# 24hpf\_pos

## **Global Summary**

```
%DE = 0.58

# genes with fdr < 0.2 = 8239 (3273 + /4966 -)

# genes with fdr < 0.1 = 0 (0 + /0 -)

# genes with fdr < 0.05 = 0 (0 + /0 -)

# genes with fdr < 0.01 = 0 (0 + /0 -)

# genes in genesets = 21072

<FC> = 0

<t-score> = -7.61

<p-value> = 0.18

<fdr> = 0.42
```

#### 

### Global Genelist

| Rank<br>ID |            | log(FC)<br>p-val |       | fdr<br>lue | Description<br>Metagene |   |
|------------|------------|------------------|-------|------------|-------------------------|---|
| 1          | ENSDARG000 | -2.95            | 3e-05 | 0.1        | 3 x 37                  | SPHK1 interactor, AKAP domain containing [Source:ZFIN;Ac    |
| 2          | ENSDARG000 | -2.34            | 4e-05 | 0.1        | 2 x 6                   | zgc:136870 [Source:ZFIN;Acc:ZDB-GENE-060312-1]              |
| 3          | ENSDARG000 | -0.01            | 4e-05 | 0.1        | 25 x 23                 | zgc:152652 [Source:ZFIN;Acc:ZDB-GENE-060818-27]             |
| 4          | ENSDARG000 | -2.81            | 6e-05 | 0.1        | 4 x 39                  | neurensin 1 [Source:ZFIN;Acc:ZDB-GENE-030131-7491]          |
| 5          | ENSDARG000 | -2.8             | 6e-05 | 0.1        | 4 x 38                  | si:ch211-14c7.2 [Source:ZFIN;Acc:ZDB-GENE-060503-856        |
| 6          | ENSDARG000 | -2.98            | 7e-05 | 0.1        | 2 x 36                  | family with sequence similarity 135 member B [Source:HGNC   |
| 7          | ENSDARG000 | 0.82             | 8e-05 | 0.1        | 40 x 24                 | RWD domain containing 4 [Source:ZFIN;Acc:ZDB-GENE-04        |
| 8          | ENSDARG000 | -2.86            | 1e-04 | 0.1        | 1 x 28                  | claudin b [Source:ZFIN;Acc:ZDB-GENE-010328-2]               |
| 9          | ENSDARG000 | -0.01            | 1e-04 | 0.1        | 24 x 23                 | U1 spliceosomal RNA [Source:RFAM;Acc:RF00003]               |
| 10         | ENSDARG000 | 0                | 1e-04 | 0.1        | 21 x 23                 |   |
| 11         | ENSDARG000 | -2.86            | 2e-04 | 0.1        | 5 x 40                  | si:dkey-191m6.4 [Source:ZFIN;Acc:ZDB-GENE-121214-18         |
| 12         | ENSDARG000 | -2.8             | 2e-04 | 0.1        | 1 x 9                   | sarcolemma associated protein b [Source:ZFIN;Acc:ZDB-GE     |
| 13         | ENSDARG000 | 0                | 2e-04 | 0.1        | 21 x 23                 |   |
| 14         | ENSDARG000 | -1.99            | 2e-04 | 0.1        | 3 x 1                   | transmembrane protein 243, mitochondrial a [Source:ZFIN;Ac  |
| 15         | ENSDARG000 | 0                | 2e-04 | 0.1        | 21 x 22                 | Vault RNA [Source:RFAM;Acc:RF00006]                         |
| 16         | ENSDARG000 | -2.84            | 2e-04 | 0.1        | 3 x 37                  | protocadherin 11 [Source:ZFIN;Acc:ZDB-GENE-140106-21]       |
| 17         | ENSDARG000 | 1.06             | 3e-04 | 0.1        | 38 x 31                 | solute carrier family 7 member 1 [Source:HGNC Symbol;Acc:   |
| 18         | ENSDARG000 | -2.39            | 3e-04 | 0.1        | 1 x 10                  | Rho GTPase activating protein 21a [Source:ZFIN;Acc:ZDB-C    |
| 19         | ENSDARG000 | -0.01            | 3e-04 | 0.1        | 25 x 23                 | si:dkey-11o1.3 [Source:ZFIN;Acc:ZDB-GENE-100921-37]         |
| 20         | ENSDARG000 | -2.63            | 3e-04 | 0.1        | 1 x 1                   | basic helix-loop-helix family, member e41 [Source:ZFIN;Acc: |

### Global Geneset Analysis

|     | Rank GSZ p                      |                | p-value #all |           | Geneset  |  |  |
|-----|---------------------------------|----------------|--------------|-----------|----------|--|--|
|     | Overexp                         | ressed         |              |           |          |  |  |
| Ac: | 1                               | 3.14           | NULL         | 13        | BP       | amino acid transport   |  |
|     | 2                               | 2.92           | NULL         | 2030      | MF       | nucleic acid binding   |  |
|     | 3                               | 2.84           | NULL         | 36        | MF       | amino acid transmembrane transporter activity                  |  |
|     | 4                               | 2.79           | NULL         | 10        | MF       | hydrolase activity, acting on acid anhydrides, in phosphorus-c |  |
|     | 5                               | 2.75           | NULL         | 39        | BP       | amino acid transmembrane transport                             |  |
|     | 6                               | 2.62           | NULL         | 11        | BP       | thrombocyte differentiation                                    |  |
|     | 2<br>3<br>4<br>5<br>6<br>7      | 2.58           | NULL         | 11        | BP       | cellular metabolic process                                     |  |
|     | 8                               | 2.4            | NULL         | 22        | BP       | double-strand break repair via homologous recombination        |  |
| 56  | 9                               | 1.95           | NULL         | 13        | BP       | miRNA mediated inhibition of translation                       |  |
| 30  | 10                              | 1.95           | NULL         | 32        | BP       | DNA duplex unwinding   |  |
|     | 11                              | 1.89           | NULL         | 2716      | CC       | nucleus  |  |
| 1C  | 12                              | 1.8            | NULL         | 36        | MF       | endonuclease activity  |  |
|     | 13                              | 1.76           | NULL         | 30        | BP       | DNA recombination  |  |
| 04  | 14                              | 1.73           | NULL         | 229       | CC       | chromosome   |  |
|     | 15                              | 1.65           | NULL         | 148       | BP       | DNA repair   |  |
|     | 16                              | 1.64           | NULL         | 23        | BP       | gene silencing by RNA  |  |
|     | 17                              | 1.63           | NULL         | 30        | BP       | RNA phosphodiester bond hydrolysis, endonucleolytic            |  |
|     | 18                              | 1.62           | NULL         | 78        | BP       | DNA replication  |  |
|     | 19                              | 1.55           | NULL         | 47        | MF       | nuclease activity  |  |
|     | 20                              | 1.52           | NULL         | 43        | BP       | ribosome biogenesis  |  |
| 18  | Underex                         | pressed        |              |           |          |  |  |
|     | 1                               | -11.57         | NULL         | 10        | BP       | cellular lipid metabolic process                               |  |
| ŝΕ  | 1<br>2<br>3<br>4<br>5<br>6<br>7 | -6.12          | NULL         | 37        | MF       | carboxylic ester hydrolase activity                            |  |
| _   | 3                               | -4.71          | NULL         | 22        | BP       | neuromast development  |  |
|     | 4                               | -3.76          | NULL         | 175       | BP       | nervous system development                                     |  |
|     | 5                               | -3.66          | NULL         | 410       | CC       | mitochondrion  |  |
| Αc  | 6                               | -3.42          | NULL         | 1427      | BP       | biological_process   |  |
| м   | 7                               | -3.38          | NULL         | 13        | BP       | dopaminergic neuron differentiation                            |  |
|     | 8                               | -2.84          | NULL         | 561       | MF       | GTP binding  |  |
|     | 9                               | -2.61          | NULL         | 24        | BP       | synapse organization   |  |
|     | 10                              | -2.55          | NULL         | 1437      | MF       | molecular_function   |  |
| 21  | 11                              | -2.37          | NULL         | 19        | BP       | transmission of nerve impulse                                  |  |
|     | 12                              | -2.28          | NULL         | 71        | CC       | bicellular tight junction                                      |  |
| C:  | 13                              | -2.19          | NULL         | 38        | BP       | negative regulation of JAK–STAT cascade                        |  |
|     | 14<br>15                        | -2.09<br>-2.03 | NULL<br>NULL | 219<br>24 | CC<br>BP | cell junction peripheral nervous system development            |  |
| -C  | 16                              | -2.03<br>-2.02 | NULL         | 24<br>12  | BP<br>BP | negative regulation of insulin receptor signaling pathway      |  |
|     | 17                              | -2.02<br>-1.94 | NULL         | 25        | MF       | phospholipid binding   |  |
| ]   | 18                              | -1.94          | NULL         | 32        | BP       | myelination  |  |
| -   | 19                              | -1.9           | NULL         | 48        | MF       | protein kinase inhibitor activity                              |  |
| cc: | 20                              | -1.85          | NULL         | 40        | BP       | intracellular receptor signaling pathway                       |  |
|     |                                 |                |              | -         | ٥.       | 31 44 43 44 31 44  |  |

