72hpf_pos_hand2

Global Summary

```
%DE = 0.16
# genes with fdr < 0.2 = 3582 (1910 + /1672 -)
# genes with fdr < 0.1 = 3006 (1646 + /1360 -)
# genes with fdr < 0.05 = 2649 (1457 + /1192 -)
# genes with fdr < 0.01 = 1906 (1118 + /788 -)
# genes in genesets = 21072

<FC> = 0
<t-score> = 0.02
<p-value> = 0.07
<fdr> = 0.84
```

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		
			•			_
1	ENSDARG000	2.29	2e-16	2e-14	8 x 1	nuclear receptor subfamily 4, group A, member 1 [Source:ZFI
2	ENSDARG000	2.92	2e-16	2e-14	8 x 8	T-cell activation RhoGTPase activating protein a [Source:ZFI
3	ENSDARG000	3.24	2e-16	2e-14	6 x 1	ryanodine receptor 2b (cardiac) [Source:ZFIN;Acc:ZDB-GEN
4	ENSDARG000	3.68	2e-16	2e-14	1 x 4	cathepsin L.1 [Source:ZFIN;Acc:ZDB-GENE-040718-61]
5	ENSDARG000	3.28	2e-16	2e-14	1 x 3	granulin a [Source:ZFIN;Acc:ZDB-GENE-030131-8434]
6	ENSDARG000	2.65	2e-16	2e-14	1 x 4	nuclear factor of kappa light polypeptide gene enhancer in B-
7	ENSDARG000	2.76	2e-16	2e-14	1 x 1	aldo-keto reductase family 1, member B1 (aldose reductase)
8	ENSDARG000	-3.12	2e-16	2e-14	3 x 40	amphiphysin [Source:ZFIN;Acc:ZDB-GENE-040426-1711]
9	ENSDARG000	-2.55	2e-16	2e-14	29 x 7	heart and neural crest derivatives expressed 2 [Source:ZFIN;
10	ENSDARG000	-4.09	2e-16	2e-14	40 x 40	zinc finger-like gene 2a [Source:ZFIN;Acc:ZDB-GENE-0308
11	ENSDARG000	-3.07	2e-16	2e-14	4 x 40	LIM domain only 3 [Source:ZFIN;Acc:ZDB-GENE-050522-2
12	ENSDARG000	2.68	2e-16	2e-14	1 x 5	fibrinogen beta chain [Source:ZFIN;Acc:ZDB-GENE-030131
13	ENSDARG000	-2.67	2e-16	2e-14	3 x 40	diencephalon/mesencephalon homeobox 1a [Source:ZFIN;Ac
14	ENSDARG000	-2.27	2e-16	2e-14	4 x 38	dynamin 1a [Source:ZFIN;Acc:ZDB-GENE-081104-27]
15	ENSDARG000	2.51	2e-16	2e-14	1 x 1	RAB34, member RAS oncogene family b [Source:ZFIN;Acc:Z
16	ENSDARG000	-2.47	2e-16	2e-14	40 x 40	carbonic anhydrase [Source:ZFIN;Acc:ZDB-GENE-980526-
17	ENSDARG000	4.42	2e-16	2e-14	4 x 1	troponin C type 1a (slow) [Source:ZFIN;Acc:ZDB-GENE-030
18	ENSDARG000	3.41	2e-16	2e-14	7 x 1	myosin binding protein C, cardiac [Source:ZFIN;Acc:ZDB-GE
19	ENSDARG000	2.33	2e-16	2e-14	1 x 5	complement component c3a, duplicate 1 [Source:ZFIN;Acc:Z
20	ENSDARG000	-3.14	2e-16	2e-14	40 x 40	solute carrier family 4 (anion exchanger), member 1a (Diego I

Docorintion

Global Geneset Analysis

	Rank	GSZ	p-value	#all	Gene	eset
	Overexp	ressed				
FI	1	12.51	NULL	712	BP	oxidation-reduction process
	2	12.46	NULL	522	MF	oxidoreductase activity
=1	3	11.53	NULL	35	BP	sarcomere organization
		10.55	NULL	54	BP	heart contraction
N	5	9.3	NULL	231	MF	actin binding
	4 5 6	8.91	NULL	12	BP	cardiac muscle tissue development
	7	8.67	NULL	414	BP	metabolic process
	8	8.51	NULL	70	CC	myosin complex
	9	8.4	NULL	96	CC	lysosome
	10	8.19	NULL	23	CC	troponin complex
	11	8.17	NULL	11	BP	striated muscle contraction
i-	12	8.12	NULL	39	CC	Z disc
	13	8.11	NULL	480	MF	catalytic activity
)	14	7.99	NULL	33	MF	endopeptidase inhibitor activity
	15	7.94	NULL	27	BP	response to bacterium
	16	7.66	NULL	15	BP	cardiac muscle contraction
	17	7.62	NULL	13	BP	response to cadmium ion
I;.	18	7.56	NULL	13	BP	cardiac muscle cell proliferation
	19	7.37	NULL	30	BP	pigmentation
8(20	7.24	NULL	23	BP	lipoprotein metabolic process
	20	7.24	NOLL		Di.	
2	Underex	pressea	1			
	1	-17.96	NULL	168	CC	nucleosome
1	2	-17.47	NULL	229	CC	chromosome
	3	-16.7	NULL	1484	MF	DNA binding
۸c	4	-15.71	NULL	2716	CC	nucleus
	2 3 4 5 6 7	-15.16		117	BP	nucleosome assembly
	<u>6</u>	-13	NULL	232	MF	protein heterodimerization activity
	(-12.74		14	CC	hemoglobin complex
-	8	-11.02		37	MF	nucleosomal DNA binding
Z	9	-10.98		2030	MF	nucleic acid binding
	10	-10.93		19	MF	oxygen binding
-	11 12	-10.93 -10.93		19 19	BP MF	oxygen transport oxygen transporter activity
	13	-10.93		537	MF	sequence–specific DNA binding
BC	14	-9.68	NULL NULL	1239	BP	regulation of transcription, DNA-templated
	15	-9.06 -9.27	NULL	454	BP	multicellular organism development
Е	16	-8.71	NULL	175	BP	nervous system development
	17	-8.04	NULL	173	BP	homophilic cell adhesion via plasma membrane adhesion molec
Z	18	-7.94	NULL	43	BP	DNA-templated transcription, initiation
	19	-7.31	NULL	155	CC	synapse
ı	20	-7.13	NULL	153	CC	proteinaceous extracellular matrix
			-		-	

