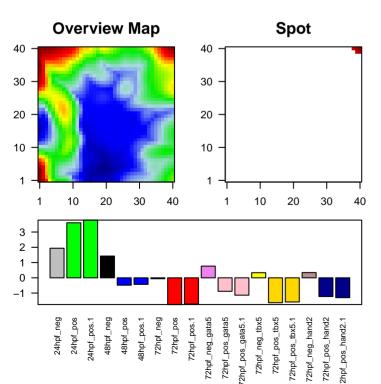


## Spot Summary: A

# metagenes = 5 # genes = 125 <r> metagenes = 1 <r> genes = 0.73 beta: r2= 28.87 / log p= -Inf # samples with spot = 3 ( 16.7 %) 24hpf\_neg : 1 ( 100 %)

24hpf\_pos : 2 ( 100 %)



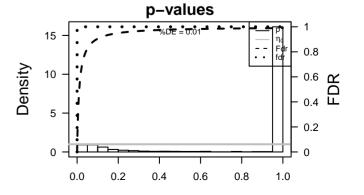
## **Spot Genelist**

Raı	nk ID	max e min e		r e	Symb	Description bol						
1	ENSDARG000	8.12	-6.4	0.89	hbbe3	hemoglobin beta embryonic-3 [Source:ZFIN;Acc:ZDB-GENE						
2	ENSDARG000	7.83	-4.49	0.96	drl	draculin [Source:ZFIN;Acc:ZDB-GENE-991213-3]						
3	ENSDARG000	7.36	-4.55	0.95	si:dkey-	26/19/kely-261j4.4 [Source:ZFIN;Acc:ZDB-GENE-060531-125]						
4	ENSDARG000	7.35	-4.2	0.9	blf	bloody fingers [Source:ZFIN;Acc:ZDB-GENE-050721-1]						
5	ENSDARG000	7.06	-5.06	0.95	si:dkey-	26/1前k会y-261j4.3 [Source:ZFIN;Acc:ZDB-GENE-060531-124]						
6	ENSDARG000	6.46	-4.6	0.75		protogenin homolog b (Gallus gallus) [Source:ZFIN;Acc:ZDB-						
7	ENSDARG000	6.43	-3.22	0.88	stab2	stabilin 2 [Source:ZFIN;Acc:ZDB-GENE-041210-336]						
8	ENSDARG000	6.31	-1.79	0.87	ela2l	elastase 2 like [Source:ZFIN;Acc:ZDB-GENE-040511-1]						
9	ENSDARG000	6.11	-4.16	0.95	tfr1a	transferrin receptor 1a [Source:ZFIN;Acc:ZDB-GENE-04122						
10	ENSDARG000	6	-2.33	0.92		si:ch73-299h12.2 [Source:ZFIN;Acc:ZDB-GENE-081031-7]						
11	ENSDARG000	5.97	-3.89	0.91	klf17	Kruppel-like factor 17 [Source:ZFIN;Acc:ZDB-GENE-01012!						
12	ENSDARG000	5.69	-3.46	0.93	gata1a	GATA binding protein 1a [Source:ZFIN;Acc:ZDB-GENE-980!						
13	ENSDARG000	5.69	-3.04	0.91	gfi1b	growth factor independent 1B transcription repressor [Source						
14	ENSDARG000	5.53	-3.53	0.83								
15	ENSDARG000	5.51	-4.09	0.89	znfl2a	zinc finger-like gene 2a [Source:ZFIN;Acc:ZDB-GENE-0308						
16	ENSDARG000	5.45	-1.91	0.76	срох	coproporphyrinogen oxidase [Source:ZFIN;Acc:ZDB-GENE-						
17	ENSDARG000	5.42	-2.18	0.8	hmbsb	hydroxymethylbilane synthase, b [Source:ZFIN;Acc:ZDB-GEI						
18	ENSDARG000	5.39	-4.85	0.92	hdr	hematopoietic death receptor [Source:ZFIN;Acc:ZDB-GENE-						
19	ENSDARG000	5.3	-2.88	0.84	tbx6l	T-box 6, like [Source:ZFIN;Acc:ZDB-GENE-980526-171]						
20	ENSDARG000	5.29	-4.07	0.89	susd1	sushi domain containing 1 [Source:ZFIN;Acc:ZDB-GENE-06						

### **Geneset Overrepresentation**

Rank p-value #in/all Geneset

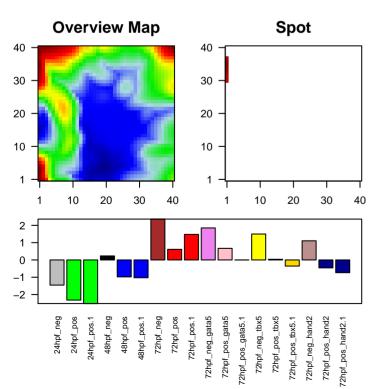
1	2e-21	10 / 14	СС	hemoglobin complex
2	2e-19	10 / 19	MF	oxygen binding
3	2e-19	10 / 19	BP	oxygen transport
4	2e-19	10 / 19	MF	oxygen transporter activity
5	3e-17	10 / 28	BP	embryonic hemopoiesis
6	1e-13	13 / 145	MF	heme binding
7	1e-13	9 / 40	BP	erythrocyte differentiation
8	3e-11	12 / 178	MF	iron ion binding
9	9e-10	6/24	BP	myeloid cell differentiation
10	3e-09	7 / 52	BP	blood vessel development
11	5e-07	4 / 15	BP	heme biosynthetic process
12	1e-06	6 / 75	BP	hemopoiesis
13	2e-06	4 / 21	BP	erythrocyte development
14	3e-06	23 / 1761	MF	metal ion binding
15	5e-06	8/210	MF	protein binding
16	2e-05	3 / 12	BP	hemoglobin biosynthetic process
17	2e-05	4/38	BP	vasculogenesis
18	3e-05	16 / 1084	BP	transport
19	4e-05	10 / 454	BP	multicellular organism development
20	7e-05	4 / 50	BP	vasculature development
21	6e-04	3/37	BP	definitive hemopoiesis
22	7e-04	9 / 537	MF	sequence-specific DNA binding
23	1e-03	3 / 47	MF	structural constituent of cytoskeleton
24	1e-03	14 / 1239	BP	regulation of transcription, DNA-templated
25	1e-03	5 / 183	MF	RNA polymerase II transcription factor activity, sequence-specific DNA
26	1e-03	2 / 13	BP	gastrulation with mouth forming second
27	2e-03	4 / 116	MF	metalloendopeptidase activity
28	2e-03	2/16	BP	defense response
29	2e-03	2/16	BP	vascular endothelial growth factor receptor signaling pathway
30	3e-03	2 / 18	BP	neutrophil differentiation
31	3e-03	2/19	BP	neuron migration
32	4e-03	2/20	BP	positive regulation of gene expression
33	5e-03	2 / 23	MF	hyaluronic acid binding
34	5e-03	2/24	BP	primitive hemopoiesis
35	8e-03	3 / 90	BP	positive regulation of transcription, DNA-templated
36	9e-03	2/32	BP	retinal ganglion cell axon guidance
37	9e-03	2/33	BP	blood vessel morphogenesis
38	9e-03	2/33	BP	hindbrain development
39	1e-02	3 / 109	BP	chordate embryonic development
40	1e-02	2 / 40	BP	heart morphogenesis



BP				СС				MF			
Rank	p-value	#in/all	Geneset	Rank	p-value	#in/all	Geneset	Rank	p-value	#in/all	Geneset
1	2e-19	10 / 19	oxygen transport	1	2e-21	10 / 14	hemoglobin complex	1	2e-19	10 / 19	oxygen binding
2	3e-17	10 / 28	embryonic hemopoiesis	2	2e-02	2/51	lysosomal membrane	2	2e-19	10 / 19	oxygen transporter activity
3	1e-13	9 / 40	erythrocyte differentiation	3	3e-02	4 / 268	cytoskeleton	3	1e-13	13 / 145	heme binding
4	9e-10	6 / 24	myeloid cell differentiation	4	4e-02	3 / 161	mitochondrial inner membrane	4	3e-11	12 / 178	iron ion binding
5	3e-09	7 / 52	blood vessel development	5	5e-02	1/11	exocytic vesicle	5	3e-06	23 / 1761	metal ion binding
6	5e-07	4 / 15	heme biosynthetic process	6	7e-02	7 / 809	integral component of plasma membrane	6	5e-06	8 / 210	protein binding
7	1e-06	6 / 75	hemopoiesis	7	7e-02	1 / 17	external side of plasma membrane	7	7e-04	9 / 537	sequence–specific DNA binding
8	2e-06	4 / 21	erythrocyte development	8	7e-02	1 / 17	integral component of nuclear inner membrane	8	1e-03	3 / 47	structural constituent of cytoskeleton
9	2e-05	3 / 12	hemoglobin biosynthetic process	9	7e-02	2/101	endosome	9	1e-03	5 / 183	RNA polymerase II transcription factor activity, sequence–specific DNA bindir
10	2e-05	4 / 38	vasculogenesis	10	8e-02	35 / 6248	integral component of membrane	10	2e-03	4 / 116	metalloendopeptidase activity
11	3e-05	16 / 1084	transport	11	9e-02	17 / 2716	nucleus	11	5e-03	2 / 23	hyaluronic acid binding
12	4e-05	10 / 454	multicellular organism development	12	1e-01	1 / 24	early endosome	12	1e-02	8 / 717	calcium ion binding
13	7e-05	4 / 50	vasculature development	13	1e-01	1/26	vesicle	13	2e-02	3 / 128	metallopeptidase activity
14	6e-04	3 / 37	definitive hemopoiesis	14	1e-01	1 / 32	chromatin	14	2e-02	2 / 52	transmembrane receptor protein tyrosine kinase activity
15	1e-03	14 / 1239	regulation of transcription, DNA-templated	15	1e-01	1 / 36	P-body	15	2e-02	7 / 633	transcription factor activity, sequence–specific DNA binding

### Spot Summary: B

72hpf\_neg\_gata5 : 1 ( 100 %)



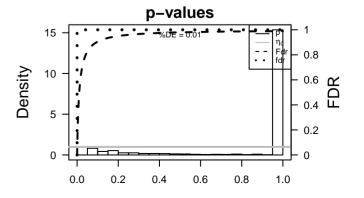
## **Spot Genelist**

Rai	nk ID	max	e min e	r ∋	Symb	Description ool
1	ENSDARG000	11.88	-0.87	0.42		
2	ENSDARG000	5.44	-2.17	0.81	opn1sw2	2 opsin 1 (cone pigments), short-wave-sensitive 2 [Source:ZFI
3	ENSDARG000	5.34	-6.98	0.93	matn1	matrilin 1 [Source:ZFIN;Acc:ZDB-GENE-050307-3]
4	ENSDARG000	5.22	-3.71	0.82	opn1mw	1opsin 1 (cone pigments), medium-wave-sensitive, 1 [Source:
5	ENSDARG000	5.16	-4.48	0.78	opn1sw1	opsin 1 (cone pigments), short-wave-sensitive 1 [Source:ZFI
6	ENSDARG000	5.14	-4.55	0.96	rho	rhodopsin [Source:ZFIN;Acc:ZDB-GENE-990415-271]
7	ENSDARG000	5.09	-5.91	0.88	and2	actinodin2 [Source:ZFIN;Acc:ZDB-GENE-041105-2]
8	ENSDARG000	5.01	-4.88	0.95	opn1lw2	opsin 1 (cone pigments), long-wave-sensitive, 2 [Source:ZFI
9	ENSDARG000	4.9	-3.66	0.87	and1	actinodin1 [Source:ZFIN;Acc:ZDB-GENE-030131-9105]
10	ENSDARG000	4.83	-5.45	0.97	arr3a	arrestin 3a, retinal (X-arrestin) [Source:ZFIN;Acc:ZDB-GENE
11	ENSDARG000	4.82	-3.89	0.9	gnb3b	guanine nucleotide binding protein (G protein), beta polypepti
12	ENSDARG000	4.71	-3.52	0.92	rcvrn3	recoverin 3 [Source:ZFIN;Acc:ZDB-GENE-040426-1661]
13	ENSDARG000	4.57	-3.71	0.85	pde6c	phosphodiesterase 6C, cGMP-specific, cone, alpha prime [Si
14	ENSDARG000	4.55	-3.73	0.85		
15	ENSDARG000	4.55	-4.06	0.87	gnat2	guanine nucleotide binding protein (G protein), alpha transdu
16	ENSDARG000	4.25	-2.5	0.83	opn1lw1	opsin 1 (cone pigments), long-wave-sensitive, 1 [Source:ZFI
17	ENSDARG000	4.23	-1.93	0.68	fbp2	fructose-1,6-bisphosphatase 2 [Source:ZFIN;Acc:ZDB-GEN
18	ENSDARG000	4.19	-2.48	0.74	and3	actinodin3 [Source:ZFIN;Acc:ZDB-GENE-040724-185]
19	ENSDARG000	4.19	-3.55	0.84	scn4ab	sodium channel, voltage-gated, type IV, alpha, b [Source:ZFI
20	ENSDARG000	4.16	-2.83	0.78	pde6h	phosphodiesterase 6H, cGMP-specific, cone, gamma [Sourc

## Geneset Overrepresentation

Rank p-value #in/all Geneset

rtanit	p	// III // CIII	001	110001
1	3e-19	16 / 83	BP	visual perception
	2e-09	7 / 33	MF	photoreceptor activity
3	3e-08	6 / 28	BP	phototransduction
4	4e-08	7 / 49	MF	extracellular matrix structural constituent
5	5e-08	6/31	CC	photoreceptor outer segment
2 3 4 5 6 7	5e-08	6 / 31	BP	protein-chromophore linkage
7	2e-07	7 / 62	CC	intermediate filament
8	2e-06	17 / 634	CC	extracellular region
9	2e-06	5 / 31	MF	G-protein coupled photoreceptor activity
10	6e-06	7 / 102	BP	response to stimulus
11	8e-06	17 / 717	MF	calcium ion binding
12	1e-05	8 / 153	CC	proteinaceous extracellular matrix
13	3e-05	5 / 55	BP	central nervous system development
14	3e-05	3 / 10	MF	small molecule binding
15	5e-05	20 / 1084	BP	transport
16	5e-05	4 / 30	BP	detection of visible light
17	1e-04	7 / 159	MF	structural molecule activity
18	2e-04	4 / 41	MF	copper ion binding
19	2e-04	8 / 229	MF	transporter activity
20	3e-04	3 / 20	BP	fin development
21	5e-04	3 / 23	MF	hyaluronic acid binding
22	6e-04	11 / 499	BP	ion transport
23	8e-04	5 / 106	BP	calcium ion transmembrane transport
24	9e-04	3 / 28	BP	skeletal system development
25	1e-03	3 / 29	MF	3',5'-cyclic-nucleotide phosphodiesterase activity
26	1e-03	4 / 65	BP	sodium ion transport
27	1e-03	4 / 70	BP	sodium ion transmembrane transport
28	2e-03	4 / 74	CC	neuron projection
29	2e-03	3 / 35	BP	cellular calcium ion homeostasis
30	2e-03	4 / 79	MF	calcium channel activity
31	2e-03	63 / 6723	CC	membrane
32	2e-03	2 / 11	MF	oxidoreductase activity, acting on the CH-NH2 group of donors, oxygen
33	3e-03	2 / 12	BP	photoreceptor cell maintenance
34	3e-03	18 / 1295	BP	signal transduction
35	3e-03	2 / 13	BP	synaptic vesicle endocytosis
36	4e-03	2 / 14	BP	inner ear morphogenesis
37	4e-03	2 / 14	BP	regulation of cytosolic calcium ion concentration
38	4e-03	2/14	MF	sodium:bicarbonate symporter activity
39	4e-03	58 / 6248	CC	integral component of membrane
40	5e-03	6 / 231	MF	actin binding



ВР				СС				MF			
Rank	p-value	#in/all	Geneset	Rank	p-value	#in/all	Geneset	Rank	p-value	#in/all	Geneset
1	3e-19	16 / 83	visual perception	1	5e-08	6/31	photoreceptor outer segment	1	2e-09	7 / 33	photoreceptor activity
2	3e-08	6 / 28	phototransduction	2	2e-07	7 / 62	intermediate filament	2	4e-08	7 / 49	extracellular matrix structural constituent
3	5e-08	6/31	protein-chromophore linkage	3	2e-06	17 / 634	extracellular region	3	2e-06	5 / 31	G-protein coupled photoreceptor activity
4	6e-06	7 / 102	response to stimulus	4	1e-05	8 / 153	proteinaceous extracellular matrix	4	8e-06	17 / 717	calcium ion binding
5	3e-05	5 / 55	central nervous system development	5	2e-03	4 / 74	neuron projection	5	3e-05	3 / 10	small molecule binding
6	5e-05	20 / 1084	transport	6	2e-03	63 / 6723	membrane	6	1e-04	7 / 159	structural molecule activity
7	5e-05	4/30	detection of visible light	7	4e-03	58 / 6248	integral component of membrane	7	2e-04	4 / 41	copper ion binding
8	3e-04	3 / 20	fin development	8	1e-02	2/22	synaptic vesicle membrane	8	2e-04	8 / 229	transporter activity
9	6e-04	11 / 499	ion transport	9	1e-02	3/70	myosin complex	9	5e-04	3 / 23	hyaluronic acid binding
10	8e-04	5 / 106	calcium ion transmembrane transport	10	3e-02	2/38	apical plasma membrane	10	1e-03	3 / 29	3',5'-cyclic-nucleotide phosphodiesterase activity
11	9e-04	3 / 28	skeletal system development	11	4e-02	2 / 48	heterotrimeric G-protein complex	11	2e-03	4/79	calcium channel activity
12	1e-03	4 / 65	sodium ion transport	12	5e-02	10 / 809	integral component of plasma membrane	12	2e-03	2/11	oxidoreductase activity, acting on the CH-NH2 group of donors, oxygen as ac
13	1e-03	4/70	sodium ion transmembrane transport	13	5e-02	13 / 1162	plasma membrane	13	4e-03	2 / 14	sodium:bicarbonate symporter activity
14	2e-03	3 / 35	cellular calcium ion homeostasis	14	7e-02	1/11	BLOC-1 complex	14	5e-03	6 / 231	actin binding
15	3e-03	2 / 12	photoreceptor cell maintenance	15	7e-02	1/11	membrane attack complex	15	5e-03	2 / 16	anion transmembrane transporter activity

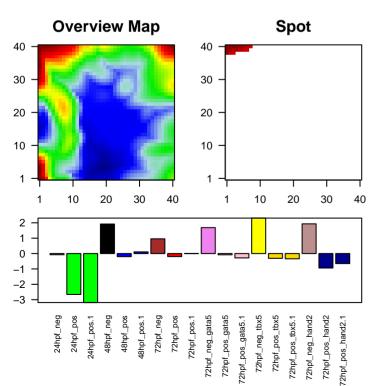
### Spot Summary: C

# genes = 474

# metagenes = 18

<r> metagenes = 0.97</r> <r> genes = 0.77</ri> beta: r2= 31.1 / log p= -Inf

# samples with spot = 3 ( 16.7 %)
48hpf\_neg : 1 ( 100 %)
72hpf\_neg\_tbx5 : 1 ( 100 %)
72hpf\_neg\_hand2 : 1 ( 100 %)



## **Spot Genelist**

19 ENSDARG000 3.61

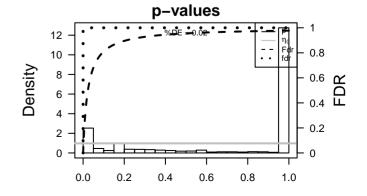
Rar	nk ID	max	e min e	r e	Symb	Description ool	Rank	p-value	#in/all	Ger	neset
1	ENSDARG000	5.4	-5.6	0.79	muc5.1	mucin 5.1, oligomeric mucus/gel-forming [Source:ZFIN;Acc:Z	1 2	2e-23 1e-22	51 / 537 31 / 175	MF BP	sequeno
2	ENSDARG000	5.19	-6.04	0.53	atp1a1a.	2ATPase, Na+/K+ transporting, alpha 1a polypeptide, tandem (	3	5e-16 3e-14	65 / 1239 22 / 158	BP MF	regulation
3	ENSDARG000	4.85	-4.47	0.72	npas4a	neuronal PAS domain protein 4a [Source:ZFIN;Acc:ZDB-GEI	5	1e-13 2e-12	35 / 454 21 / 172	BP BP	multicellu homophi
4	ENSDARG000	4.76	-5.55	0.77	col10a1a	acollagen, type X, alpha 1a [Source:ZFIN;Acc:ZDB-GENE-03	7 8	2e-12 2e-11	65 / 1484 19 / 155	MF CC	DNA bind
5	ENSDARG000	4.72	-8.26	0.87	col11a2	collagen, type XI, alpha 2 [Source:ZFIN;Acc:ZDB-GENE-000	9 10	3e-11 2e-10	93 / 2716 52 / 1162	CC	nucleus plasma r
6	ENSDARG000	4.49	-6.7	0.85		si:dkey-65b12.6 [Source:ZFIN;Acc:ZDB-GENE-060526-329	11 12	4e-10 8e-10	15 / 108 19 / 193	CC BP	microtub positive r
7	ENSDARG000	4.01	-3.22	0.94	sv2a	synaptic vesicle glycoprotein 2A [Source:ZFIN;Acc:ZDB-GEN	13 14	3e-09 7e-09	24 / 333 14 / 113	BP BP	cell adhe transcrip
8	ENSDARG000	4.01	-6.39	0.88	col9a3	collagen, type IX, alpha 3 [Source:ZFIN;Acc:ZDB-GENE-03(	15 16	2e-08 2e-08	33 / 643 35 / 717	BP MF	transcrip calcium i
9	ENSDARG000	4	-6.25	0.81	ерус	epiphycan [Source:ZFIN;Acc:ZDB-GENE-041008-9]	17 18	5e-08 5e-08	8 / 32 8 / 32	MF MF	ionotropi
10	ENSDARG000	3.9	-5.96	0.97	stx1b	syntaxin 1B [Source:ZFIN;Acc:ZDB-GENE-000330-4]	19 20	5e-08 1e-07	8 / 32 9 / 49	BP MF	extracelli
11	ENSDARG000	3.88	-5.45	0.91	grin1b	glutamate receptor, ionotropic, N-methyl D-aspartate 1b [Soi	21 22	1e-07 4e-07	27 / 499 9 / 57	BP BP	ion trans
12	ENSDARG000	3.88	-6.3	0.95	pclob	piccolo presynaptic cytomatrix protein b [Source:ZFIN;Acc:ZC	23 24 25	5e-07 8e-07	30 / 633 10 / 78	MF BP BP	axon gui
13	ENSDARG000	3.79	-5.15	0.82	fgfbp2b	fibroblast growth factor binding protein 2b [Source:ZFIN;Acc:2	26 27	1e-06 3e-06 3e-06	13 / 147 14 / 183 157 / 6723	MF CC	RNA poly
14	ENSDARG000	3.75	-3.97	0.91	slc32a1	solute carrier family 32 (GABA vesicular transporter), membe	28 29	4e-06 4e-06	7/39 9/74	BP CC	neuron p
15	ENSDARG000	3.71	-5.4	0.95	slc6a1b	solute carrier family 6 (neurotransmitter transporter), member	30 31	5e-06 7e-06	15 / 219 5 / 17	CC BP	cell junct
16	ENSDARG000	3.69	-4.33	0.95	gad2	glutamate decarboxylase 2 [Source:ZFIN;Acc:ZDB-GENE-0:	32 33	7e-06 7e-06	5 / 17 9 / 79	CC BP	presynap
17	ENSDARG000	3.68	-6.04	0.66	atp1b1b	ATPase, Na+/K+ transporting, beta 1b polypeptide [Source:ZI	34	8e-06	7 / 44	BP	neuron d

atp2b3a ATPase, Ca++ transporting, plasma membrane 3a [Source:Zf

adenylate cyclase activating polypeptide 1a (pituitary) receptor synaptotagmin Ia [Source:ZFIN;Acc:ZDB-GENE-040718-16

#### **Geneset Overrepresentation**

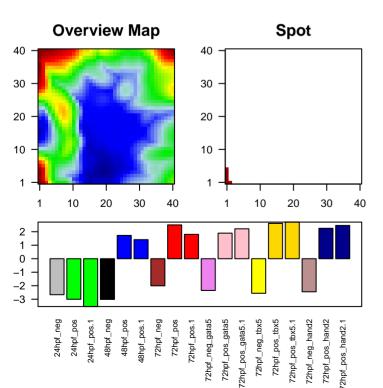
rtaint	p raide	min, an	001	
4	2- 22	E4 / E07	MF	sequence–specific DNA binding
1	2e-23 1e-22	51 / 537 31 / 175	BP	nervous system development
2 3 4 5 6 7	5e-16	65 / 1239	BP	regulation of transcription, DNA-templated
3 1	3e-16		MF	microtubule binding
4	1e-13	22 / 158 35 / 454	BP	multicellular organism development
5	2e-12	21 / 172	BP	homophilic cell adhesion via plasma membrane adhesion molecules
0	2e-12 2e-12	65 / 1484	MF	DNA binding
8	2e-12 2e-11	19 / 155	CC	synapse
9	3e-11	93 / 2716	CC	nucleus
10	2e-10	52 / 1162	CC	plasma membrane
11	4e-10	15 / 108	CC	microtubule
12	8e-10	19 / 193	BP	positive regulation of transcription from RNA polymerase II promoter
13	3e-09	24 / 333	BP	cell adhesion
14	7e-09	14 / 113	BP	transcription from RNA polymerase II promoter
15	2e-08	33 / 643	BP	transcription, DNA-templated
16	2e-08	35 / 717	MF	calcium ion binding
17	5e-08	8 / 32	MF	extracellular-glutamate-gated ion channel activity
18	5e-08	8 / 32	MF	ionotropic glutamate receptor activity
19	5e-08	8 / 32	BP	ionotropic glutamate receptor signaling pathway
20	1e-07	9 / 49	MF	extracellular matrix structural constituent
21	1e-07	27 / 499	BP	ion transport
22	4e-07	9 / 57	BP	microtubule cytoskeleton organization
23	5e-07	30 / 633	MF	transcription factor activity, sequence–specific DNA binding
24	8e-07	10 / 78	BP	axon guidance
25	1e-06	13 / 147	BP	brain development
26	3e-06	14 / 183	MF	RNA polymerase II transcription factor activity, sequence-specific DNA
27	3e-06	157 / 6723	CC	membrane
28	4e-06	7 / 39	BP	neuron projection development
29	4e-06	9/74	CC	neuron projection
30	5e-06	15 / 219	CC	cell junction
31	7e-06	5 / 17	BP	cytoskeleton-dependent intracellular transport
32	7e-06	5 / 17	CC	presynaptic active zone
33	7e-06	9 / 79	BP	excitatory postsynaptic potential
34	8e-06	7 / 44	BP	neuron development
35	1e-05	5 / 18	MF	tubulin binding
36	1e-05	7 / 46	BP	eye development
37	1e-05	8 / 65	BP	sodium ion transport
38	2e-05	16 / 270	MF	ion channel activity
39	2e-05	6 / 33	BP	hindbrain development
40	2e-05	4 / 11	MF	spectrin binding



BP				СС				MF			
Rank	p-value	#in/all	Geneset	Rank	p-value	#in/all	Geneset	Rank	p-value	#in/all	Geneset
1	1e-22	31 / 175	nervous system development	1	2e-11	19 / 155	synapse	1	2e-23	51 / 537	sequence–specific DNA binding
2	5e-16	65 / 1239	regulation of transcription, DNA-templated	2	3e-11	93 / 2716	nucleus	2	3e-14	22 / 158	microtubule binding
3	1e-13	35 / 454	multicellular organism development	3	2e-10	52 / 1162	plasma membrane	3	2e-12	65 / 1484	DNA binding
4	2e-12	21 / 172	homophilic cell adhesion via plasma membrane adhesion molecules	4	4e-10	15 / 108	microtubule	4	2e-08	35 / 717	calcium ion binding
5	8e-10	19 / 193	positive regulation of transcription from RNA polymerase II promoter	5	3e-06	157 / 6723	membrane	5	5e-08	8 / 32	extracellular-glutamate-gated ion channel activity
6	3e-09	24 / 333	cell adhesion	6	4e-06	9/74	neuron projection	6	5e-08	8 / 32	ionotropic glutamate receptor activity
7	7e-09	14 / 113	transcription from RNA polymerase II promoter	7	5e-06	15 / 219	cell junction	7	1e-07	9 / 49	extracellular matrix structural constituent
8	2e-08	33 / 643	transcription, DNA-templated	8	7e-06	5 / 17	presynaptic active zone	8	5e-07	30 / 633	transcription factor activity, sequence–specific DNA binding
9	5e-08	8 / 32	ionotropic glutamate receptor signaling pathway	9	3e-05	6/36	synaptic vesicle	9	3e-06	14 / 183	RNA polymerase II transcription factor activity, sequence–specific DNA bindir
10	1e-07	27 / 499	ion transport	10	6e-05	8 / 80	postsynaptic membrane	10	1e-05	5 / 18	tubulin binding
11	4e-07	9/57	microtubule cytoskeleton organization	11	1e-04	140 / 6248	integral component of membrane	11	2e-05	16 / 270	ion channel activity
12	8e-07	10 / 78	axon guidance	12	2e-04	4/17	AMPA glutamate receptor complex	12	2e-05	4/11	spectrin binding
13	1e-06	13 / 147	brain development	13	5e-04	3/10	clathrin-coated vesicle	13	4e-05	10 / 120	motor activity
14	4e-06	7 / 39	neuron projection development	14	7e-04	13 / 268	cytoskeleton	14	5e-05	10 / 124	receptor activity
15	7e-06	5 / 17	cytoskeleton-dependent intracellular transport	15	9e-04	4 / 26	microtubule cytoskeleton	15	1e-04	6 / 47	structural constituent of cytoskeleton

### Spot Summary: D

# metagenes = 6 # genes = 189 <r> metagenes = 0.98 <r> genes = 0.81 beta: r2= 70.07 / log p= -Inf # samples with spot = 8 ( 44.4 %) 72hpf\_pos: 2 ( 100 %) 72hpf\_pos\_gata5: 2 ( 100 %) 72hpf\_pos\_hand2: 2 ( 100 %)



## **Spot Genelist**

max e

Rank

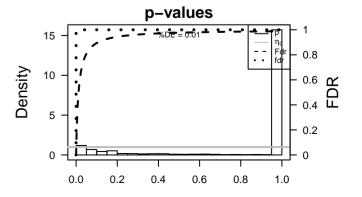
Nai	ID	min e			Syml	ool
1	ENSDARG000	5.16	-6.13	0.97	oacyl	O-acyltransferase like [Source:ZFIN;Acc:ZDB-GENE-09071
2	ENSDARG000	4.98	-7.11	0.95	wu:fc46	h 1/2u:fc46h12 [Source:ZFIN;Acc:ZDB-GENE-030131-3611]
3	ENSDARG000	4.9	-4.2	0.73	zgc:112	2@gc:112265 [Source:ZFIN;Acc:ZDB-GENE-050626-133]
4	ENSDARG000	4.88	-6.93	0.94	si:dkey-	25/1dtk@2-251i10.2 [Source:ZFIN;Acc:ZDB-GENE-050506-10:
5	ENSDARG000	4.84	-5.75	0.81	serpina <sup>2</sup>	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	4.71	-7.81	0.91	gch2	GTP cyclohydrolase 2 [Source:ZFIN;Acc:ZDB-GENE-00120:
8	ENSDARG000	4.69	-4.69	0.69	agxtb	alanine-glyoxylate aminotransferase b [Source:ZFIN;Acc:ZDI
9	ENSDARG000	4.67	-4.1	0.8	plg	plasminogen [Source:ZFIN;Acc:ZDB-GENE-030131-1411]
10	ENSDARG000	4.58	-3.93	0.72	fga	fibrinogen alpha chain [Source:ZFIN;Acc:ZDB-GENE-03101
11	ENSDARG000	4.57	-5.01	0.84	serpina <sup>4</sup>	1 serpin peptidase inhibitor, clade A (alpha-1 antiproteinase, ar
12	ENSDARG000	4.53	-5.75	0.99		si:dkey-73n8.3 [Source:ZFIN;Acc:ZDB-GENE-141219-27]
13	ENSDARG000	4.53	-4.41	0.83	fgb	fibrinogen beta chain [Source:ZFIN;Acc:ZDB-GENE-030131
14	ENSDARG000	4.51	-4.97	0.95	zgc:113	14gc:113142 [Source:ZFIN;Acc:ZDB-GENE-050220-2]
15	ENSDARG000	4.47	-7.23	0.96	xdh	xanthine dehydrogenase [Source:ZFIN;Acc:ZDB-GENE-070
16	ENSDARG000	4.44	-6.92	0.95	zgc:162	15gc:162150 [Source:ZFIN;Acc:ZDB-GENE-070410-23]
17	ENSDARG000	4.4	-6.51	0.98	bscl2l	Bernardinelli-Seip congenital lipodystrophy 2, like [Source:ZF
18	ENSDARG000	4.4	-5.48	0.94	uraha	urate (5-hydroxyiso-) hydrolase a [Source:ZFIN;Acc:ZDB-Gl
19	ENSDARG000	4.39	-5.45	0.95	sprb	sepiapterin reductase b [Source:ZFIN;Acc:ZDB-GENE-0707
20	ENSDARG000	4.38	-5.44	0.9		6-pyruvoyltetrahydropterin synthase [Source:ZFIN;Acc:ZDB-

Description

### **Geneset Overrepresentation**

Rank p-value #in/all Geneset

1	9e-13	11 / 67	BP	lipid transport
2	2e-12	8 / 23	BP	lipoprotein metabolic process
3	6e-11	23 / 634	CC	extracellular region
4	3e-09	5/10	CC	chylomicron
5	2e-08	21 / 712	BP	oxidation-reduction process
6	6e-08	9 / 109	BP	negative regulation of endopeptidase activity
7	8e-08	6/33	MF	endopeptidase inhibitor activity
8	4e-07	4/10	CC	high-density lipoprotein particle
9	4e-07	4/10	CC	melanosome
10	4e-07	4/10	BP	triglyceride catabolic process
11	6e-07	5 / 25	BP	cellular response to estrogen stimulus
12	6e-07	4/11	BP	cholesterol homeostasis
13	9e-07	4 / 12	BP	cholesterol biosynthetic process
14	1e-06	4 / 13	BP	cholesterol efflux
15	3e-06	15 / 522	MF	oxidoreductase activity
16	4e-06	4 / 17	CC	blood microparticle
17	4e-06	4 / 17	MF	cholesterol binding
18	4e-06	4 / 17	MF	cholesterol transporter activity
19	7e-06	7 / 105	MF	lipid binding
20	3e-05	3 / 10	MF	protein binding, bridging
21	4e-05	13 / 500	CC	extracellular space
22	5e-05	3 / 11	BP	melanosome organization
23	6e-05	3 / 12	BP	aromatic amino acid family metabolic process
24	6e-05	3 / 12	BP	platelet activation
25	7e-05	10 / 321	MF	GTPase activity
26	1e-04	3 / 15	CC	secretory granule
27	4e-04	3 / 21	MF	substrate-specific transmembrane transporter activity
28	4e-04	12 / 561	MF	GTP binding
29	7e-04	3 / 26	BP	melanosome transport
30	7e-04	3 / 26	CC	vesicle
31	8e-04	3 / 27	BP	response to bacterium
32	1e-03	3 / 30	BP	pigmentation
33	1e-03	4 / 67	MF	transmembrane transporter activity
34	1e-03	3 / 31	BP	protein-chromophore linkage
35	1e-03	3 / 33	MF	photoreceptor activity
36	2e-03	3 / 35	CC	peroxisome
37	2e-03	4 / 80	BP	liver development
38	2e-03	3 / 38	CC	trans-Golgi network
39	3e-03	2/12	BP	regulation of axon extension
40	3e-03	3 / 43	MF	iron-sulfur cluster binding



BP				СС				MF			
Rank	p-value	#in/all	Geneset	Rank	p-value	#in/all	Geneset	Rank	p-value	#in/all	Geneset
1	9e-13	11 / 67	lipid transport	1	6e-11	23 / 634	extracellular region	1	8e-08	6/33	endopeptidase inhibitor activity
2	2e-12	8 / 23	lipoprotein metabolic process	2	3e-09	5/10	chylomicron	2	3e-06	15 / 522	oxidoreductase activity
3	2e-08	21 / 712	oxidation-reduction process	3	4e-07	4/10	high-density lipoprotein particle	3	4e-06	4 / 17	cholesterol binding
4	6e-08	9 / 109	negative regulation of endopeptidase activity	4	4e-07	4/10	melanosome	4	4e-06	4 / 17	cholesterol transporter activity
5	4e-07	4 / 10	triglyceride catabolic process	5	4e-06	4 / 17	blood microparticle	5	7e-06	7 / 105	lipid binding
6	6e-07	5 / 25	cellular response to estrogen stimulus	6	4e-05	13 / 500	extracellular space	6	3e-05	3/10	protein binding, bridging
7	6e-07	4/11	cholesterol homeostasis	7	1e-04	3 / 15	secretory granule	7	7e-05	10 / 321	GTPase activity
8	9e-07	4 / 12	cholesterol biosynthetic process	8	7e-04	3 / 26	vesicle	8	4e-04	3 / 21	substrate-specific transmembrane transporter activity
9	1e-06	4 / 13	cholesterol efflux	9	2e-03	3 / 35	peroxisome	9	4e-04	12 / 561	GTP binding
10	5e-05	3/11	melanosome organization	10	2e-03	3/38	trans-Golgi network	10	1e-03	4 / 67	transmembrane transporter activity
11	6e-05	3 / 12	aromatic amino acid family metabolic process	11	1e-02	3/70	myosin complex	11	1e-03	3/33	photoreceptor activity
12	6e-05	3 / 12	platelet activation	12	1e-02	59 / 6723	membrane	12	3e-03	3 / 43	iron-sulfur cluster binding
13	7e-04	3 / 26	melanosome transport	13	2e-02	55 / 6248	integral component of membrane	13	3e-03	2/13	amyloid-beta binding
14	8e-04	3 / 27	response to bacterium	14	3e-02	2 / 42	mitochondrial membrane	14	4e-03	2/15	transaminase activity
15	1e-03	3 / 30	pigmentation	15	4e-02	17 / 1580	cellular_component	15	5e-03	6 / 229	transporter activity