Electronic Supplementary Information

Transcriptomic analysis of thermotolerant yeast *Kluyveromyces marxianus* in multiple inhibitors tolerance

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## Table S1 Summary of mapping results from RNA-seq of *K. marxianus*

| Sample | Clean reads (bp) | Clean base > Q20 (%) | > Q30 (%) | GC (%) | Uniquely Mapping reads | Mapping rate (%) |
|--------|------------------|----------------------|-----------|--------|------------------------|------------------|
| I      | 13,622,794       | 97.68                | 92.79     | 44.57  | 12,490,287             | 91.69            |
| C      | 17,697,296       | 97.31                | 91.87     | 46.27  | 16,279,803             | 91.99            |

Note: I and C represent samples of yeast grown on medium with or without multiple fermentation inhibitors in YPD under aerobic condition. Q20, Q30 refer to the proportion of base calls with Phred scores >20 or 30 in the total bases.
| ID          | Description                                                | DEGs in study | Background | Ratio in background | Number up | Number down |
|------------|-------------------------------------------------------------|---------------|------------|---------------------|-----------|-------------|
| GO:0006096 | glycolytic process                                         | 16            | 26         | 0.62                | 2         | 14          |
| GO:0032787 | monocarboxylic acid metabolic process                      | 40            | 90         | 0.44                | 13        | 27          |
| GO:0006090 | pyruvate metabolic process                                 | 22            | 42         | 0.52                | 6         | 16          |
| GO:0006094 | gluconeogenesis                                            | 17            | 31         | 0.55                | 3         | 14          |
| GO:0006091 | generation of precursor metabolites and energy             | 27            | 71         | 0.38                | 11        | 16          |
| GO:0055114 | oxidation-reduction process                                | 69            | 304        | 0.23                | 33        | 36          |
| GO:0016491 | oxidoreductase activity                                    | 65            | 286        | 0.23                | 36        | 29          |
| GO:0043436 | oxoacid metabolic process                                  | 77            | 394        | 0.20                | 26        | 51          |
| GO:0006082 | organic acid metabolic process                              | 77            | 395        | 0.19                | 26        | 51          |
| GO:0019319 | hexose biosynthetic process                                | 17            | 32         | 0.53                | 3         | 14          |
| GO:0046364 | monosaccharide biosynthetic process                        | 17            | 32         | 0.53                | 3         | 14          |
| GO:0042815 | small molecule metabolic process                           | 115           | 689        | 0.17                | 42        | 73          |
| GO:0019752 | carboxylic acid metabolic process                          | 77            | 393        | 0.20                | 26        | 51          |
| GO:0044763 | single-organism cellular process                           | 184           | 1329       | 0.14                | 89        | 95          |
| GO:0044710 | single-organism metabolic process                          | 171           | 1138       | 0.15                | 80        | 91          |
| GO:0006099 | tricarboxylic acid cycle                                   | 16            | 29         | 0.55                | 16        | 0           |
| GO:0044699 | single-organism process                                    | 220           | 1602       | 0.14                | 113       | 107         |
| GO:0044711 | single-organism biosynthetic process                       | 64            | 344        | 0.19                | 12        | 52          |
| GO:0006006 | glucose metabolic process                                  | 18            | 43         | 0.42                | 3         | 15          |
| GO:0003824 | catalytic activity                                         | 212           | 1754       | 0.12                | 112       | 100         |
| GO:1901564 | organonitrogen compound metabolic process                  | 98            | 641        | 0.15                | 34        | 64          |
| GO:0016051 | carbohydrate biosynthetic process                          | 18            | 47         | 0.38                | 3         | 15          |
| GO:0044724 | carbohydrate catabolic process                             | 17            | 43         | 0.40                | 2         | 15          |
| GO:0016614 | acting on CH-OH group of donors                            | 18            | 51         | 0.35                | 9         | 9           |
| GO:0016052 | carbohydrate catabolic process | 17 | 47 | 0.36 | 2 | 15 |
| GO:0019318 | hexose metabolic process | 19 | 58 | 0.33 | 4 | 15 |
| GO:0016616 | oxidoreductase activity, acting on the CH-OH group of donors, NAD or NADP as acceptor | 17 | 48 | 0.35 | 8 | 9 |
| GO:0005996 | monosaccharide metabolic process | 19 | 60 | 0.32 | 4 | 15 |
| GO:0068152 | metabolic process | 243 | 2176 | 0.11 | 126 | 117 |
| GO:0044262 | cellular carbohydrate metabolic process | 17 | 50 | 0.34 | 7 | 10 |
| GO:0055085 | transmembrane transport | 49 | 269 | 0.18 | 35 | 14 |
| GO:0048037 | cofactor binding | 31 | 138 | 0.22 | 16 | 15 |
| GO:0009987 | cellular process | 230 | 2047 | 0.11 | 118 | 112 |
| GO:1990204 | oxidoreductase complex | 10 | 20 | 0.50 | 10 | 0 |
| GO:0051186 | cofactor metabolic process | 27 | 118 | 0.23 | 7 | 20 |
| GO:0015976 | carbon utilization | 8 | 13 | 0.62 | 4 | 4 |
| GO:0046487 | glyoxylate metabolic process | 8 | 13 | 0.62 | 6 | 2 |
| GO:0068152 | metabolic process | 35 | 178 | 0.20 | 14 | 21 |
| GO:1901566 | organic substance biosynthetic process | 84 | 599 | 0.14 | 18 | 66 |
| GO:0044712 | single-organism catabolic process | 39 | 214 | 0.18 | 11 | 28 |
| GO:0009058 | biosynthetic process | 86 | 626 | 0.14 | 19 | 67 |
| GO:0006732 | coenzyme metabolic process | 22 | 93 | 0.24 | 5 | 17 |
| GO:0044723 | carbohydrate metabolic process | 27 | 128 | 0.21 | 9 | 18 |
| GO:003674 | molecular_function | 291 | 2817 | 0.10 | 166 | 125 |
| GO:0044237 | cellular metabolic process | 181 | 1595 | 0.11 | 82 | 99 |
| GO:1901566 | organonitrogen compound biosynthetic process | 39 | 223 | 0.17 | 8 | 31 |
| GO:0051287 | NAD binding | 9 | 21 | 0.43 | 4 | 5 |
| GO:0006081 | cellular aldehyde metabolic process | 9 | 21 | 0.43 | 6 | 3 |
| GO:1901070 | compound biosynthetic process | 4 | 4 | 1.00 | 1 | 3 |
| GO:0008150 | biological_process | 314 | 3115 | 0.10 | 180 | 134 |
| GO:0044283 | small molecule biosynthetic process | 33 | 185 | 0.18 | 5 | 28 |
| GO:0050662  | coenzyme binding       | 20  | 91  | 0.22 | 10  | 10 |
|-------------|-------------------------|-----|-----|------|-----|----|
| GO:0071704  | organic substance metabolic process | 186 | 1677 | 0.11 | 81  | 105 |
| GO:0006740  | NADPH regeneration      | 8   | 19  | 0.42 | 1   | 7  |
| GO:0006007  | glucose catabolic process | 8   | 19  | 0.42 | 1   | 7  |
| GO:0019320  | hexose catabolic process | 8   | 19  | 0.42 | 1   | 7  |
| GO:0006098  | pentose-phosphate shunt | 8   | 19  | 0.42 | 1   | 7  |
| GO:0006753  | nucleoside phosphate metabolic process | 37  | 222 | 0.17 | 14  | 23 |
| GO:0005985  | sucrose metabolic process | 7   | 15  | 0.47 | 3   | 4  |
| GO:0005982  | starch metabolic process | 7   | 15  | 0.47 | 3   | 4  |
| GO:0043169  | cation binding          | 73  | 543 | 0.13 | 41  | 32 |
| GO:0043167  | ion binding             | 132 | 1127| 0.12 | 73  | 59 |
| GO:0009117  | nucleotide metabolic process | 36  | 218 | 0.17 | 13  | 23 |
| GO:0046872  | metal ion binding       | 72  | 539 | 0.13 | 40  | 32 |
| GO:0006000  | fructose metabolic process | 7   | 16  | 0.44 | 2   | 5  |
| GO:0006013  | mannose metabolic process | 7   | 16  | 0.44 | 2   | 5  |
| GO:0006739  | NADP metabolic process  | 8   | 21  | 0.38 | 1   | 7  |
| GO:0046365  | monosaccharide catabolic process | 8   | 21  | 0.38 | 1   | 7  |
| GO:0009152  | purine ribonucleotide biosynthetic process | 10  | 32  | 0.31 | 3   | 7  |
| GO:0006164  | purine nucleotide biosynthetic process | 10  | 32  | 0.31 | 3   | 7  |
| GO:0046496  | nicotinamide nucleotide metabolic process | 9   | 27  | 0.33 | 2   | 7  |
| GO:0005984  | disaccharide metabolic process | 7   | 17  | 0.41 | 3   | 4  |
| GO:0009063  | cellular amino acid catabolic process | 8   | 22  | 0.36 | 3   | 5  |
| GO:0009260  | ribonucleotide biosynthetic process | 11  | 40  | 0.28 | 3   | 8  |
| GO:0046912  | transferase activity, transferring acyl groups, acyl groups converted into alkyl on transfer | 5   | 9   | 0.56 | 2   | 3  |
| GO:0006790  | sulfur compound metabolic process | 15  | 67  | 0.22 | 3   | 12 |
| GO:0009168  | monophosphate biosynthetic process | 9   | 29  | 0.31 | 2   | 7  |
| GO:0009127  | monophosphate biosynthetic process | 9   | 29  | 0.31 | 2   | 7  |
| GO               | Description                                                                 | Count1 | Count2 | p-Value | Count3 | Count4 |
|------------------|-----------------------------------------------------------------------------|--------|--------|---------|--------|--------|
| GO:0000287       | magnesium ion binding                                                       | 11     | 41     | 0.27    | 3      | 8      |
| GO:0046390       | ribose phosphate biosynthetic process                                       | 11     | 41     | 0.27    | 3      | 8      |
| GO:0046037       | GMP metabolic process                                                        | 3      | 3      | 1.00    | 0      | 3      |
| GO:0004365       | dehydrogenase (NAD+) (phosphorylating) activity                             | 3      | 3      | 1.00    | 1      | 2      |
| GO:0006177       | GMP biosynthetic process                                                     | 3      | 3      | 1.00    | 0      | 3      |
| GO:0046395       | carboxylic acid catabolic process                                            | 8      | 24     | 0.33    | 3      | 5      |
| GO:0016054       | organic acid catabolic process                                               | 8      | 24     | 0.33    | 3      | 5      |
| GO:0072522       | purine-containing compound biosynthetic process                             | 10     | 36     | 0.28    | 3      | 7      |
| GO:0006144       | purine nucleobase metabolic process                                          | 16     | 77     | 0.21    | 4      | 12     |
| GO:0006733       | oxidoreduction coenzyme metabolic process                                    | 10     | 37     | 0.27    | 2      | 8      |
| GO:0019362       | pyridine nucleotide metabolic process                                       | 9      | 31     | 0.29    | 2      | 7      |
| GO:0055086       | nucleobase-containing small molecule metabolic process                       | 41     | 281    | 0.15    | 16     | 25     |
| GO:0006073       | cellular glucan metabolic process                                           | 7      | 20     | 0.35    | 3      | 4      |
| GO:1901606       | alpha-amino acid catabolic process                                          | 7      | 20     | 0.35    | 3      | 4      |
| GO:0009311       | oligosaccharide metabolic process                                           | 7      | 20     | 0.35    | 3      | 4      |
| GO:0044042       | glucan metabolic process                                                     | 7      | 20     | 0.35    | 3      | 4      |
| GO:0072524       | compound metabolic process                                                   | 10     | 38     | 0.26    | 2      | 8      |
| GO:0005829       | cytosol                                                                      | 8      | 26     | 0.31    | 4      | 4      |
| GO:0009167       | monophosphate metabolic process                                             | 21     | 117    | 0.18    | 10     | 11     |
| GO:0009126       | monophosphate metabolic process                                             | 21     | 117    | 0.18    | 10     | 11     |
| GO:0008483       | transaminase activity                                                        | 7      | 21     | 0.33    | 3      | 4      |
| GO:0044264       | cellular polysaccharide metabolic process                                    | 7      | 21     | 0.33    | 3      | 4      |
| GO:0005976       | polysaccharide metabolic process                                            | 7      | 21     | 0.33    | 3      | 4      |
| GO:0016769 | transferase activity, transferring nitrogenous groups | 7 | 21 | 0.33 | 3 | 4 |
| GO:0044765 | single-organism transport respiratory chain complex III | 53 | 394 | 0.13 | 37 | 16 |
| GO:0006553 | lysine metabolic process monocarboxylic acid biosynthetic process cofactor biosynthetic process | 8 | 27 | 0.30 | 1 | 7 |
| GO:0051188 | carboxylic acid biosynthetic process | 14 | 67 | 0.21 | 5 | 9 |
| GO:0046394 | monophosphate biosynthetic process | 25 | 151 | 0.17 | 4 | 21 |
| GO:0009161 | monophosphate metabolic process | 22 | 128 | 0.17 | 10 | 12 |
| GO:0006520 | cellular amino acid metabolic process nucleoside monophosphate metabolic process alcohol dehydrogenase (NAD) activity | 45 | 325 | 0.14 | 14 | 31 |
| GO:0009123 | branched-chain amino acid metabolic process | 22 | 130 | 0.17 | 10 | 12 |
| GO:0004022 | glycosyl compound biosynthetic process | 9 | 35 | 0.26 | 3 | 6 |
| GO:0009081 | small molecule catabolic process | 7 | 23 | 0.30 | 0 | 7 |
| GO:0044282 | intracellular organelle lumen | 8 | 29 | 0.28 | 3 | 5 |
| GO:0043233 | organelle lumen | 8 | 29 | 0.28 | 8 | 0 |
| GO:0019637 | nucleoside monophosphate metabolic process | 41 | 294 | 0.14 | 15 | 26 |
| GO:0009124 | nucleoside monophosphate biosynthetic process aspartate family amino acid metabolic process | 10 | 42 | 0.24 | 2 | 8 |
| GO:0009066 | oxidative phosphorylation | 15 | 77 | 0.19 | 3 | 12 |
| GO:0006119 | antioxidant activity | 6 | 18 | 0.33 | 4 | 2 |
| GO:0051539 | 4 iron, 4 sulfur cluster binding | 5  | 13 | 0.38 | 3  | 2  |
| GO:0016021 | integral component of membrane | 60 | 479 | 0.13 | 41 | 19 |
| GO:0044425 | membrane part | 74 | 617 | 0.12 | 51 | 23 |
| GO:006793  | phosphorous metabolic process | 61 | 487 | 0.13 | 24 | 37 |
| GO:0009112 | nucleobase metabolic process | 17 | 93  | 0.18 | 4  | 13 |
| GO:0046129 | purine ribonucleoside biosynthetic process | 7  | 25  | 0.28 | 3  | 4  |
| GO:0042451 | purine nucleoside biosynthetic process | 7  | 25  | 0.28 | 3  | 4  |
| GO:0031974 | membrane-enclosed lumen | 9  | 38  | 0.24 | 9  | 0  |
| GO:1901362 | organic cyclic compound biosynthetic process | 34 | 240 | 0.14 | 9  | 25 |
| GO:0034614 | cellular response to reactive oxygen species transmembrane transporter activity | 4  | 9   | 0.44 | 2  | 2  |
| GO:0022857 | heme binding | 8  | 32  | 0.25 | 1  | 7  |
| GO:0046906 | tetrapyrole binding nucleoside biosynthetic process | 8  | 32  | 0.25 | 3  | 5  |
| GO:0009163 | ribonucleoside biosynthetic process | 8  | 32  | 0.25 | 3  | 5  |
| GO:0042455 | catabolic process | 42 | 315 | 0.13 | 13 | 29 |
| GO:0043604 | amide biosynthetic process | 7  | 26  | 0.27 | 1  | 6  |
| GO:0005215 | transporter activity thiamine-containing | 33 | 232 | 0.14 | 23 | 10 |
| GO:0042723 | compound metabolic process | 3  | 5   | 0.60 | 0  | 3  |
| GO:1990351 | transporter complex | 3  | 5   | 0.60 | 3  | 0  |
| GO:0030976 | thiamine pyrophosphate binding | 3  | 5   | 0.60 | 2  | 1  |
| GO:0006772 | thiamine metabolic process | 3  | 5   | 0.60 | 0  | 3  |
| GO:0070469 | respiratory chain transmembrane transporter complex | 3  | 5   | 0.60 | 3  | 0  |
| GO:1902495 | cellular biosynthetic process | 69 | 573 | 0.12 | 15 | 54 |
| GO:0044249 | hydro-lyase activity phosphate-containing | 6  | 20  | 0.30 | 4  | 2  |
| GO:0006796 | compound metabolic process | 59 | 479 | 0.12 | 23 | 36 |
| GO          | Description                                                      | Term Count | Gene Count | Benjamini Adjusted | FDR Count | Gene Count |
|-------------|------------------------------------------------------------------|------------|------------|--------------------|-----------|------------|
| GO:1901605  | alpha-amino acid metabolic process                               | 39         | 289        | 0.13               | 11        | 28         |
| GO:0006066  | alcohol metabolic process                                        | 7          | 27         | 0.26               | 0         | 7          |
| GO:0009108  | coenzyme biosynthetic process                                    | 11         | 55         | 0.20               | 3         | 8          |
| GO:0004449  | isocitrate dehydrogenase (NAD\(^+\)) activity                  | 2          | 2          | 1.00               | 2         | 0          |
| GO:0003872  | 6-phosphofructokinase activity                                   | 2          | 2          | 1.00               | 0         | 2          |
| GO:0006002  | fructose 6-phosphate metabolic process                           | 2          | 2          | 1.00               | 0         | 2          |
| GO:0016801  | hydrolase activity, acting on ether bonds                        | 2          | 2          | 1.00               | 0         | 2          |
| GO:0016805  | dipeptidase activity                                             | 2          | 2          | 1.00               | 0         | 2          |
| GO:0070283  | radical SAM enzyme activity                                      | 2          | 2          | 1.00               | 1         | 1          |
| GO:1903289  | regulation of ATP catabolic process                              | 2          | 2          | 1.00               | 2         | 0          |
| GO:0004410  | homocitrate synthase activity                                    | 2          | 2          | 1.00               | 0         | 2          |
| GO:0043171  | peptide catabolic process                                        | 2          | 2          | 1.00               | 0         | 2          |
| GO:0006510  | ATP-dependent proteolysis                                        | 2          | 2          | 1.00               | 2         | 0          |
| GO:004176   | ATP-dependent peptidase activity                                 | 2          | 2          | 1.00               | 2         | 0          |
| GO:0004347  | glucose-6-phosphate isomerase activity                           | 2          | 2          | 1.00               | 0         | 2          |
| GO:0032781  | positive regulation of ATPase activity                           | 2          | 2          | 1.00               | 2         | 0          |
| GO:003938   | IMP dehydrogenase activity                                       | 2          | 2          | 1.00               | 0         | 2          |
| GO:0001671  | ATPase activator activity                                        | 2          | 2          | 1.00               | 2         | 0          |
| GO:0043462  | regulation of ATPase activity                                    | 2          | 2          | 1.00               | 2         | 0          |
| GO:0005945  | 6-phosphofructokinase complex                                    | 2          | 2          | 1.00               | 0         | 2          |
| GO:0006633  | fatty acid biosynthetic process transferase activity             | 6          | 21         | 0.29               | 1         | 5          |
| GO:0016765  | transferring alkyl or aryl (other than methyl) groups            | 6          | 21         | 0.29               | 1         | 5          |
| GO:0044445  | cytosolic part                                                   | 6          | 21         | 0.29               | 0         | 6          |
| GO:1901615  | organic hydroxy compound metabolic process                       | 8          | 34         | 0.24               | 0         | 8          |
| GO:0009110  | vitamin biosynthetic process                                     | 9          | 41         | 0.22               | 1         | 8          |
| GO:0042364  | water-soluble vitamin                                            | 9          | 41         | 0.22               | 1         | 8          |
| GO:0030170 | biosynthetic process | pyridoxal phosphate binding | 9 | 41 | 0.22 | 4 | 5 |
|------------|---------------------|----------------------------|---|----|------|---|---|
| GO:0072593 | reactive oxygen species | metabolic process | 4 | 10 | 0.40 | 2 | 2 |
| GO:0008299 | isoprenoid biosynthetic process | 4 | 10 | 0.40 | 0 | 4 |
| GO:0000302 | response to reactive oxygen species | 4 | 10 | 0.40 | 2 | 2 |
| GO:1901701 | cellular response to oxygen-containing compound | 4 | 10 | 0.40 | 2 | 2 |
| GO:006720  | isoprenoid metabolic process | 4 | 10 | 0.40 | 0 | 4 |
| GO:0016684 | oxidoreductase activity, acting on peroxide as acceptor | 4 | 10 | 0.40 | 2 | 2 |
| GO:0019751 | polyol metabolic process | 4 | 10 | 0.40 | 0 | 4 |
| GO:0044271 | cellular nitrogen compound biosynthetic process | 32 | 230 | 0.14 | 9 | 23 |
| GO:0006631 | fatty acid metabolic process | 7 | 28 | 0.25 | 1 | 6 |
| GO:0051536 | iron-sulfur cluster binding | 7 | 28 | 0.25 | 5 | 2 |
| GO:0051540 | metal cluster binding | 7 | 28 | 0.25 | 5 | 2 |
| GO:0006766 | vitamin metabolic process | 12 | 61 | 0.20 | 2 | 10 |
| GO:0006767 | water-soluble vitamin metabolic process | 12 | 61 | 0.20 | 2 | 10 |
| GO:0022891 | transmembrane transporter activity | 24 | 159 | 0.15 | 15 | 9 |
| GO:0042221 | response to chemical organic substance catabolic process | 8 | 35 | 0.23 | 5 | 3 |
| GO:1901575 | NADP binding oxidoreductase activity, acting on the aldehyde or oxo group of donors | 38 | 287 | 0.13 | 11 | 27 |
| GO:0016903 | purine nucleotide metabolic process | 6 | 22 | 0.27 | 3 | 3 |
| GO:0006163 | purine-containing compound metabolic process | 24 | 163 | 0.15 | 11 | 13 |
| GO:0072521 | lysine biosynthetic process via aminoadipic acid tricarboxylic acid cycle enzyme complex | 3 | 6 | 0.50 | 0 | 3 |
| GO:0019878 | chaperone binding | 3 | 6 | 0.50 | 3 | 0 |
| GO:001681  | sulfur compound binding | 3 | 6 | 0.50 | 2 | 1 |
| GO:1901700 | response to oxygen-containing compound | 4 | 11 | 0.36 | 2 | 2 |
| GO:0009085 | lysine biosynthetic process | 4 | 11 | 0.36 | 0 | 4 |
| GO:0010035 | response to inorganic substance | 4 | 11 | 0.36 | 2 | 2 |
| GO:006694 | steroid biosynthetic process oxidoreductase activity, acting on the aldehyde or oxo group of donors, NAD or NADP as acceptor | 5 | 17 | 0.29 | 0 | 5 |
| GO:0006807 | nitrogen compound metabolic process | 115 | 1071 | 0.11 | 47 | 68 |
| GO:0016835 | carbon-oxygen lyase activity | 6 | 24 | 0.25 | 4 | 2 |
| GO:0005759 | mitochondrial matrix | 6 | 24 | 0.25 | 6 | 0 |
| GO:0009165 | nucleotide biosynthetic process | 11 | 58 | 0.19 | 3 | 8 |
| GO:0034599 | cellular response to oxidative stress | 5 | 18 | 0.28 | 3 | 2 |
| GO:0008202 | steroid metabolic process | 5 | 18 | 0.28 | 0 | 5 |
| GO:1901293 | nucleoside phosphate biosynthetic process | 11 | 60 | 0.18 | 3 | 8 |
| GO:0031072 | heat shock protein binding | 3 | 7 | 0.43 | 3 | 0 |
| GO:0044272 | sulfur compound biosynthetic process | 8 | 39 | 0.21 | 2 | 6 |
| GO:0009259 | ribonucleotide metabolic process | 24 | 170 | 0.14 | 11 | 13 |
| GO:0008643 | carbohydrate transport | 6 | 25 | 0.24 | 4 | 2 |
| GO:0005739 | mitochondrion | 16 | 101 | 0.16 | 11 | 5 |
| GO:0019693 | ribose phosphate metabolic process | 24 | 172 | 0.14 | 11 | 13 |
| GO:0016829 | lyase activity pyrimidine-containing compound biosynthetic process | 11 | 62 | 0.18 | 7 | 4 |
| GO:0072528 | ATPase regulator activity | 5 | 19 | 0.26 | 1 | 4 |
| GO:0006551 | leucine metabolic process | 5 | 19 | 0.26 | 0 | 5 |
| GO:0016310 | phosphorylation | 27 | 200 | 0.14 | 13 | 14 |
| GO:0009266 | response to temperature stimulus oxidoreductase activity, acting on the CH-CH group of donors, quinone or related compound as acceptor | 2 | 3 | 0.67 | 2 | 0 |
| GO:0016635 | ATPase regulator activity | 2 | 3 | 0.67 | 1 | 1 |
| GO:0004888 | transmembrane signaling | 2 | 3 | 0.67 | 2 | 0 |
| GO:0003984 | receptor activity | acetalactate synthase activity | 2 | 3 | 0.67 | 0 | 2 |
|------------|------------------|-------------------------------|---|---|-------|---|---|
| GO:0045252 | acetolactate synthase activity | oxoglutarate dehydrogenase complex | 2 | 3 | 0.67 | 2 | 0 |
| GO:0004096 | catalase activity | aconitate hydratase activity | 2 | 3 | 0.67 | 2 | 0 |
| GO:0003994 | succinate dehydrogenase complex | dihydrolipoyl dehydrogenase complex | 2 | 3 | 0.67 | 2 | 0 |
| GO:0045240 | oxoglutarate dehydrogenase complex | response to heat | 2 | 3 | 0.67 | 2 | 0 |
| GO:0009083 | branched-chain amino acid catabolic process | succinate dehydrogenase activity | 2 | 3 | 0.67 | 2 | 0 |
| GO:0000104 | peptidyl-lysine modification to peptidyl-hypusine | mitochondrial respiratory chain complex III | 2 | 3 | 0.67 | 2 | 0 |
| GO:0008612 | dehydrogenase (NADP+) activity | glyoxylate cycle | 2 | 3 | 0.67 | 2 | 0 |
| GO:0006552 | leucine catabolic process | acetalactate synthase complex | 2 | 3 | 0.67 | 2 | 0 |
| GO:0005948 | intramolecular oxidoreductase activity | cellular modified amino acid biosynthetic process | 4 | 13 | 0.31 | 1 | 3 |
| GO:0016860 | cellular response to chemical stimulus | purine ribonucleotide metabolic process | 7 | 33 | 0.21 | 1 | 6 |
| GO:0009150 | iron ion binding | branched-chain amino acid biosynthetic process | 7 | 34 | 0.21 | 2 | 5 |
| GO:0051537 | 2 iron, 2 sulfur cluster binding | ergosterol metabolic process | 5 | 20 | 0.25 | 0 | 5 |
| GO:0008204 | prenyltransferase activity | 2 iron, 2 sulfur cluster binding | 3 | 8 | 0.38 | 2 | 1 |
| GO:0016776 | phosphotransferase activity, phosphate group as acceptor | 3 | 8 | 0.38 | 1 | 2 |
| GO:0016128 | phytosteroid metabolic process | 3 | 8 | 0.38 | 0 | 3 |
| GO:0016129 | phytosteroid biosynthetic process | 3 | 8 | 0.38 | 0 | 3 |
| GO:0019842 | vitamin binding | 3 | 8 | 0.38 | 2 | 1 |
| GO:0006696 | ergosterol biosynthetic process | 3 | 8 | 0.38 | 0 | 3 |
| GO:0006189 | 'de novo' IMP biosynthetic process | 3 | 8 | 0.38 | 0 | 3 |
| GO:0006541 | glutamine metabolic process | 3 | 8 | 0.38 | 0 | 3 |
| GO:0044107 | cellular alcohol metabolic process | 3 | 8 | 0.38 | 0 | 3 |
| GO:0044108 | cellular alcohol biosynthetic process | 3 | 8 | 0.38 | 0 | 3 |
| GO:0019643 | reductive tricarboxylic acid cycle | 4 | 14 | 0.29 | 4 | 0 |
| GO:0015977 | carbon fixation | 4 | 14 | 0.29 | 4 | 0 |
| GO:0018130 | heterocycle biosynthetic process | 29 | 223 | 0.13 | 9 | 20 |
| GO:0016861 | intramolecular oxidoreductase activity, interconverting aldoses and ketoses | 3 | 9 | 0.33 | 0 | 3 |
| GO:0006575 | cellular modified amino acid | 9 | 50 | 0.18 | 1 | 8 |
| GO:0030554  | metabolic process | 53  | 462 | 0.11 | 30  | 23  |
|-------------|-------------------|-----|-----|------|-----|-----|
| GO:0016830  | carbon-carbon lyase activity | 5   | 22  | 0.23 | 3   | 2   |
| GO:0036094  | small molecule binding | 78  | 718 | 0.11 | 39  | 39  |
| GO:0006020  | inositol metabolic process | 2   | 4   | 0.50 | 0   | 2   |
| GO:0042724  | compound biosynthetic process | 2   | 4   | 0.50 | 0   | 2   |
| GO:0004448  | isocitrate dehydrogenase activity | 2   | 4   | 0.50 | 2   | 0   |
| GO:0043446  | cellular alkane metabolic process | 2   | 4   | 0.50 | 0   | 2   |
| GO:0006108  | malate metabolic process | 2   | 4   | 0.50 | 2   | 0   |
| GO:0016615  | malate dehydrogenase activity | 2   | 4   | 0.50 | 2   | 0   |
| GO:0009228  | thiamine biosynthetic process | 2   | 4   | 0.50 | 0   | 2   |
| GO:0015947  | methane metabolic process | 2   | 4   | 0.50 | 0   | 2   |
| GO:0004784  | superoxide dismutase activity | 2   | 4   | 0.50 | 2   | 0   |
| GO:0042743  | hydrogen peroxide metabolic process | 2   | 4   | 0.50 | 0   | 2   |
| GO:0016721  | acting on superoxide radicals as acceptor | 2   | 4   | 0.50 | 2   | 0   |
| GO:0008144  | drug binding | 2   | 4   | 0.50 | 0   | 2   |
| GO:0018065  | protein-cofactor linkage | 2   | 4   | 0.50 | 2   | 0   |
| GO:0016114  | terpenoid biosynthetic process | 2   | 4   | 0.50 | 0   | 2   |
| GO:0006515  | synthesized protein catabolic process | 2   | 4   | 0.50 | 2   | 0   |
| GO:0006721  | terpenoid metabolic process | 2   | 4   | 0.50 | 0   | 2   |
| GO:0008121  | ubiquinol-cytochrome-c reductase activity | 2   | 4   | 0.50 | 2   | 0   |
| GO:0016681  | acting on diphenols and related substances as donors, cytochrome as acceptor oxidoreductase activity, | 2   | 4   | 0.50 | 2   | 0   |
| GO:0016679  | acting on diphenols and related substances as donors | 2   | 4   | 0.50 | 2   | 0   |
| GO:0009071  | serine family amino acid catabolic process | 2   | 4   | 0.50 | 0   | 2   |
| GO               | Description                                      | Up | Down | Ratio | Background | Up | Down |
|------------------|--------------------------------------------------|----|------|-------|------------|----|------|
| GO:0070301       | cellular response to hydrogen peroxide           | 2  | 4    | 0.50  | 0          | 0  | 2    |
| GO:0006546       | glycine catabolic process                        | 2  | 4    | 0.50  | 0          | 0  | 2    |
| GO:0006563       | L-serine metabolic process                       | 6  | 30   | 0.20  | 1          | 5  |      |
| GO:0043603       | cellular amide metabolic process                 | 9  | 52   | 0.17  | 1          | 8  |      |
| GO:0005737       | cytoplasm                                       | 33 | 266  | 0.12  | 8          | 25 |      |
| GO:0015940       | pantothenate biosynthetic process                | 4  | 16   | 0.25  | 1          | 3  |      |
| GO:0015939       | pantothenate metabolic process                   | 4  | 16   | 0.25  | 1          | 3  |      |
| GO:0016740       | transferase activity                             | 67 | 607  | 0.11  | 30         | 37 |      |
| GO:0006950       | response to stress                               | 22 | 164  | 0.13  | 19         | 3  |      |

Note: Ratio in background represents the ratio of DEGs in the specific GO categories (background genes). Number up or down represent the number of DEG up- or down-regulated in response to the multiple inhibitors stress.
| ID     | Term                                           | DEGs | Background genes | DEGs/backgroud genes |
|--------|------------------------------------------------|------|------------------|----------------------|
| ko01220| Degradation of aromatic compounds              | 4    | 6                | 0.667                |
| ko00830| Retinol metabolism                             | 3    | 5                | 0.600                |
| ko0983 | Drug metabolism - other enzymes                | 4    | 7                | 0.571                |
| ko0010 | Glycolysis / Gluconeogenesis                    | 25   | 44               | 0.568                |
| ko0680 | Methane metabolism                             | 11   | 20               | 0.550                |
| ko0710 | Carbon fixation in photosynthetic organisms     | 9    | 17               | 0.529                |
| ko0020 | Citrate cycle (TCA cycle)                      | 14   | 28               | 0.500                |
| ko0630 | Glyoxylate and dicarboxylate metabolism         | 10   | 20               | 0.500                |
| ko0130 | Ubiquinone and other terpenoid-quinone biosynthesis | 5    | 10               | 0.500                |
| ko0625 | Chloroalkane and chloroalkene degradation       | 4    | 8                | 0.500                |
| ko0626 | Naphthalene degradation                        | 3    | 6                | 0.500                |
| ko0300 | Lysine biosynthesis                            | 6    | 13               | 0.462                |
| ko01200| Carbon metabolism                              | 42   | 92               | 0.457                |
| ko01210| 2-Oxocarboxylic acid metabolism                | 15   | 35               | 0.429                |
| ko0730 | Thiamine metabolism                            | 3    | 7                | 0.429                |
| ko04626| Plant-pathogen interaction                     | 2    | 5                | 0.400                |
| ko04612| Antigen processing and presentation             | 2    | 5                | 0.400                |
| ko04621| NOD-like receptor signaling pathway             | 2    | 5                | 0.400                |
| ko0950 | Isoquinoline alkaloid biosynthesis              | 2    | 5                | 0.400                |
| ko0521 | Streptomycin biosynthesis                       | 2    | 5                | 0.400                |
| ko0030 | Pentose phosphate pathway                       | 9    | 23               | 0.391                |
| ko0550 | Starch and sucrose metabolism                   | 12   | 31               | 0.387                |
| ko0052 | Galactose metabolism                           | 5    | 13               | 0.385                |
| ko0380 | Tryptophan metabolism                          | 6    | 16               | 0.375                |
| ko0750 | Vitamin B6 metabolism                          | 3    | 8                | 0.375                |
| ko0280 | Valine, leucine and isoleucine degradation      | 4    | 11               | 0.364                |
| ko0650 | Butanoate metabolism                           | 4    | 11               | 0.364                |
| ko0230 | Central carbon metabolism in cancer            | 5    | 14               | 0.357                |
| ko0051 | Fructose and mannose metabolism                | 6    | 17               | 0.353                |
| ko0910 | Nitrogen metabolism                            | 2    | 6                | 0.333                |
| ko0260 | Glycine, serine and threonine metabolism        | 10   | 32               | 0.313                |
| ko0670 | One carbon pool by folate                      | 5    | 16               | 0.313                |
| ko0290 | Valine, leucine and isoleucine biosynthesis     | 4    | 13               | 0.308                |
| ko0980 | Metabolism of xenobiotics by cytochrome P450    | 3    | 10               | 0.300                |
| ko0982 | Drug metabolism - cytochrome P450               | 3    | 10               | 0.300                |
| ko01200| Biosynthesis of amino acids                     | 33   | 112              | 0.295                |
| ko0071 | Fatty acid degradation                         | 5    | 17               | 0.294                |
| ko0350 | Tyrosine metabolism                            | 5    | 17               | 0.294                |
| ko0780 | Biotin metabolism                              | 2    | 7                | 0.286                |
| KEGG ID  | Pathway Description                                      | ID   | FD  | FDR  |
|---------|---------------------------------------------------------|------|-----|------|
| ko00620 | Pyruvate metabolism                                     | 11   | 39  | 0.282|
| ko04152 | AMPK signaling pathway                                  | 7    | 25  | 0.280|
| ko04066 | HIF-1 signaling pathway                                 | 5    | 18  | 0.278|
| ko00040 | Pentose and glucuronate interconversions                | 3    | 11  | 0.273|
| ko04260 | Cardiac muscle contraction                              | 5    | 20  | 0.250|
| ko04068 | FoxO signaling pathway                                  | 4    | 16  | 0.250|
| ko00770 | Pantothenate and CoA biosynthesis                       | 4    | 16  | 0.250|
| ko00040 | Pentose and glucuronate interconversions                | 3    | 11  | 0.273|
| ko00190 | Oxidative phosphorylation                              | 7    | 39  | 0.241|
| ko00900 | Terpenoid backbone biosynthesis                         | 4    | 17  | 0.235|
| ko00040 | Pentose and glucuronate interconversions                | 3    | 11  | 0.273|
| ko00190 | Oxidative phosphorylation                              | 7    | 39  | 0.241|
| ko00900 | Terpenoid backbone biosynthesis                         | 4    | 17  | 0.235|
| ko00550 | GABAergic synapse                                       | 3    | 13  | 0.231|
| ko00903 | Tropane, piperidine and pyridine alkaloid biosynthesis  | 2    | 9   | 0.222|
| ko03320 | PPAR signaling pathway                                 | 2    | 9   | 0.222|
| ko00250 | Alanine, aspartate and glutamate metabolism             | 5    | 24  | 0.208|
| ko02020 | Two-component system                                   | 3    | 15  | 0.200|
| ko00410 | beta-Alanine metabolism                                | 3    | 15  | 0.200|
| ko00100 | Steroid biosynthesis                                   | 3    | 15  | 0.200|
| ko04727 | GABAergic synapse                                       | 2    | 10  | 0.200|
| ko00903 | Limonene and pinene degradation                        | 1    | 5   | 0.200|
| ko00860 | Porphyrin and chlorophyll metabolism                   | 3    | 16  | 0.188|
| ko00310 | Lysine degradation                                     | 3    | 16  | 0.188|
| ko00250 | Alanine, aspartate and glutamate metabolism             | 5    | 24  | 0.208|
| ko02020 | Two-component system                                   | 3    | 15  | 0.200|
| ko00410 | beta-Alanine metabolism                                | 3    | 15  | 0.200|
| ko00100 | Steroid biosynthesis                                   | 3    | 15  | 0.200|
| ko04727 | GABAergic synapse                                       | 2    | 10  | 0.200|
| ko00903 | Limonene and pinene degradation                        | 1    | 5   | 0.200|
| ko00860 | Porphyrin and chlorophyll metabolism                   | 3    | 16  | 0.188|
| ko00310 | Lysine degradation                                     | 3    | 16  | 0.188|
| ko00250 | Alanine, aspartate and glutamate metabolism             | 5    | 24  | 0.208|
| ko02020 | Two-component system                                   | 3    | 15  | 0.200|
| ko00410 | beta-Alanine metabolism                                | 3    | 15  | 0.200|
| ko00100 | Steroid biosynthesis                                   | 3    | 15  | 0.200|
| ko04727 | GABAergic synapse                                       | 2    | 10  | 0.200|
| ko00903 | Limonene and pinene degradation                        | 1    | 5   | 0.200|
| ko00860 | Porphyrin and chlorophyll metabolism                   | 3    | 16  | 0.188|
| ko00310 | Lysine degradation                                     | 3    | 16  | 0.188|
| ko00250 | Alanine, aspartate and glutamate metabolism             | 5    | 24  | 0.208|
| ko02020 | Two-component system                                   | 3    | 15  | 0.200|
| ko00410 | beta-Alanine metabolism                                | 3    | 15  | 0.200|
| ko00100 | Steroid biosynthesis                                   | 3    | 15  | 0.200|
| ko04727 | GABAergic synapse                                       | 2    | 10  | 0.200|
| ko00903 | Limonene and pinene degradation                        | 1    | 5   | 0.200|
| ko00860 | Porphyrin and chlorophyll metabolism                   | 3    | 16  | 0.188|
| ko00310 | Lysine degradation                                     | 3    | 16  | 0.188|
| ko00250 | Alanine, aspartate and glutamate metabolism             | 5    | 24  | 0.208|
| ko02020 | Two-component system                                   | 3    | 15  | 0.200|
| ko00410 | beta-Alanine metabolism                                | 3    | 15  | 0.200|
| ko00100 | Steroid biosynthesis                                   | 3    | 15  | 0.200|
| ko04727 | GABAergic synapse                                       | 2    | 10  | 0.200|
| ko00903 | Limonene and pinene degradation                        | 1    | 5   | 0.200|
| ko00860 | Porphyrin and chlorophyll metabolism                   | 3    | 16  | 0.188|
| ko00310 | Lysine degradation                                     | 3    | 16  | 0.188|
| ko00250 | Alanine, aspartate and glutamate metabolism             | 5    | 24  | 0.208|
| ko02020 | Two-component system                                   | 3    | 15  | 0.200|
| ko00410 | beta-Alanine metabolism                                | 3    | 15  | 0.200|
| ko00100 | Steroid biosynthesis                                   | 3    | 15  | 0.200|
| ko04727 | GABAergic synapse                                       | 2    | 10  | 0.200|
| ko00903 | Limonene and pinene degradation                        | 1    | 5   | 0.200|
| ko00860 | Porphyrin and chlorophyll metabolism                   | 3    | 16  | 0.188|
| ko00310 | Lysine degradation                                     | 3    | 16  | 0.188|
| ko00250 | Alanine, aspartate and glutamate metabolism             | 5    | 24  | 0.208|
| ko02020 | Two-component system                                   | 3    | 15  | 0.200|
| ko00410 | beta-Alanine metabolism                                | 3    | 15  | 0.200|
| ko00100 | Steroid biosynthesis                                   | 3    | 15  | 0.200|
| ko04727 | GABAergic synapse                                       | 2    | 10  | 0.200|
| ko00903 | Limonene and pinene degradation                        | 1    | 5   | 0.200|
| ko00860 | Porphyrin and chlorophyll metabolism                   | 3    | 16  | 0.188|
| ko00310 | Lysine degradation                                     | 3    | 16  | 0.188|
| ko00250 | Alanine, aspartate and glutamate metabolism             | 5    | 24  | 0.208|
| ko02020 | Two-component system                                   | 3    | 15  | 0.200|
| ko00410 | beta-Alanine metabolism                                | 3    | 15  | 0.200|
| ko00100 | Steroid biosynthesis                                   | 3    | 15  | 0.200|
| ko04727 | GABAergic synapse                                       | 2    | 10  | 0.200|
| ko00903 | Limonene and pinene degradation                        | 1    | 5   | 0.200|
| ko00860 | Porphyrin and chlorophyll metabolism                   | 3    | 16  | 0.188|
| ko00310 | Lysine degradation                                     | 3    | 16  | 0.188|
| ko00250 | Alanine, aspartate and glutamate metabolism             | 5    | 24  | 0.208|
ko04071  Sphingolipid signaling pathway  2  17  0.118
ko00790  Folate biosynthesis  1  9  0.111
ko03450  Non-homologous end-joining  1  9  0.111
ko00450  Selenocompound metabolism  1  9  0.111
ko04151  PI3K-Akt signaling pathway  2  20  0.100
ko01212  Fatty acid metabolism  2  21  0.095
ko04020  Calcium signaling pathway  1  11  0.091
ko01040  Biosynthesis of unsaturated fatty acids  1  12  0.083
ko00514  Other types of O-glycan biosynthesis  1  12  0.083
ko04022  cGMP-PKG signaling pathway  1  12  0.083
ko04966  Collecting duct acid secretion  1  12  0.083
ko00340  Histidine metabolism  1  12  0.083
ko03018  RNA degradation  4  49  0.082
ko04141  Protein processing in endoplasmic reticulum  6  76  0.079
ko00920  Sulfur metabolism  1  13  0.077
ko04666  Fc gamma R-mediated phagocytosis  1  13  0.077
ko00562  Inositol phosphate metabolism  1  13  0.077
ko04144  Endocytosis  3  40  0.075
ko04113  Meiosis - yeast  7  99  0.071
ko03040  Spliceosome  4  63  0.063
ko00760  Nicotinate and nicotinamide metabolism  1  16  0.063
ko03022  Basal transcription factors  2  32  0.063
ko00564  Glycerocephospholipid metabolism  2  33  0.061
ko03440  Homologous recombination  1  18  0.056
ko03460  Fanconi anemia pathway  1  18  0.056
ko04810  Regulation of actin cytoskeleton  1  18  0.056
ko03060  Protein export  1  18  0.056
ko04010  MAPK signaling pathway  1  18  0.056
ko00400  Phenylalanine, tyrosine and tryptophan biosynthesis  1  19  0.053
ko04921  Oxytocin signaling pathway  1  19  0.053
ko04914  Progesterone-mediated oocyte maturation  1  19  0.053
ko04721  Synaptic vesicle cycle  1  22  0.045
ko00240  Pyrimidine metabolism  3  68  0.044
ko00513  Various types of N-glycan biosynthesis  1  32  0.031
ko04145  Phagosome  1  32  0.031
ko03420  Nucleotide excision repair  1  36  0.028
ko04111  Cell cycle - yeast  3  110  0.027
ko04011  MAPK signaling pathway - yeast  1  37  0.027
ko00970  Aminoacyl-tRNA biosynthesis  1  38  0.026
ko03013  RNA transport  1  79  0.013

Note: The ratio of DEGs/background genes indicates the effects of the DEGs in the specific KEGG pathway (background genes).
| ID        | Gene               | NR_Description                                           | Primer | Sequence (5'→3')                  |
|-----------|--------------------|----------------------------------------------------------|--------|-----------------------------------|
| KMAR_10772 | uncharacterized abhydrolase domain-containing protein YGR015C | Forward | CCCTTGTGAATCTTGCGTTAAGTTG         |
|           |                    | Reverse                                                 |        | AATGTAGCATACGTCGTCATAGTTG         |
| KMAR_80057 | RPB1              | DNA-directed RNA polymerase II subunit RPB1             | Forward | CCCTGGTAAACACTTCTCCTCAG           |
|           |                    | Reverse                                                 |        | GAGCAGAGTACGTTGTAAGTTG            |
| KMAR_50053 | IRC8              | uncharacterized protein IRC8                           | Forward | GCAACAGAAACACTCAACAAAG             |
|           |                    | Reverse                                                 |        | TCCCTTCCCACCCGAAAC                |
| KMAR_10795 | NQO2              | ribosylhydronicotinamide dehydrogenase                 | Forward | GCACCCAGAATTAGTGATCCAGAAG          |
|           |                    | Reverse                                                 |        | AATCCAAAACCCGAGTAACCGAAAG          |
| KMAR_80139 | carbonic anhydrase | Forward                                                 |        | TGAAGGTAACAAAGTCGTCACTTG           |
|           |                    | Reverse                                                 |        | TCGTCAAGGTCACCCTGAGTAG             |
| KMAR_50521 | SDH4              | succinate dehydrogenase                                | Forward | CCACCTCGTCCTCGTCCTATTG            |
|           |                    | Reverse                                                 |        | CCCATGATACACCTCTTTGTTC            |
| KMAR_10054 | HBN1              | putative nitroreductase HBN1                           | Forward | GGCTTCTGTACCGTGATCGTGTTG          |
|           |                    | Reverse                                                 |        | TGGATTGGTCTGCGAAGGATGG             |
| KMAR_20313 | MCH5              | riboflavin transporter MCH5                            | Forward | ACACCTTAAACCTCTGCTC              |
|           |                    | Reverse                                                 |        | GCACCAGATAGAAGAAC                |
| KMAR_70277 | CTR1              | copper transport protein CTR1                          | Forward | CCGTCTCTTAATACATCTCAG             |
|           |                    | Reverse                                                 |        | CCATCGTCATCTCCTAGGA              |
| KMAR_40093 | ARN2              | siderophore iron transporter ARN2                      | Forward | TTCAAGGCAGTGATGAAGATT            |
|           |                    | Reverse                                                 |        | CGAAGGTGATAGGTGATGG               |
| KMAR_10790 | SIT1              | major facilitator superfamily                          | Forward | CTATCTGGACCTCCTTAACCT            |
|           |                    | Reverse                                                 |        | AATAGAACACACACAAAC               |
| KMAR_30337 | PDR12             | ATP-dependent permease PDR12                           | Forward | CTGCCTACTTCTGCTTCTA         |
|           |                    | Reverse                                                 |        | CAGAACAAACAACATACCA               |
| KMAR_80266 | ITR2              | myo-inositol transporter 2                             | Forward | CTCTGGCTACTTGTGTATCC            |
|           |                    | Reverse                                                 |        | TCCTCTTGCTGCTAGTTGT              |
| KMAR_20248 | JEN2              | putative sialic acid transporter                       | Forward | GTGCTCTCTCTAGATGTTGA             |
|           |                    | Reverse                                                 |        | CAGTCTGATAGGTAAGTAAGGA             |
| KMAR_60075 | JEN1              | carboxylic acid transporter protein homolog            | Forward | AAGAAGGATTACGCTAAGGT            |
|           |                    | Reverse                                                 |        | GAGATGGAAGTACGTTGAGGAC            |
| KMAR_50130 | FNX1              | multidrug resistance protein fnx1                      | Forward | CGGTCAATGGGCAATAGGA             |
|           |                    | Reverse                                                 |        | AGCGAGAGAGTAACAGTAA               |
| KMAR_70043 | ACT1              | Actin                                                   | Forward | TTGGCTCTTGAGAGACATCATCAG           |
|           |                    | Reverse                                                 |        | AGCGAGATGAGAAAAGCGTTT            |
Figure S1 Differentially expressed genes in GO enrichments in multiple inhibitors treated condition.
Figure S2 Differentially expressed genes in KEGG pathways in multiple inhibitors treated condition.