AAA)
- EVM0010847: Major Facilitator Superfamily
- EVM0012135: Dioxygenase
| EVM0007164 | 595.57 | 56.91 | 3.39 | 5.00E-05 | 4.28E-04 | -- | Dienelactone hydrolase family |
| EVM0002720 | 70.31  | 6.64  | 3.40 | 5.00E-05 | 4.28E-04 | -- | Serine carboxypeptidase S28 |
| EVM0008923 | 2.37   | 0.22  | 3.43 | 3.25E-03 | 1.51E-02 | -- | -- |
| EVM0009217 | 79.93  | 7.41  | 3.43 | 5.00E-05 | 4.28E-04 | Secondary metabolites biosynthesis, transport and catabolism | Cytochrome P450 |
| EVM0008962 | 324.22 | 29.98 | 3.43 | 5.00E-05 | 4.28E-04 | General function prediction only | MOSC domain |
| EVM0001489 | 592.86 | 54.70 | 3.44 | 5.00E-05 | 4.28E-04 | General function prediction only | Enoyl-(Acyl carrier protein) reductase |
| EVM0000637 | 159.66 | 14.72 | 3.44 | 5.00E-05 | 4.28E-04 | -- | Cytochrome P450 |
| EVM0006816 | 774.23 | 70.01 | 3.47 | 5.00E-05 | 4.28E-04 | -- | -- |
| EVM0004480 | 46.13  | 4.17  | 3.47 | 5.00E-05 | 4.28E-04 | -- | Glycosyl hydrolases family 15 |
| EVM0011006 | 171.49 | 15.43 | 3.47 | 5.00E-05 | 4.28E-04 | -- | Protein of unknown function (DUF1524) |
| EVM0010117 | 72.60  | 6.47  | 3.49 | 5.00E-05 | 4.28E-04 | -- | -- |
| EVM0010473 | 225.11 | 19.98 | 3.49 | 5.00E-05 | 4.28E-04 | Secondary metabolites biosynthesis, transport and catabolism | Multicopper oxidase |
General function prediction only

O-methyltransferase

Velvet factor

Alpha/beta hydrolase family

Posttranslational modification, protein turnover, chaperones

Prolyl oligopeptidase, N-terminal beta-propeller domain

Lipid transport and metabolism

C2 domain

Posttranslational modification, protein turnover, chaperones

ATPase family associated with various cellular activities (AAA)

Carbohydrate transport and metabolism

Major Facilitator Superfamily

Cytochrome P450
| Accession     | EVM0010121 | EVM0007799 | EVM0011914 | EVM0008614 | EVM0008197 | EVM0002710 | EVM0011914 | EVM0002822 | EVM0005498 | EVM0000510 | EVM0000680 | EVM00009154 | EVM0000510 |
|--------------|------------|------------|------------|------------|------------|------------|------------|------------|------------|------------|------------|------------|------------|
| Gene ID      | EVM0010121 | EVM0007799 | EVM0011914 | EVM0008614 | EVM0008197 | EVM0002710 | EVM0011914 | EVM0002822 | EVM0005498 | EVM0000510 | EVM0000680 | EVM00009154 | EVM0000510 |
| Description  | Glycosyl hydrolases family 18 | Amino acid transport and metabolism | Cerato-platanin | Fungal Zn(2)-Cys(6) binuclear cluster domain | -- | Aldo/keto reductase family | Secondary metabolites biosynthesis, transport and catabolism | Caspase domain | -- | -- | -- | -- | -- |
| **Values**   | 83.49      | 7.54       | 19.87      | 59.00      | 143.10     | 219.48     | 19.87      | 190.24     | 381.86     | 171.85     | 114.15     | 182.54     | 171.85     |
| **Values**   | 6.31       | 0.57       | 1.42       | 4.20       | 10.63      | 16.10      | 1.42       | 13.16      | 26.37      | 11.80      | 7.99       | 12.76      | 11.80      |
| **Values**   | 3.72       | 3.73       | 3.80       | 3.81       | 3.75       | 3.77       | 3.80       | 3.85       | 3.86       | 3.86       | 3.84       | 3.84       | 3.86       |
| **Values**   | 5.00E-05   | 5.00E-05   | 1.50E-04   | 5.00E-05   | 5.00E-05   | 5.00E-05   | 1.50E-03   | 5.00E-05   | 5.00E-05   | 5.00E-05   | 5.00E-05   | 5.00E-05   | 5.00E-05   |
| **Values**   | 4.28E-04   | 4.28E-04   | 1.14E-03   | 4.28E-04   | 4.28E-04   | 4.28E-04   | 4.28E-03   | 4.28E-04   | 4.28E-04   | 4.28E-04   | 4.28E-04   | 4.28E-04   | 4.28E-04   | 4.28E-04   |
| **Values**   | --         | --         | --         | --         | --         | --         | --         | --         | --         | --         | --         | --         | --         | --         |
| EVM0008821  | 44.97 | 3.05 | 3.88 | 5.00E-05 | 4.28E-04 | --                               | Glycosyl hydrolases family 25 |
| EVM0008117  | 181.98| 12.00| 3.92 | 5.00E-05 | 4.28E-04 | --                               | --                             |
| EVM0008284  | 46.22 | 3.02 | 3.93 | 5.00E-05 | 4.28E-04 | Amino acid transport and metabolism | Arginase family                 |
| EVM0008750  | 118.92| 7.76 | 3.94 | 5.00E-05 | 4.28E-04 | General function prediction only   | Major Facilitator Superfamily  |
| EVM0122233  | 79.77 | 5.11 | 3.97 | 5.00E-05 | 4.28E-04 | --                               | --                             |
| EVM0009138  | 66.41 | 4.25 | 3.97 | 5.00E-05 | 4.28E-04 | --                               | --                             |
| EVM003104   | 443.70| 28.10| 3.98 | 5.00E-05 | 4.28E-04 | General function prediction only   | Major Facilitator Superfamily  |
| EVM012248   | 15.02 | 0.93 | 4.01 | 5.00E-05 | 4.28E-04 | --                               | Protein of unknown function (DUF1399) |
| EVM0005724  | 417.58| 25.34| 4.04 | 5.00E-05 | 4.28E-04 | --                               | Protein of unknown function (Ytp1) |
| EVM0001981  | 378.57| 22.43| 4.08 | 5.00E-05 | 4.28E-04 | --                               | HD domain                      |
| EVM0002854  | 137.65| 8.14 | 4.08 | 5.00E-05 | 4.28E-04 | Secondary metabolites biosynthesis, transport and catabolism | Multicopper oxidase |
| EVM0009418  | 2053.38| 120.46| 4.09 | 5.00E-05 | 4.28E-04 | --                               | --                             |
| EVM0008010 | 24.07 | 1.41 | 4.09 | 5.00E-05 | 4.28E-04 | -- | -- |
| EVM0007102 | 572.04 | 32.96 | 4.12 | 5.00E-05 | 4.28E-04 | -- | -- |
| EVM0003903 | 75.22 | 4.32 | 4.12 | 5.00E-05 | 4.28E-04 | -- | -- |
| EVM0009696 | 63.62 | 3.64 | 4.13 | 5.00E-05 | 4.28E-04 | Amino acid transport and metabolism | Aminotransferase class-V |
| EVM0004904 | 86.10 | 4.84 | 4.15 | 5.00E-05 | 4.28E-04 | -- | FAD binding domain |
| EVM0008387 | 394.95 | 22.13 | 4.16 | 5.00E-05 | 4.28E-04 | -- | -- |
| EVM0002281 | 218.98 | 12.27 | 4.16 | 5.00E-05 | 4.28E-04 | -- | -- |
| EVM0004458 | 89.15 | 4.94 | 4.17 | 5.00E-05 | 4.28E-04 | -- | -- |
| EVM0011894 | 1198.07 | 65.91 | 4.18 | 5.00E-05 | 4.28E-04 | Secondary metabolites biosynthesis, transport and catabolism | Cytochrome P450 |
| EVM0011907 | 188.82 | 10.31 | 4.19 | 5.00E-05 | 4.28E-04 | Coenzyme transport and metabolism | Polyprenyl synthetase |
| EVM0006935 | 56.65 | 3.08 | 4.20 | 5.00E-05 | 4.28E-04 | -- | UbiA prenyltransferase family |
| EVM0007914 | 24.61 | 1.33 | 4.21 | 5.00E-05 | 4.28E-04 | -- | -- |
| EVM0003022  | 4138.79 | 216.17 | 4.26 | 5.00E-05 | 4.28E-04 | Amino acid transport and metabolism | FAD dependent oxidoreductase |
| EVM0007317  | 11.61   | 0.60   | 4.26 | 5.00E-05 | 4.28E-04 | -- | Protein of unknown function (DUF1399) |
| EVM0010171  | 201.24  | 10.28  | 4.29 | 5.00E-05 | 4.28E-04 | Energy production and conversion | Aldo/keto reductase family |
| EVM0004633  | 48.08   | 2.42   | 4.31 | 1.65E-03 | 8.65E-03 | -- | -- |
| EVM0007038  | 9.24    | 0.45   | 4.35 | 6.50E-04 | 3.98E-03 | -- | -- |
| EVM0009981  | 11.99   | 0.59   | 4.35 | 5.00E-05 | 4.28E-04 | -- | -- |
| EVM0011428  | 100.27  | 4.75   | 4.40 | 5.00E-05 | 4.28E-04 | Inorganic ion transport and metabolism | Sulfate transporter family |
| EVM0010332  | 44.42   | 2.09   | 4.41 | 5.00E-05 | 4.28E-04 | -- | -- |
| EVM0005069  | 23.11   | 1.08   | 4.42 | 5.00E-05 | 4.28E-04 | Energy production and conversion | FAD binding domain |
| EVM0012182  | 52.35   | 2.43   | 4.43 | 5.00E-05 | 4.28E-04 | -- | Glutathione S-transferase, N-terminal domain |
| EVM0006219  | 197.00  | 9.00   | 4.45 | 5.00E-05 | 4.28E-04 | -- | Serine carboxypeptidase |
| EVM0004142  | 1201.01 | 54.82  | 4.45 | 5.00E-05 | 4.28E-04 | Intracellular trafficking, secretion, and vesicular transport | Vacuolar sorting protein 39 domain 1 |
| EVM0006589 | 3.77  | 0.17  | 4.46  | 5.75E-03 | 2.41E-02 | Carbohydrate transport and metabolism | Transaldolase |
|------------|-------|-------|-------|----------|----------|--------------------------------------|---------------|
| EVM0007634 | 191.31| 8.67  | 4.46  | 5.00E-05 | 4.28E-04 | --                                   | --            |
| EVM0003422 | 753.46| 33.74 | 4.48  | 5.00E-05 | 4.28E-04 | General function prediction only     | Zinc-binding dehydrogenase |
| EVM0009739 | 636.83| 27.95 | 4.51  | 5.00E-05 | 4.28E-04 | Energy production and conversion     | Aldo/keto reductase family |
| EVM0008958 | 109.72| 4.48  | 4.61  | 5.00E-05 | 4.28E-04 | --                                   | --            |
| EVM0002125 | 126.72| 4.99  | 4.67  | 5.00E-05 | 4.28E-04 | General function prediction only     | Major Facilitator Superfamily |
| EVM0007544 | 25.66 | 1.00  | 4.68  | 5.00E-05 | 4.28E-04 | Posttranslational modification, protein turnover, chaperones | Eukaryotic aspartyl protease |
| EVM0002085 | 822.30| 30.87 | 4.74  | 5.00E-05 | 4.28E-04 | --                                   | Major Facilitator Superfamily |
| EVM0003690 | 58.60 | 2.03  | 4.85  | 5.00E-05 | 4.28E-04 | --                                   | Caspase domain |
| EVM0006864 | 967.54| 32.73 | 4.89  | 5.00E-05 | 4.28E-04 | --                                   | Glyoxal oxidase N-terminus |
| EVM0009934 | 425.94| 13.64 | 4.96  | 5.00E-05 | 4.28E-04 | --                                   | Uncharacterized conserved protein (DUF2183) |
| EVM0009784 | 110.14| 3.49  | 4.98  | 5.00E-05 | 4.28E-04 | Energy production and conversion     | D-isomer specific 2-hydroxyacid dehydrogenase, NAD binding domain |
| Accession   | EVM0002904 | EVM0000127 | EVM0003743 | EVM0001170 | EVM0003059 | EVM0007243 | EVM0005595 | EVM0000291 | EVM0003051 | EVM000195 | EVM0004715 | EVM0005846 |
|-------------|------------|------------|------------|------------|------------|------------|------------|------------|------------|------------|------------|------------|
|            | 466.31     | 1938.82    | 30.49      | 13.43      | 335.60     | 89.66      | 36.50      | 819.94     | 504.27     | 403.22     | 138.65     | 477.23     |
|            | 13.74      | 56.25      | 0.88       | 0.38       | 9.02       | 2.02       | 0.79       | 16.96      | 9.48       | 7.38       | 2.47       | 8.48       |
|            | 5.09       | 5.11       | 5.12       | 5.14       | 5.22       | 5.47       | 5.53       | 5.60       | 5.73       | 5.77       | 5.81       | 5.81       |
|            | 5.00E-05   | 5.00E-05   | 5.00E-05   | 2.65E-03   | 5.00E-05   | 5.00E-05   | 5.00E-05   | 5.00E-05   | 5.00E-05   | 5.00E-05   | 5.00E-05   | 5.00E-05   |
|            | 4.28E-04   | 4.28E-04   | 4.28E-04   | 1.28E-02   | 4.28E-04   | 4.28E-04   | 4.28E-04   | 4.28E-04   | 4.28E-04   | 4.28E-04   | 4.28E-04   | 4.28E-04   |
| Carbohydrate transport and metabolism | -- | -- | Carbohydrate transport and metabolism | Inorganic ion transport and metabolism | Carbohydrate transport and metabolism | Secondary metabolites biosynthesis, transport and catabolism | -- | General function prediction only | -- | Serine carboxypeptidase S28 | -- | -- |
| Major Facilitator Superfamily | -- | -- | ChaC-like protein | | | | Serine carboxypeptidase | GMC oxidoreductase | -- | Serine carboxypeptidase S28 | -- | -- |
| Glucosamine-6-phosphate isomerases/6-phosphogluconolactonase | -- | | | | | | | | | | | |
| EVM0011539  | 51.89 | 0.90 | 5.85 | 5.00E-05 | 4.28E-04 | General function prediction only | Uncharacterized alpha/beta hydrolase domain (DUF2235) |
| EVM0010247  | 467.59 | 7.52 | 5.96 | 5.00E-05 | 4.28E-04 | Secondary metabolites biosynthesis, transport and catabolism | Cytochrome P450 |
| EVM0001865  | 191.28 | 2.96 | 6.01 | 5.00E-05 | 4.28E-04 | -- | Pregnancy-associated plasma protein-A |
| EVM0008864  | 539.20 | 7.85 | 6.10 | 5.00E-05 | 4.28E-04 | Energy production and conversion | Acetyl-CoA hydrolase/transferase N-terminal domain |
| EVM0001256  | 165.46 | 2.17 | 6.25 | 5.00E-05 | 4.28E-04 | -- | LVIVD repeat |
| EVM0006129  | 135.47 | 1.63 | 6.38 | 1.26E-02 | 4.49E-02 | Posttranslational modification, protein turnover, chaperones | Subtilase family |
| EVM0001579  | 1118.44 | 11.76 | 6.57 | 5.00E-05 | 4.28E-04 | General function prediction only | Family of unknown function (DUF706) |
| EVM0007573  | 4893.13 | 49.42 | 6.63 | 5.00E-05 | 4.28E-04 | -- | Fungal hydrophobin |
| EVM0008755  | 1761.64 | 17.35 | 6.67 | 5.00E-05 | 4.28E-04 | -- | Cupin domain |
| EVM0000645  | 2914.00 | 26.24 | 6.79 | 5.00E-05 | 4.28E-04 | -- | Hemopexin |
| EVM0010621  | 264.23 | 2.18 | 6.92 | 5.00E-05 | 4.28E-04 | -- | Deuterolysin metalloprotease (M35) family |
| gene ID        | R1   | R2   | R3   | Z1    | Z2   | Z3    |
|---------------|------|------|------|-------|------|-------|
| EVM0011356    | 126.07 | 0.89 | 7.14 | 5.00E-05 | 4.28E-04 | --   |
|               |       |      |      | Glyoxal oxidase N-terminus |
| EVM0007266    | 2994.17 | 19.52 | 7.26 | 5.00E-05 | 4.28E-04 | --   |
|               |       |      |      | --     |
| EVM0002793    | 4387.83 | 22.24 | 7.62 | 5.00E-05 | 4.28E-04 | --   |
|               |       |      |      | Cerato-platanin |

Data Set S6 FPKM values for common DEGs of mushroom *P. eryngii* after *E. beijingensis* infection
| EVM0007670  | 30.91 | 22.98 | 19.18 | 247.19 | 153.28 | 106.90  |
| EVM0008628  | 32.71 | 20.34 | 17.86 | 9.17   | 9.18   | 7.42    |
| EVM0008224  | 180.18| 126.92| 138.01| 433.73 | 476.01 | 501.58  |
| EVM0006099  | 83.14 | 130.16| 92.45 | 241.37 | 365.45 | 395.05  |
| EVM0000147  | 0.39  | 1.57  | 0.76  | 3.17   | 4.62   | 4.78    |
| EVM0012262  | 13.02 | 10.72 | 9.14  | 29.18  | 25.85  | 30.04   |
| EVM0011230  | 8.09  | 12.94 | 17.92 | 74.23  | 98.61  | 67.68   |
| EVM0008633  | 28.94 | 34.63 | 43.13 | 88.35  | 82.00  | 87.74   |
| EVM0005216  | 46.67 | 44.31 | 46.06 | 108.37 | 110.45 | 152.40  |
| EVM0006468  | 15.66 | 16.56 | 13.60 | 37.70  | 36.95  | 49.85   |
| EVM0006335  | 118.87| 68.22 | 116.74| 245.18 | 372.66 | 422.08  |
| EVM0006895  | 2.87  | 2.96  | 2.86  | 7.03   | 6.71   | 8.34    |
| EVM0005135  | 8.93  | 11.96 | 13.43 | 20.49  | 27.52  | 30.55   |
| EVM0009047  | 17.25 | 17.78 | 19.41 | 36.39  | 42.69  | 43.44   |
| EVM0004085  | 201.70| 274.18| 1424.44| 545.36 | 814.21 | 278.23  |
| EVM0006976  | 19.35 | 13.80 | 13.03 | 41.25  | 40.89  | 44.26   |
| EVM010633   | 1350.09| 739.01| 518.20| 3170.56| 3281.28| 5169.30 |
| EVM0004688  | 26.10 | 23.99 | 18.59 | 121.36 | 93.72  | 75.99   |
| EVM0011391  | 22.54 | 30.67 | 33.33 | 64.51  | 81.24  | 73.74   |
| EVM0003817  | 5.13  | 5.59  | 4.77  | 20.70  | 20.50  | 18.81   |
| EVM0003678  | 2.80  | 4.71  | 5.28  | 9.07   | 10.64  | 12.82   |
| EVM0004031  | 11.09 | 10.64 | 9.34  | 158.24 | 124.33 | 141.70  |
| EVM0007517  | 98.50 | 55.71 | 15.36 | 392.66 | 294.22 | 224.72  |
| EVM              | 11.25 | 13.48 | 10.11 | 41.23 | 44.44 | 107.07 |
|------------------|-------|-------|-------|-------|-------|--------|
| EVM00007572      | 2.86  | 3.94  | 3.48  | 14.88 | 18.95 | 16.41  |
| EVM0001336       | 53.25 | 37.80 | 64.58 | 25.30 | 17.30 | 26.20  |
| EVM00008791      | 14.59 | 7.34  | 6.50  | 38.42 | 34.32 | 29.07  |
| EVM0003855       | 4.12  | 4.75  | 3.50  | 13.64 | 13.38 | 18.23  |
| EVM0006461       | 7.64  | 6.93  | 6.25  | 16.65 | 16.14 | 18.29  |
| EVM0006795       | 1494.96 | 860.74 | 461.49 | 3582.30 | 2314.38 | 1683.99 |
| EVM0010882       | 265.72 | 231.63 | 160.85 | 184.44 | 229.77 | 274.60 |
| EVM0000252       | 18.24 | 16.06 | 15.85 | 36.90 | 32.99 | 42.69  |
| EVM0011482       | 17.82 | 22.08 | 32.31 | 81.69 | 79.69 | 96.74  |
| EVM0010721       | 5.31  | 6.47  | 7.09  | 1.81  | 1.87  | 1.96   |
| EVM0001778       | 124.96 | 135.45 | 110.15 | 362.45 | 413.61 | 383.48 |
| EVM0011691       | 9.28  | 12.75 | 12.58 | 26.36 | 28.52 | 48.57  |
| EVM00009958      | 13.74 | 13.22 | 11.49 | 28.17 | 28.26 | 30.55  |
| EVM0005225       | 16.22 | 19.80 | 39.79 | 25.31 | 14.44 | 17.46  |
| EVM0006316       | 5.93  | 5.94  | 7.60  | 16.19 | 15.11 | 17.11  |
| EVM0009341       | 9.53  | 10.40 | 10.72 | 28.18 | 24.81 | 30.32  |
| EVM0008305       | 10.53 | 9.82  | 14.15 | 32.76 | 28.69 | 38.34  |
| EVM0006301       | 28.63 | 31.86 | 123.07 | 74.11 | 97.07 | 40.33  |
| EVM0008173       | 1.14  | 1.71  | 1.48  | 3.25  | 3.44  | 6.30   |
| EVM0011757       | 4.27  | 3.67  | 1.95  | 9.82  | 10.83 | 8.88   |
| EVM0000347       | 285.86 | 249.76 | 292.07 | 97.62 | 113.76 | 69.67  |
| EVM0008335       | 59.07 | 49.06 | 36.68 | 20.26 | 21.15 | 17.14  |
| EVM0011462       | 34.17 | 33.58 | 34.50 | 10.00 | 12.20 | 9.99   |
| EVM0001350 | 357.09 | 145.73 | 376.65 | 1686.44 | 1864.80 | 1027.81 |
| EVM0002963 | 54.85  | 100.39 | 72.68  | 21.60   | 31.23   | 31.53   |
| EVM0003818 | 15.18  | 15.05  | 14.42  | 37.33   | 40.20   | 34.63   |
| EVM0004778 | 31.63  | 62.74  | 27.45  | 194.28  | 276.37  | 352.76  |
| EVM0002814 | 132.04 | 131.54 | 94.54  | 289.05  | 305.86  | 252.69  |
| EVM0008835 | 35.82  | 55.75  | 32.71  | 88.70   | 149.26  | 136.13  |
| EVM0001119 | 40.49  | 43.58  | 40.52  | 20.03   | 19.90   | 19.39   |
| EVM0001810 | 290.27 | 190.23 | 283.77 | 124.20  | 64.65   | 104.23  |
| EVM0000800 | 428.60 | 309.62 | 162.68 | 906.54  | 760.97  | 367.38  |
| EVM0008064 | 17.02  | 12.24  | 10.34  | 35.15   | 31.56   | 33.26   |
| EVM0004677 | 131.80 | 170.33 | 972.61 | 38.71   | 58.57   | 114.42  |
| EVM0003103 | 59.11  | 58.14  | 52.01  | 297.01  | 208.62  | 237.94  |
| EVM0011882 | 66.19  | 43.81  | 28.65  | 21.58   | 16.90   | 139.63  |
| EVM0007905 | 18.04  | 19.62  | 13.87  | 39.74   | 44.43   | 55.09   |
| EVM0001437 | 19.76  | 18.61  | 21.06  | 45.14   | 41.96   | 43.52   |
| EVM0009691 | 36.99  | 31.92  | 22.42  | 76.22   | 83.08   | 75.39   |
| EVM0005968 | 6.06   | 5.69   | 2.09   | 28.61   | 23.71   | 18.53   |
| EVM0004038 | 1552.61| 1024.34| 1161.22| 4225.45| 2468.78| 3149.55|
| EVM0012015 | 15.29  | 17.15  | 20.09  | 40.16   | 42.76   | 54.81   |
| EVM0011621 | 51.54  | 60.74  | 49.66  | 138.09  | 129.47  | 108.33  |
| EVM0009995 | 5.73   | 4.67   | 6.51   | 26.87   | 25.30   | 26.74   |
| EVM0006946 | 18.89  | 10.95  | 9.90   | 67.22   | 40.71   | 30.38   |
| EVM0009527 | 4.57   | 6.09   | 5.81   | 26.90   | 22.17   | 24.15   |
| EVM0002148 | 67.67  | 32.23  | 18.94  | 851.70  | 669.23  | 844.41  |
| EVM0012244 | 0.58   | 1.18   | 0.73   | 4.57    | 4.69    | 4.64    |
| EVM0002993 | 7.18   | 10.03  | 13.20  | 17.86   | 20.82   | 27.54   |
| Item        | 1st Value | 2nd Value | 3rd Value | 4th Value | 5th Value | 6th Value |
|-------------|-----------|-----------|-----------|-----------|-----------|-----------|
| EVM0008404  | 13.39     | 15.89     | 11.35     | 44.93     | 38.43     | 39.03     |
| EVM0012102  | 17.50     | 18.46     | 18.41     | 40.60     | 41.74     | 44.99     |
| EVM0010344  | 1807.48   | 1055.50   | 1120.67   | 3862.04   | 3949.47   | 5556.24   |
| EVM0005285  | 1421.95   | 1034.32   | 755.82    | 6412.12   | 4536.14   | 5491.75   |
| EVM0007162  | 15.05     | 14.24     | 18.75     | 64.07     | 51.71     | 46.92     |
| EVM0010470  | 198.15    | 134.22    | 144.34    | 62.94     | 51.70     | 62.71     |
| EVM0002623  | 12.13     | 10.92     | 8.06      | 25.21     | 23.11     | 26.15     |
| EVM0000794  | 677.62    | 547.80    | 532.17    | 1891.66   | 1675.77   | 1984.75   |
| EVM0005353  | 1.95      | 2.27      | 1.36      | 17.43     | 15.84     | 9.61      |
| EVM0004549  | 312.60    | 324.29    | 201.58    | 1507.81   | 1646.46   | 1386.51   |
| EVM0007837  | 2567.46   | 1876.37   | 1756.10   | 5847.03   | 3928.94   | 5291.10   |
| EVM0007035  | 54.56     | 68.03     | 44.51     | 24.77     | 22.81     | 15.12     |
| EVM0007826  | 24.23     | 23.42     | 19.64     | 63.15     | 64.42     | 70.79     |
| EVM0010778  | 10.98     | 8.19      | 7.32      | 3.50      | 2.62      | 3.65      |
| EVM0004358  | 181.56    | 154.92    | 195.63    | 604.80    | 554.44    | 658.94    |
| EVM0004582  | 1.95      | 2.35      | 1.40      | 5.63      | 7.33      | 8.42      |
| EVM0009399  | 19.92     | 19.78     | 28.13     | 74.45     | 60.91     | 64.87     |
| EVM0006268  | 78.69     | 77.30     | 101.75    | 29.59     | 30.87     | 29.19     |
| EVM0001552  | 13.45     | 13.94     | 12.27     | 55.19     | 55.87     | 41.72     |
| EVM0007566  | 1914.58   | 1114.51   | 404.06    | 5997.38   | 4249.04   | 4360.24   |
| EVM0006788  | 199.54    | 204.59    | 217.88    | 72.05     | 70.28     | 59.89     |
| EVM0007065  | 120.18    | 74.32     | 45.00     | 304.16    | 195.25    | 124.25    |
| EVM0008632  | 3.35      | 6.89      | 5.35      | 24.92     | 16.97     | 37.76     |
| EVM0003548  | 9.49      | 8.36      | 6.31      | 33.24     | 31.64     | 28.99     |
| EVM0004042  | 56.20     | 63.23     | 54.48     | 133.72    | 213.16    | 193.43    |
| EVM0007796  | 29.71     | 54.09     | 23.12     | 65.68     | 181.52    | 116.93    |
| Code           | Value1 | Value2 | Value3 | Value4 | Value5 | Value6 |
|---------------|--------|--------|--------|--------|--------|--------|
| EVM0011042    | 159.57 | 149.02 | 107.56 | 487.46 | 391.77 | 321.64 |
| EVM0003373    | 3.94   | 2.09   | 0.93   | 9.27   | 7.70   | 13.38  |
| EVM0008586    | 12.89  | 12.87  | 8.70   | 77.50  | 74.08  | 68.23  |
| EVM0006314    | 2.66   | 4.06   | 1.77   | 7.89   | 9.95   | 11.01  |
| EVM0003089    | 18.34  | 11.28  | 9.06   | 2.50   | 3.23   | 1.13   |
| EVM0006561    | 6.30   | 7.62   | 4.00   | 24.23  | 21.48  | 17.61  |
| EVM0011516    | 8.26   | 11.72  | 21.39  | 44.14  | 39.93  | 47.70  |
| EVM0008302    | 76.36  | 33.75  | 49.03  | 163.78 | 84.87  | 103.98 |
| EVM0002141    | 2.78   | 5.35   | 43.68  | 11.49  | 14.73  | 21.10  |
| EVM0010493    | 7.85   | 10.22  | 26.31  | 26.03  | 24.50  | 58.24  |
| EVM0011165    | 39.96  | 29.59  | 21.32  | 119.75 | 96.16  | 87.15  |
| EVM0012070    | 1404.56| 1068.93| 1163.47| 4015.74| 2610.87| 2743.83|
| EVM0006749    | 24.96  | 19.04  | 14.17  | 65.23  | 88.66  | 95.01  |
| EVM0005012    | 2.15   | 4.61   | 3.68   | 13.66  | 10.52  | 18.32  |
| EVM0009023    | 11.18  | 9.60   | 10.77  | 42.43  | 36.89  | 35.70  |
| EVM0011687    | 37.08  | 46.34  | 33.85  | 10.72  | 9.58   | 8.79   |
| EVM0000240    | 12.62  | 10.82  | 10.98  | 37.72  | 31.75  | 33.76  |
| EVM0003528    | 111.38 | 80.61  | 21.72  | 480.04 | 456.82 | 301.01 |
| EVM0002926    | 233.05 | 93.62  | 34.17  | 1117.65| 956.06 | 725.08 |
| EVM0001935    | 22.42  | 17.61  | 16.53  | 45.90  | 46.24  | 52.97  |
| EVM0000282    | 155.66 | 157.30 | 213.49 | 1258.86| 1159.63| 1807.70|
| EVM0008890    | 11.81  | 17.09  | 18.59  | 5.85   | 8.53   | 6.96   |
| EVM0008259    | 791.35 | 1280.14| 843.42 | 251.28 | 541.81 | 294.90 |
| EVM0011107    | 137.61 | 80.25  | 91.06  | 355.39 | 266.21 | 416.56 |
| EVM0011808    | 7.72   | 8.34   | 7.83   | 5.45   | 4.25   | 6.78   |
| EVM0006645    | 485.89 | 372.93 | 360.08 | 82.89  | 58.00  | 74.72  |
| EVM0006896  | 412.41 | 214.29 | 66.84 | 1361.32 | 721.71 | 430.23 |
| EVM0001466  | 13.98  | 14.05  | 13.74 | 4.67    | 5.73   | 4.38   |
| EVM0002736  | 103.75 | 88.78  | 87.69 | 34.02   | 31.00  | 31.56  |
| EVM0007949  | 12.09  | 14.57  | 10.48 | 56.70   | 44.95  | 53.00  |
| EVM0005054  | 24.15  | 18.28  | 9.91  | 104.28  | 81.05  | 50.06  |
| EVM0006132  | 24.32  | 57.10  | 85.94 | 174.52  | 185.61 | 229.13 |
| EVM0011587  | 121.39 | 159.68 | 73.31 | 336.73  | 530.01 | 746.54 |
| EVM0009204  | 10.20  | 10.50  | 11.51 | 31.67   | 30.76  | 34.94  |
| EVM0006257  | 162.43 | 158.73 | 192.83| 451.02  | 355.70 | 494.59 |
| EVM0003296  | 214.70 | 142.35 | 183.26| 580.61  | 427.41 | 397.72 |
| EVM0008777  | 12.60  | 17.03  | 34.99 | 64.05   | 68.85  | 75.27  |
| EVM0008982  | 1.33   | 3.01   | 1.22  | 6.25    | 10.57  | 17.36  |
| EVM0007328  | 1928.08| 1376.96| 1407.82| 4802.84 | 3142.71| 4431.20|
| EVM0005703  | 18.56  | 21.51  | 24.18 | 54.75   | 59.51  | 52.82  |
| EVM0000406  | 3.96   | 4.56   | 3.54  | 15.66   | 14.95  | 19.43  |
| EVM0001342  | 29.29  | 31.02  | 26.47 | 153.60  | 144.47 | 110.10 |
| EVM0010231  | 58.52  | 76.04  | 92.02 | 21.28   | 30.59  | 23.00  |
| EVM0005865  | 439.25 | 229.42 | 356.73| 2171.68 | 3627.32| 4175.63|
| EVM0009699  | 51.54  | 59.57  | 59.94 | 308.49  | 257.35 | 227.55 |
| EVM0003543  | 68.41  | 45.44  | 58.24 | 570.23  | 365.30 | 203.55 |
| EVM0006648  | 3.63   | 4.23   | 10.86 | 11.48   | 16.81  | 3.84   |
| EVM0009974  | 84.98  | 82.68  | 106.91| 22.85   | 32.89  | 43.81  |
| EVM0008622  | 99.12  | 75.43  | 60.22 | 256.65  | 223.50 | 278.68 |
| EVM0000189  | 4.32   | 6.27   | 4.27  | 14.29   | 14.90  | 12.57  |
| EVM0006060  | 5.47   | 5.94   | 4.96  | 12.67   | 15.14  | 19.72  |
| EVM0005078  | 1.53   | 1.14   | 2.05  | 7.42    | 10.08  | 8.10   |
| EVM0009103 | 7.65 | 5.56 | 3.60 | 21.83 | 30.53 | 17.60 |
| EVM0001672 | 13.37 | 17.06 | 22.45 | 5.35 | 5.30 | 5.74 |
| EVM0012202 | 1206.18 | 1409.84 | 2781.27 | 388.20 | 485.96 | 922.93 |
| EVM0005323 | 3.08 | 5.98 | 6.86 | 18.96 | 15.72 | 23.13 |
| EVM0007046 | 5.36 | 6.70 | 4.31 | 11.19 | 13.80 | 15.36 |
| EVM0003008 | 72.60 | 55.18 | 23.24 | 208.02 | 142.78 | 237.88 |
| EVM0009044 | 73.68 | 79.78 | 102.53 | 33.29 | 28.18 | 24.39 |
| EVM0003335 | 11.31 | 11.60 | 12.09 | 43.06 | 35.03 | 50.43 |
| EVM0005614 | 29.73 | 36.17 | 29.19 | 81.43 | 80.20 | 73.73 |
| EVM0012150 | 92.97 | 93.07 | 105.86 | 27.28 | 27.97 | 27.76 |
| EVM0009153 | 31.60 | 60.01 | 29.86 | 86.14 | 120.20 | 75.35 |
| EVM0009807 | 56.94 | 26.15 | 138.17 | 3.85 | 5.75 | 13.55 |
| EVM0000264 | 2341.01 | 1276.43 | 1330.92 | 7739.50 | 7974.27 | 11531.60 |
| EVM0001405 | 143.68 | 143.94 | 169.09 | 57.08 | 56.30 | 62.70 |
| EVM0005286 | 403.44 | 425.68 | 406.86 | 182.66 | 184.96 | 173.56 |
| EVM00000264 | 0.97 | 1.10 | 0.51 | 2.37 | 5.88 | 1.37 |
| EVM0001127 | 34.01 | 30.20 | 44.96 | 130.81 | 135.73 | 126.62 |
| EVM0012049 | 3.07 | 2.62 | 3.32 | 39.20 | 39.34 | 59.99 |
| EVM0010419 | 3.65 | 4.29 | 2.25 | 15.01 | 17.40 | 14.74 |
| EVM0004577 | 27.55 | 24.45 | 24.64 | 78.20 | 52.61 | 52.64 |
| EVM0011914 | 35.25 | 105.82 | 19.87 | 4.96 | 16.29 | 1.42 |
| EVM0004173 | 11.83 | 22.04 | 66.71 | 52.31 | 57.02 | 140.40 |
| EVM0008242 | 1.04 | 1.48 | 0.81 | 6.50 | 6.41 | 7.17 |
| EVM0008112 | 670.65 | 718.63 | 1059.00 | 90.26 | 81.43 | 120.13 |
| EVM0005227 | 61.43 | 55.84 | 39.94 | 137.05 | 158.73 | 135.16 |
| EVM000938 | 23.74 | 21.00 | 18.63 | 48.64 | 43.30 | 47.64 |
| EVM0008739  | 374.83 | 362.39 | 394.01 | 120.64 | 131.42 | 101.13 |
|------------|--------|--------|--------|--------|--------|--------|
| EVM0010136 | 49.72  | 97.45  | 131.96 | 21.94  | 27.89  | 49.87  |
| EVM0005980 | 46.60  | 41.85  | 5.06   | 19.03  | 20.92  | 30.28  |
| EVM0000637 | 15.80  | 86.49  | 159.66 | 31.63  | 21.67  | 14.72  |
| EVM0005665 | 79.76  | 98.29  | 131.64 | 83.52  | 65.06  | 35.23  |
| EVM0007579 | 196.92 | 204.50 | 214.68 | 63.66  | 76.15  | 72.77  |
| EVM0002694 | 4.83   | 4.22   | 3.97   | 13.70  | 12.82  | 13.92  |
| EVM0008891 | 8.58   | 7.44   | 7.95   | 69.58  | 49.34  | 81.18  |
| EVM0009404 | 14.69  | 12.49  | 15.36  | 66.19  | 69.28  | 78.43  |
| EVM0007930 | 11.07  | 11.43  | 8.61   | 26.99  | 30.89  | 28.34  |
| EVM0007361 | 17.76  | 17.90  | 19.72  | 57.99  | 49.81  | 62.71  |
| EVM0008511 | 31.79  | 36.18  | 24.25  | 129.79 | 110.86 | 107.30 |
| EVM0008438 | 16.67  | 19.82  | 19.61  | 38.81  | 39.78  | 49.36  |
| EVM0007642 | 279.57 | 294.85 | 1836.29| 12.38  | 19.17  | 286.69 |
| EVM0009852 | 9.77   | 10.78  | 8.91   | 65.38  | 63.41  | 34.59  |
| EVM0000435 | 51.56  | 45.83  | 26.09  | 139.96 | 158.90 | 230.91 |
| EVM0000880 | 16.93  | 20.12  | 11.15  | 64.72  | 44.27  | 121.55 |
| EVM0003129 | 3.16   | 2.64   | 2.58   | 9.28   | 10.21  | 8.56   |
| EVM0003828 | 8.48   | 9.87   | 14.93  | 49.52  | 53.54  | 57.41  |
| EVM0010247 | 33.91  | 268.99 | 467.59 | 14.40  | 17.39  | 7.52   |
| EVM0007358 | 9.21   | 13.04  | 8.84   | 39.84  | 32.96  | 28.05  |
| EVM0009599 | 5.50   | 5.52   | 3.50   | 1.16   | 1.27   | 1.18   |
| EVM0006493 | 123.41 | 122.28 | 100.54 | 258.75 | 264.14 | 220.63 |
| EVM0009981 | 3.71   | 3.40   | 11.99  | 0.49   | 0.81   | 0.59   |
| EVM0010786 | 16.62  | 12.59  | 22.46  | 131.82 | 126.97 | 110.84 |
| EVM0008465 | 29.96  | 29.83  | 46.77  | 327.87 | 304.46 | 319.96 |
| EVM0000318 | 5.06  | 3.51  | 3.10  | 0.63  | 0.64  | 0.62  |
| EVM0009757 | 152.11| 77.40 | 125.51| 512.66| 360.03| 392.95|
| EVM0005744 | 12.23 | 9.94  | 8.96  | 2.07  | 2.37  | 3.90  |
| EVM0005079 | 66.24 | 59.35 | 33.60 | 187.21| 214.60| 246.26|
| EVM0011840 | 15.75 | 17.63 | 17.37 | 38.66 | 41.60 | 34.77 |
| EVM0007883 | 184.74| 170.76| 261.91| 382.04| 417.69| 605.79|
| EVM0009544 | 81.36 | 58.48 | 87.78 | 33.60 | 25.57 | 13.78 |
| EVM0006136 | 157.27| 96.87 | 84.59 | 512.60| 417.01| 410.10|
| EVM0011806 | 977.12| 609.02| 647.26| 1963.32| 1380.14| 1538.05|
| EVM0007712 | 48.98 | 37.77 | 28.42 | 9.10  | 9.99  | 8.63  |
| EVM0008406 | 13.77 | 26.64 | 47.92 | 88.54 | 79.82 | 199.36|
| EVM0002114 | 223.28| 154.53| 182.00| 80.09 | 67.49 | 65.92 |
| EVM0008562 | 182.17| 142.27| 205.37| 586.17| 865.07| 869.38|
| EVM0001738 | 1379.82| 348.42| 145.06| 4240.67| 1928.15| 2200.62|
| EVM0010867 | 1471.16| 928.29| 382.18| 3313.53| 2378.57| 1948.93|
| EVM0005272 | 811.62| 408.78| 404.12| 1751.54| 1587.89| 2535.69|
| EVM0007568 | 178.71 | 127.56| 104.78| 526.23 | 303.20 | 381.71 |
| EVM0002786 | 1913.05| 1247.12| 1521.28| 4304.47| 4081.63| 3153.75|
| EVM0005279 | 429.38| 619.87| 307.74| 1672.61| 2080.40| 1820.55|
| EVM0002125 | 8.30  | 20.91 | 126.72| 2.55  | 3.05  | 4.99  |
| EVM0010318 | 5.40  | 3.61  | 4.94  | 14.91 | 15.87 | 13.46 |
| EVM0002270 | 2.33  | 2.93  | 4.45  | 26.09 | 11.86 | 46.89 |
| EVM0005755 | 76.65 | 56.14 | 121.21| 32.65 | 21.40 | 21.02 |
| EVM0006805 | 100.27| 133.31| 107.23| 412.25| 294.00| 374.56 |
| EVM0010856 | 46.63 | 41.65 | 28.50 | 17.30 | 15.35 | 12.93 |
| EVM0003787 | 76.12 | 67.47 | 57.82 | 157.01| 150.51| 164.19 |
| EVM0006402 | 133.80 | 164.77 | 24.68 | 432.17 | 428.53 | 454.50 |
| EVM0012211 | 28.44  | 24.74  | 19.84 | 65.38  | 57.71  | 77.25  |
| EVM0008337 | 15.72  | 25.78  | 72.85 | 106.59 | 56.76  | 27.80  |
| EVM0007661 | 8.33   | 8.98   | 13.62 | 43.70  | 43.54  | 34.23  |
| EVM0000209 | 7.71   | 8.50   | 7.53  | 24.46  | 23.39  | 22.63  |
| EVM0007331 | 2.74   | 3.46   | 4.19  | 11.03  | 11.04  | 12.89  |
| EVM0011153 | 189.73 | 189.03 | 135.74| 383.39 | 441.33 | 570.89 |
| EVM0008761 | 13.32  | 21.69  | 13.60 | 47.49  | 45.37  | 59.88  |
| EVM0011971 | 10.24  | 8.85   | 9.04  | 33.93  | 30.81  | 23.05  |
| EVM0003936 | 43.31  | 77.86  | 66.45 | 150.05 | 161.09 | 172.18 |
| EVM0001178 | 20.65  | 21.49  | 27.67 | 67.30  | 78.95  | 81.84  |
| EVM0007506 | 269.85 | 189.76 | 224.15| 624.50 | 522.92 | 458.19 |
| EVM0003029 | 23.91  | 31.14  | 30.01 | 172.29 | 156.58 | 106.91 |
| EVM0011790 | 49.97  | 26.16  | 35.04 | 10.85  | 7.20   | 10.70  |
| EVM0008010 | 4.63   | 4.56   | 24.07 | 0.71   | 0.28   | 1.41   |
| EVM0010621 | 41.11  | 29.42  | 264.23| 1.54   | 1.85   | 2.18   |
| EVM0007602 | 11.40  | 10.24  | 5.84  | 30.24  | 23.67  | 18.86  |
| EVM0006689 | 17.21  | 14.87  | 12.72 | 81.39  | 72.27  | 66.24  |
| EVM00011658| 7.13   | 8.49   | 5.66  | 1.60   | 1.80   | 2.57   |
| EVM0006981 | 20.16  | 15.64  | 11.02 | 144.03 | 122.70 | 147.01 |
| EVM0004635 | 65.35  | 75.47  | 101.07| 550.54 | 464.42 | 382.58 |
| EVM0008537 | 8018.90| 9774.36| 2311.19| 20193.20| 30297.40| 14034.10|
| EVM0008710 | 157.51 | 275.29 | 369.93| 5.11   | 7.98   | 36.32  |
| EVM0001877 | 6.85   | 4.63   | 4.08  | 2.81   | 1.82   | 1.58   |
| EVM0008011 | 47.05  | 65.93  | 979.97| 98.22  | 170.62 | 193.57 |
| EVM0006845 | 17.01  | 15.45  | 10.33 | 40.29  | 33.19  | 32.38  |
| Component ID | Value 1 | Value 2 | Value 3 | Value 4 | Value 5 | Value 6 |
|--------------|---------|---------|---------|---------|---------|---------|
| EVM0000593   | 97.57   | 100.34  | 135.73  | 341.37  | 261.18  | 362.89  |
| EVM0002338   | 10.46   | 13.22   | 10.13   | 49.86   | 40.84   | 44.68   |
| EVM0001647   | 62.00   | 48.79   | 35.86   | 191.21  | 145.80  | 189.11  |
| EVM0003051   | 99.99   | 150.00  | 504.27  | 39.84   | 49.02   | 9.48    |
| EVM0008519   | 150.41  | 124.61  | 122.32  | 416.66  | 347.64  | 444.91  |
| EVM0005014   | 1.97    | 4.72    | 8.10    | 14.41   | 17.51   | 24.13   |
| EVM0007872   | 34.34   | 31.65   | 63.49   | 106.21  | 98.52   | 231.38  |
| EVM0006494   | 13.62   | 15.86   | 15.29   | 57.63   | 44.29   | 45.11   |
| EVM00011068  | 30.01   | 37.34   | 76.82   | 111.26  | 291.05  | 359.63  |
| EVM0007942   | 81.46   | 113.13  | 399.70  | 186.36  | 50.15   | 71.75   |
| EVM0009908   | 413.33  | 352.00  | 220.37  | 1253.82 | 1255.26 | 960.96  |
| EVM0010148   | 191.45  | 173.26  | 177.16  | 643.25  | 398.39  | 420.48  |
| EVM0004379   | 196.64  | 228.26  | 235.10  | 591.88  | 483.53  | 595.80  |
| EVM0004319   | 36.64   | 32.83   | 26.02   | 74.19   | 79.47   | 116.50  |
| EVM0003574   | 154.12  | 154.12  | 154.12  | 154.12  | 154.12  | 154.12  |
| EVM0004716   | 31.56   | 31.48   | 37.97   | 26.40   | 24.36   | 25.03   |
| EVM0001259   | 15.49   | 16.51   | 12.62   | 14.72   | 15.40   | 9.60    |
| EVM0006727   | 42.96   | 43.81   | 32.36   | 17.73   | 15.40   | 15.37   |
| EVM0001189   | 44.76   | 42.53   | 47.14   | 101.31  | 98.39   | 108.13  |
| EVM0002682   | 38.96   | 47.46   | 65.55   | 373.60  | 389.54  | 435.15  |
| EVM0003224   | 65.35   | 61.67   | 67.85   | 151.56  | 178.72  | 209.58  |
| EVM0006666   | 103.37  | 55.68   | 56.27   | 247.26  | 174.32  | 148.08  |
| EVM0007445   | 2.78    | 3.29    | 2.65    | 9.26    | 9.80    | 23.57   |
| EVM0001888   | 8.68    | 15.78   | 16.48   | 3.60    | 4.04    | 1.42    |
| EVM0011852   | 32.55   | 45.43   | 46.96   | 197.48  | 163.64  | 155.72  |
| EVM0005497 | 51.81 | 60.73 | 53.46 | 226.99 | 235.18 | 274.54 |
|------------|-------|-------|-------|--------|--------|--------|
| EVM0006340 | 78.81 | 52.61 | 56.11 | 19.07  | 18.99  | 23.83  |
| EVM0001591 | 1.97  | 1.17  | 1.57  | 8.24   | 5.80   | 6.29   |
| EVM0007305 | 349.97| 247.84| 332.47| 808.63 | 740.78 | 821.83 |
| EVM0000195 | 12.77 | 46.72 | 403.22| 4.71   | 7.06   | 7.38   |
| EVM0004054 | 399.42| 437.54| 2923.38| 1389.50| 965.46 | 554.24 |
| EVM0001964 | 8.12  | 7.02  | 4.59  | 38.57  | 46.30  | 29.32  |
| EVM001335  | 9.27  | 13.23 | 10.05 | 25.29  | 27.96  | 28.83  |
| EVM002673  | 29.18 | 20.51 | 4.93  | 120.27 | 57.42  | 315.29 |
| EVM007146  | 878.23| 732.45| 1280.47| 5607.20| 4368.04| 4054.33|
| EVM005500  | 16.81 | 11.98 | 13.73 | 34.99  | 38.59  | 42.56  |
| EVM004965  | 3.40  | 2.58  | 2.64  | 18.85  | 18.91  | 22.29  |
| EVM007573  | 5359.43| 3633.65| 4893.13| 1206.28| 847.04 | 49.42  |
| EVM002948  | 39.63 | 33.72 | 30.61 | 115.44 | 90.82  | 118.09 |
| EVM004840  | 490.75| 299.94| 276.31| 197.64 | 134.47 | 111.05 |
| EVM002297  | 215.72| 237.19| 271.37| 1306.69| 834.10 | 564.48 |
| EVM010605  | 962.90| 754.98| 717.39| 2217.45| 1525.74| 1870.07|
| EVM011758  | 11.07 | 10.85 | 15.85 | 12.07  | 15.52  | 13.93  |
| EVM011344  | 9.73  | 9.71  | 9.92  | 35.54  | 29.66  | 34.83  |
| EVM005557  | 73.60 | 49.62 | 46.12 | 20.38  | 21.20  | 18.52  |
| EVM009851  | 11.76 | 14.31 | 12.02 | 35.66  | 36.24  | 36.93  |
| EVM000907  | 1.40  | 2.79  | 1.60  | 6.04   | 6.73   | 5.17   |
| EVM006820  | 17.51 | 19.02 | 40.31 | 112.24 | 99.54  | 193.40 |
| EVM006726  | 302.99| 204.54| 219.90| 140.31 | 130.51 | 156.35 |
| EVM002996  | 26.17 | 22.09 | 17.46 | 61.25  | 57.76  | 62.69  |
| EVM006700  | 186.14| 162.97| 195.99| 763.41 | 638.54 | 526.28 |
| Code          | Value1 | Value2 | Value3 | Value4 | Value5 | Value6 |
|---------------|--------|--------|--------|--------|--------|--------|
| EVM0011432    | 7.75   | 9.06   | 7.16   | 52.00  | 49.27  | 43.40  |
| EVM0005691    | 0.55   | 0.43   | 0.56   | 1.94   | 1.60   | 3.42   |
| EVM0004710    | 164.60 | 186.95 | 129.07 | 370.26 | 391.17 | 506.83 |
| EVM0006122    | 32.58  | 39.58  | 26.98  | 10.04  | 9.33   | 8.83   |
| EVM0000598    | 43.49  | 51.01  | 50.04  | 106.35 | 161.48 | 193.70 |
| EVM0007667    | 30.58  | 16.32  | 25.02  | 3.36   | 5.15   | 6.37   |
| EVM0000357    | 19.19  | 96.01  | 423.46 | 241.11 | 238.04 | 192.64 |
| EVM0005915    | 24.78  | 11.51  | 12.02  | 64.70  | 29.42  | 100.28 |
| EVM0008192    | 156.48 | 232.76 | 298.23 | 76.59  | 101.56 | 43.62  |
| EVM0002257    | 28.03  | 30.87  | 26.14  | 58.63  | 67.12  | 152.50 |
| EVM0002150    | 131.46 | 170.20 | 312.70 | 745.19 | 654.75 | 639.48 |
| EVM0008163    | 4.77   | 4.18   | 1.87   | 12.71  | 12.15  | 12.12  |
| EVM0011446    | 2630.22| 1632.45| 1369.67| 7170.90| 4570.86| 6690.14|
| EVM0005976    | 75.67  | 107.64 | 183.50 | 328.96 | 373.40 | 452.68 |
| EVM0004575    | 99.93  | 139.05 | 187.92 | 42.19  | 49.21  | 64.19  |
| EVM0011121    | 3.69   | 14.51  | 145.48 | 21.23  | 33.44  | 56.01  |
| EVM0005881    | 3.51   | 4.08   | 2.01   | 18.31  | 15.48  | 19.68  |
| EVM0010521    | 22.11  | 41.02  | 159.20 | 566.26 | 126.46 | 356.79 |
| EVM000366     | 1.37   | 3.30   | 5.23   | 5.43   | 7.14   | 12.37  |
| EVM0005236    | 393.07 | 407.49 | 327.58 | 994.81 | 994.97 | 1092.18|
| EVM0003322    | 5.49   | 9.08   | 5.71   | 20.02  | 26.32  | 21.72  |
| EVM0008058    | 6.15   | 11.63  | 9.76   | 35.18  | 42.04  | 40.64  |
| EVM0005796    | 1156.13| 1012.35| 1292.18| 5651.83| 3312.97| 4545.87|
| EVM0003903    | 18.22  | 39.03  | 75.22  | 7.84   | 7.38   | 4.32   |
| EVM0010158 | 41.47 | 53.50 | 53.16 | 104.62 | 157.86 | 227.91 |
| EVM0001192 | 69.88 | 105.27 | 64.77 | 323.20 | 359.10 | 336.77 |
| EVM0005366 | 22.53 | 24.96 | 37.05 | 127.49 | 97.53 | 111.93 |
| EVM0001632 | 176.73 | 165.09 | 103.27 | 412.13 | 359.10 | 336.77 |
| EVM0007196 | 104.62 | 104.62 | 104.62 | 104.62 | 104.62 | 104.62 |
| EVM0008237 | 57.53 | 120.79 | 114.01 | 369.31 | 310.96 | 311.92 |
| EVM0003453 | 11.08 | 10.76 | 8.27 | 32.78 | 36.39 | 29.99 |
| EVM0007650 | 15.58 | 15.88 | 11.44 | 44.33 | 42.04 | 32.95 |
| EVM0010983 | 5.20 | 5.99 | 2.80 | 14.17 | 12.64 | 12.29 |
| EVM0001816 | 141.39 | 152.25 | 89.05 | 464.75 | 425.44 | 491.73 |
| EVM0011261 | 262.49 | 215.77 | 149.31 | 861.95 | 638.75 | 872.19 |
| EVM000423 | 18.07 | 30.80 | 37.16 | 162.41 | 171.23 | 90.35 |
| EVM0005583 | 13.13 | 16.59 | 16.56 | 60.65 | 47.99 | 56.97 |
| EVM0010981 | 1041.63 | 1381.82 | 290.73 | 2689.99 | 3628.46 | 1516.73 |
| EVM0011499 | 10.11 | 13.28 | 8.32 | 24.96 | 33.64 | 19.14 |
| EVM0005431 | 7.25 | 8.59 | 7.22 | 18.99 | 21.08 | 25.93 |
| EVM0011804 | 4.66 | 4.39 | 5.19 | 21.10 | 21.51 | 19.64 |
| EVM0000819 | 3.52 | 3.21 | 2.35 | 19.76 | 20.74 | 15.96 |
| EVM0002657 | 350.18 | 408.67 | 362.68 | 956.58 | 957.32 | 1066.26 |
| EVM0010558 | 19.86 | 18.17 | 13.17 | 59.63 | 54.39 | 35.02 |
| EVM0011517 | 17.34 | 15.58 | 20.19 | 65.39 | 54.91 | 48.48 |
| EVM0010061 | 78.77 | 48.69 | 55.99 | 230.53 | 166.45 | 144.62 |
| EVM0004775 | 20.46 | 19.25 | 21.60 | 98.91 | 75.95 | 44.25 |
| EVM0011006 | 4.98 | 18.23 | 171.49 | 1.50 | 2.40 | 15.43 |
| EVM0007042 | 454.36 | 296.43 | 283.50 | 913.61 | 981.43 | 1325.40 |
| EVM0012010 | 48.69 | 20.73 | 22.49 | 110.02 | 94.44 | 218.63 |
| EVM0005171 | 16.83 | 14.80 | 14.11 | 39.07 | 32.94 | 28.60 |
| EVM0009051 | 454.36 | 296.43 | 283.50 | 913.61 | 981.43 | 1325.40 |
| EVM0000184 | 110.04 | 152.63 | 59.07 | 12.76 | 14.70 | 10.70 |
| EVM0007446 | 5017.20 | 5417.96 | 3962.69 | 40681.30 | 30257.30 | 31870.50 |
| EVM00007446 | 1162.29 | 1034.64 | 1647.58 | 466.01 | 393.16 | 371.57 |
| EVM0009999 | 3.31 | 8.29 | 3.21 | 38.62 | 23.05 | 33.16 |
| EVM0000955 | 11.05 | 11.02 | 10.02 | 31.05 | 32.01 | 21.91 |
| EVM0000005 | 33.92 | 34.87 | 18.74 | 73.56 | 74.87 | 52.99 |
| EVM0004341 | 81.75 | 99.35 | 65.39 | 497.62 | 438.56 | 380.43 |
| EVM0006717 | 16.65 | 12.48 | 19.89 | 39.01 | 52.79 | 51.66 |
| EVM0006542 | 48.12 | 52.74 | 2175.70 | 288.67 | 251.58 | 466.37 |
| EVM0010012 | 6.44 | 11.95 | 11.00 | 25.48 | 24.89 | 42.92 |
| EVM0000596 | 6.54 | 6.95 | 3.89 | 14.83 | 15.62 | 14.13 |
| EVM0003992 | 15.22 | 14.16 | 17.66 | 44.33 | 44.92 | 53.99 |
| EVM0002923 | 5995.82 | 4250.88 | 2245.12 | 20036.90 | 12227.00 | 12605.60 |
| EVM0000245 | 26.13 | 24.45 | 22.88 | 63.68 | 64.79 | 47.20 |
| EVM0008872 | 1.78 | 2.84 | 1.63 | 4.78 | 6.82 | 7.39 |
| EVM0002076 | 325.41 | 184.01 | 300.25 | 839.77 | 823.43 | 1075.35 |
| EVM0008722 | 195.10 | 340.50 | 155.69 | 92.39 | 62.89 | 61.14 |
| ID       | Value 1 | Value 2 | Value 3 | Value 4 | Value 5 | Value 6 |
|----------|---------|---------|---------|---------|---------|---------|
| EVM0008782 | 25.90   | 21.60   | 25.09   | 13.10   | 10.78   | 11.03   |
| EVM0001331 | 27.81   | 36.49   | 48.73   | 8.17    | 11.22   | 11.13   |
| EVM0000062 | 20.49   | 20.77   | 12.99   | 99.66   | 113.10  | 160.27  |
| EVM0002999 | 48.51   | 53.51   | 53.99   | 22.10   | 23.77   | 18.24   |
| EVM0004233 | 26.26   | 14.27   | 16.74   | 356.42  | 447.19  |
| EVM0000062 | 20.49   | 20.77   | 12.99   | 99.66   | 113.10  | 160.27  |
| EVM0002999 | 48.51   | 53.51   | 53.99   | 22.10   | 23.77   | 18.24   |
| EVM0004233 | 26.26   | 14.27   | 16.74   | 356.42  | 447.19  |
| EVM0000062 | 20.49   | 20.77   | 12.99   | 99.66   | 113.10  | 160.27  |
| EVM0002999 | 48.51   | 53.51   | 53.99   | 22.10   | 23.77   | 18.24   |
| EVM0004233 | 26.26   | 14.27   | 16.74   | 356.42  | 447.19  |
| EVM0000062 | 20.49   | 20.77   | 12.99   | 99.66   | 113.10  | 160.27  |
| EVM0002999 | 48.51   | 53.51   | 53.99   | 22.10   | 23.77   | 18.24   |
| EVM0004233 | 26.26   | 14.27   | 16.74   | 356.42  | 447.19  |
| EVM0000062 | 20.49   | 20.77   | 12.99   | 99.66   | 113.10  | 160.27  |
| EVM0002999 | 48.51   | 53.51   | 53.99   | 22.10   | 23.77   | 18.24   |
| EVM0004233 | 26.26   | 14.27   | 16.74   | 356.42  | 447.19  |
| EVM0000062 | 20.49   | 20.77   | 12.99   | 99.66   | 113.10  | 160.27  |
| EVM0002999 | 48.51   | 53.51   | 53.99   | 22.10   | 23.77   | 18.24   |
| EVM0004233 | 26.26   | 14.27   | 16.74   | 356.42  | 447.19  |
| EVM0000062 | 20.49   | 20.77   | 12.99   | 99.66   | 113.10  | 160.27  |
| EVM0002999 | 48.51   | 53.51   | 53.99   | 22.10   | 23.77   | 18.24   |
| EVM0004233 | 26.26   | 14.27   | 16.74   | 356.42  | 447.19  |
| EVM0000062 | 20.49   | 20.77   | 12.99   | 99.66   | 113.10  | 160.27  |
| EVM0002999 | 48.51   | 53.51   | 53.99   | 22.10   | 23.77   | 18.24   |
| EVM0004233 | 26.26   | 14.27   | 16.74   | 356.42  | 447.19  |
| EVM0000062 | 20.49   | 20.77   | 12.99   | 99.66   | 113.10  | 160.27  |
| EVM0002999 | 48.51   | 53.51   | 53.99   | 22.10   | 23.77   | 18.24   |
| EVM0004233 | 26.26   | 14.27   | 16.74   | 356.42  | 447.19  |
| EVM0000062 | 20.49   | 20.77   | 12.99   | 99.66   | 113.10  | 160.27  |
| EVM0002999 | 48.51   | 53.51   | 53.99   | 22.10   | 23.77   | 18.24   |
| EVM0004233 | 26.26   | 14.27   | 16.74   | 356.42  | 447.19  |
| EVM0010446 | 15.39 | 18.81 | 36.52 | 113.29 | 101.30 | 138.75 |
| EVM0011910 | 45.62 | 57.76 | 60.21 | 19.83  | 28.09  | 20.81  |
| EVM0011085 | 39.91 | 32.62 | 23.83 | 96.40  | 82.46  | 98.97  |
| EVM0003560 | 18.66 | 19.19 | 13.70 | 77.76  | 73.30  | 72.15  |
| EVM0008363 | 46.52 | 54.23 | 43.74 | 94.51  | 113.56 | 127.52 |
| EVM0011097 | 378.34| 303.47| 183.48| 855.96 | 956.27 | 981.53 |
| EVM0003743 | 7.10  | 6.24  | 30.49 | 1.10   | 2.40   | 0.88   |
| EVM0006251 | 4.83  | 3.49  | 5.01  | 43.80  | 41.06  | 56.48  |
| EVM0007684 | 199.30| 137.09| 183.12| 36.61  | 33.25  | 36.89  |
| EVM0008651 | 112.98| 86.60 | 93.46 | 232.33 | 224.47 | 270.68 |
| EVM0001681 | 258.91| 268.76| 199.69| 863.46 | 719.84 | 965.94 |
| EVM0009732 | 14.88 | 18.80 | 10.68 | 42.98  | 60.80  | 35.72  |
| EVM0005521 | 102.86| 98.68 | 142.17| 42.74  | 36.68  | 59.70  |
| EVM0001809 | 129.36| 98.29 | 81.04 | 313.62 | 278.85 | 261.96 |
| EVM0000289 | 31.95 | 27.95 | 22.98 | 67.13  | 58.88  | 51.27  |
| EVM0007958 | 1.73  | 2.34  | 2.44  | 6.09   | 8.05   | 21.40  |
| EVM0000204 | 803.35| 890.32| 629.60| 2257.79| 2303.93| 2450.84|
| EVM0002245 | 29.50 | 24.28 | 30.43 | 83.48  | 64.74  | 73.87  |
| EVM0009138 | 2.81  | 8.14  | 66.41 | 15.19  | 2.78   | 4.25   |
| EVM0002154 | 0.68  | 1.66  | 0.84  | 2.08   | 4.29   | 3.47   |
| EVM0005312 | 0.97  | 1.12  | 1.72  | 3.34   | 2.31   | 3.82   |
| EVM0009845 | 12.24 | 13.77 | 12.95 | 53.49  | 40.20  | 40.87  |
| EVM0008746 | 49.40 | 59.21 | 89.10 | 12.72  | 12.92  | 10.32  |
| EVM0004868 | 20.24 | 18.65 | 13.62 | 46.64  | 38.84  | 39.98  |
| EVM0011907 | 18.74 | 51.08 | 188.82| 8.44   | 16.32  | 10.31  |
| Code           | Value 1 | Value 2 | Value 3 | Value 4 | Value 5 | Value 6 |
|---------------|---------|---------|---------|---------|---------|---------|
| EVM0002548    | 15.32   | 13.79   | 18.97   | 53.40   | 54.15   | 53.22   |
| EVM0008198    | 40.47   | 39.94   | 38.19   | 117.60  | 118.44  | 110.46  |
| EVM0007266    | 1958.60 | 1631.18 | 2994.17 | 24.78   | 39.90   | 19.52   |
| EVM0010589    | 69.26   | 85.97   | 174.65  | 799.29  | 462.72  | 445.54  |
| EVM0004931    | 22.57   | 20.75   | 19.92   | 59.69   | 48.64   | 46.49   |
| EVM0009512    | 19.39   | 21.18   | 22.97   | 54.50   | 76.60   | 72.49   |
| EVM0004228    | 38.60   | 31.97   | 65.17   | 125.61  | 93.52   | 144.81  |
| EVM0002723    | 6.08    | 11.98   | 42.95   | 21.03   | 53.00   | 96.28   |
| EVM0001737    | 64.51   | 97.00   | 43.05   | 15.72   | 20.42   | 9.19    |
| EVM0004887    | 2.66    | 3.64    | 7.47    | 1.18    | 1.77    | 1.66    |
| EVM0005861    | 157.11  | 76.15   | 9.29    | 450.22  | 358.24  | 197.13  |
| EVM0009798    | 42.06   | 47.15   | 18.72   | 197.31  | 176.51  | 156.91  |
| EVM0008227    | 41.23   | 34.98   | 34.62   | 12.26   | 11.47   | 13.08   |
| EVM000478     | 45.23   | 56.73   | 71.73   | 10.54   | 11.75   | 7.41    |
| EVM0011786    | 13.44   | 10.99   | 22.04   | 85.69   | 81.86   | 83.21   |
| EVM000557     | 23.01   | 12.73   | 20.43   | 53.55   | 52.98   | 67.81   |
| EVM0007751    | 100.21  | 78.58   | 116.36  | 27.07   | 30.98   | 31.79   |
| EVM0011961    | 104.37  | 145.44  | 114.49  | 348.96  | 315.05  | 315.80  |
| EVM0002743    | 16.42   | 12.34   | 9.03    | 46.85   | 48.46   | 37.61   |
| EVM0007323    | 699.26  | 429.64  | 388.35  | 2059.06 | 1877.24 | 3065.78 |
| EVM0011919 | 29.00 | 27.01 | 27.40 | 64.03 | 54.58 | 70.06 |
| EVM0009169 | 97.58 | 589.43 | 1408.42 | 44.41 | 115.82 | 586.51 |
| EVM0005073 | 11.11 | 10.32 | 11.11 | 29.62 | 32.96 | 40.97 |
| EVM0001520 | 2.87 | 4.32 | 2.40 | 11.11 | 15.87 | 33.19 |
| EVM002302 | 18.03 | 22.38 | 21.43 | 65.06 | 66.30 | 60.80 |
| EVM002044 | 53.36 | 94.18 | 40.93 | 149.08 | 225.88 | 103.39 |
| EVM011366 | 12.21 | 14.56 | 14.13 | 26.99 | 30.73 | 30.62 |
| EVM004320 | 141.78 | 149.65 | 137.75 | 62.00 | 59.82 | 63.67 |
| EVM001489 | 52.74 | 73.96 | 592.86 | 26.35 | 28.26 | 54.70 |
| EVM006748 | 105.07 | 96.81 | 78.41 | 44.52 | 41.16 | 37.40 |
| EVM000363 | 12.35 | 9.96 | 10.99 | 49.78 | 40.60 | 47.64 |
| EVM001661 | 5.76 | 6.71 | 6.38 | 64.32 | 65.06 | 55.31 |
| EVM008966 | 24.44 | 22.04 | 23.39 | 102.00 | 194.61 | 151.06 |
| EVM006677 | 24.68 | 23.91 | 12.11 | 51.24 | 51.92 | 29.64 |
| EVM004297 | 32.24 | 21.23 | 24.02 | 137.10 | 128.12 | 104.81 |
| EVM006292 | 2.18 | 5.14 | 2.78 | 10.24 | 14.73 | 10.69 |
| EVM007852 | 779.47 | 799.16 | 384.44 | 4462.47 | 3705.76 | 2074.10 |
| EVM006225 | 138.68 | 85.30 | 57.88 | 31.39 | 27.53 | 26.43 |
| EVM002910 | 10.36 | 16.37 | 11.60 | 76.95 | 73.90 | 58.76 |
| EVM001584 | 35.33 | 39.66 | 34.37 | 86.44 | 89.56 | 132.95 |
| EVM007418 | 54.66 | 43.76 | 44.52 | 147.90 | 104.37 | 125.75 |
| EVM000933 | 5.16 | 3.88 | 5.96 | 0.63 | 1.01 | 1.13 |
| EVM008748 | 5.95 | 14.50 | 48.27 | 24.02 | 29.11 | 17.70 |
| EVM008356 | 13.38 | 12.11 | 9.76 | 55.97 | 48.78 | 42.01 |
| EVM002787 | 119.17 | 1001.29 | 2575.10 | 275.13 | 323.55 | 253.63 |
| EVM007225 | 72.33 | 74.26 | 121.76 | 258.85 | 570.70 | 592.66 |
| EVM0006187 | 0.74 | 1.96 | 3.53 | 9.76 | 10.02 | 8.37 |
| EVM0003134 | 58.00 | 60.76 | 32.98 | 16.17 | 8.07 | 10.41 |
| EVM0009858 | 33.46 | 33.92 | 27.87 | 79.52 | 80.81 | 90.71 |
| EVM0006629 | 43.15 | 44.42 | 45.38 | 12.20 | 15.84 | 17.78 |
| EVM0001122 | 37.62 | 27.42 | 12.3 | 1.71 | 1.62 | 3.02 |
| EVM0008931 | 53.49 | 52.62 | 39.74 | 23.27 | 21.83 | 16.88 |
| EVM0005506 | 4.46 | 6.00 | 4.39 | 11.58 | 13.32 | 21.88 |
| EVM0009846 | 20.45 | 22.15 | 37.11 | 9.94 | 5.72 | 4.33 |
| EVM0005619 | 16.97 | 9.47 | 10.10 | 43.57 | 35.23 | 39.74 |
| EVM0008951 | 27.26 | 29.06 | 24.36 | 81.36 | 67.44 | 82.19 |
| EVM0008230 | 15.30 | 17.37 | 24.18 | 66.75 | 58.98 | 74.24 |
| EVM0006543 | 1.87 | 3.63 | 2.71 | 8.60 | 8.27 | 19.06 |
| EVM0005265 | 32.85 | 47.44 | 110.83 | 260.64 | 230.58 | 281.64 |
| EVM0003316 | 490.45 | 552.91 | 471.55 | 1118.51 | 1114.40 | 1089.32 |
| EVM0006288 | 22.63 | 22.48 | 19.08 | 51.99 | 46.42 | 38.56 |
| EVM0005679 | 23.45 | 18.98 | 70.13 | 10.16 | 8.17 | 9.42 |
| EVM0000628 | 22.06 | 17.00 | 34.15 | 94.65 | 88.10 | 112.13 |
| EVM0005515 | 2.40 | 9.55 | 17.78 | 6.77 | 3.54 | 3.90 |
| EVM0003839 | 801.48 | 516.29 | 537.50 | 1889.09 | 1370.46 | 1654.23 |
| EVM0008650 | 53.76 | 73.28 | 15.28 | 281.20 | 206.52 | 75.60 |
| EVM0001562 | 143.45 | 135.12 | 139.15 | 38.42 | 60.05 | 55.68 |
| EVM0002944 | 23.42 | 23.88 | 21.25 | 9.39 | 11.24 | 9.90 |
| EVM0008343 | 11.12 | 6.92 | 7.63 | 34.89 | 31.11 | 31.31 |
| EVM0007514 | 33.18 | 137.65 | 18.82 | 82.54 | 429.80 | 210.86 |
| EVM0011240 | 257.40 | 225.96 | 299.49 | 111.20 | 88.62 | 109.41 |
| Code          | 5.33   | 9.83   | 30.54  | 38.01  | 4.70   | 3.70   |
|---------------|--------|--------|--------|--------|--------|--------|
| EVM0003721    | 254.23 | 166.50 | 84.33  | 596.65 | 461.01 | 438.78 |
| EVM0000905    | 32.00  | 27.14  | 23.39  | 88.32  | 92.62  | 93.07  |
| EVM0005845    | 45.97  | 32.84  | 29.53  | 16.02  | 14.43  | 10.30  |
| EVM0005402    | 1.59   | 2.39   | 2.38   | 6.87   | 7.16   | 8.72   |
| EVM0002732    | 51.09  | 68.12  | 128.68 | 19.86  | 12.32  | 20.56  |
| EVM0007764    | 23.91  | 19.32  | 19.91  | 4.11   | 4.41   | 3.66   |
| EVM0004958    | 8.98   | 9.86   | 11.61  | 37.18  | 54.76  | 106.06 |
| EVM0008721    | 1.57   | 1.68   | 2.30   | 9.93   | 6.36   | 4.94   |
| EVM0002952    | 34.73  | 29.64  | 27.88  | 15.18  | 14.68  | 13.22  |
| EVM0006917    | 1.96   | 4.18   | 1.68   | 16.28  | 17.73  | 12.58  |
| EVM0005087    | 137.39 | 91.68  | 91.19  | 280.83 | 232.42 | 311.07 |
| EVM0007132    | 0.86   | 0.60   | 0.99   | 2.66   | 3.26   | 4.05   |
| EVM0005203    | 45.67  | 38.75  | 36.14  | 15.76  | 17.21  | 17.59  |
| EVM0012190    | 3.47   | 3.58   | 6.88   | 0.82   | 1.08   | 2.51   |
| EVM0011123    | 62.48  | 59.11  | 49.31  | 25.21  | 21.40  | 19.16  |
| EVM0011785    | 4.26   | 5.92   | 4.52   | 8.87   | 13.65  | 14.45  |
| EVM0009049    | 16.16  | 11.25  | 7.76   | 3.00   | 1.37   | 2.37   |
| EVM0006660    | 601.05 | 559.24 | 711.10 | 197.09 | 211.01 | 220.73 |
| EVM0003583    | 661.53 | 822.18 | 56.60  | 213.60 | 289.96 | 1326.27|
| EVM0009651    | 3.21   | 4.96   | 4.91   | 12.01  | 11.60  | 12.97  |
| EVM0006126    | 24.83  | 28.63  | 21.17  | 58.23  | 72.95  | 97.29  |
| EVM0012187    | 8.45   | 10.51  | 10.73  | 22.91  | 22.08  | 28.82  |
| EVM0003929    | 11.97  | 17.66  | 13.23  | 3.34   | 6.90   | 5.11   |
| EVM0006117    | 11.59  | 14.98  | 9.64   | 40.49  | 32.42  | 25.75  |
| EVM0010645    | 9.49   | 9.87   | 8.74   | 36.14  | 28.49  | 29.48  |
| EVM0005139 | 323.22 | 160.92 | 37.04 | 1364.38 | 877.27 | 591.64 |
| EVM0011013 | 14.04  | 11.45  | 6.39  | 67.94   | 64.79  | 55.62  |
| EVM0012127 | 23.24  | 18.30  | 19.67 | 47.84   | 41.10  | 45.57  |
| EVM0008720 | 251.03 | 239.89 | 208.73| 99.23   | 104.78 | 71.42  |
| EVM000512  | 6.92   | 9.72   | 9.27  | 3.34    | 3.52   | 3.66   |
| EVM0007593 | 128.29 | 108.89 | 110.22| 277.65  | 246.16 | 237.91 |
| EVM0009027 | 30.58  | 31.58  | 38.58 | 4.98    | 12.04  | 13.03  |
| EVM0008755 | 63.02  | 71.14  | 1761.64| 8.99    | 9.38   | 17.35  |
| EVM0010669 | 117.55 | 96.29  | 90.91 | 359.05  | 243.59 | 202.04 |
| EVM0000211 | 29.99  | 31.24  | 24.18 | 64.00   | 62.49  | 65.38  |
| EVM0003326 | 29.04  | 34.24  | 32.29 | 134.59  | 100.26 | 87.47  |
| EVM0007277 | 769.92 | 590.66 | 708.74| 1683.76 | 1235.39| 1596.78|
| EVM0012095 | 7.11   | 7.23   | 7.67  | 22.21   | 18.64  | 18.66  |
| EVM0011387 | 65.19  | 77.10  | 110.47| 28.38   | 26.65  | 18.67  |
| EVM0002121 | 25.61  | 22.65  | 19.84 | 8.95    | 7.49   | 5.97   |
| EVM0010870 | 17.58  | 14.22  | 18.91 | 119.36  | 87.23  | 90.66  |
| EVM0005036 | 19.90  | 18.21  | 14.34 | 91.96   | 89.13  | 101.37 |
| EVM0003306 | 30.60  | 37.08  | 48.58 | 185.23  | 191.95 | 169.53 |
| EVM0002558 | 11.74  | 11.05  | 11.62 | 35.51   | 27.09  | 24.16  |
| EVM0002898 | 18.52  | 13.73  | 14.77 | 68.49   | 65.76  | 84.06  |
| EVM0003416 | 22.42  | 25.30  | 22.70 | 79.59   | 51.63  | 54.03  |
| EVM0010403 | 6.85   | 4.09   | 7.81  | 29.37   | 17.08  | 22.98  |
| EVM0000419 | 56.33  | 47.31  | 44.43 | 183.64  | 163.41 | 175.18 |
| EVM0008035 | 27.70  | 24.86  | 18.88 | 11.75   | 11.08  | 8.75   |
| EVM0007187 | 2.41   | 5.62   | 3.62  | 15.76   | 25.43  | 26.03  |
| EVM0000211 | 25.61  | 22.65  | 19.84 | 8.95    | 7.49   | 5.97   |
| EVM0002760 | 6.22  | 39.53 | 178.07 | 73.45 | 15.99 | 13.98 |
|------------|-------|-------|--------|-------|-------|-------|
| EVM0003745 | 4.61  | 5.02  | 6.42   | 12.31 | 13.20 | 80.38 |
| EVM0004134 | 52.49 | 51.54 | 46.71  | 167.16| 146.79| 174.72|
| EVM0003609 | 366.16| 221.00| 122.45 | 966.62| 771.77| 1036.20|
| EVM0004301 | 1.28  | 2.59  | 27.42  | 40.53 | 52.40 | 80.38 |
| EVM0004405 | 17.40 | 13.98 | 13.10  | 97.00 | 82.97 | 94.70 |
| EVM0005253 | 643.40| 425.02| 213.46 | 2114.47| 1332.13| 1036.20|
| EVM0005127 | 77.37 | 87.46 | 51.92  | 748.41| 713.49| 657.87|
| EVM0002551 | 20.53 | 24.13 | 15.15  | 56.42 | 52.33 | 53.00 |
| EVM0002953 | 14.48 | 38.71 | 180.59 | 3.32  | 9.67  | 70.64 |
| EVM0001104 | 4.48  | 6.02  | 4.48   | 139.31| 90.23 | 41.99 |
| EVM0001256 | 98.71 | 107.28| 165.46 | 5.30  | 3.62  | 2.17  |
| EVM0008758 | 1.28  | 1.13  | 2.54   | 0.21  | 0.21  | 0.71  |
| EVM0011475 | 5.23  | 6.49  | 5.42   | 20.53 | 23.79 | 21.76 |
| EVM0010141 | 72.42 | 48.19 | 40.37  | 209.87| 178.63| 226.56|
| EVM0003167 | 14.40 | 13.76 | 37.21  | 181.82| 215.43| 516.16|
| EVM0006881 | 12.47 | 16.18 | 14.67  | 64.73 | 79.95 | 79.43 |
| EVM0007451 | 105.78| 84.78 | 78.06  | 37.32 | 34.11 | 32.40 |
| EVM0008059 | 238.02| 33.09 | 66.52  | 79.59 | 113.28| 105.69|
| EVM0002805 | 149.26| 128.92| 117.02 | 300.83| 295.79| 398.44|
| EVM0005613 | 14.14 | 18.39 | 19.51  | 50.67 | 53.56 | 76.71 |
| EVM0010422 | 5.58  | 4.63  | 4.02   | 42.54 | 42.69 | 45.67 |
| EVM0010862 | 95.69 | 90.28 | 89.85  | 231.41| 211.19| 302.39|
| EVM0006570 | 792.75| 718.07| 502.56 | 3557.49| 2755.72| 2569.12|
| EVM0001473 | 24.18 | 25.08 | 20.28  | 59.25 | 54.27 | 58.50 |
|   |    |    |    |    |    |
|---|----|----|----|----|----|
| EVM0005197 | 9.63 | 35.23 | 14.21 | 19.52 | 82.94 |
| EVM0010575 | 22.57 | 20.51 | 14.56 | 53.30 | 44.72 |
| EVM0007616 | 18.76 | 24.00 | 23.95 | 65.25 | 61.74 |
| EVM0004461 | 16.00 | 14.63 | 32.27 | 40.31 | 77.34 |
| EVM0008894 | 19.08 | 28.54 | 34.83 | 113.02 | 57.75 |
| EVM0002854 | 44.72 | 96.47 | 137.65 | 93.53 | 27.12 |
| EVM0009876 | 9.36 | 8.31 | 11.28 | 53.35 | 54.78 |
| EVM0004513 | 60.65 | 76.28 | 82.31 | 204.10 | 186.79 |
| EVM0010109 | 8.69 | 7.58 | 7.76 | 18.14 | 20.68 |
| EVM0006915 | 19.97 | 28.66 | 21.29 | 115.05 | 105.38 |
| EVM0008461 | 9.67 | 10.87 | 12.87 | 46.45 | 36.33 |
| EVM0006626 | 51.89 | 45.70 | 65.78 | 257.00 | 312.50 |
| EVM0005846 | 6.02 | 9.38 | 477.23 | 1.61 | 2.40 |
| EVM0007696 | 7.81 | 8.52 | 7.57 | 33.26 | 17.12 |
| EVM0012149 | 59.55 | 61.11 | 94.14 | 28.84 | 25.29 |
| EVM0009698 | 1577.37 | 1174.02 | 1049.89 | 4373.42 | 2720.55 |
| EVM0006874 | 30.80 | 40.47 | 13.57 | 2.54 | 3.64 |
| EVM0011734 | 5.99 | 6.18 | 2.25 | 14.73 | 20.81 |
| EVM0010265 | 33.25 | 43.39 | 35.36 | 113.06 | 108.98 |
| EVM0008481 | 11.72 | 10.28 | 7.22 | 28.45 | 29.48 |
| EVM0001981 | 5.86 | 72.41 | 378.57 | 26.02 | 10.40 |
| EVM0004142 | 1008.37 | 565.17 | 1201.01 | 56.52 | 57.81 |
| EVM0001277 | 4.40 | 4.91 | 5.83 | 22.39 | 25.03 |
| EVM0012233 | 1.25 | 12.95 | 79.77 | 3.21 | 3.31 |
| EVM0000932 | 98.37 | 62.30 | 56.84 | 271.11 | 216.15 |
| EVM0008213 | 1093.56 | 778.98 | 798.91 | 2286.68 | 2190.78 |
| EVM0002372 | 6.14 | 8.81 | 12.43 | 24.88 | 27.99 | 50.32 |
| EVM0011950 | 601.16 | 577.86 | 418.92 | 2042.67 | 2141.59 | 1347.21 |
| EVM0001725 | 24.27 | 16.94 | 9.80 | 49.91 | 35.37 | 32.87 |
| EVM0008881 | 231.32 | 197.99 | 9.80 | 49.91 | 35.37 | 32.87 |
| EVM0006028 | 2.07 | 2.45 | 3.29 | 0.58 | 1.01 | 0.58 |
| EVM0000202 | 148.92 | 149.45 | 271.29 | 47.18 | 36.66 | 42.39 |
| EVM0010213 | 7709.96 | 1148.45 | 681.01 | 2576.26 | 2672.67 | 3955.13 |
| EVM005121 | 147.61 | 166.37 | 190.59 | 469.78 | 418.83 | 448.80 |
| EVM0004221 | 7.22 | 6.81 | 1.70 | 44.37 | 40.02 | 207.12 |
| EVM0012007 | 20.42 | 17.93 | 21.95 | 56.96 | 61.23 | 72.15 |
| EVM0008313 | 21.42 | 24.55 | 27.63 | 10.18 | 9.35 | 13.63 |
| EVM001525 | 32.01 | 33.65 | 27.70 | 100.94 | 69.49 | 67.45 |
| EVM0003267 | 9620.57 | 7123.21 | 1260.86 | 46550.10 | 36948.10 | 34941.10 |
| EVM0004698 | 81.53 | 65.13 | 60.10 | 230.51 | 256.36 | 326.74 |
| EVM0007377 | 10.04 | 11.94 | 9.47 | 26.93 | 27.15 | 26.23 |
| EVM0011226 | 140.90 | 121.74 | 128.12 | 298.96 | 318.86 | 339.63 |
| EVM0011879 | 38.22 | 18.02 | 42.12 | 85.35 | 107.65 | 185.59 |
| EVM0010715 | 73.74 | 53.79 | 38.90 | 164.65 | 145.51 | 155.98 |
| EVM0011088 | 21.26 | 14.00 | 20.87 | 85.72 | 55.00 | 98.79 |
| EVM0002681 | 11.19 | 12.43 | 10.79 | 33.61 | 28.42 | 35.29 |
| EVM0005169 | 1355.12 | 1103.72 | 4332.32 | 206.52 | 164.25 | 674.83 |
| EVM0000883 | 4.16 | 3.80 | 3.86 | 14.72 | 11.15 | 10.79 |
| EVM0002674 | 9.74 | 8.85 | 4.93 | 1.52 | 2.34 | 1.53 |
| EVM0002912 | 170.90 | 156.77 | 152.57 | 655.95 | 540.40 | 503.86 |
| EVM0008150 | 5.20   | 41.66  | 80.30  | 31.31  | 16.20   | 15.36   |
| EVM0008211 | 14.80  | 17.24  | 13.55  | 36.44  | 35.84   | 28.25   |
| EVM0008292 | 16.07  | 16.60  | 12.39  | 43.43  | 37.24   | 37.02   |
| EVM0003945 | 216.14 | 205.26 | 180.22 | 101.73 | 85.30   | 76.53   |
| EVM0004809 | 43.74  | 40.01  | 39.76  | 127.43 | 118.60  | 137.53  |
| EVM0000393 | 16.07  | 16.60  | 12.39  | 43.43  | 37.24   | 37.02   |
| EVM0003951 | 36.10  | 36.31  | 58.59  | 119.44 | 124.85  | 148.43  |
| EVM0009623 | 7.20   | 26.53  | 30.69  | 310.96 | 208.31  | 548.84  |
| EVM0002451 | 2.49   | 2.84   | 2.95   | 20.67  | 20.22   | 25.34   |
| EVM0006992 | 9.57   | 12.70  | 22.34  | 43.56  | 46.74   | 56.72   |
| EVM0005649 | 178.28 | 153.19 | 123.43 | 479.93 | 407.26  | 430.64  |
| EVM0005377 | 4.34   | 6.19   | 7.43   | 18.99  | 16.93   | 15.72   |
| EVM0009546 | 73.84  | 97.32  | 270.71 | 41.52  | 42.58   | 58.81   |
| EVM0000260 | 9.50   | 8.84   | 7.30   | 48.78  | 33.00   | 36.65   |
| EVM0010935 | 21.44  | 16.37  | 16.67  | 76.02  | 72.16   | 106.17  |
| EVM0002754 | 7.81   | 10.25  | 17.95  | 64.06  | 69.76   | 71.17   |
| EVM0003280 | 3.61   | 26.67  | 36.33  | 209.01 | 144.42  | 238.27  |
| EVM0003951 | 36.10  | 36.31  | 58.59  | 119.44 | 124.85  | 148.43  |
| EVM0009347 | 15.04  | 16.22  | 15.58  | 71.76  | 52.85   | 38.60   |
| EVM0003465 | 15.24  | 23.72  | 23.61  | 49.19  | 51.36   | 58.39   |
| EVM0010235 | 2.28   | 3.00   | 1.38   | 4.86   | 6.12    | 4.71    |
| EVM0002281 | 68.12  | 47.04  | 218.98 | 14.92  | 7.08    | 12.27   |
| EVM0004156 | 0.66   | 0.96   | 0.74   | 2.67   | 2.60    | 2.20    |
| EVM0006723 | 155.42 | 135.41 | 29.57  | 794.72 | 704.37  | 1458.58 |
| Code          | 9.52  | 10.17 | 15.80 | 41.78 | 36.83 | 39.97 |
|--------------|-------|-------|-------|-------|-------|-------|
| EVM0001247   | 90.27 | 34.90 | 25.31 | 183.43| 117.26| 93.81 |
| EVM0002391   | 399.28| 207.59| 123.60| 2143.23| 1159.11| 1386.81|
| EVM0000869   | 161.53| 219.77| 474.64| 545.40| 768.15| 1314.67|
| EVM0009500   | 100.93| 121.52| 155.93| 48.23 | 51.03 | 54.85 |
| EVM0005306   | 44.42 | 52.40 | 41.70 | 117.29| 114.02| 121.68|
| EVM002711    | 20.51 | 17.89 | 15.39 | 85.56 | 93.88 | 103.19|
| EVM006159    | 40.98 | 47.41 | 136.24| 102.02| 136.47| 60.24 |
| EVM006020    | 33.57 | 40.69 | 62.17 | 103.92| 144.13| 280.92|
| EVM006479    | 40.01 | 34.65 | 19.38 | 7.56  | 9.23  | 7.04  |
| EVM000333    | 20.83 | 24.34 | 29.16 | 8.72  | 11.84 | 6.81  |
| EVM006914    | 2.53  | 5.67  | 5.04  | 8.65  | 11.63 | 14.55 |
| EVM004495    | 299.00| 260.54| 251.97| 674.21| 555.58| 534.01|
| EVM009944    | 7.36  | 8.88  | 6.66  | 22.75 | 23.15 | 19.45 |
| EVM007596    | 20.18 | 21.58 | 20.25 | 59.46 | 51.00 | 54.73 |
| EVM010264    | 22.62 | 19.41 | 12.22 | 191.62| 215.88| 226.65|
| EVM005335    | 7.90  | 17.23 | 11.32 | 26.98 | 36.23 | 32.83 |
| EVM002127    | 55.73 | 38.35 | 36.60 | 115.98| 103.06| 121.66|
| EVM010113    | 33.98 | 29.57 | 61.21 | 104.28| 139.57| 201.03|
| EVM008730    | 8.47  | 16.51 | 17.63 | 36.22 | 52.29 | 96.77 |
| EVM001016    | 3.40  | 5.47  | 5.33  | 13.39 | 18.51 | 22.66 |
| EVM004238    | 22.13 | 23.97 | 23.90 | 80.54 | 73.47 | 60.16 |
| EVM009090    | 19.21 | 25.19 | 14.37 | 118.55| 266.06| 149.64|
| EVM007527    | 271.98| 227.68| 220.25| 99.60 | 100.76| 104.46|
| EVM007254    | 8026.47| 6323.28| 7240.86| 36270.50| 24518.90| 31828.00|
| EVM000530    | 33.76 | 32.20 | 27.77 | 11.51 | 14.44 | 9.76  |
| EVM0000784  | 9.86  | 9.47  | 7.75  | 23.58 | 27.84 | 20.82  |
| EVM0008917  | 21.73 | 19.92 | 21.10 | 55.42 | 48.96 | 72.47  |
| EVM0006789  | 107.49| 83.87 | 131.04| 44.24 | 35.06 | 47.82  |
| EVM0002798  | 5.25  | 3.75  | 3.13  | 23.12 | 17.23 | 15.83  |
| EVM0011948  | 45.34 | 47.96 | 54.37 | 17.28 | 21.16 | 27.06  |
| EVM0003022  | 7.83  | 448.11| 4138.79| 2.09 | 7.75  | 216.17 |
| EVM0002867  | 30.59 | 34.56 | 34.40 | 124.43| 117.39| 87.22  |
| EVM0002582  | 321.38| 320.26| 326.95| 135.71| 120.20| 94.50  |
| EVM0011435  | 56.24 | 55.96 | 70.56 | 14.19 | 14.72 | 10.88  |
| EVM0008447  | 47.15 | 49.59 | 51.60 | 182.04| 136.13| 122.92 |
| EVM0003122  | 41.25 | 43.47 | 53.18 | 14.40 | 16.92 | 13.46  |
| EVM0005126  | 2.58  | 3.47  | 4.20  | 5.93  | 7.86  | 9.52   |
| EVM0004911  | 537.24| 415.95| 288.88| 1110.72| 1480.83| 1632.91|
| EVM0002782  | 27.83 | 25.36 | 34.88 | 12.54 | 9.81  | 13.02  |
| EVM0009733  | 8.69  | 8.04  | 12.02 | 26.23 | 34.16 | 63.75  |
| EVM0006949  | 41.28 | 68.14 | 69.91 | 222.96| 212.58| 277.54 |
| EVM0007199  | 136.75| 107.14| 167.20| 592.09| 404.82| 379.02 |
| EVM0003386  | 4.47  | 12.67 | 5.95  | 12.11 | 26.78 | 12.04  |
| EVM0011601  | 146.90| 125.16| 76.61 | 401.96| 310.07| 225.49 |
| EVM0008827  | 3.30  | 3.91  | 6.39  | 0.96  | 0.95  | 1.59   |
| EVM0006578  | 103.07| 98.13 | 93.35 | 263.57| 233.00| 272.30 |
| EVM0011492  | 260.14| 336.75| 1057.93| 639.74| 808.34| 516.65 |
| EVM0005758  | 66.90 | 58.97 | 38.11 | 152.55| 176.41| 241.58 |
| EVM0000108  | 44.65 | 60.50 | 53.59 | 22.23 | 27.61 | 22.39  |
| EVM0008637  | 27.01 | 31.67 | 74.73 | 26.63 | 20.78 | 19.82  |
| EVM0002747  | 1.62  | 1.73  | 1.61  | 0.25  | 0.38  | 0.17   |
Data Set S7 Genes involved in oxidoreductase activity and oxidation-reduction process

| oxidoreductase activity | log2(fold change R1 vs Z1) | log2(fold change R2 vs Z2) | log2(fold change R2 vs Z2) | R1 vs Z1 q value | R2 vs Z2 q value | R3 vs Z3 q value | annotation |
|-------------------------|-----------------------------|-----------------------------|-----------------------------|------------------|------------------|------------------|------------|
| EVM0000006              | -0.88                       | -0.03                       | 1.18                        | 2.08E-02         | 9.61E-01         | 7.96E-04         | Cytochrome P450 |
| EVM0000040              | 1.16                        | 0.61                        | 0.15                        | 7.96E-04         | 9.59E-02         | 7.48E-01         | Flavin-binding monooxygenase-like |
| EVM0000093              | -1.51                       | -0.45                       | 0.72                        | 4.28E-04         | 4.82E-04         | 1.01E-02         | Cytochrome b5-like Heme/Steroid binding domain |
| EVM0000151              | -1.77                       | -2.45                       | 1.10                        | 2.36E-03         | 2.92E-03         | 4.28E-04         | short chain dehydrogenase |
| EVM0000204              | -1.49                       | -1.37                       | 1.96                        | 7.55E-03         | 5.26E-02         | 2.92E-03         | Catalase |
| EVM0000295              | 1.12                        | 1.10                        | 1.75                        | 4.28E-04         | 1.46E-01         | 4.28E-04         | Fatty acid hydroxylase superfamily |
| EVM0000375              | -1.36                       | -0.59                       | 1.36                        | 7.21E-01         | 9.21E-01         | 4.28E-04         | lactate/malate dehydrogenase, NAD binding domain |
| EVM0000503              | -0.54                       | 0.06                        | 1.46                        | 3.10E-02         | 6.34E-01         | 5.51E-01         | Acyl-CoA dehydrogenase, C-terminal domain |
| EVM0000528              | -1.04                       | -0.24                       | -0.31                       | 4.28E-04         | 4.98E-03         | 9.68E-02         | Putative FMN-binding domain |
| EVM0000538              | -1.82                       | -0.75                       | 1.40                        | 7.44E-01         | 5.81E-02         | 4.28E-04         | Isocitrate/isopropylmalate dehydrogenase |
| EVM0000566              | 0.17                        | -0.71                       | 1.27                        | 6.58E-01         | 1.68E-01         | 4.28E-04         | Cytochrome P450 |
| Gene ID       | EVM0000600 | EVM0000621 | EVM0000637 | EVM0000680 | EVM0000705 | EVM0000711 | EVM0000762 | EVM0000773 | EVM0000781 | EVM0000804 | EVM0000833 | EVM0000891 | EVM0000944 | EVM0000973 | EVM0001011 | EVM0001128 | EVM0001166 | EVM0001244 | EVM0001285 | EVM0001322 | EVM0001489 | EVM0001579 | EVM0001740 | EVM0001774 |
|--------------|------------|------------|------------|------------|------------|------------|------------|------------|------------|------------|------------|------------|------------|------------|------------|------------|------------|------------|------------|------------|------------|------------|------------|
| Value        | -1.01      | 0.03       | -1.00      | 0.61       | -0.94      | 1.10       | -1.81      | -0.58      | -0.51      | -0.63      | 0.79       | -0.43      | -0.04      | 0.82       | -0.64      | -0.14      | 0.02       | -0.53      | 0.27       | 0.80       | -1.94      | 0.48       |
| Standard Dev.| -0.61      | 0.09       | 2.00       | 1.42       | -1.26      | 0.91       | -1.24      | -1.30      | 0.10       | -0.11      | 0.27       | 0.56       | -0.45      | 0.26       | 1.15       | 1.53       | 0.77       | -0.54      | -0.31      | 0.95       | 0.64       |
| Mean         | -1.42      | 1.01       | 3.44       | 3.84       | -1.78      | 0.91       | -0.64      | -2.03      | 2.18       | -1.67      | 3.16       | 1.21       | 2.13       | 2.36       | -0.43      | 0.07       | 2.21       | -1.42      | 2.15       | 1.20       | 2.15       |
| Standard Dev.| 4.23E-03   | 9.52E-01   | 8.22E-03   | 1.78E-01   | 1.30E-02   | 1.14E-03   | 4.28E-04   | 1.55E-01   | 8.22E-03   | 1.43E-01   | 2.31E-02   | 3.12E-01   | 9.49E-01   | 7.90E-02   | 6.63E-02   | 8.27E-01   | 9.76E-01   | 2.63E-01   | 5.57E-01   | 2.22E-02   | 3.98E-03   | 2.90E-01   |
| P-Value      | 9.58E-02   | 8.63E-01   | 4.28E-04   | 1.46E-03   | 4.28E-04   | 5.94E-03   | 4.28E-04   | 7.96E-03   | 8.52E-01   | 8.33E-01   | 5.36E-01   | 1.40E-01   | 2.57E-01   | 6.46E-01   | 1.14E-03   | 4.28E-04   | 3.76E-01   | 1.40E-01   | 1.25E-01   | 4.28E-04   | 1.25E-01   |
| Description  | Nitronate monooxygenase | Oxidoreductase family, NAD-binding Rossmann fold | Cytochrome P450 | Cytochrome P450 | Iron/manganese superoxide dismutases, C-terminal domain | Cytochrome P450 | Protein of unknown function (DUF1295) | NADH-ubiquinone oxidoreductase B18 subunit (NDUFB7) | FAD dependent oxidoreductase | Acyl-CoA dehydrogenase, C-terminal domain | Isocitrate/isopropylmalate dehydrogenase | Pyridoxamine 5’-phosphate oxidase | Aldo/keto reductase family | FMN-dependent dehydrogenase | Cytochrome P450 | Cytochrome P450 | Cytochrome P450 | Cytochrome P450 | Cytochrome P450 | Cytochrome P450 | Cytochrome P450 | Enoyl-(Acyl carrier protein) reductase | Family of unknown function (DUF706) | 2OG-Fe(II) oxygenase superfamily |
| Gene ID      | ExpVal1       | ExpVal2       | ExpVal3       | ExpVal4       | Description                                                                                      |
|-------------|---------------|---------------|---------------|---------------|-------------------------------------------------------------------------------------------------|
| EVM0001778  | -1.54         | -1.61         | -1.80         | 4.28E-04      | Pyridoxamine 5'-phosphate oxidase                                                                 |
| EVM0001859  | -0.20         | -0.37         | 1.01          | 6.56E-01      | D-isomer specific 2-hydroxyacid dehydrogenase, NAD binding domain                                |
| EVM0001905  | -0.92         | 0.53          | 2.57          | 5.70E-03      | GMC oxidoreductase                                                                             |
| EVM0001912  | 0.21          | 0.62          | 1.09          | 6.33E-01      | EPSP synthase (3-phosphoshikimate 1-carboxyvinyltransferase)                                    |
| EVM0002090  | 0.33          | 0.07          | 1.19          | 4.27E-01      | Taurine catabolism dioxygenase TauD, TfdA family                                               |
| EVM0002137  | 1.16          | 0.51          | 1.35          | 5.70E-03      | D-arabinono-1,4-lactone oxidase                                                                 |
| EVM0002201  | -0.95         | 0.15          | 1.65          | 1.77E-03      | short chain dehydrogenase                                                                       |
| EVM0002262  | -0.23         | -1.06         | -0.14         | 6.48E-01      | Aldehyde dehydrogenase family                                                                  |
| EVM0002281  | 2.19          | 2.73          | 4.16          | 4.28E-04      | Oxoglutarate and iron-dependent oxygenase degradation C-term                                     |
| EVM0002287  | 2.11          | -0.13         | -1.54         | 1.51E-02      | Cytochrome P450                                                                                 |
| EVM0002309  | -0.28         | -0.97         | -1.20         | 4.96E-01      | NAD-dependent glycerol-3-phosphate dehydrogenase C-terminus                                     |
| EVM0002372  | -2.02         | -1.67         | -2.02         | 4.28E-04      | Cytochrome P450                                                                                 |
| EVM0002430  | 1.10          | 0.46          | 0.77          | 3.19E-01      | Dehydrogenase E1 component                                                                      |
| EVM0002432  | -1.52         | 0.48          | -0.66         | 6.64E-03      | Cytochrome P450                                                                                 |
| EVM0002521  | -0.95         | -0.77         | -1.17         | 1.32E-02      | Acyl-CoA dehydrogenase, C-terminal domain                                                       |
| EVM0002562  | -0.92         | -0.33         | 2.38          | 6.17E-03      | AhpC/TSA family                                                                                |
| EVM0002722  | -1.79         | -0.66         | -0.67         | 4.28E-04      | Multicopper oxidase                                                                            |
| EVM0002729  | 0.09          | -0.38         | -2.16         | 8.72E-01      | Ergosterol biosynthesis ERG4/ERG24 family                                                      |
| EVM0002811  | -0.49         | -1.25         | -2.09         | 3.89E-01      | Thioredoxin                                                                                    |
| EVM0002854  | -1.06         | 1.83          | 4.08          | 2.07E-03      | Multicopper oxidase                                                                            |
| EVM0002892  | -0.93         | -0.80         | -1.03         | 1.16E-02      | FAD binding domain                                                                             |
| Gene ID | Value 1 | Value 2 | Value 3 | Value 4 | Value 5 | Value 6 | Function |
|---------|---------|---------|---------|---------|---------|---------|----------|
| EVM0002918 | 0.47 | 1.06 | 1.57 | 2.72E-01 | 1.77E-03 | 4.28E-04 | Cytochrome P450 |
| EVM0003014 | 0.62 | 1.07 | 1.63 | 7.91E-02 | 1.01E-02 | 4.28E-04 | Methyleneitetrahydrofolate reductase |
| EVM0003022 | 1.91 | 5.85 | 4.26 | 4.28E-04 | 4.28E-04 | 4.28E-04 | FAD dependent oxidoreductase |
| EVM0003034 | 0.38 | 0.90 | 1.32 | 3.13E-01 | 2.03E-02 | 2.07E-03 | Formate--tetrahydrofolate ligase |
| EVM0003191 | 0.98 | 0.28 | 1.28 | 4.98E-03 | 5.14E-01 | 2.92E-03 | Cytochrome P450 |
| EVM0003237 | 0.12 | 1.47 | 2.85 | 8.12E-04 | 4.28E-04 | 4.28E-04 | Glutamate/Leucine/Phenylalanine/Valine dehydrogenase |
| EVM0003243 | 0.77 | 0.89 | 2.38 | 2.70E-02 | 5.94E-03 | 4.28E-04 | AMP-binding enzyme |
| EVM0003304 | 1.48 | 0.58 | 0.69 | 2.29E-02 | 3.28E-01 | 3.11E-01 | Cytochrome P450 |
| EVM0003346 | -1.43 | -0.11 | -0.55 | 7.96E-04 | 8.26E-01 | 1.68E-01 | Nitronate monooxygenase |
| EVM0003361 | -2.68 | -2.67 | -0.84 | 4.28E-04 | 4.28E-04 | 1.81E-01 | Lipoxygenase |
| EVM0003398 | 0.78 | 0.19 | -1.54 | 1.00E+00 | 8.28E-01 | 4.07E-02 | Cytochrome P450 |
| EVM0003471 | -0.03 | 1.43 | 0.79 | 9.68E-01 | 2.92E-03 | 1.08E-01 | GMC oxidoreductase |
| EVM0003525 | -0.52 | -0.96 | -1.14 | 1.49E-01 | 4.73E-03 | 1.14E-03 | Enoyl-(Acyl carrier protein) reductase |
| EVM0003609 | -1.40 | -1.80 | -2.78 | 4.28E-04 | 4.28E-04 | 4.28E-04 | Cytochrome oxidase c subunit ViB |
| EVM0003803 | -1.32 | 0.54 | 0.26 | 1.34E-02 | 2.70E-01 | 6.09E-01 | NAD:flavin oxidoreductase / NADH oxidase family |
| EVM0003814 | -0.88 | 5.08 | 3.29 | 1.01E-01 | 4.28E-04 | 1.46E-03 | GMC oxidoreductase |
| EVM0003882 | -1.41 | -0.92 | 1.24 | 4.28E-04 | 5.94E-03 | 7.96E-04 | Pyridine nucleotide-disulphide oxidoreductase |
| EVM0003917 | 0.90 | 0.15 | 1.73 | 1.62E-01 | 8.50E-01 | 2.36E-03 | Aldehyde dehydrogenase family |
| EVM0003929 | 1.84 | 1.36 | 1.37 | 4.28E-04 | 1.14E-03 | 7.96E-04 | Taurine catabolism dioxygenase TauD, TfdA family |
| EVM0003976 | 1.75 | 1.80 | 1.59 | 4.28E-04 | 4.28E-04 | 4.28E-04 | Conserved region in glutamate synthase |
| EVM0004000 | 0.03 | 1.45 | 3.28 | 9.52E-01 | 4.28E-04 | 4.28E-04 | Glucose-6-phosphate dehydrogenase, C-terminal domain |
| EVM0004021 | 0.27 | 0.60 | 1.97 | 5.19E-01 | 1.17E-01 | 4.28E-04 | Cytochrome P450 |
| EVM0004069 | 0.39 | 1.00 | 0.29 | 3.25E-01 | 3.46E-03 | 4.85E-01 | FAD linked oxidases, C-terminal domain |
| EVM0004108 | -1.17 | -0.51 | -0.77 | 6.41E-03 | 2.91E-01 | 7.94E-02 | Cytochrome P450 |
| ID       | Value1 | Value2 | Value3 | Value4  | Value5  | Value6  | Description                                                                 |
|---------|--------|--------|--------|---------|---------|---------|-----------------------------------------------------------------------------|
| EVM0004177 | 0.93   | 1.22   | 2.66   | 7.77E-03| 3.98E-03| 4.28E-04| Nitrite and sulphite reductase 4Fe-4S domain                               |
| EVM0004215 | -0.59  | -1.54  | -1.65  | 1.02E-01| 4.28E-04| 4.28E-04| Cytochrome c oxidase subunit Va                                              |
| EVM0004219 | -0.34  | 2.03   | 2.28   | 3.89E-01| 4.28E-04| 4.28E-04| NADH:flavin oxidoreductase / NADH oxidase family                            |
| EVM0004285 | 0.01   | 1.57   | 1.39   | 9.87E-01| 4.28E-04| 4.28E-04| Multicopper oxidase                                                         |
| EVM0004300 | 0.10   | 3.62   | 2.87   | 9.15E-01| 4.28E-04| 4.28E-04| Cytochrome P450                                                              |
| EVM0004320 | 1.19   | 1.32   | 1.11   | 7.96E-04| 4.28E-04| 4.28E-04| Aldo/keto reductase family                                                  |
| EVM0004345 | -1.42  | -1.23  | -0.54  | 4.28E-04| 1.14E-03| 1.42E-01| Taurine catabolism dioxygenase TauD, TfdA family                             |
| EVM0004424 | 0.25   | 0.38   | 1.41   | 5.55E-01| 3.28E-01| 4.28E-04| Histidinol dehydrogenase                                                    |
| EVM0004456 | -1.27  | -1.25  | -1.71  | 6.50E-02| 8.91E-02| 2.94E-02| Alcohol dehydrogenase GroES-like domain                                     |
| EVM0004461 | -1.33  | -2.40  | -1.35  | 4.28E-04| 4.28E-04| 4.28E-04| Putative oxidoreductase C terminal                                           |
| EVM0004488 | -0.69  | -0.67  | -3.77  | 6.58E-02| 8.95E-02| 4.28E-04| Multicopper oxidase                                                         |
| EVM0004518 | -1.04  | -0.78  | 1.46   | 1.08E-02| 6.28E-02| 4.28E-04| Aldehyde dehydrogenase family                                               |
| EVM0004655 | 0.25   | 0.81   | 1.77   | 6.09E-01| 2.98E-02| 4.28E-04| Methylenetetrahydrofolate reductase                                         |
| EVM0004661 | -1.20  | -1.32  | -1.51  | 2.07E-03| 1.77E-03| 4.28E-04| Cytochrome P450                                                              |
| EVM0004712 | 0.21   | 0.98   | 2.35   | 6.95E-01| 1.06E-02| 4.28E-04| short chain dehydrogenase                                                   |
| EVM0004732 | 0.72   | -0.44  | 1.19   | 5.01E-02| 2.49E-01| 4.28E-04| Acyl-CoA dehydrogenase, C-terminal domain                                    |
| EVM0004740 | -0.43  | 0.10   | 1.57   | 3.08E-01| 8.46E-01| 4.28E-04| Iron-containing alcohol dehydrogenase                                       |
| EVM0004894 | -0.62  | -0.18  | 1.22   | 9.74E-02| 7.10E-01| 4.28E-04| FAD binding domain                                                          |
| EVM0005148 | 0.05   | 0.05   | 1.41   | 9.19E-01| 9.29E-01| 4.28E-04| 6-phosphogluconate dehydrogenase, C-terminal domain                        |
| EVM0005231 | -0.41  | 1.33   | 2.79   | 3.80E-01| 7.96E-04| 4.28E-04| FAD dependent oxidoreductase                                                |
| EVM0005275 | -1.34  | -0.96  | -1.01  | 2.08E-02| 6.50E-02| 6.15E-02| FAD binding domain                                                          |
| EVM0005310 | 0.65   | 1.92   | 2.03   | 1.00E-01| 4.28E-04| 4.28E-04| Enoyl-(Acyl carrier protein) reductase                                      |
| EVM0005316 | 0.78   | 0.76   | 1.93   | 3.30E-01| 2.66E-01| 3.58E-02| Dioxigenase                                                                 |
| EVM0005338 | -1.28  | -0.34  | 0.12   | 4.28E-04| 4.14E-01| 8.27E-01| Zinc-binding dehydrogenase                                                  |
| EVM0005390 | 0.26   | -0.36  | -1.06  | 5.39E-01| 3.65E-01| 7.96E-04| short chain dehydrogenase                                                   |
| EVM0005468 | -0.48  | 0.06   | 1.52   | 3.02E-01| 9.16E-01| 4.28E-04| Pyrroline-5-carboxylate reductase dimerisation                              |
| EVM0005495 | -0.10 | 0.85  | 1.57  | 9.13E-01 | 1.54E-01 | 6.87E-03 | Ketopantoate reductase PanE/ApbA C terminal non-haem dioxygenase in morphine synthesis N-terminal |
| EVM0005518 | -1.19 | -0.46 | -1.17 | 4.63E-02 | 4.33E-01 | 3.18E-02 | |
| EVM0005567 | 1.92  | 0.79  | 0.18  | 4.28E-04 | 4.42E-02 | 7.38E-01 | Ribonucleotide reductase, small chain |
| EVM0005612 | -0.11 | 0.38  | 1.11  | 8.30E-01 | 3.39E-01 | 7.96E-04 | Aldehyde dehydrogenase family |
| EVM0005631 | -0.93 | -0.46 | -1.77 | 1.44E-01 | 4.49E-01 | 1.08E-02 | Domain of unknown function (DUF3415) |
| EVM0005691 | -1.83 | -1.89 | -2.61 | 5.94E-03 | 1.47E-02 | 1.46E-03 | Cytochrome P450 |
| EVM0005762 | 0.01  | -0.69 | -1.40 | 9.82E-01 | 5.61E-02 | 4.28E-04 | Thioredoxin |
| EVM0005768 | 0.41  | -0.86 | -1.19 | 3.93E-01 | 3.41E-02 | 2.07E-03 | Peroxidase |
| EVM0005773 | 0.28  | 1.11  | 0.41  | 4.88E-01 | 4.28E-04 | 2.85E-01 | Cytochrome P450 |
| EVM0005861 | -1.52 | -2.23 | -4.41 | 1.14E-03 | 4.28E-04 | 4.28E-04 | Catalase Pyridine nucleotide-disulphide oxidoreductase |
| EVM0005891 | -1.32 | -1.88 | -0.63 | 4.28E-04 | 4.28E-04 | 8.10E-02 | Cytochrome P450 |
| EVM0005925 | -0.27 | 1.85  | 1.69  | 5.51E-01 | 4.28E-04 | 4.28E-04 | 3-hydroxyanthranilic acid dioxygenase |
| EVM0005970 | -1.01 | 0.51  | 1.89  | 1.28E-02 | 2.10E-01 | 4.28E-04 | Flavin-binding monooxygenase-like |
| EVM0005975 | 0.00  | 0.46  | 1.63  | 9.94E-01 | 2.10E-01 | 4.28E-04 | short chain dehydrogenase |
| EVM0006055 | -1.25 | 1.12  | 2.89  | 5.65E-02 | 3.04E-02 | 4.28E-04 | Alcohol dehydrogenase GroES-like domain |
| EVM0006084 | -0.91 | 0.38  | 2.99  | 2.20E-02 | 3.64E-01 | 4.28E-04 | Aldo/keto reductase family |
| EVM0006117 | -1.80 | -1.11 | -1.42 | 4.28E-04 | 3.72E-03 | 4.28E-04 | short chain dehydrogenase |
| EVM0006352 | -0.58 | 1.37  | 3.31  | 1.89E-01 | 4.28E-04 | 4.28E-04 | Fatty acid desaturase |
| EVM0006432 | -1.67 | 0.89  | 1.82  | 4.28E-04 | 3.95E-02 | 4.28E-04 | Cytochrome P450 |
| EVM0006458 | -1.23 | -0.45 | -0.36 | 4.28E-04 | 2.42E-01 | 3.70E-01 | Zinc-binding dehydrogenase |
| EVM0006467 | -0.65 | 0.21  | 1.24  | 1.05E-01 | 6.65E-01 | 7.96E-04 | Alcohol dehydrogenase GroES-like domain |
| EVM0006502 | -1.14 | -1.14 | -0.56 | 4.28E-04 | 7.96E-04 | 1.24E-01 | Pyridoxamine 5'-phosphate oxidase |
| EVM0006570 | -2.17 | -1.94 | -2.35 | 4.28E-04 | 4.28E-04 | 4.28E-04 | Alcohol dehydrogenase GroES-like domain |
| EVM0006605 | 0.23  | 0.15  | 1.56  | 6.09E-01 | 7.68E-01 | 4.28E-04 | Cytochrome P450 |
| EVM0006652 | -1.14 | 0.56  | 1.34  | 1.14E-03 | 1.22E-01 | 7.96E-04 |
| EVM0006662 | -1.63 | -0.55 | -0.28 | 4.28E-04 | 1.74E-01 | 5.18E-01 | Hydroxymethylglutaryl-coenzyme A reductase |
| EVM0006670 | -2.87 | -0.07 | -2.52 | 1.14E-01 | 9.55E-01 | 4.98E-02 | Cytochrome P450 |
| EVM0006718 | -0.27 | 1.25 | 0.74 | 5.78E-01 | 4.23E-03 | 2.25E-01 | FAD dependent oxidoreductase |
| EVM0006753 | -1.68 | -0.13 | 2.96 | 4.28E-04 | 8.34E-01 | 4.28E-04 | Family of unknown function (DUF706) |
| EVM0006754 | 0.17 | -1.59 | -0.19 | 7.35E-01 | 4.28E-04 | 7.93E-01 | Coproporphyrinogen III oxidase |
| EVM0006768 | -0.49 | -1.25 | 0.42 | 2.10E-01 | 4.28E-04 | 2.80E-01 | Cytochrome P450 |
| EVM0006770 | -2.56 | 0.13 | -0.29 | 4.28E-04 | 8.52E-01 | 5.71E-01 | Domain of unknown function (DUF3415) |
| EVM0006858 | -0.79 | 0.65 | 2.02 | 2.24E-02 | 8.43E-02 | 4.28E-04 | Aldehyde dehydrogenase family |
| EVM0006901 | 0.94 | -0.08 | 2.13 | 6.64E-03 | 8.77E-01 | 4.28E-04 | Acetohydroxy acid isomeroreductase, catalytic domain |
| EVM0006992 | -2.19 | -1.88 | -1.34 | 4.28E-04 | 4.28E-04 | 4.28E-04 | Cytochrome P450 |
| EVM0007015 | 1.66 | 0.94 | 1.36 | 4.28E-04 | 1.22E-02 | 4.28E-04 | Acyl transferase domain |
| EVM0007048 | -1.00 | 0.06 | 3.32 | 2.93E-02 | 9.25E-01 | 4.28E-04 | -- |
| EVM0007059 | -0.92 | -0.34 | 2.93 | 6.53E-02 | 5.05E-01 | 4.28E-04 | Domain of unknown function (DUF3415) |
| EVM0007176 | 0.48 | -0.48 | -1.64 | 1.96E-01 | 2.15E-01 | 4.28E-04 | D-isomer specific 2-hydroxyacid dehydrogenase, NAD binding domain |
| EVM0007202 | -2.74 | -0.13 | -1.07 | 4.28E-04 | 8.48E-01 | 2.56E-02 | non-haem dioxygenase in morphine synthesis N-terminal |
| EVM0007311 | -0.90 | 0.57 | 1.66 | 1.30E-02 | 1.22E-01 | 4.28E-04 | Cytochrome P450 |
| EVM0007315 | -0.07 | 0.06 | 1.25 | 8.86E-01 | 9.09E-01 | 4.28E-04 | Homoserine dehydrogenase |
| EVM0007336 | 1.59 | 0.11 | 0.74 | 4.28E-04 | 8.19E-01 | 5.69E-02 | AhpC/TSA family |
| EVM0007461 | -2.31 | -0.74 | -0.70 | 4.28E-04 | 8.26E-02 | 1.11E-01 | Aldo/keto reductase family |
| EVM0007494 | -0.38 | -0.60 | -1.31 | 3.21E-01 | 9.65E-02 | 4.28E-04 | Glutaredoxin |
| EVM0007521 | -0.07 | -0.03 | -1.10 | 8.85E-01 | 9.56E-01 | 3.19E-03 | Cytochrome P450 |
| EVM0007795 | -1.01 | 0.09 | 1.52 | 3.46E-03 | 8.62E-01 | 4.28E-04 | Cytochrome P450 |
| EVM0007958 | -1.81 | -1.78 | -3.13 | 4.28E-04 | 4.28E-04 | 4.28E-04 | Multicopper oxidase |
| EVM0008002 | -3.30 | -1.47 | 0.74 | 4.28E-04 | 4.28E-04 | 6.32E-02 | Flavodoxin |
| Accession  | Fold Change | Enzyme Name                                      |
|-----------|-------------|-------------------------------------------------|
| EVM0008061| 0.34        | GMC oxidoreductase                               |
| EVM0008150| -2.59       | Aldo/keto reductase family                       |
| EVM0008238| -0.36       | Cytochrome P450                                  |
| EVM0008251| -0.11       | Aldo/keto reductase family                       |
| EVM0008259| 1.66        | Putative oxidoreductase C terminal               |
| EVM0008262| -1.05       | NAD binding domain of 6-phosphogluconate dehydrogenase |
| EVM0008303| -0.51       | short chain dehydrogenase                        |
| EVM0008324| -1.77       | Cytochrome P450                                  |
| EVM0008383| -0.17       | NADH ubiquinone oxidoreductase subunit NDUFA12    |
| EVM0008497| -1.34       | MaoC like domain                                 |
| EVM0008503| -0.81       | short chain dehydrogenase                        |
| EVM0008522| 1.56        | FAD dependent oxidoreductase                     |
| EVM0008582| -0.98       | short chain dehydrogenase                        |
| EVM0008651| -1.04       | Copper/zinc superoxide dismutase (SODC)          |
| EVM0008666| 0.03        | Dioxygenase                                      |
| EVM0008720| 1.34        | Ribonucleotide reductase, barrel domain          |
| EVM0008803| -1.45       | FAD binding domain                               |
| EVM0008889| -1.80       | Cytochrome P450                                  |
| EVM0008945| 0.56        | Pyridine nucleotide-disulphide oxidoreductase    |
| EVM0008970| -0.42       | Cytochrome P450                                  |
| EVM0009164| -0.79       | Aldehyde dehydrogenase family                    |
| EVM0009294| -0.35       | Fatty acid hydroylase superfamily               |
| EVM0009319| 0.41        | Cytochrome P450                                  |
| EVM0009384| 0.83        | Isocitrate/isopropylmalate dehydrogenase         |
| EVM0009514 | 1.09 | 0.14 | 1.32 | 7.96E-04 | 7.66E-01 | 4.28E-04 | Glyceraldehyde 3-phosphate dehydrogenase, C-terminal domain |
| EVM0009547 | -0.80 | -0.51 | -2.15 | 4.10E-02 | 2.27E-01 | 4.28E-04 | Cytochrome P450 |
| EVM0009549 | -0.48 | 0.28 | 1.09 | 2.45E-01 | 5.42E-01 | 1.77E-03 | Zinc-binding dehydrogenase |
| EVM0009575 | -0.23 | -0.58 | -1.05 | 5.88E-01 | 9.72E-02 | 1.14E-03 | Acyl-CoA dehydrogenase, C-terminal domain |
| EVM0009632 | 0.01 | 1.40 | 1.33 | 9.86E-01 | 7.96E-04 | 4.28E-04 | Copper amine oxidase, enzyme domain |
| EVM0009683 | -0.16 | 0.09 | 2.06 | 7.55E-01 | 8.52E-01 | 4.28E-04 | Cytochrome P450 |
| EVM0009692 | -1.44 | -0.01 | 0.60 | 4.28E-04 | 9.84E-01 | 1.06E-01 | Aldo/keto reductase family |
| EVM0009701 | -0.97 | 0.83 | 2.95 | 1.32E-02 | 4.07E-02 | 4.28E-04 | Glutathione peroxidase |
| EVM0009755 | -0.60 | -0.47 | -1.67 | 2.39E-01 | 4.09E-01 | 4.28E-04 | Cytochrome P450 |
| EVM0009784 | 0.14 | 1.50 | 4.98 | 8.47E-01 | 3.46E-03 | 4.28E-04 | D-isomer specific 2-hydroxyacid dehydrogenase, NAD binding domain |
| EVM0010016 | 0.09 | -0.31 | 1.04 | 8.56E-01 | 4.62E-01 | 2.65E-03 | Oxidoreductase family, NAD-binding Rossmann fold |
| EVM0010226 | -1.37 | -0.64 | 1.32 | 4.28E-04 | 1.19E-01 | 1.14E-03 | Iron/manganese superoxide dismutases, C-terminal domain |
| EVM0010256 | -2.93 | -1.02 | -0.82 | 4.28E-04 | 2.67E-02 | 9.00E-02 | GMC oxidoreductase |
| EVM0010470 | 1.65 | 1.38 | 1.20 | 4.28E-04 | 4.28E-04 | 4.28E-04 | Proteasome/cyclosome repeat |
| EVM0010473 | -0.83 | 1.51 | 3.49 | 2.56E-02 | 4.28E-04 | 4.28E-04 | Multicopper oxidase |
| EVM0010485 | -0.64 | -1.17 | -2.45 | 6.50E-02 | 4.28E-04 | 4.28E-04 | Cytochrome P450 |
| EVM0010517 | -1.23 | -0.05 | 0.04 | 4.28E-04 | 9.30E-01 | 9.33E-01 | SeLR domain |
| EVM0010628 | 0.04 | -0.04 | 2.33 | 9.55E-01 | 9.54E-01 | 4.28E-04 | Taurine catabolism dioxygenase TauD, TfdA family |
| EVM0010699 | 0.59 | 2.41 | 2.49 | 1.09E-01 | 1.20E-02 | 4.28E-04 | Aldo/keto reductase family |
| EVM0010749 | -1.23 | 0.12 | 1.44 | 1.40E-02 | 8.55E-01 | 2.92E-03 | Cytochrome P450 |
| EVM0010820 | -0.54 | -1.89 | -2.58 | 1.47E-01 | 4.28E-04 | 4.28E-04 | Cytochrome oxidase c subunit VIIb |
| EVM0010845 | -1.30 | -0.28 | -0.37 | 4.52E-02 | 6.89E-01 | 5.91E-01 | Domain of unknown function (DUF3415) |
| EVM0010922 | -0.72 | -1.21 | -1.57 | 7.54E-02 | 7.96E-04 | 4.28E-04 | Nitrate monooxygenase |
| Accession | Rows 1 | Rows 2 | Rows 3 | Rows 4 | Columns 2 | Columns 3 | Columns 4 | Description |
|-----------|--------|--------|--------|--------|-----------|-----------|-----------|-------------|
| EVM0010946 | -1.16  | -0.18  | -0.23  | 4.63E-02 | 7.93E-01  | 7.06E-01  | Pyridine nucleotide-disulphide oxidoreductase |
| EVM0010988 | -1.24  | 0.14   | 0.47   | 4.28E-04 | 7.86E-01  | 2.60E-01  | Alcohol dehydrogenase GroES-like domain |
| EVM0011026 | -0.65  | -0.99  | -1.16  | 5.60E-02 | 2.36E-03  | 4.28E-04  | Semialdehyde dehydrogenase, dimerisation domain |
| EVM0011062 | -1.15  | -1.07  | 0.45   | 2.07E-03 | 1.46E-03  | 2.41E-01  | lactate/malate dehydrogenase, NAD binding domain |
| EVM0011151 | 0.05   | 1.06   | 1.38   | 9.30E-01 | 3.98E-03  | 4.28E-04  | Cytochrome P450 |
| EVM0011181 | -1.48  | -0.99  | -0.89  | 4.28E-04 | 9.08E-03  | 2.13E-02  | GMC oxidoreductase |
| EVM0011216 | 0.51   | 0.16   | 1.51   | 1.64E-01 | 7.31E-01  | 4.28E-04  | Oxidoreductase family, NAD-binding Rossmann fold |
| EVM0011238 | 1.18   | 0.67   | -1.85  | 7.96E-04 | 5.63E-02  | 4.28E-04  | Cytochrome P450 |
| EVM0011287 | -1.14  | 0.01   | 1.73   | 2.92E-03 | 9.84E-01  | 4.28E-04  | Cytochrome P450 |
| EVM0011343 | -1.31  | -2.00  | -4.05  | 4.28E-04 | 4.28E-04  | 4.28E-04  | Glutaredoxin |
| EVM0011359 | -0.83  | -1.30  | -2.20  | 1.44E-02 | 4.28E-04  | 4.28E-04  | ETC complex I subunit conserved region |
| EVM0011379 | -1.82  | -0.91  | -0.40  | 4.28E-04 | 1.06E-02  | 3.21E-01  | non-haem dioxygenase in morphine synthesis N-terminal |
| EVM0011422 | 0.46   | -1.11  | 1.57   | 2.58E-01 | 2.36E-03  | 6.86E-02  | Alcohol dehydrogenase GroES-like domain |
| EVM0011443 | 0.11   | -0.16  | 1.20   | 8.15E-01 | 7.42E-01  | 4.28E-04  | Saccharopine dehydrogenase |
| EVM0011505 | -0.08  | -1.19  | -1.78  | 9.26E-01 | 6.70E-02  | 3.95E-02  | Cytochrome P450 |
| EVM0011552 | -1.30  | -0.94  | -1.13  | 4.28E-04 | 7.55E-03  | 2.65E-03  | Fatty acid desaturase |
| EVM0011559 | -1.16  | 0.04   | 0.10   | 2.07E-03 | 9.35E-01  | 8.43E-01  | FAD linked oxidases, C-terminal domain |
| EVM0011689 | -1.13  | -0.09  | 0.08   | 3.72E-03 | 8.78E-01  | 8.94E-01  | non-haem dioxygenase in morphine synthesis N-terminal |
| EVM0011731 | 0.80   | -0.66  | -2.34  | 5.55E-02 | 9.27E-02  | 4.28E-04  | Peroxidase, family 2 |
| EVM0011732 | -0.28  | -0.52  | 2.54   | 6.07E-01 | 2.72E-01  | 4.28E-04  | homogentisate 1,2-dioxygenase |
| EVM0011888 | -1.33  | -0.83  | -1.45  | 4.01E-02 | 1.85E-01  | 2.82E-02  | Peroxidase |
| EVM0011894 | -0.08  | 3.47   | 4.18   | 8.80E-01 | 4.28E-04  | 4.28E-04  | Cytochrome P450 |
| EVM0011921 | -0.93  | -0.95  | -1.21  | 1.04E-01 | 6.38E-02  | 8.00E-03  | Aldehyde dehydrogenase family |
| EVM0011981 | 0.25   | 0.23   | 1.37   | 5.88E-01 | 6.37E-01  | 4.28E-04  | Aldehyde dehydrogenase family |
| EVM0012038 | -0.41 | -0.62 | -1.83 | 3.27E-01 | 9.94E-02 | 4.28E-04 | 3-beta hydroxysteroid dehydrogenase/isomerase family |
| EVM0012096 | 0.01  | -0.05 | 2.21  | 9.93E-01 | 9.45E-01 | 4.28E-04 | Glyceraldehyde 3-phosphate dehydrogenase, C-terminal domain |
| EVM0012116 | -1.95 | -1.32 | 0.87  | 4.28E-04 | 4.28E-04 | 1.28E-02 | Redoxin |
| EVM0012120 | -0.57 | -0.84 | -1.70 | 1.63E-01 | 2.27E-02 | 4.28E-04 | 3-hydroxyacyl-CoA dehydrogenase, NAD binding domain |
| EVM0012216 | 0.23  | -0.75 | 1.18  | 5.91E-01 | 2.74E-02 | 4.28E-04 | short chain dehydrogenase |
| EVM0000868 | 1.24  | 0.37  | 1.36  | 4.28E-04 | 3.35E-01 | 4.28E-04 | Aconitase family (aconitate hydratase) |
| EVM0000933 | 3.04  | 1.94  | 2.40  | 4.28E-04 | 7.96E-04 | 4.28E-04 | Malic enzyme, NAD binding domain |
| EVM0001216 | -0.72 | 0.33  | 1.26  | 5.41E-02 | 4.24E-01 | 4.28E-04 | Citrate synthase |
| EVM0001679 | 0.62  | 0.38  | 1.21  | 1.40E-01 | 4.04E-01 | 2.92E-03 | Alpha amylase, C-terminal all-beta domain |
| EVM0001730 | 0.05  | 0.07  | 2.91  | 9.33E-01 | 8.99E-01 | 4.28E-04 | Malate synthase |
| EVM0001902 | -1.09 | -0.71 | -0.57 | 1.14E-03 | 4.01E-02 | 1.12E-01 | Lyase |
| EVM0004079 | -0.95 | 0.53  | 1.01  | 9.02E-02 | 2.30E-01 | 1.30E-02 | Phosphoadenosine phosphosulfate reductase family |
| EVM0004970 | 0.18  | 0.26  | 1.06  | 6.73E-01 | 5.26E-01 | 5.70E-03 | Malic enzyme, NAD binding domain |
| EVM0005877 | -0.77 | -1.24 | -1.14 | 2.80E-02 | 4.28E-04 | 7.96E-04 | Ubiquinol-cytochrome C reductase complex 14kD subunit |
| EVM0006700 | -2.04 | -1.97 | -1.43 | 4.28E-04 | 4.28E-04 | 1.14E-03 | Aconitase family (aconitate hydratase) |
| EVM0007457 | -0.59 | -0.04 | 1.54  | 1.41E-01 | 9.49E-01 | 4.28E-04 | Malic enzyme, NAD binding domain |
| EVM0011448 | 0.48  | 0.62  | 1.64  | 1.92E-01 | 7.82E-02 | 4.28E-04 | glucanotransferase domain of human glycogen debranching enzyme |
| EVM0011502 | 0.78  | 0.72  | 1.13  | 3.29E-02 | 4.94E-02 | 1.14E-03 | Citrate synthase |
