72hpf_neg

Global Summary

```
%DE = 0.14
# genes with fdr < 0.2 = 2869 ( 1486 + / 1383 -)
# genes with fdr < 0.1 = 2365 ( 1228 + / 1137 -)
# genes with fdr < 0.05 = 2108 ( 1091 + / 1017 -)
# genes with fdr < 0.01 = 1375 ( 686 + / 689 -)
# genes in genesets = 21072

<FC> = 0
<t-score> = 0
<p-value> = 0.1
<fdr> = 0.86
```


Global Genelist

Rank ID		log(FC) fdr p-value			Description Metagene	
1	ENSDARG000	-4.32	2e-16	3e-14	8 x 1	nuclear receptor subfamily 4, group A, member 1 [Source:ZFI
2	ENSDARG000	5.14	2e-16	3e-14	1 x 37	rhodopsin [Source:ZFIN;Acc:ZDB-GENE-990415-271]
3	ENSDARG000	-3.15	2e-16	3e-14	5 x 1	solute carrier family 45, member 2 [Source:ZFIN;Acc:ZDB-G
4	ENSDARG000	4.82	2e-16	3e-14	1 x 36	guanine nucleotide binding protein (G protein), beta polypepti
5	ENSDARG000	-4.98	2e-16	3e-14	3 x 1	microphthalmia-associated transcription factor a [Source:ZFI
6	ENSDARG000	-2.64	2e-16	3e-14	2 x 1	$phosphoribosyl formyl glycinamidine\ synthase\ [Source: ZFIN; A$
7	ENSDARG000	-3.12	2e-16	3e-14	1 x 4	nuclear factor of kappa light polypeptide gene enhancer in B-
8	ENSDARG000	-4.16	2e-16	3e-14	1 x 1	cyclin-dependent kinase 15 [Source:ZFIN;Acc:ZDB-GENE-(
9	ENSDARG000	-4.06	2e-16	3e-14	1 x 1	aldo-keto reductase family 1, member B1 (aldose reductase)
10	ENSDARG000	3.67	2e-16	3e-14	1 x 40	ATPase, Na+/K+ transporting, alpha 1a polypeptide, tandem (
11	ENSDARG000	3.32	2e-16	3e-14	1 x 37	Rh family, B glycoprotein (gene/pseudogene) [Source:ZFIN;A
12	ENSDARG000	2.85	2e-16	3e-14	15 x 40	versican b [Source:ZFIN;Acc:ZDB-GENE-030131-2185]
13	ENSDARG000	4.71	2e-16	3e-14	1 x 36	recoverin 3 [Source:ZFIN;Acc:ZDB-GENE-040426-1661]
14	ENSDARG000	-3.99	2e-16	3e-14	4 x 1	troponin C type 1a (slow) [Source:ZFIN;Acc:ZDB-GENE-030
15	ENSDARG000	-3.18	2e-16	3e-14	7 x 1	myosin binding protein C, cardiac [Source:ZFIN;Acc:ZDB-GE
16	ENSDARG000	-3.82	2e-16	3e-14	1 x 3	apolipoprotein A-Ia [Source:ZFIN;Acc:ZDB-GENE-990415-
17	ENSDARG000	4.23	2e-16	3e-14	1 x 33	fructose–1,6-bisphosphatase 2 [Source:ZFIN;Acc:ZDB-GEN
18	ENSDARG000	3.45	2e-16	3e-14	1 x 38	collagen, type I, alpha 1a [Source:ZFIN;Acc:ZDB-GENE-030
19	ENSDARG000	3.54	2e-16	3e-14	1 x 39	collagen, type XI, alpha 2 [Source:ZFIN;Acc:ZDB-GENE-000
20	ENSDARG000	-3.34	2e-16	3e-14	1 x 5	phosphoenolpyruvate carboxykinase 1 (soluble) [Source:ZFIN

Global Geneset Analysis

	Rank	GSZ	p-value	#all	Gene	eset
	Overexp	ressed				
FΙ	1	19.2	NULL	49	MF	extracellular matrix structural constituent
	2	13.43	NULL	153	CC	proteinaceous extracellular matrix
	2 3 4 5 6	12.6	NULL	2716	CC	nucleus
	4	12.17	NULL	83	BP	visual perception
GI	5	12.16	NULL	1484	MF	DNA binding
-	6	11.59	NULL	20	BP	fin development
oti	7	11.52	NULL	333	BP	cell adhesion
ou	8	11.39	NULL	454	BP .	multicellular organism development
	9	11.05	NULL	537	MF	sequence-specific DNA binding
FI	10	10.7	NULL	717	MF	calcium ion binding
	11	10.51	NULL	1239	BP	regulation of transcription, DNA-templated
;A	12	10.51	NULL	76	BP	cartilage development
	13	9.4	NULL	634	CC	extracellular region
3-	14	9.21	NULL	15	CC	basement membrane
	15	8.71	NULL	46	CC	collagen trimer
-(16	8.53	NULL	78	BP	axon guidance
	17				BP	phototransduction
e)		7.91	NULL	28		•
	18	7.67	NULL	32	BP	retinal ganglion cell axon guidance
n (19	7.66	NULL	17	BP	fin morphogenesis
	20	7.56	NULL	93	BP	dorsal/ventral pattern formation
;A	Underex	pressed	1			
	1	-8.75	NULL	96	CC	lysosome
	ż	-8.56	NULL	30	BP	pigmentation
	1 2 3 4 5 6 7	-8.15	NULL	11	BP	melanosome organization
	4	-7.11	NULL	23	CC	troponin complex
	5	-7.02	NULL	712	BP	oxidation-reduction process
	6	-7	NULL	10	CC	melanosome
30	7	-6.66	NULL	480	MF	catalytic activity
	8	-6.54	NULL	522	MF	oxidoreductase activity
ЭE	9	-6.2	NULL	35	BP	sarcomere organization
	10	-6.15	NULL	54	BP	heart contraction
5-	11	-6.15	NULL	21	MF	substrate-specific transmembrane transporter activity
	12	-5.99	NULL	11	BP	purine nucleotide biosynthetic process
ΕN	13	-5.84	NULL	62	BP	proteolysis involved in cellular protein catabolic process
	14	-5.83	NULL	51	CC	lysosomal membrane
30	15	-5.78	NULL	13	BP	response to cadmium ion
	<u> 16</u>	-5.63	NULL	414	BP	metabolic process
00	17	-5.61	NULL	13	BP	regulation of muscle contraction
U	18	-5.44	NULL	15	BP	cardiac muscle contraction
	19	-5.39	NULL	15	BP	skeletal muscle contraction
IIV.	20	-5.26	NULL	410	CC	mitochondrion

