72hpf_neg_hand2

Global Summary

%DE = 0
genes with fdr < 0.2 = 0 (0 + / 0 -)# 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> = 0
<p-value> = 0.73<fdr> = 1

Global Genelist

Rank ID		log(FC) fdr p-value		Description Metagene		
1 ENS	DARG000	-5.05	0.1	1	1 x 1	solute carrier family 2 (facilitated glucose transporter), membe
2 ENS	DARG000	-4.71	0.1	1	1 x 1	GTP cyclohydrolase 2 [Source:ZFIN;Acc:ZDB-GENE-00120
3 ENS	DARG000	-4.98	0.1	1	4 x 1	ventricular myosin heavy chain-like [Source:ZFIN;Acc:ZDB-(
4 ENS	DARG000	-4.35	0.1	1	1 x 1	aldehyde oxidase 5 [Source:ZFIN;Acc:ZDB-GENE-001205-:
5 ENS	DARG000	-4.75	0.1	1	1 x 1	opsin 8, group member b [Source:ZFIN;Acc:ZDB-GENE-070
6 ENS	DARG000	-4.36	0.1	1	3 x 1	cardiac myosin light chain-1 [Source:ZFIN;Acc:ZDB-GENE-
7 ENS	DARG000	-4.11	0.1	1	1 x 1	wu:fc46h12 [Source:ZFIN;Acc:ZDB-GENE-030131-3611]
8 ENS	DARG000	-4.08	0.1	1	1 x 1	zgc:162150 [Source:ZFIN;Acc:ZDB-GENE-070410-23]
9 ENS	DARG000	-4.33	0.1	1	1 x 1	O-acyltransferase like [Source:ZFIN;Acc:ZDB-GENE-09071
10 ENS	DARG000	-4.58	0.1	1	2 x 1	connexin 30.3 [Source:ZFIN;Acc:ZDB-GENE-040406-1]
11 ENS	DARG000	-4.26	0.1	1	1 x 1	xanthine dehydrogenase [Source:ZFIN;Acc:ZDB-GENE-070
12 ENS	DARG000	-4.36	0.1	1	1 x 1	melanophilin b [Source:ZFIN;Acc:ZDB-GENE-070803-2]
13 ENS	DARG000	-4.15	0.1	1	2 x 1	myosin, heavy chain 6, cardiac muscle, alpha [Source:ZFIN;A
14 ENS	DARG000	-3.9	0.1	1	1 x 1	transmembrane protein 130 [Source:ZFIN;Acc:ZDB-GENE-(
15 ENS	DARG000	-4.24	0.1	1	1 x 1	tyrosine aminotransferase [Source:ZFIN;Acc:ZDB-GENE-03
16 ENS	DARG000	-4.1	0.1	1	1 x 1	6-pyruvoyltetrahydropterin synthase [Source:ZFIN;Acc:ZDB-
17 ENS	DARG000	-4.11	0.1	1	1 x 1	molybdenum cofactor sulfurase [Source:ZFIN;Acc:ZDB-GEN
18 ENS	DARG000	-3.79	0.1	1	1 x 1	Bernardinelli-Seip congenital lipodystrophy 2, like [Source:ZF
19 ENS	DARG000	-4.95	0.1	1	29 x 7	heart and neural crest derivatives expressed 2 [Source:ZFIN;
20 ENS	DARG000	-4.22	0.1	1	6 x 1	solute carrier family 8 (sodium/calcium exchanger), member 1

Global Geneset Analysis

	Rank	GSZ	p-value	#all	Gene	eset
	Overexp	ressed				
mbe	1	15.83	NULL	168	CC	nucleosome
	2	14.67	NULL	333	BP	cell adhesion
120	3	14.34	NULL	1484	MF	DNA binding
	4	14.1	NULL	172	BP	homophilic cell adhesion via plasma membrane adhesion m
B-(5	13.99	NULL	155	CC	synapse
	6	13.56	NULL	270	MF	ion channel activity
15–1	7	13.49	NULL	229	CC	chromosome
	8	12.92	NULL	175	BP	nervous system development
07C	9	12.86	NULL	1162	CC	plasma membrane
070	10	12.15	NULL	117	BP	nucleosome assembly
E-	11	12.08	NULL	2716	CC	nucleus
E-	12	11.75	NULL	499	BP	ion transport
_	13	11.59	NULL	717	MF	calcium ion binding
]	14	11.59	NULL	32	MF	extracellular-glutamate-gated ion channel activity
	15	11.59	NULL	32	MF	ionotropic glutamate receptor activity
	16	11.59	NULL	32	BP	ionotropic glutamate receptor signaling pathway
	17	11.41	NULL	537	MF	sequence–specific DNA binding
071	18	11.26	NULL	153	CC	proteinaceous extracellular matrix
	19	10.86	NULL	1239	BP	regulation of transcription, DNA-templated
	20	10.82	NULL	232	MF	protein heterodimerization activity
070	Underex	pressed				
	1	-13.94	NULL	712	BP	oxidation-reduction process
	1 2 3 4 5 6 7	-13.27	NULL	522	MF	oxidoreductase activity
	3	-10.67	NULL	414	BP	metabolic process
N;A	4	-9.54	NULL	96	CC	lysosome
,,	5	-7.55	NULL	43	MF	iron-sulfur cluster binding
E-(<u>6</u>	-7.22	NULL	410	CC	mitochondrion
	(-7.12	NULL	480	MF	catalytic activity
00	8	-6.97	NULL	30	BP	pigmentation
-03	9	-6.77	NULL	24	BP	nucleoside metabolic process
_	10	-6.74	NULL NULL	57 969	MF MF	flavin adenine dinucleotide binding hydrolase activity
)B-	11 12	-6.36 -6.36	NULL	11	BP	purine nucleotide biosynthetic process
	13	-6.29	NULL	67	BP	lipid transport
EN	14	-6.18	NULL	1580	CC	cellular_component
	15	-5.92	NULL	164	BP	carbohydrate metabolic process
:ZF	16	-5.87	NULL	25	MF	glutathione transferase activity
	17	-5.81	NULL	28	MF	2 iron, 2 sulfur cluster binding
IN;	18	-5.81	NULL	23	BP	lipoprotein metabolic process
	19	-5.5	NULL	35	BP	sarcomere organization
er 1	20	-5.47	NULL	209	CC	endoplasmic reticulum membrane

