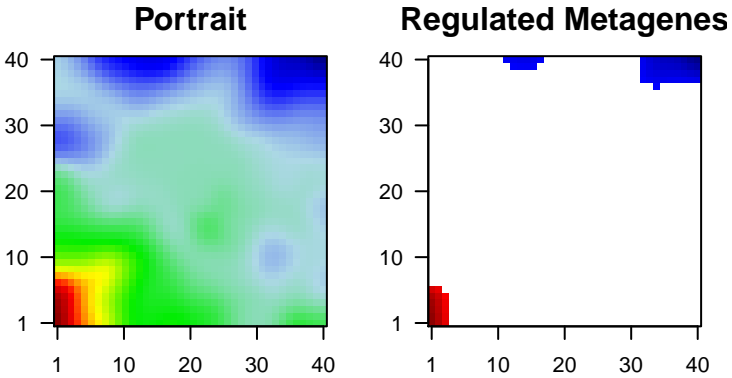


# 72hpf\_pos\_tbx5

## Global Summary

%DE = 0.39  
# 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> = -9.79  
<p-value> = 0.21  
<fdr> = 0.61



## Global Genelist

Rank	ID	log(FC)	p-value	fdr	Description
					Metagene
1	ENSDARG000	0	5e-06	0.2	21 x 22 uromodulin [Source:ZFIN;Acc:ZDB-GENE-121214-192]
2	ENSDARG000	-0.01	4e-05	0.2	25 x 23 zgc:152652 [Source:ZFIN;Acc:ZDB-GENE-060818-27]
3	ENSDARG000	0	8e-05	0.2	21 x 22 si:key-185p13.1 [Source:ZFIN;Acc:ZDB-GENE-110411-12]
4	ENSDARG000	0	9e-05	0.2	22 x 22 trace amine associated receptor 19n [Source:ZFIN;Acc:ZDB-
5	ENSDARG000	0	9e-05	0.2	21 x 22 U6 spliceosomal RNA [Source:RFAM;Acc:RF00026]
6	ENSDARG000	0	1e-04	0.2	21 x 22
7	ENSDARG000	0	1e-04	0.2	22 x 22 si:ch211-229g14.3 [Source:ZFIN;Acc:ZDB-GENE-081104-1]
8	ENSDARG000	-1.36	1e-04	0.2	35 x 37 si:ch1073-153i20.4 [Source:ZFIN;Acc:ZDB-GENE-160113-
9	ENSDARG000	1.43	1e-04	0.2	8 x 6 motile sperm domain containing 2 [Source:ZFIN;Acc:ZDB-GI-
10	ENSDARG000	-0.94	1e-04	0.2	16 x 40 cadherin 15, type 1, M-cadherin (myotubule) [Source:ZFIN;A-
11	ENSDARG000	0	2e-04	0.2	21 x 22 U6 spliceosomal RNA [Source:RFAM;Acc:RF00026]
12	ENSDARG000	0.58	2e-04	0.2	6 x 31 transient receptor potential cation channel, subfamily M, mem
13	ENSDARG000	-0.44	2e-04	0.2	5 x 27 thioredoxin-related transmembrane protein 2b [Source:ZFIN;
14	ENSDARG000	-0.57	2e-04	0.2	6 x 26 si:key-721i4.3 [Source:ZFIN;Acc:ZDB-GENE-060526-332]
15	ENSDARG000	0	2e-04	0.2	21 x 22
16	ENSDARG000	0	2e-04	0.2	21 x 22
17	ENSDARG000	1.52	3e-04	0.2	7 x 12 si:ch211-152c8.5 [Source:ZFIN;Acc:ZDB-GENE-030131-5]
18	ENSDARG000	-0.01	3e-04	0.2	25 x 23 si:key-11o1.3 [Source:ZFIN;Acc:ZDB-GENE-100921-37]
19	ENSDARG000	-0.01	3e-04	0.2	25 x 23 chloride channel accessory 5, tandem duplicate 2 [Source:ZF
20	ENSDARG000	-0.41	3e-04	0.2	34 x 22

## Global Geneset Analysis

Rank	GSZ	p-value	#all	Geneset
<i>Overexpressed</i>				
1	0.78	NULL	12	BP ADP transport
2	0.78	NULL	12	BP ATP transport
3	0.72	NULL	1084	BP transport
4	0.71	NULL	1761	MF metal ion binding
5	0.71	NULL	6723	CC membrane
6	0.7	NULL	712	BP oxidation-reduction process
7	0.67	NULL	591	BP transmembrane transport
8	0.67	NULL	11	BP digestive tract morphogenesis
9	0.65	NULL	6248	CC integral component of membrane
10	0.64	NULL	522	MF oxidoreductase activity
11	0.61	NULL	2189	CC cytoplasm
12	0.58	NULL	161	CC mitochondrial inner membrane
13	0.56	NULL	27	MF oxidoreductase activity, acting on paired donors, with incorporation
14	0.53	NULL	11	MF MAP kinase kinase kinase kinase activity
15	0.51	NULL	1787	MF ATP binding
16	0.51	NULL	10	BP mitochondrial electron transport, ubiquinol to cytochrome c
17	0.5	NULL	410	CC mitochondrion
18	0.49	NULL	1066	CC intracellular
19	0.48	NULL	1506	MF nucleotide binding
20	0.48	NULL	499	BP ion transport
<i>Underexpressed</i>				
1	-2.16	NULL	46	MF trace-amine receptor activity
2	-1.06	NULL	117	BP nucleosome assembly
3	-0.85	NULL	168	CC nucleosome
4	-0.75	NULL	229	CC chromosome
5	-0.69	NULL	153	MF ATPase activity
6	-0.69	NULL	19	BP transmission of nerve impulse
7	-0.6	NULL	24	BP peripheral nervous system development
8	-0.59	NULL	24	BP synapse organization
9	-0.53	NULL	32	BP myelination
10	-0.52	NULL	37	MF nucleosomal DNA binding
11	-0.5	NULL	751	MF G-protein coupled receptor activity
12	-0.46	NULL	666	MF signal transducer activity
13	-0.45	NULL	56	BP cell redox homeostasis
14	-0.45	NULL	853	BP G-protein coupled receptor signaling pathway
15	-0.4	NULL	64	MF hydrolase activity, acting on glycosyl bonds
16	-0.37	NULL	10	BP cellular component organization
17	-0.35	NULL	11	BP regulation of cell morphogenesis
18	-0.29	NULL	172	BP homophilic cell adhesion via plasma membrane adhesion molecule
19	-0.28	NULL	85	CC cell
20	-0.28	NULL	78	BP axon guidance

