**Supplementary Figure Legends**

**Fig. S1.** Sequencing saturation curve. The x-axis shows the number of clean reads, where unit is 100 k and extreme values are based on the sequencing volume. The y-axis shows the ratio of genes identified relative to the total number of genes reported in the database (A. D02-1, B. DO2-2, C. DO2-3, D. DO4-1, E. DO4-2, F. DO4-3, G. DO8-1, H. DO8-2, I. DO8-3).

**Fig. S2.** Distribution of reads based on reference genes. Due to the variable lengths of the reference genes, the average length of each gene was divided into N equal parts, where each equal part is called a window. The x-axis shows the relative positions of genes and the y-axis shows the number of reads in each window (A. D02-1, B. DO2-2, C. DO2-3, D. DO4-1, E. DO4-2, F. DO4-3, G. DO8-1, H. DO8-2, I. DO8-3).

**Supplementary Tables**

**Table S1.** Quality control results for each sample

|  |  |  |  |  |
| --- | --- | --- | --- | --- |
| **Sample** | **Clean Read1 Q20(%) >= 90** | **Clean Reads >= 20 (M)** | **Gene Unique Mapping Ratio(%) >= 80** | **Genome Mapping Ratio(%) >= 50** |
| DO2-1 | 97.8 (Y) | 24.06 (Y) | 69.84 (N) | 70.97 (Y) |
| DO2-2 | 98.1 (Y) | 24.08 (Y) | 68.96 (N) | 70.44 (Y) |
| DO2-3 | 97.6 (Y) | 23.97 (Y) | 71.42 (N) | 72.13 (Y) |
| DO4-1 | 95.5 (Y) | 22.83 (Y) | 70.31 (N) | 60.6 (Y) |
| DO4-2 | 95.8 (Y) | 23.81 (Y) | 71.87 (N) | 67.24 (Y) |
| DO4-3 | 97.8 (Y) | 24.05 (Y) | 70.54 (N) | 73.89 (Y) |
| DO8-1 | 97.7 (Y) | 24.06 (Y) | 69.18 (N) | 73 (Y) |
| DO8-2 | 98.1 (Y) | 23.77 (Y) | 70.00 (N) | 74.22 (Y) |
| DO8-3 | 98.0 (Y) | 23.99 (Y) | 69.37 (N) | 63.3 (Y) |

“Y” denotes that the sample passed for the QC item and “N” indicates failure.

**Table S2.** Annotated down- or upregulated DEGs based on the comparison of DO2 vs. DO4

|  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- |
| **Gene ID** | **Gene Length** | **Means-DO2** | **Means-DO4** | **log2Ratio** | **Up-Down-Regulation** | **Probability** | **Blast nr** |
| evm.model.scaffold3089.2 | 369 | 56.52 | 0.57 | -6.62 | Down | 0.84 | 60S ribosomal protein L35-like |
| evm.model.scaffold3030.2 | 369 | 56.52 | 0.57 | -6.62 | Down | 0.84 | 60S ribosomal protein L35-like |
| evm.model.scaffold3023.2 | 369 | 56.52 | 0.57 | -6.62 | Down | 0.84 | 60S ribosomal protein L35-like |
| evm.model.scaffold2928.2 | 369 | 56.52 | 0.57 | -6.62 | Down | 0.84 | 60S ribosomal protein L35-like |
| evm.model.scaffold186.13 | 549 | 14.48 | 0.01 | -10.50 | Down | 0.83 | cysteine-rich secretory protein LCCL domain containing 2-like |
| evm.model.scaffold305.2 | 945 | 93.97 | 1.77 | -5.73 | Down | 0.82 | epidermal retinol dehydrogenase 2-like |
| evm.model.scaffold955.14 | 363 | 79.93 | 1.14 | -6.13 | Down | 0.83 | fibrinogen-like protein A |
| add.evm.model.scaffold1127.8 | 807 | 176.80 | 4.76 | -5.21 | Down | 0.80 | galactosylceramide sulfotransferase-like isoform 1 |
| evm.model.scaffold2850.1 | 453 | 25.39 | 0.01 | -11.31 | Down | 0.89 | major vault protein |
| evm.model.scaffold2488.6 | 313 | 13.77 | 0.01 | -10.43 | Down | 0.82 | pituitary tumor-transforming gene 1 protein-interacting protein-like isoform 1 |
| evm.model.scaffold2224.1 | 255 | 13.37 | 0.01 | -10.39 | Down | 0.82 | Threonyl-tRNA synthetase, cytoplasmic, putative |
| evm.model.scaffold463.27 | 2328 | 13.25 | 0.01 | -10.37 | Down | 0.81 | transmembrane protease, serine 3-like, partial |
| evm.model.scaffold778.29 | 765 | 0.21 | 29.22 | 7.14 | Up | 0.83 | calcium-activated chloride channel regulator 1-like |
| evm.model.scaffold532.9 | 939 | 0.01 | 35.27 | 11.78 | Up | 0.92 | cell division cycle 2 |
| evm.model.scaffold209.31 | 1581 | 0.01 | 46.50 | 12.18 | Up | 0.94 | CUB and zona pellucida-like domain-containing protein 1-like, partial |
| evm.model.scaffold114.44 | 1353 | 0.10 | 23.94 | 7.86 | Up | 0.84 | IgGFc-binding protein, partial |
| evm.model.scaffold469.3 | 411 | 3.04 | 122.43 | 5.33 | Up | 0.80 | lysozyme |
| evm.model.scaffold1946.6 | 609 | 0.01 | 41.54 | 12.02 | Up | 0.93 | reverse transcriptase |
| evm.model.scaffold657.18 | 678 | 6.34 | 217.42 | 5.10 | Up | 0.80 | RNA-directed DNA polymerase from mobile element jockey-like |
| evm.model.scaffold716.20 | 507 | 0.32 | 164.89 | 8.99 | Up | 0.95 | RNA-directed DNA polymerase from mobile element jockey-like |
| evm.model.scaffold1647.2 | 576 | 0.01 | 17.61 | 10.78 | Up | 0.86 | spermidine synthase-like |

**Table S3.** Annotated down- or upregulated DEGs based on the comparison of DO2 vs. DO8

|  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- |
| **Gene ID** | **Gene Length** | **Means-DO2** | **Means-DO8** | **log2Ratio** | **Up-Down-Regulation** | **Probability** | **Blast nr** |
| evm.model.scaffold1306.4 | 1170 | 96.12 | 0.47 | -7.67 | Down | 0.93 | angiopoietin-related protein 4-like |
| evm.model.scaffold1341.9 | 267 | 37.66 | 0.01 | -11.87 | Down | 0.94 | ATP synthase subunit f, mitochondrial |
| evm.model.scaffold245.2 | 315 | 16.66 | 0.01 | -10.70 | Down | 0.87 | cyclophilin A isoform 1 |
| evm.model.scaffold186.13 | 549 | 14.48 | 0.01 | -10.50 | Down | 0.85 | cysteine-rich secretory protein LCCL domain containing 2-like |
| evm.model.scaffold907.21 | 627 | 185.69 | 7.25 | -4.68 | Down | 0.81 | fibrinogen-like protein 1-like |
| evm.model.scaffold955.14 | 363 | 79.93 | 1.48 | -5.75 | Down | 0.84 | fibrinogen-like protein A |
| evm.model.scaffold955.15 | 834 | 66.26 | 1.08 | -5.93 | Down | 0.85 | fibrinogen-like protein A |
| evm.model.scaffold2850.1 | 453 | 25.39 | 0.01 | -11.31 | Down | 0.91 | major vault protein |
| evm.model.scaffold118.42 | 972 | 15.30 | 0.01 | -10.58 | Down | 0.86 | phytanoyl-CoA dioxygenase, peroxisomal-like |
| evm.model.scaffold559.15 | 567 | 9.92 | 0.01 | -9.95 | Down | 0.81 | RNA-directed DNA polymerase from mobile element jockey-like |
| evm.model.scaffold2817.2 | 294 | 85.7 | 0.01 | -13.07 | Down | 0.97 | thioredoxin |
| evm.model.scaffold463.27 | 2328 | 13.25 | 0.06 | -7.71 | Down | 0.81 | transmembrane protease, serine 3-like, partial |
| evm.model.scaffold207.26 | 207 | 0.01 | 11.48 | 10.17 | Up | 0.83 | alcohol dehydrogenase [NADP+]-like |
| evm.model.scaffold778.27 | 1515 | 5.46 | 245.16 | 5.49 | Up | 0.85 | chloride channel calcium activated 3-like |
| evm.model.scaffold2429.3 | 627 | 0.01 | 14.94 | 10.55 | Up | 0.86 | counting factor associated protein D-like |
| evm.model.scaffold1002.8 | 537 | 0.01 | 18.26 | 10.83 | Up | 0.88 | CR1-3 |
| evm.model.scaffold769.20 | 2184 | 0.09 | 17.28 | 7.64 | Up | 0.83 | extracellular serine proteinase-like |
| add.evm.model.scaffold1306.4 | 342 | 0.96 | 55.67 | 5.85 | Up | 0.84 | fibrinogen-like protein 1-like |
| evm.model.scaffold1149.6 | 339 | 6.02 | 173.59 | 4.85 | Up | 0.82 | ficolin (collagen/fibrinogen domain containing) 1 precursor |
| evm.model.scaffold510.15 | 1305 | 0.01 | 10.43 | 10.03 | Up | 0.81 | gamma-aminobutyric acid type B receptor subunit 1-like |
| add.evm.model.scaffold625.13 | 552 | 0.01 | 11.95 | 9.81 | Up | 0.83 | GE18016 |
| evm.model.scaffold114.44 | 1353 | 0.10 | 19.73 | 7.58 | Up | 0.84 | IgGFc-binding protein, partial |
| evm.model.scaffold942.9 | 1422 | 2.32 | 91.51 | 5.30 | Up | 0.82 | ileal sodium/bile acid cotransporter-like |
| evm.model.scaffold469.3 | 411 | 3.04 | 145.41 | 5.58 | Up | 0.85 | lysozyme |
| evm.model.scaffold200.5 | 636 | 0.01 | 13.66 | 10.42 | Up | 0.85 | retrovirus polyprotein, putative-like |
| add.evm.model.scaffold1043.4 | 1257 | 0.52 | 54.09 | 6.69 | Up | 0.87 | reverse transcriptase-like protein-like |
| add.evm.model.scaffold560.16 | 387 | 0.01 | 28.28 | 11.47 | Up | 0.92 | RNA-directed DNA polymerase from mobile element jockey-like |
| evm.model.scaffold163.8 | 750 | 0.01 | 10.29 | 10.01 | Up | 0.81 | scavenger receptor cysteine-rich protein precursor |

**Table S4.** Annotated down- or upregulated DEGs based on the comparison of DO4 vs. DO8

|  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- |
| **Gene ID** | **Gene Length** | **Means-DO4** | **Means-DO8** | **log2Ratio** | **Up-Down-Regulation** | **Probability** | **Blast nr** |
| evm.model.scaffold1341.9 | 267 | 147.48 | 0.01 | -13.85 | Down | 0.98 | ATP synthase subunit f, mitochondrial |
| evm.model.scaffold3179.1 | 513 | 15.72 | 0.01 | -10.62 | Down | 0.86 | carboxypeptidase A2-like |
| evm.model.scaffold209.31 | 1581 | 46.50 | 0.01 | -12.18 | Down | 0.95 | CUB and zona pellucida-like domain-containing protein 1-like, partial |
| evm.model.scaffold245.2 | 315 | 37.46 | 0.01 | -11.87 | Down | 0.93 | cyclophilin A isoform 1 |
| evm.model.scaffold2777.1 | 228 | 11.43 | 0.01 | -10.16 | Down | 0.82 | fucose mutarotase |
| evm.model.scaffold118.42 | 972 | 57.83 | 0.01 | -12.50 | Down | 0.96 | phytanoyl-CoA dioxygenase, peroxisomal-like |
| evm.model.scaffold3201.1 | 384 | 11.49 | 0.01 | -10.17 | Down | 0.82 | protein C20orf11-like |
| evm.model.scaffold716.20 | 507 | 164.87 | 2.43 | -6.09 | Down | 0.86 | RNA-directed DNA polymerase from mobile element jockey-like |
| evm.model.scaffold2817.2 | 294 | 151.71 | 0.01 | -13.89 | Down | 0.98 | thioredoxin |
| evm.model.scaffold3089.2 | 369 | 0.57 | 324.11 | 9.14 | Up | 0.97 | 60S ribosomal protein L35-like |
| evm.model.scaffold3030.2 | 369 | 0.57 | 324.11 | 9.14 | Up | 0.97 | 60S ribosomal protein L35-like |
| evm.model.scaffold3023.2 | 369 | 0.57 | 324.11 | 9.14 | Up | 0.97 | 60S ribosomal protein L35-like |
| evm.model.scaffold2928.2 | 369 | 0.57 | 324.11 | 9.14 | Up | 0.97 | 60S ribosomal protein L35-like |
| evm.model.scaffold5.3 | 951 | 0.21 | 71.82 | 8.42 | Up | 0.93 | CG9164-like |
| evm.model.scaffold787.13 | 426 | 0.07 | 15.95 | 7.76 | Up | 0.81 | clarin-1-like |
| evm.model.scaffold2429.3 | 627 | 0.01 | 14.94 | 10.55 | Up | 0.85 | counting factor associated protein D-like |
| evm.model.scaffold946.7 | 594 | 0.01 | 12.33 | 10.27 | Up | 0.83 | Cubilin |
| evm.model.scaffold769.20 | 2184 | 0.01 | 17.28 | 10.75 | Up | 0.87 | extracellular serine proteinase-like |
| evm.model.scaffold561.13 | 591 | 0.01 | 26.75 | 11.39 | Up | 0.91 | Fibrinogen C domain-containing protein 1-B, partial |
| evm.model.scaffold352.13 | 999 | 0.61 | 56.14 | 6.52 | Up | 0.85 | fibrinogen-like protein A |
| evm.model.scaffold1558.1 | 1125 | 0.01 | 20.62 | 11.01 | Up | 0.89 | glucose transporter type 1-like |
| evm.model.scaffold327.41 | 456 | 0.04 | 22.13 | 9.00 | Up | 0.87 | Glutaredoxin-related protein 5 |
| evm.model.scaffold2488.6 | 313 | 0.01 | 25.02 | 11.29 | Up | 0.91 | pituitary tumor-transforming gene 1 protein-interacting protein-like isoform 1 |
| evm.model.scaffold3.4 | 1797 | 0.01 | 13.00 | 10.34 | Up | 0.83 | polyprotein |
| evm.model.scaffold169.52 | 1260 | 0.01 | 10.49 | 10.04 | Up | 0.80 | protein NLRC3-like |
| evm.model.scaffold169.42 | 1455 | 0.49 | 112.96 | 7.85 | Up | 0.92 | protein NLRC3-like, partial |
| evm.model.scaffold200.5 | 636 | 0.02 | 13.66 | 9.68 | Up | 0.83 | retrovirus polyprotein, putative-like |
| evm.model.scaffold163.8 | 750 | 0.01 | 10.29 | 10.01 | Up | 0.80 | scavenger receptor cysteine-rich protein precursor |
| evm.model.scaffold2243.2 | 306 | 1.24 | 122.51 | 6.63 | Up | 0.88 | THO complex subunit 1 |