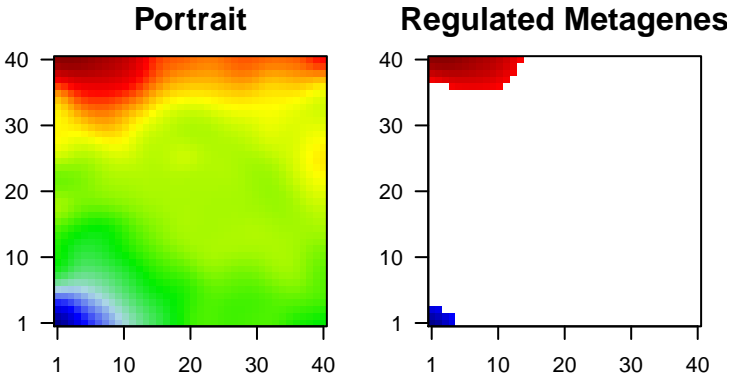


# 48hpf\_neg

## Global Summary

%DE = 0.17  
# genes with  $\text{fdr} < 0.2$  = 4194 ( 2207 + / 1987 -)  
# genes with  $\text{fdr} < 0.1$  = 3425 ( 1769 + / 1656 -)  
# genes with  $\text{fdr} < 0.05$  = 2899 ( 1491 + / 1408 -)  
# genes with  $\text{fdr} < 0.01$  = 2085 ( 1043 + / 1042 -)  
  
# genes in genesets = 21072  
  
<FC> = 0  
<t-score> = -0.01  
<p-value> = 0.07  
<fdr> = 0.83



## Global Genelist

Rank	ID	log(FC)	p-value	fdr	Description	
					Metagene	
1	ENSDARG000	-4.15	2e-16	3e-14	5 x 1	solute carrier family 45, member 2 [Source:ZFIN;Acc:ZDB-GI
2	ENSDARG000	-3.51	2e-16	3e-14	8 x 1	crystallin, lambda 1 [Source:ZFIN;Acc:ZDB-GENE-060810-
3	ENSDARG000	-3.7	2e-16	3e-14	6 x 1	ryanodine receptor 2b (cardiac) [Source:ZFIN;Acc:ZDB-GEN
4	ENSDARG000	-3.59	2e-16	3e-14	3 x 1	microphthalmia-associated transcription factor a [Source:ZFI
5	ENSDARG000	-3.15	2e-16	3e-14	2 x 1	phosphoribosylformylglycinamide synthase [Source:ZFIN;A
6	ENSDARG000	-2.67	2e-16	3e-14	1 x 7	family with sequence similarity 169, member Ab [Source:ZFI
7	ENSDARG000	-3.38	2e-16	3e-14	4 x 1	phosphoribosyl pyrophosphate amidotransferase [Source:ZFI
8	ENSDARG000	-3.14	2e-16	3e-14	1 x 4	nuclear factor of kappa light polypeptide gene enhancer in B-
9	ENSDARG000	2.8	2e-16	3e-14	2 x 40	neurocan b [Source:ZFIN;Acc:ZDB-GENE-050208-586]
10	ENSDARG000	-3.01	2e-16	3e-14	1 x 1	cyclin-dependent kinase 15 [Source:ZFIN;Acc:ZDB-GENE-(
11	ENSDARG000	-3.66	2e-16	3e-14	1 x 1	aldo-keto reductase family 1, member B1 (aldose reductase)
12	ENSDARG000	-3.8	2e-16	3e-14	2 x 1	apolipoprotein L, 1 [Source:ZFIN;Acc:ZDB-GENE-030131-3
13	ENSDARG000	-2.68	2e-16	3e-14	3 x 1	RAB3A interacting protein (rabin3)-like 1 [Source:ZFIN;Acc:Z
14	ENSDARG000	2.66	2e-16	3e-14	9 x 40	hairy-related 4, tandem duplicate 4 [Source:ZFIN;Acc:ZDB-(
15	ENSDARG000	-2.74	2e-16	3e-14	1 x 1	RAB34, member RAS oncogene family b [Source:ZFIN;Acc:Z
16	ENSDARG000	3.1	2e-16	3e-14	40 x 40	carbonic anhydrase [Source:ZFIN;Acc:ZDB-GENE-980526-
17	ENSDARG000	-4.29	2e-16	3e-14	4 x 1	troponin C type 1a (slow) [Source:ZFIN;Acc:ZDB-GENE-030
18	ENSDARG000	-3.46	2e-16	3e-14	3 x 1	cysteine and glycine-rich protein 2 [Source:ZFIN;Acc:ZDB-G
19	ENSDARG000	4.3	2e-16	3e-14	40 x 40	solute carrier family 4 (anion exchanger), member 1a (Diego I
20	ENSDARG000	-5.73	2e-16	3e-14	6 x 1	solute carrier family 8 (sodium/calcium exchanger), member 1

## Global Geneset Analysis

Rank	GSZ	p-value	#all	Geneset
<i>Overexpressed</i>				
1	19.98	NULL	1484	MF DNA binding
2	19.85	NULL	2716	CC nucleus
3	18.37	NULL	1239	BP regulation of transcription, DNA-templated
4	16.58	NULL	537	MF sequence-specific DNA binding
5	13.33	NULL	14	CC hemoglobin complex
6	13.14	NULL	172	BP homophilic cell adhesion via plasma membrane adhesion molecule
7	12.93	NULL	2030	MF nucleic acid binding
8	12.79	NULL	175	BP nervous system development
9	12.2	NULL	454	BP multicellular organism development
10	11.5	NULL	19	MF oxygen binding
11	11.5	NULL	19	BP oxygen transport
12	11.5	NULL	19	MF oxygen transporter activity
13	11	NULL	333	BP cell adhesion
14	10.59	NULL	643	BP transcription, DNA-templated
15	9.54	NULL	78	BP axon guidance
16	9.43	NULL	633	MF transcription factor activity, sequence-specific DNA binding
17	9.23	NULL	158	MF microtubule binding
18	8.46	NULL	168	CC nucleosome
19	8.4	NULL	229	CC chromosome
20	7.96	NULL	108	CC microtubule
<i>Underexpressed</i>				
1	-16.65	NULL	712	BP oxidation-reduction process
2	-15.92	NULL	522	MF oxidoreductase activity
3	-10.84	NULL	414	BP metabolic process
4	-10.06	NULL	480	MF catalytic activity
5	-9.85	NULL	30	BP pigmentation
6	-9.38	NULL	35	BP sarcomere organization
7	-9.26	NULL	54	BP heart contraction
8	-7.7	NULL	23	BP lipoprotein metabolic process
9	-7.57	NULL	33	MF endopeptidase inhibitor activity
10	-7.57	NULL	410	CC mitochondrion
11	-7.22	NULL	96	CC lysosome
12	-7.21	NULL	10	CC melanosome
13	-7.02	NULL	43	MF iron-sulfur cluster binding
14	-6.97	NULL	164	BP carbohydrate metabolic process
15	-6.94	NULL	67	BP lipid transport
16	-6.9	NULL	147	CC ribosome
17	-6.81	NULL	11	BP melanosome organization
18	-6.8	NULL	144	MF structural constituent of ribosome
19	-6.68	NULL	1580	CC cellular_component
20	-6.56	NULL	27	BP response to bacterium

