Supplementary Materials

Module-detection approaches for the integration of multilevel omics data highlight the comprehensive response of *Aspergillus fumigatus* to caspofungin

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ModuleDiscoverer (MD) provides two different techniques for identifying cliques within the protein-protein interaction network (PPIN): The single-seed approach and the multi-seed approach. The decision of identifying cliques based either on the single- or the multi-seed approach has to be made already in the first step of the MD algorithm in which the approximation of the PPIN’s community structure takes place. The term ‘single-seed’ means that the algorithm starts from only one randomly selected seed node to identify minimal cliques of size three and followed by extending them to maximal cliques which represent the basis of the final regulatory module. As reported in Vlaic et al. [1], the single-seed approach favors the enumeration of large maximal cliques in dense regions of highly overlapping cliques. Hence, some proteins, which are only part of small cliques could be missed. Addressing this issue, the multi-seed approach uses two or even more seed nodes to identify cliques. This leads to a breakdown of large maximal cliques by using multiple seeds competing for nodes during the enumeration of cliques. On the one hand, this increases the probability of identifying proteins which are only part of small cliques. On the other hand, the resulting regulatory module contains a higher number of proteins which are not associated to DEGs. Vlaic et al. showed that the multi-seed approach produces very similar results to those received by the single-seed approach. In the end, it can be regarded as a comprehensive extension of the single-seed approach due to the additionally considered small-clique-proteins.

Here, we focused on the single-seed approach for two reasons: First, this approach is comparable with other well-established maximal clique enumeration problem-based algorithms (e.g., Barrenäs et al. [2] or Gustafsson et al. [3]). Second, Vlaic et al. showed that the multi-seed identified modules can be essentially considered as an extension of the single-seed modules. Nevertheless, to estimate the comprehensiveness of the single-seed-generated regulatory modules, we performed further analyses and applied the multi-seed approach to the experimental data. The estimation of the required number of seed nodes was based on the application of MD to rat data performed by Vlaic et al.. Since the high-confidence (score > 0.7) PPIN of Aspergillus fumigatus (4 121 proteins) roughly contains a third of the nodes of the Rattus norvegicus network (15 436 proteins) used in the study of Vlaic et al. we decided to use 10 seed nodes (roughly a third). Interestingly, Vlaic et al. also showed that the values around a chosen number of seed nodes does not significantly impact the overall structure of the resulting regulatory module.
When comparing the regulatory modules received by the single- and the multi-seed approach, we observed that multi-seed-generated modules comprised 100% of all single-seed-generated modules and also contained an additional number of module components (Supplementary Table 1).

For the multi-seed overall regulatory module (ORM), we performed a generalized topological overlap measurement (as done for the single-seed ORM) to compare significantly enriched biological processes of the multi-seed- with those of the single-seed-based ORM. We found that multi-seed-based ORM clusters are significantly associated with biological processes that are also enriched for single-seed-based clusters. Such processes are, for instance, activation of kinase activity, actin-filament-based processes, response to oxidative stress, carbohydrate metabolic processes, amino acid metabolic processes, transport mechanisms and secondary and lipid metabolic process. The complete lists of significantly enriched biological processes can be found in Additional File 4. By analyzing key factors in the fungal response, we detected β-(1,3)-D-glucan synthase within the ORM, the main target of caspofungin. In addition, we identified the polyubiquitin UbiD among the top five ORM nodes ranked by both node degree and betweenness centrality. There is only a slight multi-/single-seed-difference observable for the UbiD node degree (single-seed: 111, multi-seed: 117) and betweenness centrality (single-seed: 0.396, multi-seed: 0.359). Filtering for transcription factors led to the same results for both ORM’s, including the CBF/NF-Y family transcription factor.

In conclusion, the multi-seed MD approach allows for effectively integrating multilevel omics data. It contains the regulatory modules received by the single-seed approach and provides even higher numbers of regulatory module components. The ORM generated by the multi-seed approach confirms the already observed key players and significantly associated processes. Altogether, the multi-seed MD can be considered as an extension of the single-seed MD.

[1] Vlaic S, Conrad T, Tokarski-Schnelle C, Gustafsson M, Dahmen U, Guthke R, et al. ModuleDiscoverer: Identification of regulatory modules in protein-protein interaction networks. Sci Rep. 2018;8.

[2] Barrenäs F, Chavali S, Alves AC, Coin L, Jarvelin MR, Jörnsten R, et al. Highly interconnected genes in disease-specific networks are enriched for disease-associated polymorphisms. Genome Biol. 2012 Jun 15; 13(6):R46. doi: 10.1186/gb-2012-13-6-r46.
2 Module-detecting approach KeyPathwayMiner

Background
The regulatory module-detecting KeyPathwayMiner (KPM) [4] approach was shown to be efficient for both single-level omics data analysis and the integration of multilevel omics data. It detects maximal connected sub-networks by combining differentially expressed genes (DEGs), differentially synthesized proteins (DSyPs) and differentially secreted proteins (DSePs) with non-DEG/DSyP/DSeP exception nodes acting as ‘bridges’. KPM does not make assumptions about the protein-protein interaction network’s (PPIN’s) underlying community structures.

Methods
All analyses performed for the KPM-application are based on methods described in the ‘Methods’ part of the main manuscript. KPM was applied as described in section ‘Application of module-detecting approaches’. Analyses regarding the overlap of molecular levels and time points were described in section ‘Comparison of the simple approach and a module-detecting approach’. Details on the GO-term enrichment analysis for the KPM-based ORM were shown in ‘Enrichment analysis (functional annotation of biological processes)’.

Results and Discussion
The following analyses are based on the KPM regulatory modules as presented in Table 5 in the main manuscript. Supplementary Figure 1 shows the analysis of the molecular level overlap resulting in highest values for proteome and secretome (9.5 %). We expected this result as proteome and secretome are immediately consecutive levels and are both measured by LC-MS/MS. The maximal overlap of transcriptome, proteome and secretome is 0.4 %. For estimating the best transcriptome-proteome time point match (Supplementary Figure 2), two approaches are tested: (A) comparison of module components, and (B) correlation of the module components’ regulation. Comparing only the module components (A), the results show a highest overlap of transcriptome at 1 h and proteome at 4 h (4.3 %). The comparison with the proteome at 8 h results in the best match for the transcriptome at 8 h (6.8 %). Taking into account the module components’ regulation (B),
the lowest distance can be observed for transcriptome at 1 h and proteome at 4 h. As this is in
agreement with (A) regarding the proteome at 4 h, we could assume a time delay of 3 h in the
fungal sub-responses. The much lower distance values regarding all transcriptome time points and
the proteome at 4 h (dark green) compared to those with the proteome at 8 h (light green and
yellow) point to a stronger involvement of the proteomic sub-response at 4 h than at 8 h. In contrast,
the results regarding (A) have shown higher overlap values regarding proteome at 8 h compared to
4 h. Consequently, with the KPM approach it is hard to see a clear tendency regarding the best
transcriptome-proteome time point match.

Based on a GO-term enrichment analysis regarding biological processes, we found that the KPM-
generated ORM is significantly associated with biological processes which are also enriched for the
MD-based ORM. Such processes are, for instance, (1→3)-alpha-glucan biosynthetic process,
carbohydrate catabolic process, alpha-amino acid catabolic process, lipid and secondary metabolic
processes or oxidation-reduction processes. In Supplementary Figure 3, we compared these
exemplarily selected processes regarding their MD- and KPM-based -log10 p-values and observed
highly similar values for both approaches. Complete lists of significantly enriched biological
processes as well as all components of the KPM-based ORM can be found in Additional File 5.

[4] Alcaraz N, Pauling J, Batra R, Barbosa E, Junge A, Christensen AG, Azevedo V, Ditzel HJ,
Baumbach J. KeyPathwayMiner 4.0: condition-specific pathway analysis by combining
multiple omics studies and networks with Cytoscape. BMC Syst Biol. 2014 Aug 19;8:99.
doi: 10.1186/s12918-014-0099-x.
**Supplementary Figure 1** | Overlap of molecular levels based on KeyPathwayMiner-received modules.

**Supplementary Figure 2** | Estimation of the best transcriptome-proteome time point overlap based on (A) KeyPathwayMiner-received module components and (B) their regulation.
Supplementary Figure 3 | Comparison of ModuleDiscoverer- and KeyPathwayMiner-generated overall regulatory modules regarding exemplarily selected significantly enriched biological processes. Higher values equal lower p-values.
**Supplementary Table 1** | Comparison of regulatory modules received by the single-seed (SS) and multi-seed (MS) ModuleDiscoverer approach. The overlap of module components is defined as fraction of the intersection of the respective datasets from the single-seed datasets.

| Underlying experimental dataset | Number of components of SS-based modules | Number of components of MS-based modules | Overlap of module components (SS-based modules in % of the set of MS-based modules) |
|--------------------------------|------------------------------------------|------------------------------------------|----------------------------------------------------------------------------------|
| Transcriptome 0.5h            | 511                                      | 716                                      | 511 (100 %)                                                                      |
| Transcriptome 1h              | 256                                      | 345                                      | 256 (100 %)                                                                      |
| Transcriptome 4h              | 313                                      | 413                                      | 313 (100 %)                                                                      |
| Transcriptome 8h              | 256                                      | 430                                      | 256 (100 %)                                                                      |
| Proteome 4h                   | 147                                      | 227                                      | 147 (100 %)                                                                      |
| Proteome 8h                   | 124                                      | 213                                      | 124 (100 %)                                                                      |
| Secretome 8h                  | 293                                      | 321                                      | 293 (100 %)                                                                      |
| Overall regulatory module     | 894                                      | 1119                                     | 894 (100 %)                                                                      |
| CADRE-IDs | AspGD-IDs | UniProt-IDs | Protein names | Sub-module | Cluster |
|-----------|-----------|-------------|---------------|------------|---------|
| CADAFUBP00007020 | AFUB_072030 | B0Y5B4 | Protostadienol synthase A (EC 5.4.99.32) | 1 | 1 |
| CADAFUBP00006723 | AFUB_069030 | B0Y4G7 | Terpene cyclase/mutase family member (EC 5.4.99.-) | 1 | 1 |
| CADAFUBP00005148 | AFUB_052590 | B0Y314 | Terpene cyclase/mutase family member (EC 5.4.99.-) | 1 | 1 |
| CADAFUBP00006971 | AFUB_071550 | B0Y565 | Terpene cyclase/mutase family member (EC 5.4.99.-) | 1 | 1 |
| CADAFUBP00008534 | AFUB_087800 | B0YBT9 | Farnesyl-diphosphate farnesyltransferase, putative | 1 | 1 |
| CADAFUBP00008440 | AFUB_086820 | B0YBJ5 | Terpene cyclase/mutase family member (EC 5.4.99.-) | 1 | 1 |
| CADAFUBP00006672 | AFUB_068520 | B0Y6Y0 | 3-ketosteroid reductase | 1 | 1 |
| CADAFUBP00003006 | AFUB_030680 | B0XU84 | C-3 sterol dehydrogenase/C-4 decarboxylase | 1 | 1 |
| CADAFUBP00009428 | AFUB_004350 | B0XNB3 | Cytochrome P450 sterol C-22 desaturase, putative | 1 | 1 |
| CADAFUBP00008412 | AFUB_086340 | B0Y6Y0 | O-methyltransferase, putative | 1 | 1 |
| CADAFUBP00000428 | AFUB_004350 | B0XNB3 | Cytochrome P450 sterol C-22 desaturase, putative | 1 | 1 |
| CADAFUBP00000516 | AFUB_005170 | B0Y2E5 | O-methyltransferase, putative | 1 | 1 |
| CADAFUBP00000320 | AFUB_003120 | B0XR06 | Leucine carboxyl methyltransferase superfamily | 1 | 1 |
| CADAFUBP00000980 | AFUB_009930 | B0YEY5 | O-methyltransferase, putative | 1 | 1 |
| CADAFUBP00000701 | AFUB_007010 | B0XPR6 | Cytochrome P450, putative | 1 | 1 |
| CADAFUBP00005644 | AFUB_057690 | B0Y0L0 | 3-demethylubiquinone-9 3-methyltransferase, putative | 1 | 1 |
| CADAFUBP00005641 | AFUB_055170 | B0Y3R7 | UbE/COQ5 methyltransferase, putative | 1 | 1 |
| CADAFUBP00004613 | AFUB_047060 | B0XWR6 | Homocysteine S-methyltransferase, putative | 1 | 1 |
| CADAFUBP00005423 | AFUB_046110 | B0Y6Y0 | Aromatic-L-amino-acid decarboxylase | 1 | 1 |
| CADAFUBP00000518 | AFUB_005170 | B0Y2E5 | O-methyltransferase, putative | 1 | 1 |
| CADAFUBP00000320 | AFUB_003120 | B0XR06 | Leucine carboxyl methyltransferase superfamily | 1 | 1 |
| CADAFUBP00000980 | AFUB_009930 | B0YEY5 | O-methyltransferase, putative | 1 | 1 |
| CADAFUBP00000701 | AFUB_007010 | B0XPR6 | Cytochrome P450, putative | 1 | 1 |
| CADAFUBP00005644 | AFUB_057690 | B0Y0L0 | 3-demethylubiquinone-9 3-methyltransferase, putative | 1 | 1 |

**Supplementary Table 2 | All proteins of the ModuleDiscoverer-generated overall regulatory module and their sub-module and cluster membership (see Figure 5)**
| Accession | CAUF | Description | Function | Notes |
|-----------|------|-------------|----------|-------|
| AFUB_099220 | B0YEH7 | Cytochrome P450 alkane hydroxylase, putative | Fragment | 1 1 |
| AFUB_098170 | B0YET3 | C-4 methyl sterol oxidase (Erg25), putative |  | 1 1 |
| AFUB_033070 | BOXV5 | C-3 sterol dehydrogenase/C-4 decarboxylase family protein |  | 1 1 |
| AFUB_027300 | B0XSI4 | Ergosterol biosynthesis protein Erg28, putative |  | 1 1 |
| AFUB_017380 | B0XSS0 | Sterol delta 5,6-desaturase, putative |  | 1 1 |
| AFUB_003560 | B0XMW7 | C-14 sterol reductase |  | 1 1 |
| AFUB_075810 | B0Y820 | Cytochrome P450 monoxygenase, putative |  | 1 1 |
| AFUB_062540 | B0Y0J1 | Cytochrome P450 oxygenase, putative |  | 1 1 |
| AFUB_033110 | B0XV9 | 2-amino-3-carboxymuconate-6-semialdehyde decarboxylase, putative |  | 2 2 |
| AFUB_002090 | B0XSS0 | Sterol delta 5,6-desaturase ERG3 |  | 1 1 |
| AFUB_046390 | B0Y2E3 | Sporulation-specific N-formyltyrosine oxidase Dit2, putative |  | 1 1 |
| AFUB_093140 | B0Y7A7 | 14-alpha sterol demethylase Cyp51B |  | 1 1 |
| AFUB_033120 | B0Y5N0 | 14-alpha sterol demethylase Cyp51A |  | 1 1 |
| AFUB_044030 | B0XZD5 | Cytochrome P450 monoxygenase, putative |  | 1 1 |
| AFUB_039100 | B0XXS0 | Serine/threonine protein kinase, putative |  | 1 2 |
| AFUB_006780 | B0XPK3 | cAMP-dependent protein kinase-like, putative |  | 1 2 |
| AFUB_033110 | B0XV9 | 2-amino-3-carboxymuconate-6-semialdehyde decarboxylase, putative |  | 2 2 |
| AFUB_056780 | B0V476 | Superoxide dismutase [Cu-Zn] (EC 1.15.1.1) |  | 1 2 |
| AFUB_075210 | B0Y7W1 | Protein kinase, putative |  | 2 2 |
| AFUB_026400 | B0X95 | Serine/threonine protein kinase (YPK1), putative |  | 1 2 |
| AFUB_082850 | B0Y9Z | 3-hydroxyanthranilate, 3,4-dioxygenase 1 (EC 1.13.11.6) |  | 1 2 |
| AFUB_066950 | B0Y6H | 3-hydroxyanthranilate, 3,4-dioxygenase 2 (EC 1.13.11.6) |  | 1 2 |
| AFUB_033120 | B0XVP0 | 3-hydroxyanthranilate, 3,4-dioxygenase 3 (EC 1.13.11.6) |  | 1 2 |
| AFUB_026170 | B0XS72 | 3-hydroxyanthranilate, 3,4-dioxygenase 4 (EC 1.13.11.6) |  | 1 2 |
| AFUB_073150 | B0Y7A7 | Kynureninase 1 (EC 3.7.1.3) |  | 1 2 |
| AFUB_068610 | B0Y69 | Kynureninase 2 (EC 3.7.1.3) |  | 1 2 |
| AFUB_014080 | B0XMT3 | Superoxide dismutase (EC 1.15.1.1) |  | 1 2 |
| AFUB_094400 | B0YD61 | Superoxide dismutase (EC 1.15.1.1) |  | 1 2 |
| AFUB_046060 | B0Y0G | Catalase (EC 1.11.1.6) |  | 1 2 |
| AFUB_033720 | B0XWX | Catalase (EC 1.11.1.6) |  | 1 2 |
| AFUB_001280 | B0XSRO | Catalase, putative |  | 1 2 |
| AFUB_078570 | B0Y8U | Actin cytoskeleton assembly control protein pan1 |  | 1 3 |
| AFUB_042910 | B0XZ25 | Cytochrome P450 monoxygenase, putative |  | 1 3 |
| AFUB_021180 | B0XUT3 | Cytochrome P450 monooxygenase, putative |  | 1 3 |
| AFUB_089400 | B0Y9C9 | Cytochrome P450 monooxygenase, putative |  | 1 3 |
| AFUB_082970 | B0YA11 | Cytochrome P450 monooxygenase, putative |  | 1 3 |
| AFUB_064800 | B0Y5W3 | Cytochrome P450 monooxygenase, putative |  | 1 3 |
| AFUB_012500 | B0X88 | Cytochrome P450 monooxygenase, putative |  | 1 3 |
| Accession          | Description                                                                 | Gene Symbol | Putative Function                                                                 |
|--------------------|------------------------------------------------------------------------------|-------------|-----------------------------------------------------------------------------------|
| CADAUFUB00006340   | endonuclease/exonuclease/phosphatase family protein                          | B0YSZ8      | Phosphoinositide phosphatase (Sac1), putative                                      |
| CADAUFUB00006933   | Hsp70 family protein                                                         | B0YS27      | Hsp70 chaperone Hsp88                                                             |
| CADAUFUB00001187   | 1-phosphatidylinositol-3-phosphate 5-kinase (Fab1), putative                 | B0XRX3      |                                                                                   |
| CADAUFUB00007149   | SacI domain protein                                                          | B0Y7D4      |                                                                                   |
| CADAUFUB00001512   | Vacuole-associated enzyme activator complex component (Vac14), putative      | B0XNK0      |                                                                                   |
| CADAUFUB00001850   | FMN dependent dehydrogenase, putative (EC 1.13.12-)                          | B0XM08      |                                                                                   |
| CADAUFUB00007937   | Mitochondrial cytochrome b2, putative                                        | B0Y9L8      |                                                                                   |
| CADAUFUB00001243   | Geranylgeranyl diphosphate synthase                                          | B0XRA2      |                                                                                   |
| CADAUFUB00009550   | Protein tyrosine phosphatase (Pyp1), putative                                | B0YE85      |                                                                                   |
| CADAUFUB00004231   | Protein serine/threonine kinase (Ran1), putative                             | B0XZ47      |                                                                                   |
| CADAUFUB00007386   | Mitochondrial processing peptidase beta subunit, putative                    | B0Y821      |                                                                                   |
| CADAUFUB00004989   | Telomerase reverse transcriptase, putative                                    | B0Y2C6      |                                                                                   |
| CADAUFUB00004738   | Short chain alpha-hydroxy acid oxidase, putative (EC 1.3.1.15)               | B0XH6       |                                                                                   |
| CADAUFUB00005003   | MAP kinase kinase (Mkk2), putative                                           | B0YE9       |                                                                                   |
| CADAUFUB00009550   | Protein tyrosine phosphatase (Pyp1), putative                                | B0YE85      |                                                                                   |
| CADAUFUB00004211   | MAP kinase kinase 7                                                          | B0XZ47      |                                                                                   |
| CADAUFUB00007386   | Mitochondrial processing peptidase beta subunit, putative                    | B0Y821      |                                                                                   |
| CADAUFUB00001221   | Farnesyl-pyrophosphate synthetase                                            | B0Y2C6      |                                                                                   |
| CADAUFUB00007653   | Telomerase reverse transcriptase, putative                                    | B0XT8      |                                                                                   |
| CADAUFUB00008762   | Telomerase reverse transcriptase, putative                                    | B0YCG7      |                                                                                   |
| CADAUFUB00005826   | Protein kinase C (EC 2.7.1.13)                                               | B0Y142      |                                                                                   |
| CADAUFUB00002548   | TOR pathway phosphatidylinositol 3-kinase TorA, putative                     | B0XS63      |                                                                                   |
| CADAUFUB00005134   | Protein kinase, putative                                                     | B0Y300      |                                                                                   |
| CADAUFUB00001347   | Mitochondrial processing peptidase beta subunit, putative                    | B0XMQ0      |                                                                                   |
| CADAUFUB00003998   | Pyruvate dehydrogenase complex component Pdx1, putative                      | B0XYG4      |                                                                                   |
| CADAUFUB00001483   | Succinate dehydrogenase subunit CybS, putative                               | B0XNH1      |                                                                                   |
| CADAUFUB00001519   | Glutathione reductase                                                        | B0XNK7      |                                                                                   |
| CADAUFUB00004270   | Cystathionine gamma-synthase, putative                                        | B0XZ86      |                                                                                   |
| CADAUFUB00004629   | Cystathionine beta-lyase                                                     | B0XX00      |                                                                                   |
| CADAUFUB00002565   | Prephenate dehydrogenase                                                     | B0SX80      |                                                                                   |
| CADAUFUB00005182   | NADH-ubiquinone oxidoreductase, subunit G, putative                          | B0Y348      |                                                                                   |
| CADAUFUB00005162   | Ubiquinol-cytochrome C reductase complex core protein 2, putative            | B0Y328      |                                                                                   |
| CADAUFUB00002199   | NADH-ubiquinone oxidoreductase 18 kDa subunit, putative                      | B0XVX0      |                                                                                   |
| CADAUFUB00000240   | Cytochrome C1/Cyt1, putative                                                 | B0XRX1      |                                                                                   |
| CADAUFUB00005212   | Chorismate mutase/prephenyldehydratase                                       | B0Y378      |                                                                                   |
| CADAUFUB00007286   | 2-oxoisovalerate dehydrogenase complex alpha subunit, putative               | B0Y7S1      |                                                                                   |
| CADAUFUB00008548   | Thiosulfate sulfurtransferase, putative                                       | B0YBV3      |                                                                                   |
| CADAUFUB00004640   | Tyrosinase, putative                                                         | B0XX11      |                                                                                   |
| CADAUFUB00001648   | Tyrosinase                                                                   | B0XZ86      |                                                                                   |
| CADAUFUB00004100   | Phosphopantothenate-cysteine ligase, putative                                | B0XRY6      |                                                                                   |
| CADAUFUB00008255   | Thiosulfate sulfurtransferase, putative                                       | B0YA06      |                                                                                   |
| CADAUFUB00009626   | Cystathionine beta-lyase MetG                                                  | B0YEG1      |                                                                                   |
| Accession | ID       | Name                                                                 | Description                                                                 | Location |
|-----------|----------|----------------------------------------------------------------------|-------------------------------------------------------------------------------|----------|
| CADAFUBP000008571 | AFUB_088170 | B0YBX6 Cystathionine gamma-synthase | 1 6                                                                         |          |
| CADAFUBP000008098 | AFUB_083200 | B0YA29 Cystathionine gamma-lyase | 1 6                                                                         |          |
| CADAFUBP000006068 | AFUB_062130 | B0Y2K4 Cysteine dioxygenase, putative | 1 6                                                                         |          |
| CADAFUBP000004273 | AFUB_043550 | B0XZ89 Glutamate carboxypeptidase, putative | 1 6                                                                         |          |
| CADAFUBP0000581 | AFUB_005910 | B0XP48 Cysteine dioxygenase | 1 6                                                                         |          |
| CADAFUBP00007180 | AFUB_073730 | B0Y7G5 Alanine aminotransferase, putative | 1 6                                                                         |          |
| CADAFUBP00005203 | AFUB_053140 | B0Y369 Aspartokinase (EC 2.7.2.4) | 1 6                                                                         |          |
| CADAFUBP00004387 | AFUB_044720 | B0XZP0 4-hydroxyphenylpyruvate dioxygenase, putative | 1 6                                                                         |          |
| CADAFUBP00003365 | AFUB_034410 | B0XZU5 4-hydroxyphenylpyruvate dioxygenase, putative | 1 6                                                                         |          |
| CADAFUBP000001366 | AFUB_013630 | B0XMN9 Histidinol-phosphate aminotransferase | 1 6                                                                         |          |
| CADAFUBP00001080 | AFUB_011000 | B0XQ94 5-methyltetrahydropteroyltriglutamate--homocysteine S-methyltransferase | 1 6                                                                         |          |
| CADAFUBP00004962 | AFUB_050710 | B0XZU5 Cysteine synthase B, putative | 1 6                                                                         |          |
| CADAFUBP00006575 | AFUB_067560 | B0YN3 Homocitrate synthase | 1 6                                                                         |          |
| CADAFUBP0000385 | AFUB_003920 | B0XN3 ATP synthase subunit gamma | 1 6                                                                         |          |
| CADAFUBP00007250 | AFUB_074430 | B0Y7N5 Glycerol kinase, putative | 1 6                                                                         |          |
| CADAFUBP00006676 | AFUB_068560 | B0Y6Y4 Glycerol kinase, putative | 1 6                                                                         |          |
| CADAFUBP00002543 | AFUB_026020 | B0X5S8 Glycerol dehydrogenase, putative | 1 6                                                                         |          |
| CADAFUBP0000980 | AFUB_009990 | B0XQH6 Glycerol-3-phosphate phosphatase (GppA), putative | 1 6                                                                         |          |
| CADAFUBP00005166 | AFUB_052770 | B0Y332 Homocysteine synthase CysD | 1 6                                                                         |          |
| CADAFUBP00003634 | AFUB_037120 | B0XX79 Methionine synthase, vitamin-B12 independent, putative | 1 6                                                                         |          |
| CADAFUBP0000936 | AFUB_009540 | B0XX79 Adenosylhomocysteine (EC 3.3.1.1) | 1 6                                                                         |          |
| CADAFUBP00001277 | AFUB_012980 | B0XRK3 Spermidine synthase | 1 6                                                                         |          |
| CADAFUBP00005528 | AFUB_056460 | B0Y444 Isovaleryl-CoA dehydrogenase IvdA, putative | 1 6                                                                         |          |
| CADAFUBP00007945 | AFUB_076910 | B0Y8D0 Acyl-CoA dehydrogenase family protein | 1 6                                                                         |          |
| CADAFUBP00004558 | AFUB_046490 | B0XW1 Acyl-CoA dehydrogenase, putative | 1 6                                                                         |          |
| CADAFUBP00009789 | AFUB_10820 | B0YEX4 Succinyl-CoA synthetase beta subunit, putative | 1 6                                                                         |          |
| CADAFUBP00005256 | AFUB_053690 | B0Y3C2 Succinyl-CoA synthetase alpha subunit, putative | 1 6                                                                         |          |
| CADAFUBP000006100 | AFUB_062460 | B0Y2N6 Phosphoenolpyruvate synthase, synthase | 1 6                                                                         |          |
| CADAFUBP00007568 | AFUB_077640 | B0Y8K3 Homocysteine synthase CysD | 1 6                                                                         |          |
| CADAFUBP00008222 | AFUB_090740 | B0YCM7 Fumarylacetoacetate hydrolase family protein | 1 6                                                                         |          |
| CADAFUBP00007489 | AFUB_076850 | B0Y8C4 Homogentisate 1,2-dioxygenase, putative | 1 6                                                                         |          |
| CADAFUBP00002079 | AFUB_021300 | B0XV14 Fumarylacetoacetase hydrolase FahA | 1 6                                                                         |          |
| CADAFUBP00002078 | AFUB_021290 | B0XV13 Homogentisate 1,2-dioxygenase (HmgA), putative | 1 6                                                                         |          |
| CADAFUBP00008269 | AFUB_084930 | B0YAK0 Catalase-peroxidase (CP) (EC 1.11.1.21) (Peroxidase/catalase) | 1 6                                                                         |          |
| CADAFUBP00007981 | AFUB_081980 | B0Y9R2 Acetyl-coA hydrolase Ach1, putative | 1 6                                                                         |          |
| CADAFUBP00003760 | AFUB_038380 | B0XSS6 Probable acetate kinase (EC 2.7.2.1) (Acetokinase) | 1 6                                                                         |          |
| CADAFUBP00002867 | AFUB_029270 | B0XTF9 Thiamine pyrophosphate enzyme, putative | 1 6                                                                         |          |
| CADAFUBP00004139 | AFUB_042220 | B0XY5 Aspartate-semialdehyde dehydrogenase | 1 6                                                                         |          |
| CADAFUBP00006239 | AFUB_064140 | B0Y5P7 L-lactate dehydrogenase | 1 6                                                                         |          |
| CADAFUBP00005733 | AFUB_058610 | B0Y0U9 Pantoate--beta-alanine ligase | 1 6                                                                         |          |
| CADAFUBP00007571 | AFUB_077670 | B0Y8K6 Thiamine pyrophosphate enzyme, putative | 1 6                                                                         |          |
| CADAFUBP00009633 | AFUB_099130 | B0YE8G8 Uncharacterized protein | 1 6                                                                         |          |
| CADAFUBP00008612 | AFUB_088580 | B0YC17 Indoleamine 2,3-dioxygenase family protein | 1 6                                                                         |          |
| CADAFUBP00009450 | AFUB_097230 | B0YDY5 Aminotransferase, putative | 1 6                                                                         |          |
| CADAFUBP00006590 | AFUB_067710 | B0Y6P8 4-hydroxyphenylpyruvate dioxygenase | 1 6                                                                         |          |
| CADAFUBP00002076 | AFUB_021270 | B0XV11 4-hydroxyphenylpyruvate dioxygenase | 1 6                                                                         |          |
| CADAFUBP00005265 | AFUB_053780 | B0YD1 Alcohol dehydrogenase, putative | 1 6                                                                         |          |
| CADAFUBP00001767 | AFUB_018120 | B0XT59 S-(hydroxymethyl)glutathione dehydrogenase (EC 1.1.1.284) | 1 6                                                                         |          |
| Accession       | Protein Name                                      | Description                                                                 | Location |
|-----------------|---------------------------------------------------|------------------------------------------------------------------------------|----------|
| CADAFUBP00004736| AFUB_048340 B0XXH4                                | Amine oxidase (EC 1.4.3.-)                                                   | 1 6      |
| CADAFUBP00008512| AFUB_087590 B0YBR7                                | Alcohol dehydrogenase, putative                                              | 1 6      |
| CADAFUBP00008013| AFUB_082290 B0Y9U4                                | 2-hydroxyphytanoyl-CoA lyase, putative                                       | 1 6      |
| CADAFUBP00003134| AFUB_031970 B0XUZ5                                | Dihydroxy acid dehydratase, putative                                         | 1 6      |
| CADAFUBP00000756| AFUB_007680 B0XPV2                                | Dihydroxy-acid dehydratase, putative                                         | 1 6      |
| CADAFUBP00000389| AFUB_003960 B0XN07                                | Mitochondrial dihydroxy acid dehydratase, putative                          | 1 6      |
| CADAFUBP00006349| AFUB_065240 B0Y607                                | Threonine dehydratase (EC 4.3.1.19) (Threonine deaminase)                   | 1 6      |
| CADAFUBP00008512| AFUB_087590 B0YBR7                                | Alcohol dehydrogenase, putative                                              | 1 6      |
| CADAFUBP00008205| AFUB_084300 B0YAD6                                | Aldehyde dehydrogenase ALDH                                                   | 1 6      |
| CADAFUBP00006394| AFUB_065690 B0Y652                                | Aldehyde dehydrogenase Ald3, putative                                       | 1 6      |
| CADAFUBP00005679| AFUB_056770 B0XX50                                | Aldehyde dehydratase, zinc-binding                                           | 1 6      |
| CADAFUBP00003388| AFUB_034640 B0XZW8                                | Amine oxidase (EC 1.4.3.-)                                                   | 1 6      |
| CADAFUBP00001272| AFUB_012930 B0XRJ8                                | Amine oxidase (EC 1.4.3.-)                                                   | 1 6      |
| CADAFUBP00009400| AFUB_096720 B0YD15                                | Pyruvate decarboxylase, putative                                             | 1 6      |
| CADAFUBP00008205| AFUB_084300 B0YAD6                                | Aldehyde dehydrogenase ALDH                                                   | 1 6      |
| CADAFUBP00006394| AFUB_065690 B0Y652                                | Aldehyde dehydrogenase Ald3, putative                                       | 1 6      |
| CADAFUBP00006679| AFUB_069770 B0Y4P1                                | Methylmalonate-semialdehyde dehydrogenase, putative                         | 1 6      |
| CADAFUBP00005661| AFUB_057860 B0YM07                                | Oxidoreductase, acting on the CH-OH group of donors, NAD or NADP as acceptor | 1 6      |
| CADAFUBP00004867| AFUB_049750 B0YL18                                | Oxidoreductase, putative                                                     | 1 6      |
| CADAFUBP00001736| AFUB_017800 B0XT28                                | Aldehyde dehydrogenase, putative                                             | 1 6      |
| CADAFUBP00002389| AFUB_024460 B0XWD8                                | 50S ribosomal protein L14                                                    | 1 6      |
| CADAFUBP00002292| AFUB_029830 B0XXT1                                | Mitochondrial dihydroxy acid dehydratase, putative                          | 1 6      |
| CADAFUBP00002827| AFUB_028880 B0XTB9                                | Tryptophan synthase (EC 4.2.1.20)                                            | 1 6      |
| CADAFUBP0000120| AFUB_001220 B0XNM8                                | Tryptophan synthase                                                          | 1 6      |
| CADAFUBP00008004| AFUB_082200 B0Y9T5                                | Methylenetetrahydrofolate dehydrogenase                                      | 1 6      |
| CADAFUBP00001427| AFUB_014560 B0XN47                                | 2-isopropylmalate synthase                                                   | 1 6      |
| CADAFUBP00004308| AFUB_043920 B0XZC4                                | Coenzyme A transferase, putative                                             | 1 6      |
| CADAFUBP00005942| AFUB_060830 B0YIU0                                | Protein BCP1                                                                | 1 6      |
| CADAFUBP00001998| AFUB_020450 B0XUE5                                | Alkaline serine protease                                                     | 1 6      |
| CADAFUBP00006720| AFUB_069900 B0YAG4                                | 2-oxo acid dehydrogenases acetyltransferase, putative                       | 1 6      |
| CADAFUBP00002529| AFUB_025880 B0XS44                                | Carbamoyl-phosphate synthase, large subunit                                 | 1 6      |
| CADAFUBP00008385| AFUB_086070 B0YAW6                                | Acetate-CoA ligase, putative                                                 | 1 6      |
| Accession  | Start Position | Description                                                                 | EC Numbers                           |
|------------|----------------|------------------------------------------------------------------------------|--------------------------------------|
| CADAFUBP00002325  | AFUB_023820    | Acyl-CoA synthetase, putative                                              | 1 6                                  |
| CADAFUBP00005695  | AFUB_058230    | Ubiquinol-cytochrome c reductase iron-sulfur subunit                      | 1 6                                  |
| CADAFUBP00004821  | AFUB_043630    | Dihydroliopamide succinyltransferase, putative                            | 1 6                                  |
| CADAFUBP00005950  | AFUB_067010    | Snf1 protein kinase complex subunit Snf4, putative                        | 1 6                                  |
| CADAFUBP00008812  | AFUB_090640    | Carbamoyl-phosphate synthase, small subunit                               | 1 6                                  |
| CADAFUBP00000015  | AFUB_000150    | 4-aminobutyrate aminotransferase, putative                                | 1 6                                  |
| CADAFUBP00005695  | AFUB_058230    | Ubiquinol-cytochrome c reductase iron-sulfur subunit                      | 1 6                                  |
| CADAFUBP00004821  | AFUB_043630    | Dihydroliopamide succinyltransferase, putative                            | 1 6                                  |
| CADAFUBP00005695  | AFUB_058230    | Ubiquinol-cytochrome c reductase iron-sulfur subunit                      | 1 6                                  |
| CADAFUBP00004821  | AFUB_043630    | Dihydroliopamide succinyltransferase, putative                            | 1 6                                  |
| CADAFUBP00005695  | AFUB_058230    | Ubiquinol-cytochrome c reductase iron-sulfur subunit                      | 1 6                                  |
| CADAFUBP00004821  | AFUB_043630    | Dihydroliopamide succinyltransferase, putative                            | 1 6                                  |
| CADAFUBP00005695  | AFUB_058230    | Ubiquinol-cytochrome c reductase iron-sulfur subunit                      | 1 6                                  |
| CADAFUBP00004821  | AFUB_043630    | Dihydroliopamide succinyltransferase, putative                            | 1 6                                  |
| CADAFUBP00005695  | AFUB_058230    | Ubiquinol-cytochrome c reductase iron-sulfur subunit                      | 1 6                                  |
| CADAFUBP00004821  | AFUB_043630    | Dihydroliopamide succinyltransferase, putative                            | 1 6                                  |
| Accession | Gene ID | Name | Function | Gene Name |
|-----------|---------|------|----------|-----------|
| CADAFUBP00005524 | AFUB_056420 | B0Y440 | Homoaconitase, mitochondrial (EC 4.2.1.36) | Homoaconitase, mitochondrial (EC 4.2.1.36) |
| CADAFUBP00000707 | AFUB_007190 | B0XPQ3 | Aconitate hydratase, mitochondrial (Aconitase) (EC 4.2.1.-) | Aconitate hydratase, mitochondrial (Aconitase) (EC 4.2.1.-) |
| CADAFUBP0000127 | AFUB_001300 | B0XM85 | Nitrilase | Nitrilase |
| CADAFUBP00009651 | AFUB_099310 | B0YEI6 | Uncharacterized protein | Uncharacterized protein |
| CADAFUBP00000127 | AFUB_001300 | B0XM85 | Nitrilase | Nitrilase |
| CADAFUBP00009210 | AFUB_094760 | B0YD95 | Glutamine synthetase | Glutamine synthetase |
| CADAFUBP00009735 | AFUB_081480 | B0YL6 | Glutamate dehydrogenase (EC 4.1.1.15) | Glutamate dehydrogenase (EC 4.1.1.15) |
| CADAFUBP00006867 | AFUB_070500 | B0YW1 | Gamma-glutamyltransferase | Gamma-glutamyltransferase |
| CADAFUBP00006821 | AFUB_070010 | B0Y4R5 | Glutamine synthetase (EC 6.3.1.2) | Glutamine synthetase (EC 6.3.1.2) |
| CADAFUBP00003724 | AFUB_038020 | B0XXN4 | Aconitate hydratase, mitochondrial (Aconitase) (EC 4.2.1.-) | Aconitate hydratase, mitochondrial (Aconitase) (EC 4.2.1.-) |
| CADAFUBP00003455 | AFUB_035300 | B0Y0A3 | Glutamate dehydrogenase (EC 4.1.1.15) | Glutamate dehydrogenase (EC 4.1.1.15) |
| CADAFUBP00003419 | AFUB_034950 | B0Y067 | Gamma-cysteine synthetase regulatory subunit, putative | Gamma-cysteine synthetase regulatory subunit, putative |
| CADAFUBP00003043 | AFUB_031050 | B0XU19 | FluG family protein | FluG family protein |
| CADAFUBP00003038 | AFUB_030761 | B0XPV7 | Glutamate synthase Glt1, putative | Glutamate synthase Glt1, putative |
| CADAFUBP0000123 | AFUB_001260 | B0XM77 | Glutamate dehydrogenase (EC 4.1.1.15) | Glutamate dehydrogenase (EC 4.1.1.15) |
| CADAFUBP00009314 | AFUB_095850 | B0YDJ9 | Aspartate aminotransferase (EC 2.6.1.1) | Aspartate aminotransferase (EC 2.6.1.1) |
| CADAFUBP00007278 | AFUB_074710 | B0YR3 | Delta-1-pyrroline-5-carboxylate dehydrogenase PrnC | Delta-1-pyrroline-5-carboxylate dehydrogenase PrnC |
| CADAFUBP00006570 | AFUB_067510 | B0YM8 | Aspartate aminotransferase, putative | Aspartate aminotransferase, putative |
| CADAFUBP00006223 | AFUB_063970 | B0Y5N1 | Asparagine synthetase Asn2, putative | Asparagine synthetase Asn2, putative |
| CADAFUBP00006196 | AFUB_063700 | B0Y5K4 | Glutamate dehydrogenase | Glutamate dehydrogenase |
| CADAFUBP00005448 | AFUB_055650 | B0YW4 | Arginine biosynthesis bifunctional protein ArgJ, mitochondrial | Arginine biosynthesis bifunctional protein ArgJ, mitochondrial |
| CADAFUBP00002663 | AFUB_027240 | B0XSH8 | Amino-acid acetyltransferase, mitochondrial (EC 2.3.1.1) (Arginine-requiring protein 2) (Glutamate N-acetyltransferase) (N-acetylglutamate synthase) (AGS) (NAGS) | Amino-acid acetyltransferase, mitochondrial (EC 2.3.1.1) (Arginine-requiring protein 2) (Glutamate N-acetyltransferase) (N-acetylglutamate synthase) (AGS) (NAGS) |
| CADAFUBP00002493 | AFUB_025510 | B0XS08 | Aspartate transaminase, putative | Aspartate transaminase, putative |
| CADAFUBP00002305 | AFUB_023620 | B0XW54 | Glutamate 5-kinase, putative | Glutamate 5-kinase, putative |
| CADAFUBP00002251 | AFUB_023080 | B0XVW9 | NAD-specific glutamate dehydrogenase (EC 1.4.1.2) | NAD-specific glutamate dehydrogenase (EC 1.4.1.2) |
| CADAFUBP00002086 | AFUB_021370 | B0XV21 | Argininosuccinate synthetase | Argininosuccinate synthetase |
| CADAFUBP00002083 | AFUB_021340 | B0XV18 | Asparaginase, putative | Asparaginase, putative |
| CADAFUBP00001470 | AFUB_015000 | B0XNF8 | Adenylosuccinate synthetase (AMPsase) (AdSS) (EC 6.3.4.4) (IMP--aspartate ligase) | Adenylosuccinate synthetase (AMPsase) (AdSS) (EC 6.3.4.4) (IMP--aspartate ligase) |
| CADAFUBP00000445 | AFUB_004510 | B0XND0 | Aspartate aminotransferase, putative | Aspartate aminotransferase, putative |
| CADAFUBP00000310 | AFUB_003170 | B0XML5 | L-asparaginase | L-asparaginase |
| CADAFUBP00008584 | AFUB_088300 | B0YBY9 | 3-hydroxymethyl-3-methylglutaryl-Coenzyme A lyase | 3-hydroxymethyl-3-methylglutaryl-Coenzyme A lyase |
| CADAFUBP00007628 | AFUB_078260 | B0YR3 | Succinyl-CoA:3-ketoacid-coenzyme A transferase (EC 2.8.3.5) | Succinyl-CoA:3-ketoacid-coenzyme A transferase (EC 2.8.3.5) |
| CADAFUBP00002750 | AFUB_028110 | B0XSSX3 | Hydroxymethylglutaryl-CoA lyase | Hydroxymethylglutaryl-CoA lyase |
| CADAFUBP00004441 | AFUB_004480 | B0XNC6 | Succinyl-CoA:3-ketoacid-coenzyme A transferase (EC 2.8.3.5) | Succinyl-CoA:3-ketoacid-coenzyme A transferase (EC 2.8.3.5) |
| CADAFUBP00008876 | AFUB_091290 | B0YB22 | Acetyltransferase component of pyruvate dehydrogenase complex (EC 2.3.1.12) | Acetyltransferase component of pyruvate dehydrogenase complex (EC 2.3.1.12) |
| CADAFUBP00005670 | AFUB_057960 | B0YON6 | Succinate dehydrogenase [ubiquinone] iron-sulfur subunit, mitochondrial (EC 1.3.5.1) | Succinate dehydrogenase [ubiquinone] iron-sulfur subunit, mitochondrial (EC 1.3.5.1) |
| CADAFUBP00005650 | AFUB_057230 | B0V4C1 | Succinate dehydrogenase cytochrome b560 subunit | Succinate dehydrogenase cytochrome b560 subunit |
| CADAFUBP00004046 | AFUB_041300 | B0XYL2 | Succinate dehydrogenase [ubiquinone] flavoprotein subunit, mitochondrial (EC 1.3.5.1) | Succinate dehydrogenase [ubiquinone] flavoprotein subunit, mitochondrial (EC 1.3.5.1) |
| CADAFUBP00001871 | AFUB_019180 | B0XTV0 | Dihydrolipoyl dehydrogenase (EC 1.8.1.4) | Dihydrolipoyl dehydrogenase (EC 1.8.1.4) |
| CADAFUBP00001006 | AFUB_010250 | B0XQK2 | Succinyl-CoA synthetase, alpha subunit, putative | Succinyl-CoA synthetase, alpha subunit, putative |
| CADAFUBP00007537 | AFUB_077330 | B0Y8H2 | Bifunctional pyrimidine biosynthesis protein | Bifunctional pyrimidine biosynthesis protein |
| GenBank Accession | UniProt Accession | Description | EC Numbers | Notes |
|-------------------|-------------------|-------------|------------|-------|
| CADAFUBP00000693  | AFUB_007050       | CBS domain protein (PyrABCN), putative  |           | 1     |
| CADAFUBP00009204  | AFUB_094700       | 2-methylcitrate synthase, mitochondrial (Methylcitrate synthase) (EC 2.3.3.5) ((2S,3S)-2-methylcitrate synthase) (Citrate synthase 2) (EC 2.3.3.16)  |           | 1     |
| CADAFUBP00009043  | AFUB_093060       | Malate dehydrogenase, NAD-dependent  |           | 1     |
| CADAFUBP00008879  | AFUB_091320       | Malate dehydrogenase (EC 1.1.1.37)  |           | 1     |
| CADAFUBP00007175  | AFUB_073680       | Phosphoenolpyruvate carboxylase AcuF  |           | 1     |
| CADAFUBP00006306  | AFUB_064810       | Pyruvate carboxylase (EC 6.4.1.1)  |           | 1     |
| CADAFUBP00005164  | AFUB_052750       | Citrate synthase  |           | 1     |
| CADAFUBP00004048  | AFUB_041320       | Argininosuccinate lyase  |           | 1     |
| CADAFUBP00003035  | AFUB_030970       | Citrate synthase  |           | 1     |
| CADAFUBP00002705  | AFUB_027670       | Adenylsuccinate lyase (ASL) (EC 4.3.2.2) (Adenylsuccinate)  |           | 1     |
| CADAFUBP00006327  | AFUB_065020       | D-3-phosphoglycerate dehydrogenase  |           | 1     |
| CADAFUBP00005195  | AFUB_053060       | D-3-phosphoglycerate dehydrogenase (EC 1.1.1.95)  |           | 1     |
| CADAFUBP00002101  | AFUB_021520       | Uncharacterized protein  |           | 1     |
| CADAFUBP00006423  | AFUB_065980       | Possible apospory-associated protein c  |           | 1     |
| CADAFUBP00000174  | AFUB_001790       | Ribokinase (RK) (EC 2.7.1.15)  |           | 1     |
| CADAFUBP00000958  | AFUB_095710       | Phosphoglycerate mutase family protein  |           | 1     |
| CADAFUBP00009390  | AFUB_061150       | Triosephosphate isomerase (EC 5.3.1.1)  |           | 1     |
| CADAFUBP000002619 | AFUB_026790       | Phosphoglycerate mutase, 2,3-bisphosphoglycerate-independent Triosephosphate isomerase (EC 5.3.1.1)  |           | 1     |
| CADAFUBP000008952 | AFUB_092050       | Deoxyribose-phosphate aldolase  |           | 1     |
| CADAFUBP000004163 | AFUB_042460       | Deoxyribose-phosphate aldolase  |           | 1     |
| CADAFUBP000006423 | AFUB_065980       | Possible apospory-associated protein c  |           | 1     |
| CADAFUBP000004655 | AFUB_047490       | Alpha-1,3-glucan synthase, putative  |           | 1     |
| CADAFUBP000003657 | AFUB_074460       | Phosphoglycerate mutase family protein  |           | 1     |
| CADAFUBP000002642 | AFUB_027030       | Alpha-1,3-glucan synthase, putative  |           | 1     |
| CADAFUBP000001469 | AFUB_014990       | Alpha-1,3-glucan synthase, putative  |           | 1     |
| CADAFUBP000009713 | AFUB_089700       | Alpha,alpha-trehalose-phosphate synthase subunit, putative  |           | 1     |
| CADAFUBP000008697 | AFUB_089700       | Alpha,alpha-trehalose-phosphate synthase subunit, putative  |           | 1     |
| CADAFUBP000006056 | AFUB_062010       | Alpha,alpha-trehalose-phosphate synthase subunit, putative  |           | 1     |
| CADAFUBP000004253 | AFUB_043350       | Alpha,alpha-trehalose-phosphate synthase subunit, putative  |           | 1     |
| CADAFUBP000002058 | AFUB_021090       | Alpha,alpha-trehalose-phosphate synthase subunit, putative  |           | 1     |
| CADAFUBP000002057 | AFUB_021080       | Trehalose-6-phosphate synthase (EC 2.4.1.15) (UDP-glucose-glucosyltransferase)  |           | 1     |
| CADAFUBP00000174  | AFUB_001790       | Trehalose-6-phosphate synthase (EC 2.4.1.15) (UDP-glucose-glucosyltransferase)  |           | 1     |
| CADAFUBP000007593 | AFUB_077900       | Probable beta-glucosidase J (EC 3.2.1.21) (Beta-D-glucoside glucohydrolase J) (Cellobiase J) (Gentiobiose J)  |           | 1     |
| CADAFUBP000009206 | AFUB_094720       | Probable beta-glucosidase E (EC 3.2.1.21) (Beta-D-glucoside glucohydrolase E) (Cellobiase E) (Gentiobiose E)  |           | 1     |
| CADAFUBP000004723 | AFUB_048210       | Beta-glucosidase (EC 3.2.1.21)  |           | 1     |
| CADAFUBP000009853 | AFUB_101460       | ATP-dependent 6-phosphofructokinase (ATP-PFK) (Phosphofructokinase) (EC 2.7.1.11) (Phosphofructokinase)  |           | 1     |
| CADAFUBP000009799 | AFUB_100920       | Glycosyl hydrolase, putative  |           | 1     |
| CADAFUBP000001873 | AFUB_019200       | Phosphoglucomutase, putative  |           | 1     |
| CADAFUBP000007273 | AFUB_074660       | Probable beta-glucosidase F (EC 3.2.1.21) (Beta-D-glucoside glucohydrolase F) (Cellobiase F)  |           | 1     |
| Accession         | GenBank ID   | Description                                                   |
|-------------------|--------------|---------------------------------------------------------------|
| AFUB_072510       | B0Y744       | Phosphomannomutase (EC 5.4.2.8)                               |
| AFUB_065520       | B0Y635       | Mannose-6-phosphate isomerase, class I                        |
| AFUB_045220       | B0Y009       | Phosphoglucomutase, putative                                  |
| AFUB_012770       | B0XRB5       | Mannose-6-phosphate isomerase (EC 5.3.1.8)                    |
| AFUB_015740       | B0XNU9       | Beta-glucosidase, putative                                    |
| AFUB_016780       | B0XPB8       | Probable beta-glucosidase M (EC 3.2.1.21) (Beta-D-gluco-
|                  |              | glycomutase glycolohydrolase M) (Gentiobiase M)               |
| AFUB_054750       | B0YM3M       | Probable beta-glucosidase I (EC 3.2.1.21) (Beta-D-gluco-
|                  |              | glycomutase glycolohydrolase I) (Gentiobiase I)               |
| AFUB_014260       | B0XMV0       | Beta-glucosidase, putative                                    |
| AFUB_054640       | B0Y3L5       | Beta-glucosidase, putative                                    |
| AFUB_000170       | B0XMG5       | Beta-glucosidase, putative                                    |
| AFUB_077990       | B0Y8N7       | Glycosyl hydrolase family protein                             |
| AFUB_083490       | B0YA57       | Glucosamine-6-phosphate isomerase (EC 3.5.99.6) (Gentiobiase A) |
| AFUB_072700       | B0Y763       | Enolase/allergen Asp F                                       |
| AFUB_073410       | B0Y7D3       | Fructokinase (EC 2.7.1.40)                                    |
| AFUB_068340       | B0Y6W2       | Fructose-1,6-bisphosphatase                                   |
| AFUB_075140       | B0Y7V4       | Ubiquitin-like protein ATG12                                  |
| AFUB_020300       | B0XUD0       | Alpha-amylase AmyA                                            |
| AFUB_013990       | B0XMS4       | Exo-beta,1,3-glucanase Exg0                                   |
| AFUB_001500       | B0XLY8       | Exo-beta,1,3-glucanase, putative                              |
| AFUB_075220       | B0Y7W2       | Probable glucan,1,3-beta-glucosidase D (EC 3.2.1.58) (Gentiobiase A) |
| AFUB_060350       | B0Y1H5       | Dihydroxyacetone kinase (DakA), putative                     |
| AFUB_030860       | B0XUH0       | Ribulose-phosphate 3-epimerase                               |
| AFUB_072250       | B0Y718       | Glucosamine-fructose-6-phosphate aminotransferase             |
| AFUB_017490       | B0XST0       | Exo-beta,1,3-glucanase, putative                              |
| AFUB_021900       | B0XVD8       | Pyruvate dehydrogenase E1 component alpha subunit, putative  |
| AFUB_007340       | B0XPR8       | Pyruvate dehydrogenase E1 component subunit alpha (EC 1.2.4.1) |
| AFUB_004010       | B0XN12       | Probable glucan,1,3-beta-glucosidase A (EC 3.2.1.58) (Gentiobiase A) |
| AFUB_041600       | B0XYP2       | Exo-beta,1,3-glucanase, putative                              |
| AFUB_091940       | B0Y8B7       | Malate                                                        |
| AFUB_058160       | B0Y0Q4       | 1,4-alpha-glucan branching enzyme                             |
| AFUB_012400       | B0XR78       | Alpha-1,4 glucan phosphorylase (EC 2.4.1.1)                   |
| AFUB_084020       | B0XAB0       | Glyceraldehyde-3-phosphate dehydrogenase, putative            |
| AFUB_057870       | B0Y0M8       | Fructose-bisphosphate aldolase, putative                      |
| AFUB_056770       | B0Y475       | Transaldolase (EC 2.2.1.2)                                    |
| AFUB_050490       | B0Y207       | Glyceraldehyde-3-phosphate dehydrogenase (EC 1.2.1.12)       |
| AFUB_049500       | B0Y1J3       | Glyceraldehyde-3-phosphate dehydrogenase (EC 1.2.1.12)       |
| AFUB_037500       | B0XBB7       | Fructose-bisphosphate aldolase, class II                      |
| AFUB_025630       | B0XS20       | Glucose-6-phosphate isomerase (EC 5.3.1.9)                    |
| AFUB_045340       | B0Y021       | Dihydroxyacetone synthase, putative                           |
| AFUB_040620       | B0XYE4       | Glucose-6-phosphate 1-dehydrogenase (EC 1.1.1.49)             |
| AFUB_012990       | B0XKR4       | Transketolase (EC 2.2.1.1)                                    |
| AFUB_003360       | B0XMN4       | 6-phosphogluconolactonase, putative                           |
| AFUB_067250       | B0Y6K2       | Alpha-amylase (EC 3.2.1.1)                                    |
| AFUB_029100       | B0XTE2       | Alpha-amylase, putative                                       |
| AFUB_017790       | B0XT27       | Alpha-amylase, putative                                       |
| AFUB_014700       | B0XN61       | Alpha-amylase, putative                                       |
| AFUB_095880       | B0YDK2       | Glucosamine 6-phosphate acetyltransferase, putative           |
| AFUB_083460       | B0YA54       | N-acetylglucosamine-6-phosphate deacetylase (EC 1.2.1.12)    |
| Accession          | Description                                                                 | Function                                  | Source |
|--------------------|------------------------------------------------------------------------------|-------------------------------------------|--------|
| AFUB_016850        | Glucokinase regulator family protein, putative                               | 3.5.1.25)                                 |        |
| B0XPC5             |                                                                               |                                           |        |
| AFUB_006590        | N-acetylglucosamine-phosphate mutase                                         |                                           |        |
| B0XPI4             |                                                                               |                                           |        |
| AFUB_047820        | Glucoamylase (EC 3.2.1.3) (1,4-alpha-D-glucan glucohydrolase) (Glucom 1,4-alpha-glucosidase) |                                           |        |
| B0XXS57            |                                                                               |                                           |        |
| AFUB_017770        | Glucoamylase (EC 3.2.1.3) (1,4-alpha-D-glucan glucohydrolase) (Glucom 1,4-alpha-glucosidase) |                                           |        |
| B0XSV7             |                                                                               |                                           |        |
| AFUB_002520        | Glycogen debranching enzyme Gdb1, putative                                   |                                           |        |
| B0XRH8             |                                                                               |                                           |        |
| AFUB_091720        | Probable beta-glucosidase L (EC 3.2.1.21) (Beta-D-glucoside glucohydrolase L) (Cellulbiose L) (Gentibiase L) |                                           |        |
| B0YB65             |                                                                               |                                           |        |
| AFUB_010890        | 1,3-beta-glucanosyltransferase Bgt1                                           |                                           |        |
| B0XQR5             |                                                                               |                                           |        |
| AFUB_006590        | Glycosyl hydrolases family 32 superfamily                                    |                                           |        |
| B0YCV1             |                                                                               |                                           |        |
| AFUB_080730        | Malate MalT                                                                  |                                           |        |
| B0Y9E3             |                                                                               |                                           |        |
| AFUB_077960        | Exo-beta-1,3-glucanase, putative                                             |                                           |        |
| B0Y8N4             |                                                                               |                                           |        |
| AFUB_067270        | Alpha-glucosidase AgdA, putative                                             |                                           |        |
| B0Y6K4             |                                                                               |                                           |        |
| AFUB_048930        | Exoinulinase InuD                                                           |                                           |        |
| B0Y174             |                                                                               |                                           |        |
| AFUB_018320        | Beta-fructofuranosidase, putative                                            |                                           |        |
| B0XT79             |                                                                               |                                           |        |
| AFUB_015590        | Probable alpha-beta-glucosidase agdC (EC 3.2.1.20)                           |                                           |        |
| B0XNL6             | (EC 3.2.1.21)                                                                |                                           |        |
| AFUB_006160        | Probable beta-glucosidase A (EC 3.2.1.21) (Beta-D-glucoside glucohydrolase A) (Cellulbiose A) (Gentibiase A) |                                           |        |
| B0XPE1             |                                                                               |                                           |        |
| AFUB_101570        | Acid phosphatase, putative                                                   |                                           |        |
| B0YF50             |                                                                               |                                           |        |
| AFUB_096090        | Phosphotransferase (EC 2.7.1.-)                                              |                                           |        |
| B0YDM3             |                                                                               |                                           |        |
| AFUB_094300        | Phosphotransferase (EC 2.7.1.-)                                              |                                           |        |
| B0YD52             |                                                                               |                                           |        |
| AFUB_089570        | Phosphotransferase (EC 2.7.1.-)                                              |                                           |        |
| B0YCB2             |                                                                               |                                           |        |
| AFUB_084610        | Sorbitol/xylitol dehydrogenase, putative                                     |                                           |        |
| B0YAG7             |                                                                               |                                           |        |
| AFUB_071700        | Mannitol 2-dehydrogenase (M2DH) (MDH) (EC 1.1.1.67)                          |                                           |        |
| B0Y581             |                                                                               |                                           |        |
| AFUB_059590        | Serine/threonine-protein phosphatase (EC 3.1.3.16)                           |                                           |        |
| B0Y147             |                                                                               |                                           |        |
| AFUB_044020        | 2,3-diketo-5-methylthio-1-phosphopentane phosphatase, putative               |                                           |        |
| B0XZD4             |                                                                               |                                           |        |
| AFUB_038940        | Acid phosphatase, putative                                                   |                                           |        |
| B0XXX9             |                                                                               |                                           |        |
| AFUB_032000        | Phosphotransferase (EC 2.7.1.-)                                              |                                           |        |
| B0XUZ8             |                                                                               |                                           |        |
| AFUB_022950        | Phosphotransferase (EC 2.7.1.-)                                              |                                           |        |
| B0XXV9             |                                                                               |                                           |        |
| AFUB_017510        | Phosphotransferase (EC 2.7.1.-)                                              |                                           |        |
| B0XST2             |                                                                               |                                           |        |
| AFUB_015610        | Xylitol dehydrogenase XdhB, putative                                         |                                           |        |
| B0XNT6             |                                                                               |                                           |        |
| AFUB_013930        | Zinc-dependent alcohol dehydrogenase, putative (EC 1.1.1.1-) (Fragment)     |                                           |        |
| B0XMR8             |                                                                               |                                           |        |
| AFUB_010450        | Xylitol dehydrogenase                                                        |                                           |        |
| B0XQM2             |                                                                               |                                           |        |
| AFUB_010440        | L-arabinol 4-dehydrogenase                                                   |                                           |        |
| B0XQM1             |                                                                               |                                           |        |
| AFUB_004070        | Acid phosphatase, putative                                                   |                                           |        |
| B0XN85             |                                                                               |                                           |        |
| AFUB_037100        | ADP-ribosylation factor 6, putative                                          |                                           |        |
| B0XX77             |                                                                               |                                           |        |
| AFUB_091160        | Phospholipase PdA, putative                                                  |                                           |        |
| B0YB09             |                                                                               |                                           |        |
| AFUB_043370        | Phospholipase D1 (PLD1), putative                                            |                                           |        |
| B0XZ71             |                                                                               |                                           |        |
| AFUB_032200        | Phospholipase D (PLD), putative                                              |                                           |        |
| B0XV82             |                                                                               |                                           |        |
| AFUB_066150        | Serine/threonine protein kinase (Pdd7p), putative                            |                                           |        |
| B0Y697             |                                                                               |                                           |        |
| AFUB_019610        | Meiotic regulator-interacting protein, putative                              |                                           |        |
| B0XTZ3             |                                                                               |                                           |        |
| AFUB_093370        | Formate dehydrogenase (FDH) (EC 1.2.1.2) (NAD-dependent formate dehydrogenase) |                                           |        |
| B0YC9             |                                                                               |                                           |        |
| AFUB_076160        | D-isomer specific 2-hydroxyacid dehydrogenase family protein                 |                                           |        |
| B0Y855             |                                                                               |                                           |        |
| AFUB_070430        | Isocitrate lyase                                                             |                                           |        |
| B0Y4V4             |                                                                               |                                           |        |
| AFUB_013120        | Glycerate dehydrogenase                                                      |                                           |        |
| B0XRL7             |                                                                               |                                           |        |
| AFUB_010660        | N,N-dimethylglycine oxidase                                                  |                                           |        |
| B0Y60              |                                                                               |                                           |        |
| AFUB_099260        | Glycine dehydrogenase                                                        |                                           |        |
| B0YE11             |                                                                               |                                           |        |
| AFUB_092120        | Threonine aldolase, putative                                                 |                                           |        |
| B0YBA5             |                                                                               |                                           |        |
| AFUB_076290        | FAD dependent oxidoreductase superfamily                                     |                                           |        |
| B0Y868             |                                                                               |                                           |        |
| AFUB_061650        | FAD dependent oxidoreductase superfamily                                     |                                           |        |
| B0Y286             |                                                                               |                                           |        |
| AFUB_058860        | D-amino acid oxidase                                                          |                                           |        |
| B0Y0X4             |                                                                               |                                           |        |
| Accession     | Accession2 | Accession3 | Description                                                                 | O                     |
|--------------|------------|------------|-----------------------------------------------------------------------------|-----------------------|
| CADAFUBP00005267 | AFUB_053800 | B0Y3D3    | 5-aminolevulinate synthase (EC 2.3.1.37) (5-aminolevulinic acid synthase) (Delta-ALA synthase) (Delta-aminolevulinic acid synthase) | 1                     |
| CADAFUBP00004628 | AFUB_047220 | B0XWZ9    | Serine hydroxymethyltransferase (EC 2.1.2.1)                               | 1                     |
| CADAFUBP00003900 | AFUB_039810 | B0XY66    | N,N-dimethylglycine oxidase                                                  | 1                     |
| CADAFUBP00003165 | AFUB_032290 | B0XV91    | Alanine racemase                                                            | 1                     |
| CADAFUBP00002327 | AFUB_023840 | B0XW76    | Serine hydroxymethyltransferase (EC 2.1.2.1)                               | 1                     |
| CADAFUBP00000873 | AFUB_008920 | B0XQ69    | Aminotransferase, class V, putative                                         | 1                     |
| CADAFUBP00008206 | NA         | NA        |                                                                               | 1                     |
| CADAFUBP00009209 | AFUB_094750 | B0YD94    | Malate synthase (EC 2.3.3.9)                                                | 1                     |
| CADAFUBP00007678 | AFUB_077700 | B0XW83    | Proteasome regulatory particle subunit (Rpn1), putative                     | 1                     |
| CADAFUBP00007079 | AFUB_072710 | B0Y764    | Proteasome regulatory particle subunit Rpt4, putative                       | 1                     |
| CADAFUBP00004045 | AFUB_041290 | B0XYL1    | Proteasome regulatory particle subunit Rpt1, putative                       | 1                     |
| CADAFUBP00000643 | AFUB_006550 | B0XPI0    | Proteasome regulatory particle subunit Rpt5, putative                       | 1                     |
| CADAFUBP00001446 | AFUB_014750 | B0XN66    | Hsp70 family protein                                                        | 1                     |
| CADAFUBP000001894 | AFUB_019410 | B0XTX3    | Hsp70 chaperone (BiP), putative                                              | 1                     |
| CADAFUBP00002370 | AFUB_024270 | B0XWB9    | DnaJ domain protein, putative                                                | 1                     |
| CADAFUBP000001041 | AFUB_010610 | B0XQ7N    | Heat shock protein/chaperonin HSP78, putative                               | 1                     |
| CADAFUBP00009657 | AFUB_093770 | B0YEJ2    | Ribosomes associated DnaJ chaperone Zuo1, putative                          | 1                     |
| CADAFUBP00004198 | AFUB_042810 | B0XZ14    | Translation initiation factor SUI1, putative                                | 1                     |
| CADAFUBP00009311 | AFUB_095820 | B0YD76    | Eukaryotic translation initiation factor elf-1A, putative                   | 1                     |
| CADAFUBP00000954 | AFUB_009720 | B0XOF0    | RNase L inhibitor of the ABC superfamily, putative                          | 1                     |
| CADAFUBP00000430 | AFUB_004370 | B0XNBX    | Mitochondrial translation initiation factor IF-2, putative                  | 1                     |
| CADAFUBP000008835 | AFUB_090870 | B0YRCP0   | 40S ribosomal protein S13                                                   | 1                     |
| CADAFUBP00002069 | AFUB_021200 | B0XUT5    | 40S ribosomal protein S11                                                   | 1                     |
| CADAFUBP00000460 | AFUB_004660 | B0XNE5    | 40S ribosomal protein S8                                                    | 1                     |
| CADAFUBP00006267 | AFUB_064420 | B0Y557    | ER associated DnaJ chaperone (Hlj1), putative                               | 1                     |
| CADAFUBP00005600 | AFUB_057180 | B0Y4B6    | UBA/TS-N domain protein                                                     | 1                     |
| CADAFUBP00000904 | AFUB_009220 | B0XQA0    | La domain family                                                           | 1                     |
| CADAFUBP00001453 | AFUB_014820 | B0XN73    | Heat shock protein Hsp98/Hsp104/ClaP, putative                              | 1                     |
| CADAFUBP000008163 | AFUB_083860 | B0YA94    | Translation machinery-associated protein 22                                | 1                     |
| CADAFUBP000002431 | AFUB_024880 | B0XRU6    | Eukaryotic translation initiation factor 5, putative                       | 1                     |
| CADAFUBP000006292 | AFUB_064670 | B0Y5V0    | Translation initiation factor EF-2 gamma subunit, putative                  | 1                     |
| CADAFUBP000003966 | AFUB_040500 | B0XYD2    | Translational initiation factor 2 beta                                      | 1                     |
| CADAFUBP000003495 | AFUB_035720 | B0XWF4    | Translation initiation factor 2 alpha subunit, putative                    | 1                     |
| CADAFUBP000002116 | AFUB_021670 | B0XVS1    | ER Hsp70 chaperone BiP, putative                                            | 1                     |
| CADAFUBP00000617 | AFUB_006290 | B0XPE4    | DnaJ and TPR domain protein                                                 | 1                     |
| CADAFUBP000004226 | AFUB_043080 | B0X4Z2    | Eukaryotic translation initiation factor subunit elf2A, putative             | 1                     |
| CADAFUBP000006656 | AFUB_068360 | B0Y6W4    | Aha1 domain family                                                          | 1                     |
| CADAFUBP000006019 | AFUB_061630 | B0Y284    | Hsp90 binding co-chaperone (Sba1), putative                                | 1                     |
| CADAFUBP000001866 | AFUB_019130 | B0XMT6    | Peptidyl-prolyl cis-trans isomerase Cpr7, putative                          | 1                     |
| CADAFUBP000006531 | AFUB_067120 | B0Y6I9    | Hsp90 co-chaperone Cdc37                                                   | 1                     |
| CADAFUBP000003755 | AFUB_038330 | B0XSS1    | Clustered mitochondria protein homolog (Protein TIF31 homolog)              | 1                     |
| CADAFUBP000009636 | AFUB_099160 | B0YEH1    | Eukaryotic translation initiation factor 3 subunit C (eIF3c) (Eukaryotic translation initiation factor 3 93 kDa subunit homolog) (eIF3 p93) (Translation initiation factor eIF3, p93 subunit homolog) | 1                     |
| CADAFUBP000008701 | AFUB_089510 | B0YCA6    | Eukaryotic translation initiation factor 3 subunit M (eIF3m)                | 1                     |
| CADAFUBP00003962 | AFUB_040450 | B0XVC8    | Eukaryotic translation initiation factor 3 subunit I (eIF3i) (Eukaryotic translation initiation factor 3 39 kDa subunit homolog) (eIF-3 39 kDa subunit homolog) | 1                     |
| Accession      | Description                                                                 | Length |
|---------------|------------------------------------------------------------------------------|--------|
| AFUB_039840   | Eukaryotic translation initiation factor 3 subunit K (eIF3k) (eIF-3 p25)      | 10     |
| AFUB_037810   | Eukaryotic translation initiation factor 3 subunit E (eIF3e)                  | 10     |
| AFUB_030310   | Eukaryotic translation initiation factor 3 subunit D (eIF3d)                  | 10     |
| AFUB_026190   | Eukaryotic translation initiation factor 3 subunit L (eIF3l)                  | 10     |
| AFUB_025710   | Eukaryotic translation initiation factor 3 subunit G (eIF3g)                  | 10     |
| AFUB_009410   | Eukaryotic translation initiation factor 3 subunit H (eIF3h)                  | 10     |
| AFUB_024110   | Eukaryotic translation initiation factor 3 subunit B (eIF3b)                  | 10     |
| AFUB_005560   | Eukaryotic translation initiation factor 3 subunit A (eIF3a)                  | 10     |
| AFUB_004530   | Polyadenylate-binding protein (PABP)                                         | 10     |
| AFUB_088430   | Heat shock protein (Sti1), putative                                          | 10     |
| AFUB_083640   | Hsp70 chaperone (HscA), putative                                             | 10     |
| AFUB_031960   | Dnaj domain protein (Mas5), putative                                         | 10     |
| AFUB_025800   | Mitochondrial Hsp70 chaperone (Ssc70), putative                              | 10     |
| AFUB_007770   | Molecular chaperone Hsp70                                                    | 10     |
| AFUB_005400   | Protein mitochondrial targeting protein (Mas1), putative                      | 10     |
| AFUB_006000   | 40S ribosomal protein S3, putative                                           | 10     |
| AFUB_013400   | TFIIF complex helicase Rad3, putative                                        | 10     |
| AFUB_093560   | Bifunctional purine biosynthetic protein Ade1, putative                      | 10     |
| AFUB_012440   | SCF ubiquitin ligase complex subunit CulA, putative                          | 10     |
| AFUB_020470   | Proteasome regulatory particle subunit (RpnK), putative                      | 10     |
| AFUB_074180   | SCF ubiquitin ligase subunit CulC, putative                                  | 10     |
| AFUB_047300   | GMP synthase                                                                | 10     |
| AFUB_002460   | Uridine kinase (EC 2.7.1.48)                                                 | 10     |
| AFUB_049650   | RAN small monomeric GTPase (Ran), putative                                   | 10     |
| AFUB_001470   | GTP-binding nuclear protein                                                  | 10     |
| AFUB_093230   | DUF410 domain protein                                                        | 10     |
| AFUB_003780   | ATPase get3 (EC 3.6. - - ) (Arsenical pump-driving ATPase) (Arsenite-stimulated ATPase) (Golg to ER traffic protein 3) (Guided entry of tail-anchored proteins 3) | 10     |
| AFUB_029080   | Chitin synthase ChsE                                                        | 10     |
| AFUB_091630   | DNA damage-inducible v-SNARE binding protein Ddi1, putative                  | 10     |
| AFUB_059290   | 26S proteasome regulatory subunit Mts4, putative                              | 10     |
| AFUB_063900   | SUMO-conjugating enzyme (EC 2.3.2.-)                                         | 10     |
| AFUB_059770   | Ran-specific GTPase-activating protein 1, putative                            | 10     |
| AFUB_041420   | Ran GTPase activating protein 1 (RNA1 protein)                               | 10     |
| AFUB_058070   | Adenylyltransferase and sulfurtransferase uba4 (Common component for nitrate reductase and xanthine dehydrogenase protein F) (Ubiquitin-like protein activator 4) [Includes: Molybdopterin-synthase adenylytransferase (EC 2.7.7.80) (Adenylyltransferase uba4) (Sulfur carrier protein) | 10     |
| Accession          | Gene ID | Description                                                                 | UniProt Code | GO ID |
|--------------------|---------|-----------------------------------------------------------------------------|--------------|-------|
| CADAFUBP00001008   | AFUB_010270 | MOCS2A adenylyltransferase); Molybdopterin-synthase sulfurtransferase (EC 2.8.1.11) (Sulfur carrier protein MOCS2A sulfurtransferase) (Sulfurtransferase uba4) | B0XQK4       |       |
| CADAFUBP00005016   | AFUB_051250 | Phosphoribosylformylglycinamidine synthase                                | B0Y2F3       | 1 10  |
| CADAFUBP00002805   | AFUB_028660 | Phenylalanyl-tRNA synthetase alpha subunit (PodG), putative               | B0XT97       | 1 10  |
| CADAFUBP00008549   | AFUB_087950 | Anaphase promoting complex subunit Apcl, putative                          | B0YBV4       | 1 10  |
| CADAFUBP00005556   | AFUB_056740 | Ubiquitin-conjugating enzyme (UbC), putative                               | B0Y472       | 1 10  |
| CADAFUBP00005249   | AFUB_053620 | E3 ubiquitin ligase complex SCF subunit sconC (Sulfur controller C) (Sulfur metabolite repression control protein C) | B0Y3B5       | 1 10  |
| CADAFUBP00004204   | AFUB_042860 | Anaphase-promoting complex subunit Apcl, putative                          | B0XZ20       | 1 10  |
| CADAFUBP00008997   | AFUB_091500 | Acetyl-CoA desaturase (EC 1.14.19.1)                                        | B0YB43       | 1 10  |
| CADAFUBP00006268   | AFUB_064430 | Ubiquitin fusion degradation enzyme UfdB, putative                          | B0YSS6       | 1 10  |
| CADAFUBP00003010   | AFUB_030720 | 26S proteasome regulatory subunit S5A                                        | B0XUF6       | 1 10  |
| CADAFUBP00009091   | AFUB_009280 | Hsc70 co-chaperone (SGT), putative                                          | B0XQA6       | 1 10  |
| CADAFUBP00003890   | AFUB_030270 | DNA polymerase epsilon, catalytic subunit A/POL2, putative                    | B0XX19       | 1 10  |
| CADAFUBP00005978   | AFUB_009970 | CBF/NF-Y family transcription factor, putative                              | B0XQH4       | 1 10  |
| CADAFUBP00007255   | AFUB_074480 | Adenylate cyclase AcyA                                                      | B0Y7P0       | 1 10  |
| CADAFUBP00002136   | AFUB_012570 | Multifunctional tryptophan biosynthesis protein                              | B0XR95       | 1 10  |
| CADAFUBP00002309   | AFUB_023660 | Cystathionine beta-synthase (EC 4.2.1.22)                                    | B0XW58       | 1 10  |
| CADAFUBP00005158   | AFUB_052690 | Molecular chaperone Mod-E/Hsp90                                              | B0Y324       | 1 10  |
| CADAFUBP00008589   | AFUB_008750 | Eukaryotic translation initiation factor 3 subunit F (eIF3)                  | B0XQ55       | 1 10  |
| CADAFUBP00002270   | AFUB_020690 | DNA polymerase epsilon subunit B, putative                                   | B0XUN4       | 1 10  |
| CADAFUBP00004992   | AFUB_051010 | Glycogen [starch] synthase (EC 2.4.1.11)                                    | B0Y2C9       | 1 10  |
| CADAFUBP00006607   | AFUB_067880 | 40S ribosomal protein S6                                                     | B0Y6R5       | 1 10  |
| CADAFUBP00001004   | AFUB_010230 | V-type proton ATPase subunit C                                               | B0XQK0       | 1 10  |
| CADAFUBP00004660   | NA       | NA                                                                          | NA           | 1 10  |
| CADAFUBP00003713   | AFUB_037910 | Ubiquitin (UbiC), putative                                                   | B0XXM3       | 1 10  |
| CADAFUBP00002806   | AFUB_028670 | GrpE protein homolog                                                         | B0XT98       | 1 10  |
| CADAFUBP00005247   | AFUB_053580 | UV excision repair protein (RadW), putative                                  | B0Y3B3       | 1 10  |
| CADAFUBP00000130   | AFUB_001330 | Ubiquitin-like protein DskB, putative                                        | B0XMD6       | 1 10  |
| CADAFUBP00007985   | AFUB_082020 | Fumarate reductase Osm1, putative                                            | B0Y9R6       | 1 10  |
| CADAFUBP00002644   | AFUB_027050 | Orotate phosphoribosyltransferase                                            | B0XSF9       | 1 10  |
| CADAFUBP00002618   | AFUB_026780 | Dihydroorotate reductase PyrE, putative                                      | B0XS3D       | 1 10  |
| CADAFUBP00002374   | AFUB_024310 | Orotidine 5'-phosphate dehydrogenase (EC 4.1.1.23)                          | B0XXC3       | 1 10  |
| CADAFUBP00001886   | AFUB_019330 | Allantoinase Da1, putative                                                   | B0XTW5       | 1 10  |
| CADAFUBP00008688   | AFUB_089380 | Oxidoreductase, 2-nitropropane dioxygenase family, putative                 | B0YC93       | 1 10  |
| CADAFUBP00005675   | AFUB_058010 | Nitrate reductase, putative                                                  | B0Y0P1       | 1 10  |
| CADAFUBP00003245   | AFUB_033100 | Oxidoreductase 2-nitropropane dioxygenase family, putative                  | B0XVN8       | 1 10  |
| CADAFUBP00001651   | AFUB_016830 | High affinity nitrate transporter NrtB                                       | B0XPC3       | 1 10  |
| CADAFUBP00001211   | AFUB_012320 | Nitrate transporter CrmA                                                    | B0XR70       | 1 10  |
| CADAFUBP00001210   | AFUB_012310 | Nitrite reductase NitrA                                                     | B0XR69       | 1 10  |
| CADAFUBP00001209   | AFUB_012300 | Nitrite reductase                                                           | B0XR68       | 1 10  |
| CADAFUBP00006309   | AFUB_064840 | Small nuclear ribonucleoprotein SmB, putative                               | B0Y5W7       | 1 11  |
| CADAFUBP00006844   | AFUB_070270 | U1 small nuclear ribonucleoprotein C (U1 snRNPC C) (U1-C) (U1C)             | B0Y4T8       | 1 11  |
| CADAFUBP000040875  | AFUB_008940 | RNP domain protein                                                          | B0XQ71       | 1 11  |
| CADAFUBP00009716   | AFUB_009970 | Cell cycle control protein (Cw26), putative                                 | B0YEQ1       | 1 11  |
| CADAFUBP00005715   | AFUB_058430 | RNA helicase-like splicing factor (HRH1), putative                           | B0Y0T1       | 1 11  |
| CADAFUBP00006708   | AFUB_068880 | Splicing factor 3a subunit 2, putative                                       | B0Y4F2       | 1 11  |
| CADAFUBP00007632   | AFUB_078300 | RNP domain protein                                                          | B0Y8R7       | 1 11  |
| Accession       | Description                                                                 | Protein | EC Number | Monomer | Molecular Weight |
|-----------------|------------------------------------------------------------------------------|---------|-----------|---------|------------------|
| AFUB_032070     | Translation initiation factor 4B                                            |         |           |         |                  |
| AFUB_028930     | Uncharacterized protein                                                      |         |           |         |                  |
| AFUB_07300      | FF domain protein                                                           |         |           |         |                  |
| AFUB_061210     | Cell cycle control protein (Cw8), putative                                 |         |           |         |                  |
| AFUB_052980     | Splicing factor 3b, subunit 2, 145kD                                       |         |           |         |                  |
| AFUB_050950     | Splicing factor 3a subunit 3, putative                                      |         |           |         |                  |
| AFUB_029410     | Splicing factor 3B subunit 1, putative                                      |         |           |         |                  |
| AFUB_023750     | mRNA splicing factor RNA helicase (Cdc28), putative                         |         |           |         |                  |
| AFUB_022560     | Cell division control protein (Cdc5), putative                             |         |           |         |                  |
| AFUB_059490     | U1 small nuclear ribonucleoprotein 70 kDa                                  |         |           |         |                  |
| AFUB_058570     | Small nuclear ribonucleoprotein U2, A                                       |         |           |         |                  |
| AFUB_045950     | U2 auxiliary factor small subunit, putative                                 |         |           |         |                  |
| AFUB_011600     | Translation initiation factor eIF4E, putative                               |         |           |         |                  |
| AFUB_093150     | snRNA cap binding complex subunit (Gcr3), putative                          |         |           |         |                  |
| AFUB_024500     | Small subunit of nuclear cap-binding protein complex                        |         |           |         |                  |
| AFUB_051690     | Translation initiation factor eIF4E3, putative                              |         |           |         |                  |
| AFUB_039070     | Pre-RNA splicing factor Sp2, putative                                      |         |           |         |                  |
| AFUB_064000     | Methionine aminopeptidase 2-2 (MAP 2-2) (MetAP 2-2) (EC 3.4.11.18) (Peptidase M) |         |           |         |                  |
| AFUB_073300     | Methionine aminopeptidase (EC 3.4.11.18)                                   |         |           |         |                  |
| AFUB_018820     | Methionine aminopeptidase 2-1 (MAP 2-1) (EC 3.4.11.18) (Peptidase M)        |         |           |         |                  |
| AFUB_086160     | Methionine aminopeptidase 2-3 (MAP 2-3) (EC 3.4.11.18) (Peptidase M)        |         |           |         |                  |
| AFUB_086110     | Methionine aminopeptidase (EC 3.4.11.18)                                   |         |           |         |                  |
| AFUB_053170     | 60S ribosomal protein L23                                                   |         |           |         |                  |
| AFUB_073930     | Lactoylglutathione lyase (EC 4.4.1.5) (Glyoxalase I)                       |         |           |         |                  |
| AFUB_062500     | Glyoxalase family protein                                                   |         |           |         |                  |
| AFUB_053340     | Ubiquitin ligase subunit HrtA, putative                                    |         |           |         |                  |
| AFUB_096610     | 3-hydroxybutyryl-CoA dehydrogenase, putative                              |         |           |         |                  |
| AFUB_043010     | Glutaryl-CoA dehydrogenase, putative                                       |         |           |         |                  |
| AFUB_057660     | 3-hydroxyacyl-CoA dehydrogenase, putative                                  |         |           |         |                  |
| AFUB_043030     | Glyoxalase family protein                                                   |         |           |         |                  |
| AFUB_091050     | Electron transfer flavoprotein alpha subunit, putative                     |         |           |         |                  |
| AFUB_044840     | Enoyl-CoA hydratase/isomerase family protein                               |         |           |         |                  |
| AFUB_045790     | Hybrid PKS/NRPS enzyme EqiS-like, putative                                 |         |           |         |                  |
| AFUB_041280     | T-complex protein 1 subunit delta                                           |         |           |         |                  |
| AFUB_091680     | Acyl-coenzyme A oxidase                                                     |         |           |         |                  |
| AFUB_040370     | Endosome-associated ubiquitin isopeptidase (AmsH), putative                 |         |           |         |                  |
| AFUB_084850     | Acyl-CoA oxidase, putative                                                  |         |           |         |                  |
| AFUB_011850     | WD repeat protein                                                           |         |           |         |                  |
| AFUB_014830     | Polysaccharide deacetylase family protein                                  |         |           |         |                  |
| AFUB_032310     | Acyl-CoA dehydrogenase                                                      |         |           |         |                  |
| AFUB_012780     | SAGA complex component (Sgf29), putative                                   |         |           |         |                  |
| AFUB_086030     | Hybrid NRPS/PKS enzyme EqiS-like, putative                                 |         |           |         |                  |
| AFUB_075110     | Oxidoreductase, short-chain dehydrogenase/reductase family                  |         |           |         |                  |
| AFUB_092070     | Acyl-CoA dehydrogenase, putative                                            |         |           |         |                  |
| AFUB_038620     | 3-oxoacyl-(Acyl-carrier-protein) reductase, putative                         |         |           |         |                  |
| AFUB_014390     | Acyl-CoA dehydrogenase, putative                                            |         |           |         |                  |
| AFUB_012120     | 3-ketoacyl-CoA ketothiolase (Kat1), putative                                |         |           |         |                  |
| Accession          | Enzyme Name                                                                 | Function                                                                 | Location | Gene Length |
|--------------------|------------------------------------------------------------------------------|--------------------------------------------------------------------------|----------|-------------|
| ABY441             | D-arabinitol dehydrogenase ArbD, putative                                   |                                                                          |          | 1251        |
| ABYD46             | Peroxisomal D3,D2-enoyl-CoA isomerase                                        |                                                                          |          | 1170        |
| B0YAP7             | Enoyl-CoA hydratase/isomerase family protein                                |                                                                          |          | 1285        |
| BOY0K0             | Acyl-CoA dehydrogenase, putative                                            |                                                                          |          | 1009        |
| BOXYN8             | Enoyl-CoA hydratase/isomerase family protein                                |                                                                          |          | 1288        |
| B0XSC6             | Enoyl-CoA hydratase/isomerase family protein                                |                                                                          |          | 1287        |
| B0XRF3             | Enoyl-CoA hydratase/isomerase family protein                                |                                                                          |          | 1288        |
| BOYDA0             | Nonribosomal peptide synthase, putative                                     |                                                                          |          | 1267        |
| BOY6V5             | L-aminoadipate-semialdehyde dehydrogenase (EC 1.2.1.95) (Alpha-aminoadipate reductase) |                                                                          |          | 1267        |
| BOYE9              | Oxidoreductase, short-chain dehydrogenase/reductase family                  |                                                                          |          | 1267        |
| B0Y663             | Short chain dehydrogenase, putative                                         |                                                                          |          | 1288        |
| B0XT07             | Polyketide synthase, putative                                               |                                                                          |          | 1288        |
| B0XVQ2             | 1,3,6,8-tetrahydroxynaphthalene reductase                                   |                                                                          |          | 1288        |
| BOY445             | 3-methylcrotonyl-CoA carboxylase, beta subunit (MccB), putative              |                                                                          |          | 1267        |
| BOYB13             | Polyketide synthase, putative                                               |                                                                          |          | 1267        |
| BOY488             | Small monomeric GTPase (Gtr1), putative                                     |                                                                          |          | 1267        |
| B0XWA8             | NEDD8-like protein (Ruba), putative                                         |                                                                          |          | 1267        |
| BOY53              | 15-hydroxyprostaglandin dehydrogenase (NAD(+))                              |                                                                          |          | 1288        |
| B0YO22             | Oxidoreductase, short chain dehydrogenase/reductase family, putative        |                                                                          |          | 1267        |
| B0XY51             | 3-oxoacyl-(Acyl-carrier-protein) reductase                                  |                                                                          |          | 1288        |
| BOY1F5             | Short chain dehydrogenase/reductase family                                  |                                                                          |          | 1267        |
| BOY8P5             | Nonribosomal peptide synthase, putative                                     |                                                                          |          | 1267        |
| B0YBY2             | Polyketide synthase, putative                                               |                                                                          |          | 1267        |
| BOXRE3             | Short chain oxidoreductase/dehydrogenase, putative                          |                                                                          |          | 1267        |
| BOYCE5             | Alcohol dehydrogenase                                                       |                                                                          |          | 1267        |
| BOY8R6             | PH domain protein                                                           |                                                                          |          | 1267        |
| BOYEA4             | Short chain dehydrogenase/reductase, putative                              |                                                                          |          | 1267        |
| B0YD96             | Short-chain dehydrogenase/reductase family protein, putative               |                                                                          |          | 1267        |
| BOY1J4             | Oxidoreductase, short-chain dehydrogenase/reductase family, putative        |                                                                          |          | 1267        |
| BOY1X0             | Oxidoreductase, short chain dehydrogenase/reductase family, putative        |                                                                          |          | 1267        |
| BOY8C5             | Short chain dehydrogenase/reductase family                                  |                                                                          |          | 1267        |
| BOY642             | Acyl-CoA dehydrogenase, putative                                            |                                                                          |          | 1267        |
| BOYEN6             | Short-chain dehydrogenase/reductase family protein, putative               |                                                                          |          | 1267        |
| BOXMX8             | Short chain dehydrogenase/reductase, putative                              |                                                                          |          | 1267        |
| BOY910             | Short chain dehydrogenase/reductase family protein, putative               |                                                                          |          | 1267        |
| BOYDE7             | Short chain dehydrogenase/reductase, putative                              |                                                                          |          | 1267        |
| BOXU3J             | Sorbitol/xylulose reductase Soul-like, putative                             |                                                                          |          | 1267        |
| BOXUN5             | Oxidoreductase, short chain dehydrogenase/reductase family                  |                                                                          |          | 1267        |
| BOY5C6             | Malonyl CoA-acyl carrier protein transacylase, putative                    |                                                                          |          | 1267        |
| BOY8G2             | 3-oxoacyl-(Acyl-carrier-protein) reductase                                  |                                                                          |          | 1267        |
| B0XW57             | Short chain dehydrogenase/reductase, putative                              |                                                                          |          | 1267        |
| BOY896             | 3-oxoacyl-acyl carrier protein reductase                                    |                                                                          |          | 1267        |
| BOXM5R             | 2-deoxy-D-glucuronate 3-dehydrogenase, putative                             |                                                                          |          | 1267        |
| BOY841             | Oxidoreductase, short chain dehydrogenase/reductase family                  |                                                                          |          | 1267        |
| BOY9Z6             | Oxidoreductase, short-chain dehydrogenase/reductase family, putative        |                                                                          |          | 1267        |
| BOY91              | NA                                                                           |                                                                          |          | 1267        |
| B0Y591             | Polyketide synthase, putative                                               |                                                                          |          | 1267        |
| ID                        | Accession   | Description                                                                 | Start | End |
|---------------------------|-------------|------------------------------------------------------------------------------|-------|-----|
| CADAFUBP00003312          | AFUB_033880 | Short chain dehydrogenase family protein, putative                           | 1     | 13  |
| CADAFUBP00003096          | AFUB_031590 | Uncharacterized protein                                                       | 1     | 13  |
| CADAFUBP00002484          | AFUB_025420 | Biotin apo-protein ligase, putative                                           | 1     | 13  |
| CADAFUBP00001476          | AFUB_015060 | Urea amidolysase, putative                                                   | 1     | 13  |
| CADAFUBP00000933          | AFUB_009510 | 3-oxoacyl-(Acyl-carrier-protein) reductase                                   | 1     | 13  |
| CADAFUBP00001379          | AFUB_014070 | Oxidoreductase, short-chain dehydrogenase/reductase family                   | 1     | 13  |
| CADAFUBP000008404         | AFUB_086260 | Short-chain dehydrogenase, putative                                          | 1     | 13  |
| CADAFUBP00009805          | AFUB_100980 | Short chain dehydrogenase, putative                                          | 1     | 13  |
| CADAFUBP00002110          | AFUB_021610 | Oxidoreductase, short-chain dehydrogenase/reductase family                   | 1     | 13  |
| CADAFUBP00002947          | AFUB_030080 | Oxidoreductase, short-chain dehydrogenase/reductase family                   | 1     | 13  |
| CADAFUBP00004606          | AFUB_046990 | Polyketide synthase, putative                                                | 1     | 13  |
| CADAFUBP00007980          | AFUB_081970 | Oxidoreductase, short chain dehydrogenase/reductase family                   | 1     | 13  |
| CADAFUBP00006057          | AFUB_062020 | Short chain dehydrogenase/reductase family protein                          | 1     | 13  |
| CADAFUBP00005526          | AFUB_056440 | 3-methylcrotonyl-CoA carboxylase subunit alpha (MccA), putative              | 1     | 13  |
| CADAFUBP00005398          | AFUB_055130 | Methylmalonyl-CoA decarboxylase, alpha subunit, putative                     | 1     | 13  |
| CADAFUBP00003691          | AFUB_037690 | Mitochondrial methylglutaconyl-CoA hydratase (Auh), putative                 | 1     | 13  |
| CADAFUBP00003295          | AFUB_033620 | Integral membrane protein                                                    | 1     | 13  |
| CADAFUBP00009224          | AFUB_094910 | Short-chain dehydrogenase/reductase, putative                               | 1     | 13  |
| CADAFUBP00004477          | AFUB_045640 | Polyketide synthase, putative                                                | 1     | 13  |
| CADAFUBP00006330          | AFUB_065050 | Oxidoreductase, 2-nitropropane dioxygenase family, putative                 | 1     | 13  |
| CADAFUBP000007094         | AFUB_072860 | Short chain dehydrogenase/reductase family protein                          | 1     | 13  |
| CADAFUBP00006564          | AFUB_067450 | Polyubiquitin UbiD/Ubi4, putative                                           | 1     | 13  |
| CADAFUBP00001322          | AFUB_013440 | Short-chain oxidoreductase, putative                                          | 1     | 13  |
| CADAFUBP00004898          | AFUB_050700 | Polyglutamate biosynthesis protein, putative                                 | 1     | 13  |
| CADAFUBP00009862          | AFUB_101550 | Short chain dehydrogenase, putative                                          | 1     | 13  |
| CADAFUBP00007055          | AFUB_072470 | Proteasome component (Ecm29), putative                                       | 1     | 13  |
| CADAFUBP00005366          | AFUB_054810 | COP9 signalosome subunit 6 (CsnF), putative                                 | 1     | 13  |
| CADAFUBP00003130          | AFUB_031930 | COP9 signalosome subunit 5 (CsnE), putative                                 | 1     | 13  |
| CADAFUBP00009851          | AFUB_101440 | Oxidoreductase, short chain dehydrogenase/reductase family, putative         | 1     | 13  |
| CADAFUBP0001670           | AFUB_017030 | Short chain dehydrogenase, putative                                          | 1     | 13  |
| CADAFUBP0003077           | AFUB_031390 | Short chain dehydrogenase/oxidoreductase, putative                          | 1     | 13  |
| CADAFUBP0001364           | AFUB_013920 | 3-ketoacyl-acyl carrier protein reductase                                   | 1     | 13  |
| CADAFUBP0004384           | AFUB_044690 | PKS-like enzyme, putative                                                    | 1     | 13  |
| CADAFUBP00008398          | AFUB_086200 | Polyketide synthase, putative                                                | 1     | 13  |
| CADAFUBP00009981          | AFUB_093440 | Short chain dehydrogenase/reductase family protein                          | 1     | 13  |
| CADAFUBP00009780          | AFUB_100730 | Polyketide synthase, putative                                                | 1     | 13  |
| CADAFUBP0001709           | AFUB_017520 | Short-chain dehydrogenase/reductase family, putative                        | 1     | 13  |
| CADAFUBP00004803          | AFUB_049110 | Peroxisomal dehydratase, putative                                            | 1     | 13  |
| CADAFUBP00006024          | AFUB_061680 | Oxidoreductase, short chain dehydrogenase/reductase family                   | 1     | 13  |
| CADAFUBP0001643           | AFUB_016750 | 3-oxoacyl-(Acyl-carrier-protein) reductase                                   | 1     | 13  |
| CADAFUBP0004620           | AFUB_047130 | Short-chain dehydrogenase/reductase family protein, putative                | 1     | 13  |
| CADAFUBP0001792           | AFUB_018370 | Polyketide synthase, putative                                                | 1     | 13  |
| CADAFUBP0003302           | AFUB_033690 | Short chain dehydrogenase/oxidoreductase CpoX2                              | 1     | 13  |
| CADAFUBP00006661          | AFUB_062060 | Oxidoreductase, short chain dehydrogenase/reductase family, putative         | 1     | 13  |
| CADAFUBP0001568           | AFUB_016000 | Short chain dehydrogenase family protein                                     | 1     | 13  |
| CADAFUBP00006909          | AFUB_070930 | Short chain dehydrogenase/reductase family protein                          | 1     | 13  |
| CADAFUBP0008802           | AFUB_095400 | 3-ketoacyl-acyl carrier protein reductase                                   | 1     | 13  |
| CADAFUBP0003161           | AFUB_032250 | Short chain dehydrogenase/reductase, putative                               | 1     | 13  |
| Accession          | Gene ID      | Description                                                                                           | Start | End |
|-------------------|--------------|--------------------------------------------------------------------------------------------------------|-------|-----|
| AFUB_039980       | B0XY81       | Oxidoreductase, short chain dehydrogenase/reductase family protein, putative                          | 1     | 13  |
| AFUB_087420       | B0YBQ0       | Short chain dehydrogenase/reductase, putative                                                         | 1     | 13  |
| AFUB_025690       | B0XS26       | Oxidoreductase, 2-nitropropane dioxygenase family, putative                                             | 1     | 13  |
| AFUB_083990       | B0YAA7       | Short-chain dehydrogenase/reductase 2, putative                                                        | 1     | 13  |
| AFUB_013230       | B0XRMA     | Pentafunctional AROM polypeptide [Includes: 3-dehydroquinate synthase (DHQS) (EC 4.2.3.4); 3-phosphoshikimate 1-carboxyvinyltransferase (EC 2.5.1.19); (5-enolpyruvylshikimate-3-phosphate synthase) (EPSP synthase) (EPSPS); Shikimate kinase (SK) (EC 2.7.1.71); 3-dehydroquinate dehydratase (3-dehydroquinase) (EC 4.2.1.10); Shikimate dehydrogenase (EC 1.1.1.25)] | 1     | 13  |
| AFUB_018480       | B0XTG3       | Short chain dehydrogenase/oxidoreductase, putative                                                      | 1     | 13  |
| AFUB_079910       | B0Y976       | Short-chain dehydrogenase/reductase, putative                                                         | 1     | 13  |
| AFUB_092480       | B0YBE1       | Short chain dehydrogenase/reductase, putative                                                         | 1     | 13  |
| AFUB_033290       | B0XVQ6       | Polyketide synthetase PksP                                                                             | 1     | 13  |
| AFUB_006660       | B0XPJ1       | Short-chain dehydrogenase/reductase family protein, putative                                             | 1     | 13  |
| AFUB_015500       | B0XLY5       | Oxidoreductase, short-chain dehydrogenase/reductase family                                             | 1     | 13  |
| AFUB_000900       | B0XM47       | Oxidoreductase, short-chain dehydrogenase/reductase family                                             | 1     | 13  |
| AFUB_099790       | B0YEN4       | Oxidoreductase, short-chain dehydrogenase/reductase family                                             | 1     | 13  |
| AFUB_055020       | B0Y3Q3       | Oxidoreductase, short-chain dehydrogenase/reductase family                                             | 1     | 13  |
| AFUB_056700       | B0Y468       | Oxidoreductase, short-chain dehydrogenase/reductase family                                             | 1     | 13  |
| AFUB_058390       | B0Y8S7       | Oxidoreductase, short-chain dehydrogenase/reductase family                                             | 1     | 13  |
| AFUB_089620       | B0YCB7       | 3-ketoacyl-CoA thiolase (POT1), putative                                                               | 1     | 13  |
| AFUB_068010       | B0Y6S9       | 3-ketoacyl-coA thiolase peroxisomal A                                                                  | 1     | 13  |
| AFUB_027110       | B0XSG5       | Peroxisomal 3-ketoacyl-coA thiolase (Kat1), putative                                                    | 1     | 13  |
| AFUB_090080       | B0YCG2       | Short chain dehydrogenase/reductase family                                                             | 1     | 13  |
| AFUB_052350       | B0Y2Z0       | Oxidoreductase, short-chain dehydrogenase/reductase family                                             | 1     | 13  |
| AFUB_085060       | B0YAL3       | Oxidoreductase, short-chain dehydrogenase/reductase family                                             | 1     | 13  |
| AFUB_017080       | B0XPL4       | Short chain dehydrogenase, putative                                                                    | 1     | 13  |
| AFUB_062960       | B0Y5C9       | Oxidoreductase, short-chain dehydrogenase/reductase family                                             | 1     | 13  |
| AFUB_072060       | B0Y5B7       | Short chain dehydrogenase, putative                                                                    | 1     | 13  |
| AFUB_094160       | B0YD38       | Short chain dehydrogenase/reductase family protein                                                    | 1     | 13  |
| AFUB_100680       | B0YEW1       | Short-chain dehydrogenase, putative                                                                    | 1     | 13  |
| AFUB_080930       | B0Y9G3       | Oxidoreductase, short-chain dehydrogenase/reductase family                                             | 1     | 13  |
| AFUB_083570       | B0YA65       | Acetyl-CoA acetyltransferase, putative                                                                 | 1     | 13  |
| AFUB_082740       | B0Y9Y8       | Acetoacetyl-CoA synthase                                                                                | 1     | 13  |
| AFUB_080560       | B0Y9C7       | Hydroxymethylglutaryl-CoA synthase, putative                                                           | 1     | 13  |
| AFUB_043930       | B0XZC5       | Uncharacterized protein                                                                                  | 1     | 13  |
| AFUB_038500       | B0XCT5       | Hydroxymethylglutaryl-CoA synthase, putative                                                           | 1     | 13  |
| AFUB_011330       | B0XQV8       | Acetoacetyl-CoA synthase                                                                                | 1     | 13  |
| AFUB_005550       | B0XMC1       | Acetyl-CoA-acetyltransferase, putative                                                                 | 1     | 13  |
| AFUB_014030       | B0XQM0       | Short chain oxidoreductase/dehydrogenase, putative                                                     | 1     | 13  |
| AFUB_084240       | B0YAD0       | PKS-like enzyme, putative                                                                                | 1     | 13  |
| AFUB_018340       | B0XT81       | HLH transcription factor, putative                                                                      | 1     | 13  |
| AFUB_057720       | B0YOL3       | Hybrid NRPS/PKS enzyme                                                                                 | 1     | 13  |
| AFUB_000820       | B0XM39       | Polyketide synthase, putative                                                                           | 1     | 13  |
| AFUB_046300       | B0Y013       | Short-chain dehydrogenase/reductase, putative                                                          | 1     | 13  |
| AFUB_099120       | B0YEG7       | Peroxisomal multifunctional beta-oxidation protein (MFP), putative                                      | 1     | 13  |
| Accession | Gene | Protein Name | Function | Start Position | End Position |
|-----------|------|--------------|----------|----------------|-------------|
| CADAFUBP00007032 | AFUB_072240 | B0Y717 | Histone-lysine N-methyltransferase (EC 2.1.1.43) | 1 | 13 |
| CADAFUBP00005084 | AFUB_051950 | B0Y2T9 | PHD transcription factor (Rum1), putative | 1 | 13 |
| CADAFUBP00009283 | AFUB_095530 | B0YDG8 | Short-chain dehydrogenase/reductase family protein, putative | 1 | 13 |
| CADAFUBP00005565 | AFUB_056830 | B0Y481 | NAD-dependent 15-hydroxyprostaglandin dehydrogenase | 1 | 13 |
| CADAFUBP00007474 | AFUB_076700 | B0Y8A9 | ATP citrate lyase subunit (Acl), putative | 1 | 13 |
| CADAFUBP00007473 | AFUB_076690 | B0Y8A8 | ATP citrate lyase, subunit 1, putative | 1 | 13 |
| CADAFUBP00005597 | AFUB_057150 | B0Y4B3 | 2-nitropropane dioxygenase family oxidoreductase, putative | 1 | 13 |
| CADAFUBP00002402 | AFUB_024590 | B0XRR7 | Acetyl-CoA carboxylase | 1 | 13 |
| CADAFUBP00002226 | AFUB_027790 | B0XX4 | 3-oxoacyl-[acyl-carrier-protein] synthase | 1 | 13 |
| CADAFUBP00005566 | AFUB_056940 | B0Y4B3 | Carbonyl reductase, putative | 1 | 13 |
| CADAFUBP00004404 | AFUB_044900 | B0XZQ7 | Nonribosomal peptide synthase SidE | 1 | 13 |
| CADAFUBP00009105 | AFUB_093680 | B0YCZ0 | NADH-ubiquinone oxidoreductase B14 subunit, putative | 1 | 15 |
| CADAFUBP00000343 | AFUB_005660 | B0YA54 | NADH-ubiquinone oxidoreductase 304 kDa subunit | 1 | 15 |
| CADAFUBP00006212 | AFUB_067350 | B0Y753 | Cytochrome b-c1 complex subunit 7 | 1 | 15 |
| CADAFUBP00005570 | AFUB_058380 | B0Y0S6 | Cytochrome c oxidase subunit Va, putative | 1 | 15 |
| CADAFUBP00004323 | AFUB_043140 | B0XZ48 | NADH-ubiquinone oxidoreductase 304 kDa subunit | 1 | 15 |
| CADAFUBP00005710 | AFUB_058380 | B0Y0S6 | Cytochrome c oxidase subunit Va, putative | 1 | 15 |
| CADAFUBP00002670 | AFUB_027310 | B0XSI5 | UDP-glucose 4-epimerase | 1 | 15 |
| CADAFUBP00004037 | AFUB_041210 | B0XZ48 | UDP-glucose 4-epimerase, putative | 1 | 15 |
| CADAFUBP00002670 | AFUB_027310 | B0XSI5 | UDP-glucose 4-epimerase, putative | 1 | 15 |
| CADAFUBP00000688 | AFUB_007000 | B0XPN4 | Acyl carrier protein | 1 | 15 |
| CADAFUBP00000172 | AFUB_001770 | B0X00 | Nuclear distribution protein nudF (Lissencephaly-1 homolog) (LIS-1) | 1 | 15 |
| CADAFUBP00006407 | AFUB_065820 | B0Y665 | Lysoosphopholipase 1 (EC 3.1.1.5) (Phospholipase B 1) | 1 | 15 |
| CADAFUBP00000487 | AFUB_001300 | B0XER7 | Lysoosphopholipase NTE1 (EC 3.1.1.5) (Intracellular phospholipase B) | 1 | 15 |
| CADAFUBP00009732 | AFUB_010130 | B0Y753 | MBOAT family protein, putative | 1 | 15 |
| CADAFUBP00009797 | AFUB_093420 | B0YCW4 | Glyceraldehyde diester phosphorylase family protein | 1 | 15 |
| CADAFUBP00007627 | AFUB_078250 | B0Y8R2 | Glyceraldehyde diester phosphorylase family protein | 1 | 15 |
| CADAFUBP00003378 | AFUB_034540 | B0XZV8 | Glyceraldehyde diester phosphorylase family protein | 1 | 15 |
| CADAFUBP00001763 | AFUB_018080 | B0XT55 | Glyceraldehyde diester phosphorylase family protein | 1 | 15 |
| CADAFUBP00009777 | AFUB_100690 | B0YEW2 | Fatty acid oxygenase, putative | 1 | 15 |
| CADAFUBP00006604 | AFUB_067500 | B0Y6R2 | Fatty acid oxygenase, putative | 1 | 15 |
| CADAFUBP00006379 | AFUB_065540 | B0Y637 | Patatin-like phospholipase domain-containing protein (EC 3.1.1.1) | 1 | 15 |
| CADAFUBP00003628 | AFUB_037060 | B0XX73 | Fatty acid oxygenase PpoC, putative | 1 | 15 |
| CADAFUBP00002707 | AFUB_002700 | B0XSM2 | Lysoosphopholipase (EC 3.1.1.5) | 1 | 15 |
| CADAFUBP00006555 | AFUB_006670 | B0XPJ2 | Small nucleolar ribonucleoprotein complex subunit | 1 | 15 |
| Accession | Gene ID    | Description                                                                 |
|-----------|------------|------------------------------------------------------------------------------|
| CADAFUBP00004164 | AFUB_042470 B0XY0 | (SOF1), putative WD repeat protein                                         |
| CADAFUBP00007043 | AFUB_072350 B0Y728 | rRNA processing protein (Rrp20), putative                                 |
| CADAFUBP00001840 | AFUB_018850 B0XTK0 | Small nucleolar ribonucleoprotein complex subunit Utp15, putative           |
| CADAFUBP00001234 | AFUB_012550 B0XR93 | U3 small nucleolar ribonucleoprotein protein IMP4, putative                 |
| CADAFUBP00004222 | AFUB_043040 B0XZ38 | RNA processing protein Emg1, putative                                      |
| CADAFUBP00001934 | AFUB_019810 B0XU13 | 60S ribosomal protein L24b, putative                                        |
| CADAFUBP00009106 | AFUB_093690 B0YCZ1 | DNA-directed RNA polymerase I and III 14 kDa polypeptide                    |
| CADAFUBP00008055 | AFUB_082720 B0Y9Y6 | Ribosome biogenesis protein, putative                                       |
| CADAFUBP00007233 | AFUB_074260 B0Y7L8 | DNA-directed RNA polymerase subunit (EC 2.7.7.6)                           |
| CADAFUBP00001234 | AFUB_012550 B0XR93 | U3 small nucleolar ribonucleoprotein protein IMP4, putative                 |
| CADAFUBP00001934 | AFUB_019810 B0XU13 | 60S ribosomal protein L24b, putative                                        |
| CADAFUBP00006238 | AFUB_064720 B0Y5V6 | Ribosome biogenesis protein ytm1, putative                                 |
| CADAFUBP00002875 | AFUB_029350 B0XTN4 | DNA-directed RNA polymerase I and III subunit Rrp40, putative               |
| CADAFUBP000005189 | AFUB_053000 B0Y355 | Small nuclear ribonucleoprotein complex protein Nhp2, putative              |
| CADAFUBP00002371 | AFUB_024280 B0XWC0 | U3 small nucleolar ribonucleoprotein subunit (Imp3), putative               |
| CADAFUBP00002197 | AFUB_022500 B0XVJ8 | DNA-directed RNA polymerase subunit                                          |
| CADAFUBP000007038 | AFUB_072300 B0Y723 | Methyltransferase, putative                                                 |
| CADAFUBP000005253 | AFUB_053470 B0Y3A2 | RNA processing factor 1                                                     |
| CADAFUBP000004303 | AFUB_043850 B0XZB9 | rRNA processing protein Bystin, putative                                   |
| CADAFUBP000008747 | AFUB_089980 B0YCF2 | Ribosome biogenesis protein (Rrs1), putative                               |
| CADAFUBP000006172 | AFUB_063470 B0Y510 | Ribosomal biogenesis protein Gar2                                            |
| CADAFUBP000005976 | AFUB_061170 B0Y241 | 60S acidic ribosomal protein P0, putative                                   |
| CADAFUBP000003207 | AFUB_032720 B0XV3D | DNA-directed RNA polymerase subunit                                          |
| CADAFUBP000002789 | AFUB_028500 B0XT12 | Pre-rRNA processing protein Nip7, putative                                 |
| CADAFUBP000001285 | AFUB_013060 B0XU13 | Pre-rRNA processing protein, putative                                       |
| CADAFUBP000005585 | AFUB_053000 B0Y4A1 | ABC transporter, putative                                                   |
| CADAFUBP000009863 | AFUB_015559 B0YF48 | ABC multidrug transporter, putative                                         |
| CADAFUBP000007208 | AFUB_074010 B0Y7I3 | ABC transporter, putative                                                   |
| CADAFUBP000007131 | AFUB_073240 B0Y7B6 | ABC transporter (Adp1), putative                                            |
| CADAFUBP000005583 | AFUB_057010 B0Y499 | ABC transporter, putative                                                   |
| CADAFUBP000004970 | AFUB_050970 B0Y2A7 | ABC multidrug transporter, putative                                         |
| CADAFUBP000004817 | AFUB_049250 B0YA6 | ABC multidrug transporter, putative                                         |
| CADAFUBP000004607 | AFUB_047000 B0XWR0 | ABC multidrug transporter, putative                                         |
| CADAFUBP000004094 | AFUB_041770 B0XRY0 | ABC multidrug transporter, putative                                         |
| CADAFUBP000002904 | AFUB_029650 B0XTR3 | ABC transporter, putative                                                   |
| CADAFUBP000001360 | AFUB_013880 B0XMR3 | ABC transporter, putative                                                   |
| CADAFUBP000005218 | AFUB_063920 B0Y5M6 | ABC transporter, putative                                                   |
| CADAFUBP00000576 | AFUB_065860 B0XP43 | Coenzyme A synthetase, putative                                             |
| CADAFUBP000001238 | AFUB_012590 B0XR97 | 4-coumarate-CoA ligase, putative                                            |
| CADAFUBP000002507 | AFUB_025650 B0XS22 | Mandelate racemase/muconate lactonizing enzyme family protein               |
| CADAFUBP000008564 | AFUB_088100 B0YW9 | AMP-binding enzyme, putative                                                |
| CADAFUBP000002538 | AFUB_025970 B0XS53 | Phenylacetoyl-CoA ligase, putative                                          |
| CADAFUBP000005881 | AFUB_060180 B0Y1F8 | Adenylate-forming enzyme AeA                                               |
| CADAFUBP000005483 | AFUB_056010 B0Y3Z9 | AMP-binding enzyme, putative                                                |
| CADAFUBP000006053 | AFUB_061980 B0Y2I9 | AMP dependent CoA ligase                                                   |
| CADAFUBP00000082 | AFUB_008830 B0XMR4 | Adenylate-forming enzyme, putative                                          |
| CADAFUBP000008739 | AFUB_089890 B0YCE4 | Mandelate racemase/muconate lactonizing enzyme family protein               |
| Accession     | Gene_ID       | Description                              | Count | Value |
|--------------|---------------|------------------------------------------|-------|-------|
| CADAUFUBP00001626 | AFUB_016580 B0XP98 | Long-chain-fatty-acid-CoA ligase, putative | 5     | 1     |
| CADAUFUBP00000625 | AFUB_006370 B0XPG2 | AMP-binding domain protein, putative     | 5     | 1     |
Supplementary Table 3 | Sub-module 1 cluster 1, significantly enriched GO terms (biological processes)

| GO-ID         | Term                             | Count | Size | p-value       |
|---------------|----------------------------------|-------|------|---------------|
| GO:0006694    | steroid biosynthetic process     | 14    | 21   | 2.97353E-12   |
| GO:0055114    | oxidation-reduction process      | 39    | 211  | 1.52684E-10   |
| GO:0016128    | phytosteroid metabolic process   | 11    | 17   | 1.41806E-09   |
| GO:0044107    | cellular alcohol metabolic process | 11  | 17   | 1.41806E-09   |
| GO:0006696    | ergosterol biosynthetic process  | 11    | 17   | 1.41806E-09   |
| GO:0016125    | sterol metabolic process         | 11    | 18   | 3.43632E-09   |
| GO:1902652    | secondary alcohol metabolic process | 12  | 23   | 7.25617E-09   |
| GO:0046165    | alcohol biosynthetic process     | 13    | 32   | 7.24412E-08   |
| GO:0044255    | cellular lipid metabolic process | 17    | 71   | 3.83852E-06   |
| GO:0008202    | steroid metabolic process        | 4     | 4    | 1.15868E-05   |
| GO:0006633    | fatty acid biosynthetic process  | 6     | 15   | 0.00039       |
| GO:0044699    | single-organism process          | 50    | 513  | 0.00127       |
| GO:0044711    | single-organism biosynthetic process | 26  | 206  | 0.00156       |
| GO:0016104    | triterpenoid biosynthetic process | 2     | 2    | 0.00541       |
**Supplementary Table 4** | Sub-module 1 cluster 2, significantly enriched GO terms (biological processes)

| GO-ID          | Term                                              | Count | Size  | p-value          |
|----------------|---------------------------------------------------|-------|-------|------------------|
| GO:0006979     | response to oxidative stress                      | 6     | 28    | 3.25040E-06      |
| GO:1901700     | response to oxygen-containing compound            | 5     | 16    | 3.40598E-06      |
| GO:0006801     | superoxide metabolic process                       | 3     | 3     | 3.70766E-06      |
| GO:0007571     | age-dependent general metabolic decline            | 3     | 3     | 4.54815E-06      |
| GO:0019363     | pyridine nucleotide biosynthetic process           | 3     | 4     | 1.79959E-05      |
| GO:0009435     | NAD biosynthetic process                           | 3     | 4     | 1.79959E-05      |
| GO:0006468     | protein phosphorylation                            | 4     | 17    | 0.00014          |
| GO:0006586     | indolalkylamine metabolic process                  | 3     | 7     | 0.00015          |
| GO:0001320     | age-dependent response to reactive oxygen species involved in chronological cell aging | 2     | 2     | 0.00029          |
| GO:0001315     | age-dependent response to reactive oxygen species | 2     | 2     | 0.00029          |
| GO:0070887     | cellular response to chemical stimulus             | 6     | 63    | 0.00041          |
| GO:0034354     | 'de novo' NAD biosynthetic process from tryptophan | 2     | 3     | 0.00087          |
| GO:0006796     | phosphate-containing compound metabolic process    | 7     | 104   | 0.00103          |
| GO:0036211     | protein modification process                       | 5     | 50    | 0.00116          |
| GO:0044106     | cellular amine metabolic process                   | 3     | 13    | 0.00117          |
| GO:0044699     | single-organism process                           | 15    | 513   | 0.00139          |
| GO:0010035     | response to inorganic substance                    | 3     | 14    | 0.00147          |
| GO:0042436     | indole-containing compound catabolic process       | 2     | 4     | 0.00172          |
| GO:0038202     | TORC1 signaling                                    | 2     | 4     | 0.00172          |
| GO:0006569     | tryptophan catabolic process                       | 2     | 4     | 0.00172          |
| GO:0050896     | response to stimulus                               | 5     | 70    | 0.00178          |
| GO:009072      | aromatic amino acid family metabolic process       | 3     | 17    | 0.00266          |
| GO:0042402     | cellular biogenic amine catabolic process           | 2     | 5     | 0.00284          |
| GO:0010648     | negative regulation of cell communication          | 2     | 5     | 0.00284          |
| GO:0023057     | negative regulation of signaling                   | 2     | 5     | 0.00284          |
| GO:1901293     | nucleoside phosphate biosynthetic process          | 3     | 18    | 0.00315          |
| GO:0001302     | replicative cell aging                             | 2     | 6     | 0.00422          |
| GO:0043620     | regulation of DNA-templated transcription in response to stress | 2     | 6     | 0.00422          |
| GO:0070301     | cellular response to hydrogen peroxide             | 2     | 6     | 0.00422          |
| GO:0019438     | aromatic compound biosynthetic process             | 6     | 97    | 0.00428          |
| GO:0018130     | heterocycle biosynthetic process                   | 6     | 106   | 0.00467          |
| GO:0051188     | cofactor biosynthetic process                      | 3     | 23    | 0.00648          |
| GO:0046496     | nicotinamide nucleotide metabolic process          | 3     | 26    | 0.00921          |
| GO:0072524     | pyridine-containing compound metabolic process      | 3     | 26    | 0.00921          |
**Supplementary Table 5** | Sub-module 1 cluster 3, significantly enriched GO terms (biological processes)

| GO-ID          | Term                              | Count | Size | p-value       |
|----------------|-----------------------------------|-------|------|---------------|
| GO:0006897     | endocytosis                       | 5     | 6    | 2.40413E-08   |
| GO:0030029     | actin filament-based process       | 5     | 6    | 2.40413E-08   |
| GO:0007010     | cytoskeleton organization          | 5     | 9    | 4.82736E-07   |
| GO:0007015     | actin filament organization        | 4     | 5    | 1.06152E-06   |
| GO:0016311     | dephosphorylation                 | 4     | 7    | 7.20793E-06   |
| GO:0000147     | actin cortical patch assembly      | 3     | 3    | 1.08019E-05   |
| GO:0046856     | phosphatidylinositol dephosphorylation | 3  | 3    | 1.08019E-05   |
| GO:0030258     | lipid modification                 | 4     | 8    | 1.41981E-05   |
| GO:1902589     | single-organism organelle organization | 5 | 16   | 1.50689E-05   |
| GO:0051234     | establishment of localization      | 5     | 24   | 7.00960E-05   |
| GO:0006650     | glycerophospholipid metabolic process | 4 | 12   | 9.44658E-05   |
| GO:0030242     | pexophagy                         | 2     | 3    | 0.00152       |
| GO:0045324     | late endosome to vacuole transport | 2     | 3    | 0.00152       |
| GO:0016043     | cellular component organization    | 7     | 92   | 0.00317       |
| GO:0072665     | protein localization to vacuole   | 2     | 5    | 0.00492       |
| GO:0030010     | establishment of cell polarity     | 2     | 5    | 0.00492       |
| GO:0016236     | macroautophagy                     | 2     | 6    | 0.00728       |
| GO:0070727     | cellular macromolecule localization | 4 | 37   | 0.0086        |
| GO-ID   | Term                          | Count | Size | p-value   |
|---------|-------------------------------|-------|------|-----------|
| GO:0008299 | isoprenoid biosynthetic process | 4     | 5    | 1.28999E-08 |
| GO:0044255 | cellular lipid metabolic process | 6     | 71   | 3.10319E-05 |
| GO-ID     | Term                                                | Count | Size | p-value     |
|-----------|-----------------------------------------------------|-------|------|-------------|
| GO:0036211| protein modification process                        | 8     | 50   | 2.07199E-08 |
| GO:0044700| single organism signaling                           | 5     | 17   | 2.66968E-08 |
| GO:0006468| protein phosphorylation                             | 5     | 13   | 3.21622E-08 |
| GO:0044764| multi-organism cellular process                     | 6     | 20   | 4.40182E-08 |
| GO:0048315| conidium formation                                  | 5     | 12   | 7.14998E-08 |
| GO:0051347| positive regulation of transferase activity         | 4     | 5    | 8.85073E-08 |
| GO:0042327| positive regulation of phosphorylation              | 4     | 5    | 8.85073E-08 |
| GO:0065007| biological regulation                               | 7     | 96   | 1.35817E-07 |
| GO:0000909| sporocarp development involved in sexual reproduction| 5    | 13   | 1.93373E-07 |
| GO:0019954| asexual reproduction                                | 6     | 26   | 2.52492E-07 |
| GO:0031135| negative regulation of conjugation                  | 4     | 7    | 6.10773E-07 |
| GO:0048608| reproductive structure development                  | 5     | 16   | 6.43530E-07 |
| GO:0044707| single-multicellular organism process               | 5     | 16   | 6.43530E-07 |
| GO:0048731| system development                                  | 5     | 16   | 6.43530E-07 |
| GO:0045930| negative regulation of mitotic cell cycle           | 4     | 8    | 1.21285E-06 |
| GO:0099628| response to abiotic stimulus                        | 6     | 34   | 1.40746E-06 |
| GO:0051716| cellular response to stimulus                       | 7     | 83   | 1.71546E-06 |
| GO:0007050| cell cycle arrest                                   | 3     | 3    | 1.78677E-06 |
| GO:0032147| activation of protein kinase activity                | 3     | 3    | 1.78677E-06 |
| GO:0071474| cellular hyperosmotic response                      | 3     | 3    | 1.78677E-06 |
| GO:0043902| positive regulation of multi-organism process       | 4     | 9    | 2.16759E-06 |
| GO:2000242| negative regulation of reproductive process         | 4     | 10   | 3.58691E-06 |
| GO:0051247| positive regulation of protein metabolic process     | 4     | 10   | 3.58691E-06 |
| GO:0048522| positive regulation of cellular process             | 5     | 34   | 6.45735E-06 |
| GO:0010647| positive regulation of cell communication           | 3     | 4    | 7.09360E-06 |
| GO:0023056| positive regulation of signaling                    | 3     | 4    | 7.09360E-06 |
| GO:1902533| positive regulation of intracellular signal transduction | 3 | 4 | 7.09360E-06 |
| GO:0044267| cellular protein metabolic process                  | 7     | 90   | 7.61259E-06 |
| GO:0071840| cellular component organization or biogenesis       | 8     | 112  | 1.40847E-05 |
| GO:0051128| regulation of cellular component organization       | 4     | 17   | 1.70837E-05 |
| GO:0032505| reproduction of a single-celled organism             | 4     | 15   | 2.24945E-05 |
| GO:0034293| sexual sporulation                                  | 4     | 15   | 2.24945E-05 |
| GO:0031139| positive regulation of conjugation with cellular fusion | 3 | 6 | 2.63568E-05 |
| GO:0044093| positive regulation of molecular function           | 3     | 6    | 2.64440E-05 |
| GO:0007154| cell communication                                  | 3     | 14   | 3.32168E-05 |
| GO:0006950| response to stress                                  | 6     | 71   | 3.41614E-05 |
| GO:0019953| sexual reproduction                                 | 3     | 11   | 4.93026E-05 |
| GO:0070787| conidiophore development                           | 3     | 7    | 6.06849E-05 |
| GO:0043455| regulation of secondary metabolic process           | 3     | 7    | 6.06849E-05 |
| GO:0042325| regulation of phosphorylation                       | 2     | 2    | 6.92127E-05 |
| GO:0051174| regulation of phosphorus metabolic process          | 2     | 2    | 6.95215E-05 |
| GO:0030435| sporulation resulting in formation of a cellular spore | 4 | 20 | 7.70249E-05 |
| GO:0048584| positive regulation of response to stimulus         | 4     | 20   | 7.70249E-05 |
| GO:0000165| MAPK cascade                                       | 2     | 2    | 8.85934E-05 |
| GO:1901990| regulation of mitotic cell cycle phase transition   | 3     | 8    | 9.63681E-05 |
| GO:0009889| regulation of biosynthetic process                  | 4     | 26   | 0.00011    |
| GO:0010605| negative regulation of macromolecule metabolic process | 4 | 22 | 0.00011 |
| GO:1903533| regulation of protein targeting                     | 2     | 2    | 0.00016    |
| GO:1902074| response to salt                                    | 2     | 2    | 0.00016    |
| GO          | Description                                                                 | Count1 | Count2 | FDR     |
|-------------|------------------------------------------------------------------------------|--------|--------|---------|
| GO:0045936  | negative regulation of phosphate metabolic process                           | 2      | 2      | 0.00016 |
| GO:0010969  | regulation of pheromone-dependent signal transduction involved in conjugation with cellular fusion | 2      | 2      | 0.00016 |
| GO:1903936  | cellular response to sodium arsenite                                          | 2      | 2      | 0.00016 |
| GO:0060240  | negative regulation of signal transduction involved in conjugation with cellular fusion | 2      | 2      | 0.00016 |
| GO:0043406  | positive regulation of MAP kinase activity                                   | 2      | 2      | 0.00016 |
| GO:0000768  | syncytium formation by plasma membrane fusion                                | 2      | 2      | 0.00016 |
| GO:0046685  | response to arsenic-containing substance                                     | 2      | 2      | 0.00016 |
| GO:0070302  | regulation of stress-activated protein kinase signaling cascade              | 2      | 2      | 0.00016 |
| GO:0071851  | mitotic G1 cell cycle arrest in response to nitrogen starvation               | 2      | 2      | 0.00016 |
| GO:0030437  | ascospore formation                                                          | 3      | 11     | 0.00021 |
| GO:0051726  | regulation of cell cycle                                                     | 2      | 3      | 0.00021 |
| GO:1903506  | regulation of nucleic acid-templated transcription                           | 4      | 26     | 0.00023 |
| GO:0051252  | regulation of RNA metabolic process                                          | 4      | 26     | 0.00023 |
| GO:006796   | phosphate-containing compound metabolic process                              | 6      | 102    | 0.00026 |
| GO:0071310  | cellular response to organic substance                                       | 3      | 12     | 0.00037 |
| GO:0010515  | negative regulation of induction of conjugation with cellular fusion         | 2      | 3      | 0.0004  |
| GO:006366   | transcription from RNA polymerase II promoter                                | 3      | 14     | 0.00046 |
| GO:0051171  | regulation of nitrogen compound metabolic process                            | 3      | 17     | 0.00047 |
| GO:1901989  | positive regulation of cell cycle phase transition                           | 2      | 3      | 0.00048 |
| GO:0060341  | regulation of cellular localization                                          | 2      | 3      | 0.00048 |
| GO:0019932  | second-messenger-mediated signaling                                          | 2      | 3      | 0.00048 |
| GO:0090087  | regulation of peptide transport                                              | 2      | 3      | 0.00048 |
| GO:1901362  | organic cyclic compound biosynthetic process                                 | 7      | 132    | 0.00051 |
| GO:2000112  | regulation of cellular macromolecule biosynthetic process                    | 4      | 35     | 0.00052 |
| GO:0080090  | regulation of primary metabolic process                                      | 3      | 28     | 0.00054 |
| GO:0045229  | external encapsulating structure organization                                | 3      | 14     | 0.0006  |
| GO:0031399  | regulation of protein modification process                                   | 2      | 5      | 0.00068 |
| GO:0043900  | regulation of multi-organism process                                         | 2      | 5      | 0.00069 |
| GO:1903046  | meiotic cell cycle process                                                   | 3      | 16     | 0.00069 |
| GO:0019438  | aromatic compound biosynthetic process                                       | 6      | 97     | 0.00071 |
| GO:0007163  | establishment or maintenance of cell polarity                                | 3      | 15     | 0.00074 |
| GO:0045931  | positive regulation of mitotic cell cycle                                    | 2      | 4      | 0.0008  |
| GO:0009651  | response to salt stress                                                      | 2      | 4      | 0.0008  |
| GO:0009893  | positive regulation of metabolic process                                     | 2      | 5      | 0.0009  |
| GO:1900436  | positive regulation of filamentous growth of a population of unicellular organisms in response to starvation | 2      | 4      | 0.00095 |
| GO:0019236  | response to pheromone                                                        | 2      | 4      | 0.00095 |
| GO:0032101  | regulation of response to external stimulus                                  | 2      | 4      | 0.00095 |
| GO:0032106  | positive regulation of response to extracellular stimulus                    | 2      | 4      | 0.00095 |
| GO:0032107  | regulation of response to nutrient levels                                    | 2      | 4      | 0.00095 |
| GO:1902749  | regulation of cell cycle G2/M phase transition                               | 2      | 4      | 0.00095 |
| GO:0090066  | regulation of anatomical structure size                                      | 2      | 4      | 0.00095 |
| GO:0090033  | positive regulation of filamentous growth                                    | 2      | 4      | 0.00095 |
| GO:0071470  | cellular response to osmotic stress                                          | 2      | 6      | 0.00102 |
| GO:0010468  | regulation of gene expression                                                 | 4      | 38     | 0.00103 |
| GO:0042221  | response to chemical                                                         | 4      | 57     | 0.00151 |
| GO:0010648  | negative regulation of cell communication                                    | 2      | 5      | 0.00158 |
| GO:0023057  | negative regulation of signaling                                             | 2      | 5      | 0.00158 |
| GO:0031329  | regulation of cellular catabolic process                                      | 2      | 5      | 0.00158 |
| GO:0030448  | hyphal growth                                                                 | 3      | 21     | 0.00207 |
| GO:1903047  | mitotic cell cycle process                                                    | 3      | 21     | 0.00207 |
| GO:0090304  | nucleic acid metabolic process                                                | 5      | 79     | 0.00217 |
| GO:0043620  | regulation of DNA-templated transcription in response to stress              | 2      | 6      | 0.00235 |
| GO ID          | Description                                                      | Count | Total | P-value   |
|----------------|------------------------------------------------------------------|-------|-------|-----------|
| GO:0051170     | nuclear import                                                   | 2     | 6     | 0.00235   |
| GO:0043937     | regulation of sporulation                                         | 2     | 6     | 0.00235   |
| GO:0044271     | cellular nitrogen compound biosynthetic process                  | 6     | 121   | 0.00236   |
| GO:0035556     | intracellular signal transduction                                 | 2     | 12    | 0.0024    |
| GO:0033044     | regulation of chromosome organization                            | 2     | 7     | 0.00274   |
| GO:1900428     | regulation of filamentous growth of a population of unicellular organisms | 2     | 7     | 0.00327   |
| GO:0032269     | negative regulation of cellular protein metabolic process        | 2     | 7     | 0.00327   |
| GO:0048585     | negative regulation of response to stimulus                      | 2     | 7     | 0.00327   |
| GO:0042542     | response to hydrogen peroxide                                    | 2     | 8     | 0.00432   |
| GO:0022414     | reproductive process                                             | 2     | 16    | 0.00444   |
| GO:0048468     | cell development                                                 | 2     | 13    | 0.00522   |
| GO:0018130     | heterocycle biosynthetic process                                  | 5     | 106   | 0.00523   |
| GO:0048285     | organelle fission                                                | 2     | 10    | 0.00684   |
| GO:0051246     | regulation of protein metabolic process                           | 2     | 15    | 0.00693   |
| GO:0031505     | fungal-type cell wall organization                                | 2     | 11    | 0.00699   |
| GO:0010564     | regulation of cell cycle process                                 | 2     | 11    | 0.00702   |
| GO:0035690     | cellular response to drug                                        | 3     | 32    | 0.00712   |
| GO:0031668     | cellular response to extracellular stimulus                      | 3     | 33    | 0.00777   |
| GO:1902582     | single-organism intracellular transport                           | 2     | 11    | 0.0083    |
| GO:0045893     | positive regulation of transcription, DNA-templated              | 2     | 12    | 0.00989   |
| GO:0040008     | regulation of growth                                             | 2     | 12    | 0.00989   |
| GO:1902680     | positive regulation of RNA biosynthetic process                  | 2     | 12    | 0.00989   |
| GO:0034248     | regulation of cellular amide metabolic process                   | 2     | 12    | 0.00989   |
Supplementary Table 8 | Sub-module 1 cluster 6, significantly enriched GO terms (biological processes)

| GO-ID     | Term                                                      | Count | Size  | p-value     |
|-----------|-----------------------------------------------------------|-------|-------|-------------|
| GO:0006082| organic acid metabolic process                            | 111   | 191   | 6.43205E-29 |
| GO:0006520| cellular amino acid metabolic process                     | 51    | 66    | 4.18215E-22 |
| GO:1901607| alpha-amino acid biosynthetic process                     | 26    | 30    | 3.36716E-13 |
| GO:0046394| carboxylic acid biosynthetic process                      | 52    | 93    | 1.91656E-11 |
| GO:0006807| nitrogen compound metabolic process                       | 112   | 293   | 7.17667E-10 |
| GO:0055114| oxidation-reduction process                               | 88    | 211   | 9.17399E-10 |
| GO:0046395| carboxylic acid catabolic process                         | 29    | 44    | 5.79554E-09 |
| GO:0009066| aspartate family amino acid metabolic process             | 18    | 21    | 6.17613E-09 |
| GO:0044710| single-organism metabolic process                         | 75    | 236   | 7.19873E-08 |
| GO:0044283| small molecule biosynthetic process                       | 56    | 124   | 7.66122E-08 |
| GO:1901565| organonitrogen compound catabolic process                 | 21    | 30    | 1.53891E-07 |
| GO:0006099| tricarboxylic acid cycle                                 | 12    | 14    | 2.87753E-06 |
| GO:0044282| small molecule catabolic process                          | 30    | 58    | 6.39517E-06 |
| GO:1901566| organonitrogen compound biosynthetic process              | 51    | 125   | 9.3497E-06  |
| GO:1901606| alpha-amino acid catabolic process                        | 14    | 20    | 2.09419E-05 |
| GO:0044272| sulfur compound biosynthetic process                     | 11    | 14    | 3.14417E-05 |
| GO:0072350| tricarboxylic acid metabolic process                      | 10    | 12    | 3.22308E-05 |
| GO:0045333| cellular respiration                                     | 14    | 21    | 6.02294E-05 |
| GO:0009064| glutamine family amino acid metabolic process             | 6     | 6     | 0.00019     |
| GO:0009086| methionine biosynthetic process                           | 7     | 8     | 0.00038     |
| GO:0000096| sulfur amino acid metabolic process                       | 5     | 5     | 0.00089     |
| GO:0006536| glutamate metabolic process                               | 5     | 5     | 0.00092     |
| GO:0044273| sulfur compound catabolic process                         | 5     | 5     | 0.00098     |
| GO:0009098| leucine biosynthetic process                              | 5     | 5     | 0.00098     |
| GO:0009065| glutamine family amino acid catabolism                    | 5     | 5     | 0.00098     |
| GO:0006767| water-soluble vitamin metabolic process                  | 5     | 5     | 0.00098     |
| GO:0006526| arginine biosynthetic process                             | 5     | 5     | 0.00098     |
| GO:0043648| dicarboxylic acid metabolic process                       | 6     | 7     | 0.00104     |
| GO:0006637| acyl-CoA metabolic process                                | 8     | 11    | 0.00117     |
| GO:0006575| cellular modified amino acid metabolic process             | 6     | 7     | 0.00123     |
| GO:0006067| ethanol metabolic process                                 | 6     | 7     | 0.00134     |
| GO:0006534| cysteine metabolic process                                | 6     | 7     | 0.00134     |
| GO:0009082| branched-chain amino acid biosynthetic process            | 4     | 4     | 0.00354     |
| GO:0042398| cellular modified amino acid biosynthetic process         | 4     | 4     | 0.00379     |
| GO:1902221| erythrose 4-phosphate/phosphoenolpyruvate family amino acid metabolic process | 4     | 4     | 0.00395     |
| GO:0006108| malate metabolic process                                  | 4     | 4     | 0.00395     |
| GO:0009110| vitamin biosynthetic process                              | 4     | 4     | 0.00395     |
| GO:0006570| tyrosine metabolic process                                | 4     | 4     | 0.00395     |
| GO:0006537| glutamate biosynthetic process                            | 4     | 4     | 0.00395     |
| GO:0006085| acetyl-CoA biosynthetic process                           | 5     | 6     | 0.00467     |
| GO:0009092| homoserine metabolic process                              | 5     | 6     | 0.00467     |
| GO:0035384| thioester biosynthetic process                            | 5     | 6     | 0.00467     |
| GO:0006749| glutathione metabolic process                             | 5     | 6     | 0.00467     |
| GO:0006567| threonine catabolic process                               | 5     | 6     | 0.00467     |
| GO:0019752| carboxylic acid metabolic process                         | 8     | 19    | 0.00829     |
| GO:0009072| aromatic amino acid family metabolic process              | 6     | 9     | 0.00915     |
| GO:0006090| pyruvate metabolic process                                | 10    | 20    | 0.01369     |
Supplementary Table 9 | Sub-module 1 cluster 7, significantly enriched GO terms (biological processes)

| GO-ID         | Term                                           | Count | Size | p-value       |
|---------------|------------------------------------------------|-------|------|---------------|
| GO:0005975    | carbohydrate metabolic process                 | 32    | 41   | 7.8925E-34    |
| GO:0044723    | single-organism carbohydrate metabolic process | 28    | 43   | 8.66977E-19   |
| GO:0016052    | carbohydrate catabolic process                 | 17    | 18   | 2.58370E-16   |
| GO:0005984    | disaccharide metabolic process                 | 13    | 16   | 4.32191E-10   |
| GO:0066165    | nucleoside diphosphate phosphorylation         | 10    | 10   | 7.04419E-10   |
| GO:0072524    | pyridine-containing compound metabolic process | 15    | 26   | 3.13769E-08   |
| GO:0046031    | ADP metabolic process                          | 10    | 12   | 3.71878E-08   |
| GO:0009185    | ribonucleoside diphosphate metabolic process   | 10    | 12   | 3.71878E-08   |
| GO:0009135    | purine nucleoside diphosphate metabolic process| 10    | 12   | 3.71878E-08   |
| GO:0066096    | glycolytic process                             | 8     | 8    | 4.47368E-08   |
| GO:0066733    | oxidoreduction coenzyme metabolic process      | 15    | 27   | 6.31905E-08   |
| GO:0005992    | trehalose biosynthetic process                 | 8     | 9    | 4.09715E-07   |
| GO:0009312    | oligosaccharide biosynthetic process           | 8     | 9    | 4.09715E-07   |
| GO:0005976    | polysaccharide metabolic process               | 11    | 18   | 8.53380E-07   |
| GO:0044712    | single-organism catabolic process              | 27    | 89   | 2.07454E-06   |
| GO:0046835    | carbohydrate phosphorylation                   | 6     | 6    | 3.55357E-06   |
| GO:0044275    | cellular carbohydrate catabolic process        | 9     | 14   | 4.59487E-06   |
| GO:0034637    | cellular carbohydrate biosynthetic process     | 7     | 9    | 8.26346E-06   |
| GO:0033500    | carbohydrate homeostasis                       | 7     | 9    | 1.23321E-05   |
| GO:0001678    | cellular glucose homeostasis                   | 7     | 9    | 1.23322E-05   |
| GO:0005996    | monosaccharide metabolic process               | 9     | 16   | 1.65953E-05   |
| GO:0046034    | ATP metabolic process                          | 10    | 21   | 7.27782E-05   |
| GO:0009199    | ribonucleoside triphosphate metabolic process  | 10    | 21   | 7.27782E-05   |
| GO:0009144    | purine nucleoside triphosphate metabolic process| 10    | 21   | 7.27782E-05   |
| GO:0006098    | pentose-phosphate shunt                        | 6     | 9    | 0.00022       |
| GO:0046164    | alcohol catabolic process                      | 6     | 9    | 0.00022       |
| GO:0055086    | nucleobase-containing small molecule metabolic process | 17 | 56 | 0.00022 |
| GO:0005987    | sucrose catabolic process                      | 4     | 4    | 0.00024       |
| GO:0006013    | mannose metabolic process                      | 4     | 4    | 0.00024       |
| GO:0000272    | polysaccharide catabolic process               | 4     | 4    | 0.00024       |
| GO:0006091    | generation of precursor metabolites and energy  | 14    | 42   | 0.00029       |
| GO:0006006    | glucose metabolic process                      | 6     | 10   | 0.00036       |
| GO:0065008    | regulation of biological quality               | 14    | 43   | 0.00038       |
| GO:0051186    | cofactor metabolic process                     | 15    | 49   | 0.00049       |
| GO:0046365    | monosaccharide catabolic process               | 5     | 7    | 0.0005        |
| GO:0009313    | oligosaccharide catabolic process              | 5     | 7    | 0.0005        |
| GO:0009225    | nucleotide-sugar metabolic process             | 5     | 7    | 0.0005        |
| GO:0006793    | phosphorus metabolic process                   | 26    | 113  | 0.0007        |
| GO:0044419    | interspecies interaction between organisms     | 14    | 46   | 0.00083       |
| GO:0009126    | purine nucleoside monophosphate metabolic process | 10    | 27   | 0.00089       |
| GO:0019405    | alditol catabolic process                      | 4     | 5    | 0.00102       |
| GO:0071554    | cell wall organization or biogenesis           | 8     | 19   | 0.00114       |
| GO:0046364    | monosaccharide biosynthetic process            | 5     | 8    | 0.0012        |
| GO:0009161    | ribonucleoside monophosphate metabolic process | 10    | 29   | 0.00169       |
| GO:0019725    | cellular homeostasis                           | 8     | 20   | 0.0017        |
| GO:0051817    | modification of morphology or physiology of other organism involved in symbiotic interaction | 6 | 12 | 0.00172 |
| GO:0044416    | induction by symbiont of host defense response | 6     | 12   | 0.00172       |
| GO:0052031    | modulation by symbiont of host defense response | 6     | 12   | 0.00172       |
| GO:0052510    | positive regulation by organism of defense response of other organism involved in symbiotic interaction | 6 | 12 | 0.00172 |
| GO:0031347    | regulation of defense response                 | 6     | 12   | 0.00172       |
| GO:0070596    | (1->3)-alpha-glucan biosynthetic process       | 3     | 3    | 0.00195       |
| GO:0000025 | maltose catabolic process | 3 3 0.00195 |
| GO:0006002 | fructose 6-phosphate metabolic process | 3 3 0.00195 |
| GO:0006007 | glucose catabolic process | 3 3 0.00195 |
| GO:0046348 | amino sugar catabolic process | 3 3 0.00195 |
| GO:0009298 | GDP-mannose biosynthetic process | 3 3 0.00195 |
| GO:0009056 | catabolic process | 13 53 0.00222 |
| GO:0006163 | purine nucleotide metabolic process | 10 30 0.00227 |
| GO:0052173 | response to defenses of other organism involved in symbiotic interaction | 6 13 0.00286 |
| GO:0009259 | ribonucleotide metabolic process | 10 31 0.003 |
| GO:1901135 | carbohydrate derivative metabolic process | 10 37 0.0034 |
| GO:0075136 | response to host | 6 14 0.0045 |
| GO:0043207 | response to external biotic stimulus | 6 14 0.0045 |
| GO:0009117 | nucleotide metabolic process | 6 15 0.00505 |
| GO:0006094 | gluconeogenesis | 4 7 0.00619 |
| GO:0006073 | cellular glucan metabolic process | 3 4 0.00627 |
| GO:0008152 | metabolic process | 67 606 0.00646 |
| GO:0030978 | alpha-glucan metabolic process | 3 4 0.00709 |
| GO:0046349 | amino sugar biosynthetic process | 3 4 0.00709 |
| GO:0048584 | positive regulation of response to stimulus | 7 20 0.00798 |
**Supplementary Table 10** | Sub-module 1 cluster 8, significantly enriched GO terms (biological processes)

| GO-ID          | Term                                           | Count | Size | p-value     |
|----------------|------------------------------------------------|-------|------|-------------|
| GO:0046903     | secretion                                      | 2     | 3    | 7.317E-05   |
| GO:0048856     | anatomical structure development               | 3     | 38   | 0.00065     |
| GO:0046488     | phosphatidylinositol metabolic process         | 2     | 8    | 0.00068     |
| GO:0022402     | cell cycle process                             | 3     | 40   | 0.00075     |
| GO:0046486     | glycerolipid metabolic process                 | 2     | 13   | 0.00186     |
| GO:0006644     | phospholipid metabolic process                 | 2     | 19   | 0.00246     |
| GO:0032505     | reproduction of a single-celled organism       | 2     | 15   | 0.00249     |
| GO:0034293     | sexual sporulation                             | 2     | 15   | 0.00249     |
| GO:1902589     | single-organism organelle organization         | 2     | 16   | 0.00284     |
| GO:0048646     | anatomical structure formation involved in morphogenesis | 2 | 21 | 0.00492  |
| GO:0030448     | hyphal growth                                  | 2     | 21   | 0.00492     |
| GO:0006793     | phosphorus metabolic process                   | 3     | 106  | 0.00586     |
| GO:1902578     | single-organism localization                   | 2     | 27   | 0.00811     |
| GO:0030154     | cell differentiation                           | 2     | 29   | 0.00934     |
### Supplementary Table 11

**Sub-module 1 cluster 9, significantly enriched GO terms (biological processes)**

| GO-ID       | Term                                | Count | Size  | p-value   |
|-------------|--------------------------------------|-------|-------|-----------|
| GO:0006544  | glycine metabolic process            | 2     | 2     | 0.00026   |
| GO:0044710  | single-organism metabolic process    | 7     | 236   | 0.00281   |
| GO:0006563  | L-serine metabolic process           | 2     | 6     | 0.00477   |
| GO:0055114  | oxidation-reduction process          | 9     | 211   | 0.00715   |
| GO:1901605  | alpha-amino acid metabolic process   | 5     | 75    | 0.0096    |
**Supplementary Table 12** | Sub-module 1 cluster 10, significantly enriched GO terms (biological processes)

| GO-ID          | Term                                                        | Count | Size | p-value       |
|----------------|-------------------------------------------------------------|-------|------|---------------|
| GO:0043632     | modification-dependent macromolecule catabolic process      | 20    | 23   | 4.774952E-16  |
| GO:0051603     | proteolysis involved in cellular protein catabolic process  | 20    | 24   | 2.56519E-15   |
| GO:0009059     | macromolecule biosynthetic process                          | 33    | 68   | 9.62940E-15   |
| GO:0030163     | protein catabolic process                                   | 17    | 21   | 5.97956E-13   |
| GO:0006518     | peptide metabolic process                                   | 26    | 51   | 9.83876E-12   |
| GO:0043604     | amide biosynthetic process                                  | 26    | 54   | 5.39206E-11   |
| GO:0071840     | cellular component organization or biogenesis               | 38    | 112  | 3.80132E-10   |
| GO:0044267     | cellular protein metabolic process                           | 24    | 65   | 1.95054E-09   |
| GO:0034641     | cellular nitrogen compound metabolic process                | 52    | 203  | 9.13732E-09   |
| GO:0051649     | establishment of localization in cell                       | 17    | 34   | 9.21593E-08   |
| GO:0015833     | peptide transport                                           | 17    | 35   | 1.59928E-07   |
| GO:0006457     | protein folding                                             | 8     | 9    | 3.47631E-07   |
| GO:0070727     | cellular macromolecule localization                         | 17    | 37   | 4.46409E-07   |
| GO:0034622     | cellular macromolecular complex assembly                    | 15    | 30   | 5.80739E-07   |
| GO:0070467     | protein modification by small protein conjugation or removal| 11    | 17   | 6.84696E-07   |
| GO:0010468     | regulation of gene expression                               | 17    | 38   | 7.20769E-07   |
| GO:0006511     | ubiquitin-dependent protein catabolic process               | 7     | 8    | 1.79224E-06   |
| GO:0034641     | cellular nitrogen compound metabolic process                | 13    | 26   | 2.44077E-06   |
| GO:1901566     | organonitrogen compound biosynthetic process                | 31    | 118  | 5.67628E-06   |
| GO:0006412     | translation                                                 | 7     | 10   | 1.53858E-05   |
| GO:0022613     | ribonucleoprotein complex biogenesis                        | 6     | 7    | 1.88432E-05   |
| GO:0043161     | proteasome-mediated ubiquitin-dependent protein catabolic process | 6    | 7    | 1.89654E-05   |
| GO:0051246     | regulation of protein metabolic process                     | 9     | 16   | 2.94784E-05   |
| GO:0051169     | nuclear transport                                           | 10    | 19   | 3.02865E-05   |
| GO:0071826     | ribonucleoprotein complex subunit organization              | 10    | 19   | 3.02865E-05   |
| GO:0070585     | protein localization to mitochondrion                       | 5     | 5    | 3.34880E-05   |
| GO:0001731     | formation of translation preinitiation complex              | 5     | 5    | 3.34880E-05   |
| GO:0042026     | protein refolding                                           | 5     | 5    | 3.34880E-05   |
| GO:0006886     | intracellular protein transport                             | 12    | 28   | 4.58274E-05   |
| GO:0090304     | nucleic acid metabolic process                              | 7     | 11   | 5.47941E-05   |
| GO:0072594     | establishment of protein localization to organelle          | 9     | 17   | 7.43742E-05   |
| GO:0006974     | cellular response to DNA damage stimulus                    | 6     | 8    | 9.33122E-05   |
| GO:0053085     | transmembrane transport                                     | 7     | 11   | 0.00011       |
| GO:0051171     | regulation of nitrogen compound metabolic process           | 5     | 6    | 0.00011       |
| GO:0051179     | localization                                               | 14    | 40   | 0.00013       |
| GO:0022607     | cellular component assembly                                 | 15    | 44   | 0.00017       |
| GO:0070972     | protein localization to endoplasmic reticulum               | 5     | 6    | 0.00018       |
| GO:0050658     | RNA transport                                              | 8     | 15   | 0.00018       |
| GO:0006403     | RNA localization                                            | 8     | 15   | 0.00018       |
| GO:0009266     | response to temperature stimulus                            | 8     | 15   | 0.00018       |
| GO:0015931     | nucleobase-containing compound transport                    | 8     | 15   | 0.00018       |
| GO:0006950     | response to stress                                         | 23    | 86   | 0.00021       |
| GO:0090150     | establishment of protein localization to membrane           | 4     | 4    | 0.00027       |
| GO:0030433     | ubiquitin-dependent ERAD pathway                            | 4     | 4    | 0.00027       |
| GO:0043254     | regulation of protein complex assembly                      | 4     | 4    | 0.00027       |
| GO:0006289     | nucleotide-excision repair                                  | 4     | 4    | 0.00027       |
| GO:0006996     | organelle organization                                     | 10    | 25   | 0.00031       |
| GO:0045184     | establishment of protein localization                      | 8     | 17   | 0.00035       |
| GO:0006413     | translational initiation                                   | 5     | 7    | 0.00039       |
| GO:0044249     | cellular biosynthetic process                               | 45    | 243  | 0.00067       |
| GO:0051716     | cellular response to stimulus                               | 27    | 116  | 0.0007        |
| GO:0071705 | nitrogen compound transport | 9 | 23 | 0.00074 |
| GO:0051168 | nuclear export | 7 | 14 | 0.0008 |
| GO:2000112 | regulation of cellular macromolecule biosynthetic process | 10 | 28 | 0.00087 |
| GO:1902582 | single-organism intracellular transport | 6 | 11 | 0.0011 |
| GO:0016567 | protein ubiquitination | 4 | 5 | 0.0011 |
| GO:0034976 | response to endoplasmic reticulum stress | 4 | 5 | 0.0012 |
| GO:1901659 | glycospol compound biosynthetic process | 4 | 5 | 0.0012 |
| GO:0042455 | ribonucleoside biosynthetic process | 4 | 5 | 0.0012 |
| GO:0071822 | protein complex subunit organization | 7 | 15 | 0.00122 |
| GO:0070271 | protein complex biogenesis | 7 | 15 | 0.00134 |
| GO:0051173 | positive regulation of nitrogen compound metabolic process | 8 | 19 | 0.00136 |
| GO:0002183 | cytoplasmic translational initiation | 3 | 3 | 0.00184 |
| GO:0010558 | negative regulation of macromolecule biosynthetic process | 3 | 3 | 0.00197 |
| GO:0031323 | regulation of cellular metabolic process | 6 | 13 | 0.00205 |
| GO:0044089 | positive regulation of cellular component biogenesis | 3 | 3 | 0.00211 |
| GO:0042128 | nitrate assimilation | 3 | 3 | 0.00211 |
| GO:2001057 | reactive nitrogen species metabolic process | 3 | 3 | 0.00211 |
| GO:0030150 | protein import into mitochondrial matrix | 3 | 3 | 0.00211 |
| GO:0070897 | DNA-templated transcriptional preinitiation complex assembly | 3 | 3 | 0.00211 |
| GO:0045899 | positive regulation of RNA polymerase II transcriptional preinitiation complex assembly | 3 | 3 | 0.00211 |
| GO:0070682 | proteasome regulatory particle assembly | 3 | 3 | 0.00211 |
| GO:2000144 | positive regulation of DNA-templated transcription, initiation regulation of transcription initiation from RNA polymerase II promoter | 3 | 3 | 0.00211 |
| GO:1902292 | cell cycle DNA replication initiation | 3 | 3 | 0.00211 |
| GO:0006450 | regulation of translational fidelity | 3 | 3 | 0.00211 |
| GO:0006446 | regulation of translational initiation | 3 | 3 | 0.00211 |
| GO:0046131 | pyrimidine ribonucleoside metabolic process | 3 | 3 | 0.00211 |
| GO:0046134 | pyrimidine nucleoside biosynthetic process | 3 | 3 | 0.00211 |
| GO:0060260 | posttranslational protein targeting to endoplasmic reticulum membrane | 3 | 3 | 0.00211 |
| GO:1902975 | mitotic DNA replication initiation | 3 | 3 | 0.00211 |
| GO:0006997 | nucleosome organization | 3 | 3 | 0.00211 |
| GO:0006725 | cellular aromatic compound metabolic process | 36 | 183 | 0.00246 |
| GO:0000280 | nuclear division | 5 | 9 | 0.00273 |
| GO:0010033 | response to organic substance | 7 | 17 | 0.00324 |
| GO:0007264 | small GTPase mediated signal transduction | 4 | 6 | 0.00324 |
| GO:0000070 | mitotic sister chromatid segregation | 4 | 6 | 0.00324 |
| GO:0098813 | nuclear chromosome segregation | 4 | 6 | 0.00324 |
| GO:0009116 | nucleoside metabolic process | 4 | 6 | 0.00324 |
| GO:0071824 | protein-DNA complex subunit organization | 4 | 6 | 0.00324 |
| GO:0046483 | heterocycle metabolic process | 36 | 186 | 0.00336 |
| GO:0044260 | cellular macromolecule metabolic process | 6 | 20 | 0.00384 |
| GO:0051276 | chromosome organization | 7 | 18 | 0.00434 |
| GO:1901293 | nucleoside phosphate biosynthetic process | 7 | 18 | 0.00474 |
| GO:0031325 | positive regulation of cellular metabolic process | 9 | 28 | 0.00602 |
| GO:0044770 | cell cycle phase transition | 4 | 7 | 0.00629 |
| GO:0034654 | nucleobase-containing compound biosynthetic process | 11 | 40 | 0.00654 |
| GO:0017038 | protein import | 4 | 7 | 0.00681 |
| GO:0044238 | primary metabolic process | 74 | 473 | 0.00691 |
| GO:0031327 | negative regulation of cellular biosynthetic process | 3 | 4 | 0.00716 |
| GO:0042787 | protein ubiquitination involved in ubiquitin-dependent protein catabolic process | 3 | 4 | 0.00765 |
| GO:1901988 | negative regulation of cell cycle phase transition | 3 | 4 | 0.00765 |
| GO:0051054 | positive regulation of DNA metabolic process | 3 | 4 | 0.00765 |
| GO:0031146 | SCF-dependent proteasomal ubiquitin-dependent protein | 3 | 4 | 0.00765 |
| Gene ID     | Description                                                | Count | Total | P-value  |
|------------|------------------------------------------------------------|-------|-------|----------|
| GO:0010564 | regulation of cell cycle process                           | 6     | 15    | 0.00768  |
| GO:0036211 | protein modification process                                | 13    | 50    | 0.0077   |
| GO:0009156 | ribonucleoside monophosphate biosynthetic process           | 5     | 11    | 0.00806  |
| GO:0016070 | RNA metabolic process                                       | 11    | 42    | 0.00972  |
| GO:1903047 | mitotic cell cycle process                                  | 5     | 12    | 0.00993  |
**Supplementary Table 13** | Sub-module 1 cluster 11, significantly enriched GO terms (biological processes)

| GO-ID      | Term                                           | Count | Size | p-value    |
|------------|------------------------------------------------|-------|------|------------|
| GO:0000375 | RNA splicing, via transesterification reactions | 6     | 7    | 2.70567E-09 |
| GO:0045292 | mRNA cis splicing, via spliceosome              | 5     | 5    | 1.61354E-08 |
| GO:0016070 | RNA metabolic process                           | 9     | 68   | 7.10973E-05 |
| GO:0010467 | gene expression                                 | 10    | 91   | 0.00013    |
Supplementary Table 14 | Sub-module 1 cluster 12, significantly enriched GO terms (biological processes)

| GO-ID       | Term                          | Count | Size | p-value       |
|-------------|-------------------------------|-------|------|---------------|
| GO:0006508  | proteolysis                   | 5     | 33   | 4.74361E-08   |
| GO:1902086  | fumagillin biosynthetic process | 2     | 4    | 0.00015       |
| GO:0097176  | epoxide metabolic process     | 2     | 4    | 0.00015       |
| GO:0043170  | macromolecule metabolic process | 5     | 176  | 0.00027       |
## Supplementary Table 15 | Sub-module 1 cluster 13, significantly enriched GO terms (biological processes)

| GO-ID          | Term                                      | Count | Size | p-value      |
|----------------|-------------------------------------------|-------|------|--------------|
| GO:1900815     | monodictyphenone biosynthetic process      | 13    | 13   | 5.33344E-10  |
| GO:0042180     | cellular ketone metabolic process          | 16    | 21   | 2.70294E-08  |
| GO:0042537     | benzene-containing compound metabolic process | 13 | 15   | 3.82228E-08  |
| GO:0050761     | depsipeptide metabolic process             | 9     | 9    | 4.13701E-07  |
| GO:1900557     | emericellamide biosynthetic process        | 9     | 9    | 4.13701E-07  |
| GO:1901334     | lactone metabolic process                  | 9     | 9    | 4.13701E-07  |
| GO:1900584     | o-orsellinic acid biosynthetic process     | 8     | 8    | 2.15750E-06  |
| GO:0018958     | phenol-containing compound metabolic process | 12 | 17   | 6.10997E-06  |
| GO:0019748     | secondary metabolic process                | 17    | 34   | 2.86743E-05  |
| GO:0045461     | sterigmatocystin biosynthetic process      | 13    | 22   | 4.76086E-05  |
| GO:0009404     | toxin metabolic process                    | 13    | 22   | 4.76086E-05  |
| GO:1901376     | organic heteropentacyclic compound metabolic process | 14 | 25   | 5.44246E-05  |
| GO:2001307     | xanthone-containing compound biosynthetic process | 5  | 5    | 0.0003       |
| GO:1900554     | asperfurane biosynthetic process           | 5     | 5    | 0.0003       |
| GO:1902644     | tertiary alcohol metabolic process          | 5     | 5    | 0.0003       |
| GO:0019184     | nonribosomal peptide biosynthetic process  | 7     | 10   | 0.00077      |
| GO:1901617     | organic hydroxy compound biosynthetic process | 18 | 45   | 0.00116      |
| GO:0030638     | polyketide metabolic process               | 5     | 6    | 0.0015       |
| GO:0034311     | diol metabolic process                     | 5     | 6    | 0.0015       |
| GO:0034440     | lipid oxidation                            | 4     | 4    | 0.00152      |
| GO:0006635     | fatty acid beta-oxidation                  | 4     | 4    | 0.00152      |
| GO:0008152     | metabolic process                          | 162   | 748  | 0.00172      |
| GO:0006629     | lipid metabolic process                    | 28    | 90   | 0.00518      |
| GO:0036184     | asperthecin biosynthetic process           | 3     | 3    | 0.00776      |
| GO:1900793     | shamixanthone biosynthetic process         | 3     | 3    | 0.00776      |
| GO:1900587     | arugosin biosynthetic process              | 3     | 3    | 0.00776      |
| GO:1900575     | emodin biosynthetic process                | 3     | 3    | 0.00776      |
| GO:0046173     | polyol biosynthetic process                | 5     | 8    | 0.00983      |
**Supplementary Table 16** | Sub-module 1 cluster 14, significantly enriched GO terms (biological processes)

| GO-ID       | Term                             | Count | Size | p-value   |
|-------------|----------------------------------|-------|------|-----------|
| GO:0006012  | galactose metabolic process      | 2     | 5    | 0.00051   |
| GO:0009100  | glycoprotein metabolic process   | 2     | 5    | 0.00051   |
| GO:0070085  | glycosylation                    | 2     | 5    | 0.00051   |
| GO:0036211  | protein modification process     | 3     | 50   | 0.00475   |
| GO-ID            | Term                                                      | Count | Size | p-value      |
|------------------|-----------------------------------------------------------|-------|------|--------------|
| GO:0046034       | ATP metabolic process                                     | 5     | 21   | 2.17781E-07 |
| GO:0009199       | ribonucleoside triphosphate metabolic process             | 5     | 21   | 2.17781E-07 |
| GO:0009144       | purine nucleoside triphosphate metabolic process          | 5     | 21   | 2.17781E-07 |
| GO:0009126       | purine nucleoside monophosphate metabolic process         | 5     | 27   | 8.49463E-07 |
| GO:0009161       | ribonucleoside monophosphate metabolic process            | 5     | 29   | 1.24250E-06 |
| GO:0006163       | purine nucleotide metabolic process                       | 5     | 30   | 1.48677E-06 |
| GO:0009259       | ribonucleotide metabolic process                          | 5     | 31   | 1.76766E-06 |
| GO:0042773       | ATP synthesis coupled electron transport                   | 3     | 6    | 8.98325E-06 |
| GO:0006753       | nucleoside phosphate metabolic process                    | 5     | 47   | 1.52431E-05 |
| GO:0022900       | electron transport chain                                  | 3     | 7    | 1.56552E-05 |
| GO:0006123       | mitochondrial electron transport, cytochrome c to oxygen  | 2     | 2    | 6.84496E-05 |
| GO:1901135       | carbohydrate derivative metabolic process                 | 5     | 65   | 7.78922E-05 |
| GO:0009142       | nucleoside triphosphate biosynthetic process              | 2     | 3    | 0.0002      |
| GO:0009206       | purine ribonucleoside triphosphate biosynthetic process   | 2     | 3    | 0.0002      |
| GO:0015986       | ATP synthesis coupled proton transport                     | 2     | 3    | 0.0002      |
| GO:0009060       | aerobic respiration                                       | 3     | 18   | 0.00035     |
| GO:0098660       | inorganic ion transmembrane transport                     | 2     | 4    | 0.00041     |
| GO:0098655       | cation transmembrane transport                            | 2     | 4    | 0.00041     |
| GO:1902600       | hydrogen ion transmembrane transport                      | 2     | 4    | 0.00041     |
| GO:0006818       | hydrogen transport                                       | 2     | 5    | 0.00068     |
| GO:0015672       | monovalent inorganic cation transport                     | 2     | 5    | 0.00068     |
| GO:0006793       | phosphorus metabolic process                              | 5     | 113  | 0.00115     |
| GO:0009168       | purine ribonucleoside monophosphate biosynthetic process  | 2     | 9    | 0.00239     |
| GO:0043933       | macromolecular complex subunit organization               | 3     | 35   | 0.0026      |
| GO:0006811       | ion transport                                             | 2     | 10   | 0.00297     |
| GO:0006139       | nucleobase-containing compound metabolic process          | 5     | 139  | 0.00303     |
| GO:0055085       | transmembrane transport                                   | 2     | 11   | 0.00362     |
| GO:0009152       | purine ribonucleotide biosynthetic process                | 2     | 11   | 0.00362     |
| GO:0009124       | nucleoside monophosphate biosynthetic process             | 2     | 11   | 0.00362     |
| GO:0016310       | phosphorylation                                           | 3     | 41   | 0.00413     |
| GO:0006461       | protein complex assembly                                  | 2     | 14   | 0.00448     |
| GO:0022607       | cellular component assembly                               | 3     | 44   | 0.00507     |
| GO:0046390       | ribose phosphate biosynthetic process                     | 2     | 14   | 0.00591     |
| GO:0072522       | purine-containing compound biosynthetic process           | 2     | 16   | 0.00772     |
| GO:0009165       | nucleotide biosynthetic process                           | 2     | 18   | 0.00975     |
**Supplementary Table 18** | Sub-module 2, significantly enriched GO terms (biological processes)

| GO-ID       | Term                                | Count | Size | p-value |
|-------------|-------------------------------------|-------|------|---------|
| GO:0044275  | cellular carbohydrate catabolic process | 3     | 21   | 0.00208 |
**Supplementary Table 19** | Sub-module 3, significantly enriched GO terms (biological processes)

| GO-ID         | Term                                                      | Count | Size  | p-value          |
|---------------|-----------------------------------------------------------|-------|-------|------------------|
| GO:0009395    | phospholipid catabolic process                            | 4     | 5     | 8.85073E-08      |
| GO:0016042    | lipid catabolic process                                   | 5     | 18    | 1.24586E-06      |
| GO:0046503    | glycerolipid catabolic process                            | 3     | 4     | 7.09360E-06      |
| GO:0042173    | regulation of sporulation resulting in formation of a cellular spore | 2 | 2 | 0.00016 |
| GO:1901568    | fatty acid derivative metabolic process                   | 2     | 2     | 0.00016          |
| GO:0001516    | prostaglandin biosynthetic process                        | 2     | 2     | 0.00016          |
| GO:0046456    | icosanoid biosynthetic process                            | 2     | 2     | 0.00016          |
| GO:0034306    | regulation of sexual sporulation                          | 2     | 2     | 0.00016          |
| GO:0006692    | prostanoid metabolic process                              | 2     | 2     | 0.00016          |
| GO:0031408    | oxylipin biosynthetic process                             | 2     | 2     | 0.00016          |
| GO:0043941    | positive regulation of sexual sporulation resulting in formation of a cellular spore | 2 | 2 | 0.00016 |
| GO:0043942    | negative regulation of sexual sporulation resulting in formation of a cellular spore | 2 | 2 | 0.00016 |
| GO:0043944    | negative regulation of asexual sporulation resulting in formation of a cellular spore | 2 | 2 | 0.00016 |
| GO:0043945    | positive regulation of asexual sporulation resulting in formation of a cellular spore | 2 | 2 | 0.00016 |
| GO:0006650    | glycerophospholipid metabolic process                     | 3     | 12    | 0.00037          |
| GO:0045596    | negative regulation of cell differentiation               | 2     | 3     | 0.00048          |
| GO:0045597    | positive regulation of cell differentiation               | 2     | 3     | 0.00048          |
| GO:0072338    | cellular lactam metabolic process                         | 2     | 3     | 0.00048          |
| GO:0016999    | antibiotic metabolic process                              | 2     | 3     | 0.00048          |
| GO:0006636    | unsaturated fatty acid biosynthetic process               | 2     | 3     | 0.00048          |
| GO:0043938    | positive regulation of sporulation                        | 2     | 3     | 0.00048          |
| GO:0043939    | negative regulation of sporulation                        | 2     | 3     | 0.00048          |
| GO:0042316    | penicillin metabolic process                              | 2     | 3     | 0.00048          |
| GO:0006629    | lipid metabolic process                                   | 2     | 8     | 0.00049          |
| GO:0010913    | regulation of sterigmatocystin biosynthetic process       | 2     | 4     | 0.00095          |
| GO:1903046    | meiotic cell cycle process                                | 3     | 17    | 0.00109          |
| GO:0034305    | regulation of asexual sporulation                         | 2     | 5     | 0.00158          |
| GO:0006793    | phosphorus metabolic process                              | 6     | 113   | 0.00164          |
| GO:0048646    | anatomical structure formation involved in morphogenesis  | 3     | 21    | 0.00207          |
| GO:0044702    | single organism reproductive process                      | 3     | 21    | 0.00207          |
| GO:0019954    | asexual reproduction                                      | 3     | 23    | 0.0021           |
| GO:0066071    | glycerol metabolic process                                | 2     | 7     | 0.00327          |
| GO:0043455    | regulation of secondary metabolic process                 | 2     | 7     | 0.00327          |
| GO:0045787    | positive regulation of cell cycle                         | 2     | 8     | 0.00432          |
| GO:003006     | developmental process involved in reproduction            | 3     | 27    | 0.00436          |
| GO:0006979    | response to oxidative stress                              | 3     | 28    | 0.00485          |
| GO:0044699    | single-organism process                                   | 9     | 492   | 0.00496          |
| GO:0050793    | regulation of developmental process                       | 2     | 9     | 0.00551          |
| GO:2000243    | positive regulation of reproductive process               | 2     | 9     | 0.00551          |
| GO:2000242    | negative regulation of reproductive process               | 2     | 10    | 0.00684          |
| GO:0019953    | sexual reproduction                                       | 3     | 34    | 0.00846          |
| GO-ID       | Term                                                              | Count | Size | p-value         |
|------------|-------------------------------------------------------------------|-------|------|-----------------|
| GO:0034660 | ncRNA metabolic process                                          | 16    | 23   | 2.4256E-24      |
| GO:006396  | RNA processing                                                   | 18    | 35   | 8.2480E-22      |
| GO:0090304 | nucleic acid metabolic process                                   | 22    | 79   | 1.5056E-20      |
| GO:0044085 | cellular component biogenesis                                     | 21    | 73   | 1.1911E-19      |
| GO:006364  | rRNA processing                                                  | 11    | 18   | 6.9388E-16      |
| GO:0044260 | cellular macromolecule metabolic process                         | 16    | 80   | 1.9958E-13      |
| GO:0042274 | ribosomal small subunit biogenesis                               | 10    | 15   | 2.4030E-13      |
| GO:006725  | cellular aromatic compound metabolic process                     | 22    | 183  | 5.7361E-12      |
| GO:0046483 | heterocycle metabolic process                                    | 22    | 186  | 8.2225E-12      |
| GO:0034641 | cellular nitrogen compound metabolic process                     | 22    | 203  | 5.6265E-11      |
| GO:0044260 | endonucleolytic cleavage involved in rRNA processing            | 6     | 6    | 3.9442E-10      |
| GO:1901360 | organic cyclic compound metabolic process                        | 22    | 224  | 4.7659E-10      |
| GO:000447  | ncRNA and LSU-rRNA from tricistronic rRNA transcript (SSU-rRNA, 5.8S rRNA, LSU-rRNA) | 5     | 5    | 1.6135E-08      |
| GO:0071826 | ribonucleoprotein complex subunit organization                   | 7     | 19   | 3.6627E-07      |
| GO:0042273 | ribosomal large subunit biogenesis                               | 4     | 5    | 1.6027E-06      |
| GO:0000027 | ribosomal large subunit assembly                                 | 4     | 5    | 3.0959E-06      |
| GO:0070925 | organelle assembly                                               | 5     | 12   | 1.1063E-05      |
| GO:0034622 | cellular macromolecular complex assembly                         | 7     | 30   | 1.1888E-05      |
| GO:0000463 | maturation of LSU-rRNA from tricistronic rRNA transcript (SSU-rRNA, 5.8S rRNA, LSU-rRNA) | 3     | 3    | 2.3756E-05      |
| GO:1902626 | assembly of large subunit precursor of preribosome               | 3     | 3    | 2.3756E-05      |
| GO:0097659 | nucleic acid-templated transcription                             | 6     | 30   | 0.00014         |
| GO:0071166 | ribonucleoprotein complex localization                          | 4     | 12   | 0.00027         |
| GO:0006405 | RNA export from nucleus                                          | 4     | 13   | 0.00038         |
| GO:0006611 | protein export from nucleus                                      | 4     | 13   | 0.00038         |
| GO:0000462 | maturation of SSU-rRNA from tricistronic rRNA transcript (SSU-rRNA, 5.8S rRNA, LSU-rRNA) | 3     | 7    | 0.00042         |
| GO:0033753 | establishment of ribosome localization                           | 3     | 6    | 0.00045         |
| GO:0071428 | rRNA-containing ribonucleoprotein complex export from nucleus    | 3     | 6    | 0.00045         |
| GO:0000466 | maturation of 5.8S rRNA from tricistronic rRNA transcript (SSU-rRNA, 5.8S rRNA, LSU-rRNA) | 2     | 2    | 0.00057         |
| GO:0050657 | nucleic acid transport                                           | 4     | 15   | 0.00069         |
| GO:0051236 | establishment of RNA localization                                | 4     | 15   | 0.00069         |
| GO:0098781 | ncRNA transcription                                             | 2     | 2    | 0.00074         |
| GO:001640  | organelle localization                                           | 3     | 7    | 0.00077         |
| GO:0000154 | rRNA modification                                               | 2     | 2    | 0.0008          |
| GO:0042797 | tRNA transcription from RNA polymerase III promoter              | 2     | 2    | 0.00086         |
| GO:0000055 | ribosomal large subunit export from nucleus                      | 2     | 2    | 0.00086         |
| GO:0000472 | endonucleolytic cleavage to generate mature 5'-end of SSU-rRNA from (SSU-rRNA, 5.8S rRNA, LSU-rRNA) | 2     | 2    | 0.00086         |
| GO:0001510 | RNA methylation                                                 | 2     | 2    | 0.00086         |
| GO:0034471 | ncRNA 5'-end processing                                         | 2     | 2    | 0.00086         |
| GO:0010467 | gene expression                                                  | 3     | 23   | 0.00093         |
| GO:0016403 | cellular component organization                                  | 8     | 81   | 0.00097         |
| GO:0044238 | primary metabolic process                                        | 22    | 473  | 0.00142         |
| GO:0006913 | nucleocytoplasmic transport                                     | 4     | 19   | 0.0018          |
| GO:0006402 | mRNA catabolic process                                          | 2     | 3    | 0.00253         |
| GO:0010605 | negative regulation of macromolecule metabolic process           | 4     | 22   | 0.00319         |
| GO:0006360 | transcription from RNA polymerase I promoter                     | 2     | 4    | 0.00461         |
| GO:0034654 | nucleobase-containing compound biosynthetic process             | 6     | 58   | 0.00550         |
Supplementary Table 21 | Sub-module 5, significantly enriched GO terms (biological processes)

| GO-ID     | Term    | Count | Size  | p-value     |
|-----------|---------|-------|-------|-------------|
| GO:0006810| transport | 7     | 60    | 4.1011E-07  |
| GO:0051179| localization | 7     | 67    | 9.0371E-07  |