24hpf_pos.1

Global Summary

```
%DE = 0.25
# genes with fdr < 0.2 = 6065 ( 3212 + / 2853 -)
# genes with fdr < 0.1 = 5008 ( 2457 + / 2551 -)
# genes with fdr < 0.05 = 4252 ( 1919 + / 2333 -)
# genes with fdr < 0.01 = 3168 ( 1239 + / 1929 -)
# genes in genesets = 21072

<FC> = 0
<t-score> = -0.04
<p-value> = 0.02
<fdr> = 0.75
```


Global Genelist

| Rank ID | | log(FC) fdr p-value | | | Description Metagene | |
|------------|------------|------------------------|-------|-------|-------------------------|---|
| 1 | ENSDARG000 | -4.29 | 2e-16 | 7e-15 | 1 x 29 | keratin 97 [Source:ZFIN;Acc:ZDB-GENE-040718-78] |
| 2 | ENSDARG000 | -5.96 | 2e-16 | 7e-15 | 1 x 40 | syntaxin 1B [Source:ZFIN;Acc:ZDB-GENE-000330-4] |
| 3 | ENSDARG000 | -3.37 | 2e-16 | 7e-15 | 5 x 38 | solute carrier family 17 (vesicular glutamate transporter), mer |
| 4 | ENSDARG000 | -5.44 | 2e-16 | 7e-15 | 1 x 8 | actinin alpha 3b [Source:ZFIN;Acc:ZDB-GENE-030131-204 |
| 5 | ENSDARG000 | -3.41 | 2e-16 | 7e-15 | 1 x 11 | inositol polyphosphate phosphatase-like 1b [Source:ZFIN;Ac |
| 6 | ENSDARG000 | -2.88 | 2e-16 | 7e-15 | 1 x 10 | glycoprotein M6Bb [Source:ZFIN;Acc:ZDB-GENE-030710-1 |
| 7 | ENSDARG000 | 5.19 | 2e-16 | 7e-15 | 40 x 39 | otoconin 90 [Source:ZFIN;Acc:ZDB-GENE-070912-300] |
| 8 | ENSDARG000 | -5.21 | 2e-16 | 7e-15 | 1 x 37 | tenascin XBa [Source:ZFIN;Acc:ZDB-GENE-070103-5] |
| 9 | ENSDARG000 | -3.61 | 2e-16 | 7e-15 | 1 x 8 | ATPase, Na+/K+ transporting, alpha 1a polypeptide, tandem ε |
| 10 | ENSDARG000 | -4.07 | 2e-16 | 7e-15 | 1 x 9 | RAR-related orphan receptor A, paralog b [Source:ZFIN;Acc |
| 11 | ENSDARG000 | -5.36 | 2e-16 | 7e-15 | 1 x 36 | myosin, heavy chain b [Source:ZFIN;Acc:ZDB-GENE-08112 |
| 12 | ENSDARG000 | -3.3 | 2e-16 | 7e-15 | 4 x 40 | syntaxin binding protein 1a [Source:ZFIN;Acc:ZDB-GENE-0! |
| 13 | ENSDARG000 | -4.55 | 2e-16 | 7e-15 | 1 x 37 | rhodopsin [Source:ZFIN;Acc:ZDB-GENE-990415-271] |
| 14 | ENSDARG000 | 4.64 | 2e-16 | 7e-15 | 40 x 40 | Rh blood group, D antigen [Source:ZFIN;Acc:ZDB-GENE-05 |
| 15 | ENSDARG000 | -4 | 2e-16 | 7e-15 | 1 x 38 | synaptophysin b [Source:ZFIN;Acc:ZDB-GENE-040718-205 |
| 16 | ENSDARG000 | -6.61 | 2e-16 | 7e-15 | 1 x 3 | synaptogyrin 1a [Source:ZFIN;Acc:ZDB-GENE-041010-169 |
| 17 | ENSDARG000 | -5 | 2e-16 | 7e-15 | 1 x 7 | myosin light chain, phosphorylatable, fast skeletal muscle b [\S |
| 18 | ENSDARG000 | -3.89 | 2e-16 | 7e-15 | 1 x 36 | guanine nucleotide binding protein (G protein), beta polypepti |
| 19 | ENSDARG000 | -6.62 | 2e-16 | 7e-15 | 1 x 6 | parvalbumin 2 [Source:ZFIN;Acc:ZDB-GENE-000322-4] |
| 20 | ENSDARG000 | -4.93 | 2e-16 | 7e-15 | 1 x 8 | adenosine deaminase [Source:ZFIN;Acc:ZDB-GENE-04071 |

Global Geneset Analysis

| Rank | GSZ p-value #all | | Geneset | | | | | | | |
|---|------------------|------|------------|----------|---|--|--|--|--|--|
| Overexpressed | | | | | | | | | | |
| 1 | 14.09 | NULL | 2030 | MF | nucleic acid binding | | | | | |
| | 10.31 | NULL | 14 | CC | hemoglobin complex | | | | | |
| 3 | 10.19 | NULL | 28 | BP | embryonic hemopoiesis | | | | | |
| 4 | 8.03 | NULL | 78 | BP | DNA replication | | | | | |
| 2 3 4 5 6 7 | 7.99 | NULL | 229 | CC | chromosome | | | | | |
| 6 | 7.93 | NULL | 40 | BP | erythrocyte differentiation | | | | | |
| 7 | 7.83 | NULL | 15 | BP | heme biosynthetic process | | | | | |
| 8 | 7.39 | NULL | 19 | MF | oxygen binding | | | | | |
| 9 | 7.39 | NULL | 19 | BP | oxygen transport | | | | | |
| 10 | 7.39 | NULL | 19 | MF | oxygen transporter activity | | | | | |
| 11 | 7.09 | NULL | 24 | BP | myeloid cell differentiation | | | | | |
| 12 | 6.59 | NULL | 22 | BP | DNA replication initiation | | | | | |
| 13 | 6.43 | NULL | 32 | BP | DNA duplex unwinding | | | | | |
| 14 | 6.39 | NULL | 168 | CC | nucleosome | | | | | |
| 15 | 6.21 | NULL | 148 | BP | DNA repair | | | | | |
| 16 | 6.1 | NULL | 52 | BP | blood vessel development | | | | | |
| 17 | 6.08 | NULL | 110 | BP | cell cycle | | | | | |
| 18 | 6.07 | NULL | 46 | BP | mitotic cell cycle | | | | | |
| 19 | 6.02 | NULL | 140 | CC | nucleolus | | | | | |
| 20 | 5.62 | NULL | 29 | CC | kinetochore | | | | | |
| Undere | oresseo | 1 | | | | | | | | |
| | –11.75 | | 717 | MF | calcium ion binding | | | | | |
| 2 | -10.28 | | 62 | CC | intermediate filament | | | | | |
| 2 | -9.94 | NULL | 499 | BP | ion transport | | | | | |
| 4 | -9.85 | NULL | 172 | BP BP | homophilic cell adhesion via plasma membrane adhesion molec | | | | | |
| 1 2 3 4 5 6 7 8 9 | -9.77 | NULL | 6723 | CC | membrane | | | | | |
| 6 | -9.22 | NULL | 175 | BP | nervous system development | | | | | |
| 7 | -9.13 | NULL | 1162 | CC | plasma membrane | | | | | |
| 8 | -8.82 | NULL | 155 | CC | synapse | | | | | |
| 9 | -8.72 | NULL | 6248 | CC | integral component of membrane | | | | | |
| 10 | -8.67 | NULL | 333 | BP | cell adhesion | | | | | |
| 11 | -8.58 | NULL | 49 | MF | extracellular matrix structural constituent | | | | | |
| 12 | -8.19 | NULL | 32 | MF | extracellular-glutamate-gated ion channel activity | | | | | |
| 13 | -8.19 | NULL | 32 | MF | ionotropic glutamate receptor activity | | | | | |
| 14 | -8.19 | NULL | 32 | BP | ionotropic glutamate receptor signaling pathway | | | | | |
| 15 | -8.14 | NULL | 159 | MF | structural molecule activity | | | | | |
| 16 | -8.03 | NULL | 70 | CC | myosin complex | | | | | |
| 17 | -7.76 | NULL | 18 | MF | tubulin binding | | | | | |
| 18 | -7.7 | NULL | 1084 | BP | transport motor activity | | | | | |
| 19 20 | -7.23 -7.18 | NULL | 120 270 | MF MF | motor activity ion channel activity | | | | | |
| 20 | -7.18 | NULL | 210 | IVIT | ion onariio activity | | | | | |

