**S2 Table.**

| Module | Top Molecular Function | Ref. list 6322 genes | # Hits | Fold Enrich. | p-value | p.adjust |
|---|---|---|---|---|---|---|
| black<br>164 genes | RNA polym. II basal transcription factor binding (GO:0001091) | 5 | 2 | 15.42 | 7.7E-03 | 4.3E-02 |
| | 3-hydroxyacyl-CoA dehydrogenase activity (GO:0003857) | 6 | 2 | 12.85 | 1.1E-02 | 4.3E-02 |
| | DNA replication origin binding (GO:0003688) | 6 | 2 | 12.85 | 1.1E-02 | 4.3E-02 |
| | Tat protein binding (GO:0030957) | 6 | 2 | 12.85 | 1.1E-02 | 4.3E-02 |
| | promoter-specific chromatin binding (GO:1990841) | 6 | 2 | 12.85 | 1.1E-02 | 4.3E-02 |
| | organic cyclic compound binding (GO:0097159) | 2519 | 78 | 1.19 | 2.7E-02 | 4.7E-02 |
| | heterocyclic compound binding (GO:1901363) | 2499 | 77 | 1.19 | 3.2E-02 | 4.7E-02 |
| | ATPase activity (GO:0016887) | 197 | 10 | 1.96 | 3.4E-02 | 4.7E-02 |
| | unfolded protein binding (GO:0051082) | 49 | 4 | 3.15 | 4.0E-02 | 4.7E-02 |
| | nucleic acid binding (GO:0003676) | 1758 | 56 | 1.23 | 4.4E-02 | 4.7E-02 |
| salmon<br>68 genes | adenylyltransferase activity (GO:0070566) | 15 | 4 | 24.79 | 2.3E-05 | 1.2E-04 |
| | double-stranded RNA binding (GO:0003725) | 47 | 5 | 9.89 | 1.6E-04 | 7.0E-04 |
| | threonine-type endopeptidase activity (GO:0004298) | 13 | 3 | 21.45 | 3.9E-04 | 1.6E-03 |
| | threonine-type peptidase activity (GO:0070003) | 13 | 3 | 21.45 | 3.9E-04 | 1.6E-03 |
| | tumor necrosis factor receptor binding (GO:0005164) | 15 | 3 | 18.59 | 6.0E-04 | 2.3E-03 |
| | RNA polym. II core promoter seq.-spec. DNA bind. (GO:0000979) | 21 | 3 | 13.28 | 1.6E-03 | 4.8E-03 |
| | tumor necrosis factor receptor superfamily binding (GO:0032813) | 24 | 3 | 11.62 | 2.3E-03 | 6.2E-03 |
| | nucleotidyltransferase activity (GO:0016779) | 64 | 4 | 5.81 | 5.1E-03 | 1.1E-02 |
| | zinc ion binding (GO:0008270) | 503 | 12 | 2.22 | 7.0E-03 | 1.3E-02 |
| | transition metal ion binding (GO:0046914) | 572 | 13 | 2.11 | 7.4E-03 | 1.4E-02 |
| red<br>168 genes | receptor activity (GO:0004872) | 252 | 19 | 2.84 | 4.7E-05 | 1.4E-03 |
| | molecular transducer activity (GO:0060089) | 252 | 19 | 2.84 | 4.7E-05 | 1.4E-03 |
| | monoval. inorg. cation transmemb. transp. activity (GO:0015077) | 75 | 9 | 4.52 | 2.0E-04 | 3.4E-03 |
| | active transmembrane transporter activity (GO:0022804) | 106 | 10 | 3.55 | 6.0E-04 | 6.8E-03 |
| | receptor binding (GO:0005102) | 448 | 24 | 2.02 | 8.3E-04 | 8.3E-03 |
| | actin binding (GO:0003779) | 154 | 12 | 2.93 | 9.3E-04 | 8.8E-03 |
| | hydrogen-exporting ATPase activity (GO:0036442) | 19 | 4 | 7.92 | 1.8E-03 | 1.3E-02 |
| | protein phosphatase 1 binding (GO:0008157) | 10 | 3 | 11.29 | 2.5E-03 | 1.5E-02 |
| | hydrogen ion transmembrane transporter activity (GO:0015078) | 51 | 6 | 4.43 | 2.6E-03 | 1.5E-02 |
| | secondary active transmemb. transporter activity (GO:0015291) | 52 | 6 | 4.34 | 2.9E-03 | 1.6E-02 |
| greenyellow<br>100 genes | peptidase regulator activity (GO:0061134) | 58 | 6 | 6.54 | 3.4E-04 | 6.6E-03 |
| | endopeptidase inhibitor activity (GO:0004866) | 39 | 5 | 8.11 | 4.1E-04 | 6.6E-03 |
| | peptidase inhibitor activity (GO:0030414) | 39 | 5 | 8.11 | 4.1E-04 | 6.6E-03 |
| | monosaccharide binding (GO:0048029) | 24 | 4 | 10.54 | 6.1E-04 | 7.6E-03 |
| | endopeptidase regulator activity (GO:0061135) | 43 | 5 | 7.35 | 6.4E-04 | 7.6E-03 |
| | carbohydrate binding (GO:0030246) | 77 | 6 | 4.93 | 1.5E-03 | 1.1E-02 |
| | cysteine-type endopeptidase inhibitor activity (GO:0004869) | 22 | 3 | 8.62 | 5.3E-03 | 2.0E-02 |
| | protease binding (GO:0002020) | 44 | 4 | 5.75 | 5.4E-03 | 2.0E-02 |
| | cytokine activity (GO:0005125) | 29 | 3 | 6.54 | 1.1E-02 | 2.6E-02 |
| | antioxidant activity (GO:0016209) | 30 | 3 | 6.32 | 1.2E-02 | 2.7E-02 |