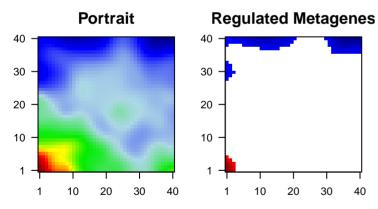
72hpf_pos_hand2.1

Global Summary

```
%DE = 0.15
# genes with fdr < 0.2 = 3273 ( 1700 + / 1573 -)
# genes with fdr < 0.1 = 2639 ( 1401 + / 1238 -)
# genes with fdr < 0.05 = 2315 ( 1257 + / 1058 -)
# genes with fdr < 0.01 = 1668 ( 961 + / 707 -)
# genes in genesets = 21072

<FC> = 0
<t-score> = 0.01
<p-value> = 0.09
<fdr> = 0.85
```



Global Genelist

Rank ID		log(FC) fdr p-value		Description Metagene			
	1	ENSDARG000	-2.98	2e-16	4e-14	1 x 37	rhodopsin [Source:ZFIN;Acc:ZDB-GENE-990415-271]
	2	ENSDARG000	2.77	2e-16	4e-14	8 x 8	T-cell activation RhoGTPase activating protein a [Source:ZFI
	3	ENSDARG000	4.08	2e-16	4e-14	1 x 4	cathepsin L.1 [Source:ZFIN;Acc:ZDB-GENE-040718-61]
	4	ENSDARG000	3.63	2e-16	4e-14	1 x 3	granulin a [Source:ZFIN;Acc:ZDB-GENE-030131-8434]
	5	ENSDARG000	2.94	2e-16	4e-14	1 x 4	nuclear factor of kappa light polypeptide gene enhancer in B-
	6	ENSDARG000	2.79	2e-16	4e-14	1 x 1	aldo-keto reductase family 1, member B1 (aldose reductase)
	7	ENSDARG000	-5.7	2e-16	4e-14	29 x 7	heart and neural crest derivatives expressed 2 [Source:ZFIN;
	8	ENSDARG000	3.11	2e-16	4e-14	1 x 5	fibrinogen beta chain [Source:ZFIN;Acc:ZDB-GENE-030131
	9	ENSDARG000	2.45	2e-16	4e-14	1 x 1	RAB34, member RAS oncogene family b [Source:ZFIN;Acc:Z
	10	ENSDARG000	-2.51	2e-16	4e-14	40 x 40	carbonic anhydrase [Source:ZFIN;Acc:ZDB-GENE-980526-
	11	ENSDARG000	3.16	2e-16	4e-14	4 x 1	troponin C type 1a (slow) [Source:ZFIN;Acc:ZDB-GENE-030
	12	ENSDARG000	2.66	2e-16	4e-14	3 x 1	cysteine and glycine-rich protein 2 [Source:ZFIN;Acc:ZDB-G
	13	ENSDARG000	2.62	2e-16	4e-14	1 x 3	apolipoprotein A-la [Source:ZFIN;Acc:ZDB-GENE-990415-
	14	ENSDARG000	-2.89	2e-16	4e-14	8 x 39	NAC alpha domain containing [Source:ZFIN;Acc:ZDB-GENE
	15	ENSDARG000	2.57	2e-16	4e-14	1 x 5	complement component c3a, duplicate 1 [Source:ZFIN;Acc:Z
	16	ENSDARG000	-2.64	2e-16	4e-14	40 x 40	solute carrier family 4 (anion exchanger), member 1a (Diego I
	17	ENSDARG000	-3.21	2e-16	4e-14	40 x 40	GATA binding protein 1a [Source:ZFIN;Acc:ZDB-GENE-980!
	18	ENSDARG000	3.94	2e-16	4e-14	1 x 3	tumor necrosis factor b (TNF superfamily, member 2) [Source
	19	ENSDARG000	2.95	2e-16	4e-14	1 x 4	apolipoprotein A-II [Source:ZFIN;Acc:ZDB-GENE-030131-1
	20	ENSDARG000	3.01	2e-16	4e-14	1 x 5	fibrinogen alpha chain [Source:ZFIN;Acc:ZDB-GENE-03101

Global Geneset Analysis

	Rank	GSZ	p-value	#all	Gene	eset					
Overexpressed											
	1	11.53	NULL	712	BP	oxidation-reduction process					
	2	11.36	NULL	522	MF	oxidoreductase activity					
ΈI	2	9.46	NULL	414	BP	metabolic process					
	4	9.38	NULL	33	MF	endopeptidase inhibitor activity					
	5	9.21	NULL	480	MF	catalytic activity					
	6	8.91	NULL	23	BP	lipoprotein metabolic process					
	4 5 6 7	8.64	NULL	10	CC	chylomicron					
	8	8.46	NULL	10	BP	triglyceride catabolic process					
_	9	8.45	NULL	96	CC	lysosome					
B-	Ĭ0	7.95	NULL	10	CC	high-density lipoprotein particle					
	11	7.85	NULL	67	BP	lipid transport					
e)	12	7.54	NULL	12	BP	cholesterol biosynthetic process					
	13	7.43	NULL	11	BP	cholesterol homeostasis					
N;	14		NULL			response to bacterium					
		7.26		27	BP	•					
31	15	7.11	NULL	410	CC	mitochondrion					
	16	7.09	NULL	30	BP	pigmentation					
:Z	17	7	NULL	13	BP	cholesterol efflux					
	18	6.62	NULL	561	MF	GTP binding					
6–	19	6.48	NULL	17	CC	blood microparticle					
0-	20	6.36	NULL	297	BP	immune response					
30	Underex	oressed									
	1	-17.68	NULL	1484	MF	DNA binding					
-G	2	-15.58	NULL	168	CC	nucleosome					
	3	-15.4	NULL	2716	CC	nucleus					
5-	2 3 4 5 6 7	-14.51	NULL	229	CC	chromosome					
J-	5	-13.59	NULL	14	CC	hemoglobin complex					
	6	-12.78	NULL	117	BP	nucleosome assembly					
٧E	7	-12.6	NULL	1239	BP	regulation of transcription, DNA-templated					
	8	-12.24	NULL	454	BP	multicellular organism development					
::Z	9	-12.02	NULL	537	MF	sequence-specific DNA binding					
	10	-11.83	NULL	19	MF	oxygen binding					
οl	11	-11.83	NULL	19	BP	oxygen transport					
	12	-11.83	NULL	19	MF	oxygen transporter activity					
308	13	-11.46	NULL	232	MF	protein heterodimerization activity					
	14	-10.88	NULL	49	MF	extracellular matrix structural constituent					
се	15	-9.86	NULL	2030	MF	nucleic acid binding					
00	<u> 16</u>	-9.81	NULL	333	BP	cell adhesion					
,	17	-9.61	NULL	37	MF	nucleosomal DNA binding					
-1	18	-9.21	NULL	34	BP	ephrin receptor signaling pathway					
	19	-9.19	NULL	153	CC	proteinaceous extracellular matrix					
01	20	-8.77	NULL	19	ME	ephrin receptor activity					

