72hpf_pos_gata5

Global Summary

```
%DE = 0.32

# 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

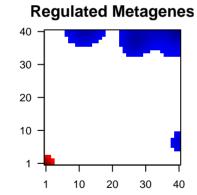
\langle FC \rangle = 0

\langle t-score \rangle = -153.11

\langle p-value \rangle = 0.26

\langle fdr \rangle = 0.68
```

Portrait 40 30 20 10 1 10 20 30 40



Global Genelist

Rank ID		log(FC) f p-valu		fdr lue	Description Metagene	
1	ENSDARG000	0	2e-07	0.3	21 x 22	U6 spliceosomal RNA [Source:RFAM;Acc:RF00026]
2	ENSDARG000	0	1e-05	0.3	21 x 22	U6 spliceosomal RNA [Source:RFAM;Acc:RF00026]
3	ENSDARG000	0	6e-05	0.3	21 x 22	si:dkey-185p13.1 [Source:ZFIN;Acc:ZDB-GENE-110411-12
4	ENSDARG000	0	9e-05	0.3	21 x 22	U6 spliceosomal RNA [Source:RFAM;Acc:RF00026]
5	ENSDARG000	0.67	1e-04	0.3	1 x 20	cytochrome P450, family 1, subfamily C, polypeptide 2 [Sourc
6	ENSDARG000	0	1e-04	0.3	21 x 23	odorant receptor, family E, subfamily 128, member 3 [Source:
7	ENSDARG000	0	2e-04	0.3	21 x 23	
8	ENSDARG000	0	2e-04	0.3	21 x 23	si:dkey-31m5.7 [Source:ZFIN;Acc:ZDB-GENE-070912-519
9	ENSDARG000	0	2e-04	0.3	21 x 23	
10	ENSDARG000	0	3e-04	0.3	21 x 23	kelch-like family member 10b, tandem duplicate 2 [Source:ZF
11	ENSDARG000	0	3e-04	0.3	21 x 21	
12	ENSDARG000	-1.13	3e-04	0.3	26 x 39	protein phosphatase 1, regulatory subunit 26 [Source:ZFIN;A
13	ENSDARG000	0	3e-04	0.3	21 x 23	si:dkey-31m5.5 [Source:ZFIN;Acc:ZDB-GENE-070912-517]
14	ENSDARG000	0.31	3e-04	0.3	20 x 10	finTRIM family, member 53 [Source:ZFIN;Acc:ZDB-GENE-0;
15	ENSDARG000	-0.15	3e-04	0.3	13 x 3	solute carrier family 25 (mitochondrial carrier; peroxisomal me
16	ENSDARG000	0	3e-04	0.3	21 x 22	
17	ENSDARG000	0	4e-04	0.3	20 x 23	
18	ENSDARG000	0	4e-04	0.3	21 x 23	
19	ENSDARG000	0	4e-04	0.3	21 x 23	carboxypeptidase A2 (pancreatic) [Source:ZFIN;Acc:ZDB-GE
20	ENSDARG000	0	4e-04	0.3	21 x 23	dopamine receptor D6b [Source:ZFIN;Acc:ZDB-GENE-1212

Global Geneset Analysis

	Rank	GSZ	p-value	#all	Gene	eset
	Overexp	ressed				
	1	0.57	NULL	6723	CC	membrane
	2	0.54	NULL	6248	CC	integral component of membrane
	2	0.33	NULL	2716	CC	nucleus
	4	0.29	NULL	2189	CC	cytoplasm
12	5	0.28	NULL	2030	MF	nucleic acid binding
-	6	0.27	NULL	1761	MF	metal ion binding
	5 6 7	0.26	NULL	1787	MF	ATP binding
	8	0.25	NULL	1580	CC	cellular component
	9	0.24	NULL	1437	MF	molecular function
rc	10	0.24	NULL	1484	MF	DNA binding
	11	0.24	NULL	1506	MF	nucleotide binding
9:	12	0.24	NULL	1427	BP	biological process
	13	0.22	NULL	1239	BP	regulation of transcription, DNA-templated
	14	0.22	NULL	1295	BP	signal transduction
	15	0.21	NULL	1066	CC	intracellular
9	16	0.21	NULL	1162	CC	plasma membrane
	17	0.21	NULL	1063	MF	transferase activity
	18	0.2	NULL	1084	BP	transport
	19	0.2	NULL	969	MF	hydrolase activity
ZF	20	0.19	NULL	947	BP	protein phosphorylation
	20	0.10	NULL	947	ВР	protein priosprioryiation
	Underex	pressed	1			
	1	0	NULL	10	CC	integral component of peroxisomal membrane
A,	ż	0	NULL	14	BP	spermatid development
	3	0	NULL	12	BP	ADP transport
_	4	0	NULL	12	BP	ATP transport
7	5	0	NULL	17	MF	protein phosphatase inhibitor activity
	2 3 4 5 6 7	0.01	NULL	13	MF	dopamine neurotransmitter receptor activity
0;	7	0.01	NULL	15	MF	carboxypeptidase activity
	8	0.01	NULL	42	BP	detection of chemical stimulus involved in sensory perception
٦ŧ	9	0.01	NULL	13	BP	B cell receptor signaling pathway
	10	0.01	NULL	19	BP	organic anion transport
	11	0.01	NULL	14	BP	inner ear morphogenesis
	12	0.01	NULL	10	BP	retinal cone cell development
	13	0.01	NULL	18	BP	phospholipase C-activating dopamine receptor signaling pathwa
	14	0.01	NULL	19	BP	dopamine receptor signaling pathway
	15	0.01	NULL	17	CC	mitochondrial respiratory chain complex IV
	<u> 16</u>	0.01	NULL	17	CC	external side of plasma membrane
Ε	17	0.01	NULL	17	CC	blood microparticle
,.	18	0.01	NULL	11	BP	peptide metabolic process
_	19	0.01	NULL	13	BP	atrioventricular canal development
2	20	0.02	NULL	10	BP	positive regulation of DNA repair

