48hpf_pos

Global Summary

```
%DE = 0.36

# genes with fdr < 0.2 = 3363 (723 + /2640 -)

# 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> = -14.21

<p-value> = 0.19

<fdr> = 0.64
```

Portrait Regulated Metagenes 40 30 -30 20 20 10 10 20 30 20 30 10 40 10

Global Genelist

Rank ID		log(FC) fd p-value		fdr lue	Description Metagene	
1	ENSDARG000	0	2e-05	0.1	22 x 22	dre-mir-430a-4 [Source:miRBase;Acc:MI0002113]
2	ENSDARG000	0	2e-05	0.1	22 x 22	dre-mir-430a-4 [Source:miRBase;Acc:MI0002113]
3	ENSDARG000	0	3e-05	0.1	22 x 22	si:dkey-241I7.5 [Source:ZFIN;Acc:ZDB-GENE-041014-237]
4	ENSDARG000	-0.01	4e-05	0.1	25 x 23	zgc:152652 [Source:ZFIN;Acc:ZDB-GENE-060818-27]
5	ENSDARG000	-0.02	6e-05	0.1	25 x 23	
6	ENSDARG000	0	1e-04	0.1	21 x 22	si:dkeyp-13d12.16 [Source:ZFIN;Acc:ZDB-GENE-141212-1
7	ENSDARG000	1.32	1e-04	0.1	3 x 13	coronin, actin binding protein, 2Ba [Source:ZFIN;Acc:ZDB-G
8	ENSDARG000	3.82	1e-04	0.1	4 x 1	troponin T type 2a (cardiac) [Source:ZFIN;Acc:ZDB-GENE-C
9	ENSDARG000	-0.43	2e-04	0.1	8 x 25	calcium binding protein 1b [Source:ZFIN;Acc:ZDB-GENE-04
10	ENSDARG000	-0.02	2e-04	0.1	21 x 27	Vault RNA [Source:RFAM;Acc:RF00006]
11	ENSDARG000	2.97	2e-04	0.1	4 x 1	phosphoribosyl pyrophosphate amidotransferase [Source:ZFI
12	ENSDARG000	-0.45	2e-04	0.1	17 x 33	potassium channel, subfamily V, member 2b [Source:ZFIN;Ac
13	ENSDARG000	-0.46	2e-04	0.1	19 x 7	si:dkey-26m3.3 [Source:ZFIN;Acc:ZDB-GENE-070705-445
14	ENSDARG000	0	2e-04	0.1	21 x 22	zmp:0000001233 [Source:ZFIN;Acc:ZDB-GENE-140106-19
15	ENSDARG000	-0.75	2e-04	0.1	5 x 31	si:ch211-276i12.4 [Source:ZFIN;Acc:ZDB-GENE-141216-2
16	ENSDARG000	-0.01	2e-04	0.1	25 x 23	si:dkey-11o1.3 [Source:ZFIN;Acc:ZDB-GENE-100921-37]
17	ENSDARG000	1.57	3e-04	0.1	1 x 3	heme-binding protein soul5 [Source:ZFIN;Acc:ZDB-GENE-1
18	ENSDARG000	-1.61	3e-04	0.1	5 x 27	neurocalcin delta b [Source:ZFIN;Acc:ZDB-GENE-040808-
19	ENSDARG000	-0.42	3e-04	0.1	40 x 14	family with sequence similarity 19 member A2, C-C motif che
20	ENSDARG000	-0.43	3e-04	0.1	5 x 26	calcium/calmodulin-dependent protein kinase IGa [Source:Zf

Global Geneset Analysis

	Rank	GSZ	p-value	#all	Gene	eset
	Overexp	ressed				
	1	4.6	NULL	11	BP	striated muscle contraction
	2	4.51	NULL	11	BP	artery development
	2	4.5	NULL	13	BP	regulation of muscle contraction
	4	3.98	NULL	14	BP	branching involved in blood vessel morphogenesis
7	4 5 6 7	3.88	NULL	15	BP	ventricular system development
	6	3.83	NULL	54	CC	actin cytoskeleton
	7	3.55	NULL	11	BP	purine nucleotide biosynthetic process
	8	3.26	NULL	17	BP	blood circulation
	9	3.17	NULL	23	CC	troponin complex
	10	2.97	NULL	24	BP	regulation of heart contraction
	11	2.63	NULL	32	BP	hematopoietic stem cell differentiation
1	12	2.6	NULL	35	BP	sarcomere organization
	13	2.37	NULL	76	BP	actin cytoskeleton organization
il	14	2.35	NULL	108	MF	actin filament binding
	15	2.32	NULL	54	BP	heart contraction
C	16	2.32	NULL	52	BP	blood vessel development
	17	2.17	NULL	50	BP	vasculature development
4	18	2.16	NULL	24	BP	nucleoside metabolic process
	19	2.01	NULL	12	BP	cardiac muscle tissue development
	20	1.72	NULL	2030	MF	nucleic acid binding
	_					
1	Underex	•				
	1	-3	NULL	34	BP	peptidyl-threonine phosphorylation
c	2	-2.43	NULL	27	MF	calmodulin-dependent protein kinase activity
	3	-2.13	NULL	24	BP	peripheral nervous system development
5	4	-1.98	NULL	19	BP	transmission of nerve impulse
	5	-1.85	NULL	13	BP	NAD biosynthetic process
9	2 3 4 5 6 7	-1.72	NULL	24	BP	synapse organization
	/	-1.67	NULL	27	MF	cytokine receptor activity
2	8	-1.63	NULL	12	BP	exocyst localization
_	9	-1.48	NULL	94	BP	peptidyl-serine phosphorylation
	10	-1.38 -1.38	NULL NULL	56 32	CC BP	voltage–gated potassium channel complex myelination
	11 12	-1.38	NULL	634	CC	extracellular region
	13	-1.36	NULL	17	BP	ceramide biosynthetic process
1	14	-1.29	NULL	71	MF	calmodulin binding
	15	-1.29 -1.29	NULL	90	MF	potassium channel activity
5	16	-1.29	NULL	22	MF	neuropeptide hormone activity
	17	-1.22	NULL	26	MF	neuropeptide binding
Е	18	-1.22	NULL	20	CC	exocyst
	19	-1.14	NULL	23	MF	NADP binding
F	20	-1.13	NULL	20	BP	G-protein coupled receptor signaling pathway, coupled to cyclic

