1. **GO analysis of mRNA\_up\_*dcp2*△ (n=1376)**

|  |  |  |  |
| --- | --- | --- | --- |
| **Functional category** | **P-value** | **k** | **f** |
| metabolism of energy reserves | 6 x 10-8 | 30 | 56 |
| sugar, glucoside, polyol and  carboxylate catabolism | 4 x 10-7 | 37 | 81 |
| tricarboxylic-acid pathway | 1 x 10-6 | 19 | 31 |
| c-compound and carbohydrate transport | 1 x 10-6 | 20 | 34 |
| c-compound and carbohydrate metabolism | 8 x 10-6 | 74 | 223 |
| stress response | 1 x 10-5 | 57 | 162 |
| meiotic recombination | 1 x 10-5 | 20 | 38 |

1. **GO analysis of mRNA\_dn\_*dcp2*△ (n=1281)**

|  |  |  |  |
| --- | --- | --- | --- |
| **Functional category** | **P-value** | **k** | **f** |
| ribosomal proteins | < 10-14 | 153 | 246 |
| rRNA processing | < 10-14 | 90 | 169 |
| RNA binding | 1 X 10-14 | 82 | 189 |
| ribosome biogenesis | 1 X 10-12 | 38 | 64 |
| translation initiation | 4 X 10-11 | 27 | 40 |
| N-directed glycosylation, deglycosylation | 6 X 10-7 | 23 | 43 |
| unfolded protein response | 1 X 10-6 | 31 | 69 |
| protein folding and stabilization | 1 X 10-6 | 38 | 93 |
| rRNA synthesis | 2 X 10-6 | 26 | 55 |
| tRNA synthesis | 4 X 10-6 | 20 | 38 |
| peptidoglycan anabolism | 6 X 10-6 | 12 | 17 |
| non-vesicular ER transport | 8 X 10-6 | 11 | 15 |
| rRNA modification | 2 X 10-5 | 12 | 18 |
| translation elongation | 2 X 10-5 | 13 | 21 |
| aminoacyl-tRNA-synthetases | 3 X 10-5 | 19 | 39 |
| tRNA modification | 5 X 10-5 | 20 | 43 |
| biosynthesis of methionine | 5 X 10-5 | 6 | 6 |

1. **GO analysis of Dhh1-dep. mRNA\_up\_*dcp2*△ (n=752)**

|  |  |  |  |
| --- | --- | --- | --- |
| **Functional category** | **P-value** | **k** | **f** |
| sugar, glucoside, polyol and  carboxylate catabolism | 9 x 10-12 | 33 | 81 |
| metabolism of energy reserves | 3 x 10-10 | 25 | 56 |
| tricarboxylic-acid pathway | 4 x 10-9 | 17 | 31 |
| stress response | 2 x 10-7 | 42 | 162 |
| c-compound and carbohydrate metabolism | 2 x 10-7 | 52 | 223 |
| sugar, glucoside, polyol and  carboxylate anabolism | 2 x 10-6 | 15 | 35 |
| c-compound and carbohydrate transport | 5 x 10-6 | 14 | 34 |
| Oxidative stress response | 8 x 10-5 | 17 | 55 |
| biosynthesis of glutamate | 8 x 10-5 | 8 | 15 |
| regulation of glycolysis and gluconeogenesis | 9 x 10-5 | 9 | 19 |

1. **GO analysis of Dhh1-indep. mRNA\_up\_*dcp2*△ (n=607)**

|  |  |  |  |
| --- | --- | --- | --- |
| **Functional category** | **P-value** | **k** | **f** |
| DNA repair | 6 x 10-9 | 39 | 159 |
| meiotic recombination | 7 x 10-8 | 16 | 38 |
| DNA damage response | 5 x 10-5 | 19 | 77 |
| Cell-cell adhesion | 9 x 10-5 | 6 | 10 |

1. **GO analysis of TE\_up\_*dcp2*△ (n=541)**

|  |  |  |  |
| --- | --- | --- | --- |
| **Functional category** | **P-value** | **k** | **f** |
| electron transport and membrane-  associated energy conservation | < 10-14 | 28 | 58 |
| electron transport | 6 X 10-13 | 30 | 83 |
| ribosomal proteins | 3 X 10-10 | 51 | 246 |
| energy generation | 7 X 10-10 | 13 | 21 |
| mitochondrion | 6 X 10-9 | 38 | 170 |
| aerobic respiration | 2 X 10-8 | 23 | 77 |
| respiration | 6 X 10-5 | 15 | 59 |

1. **GO analysis of TE\_dn\_*dcp2*△ (n=659)**

|  |  |  |  |
| --- | --- | --- | --- |
| **Functional category** | **P-value** | **k** | **f** |
| anion transport | 2 X 10-5 | 7 | 11 |
| transcription activation | 3 X 10-5 | 14 | 42 |

1. **GO analysis of Ribo\_up\_*dcp2*△ (n=1261)**

|  |  |  |  |
| --- | --- | --- | --- |
| **Functional category** | **P-value** | **k** | **f** |
| aerobic respiration | 8 X 10-11 | 40 | 77 |
| sugar, glucoside, polyol and  carboxylate catabolism | 6 X 10-10 | 40 | 81 |
| tricarboxylic-acid pathway | 4 X 10-9 | 21 | 31 |
| mitochondrion | 6 X 10-8 | 62 | 170 |
| metabolism of energy reserves | 7 X 10-7 | 27 | 56 |
| oxidative stress response | 2 X 10-6 | 26 | 55 |
| electron transport chain and membrane-  associated energy Conservation | 2 X 10-5 | 25 | 58 |
| metabolism of vitamins, cofactors, and  prosthetic groups | 4 X 10-5 | 20 | 43 |
| biosynthesis of glutamate | 7 X 10-5 | 10 | 15 |
| sugar, glucoside, polyol and  carboxylate anabolism | 7 X 10-5 | 17 | 35 |

1. **GO analysis of Ribo\_dn\_*dcp2*△ (n=1326)**

|  |  |  |  |
| --- | --- | --- | --- |
| **Functional category** | **P-value** | **k** | **f** |
| ribosomal proteins | < 10-14 | 139 | 246 |
| N-directed glycosylation, deglycosylation | 2 X 10-13 | 31 | 43 |
| peptidoglycan anabolism | 9 X 10-7 | 13 | 17 |
| RNA binding | 1 X 10-6 | 66 | 189 |
| O-directed glycosylation, deglycosylation | 1 X 10-6 | 12 | 15 |
| rRNA processing | 4 X 10-6 | 59 | 169 |
| translation elongation | 5 X 10-6 | 14 | 21 |
| ribosome biogenesis | 4 X 10-5 | 27 | 64 |
| unfolded protein response | 7 X 10-5 | 28 | 69 |
| translation initiation | 9 X 10-5 | 19 | 40 |
| sulfate assimilation | 9 X 10-5 | 7 | 8 |