24hpf_neg

Global Summary

```
%DE = 0.15
# genes with fdr < 0.2 = 3155 (1407 + /1748 -)
# genes with fdr < 0.1 = 2632 (1111 + /1521 -)
# genes with fdr < 0.05 = 2288 (918 + /1370 -)
# genes with fdr < 0.01 = 1497 (526 + /971 -)
# genes in genesets = 21072

<FC> = 0
<t-score> = -0.01
<p-value> = 0.1
<fdr> = 0.85
```

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

Global Genelist

Ina(EC)

Rank ID		log(FC) fdr p-value			Description Metagene		
	10		ρ			900	
1	ENSDARG000	-3.37	2e-16	4e-14	1 x 36	myosin, heavy chain b [Source:ZFIN;Acc:ZDB-GENE-08112	
2	ENSDARG000	-3.82	2e-16	4e-14	1 x 37	rhodopsin [Source:ZFIN;Acc:ZDB-GENE-990415-271]	
3	ENSDARG000	-4.26	2e-16	4e-14	1 x 6	parvalbumin 2 [Source:ZFIN;Acc:ZDB-GENE-000322-4]	
4	ENSDARG000	-3.15	2e-16	4e-14	1 x 9	nuclear receptor subfamily 1, group D, member 2a [Source:Zf	
5	ENSDARG000	-4.54	2e-16	4e-14	1 x 4	cathepsin L.1 [Source:ZFIN;Acc:ZDB-GENE-040718-61]	
6	ENSDARG000	-4.32	2e-16	4e-14	1 x 3	granulin a [Source:ZFIN;Acc:ZDB-GENE-030131-8434]	
7	ENSDARG000	-3.19	2e-16	4e-14	5 x 5	programmed cell death 6 [Source:ZFIN;Acc:ZDB-GENE-040	
8	ENSDARG000	-3.61	2e-16	4e-14	12 x 8	coagulation factor IIIb [Source:ZFIN;Acc:ZDB-GENE-050417	
9	ENSDARG000	-4.75	2e-16	4e-14	1 x 4	si:ch211-251b21.1 [Source:ZFIN;Acc:ZDB-GENE-060809-{	
10	ENSDARG000	-4.61	2e-16	4e-14	2 x 1	apolipoprotein L, 1 [Source:ZFIN;Acc:ZDB-GENE-030131-3	
11	ENSDARG000	-3.71	2e-16	4e-14	1 x 5	fibrinogen beta chain [Source:ZFIN;Acc:ZDB-GENE-030131	
12	ENSDARG000	-3.87	2e-16	4e-14	1 x 35	synaptotagmin Vb [Source:ZFIN;Acc:ZDB-GENE-050522-1:	
13	ENSDARG000	-4.32	2e-16	4e-14	1 x 39	cone-rod homeobox [Source:ZFIN;Acc:ZDB-GENE-010403-	
14	ENSDARG000	-3.51	2e-16	4e-14	6 x 1	solute carrier family 8 (sodium/calcium exchanger), member 1	
15	ENSDARG000	-3.15	2e-16	4e-14	1 x 7	betaine-homocysteine methyltransferase [Source:ZFIN;Acc:Z	
16	ENSDARG000	-3.66	2e-16	4e-14	1 x 3	tumor necrosis factor b (TNF superfamily, member 2) [Source	
17	ENSDARG000	-4.74	2e-16	4e-14	1 x 4	apolipoprotein A-II [Source:ZFIN;Acc:ZDB-GENE-030131-1	
18	ENSDARG000	-3.53	2e-16	4e-14	1 x 4	si:ch211-195b13.1 [Source:ZFIN;Acc:ZDB-GENE-030131-;	
19	ENSDARG000	-5.24	2e-16	4e-14	1 x 4	transferrin-a [Source:ZFIN;Acc:ZDB-GENE-980526-35]	
20	ENSDARG000	-4.09	2e-16	4e-14	6 x 1	myosin, light chain 7, regulatory [Source:ZFIN;Acc:ZDB-GEN	

Global Geneset Analysis

	Rank	GSZ	p-value	#all	Gene	eset
	Overexp	ressed				
12	1	25.37	NULL	2030	MF	nucleic acid binding
		23.38	NULL	2716	CC	nucleus
	3	23.24	NULL	229	CC	chromosome
	4	22.67	NULL	168	CC	nucleosome
	5	22.25	NULL	1484	MF	DNA binding
	6	18.21	NULL	117	BP	nucleosome assembly
:ZF	2 3 4 5 6 7	16.93	NULL	232	MF	protein heterodimerization activity
	8	13.11	NULL	37	MF	nucleosomal DNA binding
	9	12.23	NULL	454	BP	multicellular organism development
	10	11.68	NULL	1239	BP	regulation of transcription, DNA-templated
	11	11.02	NULL	78	BP	DNA replication
	12	10.91	NULL	608	MF	RNA binding
	13	10.01	NULL	43	BP	DNA-templated transcription, initiation
040	14	9.17	NULL	148	BP	DNA repair
	15	8.97	NULL	537	MF	sequence-specific DNA binding
417	16	8.62	NULL	22	BP	DNA replication initiation
	17	8.51	NULL	25	BP	membrane disruption in other organism
9–!	18	8.15	NULL	32	BP	DNA duplex unwinding
	19	8.04	NULL	140	CC	nucleolus
1–3	20	8.01	NULL	643	BP	transcription, DNA-templated
31	Underex	pressed	,			
31	1	-14.05	NULL	6723	CC	membrane
-1:		-12.8	NULL	6248	CC	integral component of membrane
-1.	2 3 4 5 6 7	-9.92	NULL	712	BP	oxidation-reduction process
	4	-9.79	NULL	1084	BP	transport
03-	5	-9.59	NULL	522	MF	oxidoreductase activity
	6	-8.32	NULL	591	BP	transmembrane transport
er 1	7	-8.17	NULL	499	BP	ion transport
	8	-7.99	NULL	19	BP	gluconeogenesis
c:Z	9	-7.87	NULL	67	BP	lipid transport
	10	-7.64	NULL	27	BP	response to bacterium
rce	11	-7.37	NULL	23	CC	troponin complex
	12	-7.36	NULL	414	BP	metabolic process
1-1	13	-7.19	NULL	23	BP	lipoprotein metabolic process
	14	-7.16	NULL	34	BP	glycolytic process
1–1	15	-6.95	NULL	231	MF	actin binding
	16	-6.93	NULL	54	BP	heart contraction
	17	-6.92	NULL	13	BP	response to cadmium ion
	18	-6.85	NULL	480	MF	catalytic activity
ΕN	19	-6.79 6.66	NULL	12	BP	negative regulation of insulin receptor signaling pathway

