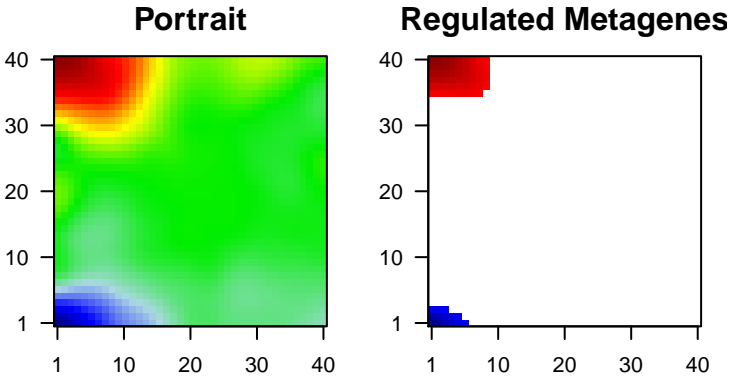


# 72hpf\_neg\_tbx5

## Global Summary

%DE = 0  
# genes with  $fdr < 0.2 = 0$  ( 0 + / 0 - )  
# 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> = 0  
<p-value> = 0.72  
<fdr> = 1



## Global Genelist

Rank	ID	log(FC)	p-value	fdr	Description
					Metagene
1	ENSDARG0000000001	-5.63	0.09	1	1 x 1 si:dkkey-251i10.2 [Source:ZFIN;Acc:ZDB-GENE-050506-10]
2	ENSDARG0000000002	-5.49	0.09	1	1 x 1 zgc:162150 [Source:ZFIN;Acc:ZDB-GENE-070410-23]
3	ENSDARG0000000003	-5.33	0.10	1	1 x 1 aldehyde oxidase 5 [Source:ZFIN;Acc:ZDB-GENE-001205-01]
4	ENSDARG0000000004	-5.27	0.10	1	3 x 1 cardiac myosin light chain-1 [Source:ZFIN;Acc:ZDB-GENE-001205-01]
5	ENSDARG0000000005	-4.75	0.10	1	1 x 1 wu:fc46h12 [Source:ZFIN;Acc:ZDB-GENE-030131-36111]
6	ENSDARG0000000006	-4.55	0.11	1	1 x 1 GTP cyclohydrolase 2 [Source:ZFIN;Acc:ZDB-GENE-001205-01]
7	ENSDARG0000000007	-4.55	0.11	1	1 x 1 xanthine dehydrogenase [Source:ZFIN;Acc:ZDB-GENE-070410-23]
8	ENSDARG0000000008	-4.38	0.11	1	1 x 1 transmembrane protein 130 [Source:ZFIN;Acc:ZDB-GENE-001205-01]
9	ENSDARG0000000009	-4.29	0.12	1	1 x 1 solute carrier family 2 (facilitated glucose transporter), member 1
10	ENSDARG0000000010	-4.33	0.12	1	1 x 1 cation/H+ exchanger protein 1 [Source:ZFIN;Acc:ZDB-GENE-001205-01]
11	ENSDARG0000000011	-4.19	0.12	1	1 x 1 solute carrier family 2 (facilitated glucose transporter), member 1
12	ENSDARG0000000012	-4.11	0.12	1	1 x 1 Bernardinelli-Seip congenital lipodystrophy 2, like [Source:ZFIN;Acc:ZDB-GENE-001205-01]
13	ENSDARG0000000013	-4.09	0.12	1	1 x 1 O-acetyltransferase like [Source:ZFIN;Acc:ZDB-GENE-090710-01]
14	ENSDARG0000000014	-4.19	0.12	1	1 x 1 si:dkkey-106n21.1 [Source:ZFIN;Acc:ZDB-GENE-131120-16]
15	ENSDARG0000000015	-4.15	0.12	1	4 x 1 ventricular myosin heavy chain-like [Source:ZFIN;Acc:ZDB-GENE-001205-01]
16	ENSDARG0000000016	-3.89	0.12	1	1 x 1 solute carrier family 22 (organic anion transporter), member 7
17	ENSDARG0000000017	-3.83	0.13	1	1 x 1 melanophilin a [Source:ZFIN;Acc:ZDB-GENE-050208-724]
18	ENSDARG0000000018	-4.02	0.13	1	1 x 1 zgc:113142 [Source:ZFIN;Acc:ZDB-GENE-050220-2]
19	ENSDARG0000000019	-3.96	0.13	1	1 x 1 sepiapterin reductase b [Source:ZFIN;Acc:ZDB-GENE-070710-01]
20	ENSDARG0000000020	-3.7	0.13	1	1 x 1 RAS and EF-hand domain containing [Source:ZFIN;Acc:ZDB-GENE-001205-01]

## Global Geneset Analysis

Rank	GSZ	p-value	#all	Geneset
<i>Overexpressed</i>				
1	18.22	NULL	155	CC synapse
2	17.86	NULL	172	BP homophilic cell adhesion via plasma membrane adhesion molecules
3	17.58	NULL	1162	CC plasma membrane
4	16.58	NULL	270	MF ion channel activity
5	16.45	NULL	499	BP ion transport
6	15.86	NULL	333	BP cell adhesion
7	15.74	NULL	175	BP nervous system development
8	14.06	NULL	32	MF extracellular-glutamate-gated ion channel activity
9	14.06	NULL	32	MF ionotropic glutamate receptor activity
10	14.06	NULL	32	BP ionotropic glutamate receptor signaling pathway
11	12.84	NULL	717	MF calcium ion binding
12	12.25	NULL	1239	BP regulation of transcription, DNA-templated
13	12.14	NULL	537	MF sequence-specific DNA binding
14	12.1	NULL	130	BP regulation of ion transmembrane transport
15	12.1	NULL	130	MF voltage-gated ion channel activity
16	12.09	NULL	79	BP excitatory postsynaptic potential
17	11.73	NULL	80	CC postsynaptic membrane
18	11.56	NULL	6248	CC integral component of membrane
19	11.5	NULL	6723	CC membrane
20	11.25	NULL	176	BP ion transmembrane transport
<i>Underexpressed</i>				
1	-15.56	NULL	712	BP oxidation-reduction process
2	-14.77	NULL	522	MF oxidoreductase activity
3	-10.01	NULL	410	CC mitochondrion
4	-9.05	NULL	414	BP metabolic process
5	-8.81	NULL	214	BP translation
6	-8.25	NULL	147	CC ribosome
7	-8.19	NULL	144	MF structural constituent of ribosome
8	-7.98	NULL	33	MF endopeptidase inhibitor activity
9	-7.79	NULL	480	MF catalytic activity
10	-7.53	NULL	96	CC lysosome
11	-7.33	NULL	43	MF iron-sulfur cluster binding
12	-6.85	NULL	1580	CC cellular_component
13	-6.74	NULL	30	BP pigmentation
14	-6.49	NULL	23	BP lipoprotein metabolic process
15	-6.31	NULL	164	BP carbohydrate metabolic process
16	-6.21	NULL	57	MF flavin adenine dinucleotide binding
17	-6.15	NULL	62	BP proteolysis involved in cellular protein catabolic process
18	-6.15	NULL	34	MF electron carrier activity
19	-5.87	NULL	10	CC chylomicron
20	-5.84	NULL	1437	MF molecular_function

