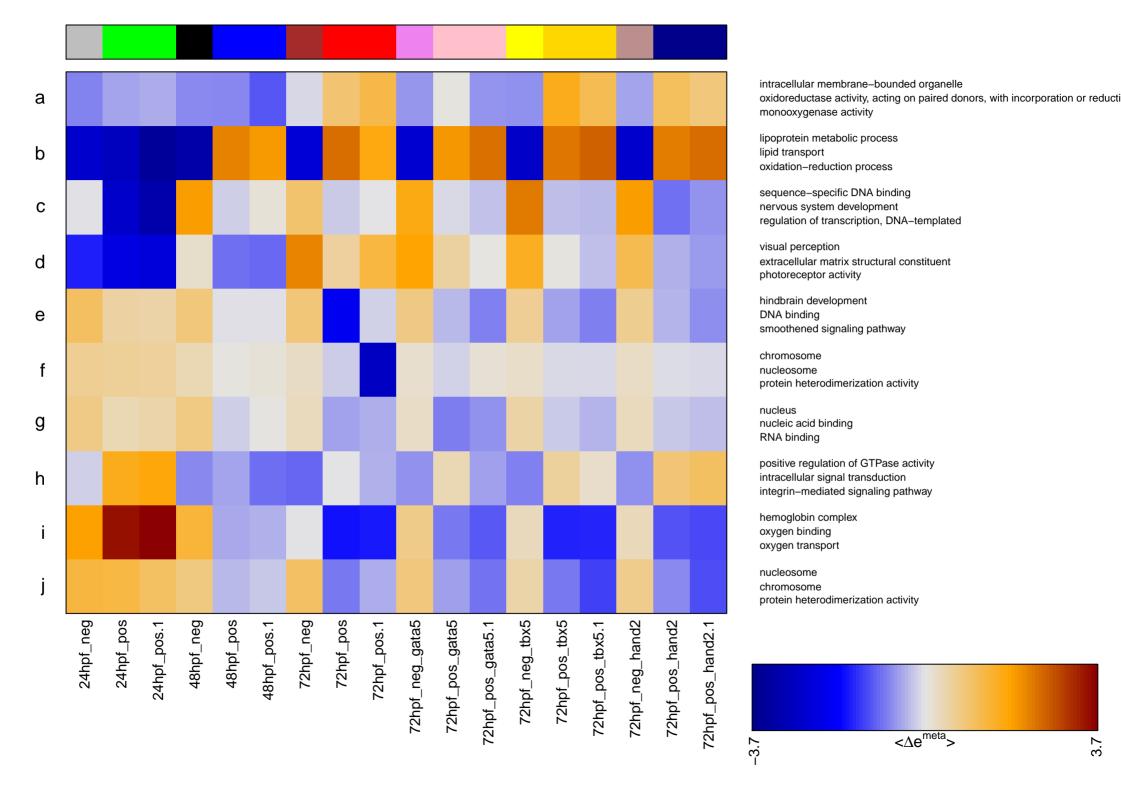


- a intracellular membrane—bounded organelle oxidoreductase activity, acting on paired donors, with incorp monooxygenase activity
 b lipoprotein metabolic process lipid transport oxidation—reduction process
 c sequence—specific DNA binding nervous system development regulation of transcription, DNA—templated
 d visual perception extracellular matrix structural constituent
- extracellular matrix structural constitue photoreceptor activity

 e hindbrain development
- DNA binding smoothened signaling pathway
- f chromosome nucleosome protein heterodimerization activity
- g nucleus
 nucleic acid binding
 RNA binding
- h positive regulation of GTPase activity intracellular signal transduction integrin-mediated signaling pathway
- i hemoglobin complex oxygen binding oxygen transport
- j nucleosome chromosome protein heterodimerization activity



3.7

Spot Summary: a

metagenes = 2 # genes = 32

<r> metagenes = 1

<r> genes = 0.71 beta: r2= 7.04 / log p= -Inf

samples with spot = 0 (0 %)

Overview Map Spot 30 30 20 20 10 10 20 30 30 40 10 20 1.5 1.0 0.5 0.0 -0.5 72hpf_neg_gata5 72hpf_pos_gata5 48hpf_pos.1 48hpf_pos 72hpf_neg 72hpf_pos 72hpf_pos.1 72hpf_neg_tbx5 72hpf_pos_hand2 72hpf_pos_gata5.1

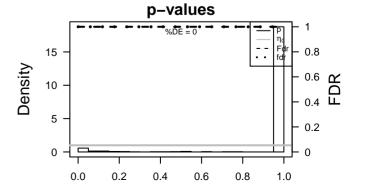
Spot Genelist

Rank ID	max	e min e	r e	Symb	Description ool
1 ENSDARGOO	3.22	-3.48	0.91	cfh	complement factor H [Source:ZFIN;Acc:ZDB-GENE-050208
2 ENSDARGOO	2.84	-3.3	0.8	cyp24a1	cytochrome P450, family 24, subfamily A, polypeptide 1 [Sour
3 ENSDARGOO	2.67	-2.47	0.88	cyp1a	cytochrome P450, family 1, subfamily A [Source:ZFIN;Acc:ZD
4 ENSDARGOO	3.14	-2.4	0.69	cyp1b1	cytochrome P450, family 1, subfamily B, polypeptide 1 [Sourc
5 ENSDARGOO	2.12	-2.31	0.9	nfil3-6	nuclear factor, interleukin 3 regulated, member 6 [Source:ZFI
6 ENSDARGOO	1.4	-1.84	0.86	ugt2a2	UDP glucuronosyltransferase 2 family, polypeptide A1 [Source
7 ENSDARGOO	1.78	-1.81	0.88		si:ch211-93f2.1 [Source:ZFIN;Acc:ZDB-GENE-041014-96]
8 ENSDARGO	2.52	-1.7	0.89	abcc2	ATP-binding cassette, sub-family C (CFTR/MRP), member 2
9 ENSDARGOO	2.2	-1.68	0.63	tnni2a.1	troponin I type 2a (skeletal, fast), tandem duplicate 1 [Source:
10 ENSDARGOO	1.18	-1.56	0.86	cxcr3.3	chemokine (C-X-C motif) receptor 3, tandem duplicate 3 [So
11 ENSDARGOO	1.45	-1.4	0.83	rbm47	RNA binding motif protein 47 [Source:ZFIN;Acc:ZDB-GENE-
12 ENSDARGOO	2.49	-1.39	0.85	adamts1	ADAM metallopeptidase with thrombospondin type 1 motif, 15
13 ENSDARGOO	1.77	-1.39	0.87	si:dkey-	194446.1 [Source:ZFIN;Acc:ZDB-GENE-100922-43]
14 ENSDARGOO	1.41	-1.37	0.88	enpp1	ectonucleotide pyrophosphatase/phosphodiesterase 1 [Sourc
15 ENSDARGOO	1.57	-1.36	0.9	cx32.3	connexin 32.3 [Source:ZFIN;Acc:ZDB-GENE-030131-1337]
16 ENSDARGOO	2.61	-1.31	0.77	zgc:9218	84i:dkeyp-52c3.2 [Source:ZFIN;Acc:ZDB-GENE-110411-46]
17 ENSDARGOO	2.42	-1.3	0.87	serpind1	serpin peptidase inhibitor, clade D (heparin cofactor), membe
18 ENSDARGOO	1.29	-1.24	0.86	suclg2	succinate-CoA ligase, GDP-forming, beta subunit [Source:ZI
19 ENSDARGOO	1.3	-1.22	0.81	dusp1	dual specificity phosphatase 1 [Source:ZFIN;Acc:ZDB-GENE
20 ENSDARGOO	1.98	-1.19	0.91	LOC100	002960

Geneset Overrepresentation

Rank p-value #in/all Geneset

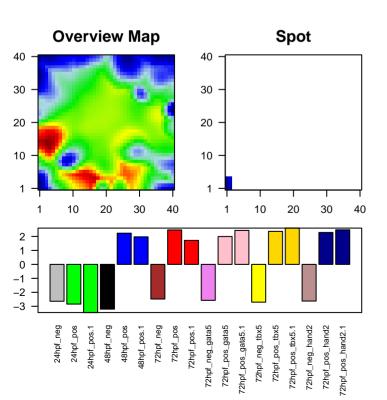
	•			
1	4e-05	3 / 59	СС	intracellular membrane-bounded organelle
2	3e-04	3 / 110	MF	oxidoreductase activity, acting on paired donors, with incorporation or
3	3e-04	3 / 119	MF	monooxygenase activity
4	4e-04	2 / 27	MF	oxidoreductase activity, acting on paired donors, with incorporation or
5	6e-04	3 / 145	MF	heme binding
2 3 4 5 6 7	9e-04	2/39	CC	connexin complex
7	1e-03	3 / 178	MF	iron ion binding
8	1e-03	2 / 44	CC	gap junction
9	2e-03	2/53	BP	chemotaxis
10	2e-03	2/58	BP	chemokine-mediated signaling pathway
11	2e-03	2 / 64	BP	cell communication
12	3e-03	2/72	BP	nucleic acid phosphodiester bond hydrolysis
13	3e-03	7 / 1761	MF	metal ion binding
14	5e-03	3 / 297	BP	immune response
15	9e-03	2 / 128	MF	metallopeptidase activity
16	1e-02	1 / 10	BP	circadian regulation of gene expression
17	1e-02	3 / 414	BP	metabolic process
18	1e-02	1 / 12	BP	head development
19	1e-02	1 / 12	BP	response to xenobiotic stimulus
20	2e-02	1 / 15	BP	cardiac muscle contraction
21	2e-02	1 / 15	MF	MAP kinase tyrosine/serine/threonine phosphatase activity
22	2e-02	1 / 15	BP	retinol metabolic process
23	2e-02	1 / 15	BP	skeletal muscle contraction
24	2e-02	3 / 480	MF	catalytic activity
25	2e-02	1 / 16	BP	inactivation of MAPK activity
26	2e-02	1 / 16	MF	polysaccharide binding
27	2e-02	1 / 17	MF	organic anion transmembrane transporter activity
28	2e-02	1 / 17	MF	transcriptional repressor activity, RNA polymerase II core promoter pro-
29	2e-02	1 / 18	MF	steroid binding
30	2e-02	3 / 522	MF	oxidoreductase activity
31	2e-02	1 / 19	BP	organic anion transport
32	2e-02	1 / 20	BP	steroid metabolic process
33	2e-02	4 / 969	MF	hydrolase activity
34	2e-02	2/209	CC	endoplasmic reticulum membrane
35	2e-02	1 / 22	MF	chemokine receptor activity
36	3e-02	2/219	CC	cell junction
37	3e-02	1 / 23	CC	troponin complex
38	3e-02	1 / 25	BP	tricarboxylic acid cycle
39	3e-02	1 / 29	BP	cellular response to xenobiotic stimulus
40	3e-02	1 / 29	MF	glucuronosyltransferase activity



BP				СС				MF			
Rank	p-value	#in/all	Geneset	Rank	p-value	#in/all	Geneset	Rank	p-value	#in/all	Geneset
1	0.002	2/53	chemotaxis	1	4e-05	3/59	intracellular membrane-bounded organelle	1	3e-04	3/110	oxidoreductase activity, acting on paired donors, with incorporation or reduction
2	0.002	2 / 58	chemokine-mediated signaling pathway	2	9e-04	2/39	connexin complex	2	3e-04	3/119	monooxygenase activity
3	0.002	2 / 64	cell communication	3	1e-03	2 / 44	gap junction	3	4e-04	2 / 27	oxidoreductase activity, acting on paired donors, with incorporation or reduction
4	0.003	2 / 72	nucleic acid phosphodiester bond hydrolysis	4	2e-02	2 / 209	endoplasmic reticulum membrane	4	6e-04	3 / 145	heme binding
5	0.005	3 / 297	immune response	5	3e-02	2/219	cell junction	5	1e-03	3 / 178	iron ion binding
6	0.011	1 / 10	circadian regulation of gene expression	6	3e-02	1/23	troponin complex	6	3e-03	7 / 1761	metal ion binding
7	0.011	3 / 414	metabolic process	7	4e-02	1 / 35	peroxisome	7	9e-03	2 / 128	metallopeptidase activity
8	0.014	1 / 12	head development	8	6e-02	2/337	endoplasmic reticulum	8	2e-02	1 / 15	MAP kinase tyrosine/serine/threonine phosphatase activity
9	0.014	1 / 12	response to xenobiotic stimulus	9	2e-01	10 / 6248	integral component of membrane	9	2e-02	3 / 480	catalytic activity
10	0.017	1 / 15	cardiac muscle contraction	10	2e-01	10 / 6723	membrane	10	2e-02	1 / 16	polysaccharide binding
11	0.017	1 / 15	retinol metabolic process	11	4e-01	1 / 410	mitochondrion	11	2e-02	1 / 17	organic anion transmembrane transporter activity
12	0.017	1 / 15	skeletal muscle contraction	12	4e-01	2 / 1162	plasma membrane	12	2e-02	1 / 17	transcriptional repressor activity, RNA polymerase II core promoter proximal r
13	0.018	1 / 16	inactivation of MAPK activity	13	4e-01	1 / 500	extracellular space	13	2e-02	1 / 18	steroid binding
14	0.021	1 / 19	organic anion transport	14	5e-01	1 / 634	extracellular region	14	2e-02	3 / 522	oxidoreductase activity
15	0.023	1 / 20	steroid metabolic process	15	5e-01	2 / 1580	cellular_component	15	2e-02	4 / 969	hydrolase activity

Spot Summary: b

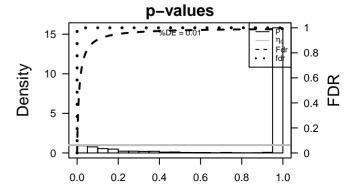
```
# metagenes = 8
# genes = 167
<r> metagenes = 0.99
<r> genes = 0.85
beta: r2= 74.8 / log p= -Inf
# samples with spot = 8 ( 44.4 %)
   24hpf_neg: 1 (100%)
   24hpf_pos: 2 (100 %)
   48hpf_neg: 1 (100%)
   72hpf_neg: 1 (100%)
   72hpf_neg_gata5 : 1 ( 100 %)
   72hpf_neg_hand2:1(100%)
```



Spot G

Genelist			Geneset Overrepresentation
may e	r	Description	Pank n-value #in/all Geneset

Ra	nk ID	max	e min	r e	Sym	Description bol	Rank	p-value	#in/all	Ge	neset
1	ENSDARG000	4.71	-7.81	0.94	gch2	GTP cyclohydrolase 2 [Source:ZFIN;Acc:ZDB-GENE-00120]	1	5e-11	7 / 23	BP	lipoprotein metabolic process
							2	6e-09	8 / 67	BP	lipid transport
2	ENSDARG000	4.34	-7.46	0.97	slc22a7	a solute carrier family 22 (organic anion transporter), member 7	3	5e-08	19 / 712	BP	oxidation-reduction process
							4	2e-07	4 / 10	CC	melanosome
3	ENSDARG000	4.47	-7.23	0.98	xdh	xanthine dehydrogenase [Source:ZFIN;Acc:ZDB-GENE-070	5	3e-06	14 / 522	MF	oxidoreductase activity
							6	2e-05	10 / 321	MF	GTPase activity
4	ENSDARG000	4.98	-7.11	0.97	wu:fc46	6h1/2u:fc46h12 [Source:ZFIN;Acc:ZDB-GENE-030131-3611]	7	2e-05	3 / 10	CC	chylomicron
							8	2e-05	3 / 10	CC	high-density lipoprotein particle
5	ENSDARG000	3.92	-7.09	0.77	pah	phenylalanine hydroxylase [Source:ZFIN;Acc:ZDB-GENE-03	9	2e-05	3 / 10	BP	triglyceride catabolic process
							10	3e-05	3 / 11	BP	cholesterol homeostasis
6	ENSDARG000	3.79	-7.08	0.98	zgc:113	333gc:113337 [Source:ZFIN;Acc:ZDB-GENE-050306-20]	11	3e-05	3 / 11	BP	melanosome organization
							12	4e-05	6 / 105	MF	lipid binding
7	ENSDARG000	3.75	-6.94	0.96	si:ch21	1-si086512-108c6.2 [Source:ZFIN;Acc:ZDB-GENE-040724-7]	13	4e-05	3 / 12	BP	cholesterol biosynthetic process
							14	6e-05	3 / 13	BP	cholesterol efflux
8	ENSDARG000	4.88	-6.93	0.96	si:dkey-	-25i1dtk@;2-251i10.2 [Source:ZFIN;Acc:ZDB-GENE-050506-10:	15	6e-05	3 / 13	BP	response to toxic substance
-							16	9e-05	3 / 15	CC	secretory granule
9	ENSDARG00	4.44	-6.92	0.97	zgc:162	21 50 c:162150 [Source:ZFIN;Acc:ZDB-GENE-070410-23]	17	1e-04	13 / 634	CC	extracellular region
Ū					-		18	1e-04	3 / 17	CC	blood microparticle
10	ENSDARG000	4.09	-6.89	0.83	apoa2	apolipoprotein A-II [Source:ZFIN;Acc:ZDB-GENE-030131-1	19	1e-04	3 / 17	MF	cholesterol binding
10						7	20	1e-04	3 / 17	MF	cholesterol transporter activity
11	ENSDARG00	4 14	-6.83	0.95	cax1	cation/H+ exchanger protein 1 [Source:ZFIN;Acc:ZDB-GENE	21	3e-04	3 / 21	MF	substrate-specific transmembrane transporter activity
	2110271110001		0.00	0.00	ouxi		22	4e-04	3 / 24	BP	nucleoside metabolic process
12	ENSDARG000	3 63	-6.81	0.97	tat	tyrosine aminotransferase [Source:ZFIN;Acc:ZDB-GENE-03	23	5e-04	3 / 26	BP	melanosome transport
12	LINSDAIRGOON	3.03	-0.01	0.51	tat	tyroomo ammonanoiotaco (coaroo.e. mt, too.e.b.b. Oe.te. oo	24	5e-04	3 / 26	CC	vesicle
13	ENSDARG000	2.05	-6.8	0.96	fmn2a	formin 2a [Source:ZFIN;Acc:ZDB-GENE-101107-1]	25	6e-04	11 / 561	MF	GTP binding
13	ENSDARGOO	3.03	-0.0	0.90	IIIIIZa	IOTHIIT 2a [Goulde.21 IN,Acc.2DB-GENE-101107-1]	26	7e-04	4 / 67	MF	transmembrane transporter activity
11	ENCDARCOO!	2.54	-6.75	0.83	oirob21	1-sis:tis2t1.4251b21.1 [Source:ZFIN;Acc:ZDB-GENE-060809-{	27	7e-04	3 / 30	BP	pigmentation
14	ENSDARG000	2.34	-0.75	0.03	SI.CHZ I	1-23/12/11/201021:1 [Godice.21 IN,Acc.200-GENE-000009-0	28	8e-04	3 / 31	BP	protein-chromophore linkage
15	ENODA DOSS	0.40	0.00	0.00	asip2b	#: -ili#: bl () 2h [C	29	9e-04	11 / 591	BP	transmembrane transport
15	ENSDARG000	3.10	-6.68	0.92	αδίμευ	agouti signaling protein, nonagouti homolog (mouse) 2b [Sou	30	1e-03	3 / 33	MF	photoreceptor activity
40	ENODA DOSS	0.00	0.05	0.00		4	31	1e-03	3 / 38	CC	trans-Golgi network
16	ENSDARG000	2.82	-6.65	0.83	si:cn21	1-sigst2t3.4195b13.1 [Source:ZFIN;Acc:ZDB-GENE-030131-	32	2e-03	54 / 6248	CC	integral component of membrane
47					_	THE RESIDENCE OF THE PROPERTY	33	2e-03	3 / 43	MF	iron-sulfur cluster binding
17	ENSDARG000	4.29	-6.62	0.94	aox5	aldehyde oxidase 5 [Source:ZFIN;Acc:ZDB-GENE-001205-:	34	2e-03	2/12	BP	aromatic amino acid family metabolic process
4.0							35	3e-03	6 / 229	MF	transporter activity
18	ENSDARG000	3.14	-6.61	0.97		transmembrane protein 19 [Source:HGNC Symbol;Acc:HGNC	36	3e-03	56 / 6723	CC	membrane
							37	4e-03	5 / 178	MF	iron ion binding
19	ENSDARG000	2.75	-6.61	0.87	syngr1a	a synaptogyrin 1a [Source:ZFIN;Acc:ZDB-GENE-041010-169	38	6e-03	3 / 60	MF	scavenger receptor activity
							39	8e-03	2 / 23	MF	NADP binding
20	ENSDARG000	3.4	-6.52	0.89	tmem16	63transmembrane protein 163a [Source:ZFIN;Acc:ZDB-GENE-	40	8e-03	3 / 70	CC	myosin complex



BP				СС				MF			
Rank	p-value	#in/all	Geneset	Rank	p-value	#in/all	Geneset	Rank	p-value	#in/all	Geneset
1	5e-11	7 / 23	lipoprotein metabolic process	1	2e-07	4 / 10	melanosome	1	3e-06	14 / 522	oxidoreductase activity
2	6e-09	8 / 67	lipid transport	2	2e-05	3 / 10	chylomicron	2	2e-05	10 / 321	GTPase activity
3	5e-08	19 / 712	oxidation-reduction process	3	2e-05	3/10	high-density lipoprotein particle	3	4e-05	6 / 105	lipid binding
4	2e-05	3 / 10	triglyceride catabolic process	4	9e-05	3/15	secretory granule	4	1e-04	3 / 17	cholesterol binding
5	3e-05	3/11	cholesterol homeostasis	5	1e-04	13 / 634	extracellular region	5	1e-04	3 / 17	cholesterol transporter activity
6	3e-05	3/11	melanosome organization	6	1e-04	3/17	blood microparticle	6	3e-04	3 / 21	substrate-specific transmembrane transporter activity
7	4e-05	3/12	cholesterol biosynthetic process	7	5e-04	3 / 26	vesicle	7	6e-04	11 / 561	GTP binding
8	6e-05	3/13	cholesterol efflux	8	1e-03	3/38	trans-Golgi network	8	7e-04	4 / 67	transmembrane transporter activity
9	6e-05	3/13	response to toxic substance	9	2e-03	54 / 6248	integral component of membrane	9	1e-03	3/33	photoreceptor activity
10	4e-04	3/24	nucleoside metabolic process	10	3e-03	56 / 6723	membrane	10	2e-03	3 / 43	iron-sulfur cluster binding
11	5e-04	3 / 26	melanosome transport	11	8e-03	3/70	myosin complex	11	3e-03	6 / 229	transporter activity
12	7e-04	3 / 30	pigmentation	12	4e-02	5/317	Golgi apparatus	12	4e-03	5 / 178	iron ion binding
13	8e-04	3 / 31	protein-chromophore linkage	13	5e-02	15 / 1580	cellular_component	13	6e-03	3/60	scavenger receptor activity
14	9e-04	11 / 591	transmembrane transport	14	6e-02	5 / 355	cytosol	14	8e-03	2 / 23	NADP binding
15	2e-03	2/12	aromatic amino acid family metabolic process	15	7e-02	2/71	endomembrane system	15	1e-02	2 / 25	glutathione transferase activity

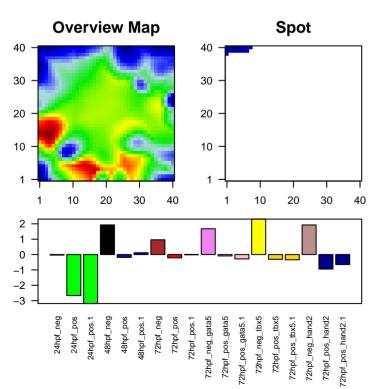
Spot Summary: c

metagenes = 16 # genes = 457

```
<r> metagenes = 0.97</r> <r> genes = 0.77

 beta: r2= 31.01 / log p= -Inf
```

samples with spot = 2 (11.1 %) 24hpf_pos : 2 (100 %)



Spot Genelist

max e

Rank

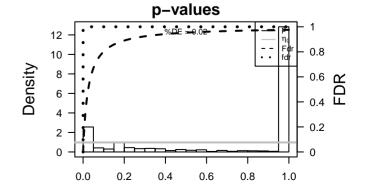
Ital	ID	max v	min e)	Symb	ool
1	ENSDARG000	2.06	-9.48	0.66	myhz1.1	myosin, heavy polypeptide 1.1, skeletal muscle [Source:ZFIN
2	ENSDARG000	4.72	-8.26	0.86	col11a2	collagen, type XI, alpha 2 [Source:ZFIN;Acc:ZDB-GENE-000
3	ENSDARG000	3.03	-7.84	0.76	krt91	keratin 17 [Source:ZFIN;Acc:ZDB-GENE-060503-86]
4	ENSDARG000	2.86	-7.73	0.92	stmn1b	stathmin 1b [Source:ZFIN;Acc:ZDB-GENE-050417-397]
5	ENSDARG000	3.2	-7.21	0.96	gpm6aa	glycoprotein M6Aa [Source:ZFIN;Acc:ZDB-GENE-030710-7
6	ENSDARG000	2.35	-6.78	0.84	сре	carboxypeptidase E [Source:ZFIN;Acc:ZDB-GENE-090313-
7	ENSDARG00	4.49	-6.7	0.85		si:dkey-65b12.6 [Source:ZFIN;Acc:ZDB-GENE-060526-329
8	ENSDARG000	2.15	-6.69	0.66	fkbp5	FK506 binding protein 5 [Source:ZFIN;Acc:ZDB-GENE-0306
9	ENSDARG000	2.83	-6.67	0.93		neuronal differentiation 1 [Source:ZFIN;Acc:ZDB-GENE-990
10	ENSDARG000	2.41	-6.61	0.87	atp1a1b	ATPase, Na+/K+ transporting, alpha 1b polypeptide [Source:2
11	ENSDARG000	1.97	-6.47	0.73	gfap	glial fibrillary acidic protein [Source:ZFIN;Acc:ZDB-GENE-9§
12	ENSDARG000	3.37	-6.4	0.97	si:dkey-	46iral8a8y-40m6.8 [Source:ZFIN;Acc:ZDB-GENE-100922-162
13	ENSDARG00	4.01	-6.39	0.88	col9a3	collagen, type IX, alpha 3 [Source:ZFIN;Acc:ZDB-GENE-03(
14	ENSDARG000	3.14	-6.34	0.9	slc1a3b	solute carrier family 1 (glial high affinity glutamate transporter
15	ENSDARG00	3.23	-6.31	0.88	map1aa	microtubule-associated protein 1Aa [Source:ZFIN;Acc:ZDB-
16	ENSDARG000	3.88	-6.3	0.95	pclob	piccolo presynaptic cytomatrix protein b [Source:ZFIN;Acc:ZE
17	ENSDARG000	3.24	-6.26	0.96		Down syndrome cell adhesion molecule like 1 [Source:ZFIN;/
18	ENSDARG000	4	-6.25	0.81	ерус	epiphycan [Source:ZFIN;Acc:ZDB-GENE-041008-9]
19	ENSDARG000	3.32	-6.25	0.96	kif5aa	kinesin family member 5A, a [Source:ZFIN;Acc:ZDB-GENE-
20	ENSDARG000	3.36	-6.19	0.97	kif1ab	kinesin family member 1Ab [Source:ZFIN;Acc:ZDB-GENE-0]

Description

Geneset Overrepresentation

Rank p-value #in/all Geneset

1	2e-23	50 / 537	MF	sequence–specific DNA binding
2	4e-23	31 / 175	BP	nervous system development
3	1e-15	63 / 1239	BP	regulation of transcription, DNA-templated
4	3e-14	35 / 454	BP	multicellular organism development
5	2e-13	21 / 158	MF	microtubule binding
6	1e-12	64 / 1484	MF	DNA binding
Ž	8e-12	20 / 172	BP	homophilic cell adhesion via plasma membrane adhesion molecules
8	1e-11	19 / 155	CC	synapse
9	2e-11	91 / 2716	CC	nucleus
10	3e-10	15 / 108	CC	microtubule
11	5e-10	19 / 193	BP	positive regulation of transcription from RNA polymerase II promoter
12	4e-09	48 / 1162	CC	plasma membrane
13	5e-09	14 / 113	BP	transcription from RNA polymerase II promoter
14	7e-09	23 / 333	BP	cell adhesion
15	8e-09	33 / 643	BP	transcription, DNA-templated
16	3e-08	8 / 32	MF	extracellular-glutamate-gated ion channel activity
17	3e-08	8 / 32	MF	ionotropic glutamate receptor activity
18	3e-08	8/32	BP	ionotropic glutamate receptor signaling pathway
19	6e-08	27 / 499	BP	ion transport
20	1e-07	33 / 717	MF	calcium ion binding
21	3e-07	9 / 57	BP	microtubule cytoskeleton organization
22	5e-07	10 / 78	BP	axon guidance
23	7e-07	29 / 633	MF	transcription factor activity, sequence-specific DNA binding
24	9e-07	13 / 147	BP	brain development
25	1e-06	8 / 49	MF	extracellular matrix structural constituent
26	2e-06	14 / 183	MF	RNA polymerase II transcription factor activity, sequence-specific DNA
27	3e-06	7 / 39	BP	neuron projection development
28	3e-06	9/74	CC	neuron projection
29	3e-06	15 / 219	CC	cell junction
30	5e-06	151 / 6723	CC	membrane
31	6e-06	9 / 79	BP	excitatory postsynaptic potential
32	6e-06	5 / 17	BP	cytoskeleton-dependent intracellular transport
33	6e-06	5 / 17	CC	presynaptic active zone
34	7e-06	7 / 44	BP	neuron development
35	8e-06	5 / 18	MF	tubulin binding
36	9e-06	7 / 46	BP	eye development
37	1e-05	16 / 270	MF	ion channel activity
38	1e-05	8 / 65	BP	sodium ion transport
39	1e-05	6 / 33	BP	hindbrain development
40	2e-05	4 / 11	MF	spectrin binding

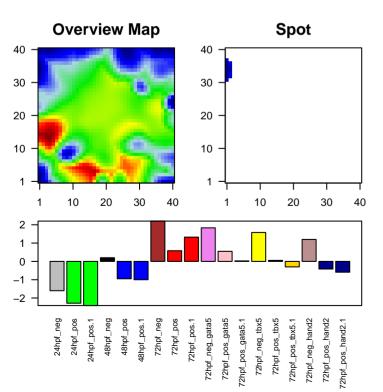


ВР				СС				MF			
Rank	p-value	#in/all	Geneset	Rank	p-value	#in/all	Geneset	Rank	p-value	#in/all	Geneset
1	4e-23	31 / 175	nervous system development	1	1e–11	19 / 155	synapse	1	2e-23	50 / 537	sequence–specific DNA binding
2	1e-15	63 / 1239	regulation of transcription, DNA-templated	2	2e-11	91 / 2716	nucleus	2	2e-13	21 / 158	microtubule binding
3	3e-14	35 / 454	multicellular organism development	3	3e-10	15 / 108	microtubule	3	1e-12	64 / 1484	DNA binding
4	8e-12	20 / 172	homophilic cell adhesion via plasma membrane adhesion molecules	4	4e-09	48 / 1162	plasma membrane	4	3e-08	8 / 32	extracellular-glutamate-gated ion channel activity
5	5e-10	19 / 193	positive regulation of transcription from RNA polymerase II promoter	5	3e-06	9/74	neuron projection	5	3e-08	8 / 32	ionotropic glutamate receptor activity
6	5e-09	14 / 113	transcription from RNA polymerase II promoter	6	3e-06	15 / 219	cell junction	6	1e-07	33 / 717	calcium ion binding
7	7e-09	23 / 333	cell adhesion	7	5e-06	151 / 6723	membrane	7	7e-07	29 / 633	transcription factor activity, sequence–specific DNA binding
8	8e-09	33 / 643	transcription, DNA-templated	8	6e-06	5 / 17	presynaptic active zone	8	1e-06	8 / 49	extracellular matrix structural constituent
9	3e-08	8 / 32	ionotropic glutamate receptor signaling pathway	9	2e-05	6 / 36	synaptic vesicle	9	2e-06	14 / 183	RNA polymerase II transcription factor activity, sequence–specific DNA bindir
10	6e-08	27 / 499	ion transport	10	5e-05	8 / 80	postsynaptic membrane	10	8e-06	5 / 18	tubulin binding
11	3e-07	9 / 57	microtubule cytoskeleton organization	11	1e-04	4 / 17	AMPA glutamate receptor complex	11	1e-05	16 / 270	ion channel activity
12	5e-07	10 / 78	axon guidance	12	1e-04	135 / 6248	integral component of membrane	12	2e-05	4/11	spectrin binding
13	9e-07	13 / 147	brain development	13	5e-04	3/10	clathrin-coated vesicle	13	3e-05	10 / 120	motor activity
14	3e-06	7 / 39	neuron projection development	14	5e-04	13 / 268	cytoskeleton	14	4e-05	10 / 124	receptor activity
15	6e-06	9 / 79	excitatory postsynaptic potential	15	8e-04	3 / 12	microtubule associated complex	15	1e-04	6 / 47	structural constituent of cytoskeleton

Spot Summary: d

metagenes = 12

24hpf_pos : 2 (100 %)



Spot Genelist

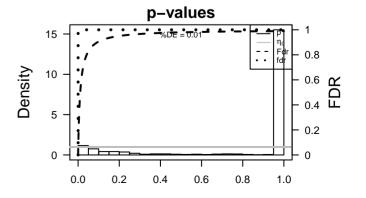
max e

Rank

Nai	ID .	III CX	min e	;	Symb	ool	Na
1	ENSDARG000	5.34	-6.98	0.94	matn1	matrilin 1 [Source:ZFIN;Acc:ZDB-GENE-050307-3]	1 2
2	ENSDARG000	3.36	-6.43	0.86	rbp4	retinol binding protein 4, plasma [Source:ZFIN;Acc:ZDB-GEN	3
3	ENSDARG000	5.09	-5.91	0.88	and2	actinodin2 [Source:ZFIN;Acc:ZDB-GENE-041105-2]	5
4	ENSDARG000	2.67	-5.74	0.89	lect1	leukocyte cell derived chemotaxin 1 [Source:ZFIN;Acc:ZDB-(7 8
5	ENSDARG000	2.52	-5.65	0.88	chd3	chromodomain helicase DNA binding protein 3 [Source:ZFIN;	9 10
6	ENSDARG000	3.56	-5.56	0.75	krtt1c19	ekeratin type 1 c19e [Source:ZFIN;Acc:ZDB-GENE-050506-9	11 12
7	ENSDARG000	3.82	-5.55	0.95	acana	aggrecan a [Source:ZFIN;Acc:ZDB-GENE-050208-221]	13 14
8	ENSDARG000	1.93	-5.48	0.82	cdkn1d	cyclin-dependent kinase inhibitor 1D [Source:ZFIN;Acc:ZDB-	15 16
9	ENSDARG000	4.83	-5.45	0.97	arr3a	arrestin 3a, retinal (X-arrestin) [Source:ZFIN;Acc:ZDB-GENE	17 18
10	ENSDARG000	2.41	-5.42	0.78			19 20
11	ENSDARG000	3.69	-5.36	0.77	myhb	myosin, heavy chain b [Source:ZFIN;Acc:ZDB-GENE-08112	21 22 23
12	ENSDARG000	2.57	-5.36	0.86	prss35	protease, serine, 35 [Source:ZFIN;Acc:ZDB-GENE-040704-	23 24 25
13	ENSDARG000	2.64	-5.25	0.88	snap25b	synaptosomal-associated protein, 25b [Source:ZFIN;Acc:ZDI	26 27
14	ENSDARG000	3.5	-5.21	0.94		tenascin XBa [Source:ZFIN;Acc:ZDB-GENE-070103-5]	28 29
15	ENSDARG000	2.33	-5.17	0.79	ngfra	nerve growth factor receptor a (TNFR superfamily, member 1)	30 31
16	ENSDARG000	3.39	-5.13	0.82	col17a1a	acollagen, type XVII, alpha 1a [Source:ZFIN;Acc:ZDB-GENE-	32 33
17	ENSDARG000	3.77	-5.03	0.81	si:dkey-	1 %治脓癌y -183i3.5 [Source:ZFIN;Acc:ZDB-GENE-030131-856	34 35
18	ENSDARG000	3.59	-4.99	0.95		periostin, osteoblast specific factor a [Source:ZFIN;Acc:ZDB-	36 37
19	ENSDARG000	2.32	-4.92	0.81	sgip1a	SH3-domain GRB2-like (endophilin) interacting protein 1a [S	38 39
20	ENSDARG000	5.01	-4.88	0.95	opn1lw2	opsin 1 (cone pigments), long-wave-sensitive, 2 [Source:ZFI	40

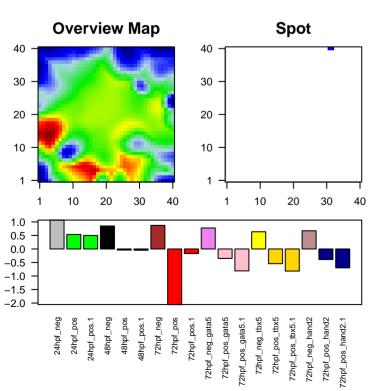
Description

	Rank	p-value	#in/all	Ge	neset
	1	4e-17	15 / 83	BP	visual perception
	2	2e-09	8 / 49	MF	extracellular matrix structural constituent
٩	3	3e-09	7 / 33	MF	photoreceptor activity
	3 4 5	4e-08	6 / 28	BP	phototransduction
	5	9e-08	6 / 31	CC	photoreceptor outer segment
	6 7	9e-08	6 / 31	BP	protein-chromophore linkage
-(7	1e-06	19 / 717	MF	calcium ion binding
	8	2e-06	9 / 153	CC	proteinaceous extracellular matrix
N;	9	3e-06	5 / 31	MF	G-protein coupled photoreceptor activity
	10	4e-06	17 / 634	CC	extracellular region
_(11	1e-05	7 / 102	BP	response to stimulus
	12	4e-05	3 / 10	MF	small molecule binding
	13	6e-05	4 / 30	BP	detection of visible light
	14	8e-05	13 / 499	BP	ion transport
3-	15	9e-05	5 / 62	CC	intermediate filament
	16	1e-04	20 / 1084	BP	transport
JE.	17	2e-04	5 / 76	BP	cartilage development
WL.	18	3e-04	8 / 229	MF	transporter activity
	19	3e-04	7 / 176	BP	ion transmembrane transport
	20	4e-04	3 / 20	BP	fin development
_	21	5e-04	3 / 21	BP	negative regulation of angiogenesis
2	22	6e-04	3 / 23	MF	hyaluronic acid binding
	23	7e-04	4 / 55	BP	central nervous system development
-	24	8e-04	8 / 270	MF	ion channel activity
	25	9e-04	65 / 6248	CC	integral component of membrane
)I	26	1e-03	5 / 106	BP	calcium ion transmembrane transport
	27	1e-03	3 / 28	BP	skeletal system development
	28	1e-03	3 / 29	MF	3',5'-cyclic-nucleotide phosphodiesterase activity
	29	1e-03	4 / 64	MF	serine-type endopeptidase inhibitor activity
1(30	1e-03	20 / 1295	BP	signal transduction
	31	1e-03	4 / 65	BP	sodium ion transport
-	32	1e-03	68 / 6723	CC	membrane
	33	2e-03	4 / 70	BP	sodium ion transmembrane transport
6	34	2e-03	3 / 35	BP	cellular calcium ion homeostasis
	35	2e-03	4 / 74	CC	neuron projection
-	36	3e-03	4/79	MF	calcium channel activity
	37	3e-03	2/11	MF	oxidoreductase activity, acting on the CH-NH2 group of donors, oxygen
S	38	3e-03	8 / 333	BP	cell adhesion
	39	3e-03	3 / 41	MF	copper ion binding
FI	40	4e-03	2/13	BP	synaptic vesicle endocytosis



ВР				СС				MF			
Rank	p-value	#in/all	Geneset	Rank	p-value	#in/all	Geneset	Rank	p-value	#in/all	Geneset
1	4e-17	15 / 83	visual perception	1	9e-08	6/31	photoreceptor outer segment	1	2e-09	8 / 49	extracellular matrix structural constituent
2	4e-08	6 / 28	phototransduction	2	2e-06	9 / 153	proteinaceous extracellular matrix	2	3e-09	7 / 33	photoreceptor activity
3	9e-08	6 / 31	protein-chromophore linkage	3	4e-06	17 / 634	extracellular region	3	1e-06	19 / 717	calcium ion binding
4	1e-05	7 / 102	response to stimulus	4	9e-05	5 / 62	intermediate filament	4	3e-06	5 / 31	G-protein coupled photoreceptor activity
5	6e-05	4 / 30	detection of visible light	5	9e-04	65 / 6248	integral component of membrane	5	4e-05	3 / 10	small molecule binding
6	8e-05	13 / 499	ion transport	6	1e-03	68 / 6723	membrane	6	3e-04	8 / 229	transporter activity
7	1e-04	20 / 1084	transport	7	2e-03	4/74	neuron projection	7	6e-04	3 / 23	hyaluronic acid binding
8	2e-04	5 / 76	cartilage development	8	5e-03	3 / 48	heterotrimeric G-protein complex	8	8e-04	8 / 270	ion channel activity
9	3e-04	7 / 176	ion transmembrane transport	9	6e-03	5 / 155	synapse	9	1e-03	3 / 29	3',5'-cyclic-nucleotide phosphodiesterase activity
10	4e-04	3 / 20	fin development	10	1e-02	16 / 1162	plasma membrane	10	1e-03	4 / 64	serine-type endopeptidase inhibitor activity
11	5e-04	3 / 21	negative regulation of angiogenesis	11	1e-02	2/22	synaptic vesicle membrane	11	3e-03	4 / 79	calcium channel activity
12	7e-04	4 / 55	central nervous system development	12	2e-02	2 / 26	neuronal cell body	12	3e-03	2/11	oxidoreductase activity, acting on the CH-NH2 group of donors, oxygen as ac
13	1e-03	5 / 106	calcium ion transmembrane transport	13	3e-02	2/38	apical plasma membrane	13	3e-03	3 / 41	copper ion binding
14	1e-03	3 / 28	skeletal system development	14	3e-02	11 / 809	integral component of plasma membrane	14	5e-03	2 / 14	sodium:bicarbonate symporter activity
15	1e-03	20 / 1295	signal transduction	15	8e-02	4/219	cell junction	15	6e-03	2/16	anion transmembrane transporter activity

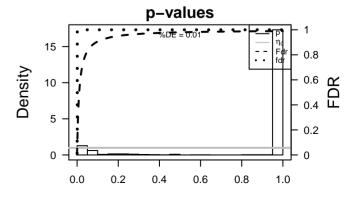
Spot Summary: e



Spot Genelist

Rar	nk ID	max	e min e	r Ə	Symb	Description pol	Rank	p-value	#in/all	Ge	neset
1	ENSDARG000	1.75	-5.1	0.91		poliovirus receptor-related 1b [Source:ZFIN;Acc:ZDB-GENE	1	1e-06	4 / 33	BP	hindbrair
0	FNODADOGG	4.40	4.50	0.00			2	1e-05	14 / 1484	MF	DNA bin
2	ENSDARG000	1.42	-4.58	0.82			3 4	2e-05 7e-05	3 / 21	BP BP	smoothe inner ear
2	FNODADOOG	4.00	4.54	0.05	l17	Journal rich report containing 17 (Source: 75IN: Acc: 70P, CEI	5	1e-03	3 / 32 4 / 104	BP	transmei
3	ENSDARG000	1.33	-4.54	0.85	Irrc17	leucine rich repeat containing 17 [Source:ZFIN;Acc:ZDB-GEI	6	2e-04	11 / 1239	BP	regulatio
	=					The second of the second secon	7	3e-04	2/10	BP	adenohy
4	ENSDARG000	3.22	-4.34	0.73		collagen, type XIV, alpha 1b [Source:ZFIN;Acc:ZDB-GENE-(8	3e-04 3e-04	5 / 232	MF	protein h
_	=					FERM I AND STATE OF THE STATE O	9	4e-04	7 / 537	MF	sequenc
5	ENSDARG000	1.95	-3.69	0.93	frmd6	FERM domain containing 6 [Source:ZFIN;Acc:ZDB-GENE-0	10	4e-04 4e-04	2/12	BP	determin
_						TEN A	11	5e-04	2/12	BP	inner ear
6	ENSDARG000	1.14	-3.33	8.0	pacs2	phosphofurin acidic cluster sorting protein 2 [Source:ZFIN;Ac	12	7e-04	3/70	CC	cell proje
_							13	7e-04 7e-04	3/70	BP	signal tra
7	ENSDARG000	1.85	-3.11	0.82	ablim1a	actin binding LIM protein 1a [Source:ZFIN;Acc:ZDB-GENE-(14	8e-04	2/17	MF	transmer
_							15	9e-04	16 / 2716	CC	nucleus
8	ENSDARG000	1.51	-2.94	0.93	sncaip	synuclein, alpha interacting protein [Source:ZFIN;Acc:ZDB-G	16	9e-04	3/76	BP	cartilage
							17	9e-04	3/76	CC	cilium
9	ENSDARG000	1.69	-2.9	0.78	si:ch211	-sich216-161c3.6 [Source:ZFIN;Acc:ZDB-GENE-131126-51	18	1e-03	3 / 78	BP	axon gui
							19	1e-03	2/19	BP	positive
10	ENSDARG000	1.77	-2.88	0.85		iroquois homeobox 3b [Source:ZFIN;Acc:ZDB-GENE-03013	20	1e-03	2/19	BP	transmer
							21	1e-03	2/21	BP	negative
11	ENSDARG000	0.85	-2.75	0.84	dcp1a	decapping mRNA 1A [Source:ZFIN;Acc:ZDB-GENE-030723	22	1e-03	2/21	MF	signal tra
							23	1e-03	6 / 491	MF	kinase a
12	ENSDARG000	1.6	-2.74	0.85	si:dkey-	18i8iii2iiy4108k21.11 [Source:ZFIN;Acc:ZDB-GENE-131127-1	24	1e-03	2 / 23	MF	dynein li
							25	2e-03	3/91	BP	heart loc
13	ENSDARG000	1.42	-2.73	8.0	zgc:163	040stone 1, H4, like [Source:ZFIN;Acc:ZDB-GENE-070927-10	26	2e-03	6 / 522	BP	phospho
							27	2e-03	8/914	MF	protein k
14	ENSDARG000	1.26	-2.63	0.88		nephronophthisis 4 [Source:ZFIN;Acc:ZDB-GENE-060503-7	28	2e-03	3 / 100	BP	peptidyl-
							29	2e-03	2 / 29	BP	hematop
15	ENSDARG000	1.27	-2.61	0.86	ror1	receptor tyrosine kinase-like orphan receptor 1 [Source:ZFIN	30	2e-03	8 / 947	BP	protein p
							31	3e-03	2/30	BP	pigmenta
16	ENSDARG000	1.41	-2.6	0.82	fam168b	family with sequence similarity 168, member B [Source:ZFIN;	32	3e-03	3/110	MF	protein t
							33	3e-03	2/31	BP	pancreas
17	ENSDARG000	1.19	-2.57	0.7	prkx	protein kinase, X-linked [Source:ZFIN;Acc:ZDB-GENE-0903	34	3e-03	3/116	MF	metalloe
• • •					•		35	3e-03	3/117	BP	Wnt sign
18	ENSDARG00	1.2	-2.51	0.88	si:ch211	-si69p2f10l.4169p10.1 [Source:ZFIN;Acc:ZDB-GENE-081104-	36	3e-03	2/34	BP	ephrin re
							37	3e-03	2/35	BP	cell proje
19	ENSDARG00	1.85	-2.51	0.88	tbx15	T-box 15 [Source:ZFIN;Acc:ZDB-GENE-020529-1]	38	4e-03	2/39	BP	skeletal
13			2.01	3.00	200.10	1	39	5e-03	4 / 268	CC	cytoskel
20	ENSDARG000	1 49	-2.48	0.67		pregnancy-associated plasma protein A, pappalysin 1a [Soul	40	5e-03	2 / 43	BP	DNA-ter
20	LINODAING001	1.40	-2.40	3.07		processing processing property and the total	40	33-00	2/40	DI	2.0. 101

1		1e-06	4 / 33	BP	hindbrain development
		1e-05	14 / 1484	MF	DNA binding
2 3 4 5 6 7	3	2e-05	3 / 21	BP	smoothened signaling pathway
4	ĺ	7e-05	3/32	BP	inner ear development
5	5	1e-04	4 / 104	BP	transmembrane receptor protein tyrosine kinase signaling pathway
6	3	2e-04	11 / 1239	BP	regulation of transcription, DNA-templated
ž	,	3e-04	2/10	BP	adenohypophysis development
8		3e-04	5 / 232	MF	protein heterodimerization activity
ğ)	4e-04	7 / 537	MF	sequence-specific DNA binding
1	0	4e-04	2/12	BP	determination of liver left/right asymmetry
1	1	5e-04	2 / 14	BP	inner ear morphogenesis
1	2	7e-04	3/70	CC	cell projection
1	3	7e-04	3 / 71	BP	signal transduction by protein phosphorylation
1	4	8e-04	2 / 17	MF	transmembrane receptor protein serine/threonine kinase activity
1	5	9e-04	16 / 2716	CC	nucleus
1	6	9e-04	3 / 76	BP	cartilage development
1	7	9e-04	3 / 76	CC	cilium
1	8	1e-03	3 / 78	BP	axon guidance
	9	1e-03	2 / 19	BP	positive regulation of BMP signaling pathway
	20	1e-03	2 / 20	BP	transmembrane receptor protein serine/threonine kinase signaling pat
	21	1e-03	2 / 21	BP	negative regulation of canonical Wnt signaling pathway
	22	1e-03	2 / 21	MF	signal transducer, downstream of receptor, with serine/threonine kinas
	23	1e-03	6 / 491	MF	kinase activity
	24	1e-03	2 / 23	MF	dynein light intermediate chain binding
	25	2e-03	3 / 91	BP	heart looping
	26	2e-03	6 / 522	BP	phosphorylation
	27	2e-03	8/914	MF	protein kinase activity
	28	2e-03	3 / 100	BP	peptidyl-tyrosine phosphorylation
	29	2e-03	2 / 29	BP	hematopoietic progenitor cell differentiation
	30	2e-03	8 / 947	BP	protein phosphorylation
	31	3e-03	2/30	BP	pigmentation
	32	3e-03	3 / 110	MF	protein tyrosine kinase activity
	33	3e-03	2/31	BP	pancreas development
	34	3e-03	3 / 116	MF	metalloendopeptidase activity
	35	3e-03	3 / 117	BP	Wnt signaling pathway
	<u>86</u>	3e-03	2/34	BP	ephrin receptor signaling pathway
	37	3e-03	2 / 35	BP	cell projection organization
	88	4e-03	2/39	BP	skeletal muscle fiber development
	39	5e-03	4 / 268	CC	cytoskeleton
4	10	5e-03	2 / 43	BP	DNA-templated transcription, initiation



BP				СС				MF			
Rank	p-value	#in/all	Geneset	Rank	p-value	#in/all	Geneset	Rank	p-value	#in/all	Geneset
1	1e-06	4 / 33	hindbrain development	1	7e-04	3/70	cell projection	1	1e-05	14 / 1484	DNA binding
2	2e-05	3 / 21	smoothened signaling pathway	2	9e-04	16 / 2716	nucleus	2	3e-04	5 / 232	protein heterodimerization activity
3	7e-05	3 / 32	inner ear development	3	9e-04	3/76	cilium	3	4e-04	7 / 537	sequence-specific DNA binding
4	1e-04	4 / 104	transmembrane receptor protein tyrosine kinase signaling pathway	4	5e-03	4 / 268	cytoskeleton	4	8e-04	2 / 17	transmembrane receptor protein serine/threonine kinase activity
5	2e-04	11 / 1239	regulation of transcription, DNA-templated	5	7e-03	2/49	microtubule organizing center	5	1e-03	2 / 21	signal transducer, downstream of receptor, with serine/threonine kinase activi
6	3e-04	2 / 10	adenohypophysis development	6	9e-03	3 / 168	nucleosome	6	1e-03	6 / 491	kinase activity
7	4e-04	2 / 12	determination of liver left/right asymmetry	7	2e-02	2/80	centrosome	7	1e-03	2 / 23	dynein light intermediate chain binding
8	5e-04	2 / 14	inner ear morphogenesis	8	2e-02	3 / 229	chromosome	8	2e-03	8 / 914	protein kinase activity
9	7e-04	3 / 71	signal transduction by protein phosphorylation	9	3e-02	1 / 13	adherens junction	9	3e-03	3 / 110	protein tyrosine kinase activity
10	9e-04	3 / 76	cartilage development	10	4e-02	1 / 16	midbody	10	3e-03	3 / 116	metalloendopeptidase activity
11	1e-03	3 / 78	axon guidance	11	5e-02	1 / 19	axon	11	7e-03	2 / 52	transmembrane receptor protein tyrosine kinase activity
12	1e-03	2 / 19	positive regulation of BMP signaling pathway	12	5e-02	5 / 809	integral component of plasma membrane	12	1e-02	10 / 1787	ATP binding
13	1e-03	2 / 20	transmembrane receptor protein serine/threonine kinase signaling pathway	13	5e-02	1/22	dynein complex	13	2e-02	1 / 10	ion channel binding
14	1e-03	2/21	negative regulation of canonical Wnt signaling pathway	14	6e-02	1 / 26	microtubule cytoskeleton	14	3e-02	1 / 13	ATP-dependent microtubule motor activity, minus-end-directed
15	2e-03	3/91	heart looping	15	7e-02	1/30	ciliary basal body	15	3e-02	1 / 14	enzyme activator activity

Spot Summary: f

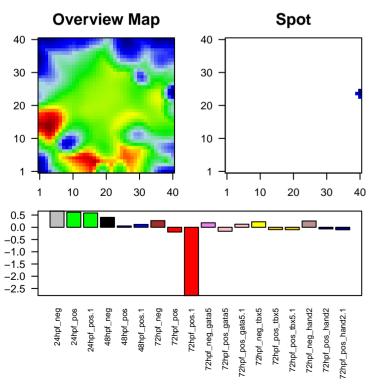
metagenes = 4

genes = 149

<r> metagenes = 0.99
<r> genes = 0.67
beta: r2= 5.43 / log p= -Inf

samples with spot = 1 (5.6 %)

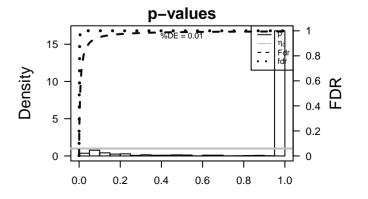
72hpf_pos: 1 (50 %)



Spot Genelist

Raı	Rank max e r ID min e		-	Symb	Description ool	Rank	p-value	#in/all	Ge	neset	
1	ENSDARG000	1.16	-5.89	0.87	rps26l	ribosomal protein S26, like [Source:ZFIN;Acc:ZDB-GENE-04	1	4e-07	10 / 229	CC	chromos
2	ENSDARG000	1.38	-5.67	0.95	zgc:112	234gc:112234 [Source:NCBI gene;Acc:554097]	2 3 4	3e-06 4e-06 3e-04	8 / 168 9 / 232 3 / 25	CC MF BP	protein h membra
3	ENSDARG000	1.71	-5.65	0.78		Nuclear RNase P [Source:RFAM;Acc:RF00009]	5 6	5e-04 5e-04	3/30 3/30	CC BP	ciliary ba
4	ENSDARG000	1.79	-4.69	0.92	si:dkey-	26/1dth@j6-261m9.6 [Source:ZFIN;Acc:ZDB-GENE-131127-10	7 8	8e-04 1e-03	3/34	BP BP	chromat protein k
5	ENSDARG000	1.84	-4.62	0.78	zc3h12b	zinc finger CCCH-type containing 12B [Source:ZFIN;Acc:ZDI	9 10	1e-03 2e-03	2/11	MF CC	diacylgly integral
6	ENSDARG000	1.04	-4.56	0.91	lsm12a	LSM12 homolog a [Source:ZFIN;Acc:ZDB-GENE-040516-1	11 12	2e-03 3e-03	3 / 49	CC BP	nuclear o
7	ENSDARG000	1.23	-4.5	0.86	pigs	phosphatidylinositol glycan anchor biosynthesis, class S [Sou	13 14	3e-03 5e-03	3 / 57 2 / 19	MF BP	mRNA b
8	ENSDARG000	1.8	-4.24	0.88	cd82b	CD82 molecule b [Source:ZFIN;Acc:ZDB-GENE-030131-28	15 16	5e-03 5e-03	2 / 20 2 / 20	MF MF	MAP kin NAD+ ki
9	ENSDARG000	1.12	-4.19	0.93	traf2a	Tnf receptor–associated factor 2a [Source:ZFIN;Acc:ZDB–GE	17 18	5e-03 7e-03	2 / 21 4 / 140	CC	axonem nucleolu
10	ENSDARG000	1.84	-4.19	0.6		Small nucleolar RNA SNORA53 [Source:RFAM;Acc:RF00565	19 20	7e-03 9e-03	2 / 24 24 / 2716	CC	cell-cell nucleus
11	ENSDARG000	1.51	-4.15	0.94	zgc:114	04gc:114046 [Source:ZFIN;Acc:ZDB-GENE-050320-24]	21 22	1e-02 1e-02	19 / 2030 2 / 31	MF BP	nucleic a autopha
12	ENSDARG000	0.87	-4.13	0.85	rwdd	RWD domain containing 4 [Source:ZFIN;Acc:ZDB-GENE-04	23 24	2e-02 2e-02	2 / 42 2 / 43	BP BP	determin DNA-ter
13	ENSDARG000	1.2	-4.1	0.92	dachc	dachshund c [Source:ZFIN;Acc:ZDB-GENE-020402-5]	25 26	3e-02 3e-02	14 / 1484 11 / 1066	MF CC	DNA bin intracellu
14	ENSDARG000	1.92	-4.01	0.92	zgc:163	Othicstone 1, H4, like [Source:ZFIN;Acc:ZDB-GENE-070927-10	27 28	3e-02 4e-02	3 / 128	BP BP	innate in
15	ENSDARG000	1.23	-4.01	0.96	cdc23	CDC23 (cell division cycle 23, yeast, homolog) [Source:ZFIN;	29 30 31	5e-02 5e-02	1/10	BP CC BP	activatio anaphas artery m
16	ENSDARG000	1.68	-3.95	0.82	egln2	egl-9 family hypoxia-inducible factor 2 [Source:ZFIN;Acc:ZDI	32 33	5e-02 5e-02 5e-02	1 / 10 1 / 10 1 / 10	CC BP	intracilia muscle o
17	ENSDARG000	1.49	-3.9	0.92	rab23	RAB23, member RAS oncogene family [Source:ZFIN;Acc:ZD	34 35	5e-02 5e-02	1/10	BP CC	protein (
18	ENSDARG000	0.88	-3.84	0.97	tmem18	3tansmembrane protein 183A [Source:ZFIN;Acc:ZDB-GENE-	36 37	5e-02 6e-02	2/70	BP MF	RNA pro
19	ENSDARG000	1.36	-3.83	0.94	wtip	WT1 interacting protein [Source:ZFIN;Acc:ZDB-GENE-0504	38 39	6e-02 6e-02	1/11	BP BP	establish fructose
20	ENSDARG000	1.37	-3.7	0.93	anapc2	anaphase promoting complex subunit 2 [Source:ZFIN;Acc:ZD	40	6e-02	1/11	BP	glutathio

1	4e-07	10 / 229	СС	chromosome
2	3e-06	8 / 168	CC	nucleosome
3	4e-06	9 / 232	MF	protein heterodimerization activity
4	3e-04	3 / 25	BP	membrane disruption in other organism
5	5e-04	3/30	CC	ciliary basal body
6	5e-04	3/30	BP	defense response to Gram–positive bacterium
Ž	8e-04	3 / 34	BP	chromatin silencing
8	1e-03	2/10	BP	protein kinase C-activating G-protein coupled receptor signaling pathway
9	1e-03	2/11	MF	diacylglycerol kinase activity
10	2e-03	3 / 47	CC	integral component of endoplasmic reticulum membrane
11	2e-03	3 / 49	CC	nuclear chromatin
12	3e-03	3 / 54	BP	MAPK cascade
13	3e-03	3 / 57	MF	mRNA binding
14	5e-03	2/19	BP	determination of left/right asymmetry in lateral mesoderm
15	5e-03	2/20	MF	MAP kinase activity
16	5e-03	2/20	MF	NAD+ kinase activity
17	5e-03	2/21	CC	axoneme
18	7e-03	4 / 140	CC	nucleolus
19	7e-03	2/24	CC	cell-cell junction
20	9e-03	24 / 2716	CC	nucleus
21	1e-02	19 / 2030	MF	nucleic acid binding
22	1e-02	2 / 31	BP	autophagosome assembly
23	2e-02	2 / 42	BP	determination of heart left/right asymmetry
24	2e-02	2 / 43	BP	DNA-templated transcription, initiation
25	3e-02	14 / 1484	MF	DNA binding
26	3e-02	11 / 1066	CC	intracellular
27	3e-02	3 / 128	BP	innate immune response
28	4e-02	3 / 138	BP	cilium assembly
29	5e-02	1 / 10	BP	activation of MAPK activity
30	5e-02	1 / 10	CC	anaphase-promoting complex
31	5e-02	1 / 10	BP	artery morphogenesis
32	5e-02	1 / 10	CC	intraciliary transport particle B
33	5e-02	1 / 10	BP	muscle cell development
34	5e-02	1 / 10	BP	protein O-linked mannosylation
35	5e-02	2/70	CC	cell projection
36	5e-02	2/70	BP	RNA processing
37	6e-02	1 / 11	MF	5'-nucleotidase activity
38	6e-02	1 / 11	BP	establishment of mitotic spindle orientation
39	6e-02	1 / 11	BP	fructose 6-phosphate metabolic process
40	6e-02	1 / 11	BP	glutathione metabolic process



ВР				CC				MF			
Rank	p-value	#in/all	Geneset	Rank	p-value	#in/all	Geneset	Rank	p-value	#in/all	Geneset
1	3e-04	3 / 25	membrane disruption in other organism	1	4e-07	10 / 229	chromosome	1	4e-06	9 / 232	protein heterodimerization activity
2	5e-04	3 / 30	defense response to Gram-positive bacterium	2	3e-06	8 / 168	nucleosome	2	1e-03	2/11	diacylglycerol kinase activity
3	8e-04	3 / 34	chromatin silencing	3	5e-04	3/30	ciliary basal body	3	3e-03	3 / 57	mRNA binding
4	1e-03	2/10	protein kinase C-activating G-protein coupled receptor signaling pathway	4	2e-03	3 / 47	integral component of endoplasmic reticulum membrane	4	5e-03	2/20	MAP kinase activity
5	3e-03	3 / 54	MAPK cascade	5	2e-03	3 / 49	nuclear chromatin	5	5e-03	2/20	NAD+ kinase activity
6	5e-03	2/19	determination of left/right asymmetry in lateral mesoderm	6	5e-03	2/21	axoneme	6	1e-02	19 / 2030	nucleic acid binding
7	1e-02	2/31	autophagosome assembly	7	7e-03	4 / 140	nucleolus	7	3e-02	14 / 1484	DNA binding
8	2e-02	2 / 42	determination of heart left/right asymmetry	8	7e-03	2/24	cell-cell junction	8	6e-02	1/11	5'-nucleotidase activity
9	2e-02	2/43	DNA-templated transcription, initiation	9	9e-03	24 / 2716	nucleus	9	6e-02	1 / 12	transcription factor activity, RNA polymerase II transcription factor recruiting
10	3e-02	3 / 128	innate immune response	10	3e-02	11 / 1066	intracellular	10	7e-02	1 / 13	SH3 domain binding
11	4e-02	3 / 138	cilium assembly	11	5e-02	1 / 10	anaphase–promoting complex	11	8e-02	1 / 15	alpha-(1->3)-fucosyltransferase activity
12	5e-02	1 / 10	activation of MAPK activity	12	5e-02	1 / 10	intraciliary transport particle B	12	8e-02	1 / 15	manganese ion binding
13	5e-02	1 / 10	artery morphogenesis	13	5e-02	2/70	cell projection	13	8e-02	12 / 1437	molecular_function
14	5e-02	1 / 10	muscle cell development	14	6e-02	2/76	cilium	14	9e-02	1 / 17	regulatory region DNA binding
15	5e-02	1 / 10	protein O-linked mannosylation	15	6e-02	1 / 12	pre-autophagosomal structure	15	1e-01	1 / 19	fucosyltransferase activity

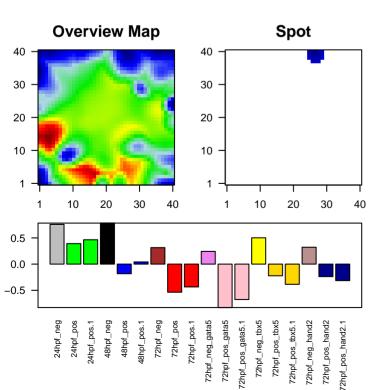
Spot Summary: g

metagenes = 18 # genes = 327

<r> metagenes = 0.97</r> <r> genes = 0.61

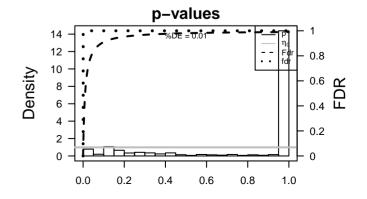
 beta: r2= 3.63 / log p= -Inf

samples with spot = 0 (0 %)



Spot Genelist

Rank ID		max	e min e	r ∋	Description Symbol	Rank	p-value	#in/all	Ger	neset	
	1	ENSDARG000	1.29	-3.05	0.62	LOC796000	1	3e-13	76 / 2716	СС	nucleus
							2	6e-11	59 / 2030	MF	nucleic acid binding
	2	ENSDARG000	1.04	-2.7	0.61	abcg2c ATP-binding cassette, sub-family G (WHITE), member 2c [S	3	9e-07	23 / 608	MF	RNA binding
	_						4	1e-06	6/30	MF	transcription cofactor activity
	3	ENSDARG000	1.69	-2.6	0.59	si:ch73-334d15.1 [Source:ZFIN;Acc:ZDB-GENE-091118-3	5	4e-06	34 / 1239 6 / 42	BP	regulation of transcription, DNA-templated histone binding
		=					6	9e-06 9e-06	5 / 25	MF MF	histone acetyltransferase activity
	4	ENSDARG000	1.64	-2.42	0.74	enpp5 ectonucleotide pyrophosphatase/phosphodiesterase 5 [Sourc	8	1e-05	5 / 27	BP	histone acetylation
	_	ENCDARCOO!	0.05	0.00	0.0	LOCADOSelfstanmodin like 2A [Source:HCNC Symbol: Apr;HCNC:2727	9	2e-05	4/14	BP	ATP-dependent chromatin remodeling
	5	ENSDARG000	0.95	-2.39	0.6	LOC10033/fa30 medin like 2A [Source:HGNC Symbol;Acc:HGNC:2727	10	3e-05	36 / 1484	MF	DNA binding
	6	ENCDARCOO!	0.89	-2.37	0.69	znf438 zinc finger protein 438 [Source:ZFIN;Acc:ZDB-GENE-06092	11	6e-05	8 / 115	MF	chromatin binding
	6	ENSDARG000	0.69	-2.31	0.09	ZNI438 Zinc iniger protein 436 [Source.21 IN,Acc.2DB-GENE-00052	12	9e-05	39 / 1761	MF	metal ion binding
	7	ENSDARG000	1 1 1	-2.33	0.81	fus FUS RNA binding protein [Source:ZFIN;Acc:ZDB-GENE-040	13	2e-04	4/24	BP	histone lysine methylation
	′	ENSDARGOO	1.14	-2.33	0.61	lus 1 00 KNA billuling protein [Source.21 IN,Acc.200=GENE=04K	14	4e-04	4 / 30	BP	chromatin remodeling
	8	ENSDARG000	0.7	-2.32	0.63	adnp2a ADNP homeobox 2a [Source:ZFIN;Acc:ZDB-GENE-040914-	15	4e-04	4 / 31	MF	histone-lysine N-methyltransferase activity
	O	LINSDARGOON	0.7	-2.52	0.03	adilp2d 7/D14 Hollicobox 2d [Godice:21 H4,760:2DD-GE14E-040514	16	5e-04	21 / 800	MF	zinc ion binding
	9	ENSDARG000	1.09	-2.32	0.52	sall3a spalt-like transcription factor 3a [Source:ZFIN;Acc:ZDB-GEN	17	1e-03	5 / 65	MF	transcription coactivator activity
	3	LINSDARGOON	1.00	-2.02	0.02	Salida spark into danostipadri dator da (obaros.E.) 117, 166.E.B.B. GEN	18	1e-03	7 / 135	MF	methyltransferase activity
	10	ENSDARG000	1 29	-2.26	0.52	fam117bbfamily with sequence similarity 117, member Bb [Source:ZFIN	19	1e-03	4 / 39	MF	protein serine/threonine phosphatase activity
	10	2110271110001	1.20	2.20	0.02		20	2e-03	7 / 144	BP	methylation
	11	ENSDARG000	1.21	-2.2	0.81	tmtc2a transmembrane and tetratricopeptide repeat containing 2a [S	21	2e-03	4 / 43	BP	DNA-templated transcription, initiation
	٠.					3 - 1-	22	2e-03	3 / 21	CC	nuclear membrane
	12	ENSDARG000	1.39	-2.11	0.74	marcksa myristoylated alanine-rich protein kinase C substrate a [Sour	23	2e-03	8 / 193	BP	positive regulation of transcription from RNA polymerase II promote
	12	2110271110001	1.00		0	maiolog ,, , ,	24	3e-03	3 / 25	BP	regulation of nucleic acid-templated transcription
	13	ENSDARG000	1.62	-2.05	0.59	zgc:158689 [Source:ZFIN;Acc:ZDB-GENE-070112-1902]	25	3e-03	23 / 1063	MF	transferase activity
	10					3 , , , , , ,	26	6e-03	6 / 138	BP	cilium assembly
	14	ENSDARG00	1.35	-2.04	0.86	usp49 ubiquitin specific peptidase 49 [Source:ZFIN;Acc:ZDB-GENE	27	7e-03	4 / 65	MF	RNA polymerase II regulatory region sequence–specific DNA bindi
	• •						28	8e-03 8e-03	2/12	BP CC	left/right pattern formation transcription factor TFIID complex
	15	ENSDARG000	0.99	-2.02	0.6	alx4a ALX homeobox 4a [Source:ZFIN;Acc:ZDB-GENE-070712-3	29 30	9e-03	4/70	CC	cell projection
							31	1e-02	2/13	BP	erythrocyte maturation
	16	ENSDARG000	1.2	-2	0.83	si:ch73-2si10e17.3-211e3.1 [Source:ZFIN;Acc:ZDB-GENE-160728-51]	32	1e-02	2/13	MF	p53 binding
							33	1e-02	2/13	MF	signal transducer activity, downstream of receptor
	17	ENSDARG000	0.9	-1.99	0.59	si:dkey-18i1qilk@6-121j17.6 [Source:ZFIN;Acc:ZDB-GENE-121214-36	34	1e-02	4 / 72	MF	helicase activity
							35	1e-02	2/14	BP	RNA polymerase II transcriptional preinitiation complex assembly
	18	ENSDARG000	0.95	-1.98	0.51		36	1e-02	2 / 15	BP	dorsal convergence
							37	1e-02	2 / 15	CC	histone acetyltransferase complex
	19	ENSDARG000	0.99	-1.98	0.78	round spermatid basic protein 1 [Source:HGNC Symbol;Acc:l	38	1e-02	3 / 43	BP	canonical Wnt signaling pathway
	-						39	1e-02	2/16	BP	negative regulation of translation
	20	ENSDARG000	1.25	-1.96	0.65	PAP associated domain containing 7 [Source:ZFIN;Acc:ZDB-	40	2e-02	2/17	MF	protein phosphatase inhibitor activity



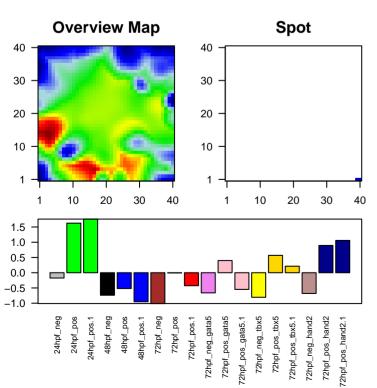
BP				CC				MF			
Rank	p-value	#in/all	Geneset	Rank	p-value	#in/all	Geneset	Rank	p-value	#in/all	Geneset
1	4e-06	34 / 1239	regulation of transcription, DNA-templated	1	3e-13	76 / 2716	nucleus	1	6e-11	59 / 2030	nucleic acid binding
2	1e-05	5 / 27	histone acetylation	2	2e-03	3/21	nuclear membrane	2	9e-07	23 / 608	RNA binding
3	2e-05	4 / 14	ATP-dependent chromatin remodeling	3	8e-03	2/12	transcription factor TFIID complex	3	1e-06	6/30	transcription cofactor activity
4	2e-04	4 / 24	histone lysine methylation	4	9e-03	4 / 70	cell projection	4	9e-06	6 / 42	histone binding
5	4e-04	4 / 30	chromatin remodeling	5	1e-02	2/15	histone acetyltransferase complex	5	9e-06	5 / 25	histone acetyltransferase activity
6	2e-03	7 / 144	methylation	6	2e-02	2/19	axon	6	3e-05	36 / 1484	DNA binding
7	2e-03	4 / 43	DNA-templated transcription, initiation	7	6e-02	3/76	cilium	7	6e-05	8 / 115	chromatin binding
8	2e-03	8 / 193	positive regulation of transcription from RNA polymerase II promoter	8	7e-02	2/36	P-body	8	9e-05	39 / 1761	metal ion binding
9	3e-03	3 / 25	regulation of nucleic acid-templated transcription	9	1e-01	1/10	chaperonin-containing T-complex	9	4e-04	4/31	histone–lysine N–methyltransferase activity
10	6e-03	6 / 138	cilium assembly	10	1e-01	2/51	lysosomal membrane	10	5e-04	21 / 800	zinc ion binding
11	8e-03	2/12	left/right pattern formation	11	1e-01	1/11	clathrin-coated pit	11	1e-03	5 / 65	transcription coactivator activity
12	1e-02	2/13	erythrocyte maturation	12	1e-01	1/11	commitment complex	12	1e-03	7 / 135	methyltransferase activity
13	1e-02	2/14	RNA polymerase II transcriptional preinitiation complex assembly	13	1e-01	5 / 229	chromosome	13	1e-03	4/39	protein serine/threonine phosphatase activity
14	1e-02	2/15	dorsal convergence	14	1e-01	1/12	histone deacetylase complex	14	3e-03	23 / 1063	transferase activity
15	1e-02	3 / 43	canonical Wnt signaling pathway	15	1e-01	1/12	lamellipodium	15	7e-03	4 / 65	RNA polymerase II regulatory region sequence–specific DNA binding

Spot Summary: h

metagenes = 2 # genes = 117

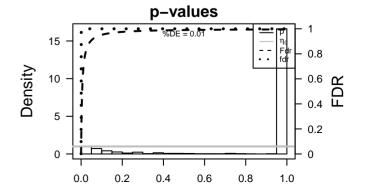
<r> metagenes = 1 <r> genes = 0.66 beta: r2= 8.08 / log p= -Inf

samples with spot = 0 (0 %)



Spot Genelist

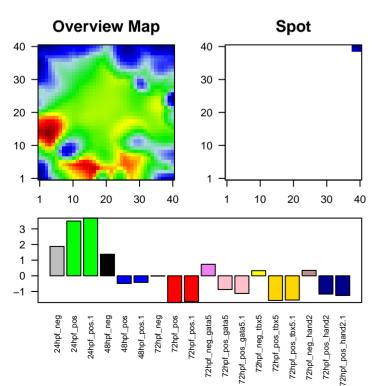
Rank ID		max	e min	r e	Sym	Description bol	Rank	p-value	#in/all	Ge	neset
1	ENSDARG000	3.07	-4.2	0.8	f5	coagulation factor V [Source:ZFIN;Acc:ZDB-GENE-030131-	1	5e-07	11 / 375	BP	positive regulation of GTPase activity
							2	1e-06	11 / 413	BP	intracellular signal transduction
2	ENSDARG000	3.47	-3.88	0.79	il6r	interleukin 6 receptor [Source:ZFIN;Acc:ZDB-GENE-080107	3	2e-05	4 / 38	BP	integrin-mediated signaling pathway
							4	4e-05	7 / 217	MF	GTPase activator activity
3	ENSDARG000	2.53	-3.71	0.83	glipr2	GLI pathogenesis-related 2 [Source:ZFIN;Acc:ZDB-GENE-(5	9e-05	16 / 1295	BP	signal transduction
							6	5e-04	42 / 6248	CC	integral component of membrane
4	ENSDARG000	2.14	-3.6	0.88	ncf1	neutrophil cytosolic factor 1 [Source:ZFIN;Acc:ZDB-GENE-0	7	6e-04	44 / 6723	CC	membrane
							8	8e-04	2/10	MF	GDP-dissociation inhibitor activity
5	ENSDARG000	1.78	-3.54	0.69		RAB11 family interacting protein 1 (class I) b [Source:ZFIN;Ar	9	8e-04	2/10	MF	GTPase regulator activity
							10	9e-04	2/11	BP	spindle organization
6	ENSDARG000	3.75	-3.16	0.77	dnase1	14.deoxyribonuclease 1 like 4, tandem duplicate 1 [Source:ZFIN	11	1e-03	3 / 49	MF	non-membrane spanning protein tyrosine kinase activity
							12	1e-03	2/13	BP	germ cell migration
7	ENSDARG000	3.53	-3.11	0.81	ikzf1	IKAROS family zinc finger 1 (Ikaros) [Source:ZFIN;Acc:ZDB-	13	1e-03	2/13	MF	signal transducer activity, downstream of receptor
							14	2e-03	3 / 58	BP	chemokine-mediated signaling pathway
8	ENSDARG000	2.9	-3.03	0.89	btk	Bruton agammaglobulinemia tyrosine kinase [Source:ZFIN;Ac	15	4e-03	2 / 23	MF	CCR chemokine receptor binding
							16	4e-03	2 / 23	BP	cellular response to interferon–gamma
9	ENSDARG000	1.8	-3	0.48	slc20a1	a solute carrier family 20, member 1a [Source:ZFIN;Acc:ZDB-C	17	4e-03	2/23	BP	lymphocyte chemotaxis
							18	4e-03	2 / 23	BP	monocyte chemotaxis
10	ENSDARG000	4.13	-2.81	0.87	mrc1a	mannose receptor, C type 1a [Source:ZFIN;Acc:ZDB-GENE-	19	4e-03	2/24	BP	cellular response to interleukin–1
							20	4e-03	2/24	BP	cellular response to tumor necrosis factor
11	ENSDARG000	2.96	-2.8	0.84	zgc:101	16@gc:101663 [Source:ZFIN;Acc:ZDB-GENE-041114-149]	21	6e-03	2/29	CC	integrin complex
							22	7e-03	3/91	BP	heart looping
12	ENSDARG000	1.84	-2.78	0.65	si:ch21	1-2/70862/31.5276a23.5 [Source:ZFIN;Acc:ZDB-GENE-141215-4	23	7e-03	4 / 178	MF	iron ion binding
							24	8e-03	3/96	MF	Rho guanyl-nucleotide exchange factor activity
13	ENSDARG000	2.53	-2.78	0.82	si:cabz(018774814601074946.1 [Source:ZFIN;Acc:ZDB-GENE-160113-1	25	8e-03	2/33	BP	positive regulation of ERK1 and ERK2 cascade
. •						•	26	8e-03	3 / 100	BP	peptidyl-tyrosine phosphorylation regulation of Rho protein signal transduction
14	ENSDARG00	3,44	-2.62	0.78			27 28	8e-03 9e-03	3 / 100 2 / 34	BP BP	fatty acid biosynthetic process
							26 29	9e-03 9e-03	4/194	BP	lipid metabolic process
15	ENSDARG000	3.13	-2.54	0.7	scarf1	scavenger receptor class F, member 1 [Source:ZFIN;Acc:ZDE	30	1e-02	8/712	BP	oxidation-reduction process
							31	1e-02 1e-02	3/110	MF	oxidoreductase activity, acting on paired donors, with incorporation or r
16	ENSDARG000	3.1	-2.52	0.93	si:ch73-	-2s/8s/2737248e21.7 [Source:ZFIN;Acc:ZDB-GENE-120215-2;	32	1e-02 1e-02	3/110	MF	protein tyrosine kinase activity
						•	33	1e-02 1e-02	2/39	BP	neutrophil chemotaxis
17	ENSDARG00	3.08	-2.4	0.77	fam117	alfamily with sequence similarity 117, member Ab [Source:ZFIN	34	1e-02 1e-02	2/41	BP	peptidyl–tyrosine autophosphorylation
• • •							35	1e-02 1e-02	2/43	CC	extrinsic component of cytoplasmic side of plasma membrane
18	ENSDARG000	1.58	-2.37	0.79	si:cabz(0183840201036022.1 [Source:ZFIN;Acc:ZDB-GENE-160113-1	36	1e-02 1e-02	2/43	BP	fatty acid metabolic process
10	2110271110001	1.00	2.01	00	OI.OUDE		37	1e-02 1e-02	3 / 122	BP	inflammatory response
19	ENSDARG000	1.42	-2.36	0.78	elovl5	ELOVL fatty acid elongase 5 [Source:ZFIN;Acc:ZDB-GENE-	38	2e-02	2/47	MF	chemokine activity
13			2.00	00	0.01.0	,	39	2e-02 2e-02	3 / 128	BP	innate immune response
20	ENSDARG000	1.86	-2.3	0.84	ltb4r	leukotriene B4 receptor [Source:ZFIN;Acc:ZDB-GENE-0707	40	2e-02 2e-02	2/50	BP	lipid catabolic process
20	2.102/110001			0.0.	100-11	Control of the contro	70		2,00	Di	1



BP				СС				MF			
Rank	p-value	#in/all	Geneset	Rank	p-value	#in/all	Geneset	Rank	p-value	#in/all	Geneset
1	5e-07	11 / 375	positive regulation of GTPase activity	1	5e-04	42 / 6248	integral component of membrane	1	4e-05	7 / 217	GTPase activator activity
2	1e-06	11 / 413	intracellular signal transduction	2	6e-04	44 / 6723	membrane	2	8e-04	2/10	GDP-dissociation inhibitor activity
3	2e-05	4 / 38	integrin-mediated signaling pathway	3	6e-03	2 / 29	integrin complex	3	8e-04	2 / 10	GTPase regulator activity
4	9e-05	16 / 1295	signal transduction	4	1e-02	2 / 43	extrinsic component of cytoplasmic side of plasma membrane	4	1e-03	3 / 49	non-membrane spanning protein tyrosine kinase activity
5	9e-04	2/11	spindle organization	5	3e-02	9 / 1066	intracellular	5	1e-03	2/13	signal transducer activity, downstream of receptor
6	1e-03	2/13	germ cell migration	6	4e-02	4/317	Golgi apparatus	6	4e-03	2 / 23	CCR chemokine receptor binding
7	2e-03	3 / 58	chemokine-mediated signaling pathway	7	5e-02	3 / 198	Golgi membrane	7	7e-03	4 / 178	iron ion binding
8	4e-03	2 / 23	cellular response to interferon–gamma	8	6e-02	1 / 15	intrinsic component of the cytoplasmic side of the plasma membrane	8	8e-03	3 / 96	Rho guanyl-nucleotide exchange factor activity
9	4e-03	2/23	lymphocyte chemotaxis	9	8e-02	1 / 20	exocyst	9	1e-02	3/110	oxidoreductase activity, acting on paired donors, with incorporation or reduction
10	4e-03	2/23	monocyte chemotaxis	10	8e-02	1/21	dendrite	10	1e-02	3/110	protein tyrosine kinase activity
11	4e-03	2 / 24	cellular response to interleukin-1	11	1e-01	1/27	guanylate cyclase complex, soluble	11	2e-02	2 / 47	chemokine activity
12	4e-03	2/24	cellular response to tumor necrosis factor	12	1e-01	1/27	integral component of Golgi membrane	12	2e-02	2 / 54	transferase activity, transferring hexosyl groups
13	7e-03	3/91	heart looping	13	2e-01	4 / 500	extracellular space	13	2e-02	3 / 145	heme binding
14	8e-03	2/33	positive regulation of ERK1 and ERK2 cascade	14	2e-01	1 / 47	integral component of endoplasmic reticulum membrane	14	3e-02	2 / 60	scavenger receptor activity
15	8e-03	3 / 100	peptidyl-tyrosine phosphorylation	15	2e-01	2 / 209	endoplasmic reticulum membrane	15	3e-02	3 / 158	microtubule binding

Spot Summary: i

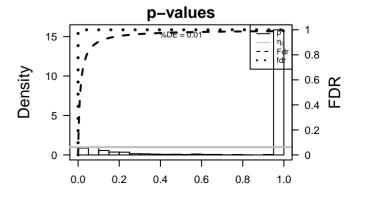
metagenes = 6 # genes = 134 <r> metagenes = 1 <r> genes = 0.73 beta: r2= 28.11 / log p= -Inf # samples with spot = 4 (22.2 %) 72hpf_pos : 2 (100 %)



Spot Genelist

Rar	nk ID	max	e min e	r e	Symb	Description ool	Rank	p-value	#in/all	Ger	neset
1	ENSDARG000	8.12	-6.4	0.89	hbbe3	hemoglobin beta embryonic-3 [Source:ZFIN;Acc:ZDB-GENE	1	4e-21	10 / 14	СС	hemoglo
2	ENSDARG000	4.82	-5.94	0.9	nmt1b	N-myristoyltransferase 1b [Source:ZFIN;Acc:ZDB-GENE-08	2 3 4	4e-19 4e-19 4e-19	10 / 19 10 / 19 10 / 19	MF BP MF	oxygen to oxygen to
3	ENSDARG000	3.63	-5.74	0.8	cxcl12b	chemokine (C-X-C motif) ligand 12b (stromal cell-derived fa	5	5e-17 2e-13	10 / 19	BP BP	embryon
4	ENSDARG000	7.06	-5.06	0.95	si:dkey-	26/1/14/89-2611/4.3 [Source:ZFIN;Acc:ZDB-GENE-060531-124]	7 8	2e-13 2e-13 6e-11	13 / 145 12 / 178	MF MF	heme bir
5	ENSDARG000	5.26	-4.98	0.9	tubb1	tubulin, beta 1 class VI [Source:ZFIN;Acc:ZDB-GENE-11040	9 10	1e-09 5e-09	6 / 24 7 / 52	BP BP	myeloid blood ve
6	ENSDARG000	5.39	-4.85	0.92	hdr	hematopoietic death receptor [Source:ZFIN;Acc:ZDB-GENE-	11 12	6e-07 8e-07	4/15 9/210	BP MF	heme bid
7	ENSDARG000	4.79	-4.79	0.92	slc4a1a	solute carrier family 4 (anion exchanger), member 1a (Diego I	13 14	2e-06 3e-06	6/75 4/21	BP BP	hemopoi
8	ENSDARG000	6.46	-4.6	0.75		protogenin homolog b (Gallus gallus) [Source:ZFIN;Acc:ZDB-	15 16	3e-06 1e-05	24 / 1761 11 / 454	MF BP	metal ior
9	ENSDARG000	2.43	-4.56	0.69	meis3	myeloid ecotropic viral integration site 3 [Source:ZFIN;Acc:ZC	17 18	2e-05 3e-05	3 / 12 4 / 38	BP BP	hemoglo vasculog
10	ENSDARG000	7.36	-4.55	0.95	si:dkey-	-26/1ず株ely-261j4.4 [Source:ZFIN;Acc:ZDB-GENE-060531-125]	19 20	6e-05 1e-04	16 / 1084 4 / 50	BP BP	transpor
11	ENSDARG000	3.58	-4.55	0.79	hif1al2	hypoxia-inducible factor 1, alpha subunit, like 2 [Source:ZFIN	21 22	3e-04 7e-04	10 / 537 3 / 37	MF BP	sequenc definitive
12	ENSDARG000	3.84	-4.5	0.83	mllt3	myeloid/lymphoid or mixed-lineage leukemia (trithorax homol	23 24	9e-04 1e-03	15 / 1239 3 / 47	BP MF	regulatio structura
13	ENSDARG000	7.83	-4.49	0.96	drl	draculin [Source:ZFIN;Acc:ZDB-GENE-991213-3]	25 26	2e-03 2e-03	2 / 13 2 / 13	BP BP	gastrulat semiciro
14	ENSDARG000	2.88	-4.44	0.79	glcci1	glucocorticoid induced 1 [Source:ZFIN;Acc:ZDB-GENE-031	27 28	2e-03 2e-03	5 / 183 4 / 116	MF MF	RNA pol metalloe
15	ENSDARG000	3.63	-4.42	0.85	egfl7	EGF-like-domain, multiple 7 [Source:ZFIN;Acc:ZDB-GENE-	29 30	3e-03 3e-03	2 / 16 2 / 16	BP BP	defense vascular
16	ENSDARG000	4.72	-4.38	0.89	epor	erythropoietin receptor [Source:ZFIN;Acc:ZDB-GENE-07111	31 32	3e-03 4e-03	2/18 2/19	BP BP	neutroph embryon
17	ENSDARG000	2.81	-4.37	0.75	gdf6a	growth differentiation factor 6a [Source:ZFIN;Acc:ZDB-GENE	33 34	4e-03 4e-03	2 / 19 2 / 20	BP BP	neuron r
18	ENSDARG000	3.2	-4.37	0.82	nt5c2l1	5'-nucleotidase, cytosolic II, like 1 [Source:ZFIN;Acc:ZDB-GI	35 36	5e-03 6e-03	2 / 23 2 / 24	MF BP	hyaluron
19	ENSDARG000	4.05	-4.36	0.78	LOC100	0537032	37 38	7e-03 9e-03	4 / 160 3 / 90	BP BP	positive
20	ENSDARG000	5.21	-4.29	0.89	rfesd	Rieske (Fe-S) domain containing [Source:ZFIN;Acc:ZDB-GE	39 40	1e-02 1e-02	2/32 2/33	BP BP	retinal ga blood ve

	4: 04	40/44	00	hamadahir samalay
1	4e-21	10 / 14	CC MF	hemoglobin complex oxygen binding
2	4e-19	10 / 19		, ,
3	4e-19	10 / 19	BP	oxygen transporter activity
4	4e-19	10 / 19	MF	oxygen transporter activity
5	5e-17	10 / 28	BP	embryonic hemopolesis
6	2e-13	9 / 40	BP	erythrocyte differentiation
7	2e-13	13 / 145	MF	heme binding
8	6e-11	12 / 178	MF	iron ion binding
9	1e-09	6 / 24	BP	myeloid cell differentiation
10	5e-09	7 / 52	BP	blood vessel development
11	6e-07	4 / 15	BP	heme biosynthetic process
12	8e-07	9/210	MF	protein binding
13	2e-06	6 / 75	BP	hemopoiesis
14	3e-06	4 / 21	BP	erythrocyte development
15	3e-06	24 / 1761	MF	metal ion binding
16	1e-05	11 / 454	BP	multicellular organism development
17	2e-05	3 / 12	BP	hemoglobin biosynthetic process
18	3e-05	4 / 38	BP	vasculogenesis
19	6e-05	16 / 1084	BP	transport
20	1e-04	4 / 50	BP	vasculature development
21	3e-04	10 / 537	MF	sequence-specific DNA binding
22	7e-04	3 / 37	BP	definitive hemopoiesis
23	9e-04	15 / 1239	BP	regulation of transcription, DNA-templated
24	1e-03	3 / 47	MF	structural constituent of cytoskeleton
25	2e-03	2 / 13	BP	gastrulation with mouth forming second
26	2e-03	2 / 13	BP	semicircular canal morphogenesis
27	2e-03	5 / 183	MF	RNA polymerase II transcription factor activity, sequence-specific DNA bind
28	2e-03	4 / 116	MF	metalloendopeptidase activity
29	3e-03	2/16	BP	defense response
30	3e-03	2/16	BP	vascular endothelial growth factor receptor signaling pathway
31	3e-03	2/18	BP	neutrophil differentiation
32	4e-03	2/19	BP	embryonic heart tube morphogenesis
33	4e-03	2/19	BP	neuron migration
34	4e-03	2/20	BP	positive regulation of gene expression
35	5e-03	2/23	MF	hyaluronic acid binding
36	6e-03	2/24	BP	primitive hemopoiesis
37	7e-03	4 / 160	BP	heart development
38	9e-03	3 / 90	BP	positive regulation of transcription, DNA-templated
39	1e-02	2/32	BP	retinal ganglion cell axon guidance
40	1e-02	2/33	BP	blood vessel morphogenesis
				, , , , , , , , , , , , , , , , , , ,



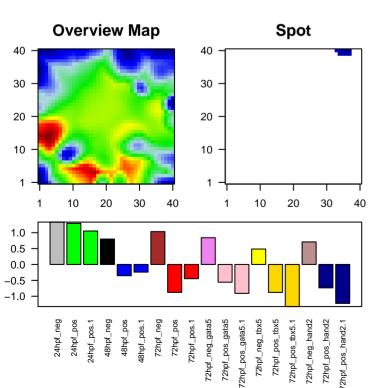
BP				СС				MF			
Rank	p-value	#in/all	Geneset	Rank	p-value	#in/all	Geneset	Rank	p-value	#in/all	Geneset
1	4e-19	10 / 19	oxygen transport	1	4e-21	10 / 14	hemoglobin complex	1	4e-19	10 / 19	oxygen binding
2	5e-17	10 / 28	embryonic hemopoiesis	2	2e-02	2/51	lysosomal membrane	2	4e-19	10 / 19	oxygen transporter activity
3	2e-13	9 / 40	erythrocyte differentiation	3	4e-02	4 / 268	cytoskeleton	3	2e-13	13 / 145	heme binding
4	1e-09	6 / 24	myeloid cell differentiation	4	4e-02	3 / 161	mitochondrial inner membrane	4	6e-11	12 / 178	iron ion binding
5	5e-09	7 / 52	blood vessel development	5	5e-02	1/11	exocytic vesicle	5	8e-07	9 / 210	protein binding
6	6e-07	4/15	heme biosynthetic process	6	6e-02	19 / 2716	nucleus	6	3e-06	24 / 1761	metal ion binding
7	2e-06	6 / 75	hemopoiesis	7	8e-02	1 / 17	external side of plasma membrane	7	3e-04	10 / 537	sequence–specific DNA binding
8	3e-06	4/21	erythrocyte development	8	8e-02	1 / 17	integral component of nuclear inner membrane	8	1e-03	3 / 47	structural constituent of cytoskeleton
9	1e-05	11 / 454	multicellular organism development	9	8e-02	2 / 101	endosome	9	2e-03	5 / 183	RNA polymerase II transcription factor activity, sequence–specific DNA bindin
10	2e-05	3 / 12	hemoglobin biosynthetic process	10	9e-02	7 / 809	integral component of plasma membrane	10	2e-03	4 / 116	metalloendopeptidase activity
11	3e-05	4 / 38	vasculogenesis	11	1e-01	1/22	dynein complex	11	5e-03	2 / 23	hyaluronic acid binding
12	6e-05	16 / 1084	transport	12	1e-01	1 / 24	early endosome	12	1e-02	8 / 633	transcription factor activity, sequence–specific DNA binding
13	1e-04	4 / 50	vasculature development	13	1e-01	1 / 26	vesicle	13	1e-02	9 / 800	zinc ion binding
14	7e-04	3 / 37	definitive hemopolesis	14	1e-01	36 / 6248	integral component of membrane	14	2e-02	3 / 115	chromatin binding
15	9e-04	15 / 1239	regulation of transcription, DNA-templated	15	1e-01	1/32	chromatin	15	2e-02	8 / 717	calcium ion binding

Spot Summary: j

metagenes = 9 # genes = 190

<r> metagenes = 0.98 <r> genes = 0.72 beta: r2= 12.14 / log p= -Inf

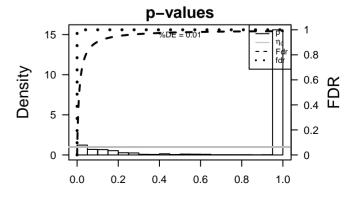
samples with spot = 1 (5.6 %)



Spot Genelist

ot Ge	enelist		Geneset Overrepresentation					
)	max e r min e	Description Symbol	Rank	p-value	#in/all	Geneset		
ICDA BC004	202 477 057	sin-boar dighter 2645 6 (Source: 75IN) Apri 7DD CENIE 091104 20		4- 45	27 / 400	00		

Rank ID		max e mi		r min e		Description Symbol		p-value	#in/all	Ge	neset
1	ENSDARG000	2.02	-4.77	0.57	si:ch211-	-នាងវង់ខេ -264f5.6 [Source:ZFIN;Acc:ZDB-GENE-081104	•	1e-45	37 / 168	СС	nucleosome
_	=					DALEDA	2	3e-40	37 / 229	CC	chromosome
2	ENSDARG000	2.19	-4.71	0.8	reps2	RALBP1 associated Eps domain containing 2 [Source:ZF	N;≜ 3 4	5e-40 1e-35	37 / 232 28 / 117	MF BP	protein heterodimerization activity nucleosome assembly
2	FNODADOGG	4.50	4.40	0.04		unc-5 netrin receptor B [Source:ZFIN;Acc:ZDB-GENE-0		9e-28	17/37	MF	nucleosomal DNA binding
3	ENSDARG000	1.53	-4.19	0.81	unc5b	unc-3 netriii receptor B [Source.ZFIN,Acc.ZDB-GENE-0	6	6e-26	55 / 1484	MF	DNA binding
1	ENSDARG000	2.16	-4.13	0.72	plch1	phospholipase C, eta 1 [Source:ZFIN;Acc:ZDB-GENE-06		8e-20	64 / 2716	CC	nucleus
4	ENSDARGOO	2.10	-4.13	0.72	piciri	phospholipase C, eta 1 [Gource.Zr IIV,Acc.ZDB=GEIVE=00	8	1e-12	9/34	BP	ephrin receptor signaling pathway
5	ENSDARG000	2.8	-4.02	0.77	cann12	calpain 12 [Source:ZFIN;Acc:ZDB-GENE-050419-245]	9	8e-11	11 / 100	BP	peptidyl-tyrosine phosphorylation
5	LINSDANGOO	2.0	-4.02	0.77	capiniz	Calpain 12 [Oodioc.21 IN,7100.200-OE112-000413-240]	10	2e-10	11 / 110	MF	protein tyrosine kinase activity
6	ENSDARG000	2 24	-3.74	0.79	emilin2h	elastin microfibril interfacer 2b [Source:ZFIN;Acc:ZDB-GE	4 4	2e-09	6/19	MF	ephrin receptor activity
O	LINODAIRCOOK	2.27	0	0.70	CITIIIIIIZD		12	2e-08	21 / 717	MF	calcium ion binding
7	ENSDARG000	1 95	-3.56	0.74	dendc1a	a DEP domain containing 1a [Source:ZFIN;Acc:ZDB-GENE	_{-0:} 13	9e-08	16 / 454	BP	multicellular organism development
,	2110271110001	1.00	0.00	0			14	6e-07	8 / 104	BP	transmembrane receptor protein tyrosine kinase signaling pathway
8	ENSDARG00	2.03	-3.47	0.8	tmem108	8transmembrane protein 108 [Source:ZFIN;Acc:ZDB-GEN	_{≣–(} 15	1e-06	6 / 52	BP	blood vessel development
O							16	3e-06	4 / 15	CC	basement membrane
9	ENSDARG00	1.71	-3.35	0.63	adamts6	ADAM metallopeptidase with thrombospondin type 1 moti	_{.6} 17	8e-06	5 / 41	BP	positive regulation of cell proliferation
J	2.102/110001				adamioo	71	18	2e-05	7 / 117	BP	Wnt signaling pathway
10	ENSDARG00	1.77	-3.26	0.71	isl2a	ISL LIM homeobox 2a [Source:ZFIN;Acc:ZDB-GENE-98	19	3e-05	5 / 52	MF	transmembrane receptor protein tyrosine kinase activity
10				***		, , , , , , , , , , , , , , , , , , , ,	20	4e-05	3 / 10	BP	adenohypophysis development
11	ENSDARG00	1.83	-3.24	0.87	bnc1	basonuclin 1 [Source:HGNC Symbol;Acc:HGNC:1081]	21	1e-04	4 / 38	BP	vasculogenesis
						, , , , , , , , , , , , , , , , , , , ,	22	1e-04	3 / 15	MF	ephrin receptor binding
12	ENSDARG00	2.38	-3.2	0.78	nr2f1b	nuclear receptor subfamily 2, group F, member 1b [Source	:ZF 23	1e-04	12 / 491	MF	kinase activity
12							24	2e-04	5/78	BP	axon guidance
13	ENSDARG00	1.55	-3.08	0.83	trabd2a	TraB domain containing 2A [Source:ZFIN;Acc:ZDB-GENE	25	2e-04	12 / 522	BP	phosphorylation
.0						• • •	20	3e-04	3/19	BP BP	non-canonical Wnt signaling pathway regulation of transcription, DNA-templated
14	ENSDARG00	1.79	-3.05	0.8		collagen type VII alpha 1-like [Source:ZFIN;Acc:ZDB-GE	NE: 27 28	3e-04	20 / 1239 13 / 634	CC	extracellular region
							26 29	4e-04 4e-04	15 / 809	CC	integral component of plasma membrane
15	ENSDARG000	1.55	-3.05	0.89	ephb4a	eph receptor B4a [Source:ZFIN;Acc:ZDB-GENE-990415	-62 30	5e-04	3 / 23	MF	Wnt-activated receptor activity
							31	7e-04	3 / 26	MF	Wnt-protein binding
16	ENSDARG000	2.69	-3.04	0.73	hbbe2	hemoglobin beta embryonic-2 [Source:ZFIN;Acc:ZDB-G		1e-03	11 / 537	MF	sequence–specific DNA binding
_							33	1e-03	12 / 633	MF	transcription factor activity, sequence–specific DNA binding
17	ENSDARG000	1.48	-3.03	0.88		signal peptide, CUB domain, EGF-like 3 [Source:ZFIN;Ac	c:Z 34	1e-03	3 / 33	BP	blood vessel morphogenesis
							35	2e-03	3 / 36	BP	fibroblast growth factor receptor signaling pathway
18	ENSDARG000	1.87	-2.92	0.73	foxf1	forkhead box F1 [Source:ZFIN;Acc:ZDB-GENE-050419-		2e-03	5 / 130	MF	growth factor activity
							37	2e-03	2/10	BP	muscle cell development
19	ENSDARG000	1.47	-2.87	0.85	fgfr1b	fibroblast growth factor receptor 1b [Source:ZFIN;Acc:ZDI	⊢G 38	2e-03	8 / 333	BP	cell adhesion
								2e-03	10 / 500	CC	extracellular space
20	ENSDARG000	2.35	-2.81	0.71	esama	endothelial cell adhesion molecule a [Source:ZFIN;Acc:ZI	39 B- 40	3e-03	3 / 40	BP	heart morphogenesis



ВР				СС				MF			
Rank	p-value	#in/all	Geneset	Rank	p-value	#in/all	Geneset	Rank	p-value	#in/all	Geneset
1	1e-35	28 / 117	nucleosome assembly	1	1e-45	37 / 168	nucleosome	1	5e-40	37 / 232	protein heterodimerization activity
2	1e-12	9/34	ephrin receptor signaling pathway	2	3e-40	37 / 229	chromosome	2	9e-28	17 / 37	nucleosomal DNA binding
3	8e-11	11 / 100	peptidyl-tyrosine phosphorylation	3	8e-20	64 / 2716	nucleus	3	6e-26	55 / 1484	DNA binding
4	9e-08	16 / 454	multicellular organism development	4	3e-06	4 / 15	basement membrane	4	2e-10	11 / 110	protein tyrosine kinase activity
5	6e-07	8 / 104	transmembrane receptor protein tyrosine kinase signaling pathway	5	4e-04	13 / 634	extracellular region	5	2e-09	6 / 19	ephrin receptor activity
6	1e-06	6 / 52	blood vessel development	6	4e-04	15 / 809	integral component of plasma membrane	6	2e-08	21 / 717	calcium ion binding
7	8e-06	5 / 41	positive regulation of cell proliferation	7	2e-03	10 / 500	extracellular space	7	3e-05	5 / 52	transmembrane receptor protein tyrosine kinase activity
8	2e-05	7 / 117	Wnt signaling pathway	8	1e-02	3 / 65	extracellular matrix	8	1e-04	3 / 15	ephrin receptor binding
9	4e-05	3 / 10	adenohypophysis development	9	2e-02	4 / 153	proteinaceous extracellular matrix	9	1e-04	12 / 491	kinase activity
10	1e-04	4 / 38	vasculogenesis	10	6e-02	52 / 6248	integral component of membrane	10	5e-04	3 / 23	Wnt–activated receptor activity
11	2e-04	5 / 78	axon guidance	11	8e-02	1 / 13	transcriptional repressor complex	11	7e-04	3 / 26	Wnt-protein binding
12	2e-04	12 / 522	phosphorylation	12	9e-02	1 / 14	hemoglobin complex	12	1e-03	11 / 537	sequence-specific DNA binding
13	3e-04	3 / 19	non-canonical Wnt signaling pathway	13	1e-01	1 / 16	midbody	13	1e-03	12 / 633	transcription factor activity, sequence–specific DNA binding
14	3e-04	20 / 1239	regulation of transcription, DNA-templated	14	1e-01	1 / 17	presynaptic active zone	14	2e-03	5 / 130	growth factor activity
15	1e-03	3 / 33	blood vessel morphogenesis	15	1e-01	53 / 6723	membrane	15	3e-03	6 / 210	protein binding