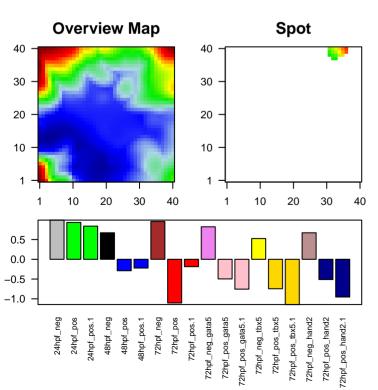


Spot Summary: A

metagenes = 19 # genes = 348

<r> metagenes = 0.98 <r> genes = 0.65 beta: r2= 9.12 / log p= -Inf

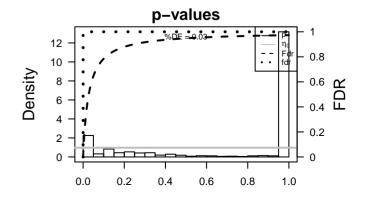
samples with spot = 1 (5.6 %) 24hpf_neg: 1 (100%)



Spot Genelist

Geneset Overrepresentation

Rank		max	е	r	Description	Rank	p-value	#in/all	Ge	neset
	ID		min e	Э	Symbol					
1	ENSDARG000	3.45	-2.09	0.84	si:ch211-si12h2f8[5212k18.5 [Source:ZFIN;Acc:ZDB-GENE-030131-(1	1e-39	40 / 168	СС	nucleosome
						2	5e-34	40 / 229	CC	chromosome
2	ENSDARG000	3.22	-4.34	0.62	collagen, type XIV, alpha 1b [Source:ZFIN;Acc:ZDB-GENE-(3	9e-34	40 / 232	MF	protein heterodimerization activity
						4	1e-32	31 / 117	BP	nucleosome assembly
3	ENSDARG000	2.85	-1.19	0.73	zic2b zic family member 2 (odd-paired homolog, Drosophila) b [Soi	5	3e-27	77 / 1484	MF	DNA binding
						6	5e-19	91 / 2716	CC	nucleus
4	ENSDARG000	2.8	-4.02	0.78	capn12 calpain 12 [Source:ZFIN;Acc:ZDB-GENE-050419-245]	7	7e-18	14 / 37	MF	nucleosomal DNA binding
						8	3e-15	32 / 454	BP	multicellular organism development
5	ENSDARG000	2.69	-3.04	0.72	hbbe2 hemoglobin beta embryonic-2 [Source:ZFIN;Acc:ZDB-GENE	9	7e-12	15 / 110	MF	protein tyrosine kinase activity
•						10	8e-12	10 / 34	BP	ephrin receptor signaling pathway
6	ENSDARG000	2.57	-1.21	0.64		11	3e-11	14 / 100	BP	peptidyl-tyrosine phosphorylation
•						12	2e-10	14 / 117	BP	Wnt signaling pathway
7	ENSDARG000	2.55	-1.55	0.83	si:dkey-26i1thte7y4261h17.1 [Source:ZFIN;Acc:ZDB-GENE-030829-14	13	7e-09	12 / 104	BP	transmembrane receptor protein tyrosine kinase signaling pathway
'					, , , , , , , , , , , , , , , , , , , ,	14	1e-08	9 / 52	MF	transmembrane receptor protein tyrosine kinase activity
8	ENSDARG00	2.48	-1.83	0.87	scube2 signal peptide, CUB domain, EGF-like 2 [Source:ZFIN:Acc:Z	15	1e-08	24 / 491	MF	kinase activity
U						16	4e-08	10 / 78	BP	axon guidance
9	ENSDARG000	2.48	-2.76	0.73	fibulin 1 [Source:HGNC Symbol;Acc:HGNC:3600]	17	5e-08	24 / 522	BP	phosphorylation
J	2.102/11000					18	7e-08	5 / 10	BP	adenohypophysis development
10	ENSDARG00	2 46	-1.44	0.82	zgc:173552gc:173552 [Source:ZFIN;Acc:ZDB-GENE-080220-24]	19	8e-08	6 / 19	BP	positive regulation of BMP signaling pathway
10	2.102/11000	2.10		0.02	-9	20	6e-07	6 / 26	MF	Wnt-protein binding
11	ENSDARG00	2 45	-2.43	0.79		21	8e-07	5 / 15	MF	ephrin receptor binding
	2.102/11000	2.10	2.10	00		22	8e-07	37 / 1239	BP	regulation of transcription, DNA-templated
12	ENSDARG000	2 44	-2.17	0.74	si:ch211-histane4.11,7H4, like [Source:ZFIN;Acc:ZDB-GENE-070927-10	23	9e-07	7 / 43	BP	DNA-templated transcription, initiation
12	LINSDAIRGOON	2.44	-2.17	0.74	31.01211-1100a to 1.1/1-1-1 line [Oddioc.21 114,700.255-02142-070327-11	24	3e-06	5 / 19	MF	ephrin receptor activity
13	ENSDARG000	2.38	-3.2	0.82	nr2f1b nuclear receptor subfamily 2, group F, member 1b [Source:ZF	25	4e-06	25 / 717	MF	calcium ion binding
13	LINSDAIRGOON	2.50	-3.2	0.02	111211b Hadical receptor Subtaining 2, group 1, member 15 (Godiec.21	26	4e-06	21 / 537	MF	sequence–specific DNA binding
14	ENSDARG000	2 27	-1.48	0.87	metrn meteorin, glial cell differentiation regulator [Source:ZFIN;Acc::	27	5e-06	5 / 21	BP	smoothened signaling pathway
14	ENSDARGOO	2.57	-1.40	0.07	meter meteorin, gilai een amerentation regulator (bouree.21 m,/toe.	28	8e-06	5 / 23	MF	Wnt-activated receptor activity
15	ENSDARG000	2.36	-1.04	0.9	hmga1a high mobility group AT-hook 1a [Source:ZFIN;Acc:ZDB-GEN	29	9e-06	8 / 83	BP	embryonic viscerocranium morphogenesis
13	ENSDARGOO	2.30	-1.04	0.9	Tilligara High Hobility group AT-Hook Ta [Source.21 IN,Acc.200-02N	30	1e-05	6 / 41	BP	positive regulation of cell proliferation
16	ENSDARG000	2.26	-1.78	0.82	si:dkey-157g16.6 [Source:ZFIN;Acc:ZDB-GENE-090313-18	31	2e-05	22 / 634	CC	extracellular region
10	ENSDARGOO	2.30	-1.70	0.02	Si.ukey=137g10.0 [30dice.21114,Acc.2DD=3E14E=030313=16	32	2e-05	10 / 149	BP	cell surface receptor signaling pathway
17	ENODA DOSS	0.05	-1.82	0.82	zqc:1735522c:173552 [Source:ZFIN:Acc:ZDB-GENE-080220-24]	33	3e-05	4 / 15	BP	posterior lateral line neuromast primordium migration
17	ENSDARG000	2.33	-1.02	0.02	2gc.17332gc.173332 [30tilde.21114,Acc.2DB=GENE=000220=24]	34	4e-05	5 / 31	BP	lymphangiogenesis
18	ENCDA DOOG	0.00	0.4	0.00	wu:fb77a06dogen 2a (osteonidogen) [Source:ZFIN;Acc:ZDB-GENE-0:	35	4e-05	5 / 32	BP	retinal ganglion cell axon guidance
10	ENSDARG000	2.32	-2.1	0.83	WU:ID77auguogen za (osteonidogen) [Source.ZFIN,Acc.ZDB-GENE-0.	36	4e-05	6 / 52	BP	blood vessel development
40	ENICOADCOO	0.0	4.70	0.00	-in-bodd dighted 200104 1 [Course: TEIN: Acc: TDD_CENE_000404_0	37	4e-05	7 / 76	BP	cartilage development
19	ENSDARG000	2.3	-1.78	0.89	si:ch211-si2th21.ti-222l21.1 [Source:ZFIN;Acc:ZDB-GENE-030131-2	38	5e-05	4 / 17	MF	transmembrane receptor protein serine/threonine kinase activity
20	ENIODADOSS	2.20	0.05	0.07	VOCADO LIBERTIA DE CONTRA DE CENTE OFICERO (C)	39	8e-05	4/19	BP	neuron migration
20	ENSDARG000	2.29	-2.25	0.87	vasna vasorin a [Source:ZFIN;Acc:ZDB-GENE-050522-43]	40	8e-05	4 / 19	BP	non-canonical Wnt signaling pathway



ВР				СС				MF			
Rank	p-value	#in/all	Geneset	Rank	p-value	#in/all	Geneset	Rank	p-value	#in/all	Geneset
1	1e-32	31 / 117	nucleosome assembly	1	1e-39	40 / 168	nucleosome	1	9e-34	40 / 232	protein heterodimerization activity
2	3e-15	32 / 454	multicellular organism development	2	5e-34	40 / 229	chromosome	2	3e-27	77 / 1484	DNA binding
3	8e-12	10 / 34	ephrin receptor signaling pathway	3	5e-19	91 / 2716	nucleus	3	7e-18	14 / 37	nucleosomal DNA binding
4	3e-11	14 / 100	peptidyl-tyrosine phosphorylation	4	2e-05	22 / 634	extracellular region	4	7e-12	15 / 110	protein tyrosine kinase activity
5	2e-10	14 / 117	Wnt signaling pathway	5	2e-04	6 / 65	extracellular matrix	5	1e-08	9 / 52	transmembrane receptor protein tyrosine kinase activity
6	7e-09	12 / 104	transmembrane receptor protein tyrosine kinase signaling pathway	6	6e-04	16 / 500	extracellular space	6	1e-08	24 / 491	kinase activity
7	4e-08	10 / 78	axon guidance	7	8e-04	3 / 15	basement membrane	7	6e-07	6 / 26	Wnt-protein binding
8	5e-08	24 / 522	phosphorylation	8	6e-03	19 / 809	integral component of plasma membrane	8	8e-07	5 / 15	ephrin receptor binding
9	7e-08	5 / 10	adenohypophysis development	9	6e-03	9 / 268	cytoskeleton	9	3e-06	5 / 19	ephrin receptor activity
10	8e-08	6 / 19	positive regulation of BMP signaling pathway	10	1e-02	6 / 153	proteinaceous extracellular matrix	10	4e-06	25 / 717	calcium ion binding
11	8e-07	37 / 1239	regulation of transcription, DNA-templated	11	2e-02	2/16	midbody	11	4e-06	21 / 537	sequence–specific DNA binding
12	9e-07	7 / 43	DNA-templated transcription, initiation	12	2e-02	2/19	axon	12	8e-06	5 / 23	Wnt-activated receptor activity
13	5e-06	5 / 21	smoothened signaling pathway	13	2e-02	3 / 49	microtubule organizing center	13	5e-05	4 / 17	transmembrane receptor protein serine/threonine kinase activity
14	9e-06	8 / 83	embryonic viscerocranium morphogenesis	14	3e-02	93 / 6248	integral component of membrane	14	1e-04	4 / 21	signal transducer, downstream of receptor, with serine/threonine kinase activi
15	1e-05	6 / 41	positive regulation of cell proliferation	15	3e-02	22 / 1162	plasma membrane	15	1e-04	20 / 633	transcription factor activity, sequence–specific DNA binding

Spot Summary: B

metagenes = 141 # genes = 2477

<r> metagenes = 0.78

beta: r2= 5.85 / log p= -Inf

samples with spot = 3 (16.7 %)

24hpf_neg : 1 (100 %) 24hpf_pos : 2 (100 %)

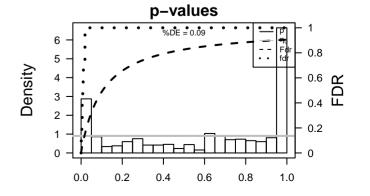
Overview Map Spot 30 30 20 20 10 30 30 20 10 20 48hpf_pos.1 72hpf_neg 72hpf_pos 48hpf_pos 72hpf_pos.1 72hpf_neg_gata5 72hpf_pos_gata5 72hpf_pos_gata5.1

Spot Genelist

Rar	nk ID	max	e min e	r)	Syml	Description bol
1	ENSDARG000	8.23	-1.2	0.54	ednrab	endothelin receptor type Ab [Source:ZFIN;Acc:ZDB-GENE-0
2	ENSDARG000	8.12	-6.4	0.84	hbbe3	hemoglobin beta embryonic-3 [Source:ZFIN;Acc:ZDB-GENE
3	ENSDARG000	7.83	-4.49	0.94	drl	draculin [Source:ZFIN;Acc:ZDB-GENE-991213-3]
4	ENSDARG000	7.74	-1.79	0.54	LOC100	0595862711-11n16.3 [Source:ZFIN;Acc:ZDB-GENE-131121-86
5	ENSDARG000	7.36	-4.55	0.92	si:dkey-	-26/19/kely-261j4.4 [Source:ZFIN;Acc:ZDB-GENE-060531-125]
6	ENSDARG000	7.35	-4.2	0.9	blf	bloody fingers [Source:ZFIN;Acc:ZDB-GENE-050721-1]
7	ENSDARG000	7.06	-5.06	0.92	si:dkey-	-26/10/14/29-261j4.3 [Source:ZFIN;Acc:ZDB-GENE-060531-124]
8	ENSDARG000	6.46	-4.6	0.78		protogenin homolog b (Gallus gallus) [Source:ZFIN;Acc:ZDB-
9	ENSDARG000	6.43	-3.22	0.88	stab2	stabilin 2 [Source:ZFIN;Acc:ZDB-GENE-041210-336]
10	ENSDARG000	6.31	-1.79	0.87	ela2l	elastase 2 like [Source:ZFIN;Acc:ZDB-GENE-040511-1]
11	ENSDARG000	6.11	-4.16	0.93	tfr1a	transferrin receptor 1a [Source:ZFIN;Acc:ZDB-GENE-04122
12	ENSDARG000	6	-2.33	0.87		si:ch73-299h12.2 [Source:ZFIN;Acc:ZDB-GENE-081031-7;
13	ENSDARG000	5.97	-3.89	0.9	klf17	Kruppel-like factor 17 [Source:ZFIN;Acc:ZDB-GENE-01012!
14	ENSDARG000	5.91	-1.27	0.64	si:dkey-	-28ig#k6y-26g8.5 [Source:ZFIN;Acc:ZDB-GENE-121214-19]
15	ENSDARG000	5.89	-1.29	0.67	zgc:174	855c:174855 [Source:ZFIN;Acc:ZDB-GENE-071004-74]
16	ENSDARG000	5.69	-3.46	0.93	gata1a	GATA binding protein 1a [Source:ZFIN;Acc:ZDB-GENE-980f
17	ENSDARG000	5.69	-3.04	0.89	gfi1b	growth factor independent 1B transcription repressor [Source
18	ENSDARG000	5.53	-3.53	0.87		
19	ENSDARG000	5.51	-4.09	0.86	znfl2a	zinc finger-like gene 2a [Source:ZFIN;Acc:ZDB-GENE-0308
20	ENSDARG000	5.48	-1.21	0.59	zgc:174	:15@c:174153 [Source:ZFIN;Acc:ZDB-GENE-080215-7]

Geneset Overrepresentation

Naiik	p-value	#III/aII	Gei	ieset
1	2e-95	569 / 2716	CC	nucleus
2	3e-67	345 / 1484	MF	DNA binding
3	5e-63	118 / 229	CC	chromosome
4	1e-59	405 / 2030	MF	nucleic acid binding
2 3 4 5 6 7	4e-58	97 / 168	CC	nucleosome
6	5e-40	95 / 232	MF	protein heterodimerization activity
7	1e-33	50 / 78	BP	DNA replication
8	2e-30	58 / 117	BP	nucleosome assembly
9	2e-21	55 / 148	BP	DNA repair
10	1e-20	22 / 25	BP	membrane disruption in other organism
11	4e-19	124 / 608	MF	RNA binding
12	5e-19	23 / 30	BP	defense response to Gram-positive bacterium
13	3e-17	199 / 1239	BP	regulation of transcription, DNA-templated
14	5e-16	18 / 22	BP	DNA replication initiation
15	2e-15	26 / 49	CC	nuclear chromatin
16	3e-15	21 / 32	BP	DNA duplex unwinding
17	6e-15	24 / 43	BP	DNA-templated transcription, initiation
18	2e-14	21 / 34	BP	chromatin silencing
19	1e-12	15 / 20	BP	DNA biosynthetic process
20	8e-12	35 / 110	BP	cell cycle
21	2e-11	17 / 29	CC	kinetochore
22	3e-11	13 / 17	MF	DNA-directed DNA polymerase activity
23	5e-11	21 / 46	BP	mitotic cell cycle
24	9e-11	30 / 91	BP	cellular response to DNA damage stimulus
25	2e-10	26 / 72	MF	helicase activity
26	3e-10	37 / 135	MF	methyltransferase activity
27	3e-09	9 / 10	BP	mitotic sister chromatid segregation
28	6e-09	15 / 30	BP	DNA recombination
29	8e-09	17 / 39	MF	single-stranded DNA binding
30	1e-08	31 / 115	MF	chromatin binding
31	1e-08	9 / 11	MF	DNA helicase activity
32	2e-08	10 / 14	CC	hemoglobin complex
33	2e-08	35 / 144	BP	methylation
34	3e-08	17 / 42	MF	histone binding
35	6e-08	40 / 183	MF	RNA polymerase II transcription factor activity, sequence-specific DNA bi
36	6e-08	12 / 22	CC	chromosome, centromeric region
37	1e-07	15 / 36	BP	protein import into nucleus
38	2e-07	23 / 79	BP	cell division
39	4e-07	95 / 643	BP	transcription, DNA-templated
40	4e-07	9 / 14	CC	condensed chromosome kinetochore



ВР				СС				MF			
Rank	p-value	#in/all	Geneset	Rank	p-value	#in/all	Geneset	Rank	p-value	#in/all	Geneset
1	1e-33	50 / 78	DNA replication	1	2e-95	569 / 2716	nucleus	1	3e-67	345 / 1484	DNA binding
2	2e-30	58 / 117	nucleosome assembly	2	5e-63	118 / 229	chromosome	2	1e-59	405 / 2030	nucleic acid binding
3	2e-21	55 / 148	DNA repair	3	4e-58	97 / 168	nucleosome	3	5e-40	95 / 232	protein heterodimerization activity
4	1e-20	22 / 25	membrane disruption in other organism	4	2e-15	26 / 49	nuclear chromatin	4	4e-19	124 / 608	RNA binding
5	5e-19	23 / 30	defense response to Gram–positive bacterium	5	2e-11	17 / 29	kinetochore	5	3e-11	13 / 17	DNA-directed DNA polymerase activity
6	3e-17	199 / 1239	regulation of transcription, DNA-templated	6	2e-08	10 / 14	hemoglobin complex	6	2e-10	26 / 72	helicase activity
7	5e-16	18 / 22	DNA replication initiation	7	6e-08	12/22	chromosome, centromeric region	7	3e-10	37 / 135	methyltransferase activity
8	3e-15	21 / 32	DNA duplex unwinding	8	4e-07	9/14	condensed chromosome kinetochore	8	8e-09	17 / 39	single-stranded DNA binding
9	6e-15	24 / 43	DNA-templated transcription, initiation	9	1e-06	22 / 80	centrosome	9	1e-08	31 / 115	chromatin binding
10	2e-14	21 / 34	chromatin silencing	10	4e-06	30 / 140	nucleolus	10	1e-08	9/11	DNA helicase activity
11	1e-12	15 / 20	DNA biosynthetic process	11	5e-06	11 / 26	nuclear pore	11	3e-08	17 / 42	histone binding
12	8e-12	35 / 110	cell cycle	12	1e-05	15 / 49	nucleoplasm	12	6e-08	40 / 183	RNA polymerase II transcription factor activity, sequence–specific DNA bindir
13	5e-11	21 / 46	mitotic cell cycle	13	2e-05	9 / 20	centriole	13	8e-07	216 / 1787	ATP binding
14	9e-11	30 / 91	cellular response to DNA damage stimulus	14	3e-05	22 / 98	transcription factor complex	14	1e-06	10 / 19	oxygen binding
15	3e-09	9 / 10	mitotic sister chromatid segregation	15	4e-05	10 / 26	nuclear speck	15	1e-06	10 / 19	oxygen transporter activity

Spot Summary: C

metagenes = 6 # genes = 180

<r> metagenes = 0.99 <r> genes = 0.63 beta: r2= 7.43 / log p= -Inf

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

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

Spot Genelist

20 ENSDARG001 2.75

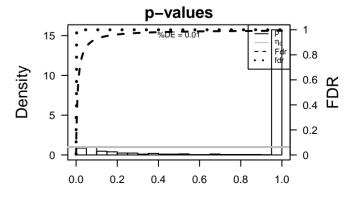
-1.6 0.84

Rai	nk ID	max	e min e	r	Symb	Description
	ID			•	Cynna	
1	ENSDARG000	5.93	-1.57	0.76	cyp7a1b	
2	ENSDARG000	4.13	-2.81	0.9	mrc1a	mannose receptor, C type 1a [Source:ZFIN;Acc:ZDB-GENE-
3	ENSDARG000	3.89	-1.94	0.79	nkx2.7	NK2 transcription factor related 7 [Source:ZFIN;Acc:ZDB-GE
4	ENSDARG000	3.75	-3.16	0.79	dnase1l4	4.deoxyribonuclease 1 like 4, tandem duplicate 1 [Source:ZFIN
5	ENSDARG000	3.53	-3.11	0.84	ikzf1	IKAROS family zinc finger 1 (Ikaros) [Source:ZFIN;Acc:ZDB-
6	ENSDARG000	3.47	-3.88	0.78	il6r	interleukin 6 receptor [Source:ZFIN;Acc:ZDB-GENE-080107
7	ENSDARG000	3.44	-2.62	0.82		
8	ENSDARG000	3.38	-2.19	0.81	ampd3b	adenosine monophosphate deaminase 3b [Source:ZFIN;Acc:
9	ENSDARG000	3.36	-3.58	0.72	slc25a37	7 solute carrier family 25 (mitochondrial iron transporter), memb
10	ENSDARG000	3.36	-1.95	0.84	slc29a1t	solute carrier family 29 (equilibrative nucleoside transporter),
11	ENSDARG000	3.35	-2.16	0.86	LOC555	35/kg/fos-2330d3.7 [Source:ZFIN;Acc:ZDB-GENE-121214-11
12	ENSDARG000	3.13	-2.54	0.74	scarf1	scavenger receptor class F, member 1 [Source:ZFIN;Acc:ZDE
13	ENSDARG000	3.1	-2.52	0.93	si:ch73-	23/8៨/2737248e21.7 [Source:ZFIN;Acc:ZDB-GENE-120215-2:
14	ENSDARG000	3.08	-2.4	0.8	fam117a	at/amily with sequence similarity 117, member Ab [Source:ZFIN
15	ENSDARG000	3.07	-4.2	0.77	f5	coagulation factor V [Source:ZFIN;Acc:ZDB-GENE-030131-
16	ENSDARG000	2.96	-2.8	0.88	zgc:1016	6@gc:101663 [Source:ZFIN;Acc:ZDB-GENE-041114-149]
17	ENSDARG000	2.9	-3.03	0.88	btk	Bruton agammaglobulinemia tyrosine kinase [Source:ZFIN;At
18	ENSDARG000	2.9	-1.95	0.91	yrk	Yes-related kinase [Source:ZFIN;Acc:ZDB-GENE-030131-5
19	ENSDARG000	2.8	-1.1	0.86	larp1b	La ribonucleoprotein domain family, member 1B [Source:ZFIN

si:ch1073sitcf04027034110a20.1 [Source:ZFIN;Acc:ZDB-GENE-121214-

Geneset Overrepresentation

	•			
1	1e-06	13 / 375	BP	positive regulation of GTPase activity
1 2 3 4 5 6 7	1e-05	69 / 6723	CC	membrane
3	2e-05	65 / 6248	CC	integral component of membrane
4	2e-05	12 / 413	BP	intracellular signal transduction
5	6e-05	15 / 712	BP	oxidation-reduction process
6	8e-05	8 / 217	MF	GTPase activator activity
	1e-04	4 / 38	BP	integrin-mediated signaling pathway
8	4e-04	3 / 22	MF	metalloaminopeptidase activity
9	9e-04	23 / 1761	MF	metal ion binding
10	2e-03	18 / 1295	BP	signal transduction
11	2e-03	2/10	MF	GDP-dissociation inhibitor activity
12	2e-03	2/10	MF	GTPase regulator activity
13	2e-03	2/11	BP	actin polymerization or depolymerization
14	2e-03	2/11	MF	deaminase activity
15	2e-03	2/11	BP	spindle organization
16	3e-03	2/12	BP	peptide catabolic process
17	3e-03	2/13	BP	erythrocyte maturation
18	3e-03	2/13	BP	germ cell migration
19	3e-03	2/13	MF	signal transducer activity, downstream of receptor
20	4e-03	2/14	BP	adaptive immune response
21	4e-03	3 / 49	MF	non-membrane spanning protein tyrosine kinase activity
22	6e-03	3 / 58	BP	chemokine-mediated signaling pathway
23	6e-03	2/19	BP	release of sequestered calcium ion into cytosol
24	8e-03	4 / 122	BP	inflammatory response
25	9e-03	4 / 128	MF	metallopeptidase activity
26	9e-03	2/23	MF	CCR chemokine receptor binding
27	9e-03	2 / 23	BP	cellular response to interferon-gamma
28	9e-03	2/23	BP	lymphocyte chemotaxis
29	9e-03	2/23	BP	monocyte chemotaxis
30	1e-02	2/24	BP	cellular response to interleukin-1
31	1e-02	2/24	BP	cellular response to tumor necrosis factor
32	1e-02	2/26	BP	positive regulation of catalytic activity
33	1e-02	2 / 27	MF	cytokine receptor activity
34	1e-02	2/28	BP	embryonic hemopoiesis
35	1e-02	2/29	BP	immune system process
36	1e-02	2/29	CC	integrin complex
37	2e-02	2/33	BP	blood coagulation
38	2e-02	2/33	BP	positive regulation of ERK1 and ERK2 cascade
39	2e-02	4 / 158	MF	microtubule binding
40	2e-02	3 / 88	MF	guanyl-nucleotide exchange factor activity



ВР				СС				MF			
Rank	p-value	#in/all	Geneset	Rank	p-value	#in/all	Geneset	Rank	p-value	#in/all	Geneset
1	1e-06	13 / 375	positive regulation of GTPase activity	1	1e-05	69 / 6723	membrane	1	8e-05	8 / 217	GTPase activator activity
2	2e-05	12 / 413	intracellular signal transduction	2	2e-05	65 / 6248	integral component of membrane	2	4e-04	3 / 22	metalloaminopeptidase activity
3	6e-05	15 / 712	oxidation-reduction process	3	1e-02	2/29	integrin complex	3	9e-04	23 / 1761	metal ion binding
4	1e-04	4 / 38	integrin-mediated signaling pathway	4	2e-02	13 / 1066	intracellular	4	2e-03	2/10	GDP-dissociation inhibitor activity
5	2e-03	18 / 1295	signal transduction	5	3e-02	2/43	extrinsic component of cytoplasmic side of plasma membrane	5	2e-03	2/10	GTPase regulator activity
6	2e-03	2/11	actin polymerization or depolymerization	6	4e-02	4 / 198	Golgi membrane	6	2e-03	2/11	deaminase activity
7	2e-03	2/11	spindle organization	7	5e-02	5/317	Golgi apparatus	7	3e-03	2 / 13	signal transducer activity, downstream of receptor
8	3e-03	2 / 12	peptide catabolic process	8	9e-02	1 / 14	M band	8	4e-03	3 / 49	non-membrane spanning protein tyrosine kinase activity
9	3e-03	2 / 13	erythrocyte maturation	9	9e-02	1 / 15	intrinsic component of the cytoplasmic side of the plasma membrane	9	9e-03	4 / 128	metallopeptidase activity
10	3e-03	2 / 13	germ cell migration	10	1e-01	2 / 85	cell	10	9e-03	2 / 23	CCR chemokine receptor binding
11	4e-03	2 / 14	adaptive immune response	11	1e-01	1/20	exocyst	11	1e-02	2 / 27	cytokine receptor activity
12	6e-03	3 / 58	chemokine-mediated signaling pathway	12	1e-01	1/21	dendrite	12	2e-02	4 / 158	microtubule binding
13	6e-03	2 / 19	release of sequestered calcium ion into cytosol	13	1e-01	1/21	membrane coat	13	2e-02	3 / 88	guanyl-nucleotide exchange factor activity
14	8e-03	4 / 122	inflammatory response	14	2e-01	1 / 27	guanylate cyclase complex, soluble	14	2e-02	2/37	peptide binding
15	9e-03	2/23	cellular response to interferon-gamma	15	2e-01	1/27	integral component of Golgi membrane	15	2e-02	3 / 96	Rho guanyl-nucleotide exchange factor activity

Spot Summary: D

```
# metagenes = 32

# genes = 571

<r> metagenes = 0.94

<r> genes = 0.73

beta: r2= 46.15 / log p= -Inf

# samples with spot = 9 (50 %)

48hpf_pos: 1 (50 %)

72hpf_pos: 2 (100 %)

72hpf_pos_gata5: 2 (100 %)

72hpf_pos_hand2: 2 (100 %)
```

Overview Map Spot 30 30 20 20 10 30 30 20 10 20 48hpf_pos.1 72hpf_neg 48hpf_pos 72hpf_pos 72hpf_neg_gata5 72hpf_pos_gata5 72hpf_pos.1 72hpf_pos_gata5.1

Spot Genelist

max e

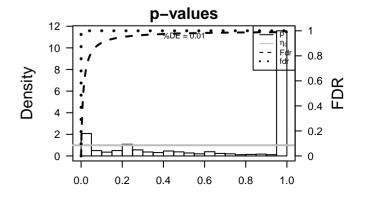
Rank

Nai	ID .	max	min e)	Symb	pol
1	ENSDARG000	5.16	-6.13	0.97	oacyl	O-acyltransferase like [Source:ZFIN;Acc:ZDB-GENE-09071
2	ENSDARG000	4.98	-7.11	0.95	wu:fc46l	n weu:fc46h12 [Source:ZFIN;Acc:ZDB-GENE-030131-3611]
3	ENSDARG000	4.9	-4.2	0.72	zgc:112	2@fjc:112265 [Source:ZFIN;Acc:ZDB-GENE-050626-133]
4	ENSDARG000	4.88	-6.93	0.95	si:dkey-	25/1d/10/2-251110.2 [Source:ZFIN;Acc:ZDB-GENE-050506-10.
5	ENSDARG000	4.84	-5.75	0.79	serpina1	Ilserine (or cysteine) proteinase inhibitor, clade A (alpha-1 anti
6	ENSDARG000	4.78	-3.37	0.83	c3a.3	complement component c3a, duplicate 3 [Source:ZFIN;Acc:Z
7	ENSDARG000	4.72	-6.07	0.64	vmhcl	ventricular myosin heavy chain-like [Source:ZFIN;Acc:ZDB-(
8	ENSDARG000	4.71	-7.81	0.92	gch2	GTP cyclohydrolase 2 [Source:ZFIN;Acc:ZDB-GENE-00120
9	ENSDARG000	4.69	-4.69	0.69	agxtb	alanine-glyoxylate aminotransferase b [Source:ZFIN;Acc:ZDI
10	ENSDARG000	4.67	-4.1	0.79	plg	plasminogen [Source:ZFIN;Acc:ZDB-GENE-030131-1411]
11	ENSDARG000	4.58	-3.93	0.71	fga	fibrinogen alpha chain [Source:ZFIN;Acc:ZDB-GENE-03101
12	ENSDARG000	4.57	-5.01	0.82	serpina1	serpin peptidase inhibitor, clade A (alpha-1 antiproteinase, ar
13	ENSDARG000	4.53	-5.75	0.99		si:dkey-73n8.3 [Source:ZFIN;Acc:ZDB-GENE-141219-27]
14	ENSDARG000	4.53	-4.41	0.82	fgb	fibrinogen beta chain [Source:ZFIN;Acc:ZDB-GENE-030131
15	ENSDARG000	4.51	-4.97	0.94	zgc:113	142c:113142 [Source:ZFIN;Acc:ZDB-GENE-050220-2]
16	ENSDARG000	4.47	-7.23	0.96	xdh	xanthine dehydrogenase [Source:ZFIN;Acc:ZDB-GENE-070
17	ENSDARG000	4.45	-2.24	0.69	plxdc1	plexin domain containing 1 [Source:ZFIN;Acc:ZDB-GENE-08
18	ENSDARG000	4.44	-6.92	0.96	zgc:162	159c:162150 [Source:ZFIN;Acc:ZDB-GENE-070410-23]
19	ENSDARG000	4.42	-4.7	0.65	tnnc1a	troponin C type 1a (slow) [Source:ZFIN;Acc:ZDB-GENE-030
20	ENSDARG000	4.4	-6.51	0.98	bscl2l	Bernardinelli-Seip congenital lipodystrophy 2, like [Source:ZF

Description

Geneset Overrepresentation

Nank	p-value	#III/aII	Gei	ieset
1	2e-14	17 / 67	BP	lipid transport
2	3e-14	50 / 712	BP	oxidation-reduction process
3	4e-14	42 / 522	MF	oxidoreductase activity
4	1e-12	12/33	MF	endopeptidase inhibitor activity
2 3 4 5 6 7	8e-12	11/30	BP	pigmentation
6	1e-11	10 / 23	BP	lipoprotein metabolic process
7	8e-11	17 / 109	BP	negative regulation of endopeptidase activity
8	2e-10	7 / 10	CC	chylomicron
9	9e-09	29 / 414	BP	metabolic process
10	1e-08	6 / 10	CC	high-density lipoprotein particle
11	1e-08	6 / 10	BP	triglyceride catabolic process
12	2e-08	7 / 17	CC	blood microparticle
13	3e-08	6 / 11	BP	cholesterol homeostasis
14	6e-08	6 / 12	BP	cholesterol biosynthetic process
15	7e-08	30 / 480	MF	catalytic activity
16	7e-08	13 / 96	CC	lysosome
17	1e-07	6 / 13	BP	cholesterol efflux
18	1e-07	35 / 634	CC	extracellular region
19	3e-07	7 / 24	BP	nucleoside metabolic process
20	7e-07	6 / 17	MF	cholesterol binding
21	7e-07	6 / 17	MF	cholesterol transporter activity
22	1e-06	5 / 11	BP	purine nucleotide biosynthetic process
23	1e-06	10 / 70	CC	myosin complex
24	5e-06	27 / 500	CC	extracellular space
25	5e-06	6 / 23	CC	troponin complex
26	9e-06	6 / 25	BP	cellular response to estrogen stimulus
27	1e-05	11 / 105	MF	lipid binding
28	1e-05	6 / 26	BP	melanocyte differentiation
29	1e-05	6 / 27	BP	response to bacterium
30	2e-05	6 / 29	BP	cellular response to xenobiotic stimulus
31	3e-05	5 / 19	BP	gluconeogenesis
32	3e-05	4 / 10	CC	melanosome
33	3e-05	13 / 164	BP	carbohydrate metabolic process
34	4e-05	56 / 1580	CC	cellular_component
35	4e-05	6/32	MF	oxidoreductase activity, acting on the CH-OH group of donors, NAD or N
36	4e-05	39 / 969	MF	hydrolase activity
37	5e-05	6 / 33	MF	NAD binding
38	6e-05	9 / 85	CC	cell
39	7e-05	6 / 35	BP	sarcomere organization
40	1e-04	4 / 13	BP	regulation of muscle contraction
-				



ВР				СС				MF			
Rank	p-value	#in/all	Geneset	Rank	p–value	#in/all	Geneset	Rank	p-value	#in/all	Geneset
1	2e-14	17 / 67	lipid transport	1	2e-10	7/10	chylomicron	1	4e-14	42 / 522	oxidoreductase activity
2	3e-14	50 / 712	oxidation-reduction process	2	1e-08	6/10	high-density lipoprotein particle	2	1e-12	12/33	endopeptidase inhibitor activity
3	8e-12	11 / 30	pigmentation	3	2e-08	7 / 17	blood microparticle	3	7e-08	30 / 480	catalytic activity
4	1e-11	10 / 23	lipoprotein metabolic process	4	7e-08	13/96	lysosome	4	7e-07	6 / 17	cholesterol binding
5	8e-11	17 / 109	negative regulation of endopeptidase activity	5	1e-07	35 / 634	extracellular region	5	7e-07	6 / 17	cholesterol transporter activity
6	9e-09	29 / 414	metabolic process	6	1e-06	10 / 70	myosin complex	6	1e-05	11 / 105	lipid binding
7	1e-08	6 / 10	triglyceride catabolic process	7	5e-06	27 / 500	extracellular space	7	4e-05	6 / 32	oxidoreductase activity, acting on the CH-OH group of donors, NAD or NADF
8	3e-08	6 / 11	cholesterol homeostasis	8	5e-06	6/23	troponin complex	8	4e-05	39 / 969	hydrolase activity
9	6e-08	6 / 12	cholesterol biosynthetic process	9	3e-05	4/10	melanosome	9	5e-05	6/33	NAD binding
10	1e-07	6 / 13	cholesterol efflux	10	4e-05	56 / 1580	cellular_component	10	2e-04	10 / 120	motor activity
11	3e-07	7 / 24	nucleoside metabolic process	11	6e-05	9 / 85	cell	11	2e-04	6 / 43	iron-sulfur cluster binding
12	1e-06	5/11	purine nucleotide biosynthetic process	12	2e-03	4/26	vesicle	12	3e-04	17 / 321	GTPase activity
13	9e-06	6 / 25	cellular response to estrogen stimulus	13	3e-03	3 / 15	secretory granule	13	4e-04	18 / 358	peptidase activity
14	1e-05	6 / 26	melanocyte differentiation	14	5e-03	4/35	peroxisome	14	6e-04	24 / 561	GTP binding
15	1e-05	6 / 27	response to bacterium	15	7e-03	4/38	trans-Golgi network	15	6e-04	8 / 92	magnesium ion binding

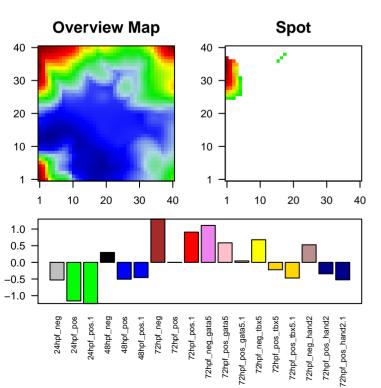
Spot Summary: E

genes = 868

<r> metagenes = 0.82
<r> genes = 0.44
beta: r2= 9.33 / log p= -Inf

metagenes = 56

samples with spot = 2 (11.1 %) 72hpf_neg : 1 (100 %) 72hpf_neg_gata5 : 1 (100 %)

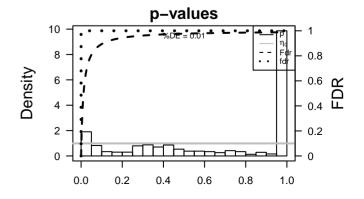


Spot Genelist

Rank ID		max	e min e	r e	Syml	Description ool
1	ENSDARG000	11.88	-0.87	0.44		
2	ENSDARG000	7.94	-1.47	0.44	cts12	cathepsin 12 [Source:ZFIN;Acc:ZDB-GENE-050208-336]
3	ENSDARG000	5.44	-2.17	0.78	opn1sw	2 opsin 1 (cone pigments), short–wave–sensitive 2 [Source:ZFI
4	ENSDARG000	5.34	-6.98	0.88	matn1	matrilin 1 [Source:ZFIN;Acc:ZDB-GENE-050307-3]
5	ENSDARG000	5.22	-3.71	0.75	opn1mv	v1opsin 1 (cone pigments), medium-wave-sensitive, 1 [Source:
6	ENSDARG000	5.16	-4.48	0.72	opn1sw	1 opsin 1 (cone pigments), short–wave–sensitive 1 [Source:ZFI
7	ENSDARG000	5.14	-4.55	0.93	rho	rhodopsin [Source:ZFIN;Acc:ZDB-GENE-990415-271]
8	ENSDARG000	5.13	-1.38	0.4	si:dkey-	29/78/769-247k7.2 [Source:ZFIN;Acc:ZDB-GENE-031118-45]
9	ENSDARG000	5.09	-5.91	0.89	and2	actinodin2 [Source:ZFIN;Acc:ZDB-GENE-041105-2]
10	ENSDARG000	5.01	-4.88	0.89	opn1lw2	2 opsin 1 (cone pigments), long-wave-sensitive, 2 [Source:ZFI
11	ENSDARG000	4.9	-3.66	0.89	and1	actinodin1 [Source:ZFIN;Acc:ZDB-GENE-030131-9105]
12	ENSDARG000	4.83	-5.45	0.9	arr3a	arrestin 3a, retinal (X-arrestin) [Source:ZFIN;Acc:ZDB-GENE
13	ENSDARG000	4.82	-3.89	0.82	gnb3b	guanine nucleotide binding protein (G protein), beta polypepti
14	ENSDARG000	4.71	-3.52	0.86	rcvrn3	recoverin 3 [Source:ZFIN;Acc:ZDB-GENE-040426-1661]
15	ENSDARG000	4.62	-1.7	0.27	kcnj1a.4	potassium inwardly-rectifying channel, subfamily J, member
16	ENSDARG000	4.57	-3.71	0.78	pde6c	phosphodiesterase 6C, cGMP-specific, cone, alpha prime [Si
17	ENSDARG000	4.55	-3.73	0.84		
18	ENSDARG000	4.55	-4.06	0.8	gnat2	guanine nucleotide binding protein (G protein), alpha transdu
19	ENSDARG000	4.25	-2.5	0.75	opn1lw1	opsin 1 (cone pigments), long-wave-sensitive, 1 [Source:ZFI
20	ENSDARG000	4.23	-1.93	0.62	fbp2	fructose-1,6-bisphosphatase 2 [Source:ZFIN;Acc:ZDB-GEN

Geneset Overrepresentation

	1	1e-18	72 / 717	MF	calcium ion binding
		3e-17	24 / 83	BP	visual perception
	2	1e-14	29 / 159	MF	structural molecule activity
2 3 4 5 6 7	<u> </u>	3e-13	18 / 62	CC	intermediate filament
	5	7e-12	55 / 634	CC	extracellular region
	6	6e-11	24 / 153	CC	proteinaceous extracellular matrix
7	7	2e-09	13 / 49	MF	extracellular matrix structural constituent
	8	5e-09	33 / 333	BP	cell adhesion
	9	5e-09	265 / 6248	CC	integral component of membrane
	10	2e-08	278 / 6723	CC	membrane
	11	1e-07	21 / 176	BP	ion transmembrane transport
	12	4e-07	68 / 1162	CC	plasma membrane
	13	6e-07	64 / 1084	BP	transport
	14	1e-06	37 / 499	BP	ion transport
	15	1e-06	9 / 36	BP	regulation of cell growth
1 1 1 1 2 2	16	2e-06	12 / 71	CC	bicellular tight junction
	17	3e-06	8 / 30	MF	insulin-like growth factor binding
	18	4e-06	11 / 64	MF	serine-type endopeptidase inhibitor activity
	19	4e-06	24 / 270	MF	ion channel activity
	20	5e-06	21 / 219	CC	cell junction
	21	6e-06	8 / 33	MF	photoreceptor activity
	22	6e-06	5 / 10	MF	small molecule binding
	23	1e-05	9 / 46	CC	collagen trimer
	24	2e-05	7 / 28	BP	phototransduction
	25	4e-05	7 / 31	MF	heparin binding
	26	4e-05	7 / 31	BP	protein-chromophore linkage
	27	4e-05	38 / 609	BP	proteolysis
	28	6e-05	5 / 15	BP	negative regulation of cell death
	29	1e-04	10 / 76	BP	cartilage development
	30	1e-04	12 / 109	BP	negative regulation of endopeptidase activity
	31	2e-04	31 / 500	CC	extracellular space
	32	3e-04	9 / 70	CC	myosin complex
	33	3e-04	9 / 70	BP	sodium ion transmembrane transport
	34	3e-04	6 / 31	MF	G-protein coupled photoreceptor activity
	35	3e-04	6 / 31	CC	photoreceptor outer segment
	36	3e-04	14 / 155	CC	synapse
38	37	4e-04	7 / 44	BP	skeletal muscle tissue development
	38	4e-04	6 / 32	BP	inner ear development
	39	5e-04	4 / 13	MF	ATP-activated inward rectifier potassium channel activity
	40	6e-04	12 / 128	MF	metallopeptidase activity



BP				СС				MF			
Rank	p-value	#in/all	Geneset	Rank	p-value	#in/all	Geneset	Rank	p-value	#in/all	Geneset
1	3e-17	24 / 83	visual perception	1	3e-13	18 / 62	intermediate filament	1	1e-18	72 / 717	calcium ion binding
2	5e-09	33 / 333	cell adhesion	2	7e-12	55 / 634	extracellular region	2	1e-14	29 / 159	structural molecule activity
3	1e-07	21 / 176	ion transmembrane transport	3	6e-11	24 / 153	proteinaceous extracellular matrix	3	2e-09	13 / 49	extracellular matrix structural constituent
4	6e-07	64 / 1084	transport	4	5e-09	265 / 6248	integral component of membrane	4	3e-06	8/30	insulin-like growth factor binding
5	1e-06	37 / 499	ion transport	5	2e-08	278 / 6723	membrane	5	4e-06	11 / 64	serine-type endopeptidase inhibitor activity
6	1e-06	9 / 36	regulation of cell growth	6	4e-07	68 / 1162	plasma membrane	6	4e-06	24 / 270	ion channel activity
7	2e-05	7 / 28	phototransduction	7	2e-06	12/71	bicellular tight junction	7	6e-06	8/33	photoreceptor activity
8	4e-05	7 / 31	protein-chromophore linkage	8	5e-06	21 / 219	cell junction	8	6e-06	5 / 10	small molecule binding
9	4e-05	38 / 609	proteolysis	9	1e-05	9 / 46	collagen trimer	9	4e-05	7 / 31	heparin binding
10	6e-05	5 / 15	negative regulation of cell death	10	2e-04	31 / 500	extracellular space	10	3e-04	6/31	G-protein coupled photoreceptor activity
11	1e-04	10 / 76	cartilage development	11	3e-04	9/70	myosin complex	11	5e-04	4 / 13	ATP-activated inward rectifier potassium channel activity
12	1e-04	12 / 109	negative regulation of endopeptidase activity	12	3e-04	6/31	photoreceptor outer segment	12	6e-04	12 / 128	metallopeptidase activity
13	3e-04	9 / 70	sodium ion transmembrane transport	13	3e-04	14 / 155	synapse	13	7e-04	12 / 130	voltage-gated ion channel activity
14	4e-04	7 / 44	skeletal muscle tissue development	14	6e-04	7 / 48	heterotrimeric G-protein complex	14	8e-04	23 / 358	peptidase activity
15	4e-04	6 / 32	inner ear development	15	4e-03	39 / 809	integral component of plasma membrane	15	9e-04	5 / 25	integrin binding

Spot Summary: F

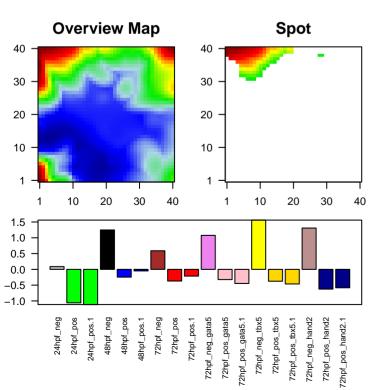
metagenes = 120 # genes = 2255

<r> metagenes = 0.82

beta: r2= 12.51 / log p= -Inf

samples with spot = 4 (22.2 %) 48hpf_neg : 1 (100 %)

72hpf_neg_gata5 : 1 (100 %) 72hpf_neg_tbx5 : 1 (100 %) 72hpf_neg_hand2 : 1 (100 %)

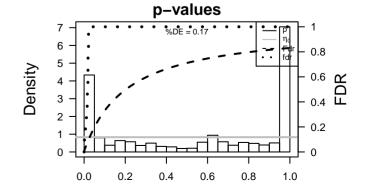


Spot Genelist

Rank ID		max e r min e			Syml	Description bol	Rank	p-value	#in/all	Geneset	
1	ENSDARG000	5.4	-5.6	0.71	muc5.1	mucin 5.1, oligomeric mucus/gel-forming [Source:ZFIN;Acc:Z	1	4e-50	123 / 333	BP	cell adhe
2	ENSDARG000	5.19	-6.04	0.35	atp1a1a	a.2ATPase, Na+/K+ transporting, alpha 1a polypeptide, tandem (2 3 4	4e-49 5e-49 5e-49	87 / 172 158 / 537	BP MF BP	homophi sequence regulation
3	ENSDARG000	4.85	-4.47	0.6	npas4a	neuronal PAS domain protein 4a [Source:ZFIN;Acc:ZDB-GEI	5 6	4e-42 1e-36	260 / 1239 81 / 175 225 / 1162	BP	nervous plasma i
4	ENSDARG000	4.76	-5.55	0.71	col10a1	acollagen, type X, alpha 1a [Source:ZFIN;Acc:ZDB-GENE-03	7 8	3e-36 5e-32	264 / 1484 776 / 6723	MF CC	DNA bin membra
5	ENSDARG000	4.72	-8.26	0.75	col11a2	collagen, type XI, alpha 2 [Source:ZFIN;Acc:ZDB-GENE-000	9 10	9e-32 2e-29	157 / 717 722 / 6248	MF CC	calcium integral
6	ENSDARG000	4.49	-6.7	0.77		si:dkey-65b12.6 [Source:ZFIN;Acc:ZDB-GENE-060526-32§	11 12	3e-25 3e-25	368 / 2716 108 / 454	CC BP	nucleus multicell
7	ENSDARG000	4.38	-2.85	0.4	col28a2	eacollagen, type XXVIII, alpha 2a [Source:ZFIN;Acc:ZDB-GENI	13 14	9e-24 3e-21	57 / 155 107 / 499	CC BP	synapse ion trans
8	ENSDARG000	4.01	-3.22	0.95	sv2a	synaptic vesicle glycoprotein 2A [Source:ZFIN;Acc:ZDB-GEN	15 16	1e-19 2e-19	71 / 270 121 / 633	MF MF	ion chan transcrip
9	ENSDARG000	4.01	-6.39	0.73	col9a3	collagen, type IX, alpha 3 [Source:ZFIN;Acc:ZDB-GENE-03(17 18	2e-18 2e-16	120 / 643 33 / 78	BP BP	transcrip axon gui
10	ENSDARG000	4	-6.25	0.67	ерус	epiphycan [Source:ZFIN;Acc:ZDB-GENE-041008-9]	19 20	5e-16 5e-16	21 / 32 21 / 32	MF MF	extracell ionotrop
11	ENSDARG000	3.9	-5.96	0.85	stx1b	syntaxin 1B [Source:ZFIN;Acc:ZDB-GENE-000330-4]	21 22	5e-16 2e-15	21 / 32 24 / 44	BP BP	ionotropi neuron o
12	ENSDARG000	3.88	-5.45	0.78	grin1b	glutamate receptor, ionotropic, N-methyl D-aspartate 1b [Soi	23 24	7e-15 3e-14	40 / 124 45 / 158	MF MF	receptor microtub
13	ENSDARG000	3.88	-6.3	0.86	pclob	piccolo presynaptic cytomatrix protein b [Source:ZFIN;Acc:ZE	25 26	7e-13 5e-12	42 / 153 37 / 130	CC BP	regulatio
14	ENSDARG000	3.87	-1.49	0.83	slc6a17	solute carrier family 6 (neutral amino acid transporter), memb	27 28	5e-12 8e-12	37 / 130 28 / 80	MF CC	voltage- postsyna
15	ENSDARG000	3.79	-5.15	0.68	fgfbp2b	fibroblast growth factor binding protein 2b [Source:ZFIN;Acc:2	29 30	1e-11 4e-11	20 / 42 37 / 138	MF BP	voltage- potassiu
16	ENSDARG000	3.75	-3.97	0.87	slc32a1	solute carrier family 32 (GABA vesicular transporter), membe	31 32 33	4e-11 6e-11 7e-11	27 / 79 31 / 103 119 / 809	BP BP CC	excitator cell-cell integral
17	ENSDARG000	3.71	-5.4	0.83	slc6a1b	solute carrier family 6 (neurotransmitter transporter), member	34 35	2e-10 3e-10	18 / 39 37 / 147	BP BP	neuron p
18	ENSDARG000	3.69	-4.33	0.88	gad2	glutamate decarboxylase 2 [Source:ZFIN;Acc:ZDB-GENE-0:	36 37	3e-10 9e-10	12 / 17 16 / 33	CC	presynaj voltage-
19	ENSDARG000	3.68	-6.04	0.51	atp1b1b	o ATPase, Na+/K+ transporting, beta 1b polypeptide [Source:ZI	38 39	3e-09 3e-09	16 / 35 29 / 106	BP BP	calcium
20	ENSDARG000	3.66	-4.73	0.88	atp2b3a	a ATPase, Ca++ transporting, plasma membrane 3a [Source:Zf	40	6e-09	9/11	BP	modulati

Geneset Overrepresentation

1	4e-50	123 / 333	BP	cell adhesion
2	4e-49	87 / 172	BP	homophilic cell adhesion via plasma membrane adhesion molecule
3	5e-49	158 / 537	MF	sequence-specific DNA binding
4	5e-49	260 / 1239	BP	regulation of transcription, DNA-templated
5	4e-42	81 / 175	BP	nervous system development
6	1e-36	225 / 1162	CC	plasma membrane
7	3e-36	264 / 1484	MF	DNA binding
8	5e-32	776 / 6723	CC	membrane
9	9e-32	157 / 717	MF	calcium ion binding
10	2e-29	722 / 6248	CC	integral component of membrane
11	3e-25	368 / 2716	CC	nucleus
12	3e-25	108 / 454	BP	multicellular organism development
13	9e-24	57 / 155	CC	synapse
14	3e-21	107 / 499	BP	ion transport
15	1e-19	71 / 270	MF	ion channel activity
16	2e-19	121 / 633	MF	transcription factor activity, sequence-specific DNA binding
17	2e-18	120 / 643	BP	transcription, DNA-templated
18	2e-16	33 / 78	BP	axon guidance
19	5e-16	21 / 32	MF	extracellular-glutamate-gated ion channel activity
20	5e-16	21 / 32	MF	ionotropic glutamate receptor activity
21	5e-16	21 / 32	BP	ionotropic glutamate receptor signaling pathway
22	2e-15	24 / 44	BP	neuron development
23	7e-15	40 / 124	MF	receptor activity
24	3e-14	45 / 158	MF	microtubule binding
25	7e-13	42 / 153	CC	proteinaceous extracellular matrix
26	5e-12	37 / 130	BP	regulation of ion transmembrane transport
27	5e-12	37 / 130	MF	voltage-gated ion channel activity
28	8e-12	28 / 80	CC	postsynaptic membrane
29	1e-11	20 / 42	MF	voltage-gated calcium channel activity
30	4e-11	37 / 138	BP	potassium ion transport
31	4e-11	27 / 79	BP	excitatory postsynaptic potential
32	6e-11	31 / 103	BP	cell-cell signaling
33	7e-11	119 / 809	CC	integral component of plasma membrane
34	2e-10	18 / 39	BP	neuron projection development
35	3e-10	37 / 147	BP	brain development
36	3e-10	12 / 17	CC	presynaptic active zone
37	9e-10	16 / 33	CC	voltage-gated calcium channel complex
38	3e-09	16 / 35	BP	calcium ion-regulated exocytosis of neurotransmitter
39	3e-09	29 / 106	BP	calcium ion transmembrane transport
40	6e-09	9/11	BP	modulation of synaptic transmission



BP				СС				MF			
Rank	p-value	#in/all	Geneset	Rank	p-value	#in/all	Geneset	Rank	p-value	#in/all	Geneset
1	4e-50	123 / 333	cell adhesion	1	1e-36	225 / 1162	plasma membrane	1	5e-49	158 / 537	sequence–specific DNA binding
2	4e-49	87 / 172	homophilic cell adhesion via plasma membrane adhesion molecules	2	5e-32	776 / 6723	membrane	2	3e-36	264 / 1484	DNA binding
3	5e-49	260 / 1239	egulation of transcription, DNA-templated	3	2e-29	722 / 6248	integral component of membrane	3	9e-32	157 / 717	calcium ion binding
4	4e-42	81 / 175	nervous system development	4	3e-25	368 / 2716	nucleus	4	1e-19	71 / 270	ion channel activity
5	3e-25	108 / 454	multicellular organism development	5	9e-24	57 / 155	synapse	5	2e-19	121 / 633	transcription factor activity, sequence–specific DNA binding
6	3e-21	107 / 499	ion transport	6	7e-13	42 / 153	proteinaceous extracellular matrix	6	5e-16	21 / 32	extracellular-glutamate-gated ion channel activity
7	2e-18	120 / 643	transcription, DNA-templated	7	8e-12	28 / 80	postsynaptic membrane	7	5e-16	21 / 32	ionotropic glutamate receptor activity
8	2e-16	33 / 78	axon guidance	8	7e-11	119 / 809	integral component of plasma membrane	8	7e-15	40 / 124	receptor activity
9	5e-16	21 / 32	ionotropic glutamate receptor signaling pathway	9	3e-10	12/17	presynaptic active zone	9	3e-14	45 / 158	microtubule binding
10	2e-15	24 / 44	neuron development	10	9e-10	16/33	voltage-gated calcium channel complex	10	5e-12	37 / 130	voltage-gated ion channel activity
11	5e-12	37 / 130	regulation of ion transmembrane transport	11	4e-08	18 / 51	presynapse	11	1e-11	20 / 42	voltage-gated calcium channel activity
12	4e-11	37 / 138	potassium ion transport	12	4e-08	22/74	neuron projection	12	2e-08	11 / 18	tubulin binding
13	4e-11	27 / 79	excitatory postsynaptic potential	13	8e-08	27 / 108	microtubule	13	2e-08	18 / 49	extracellular matrix structural constituent
14	6e-11	31 / 103	cell-cell signaling	14	1e-07	42 / 219	cell junction	14	6e-08	16 / 42	clathrin binding
15	2e-10	18 / 39	neuron projection development	15	1e-07	10 / 17	AMPA glutamate receptor complex	15	8e-08	41 / 210	protein binding