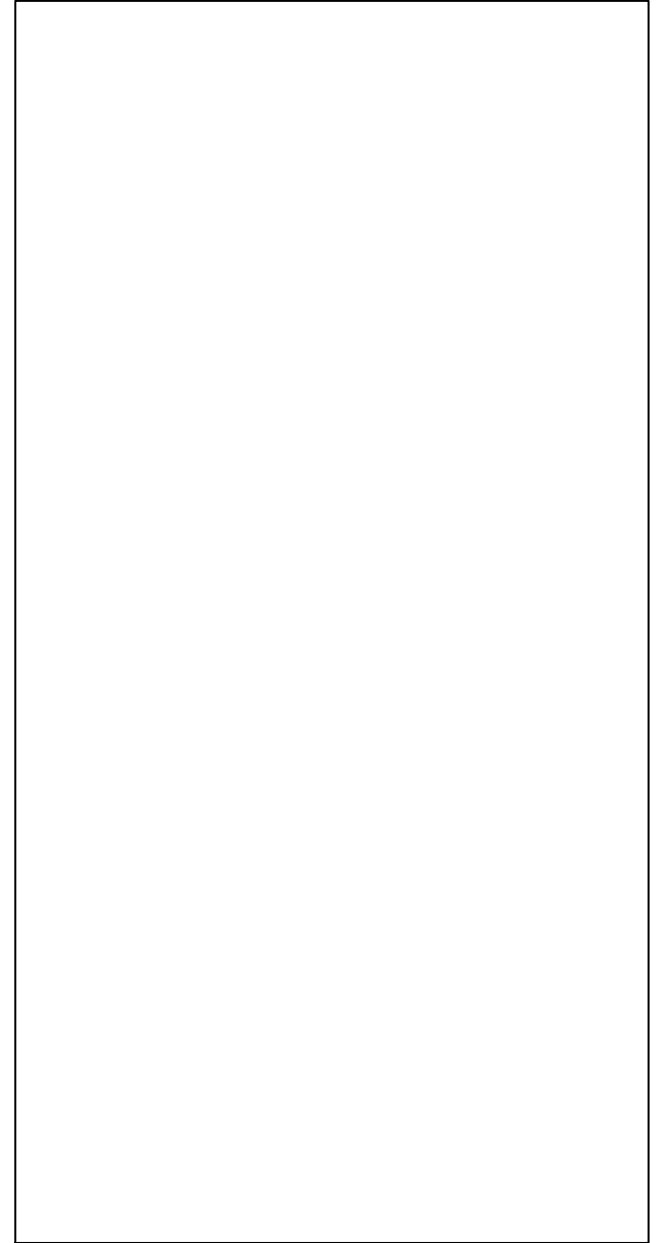
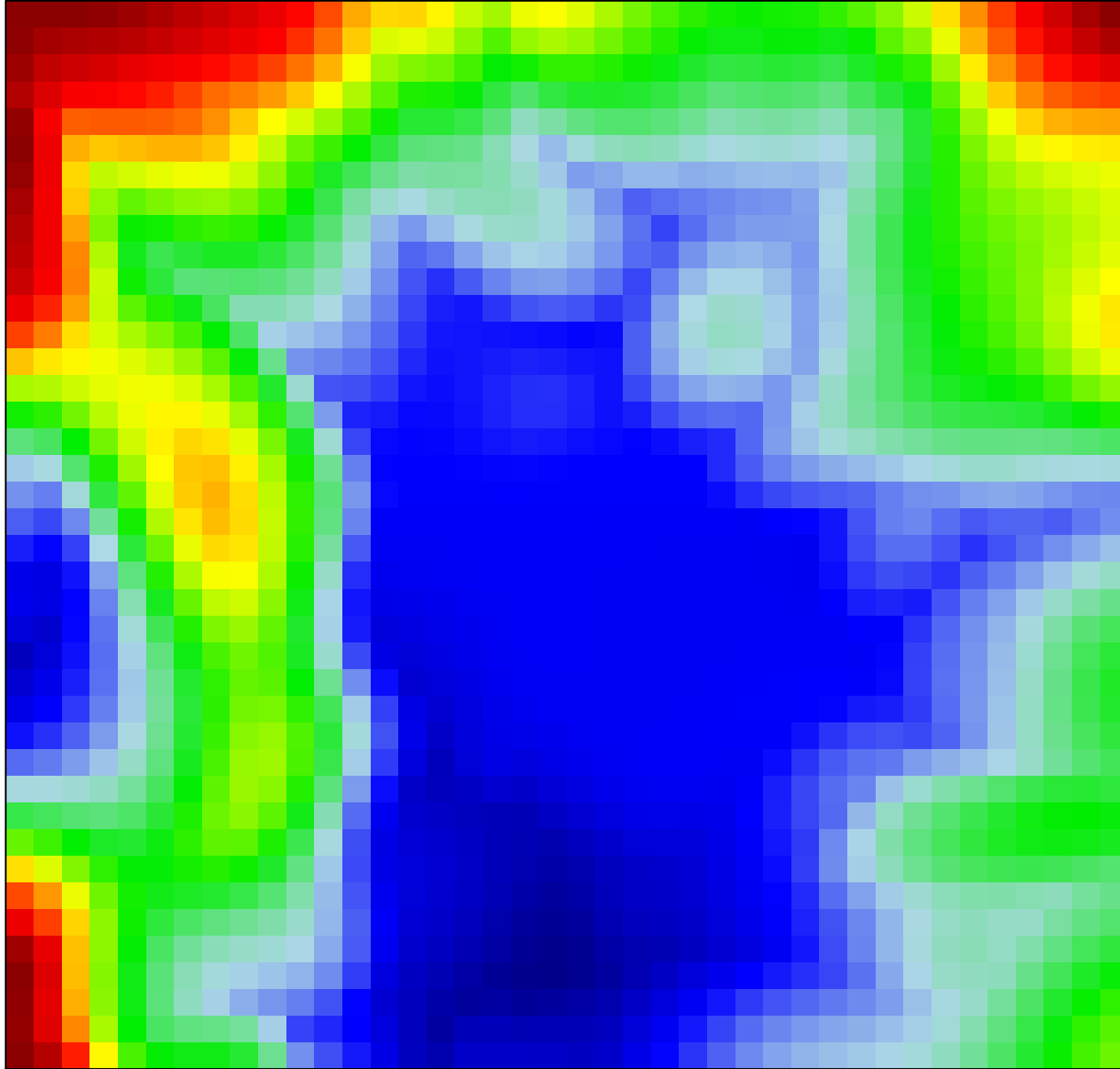
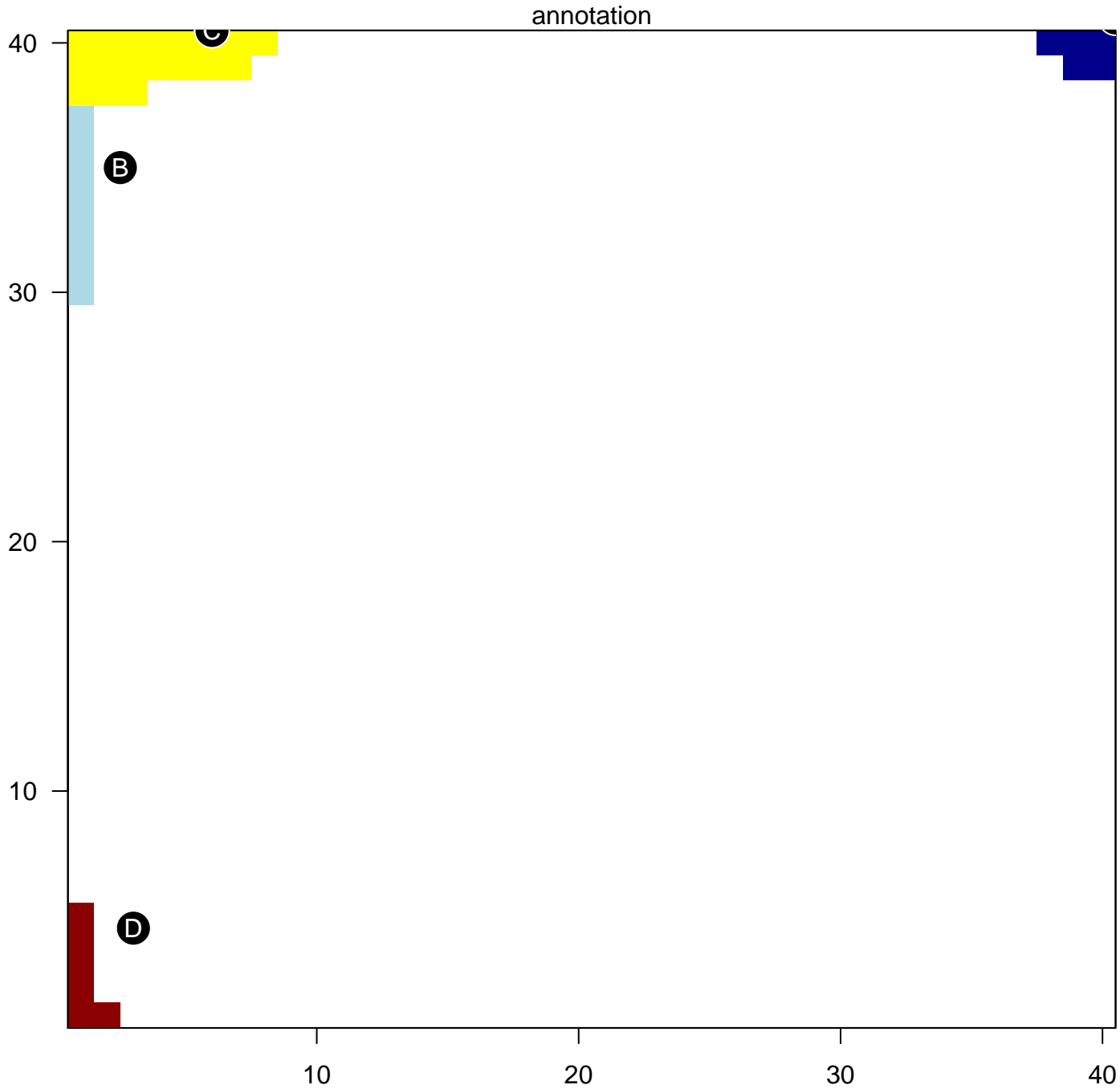


Overexpression Spots

landscape



Overexpression Spots



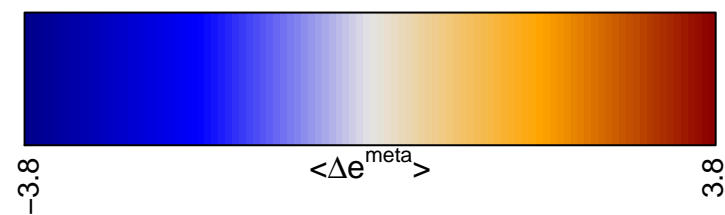
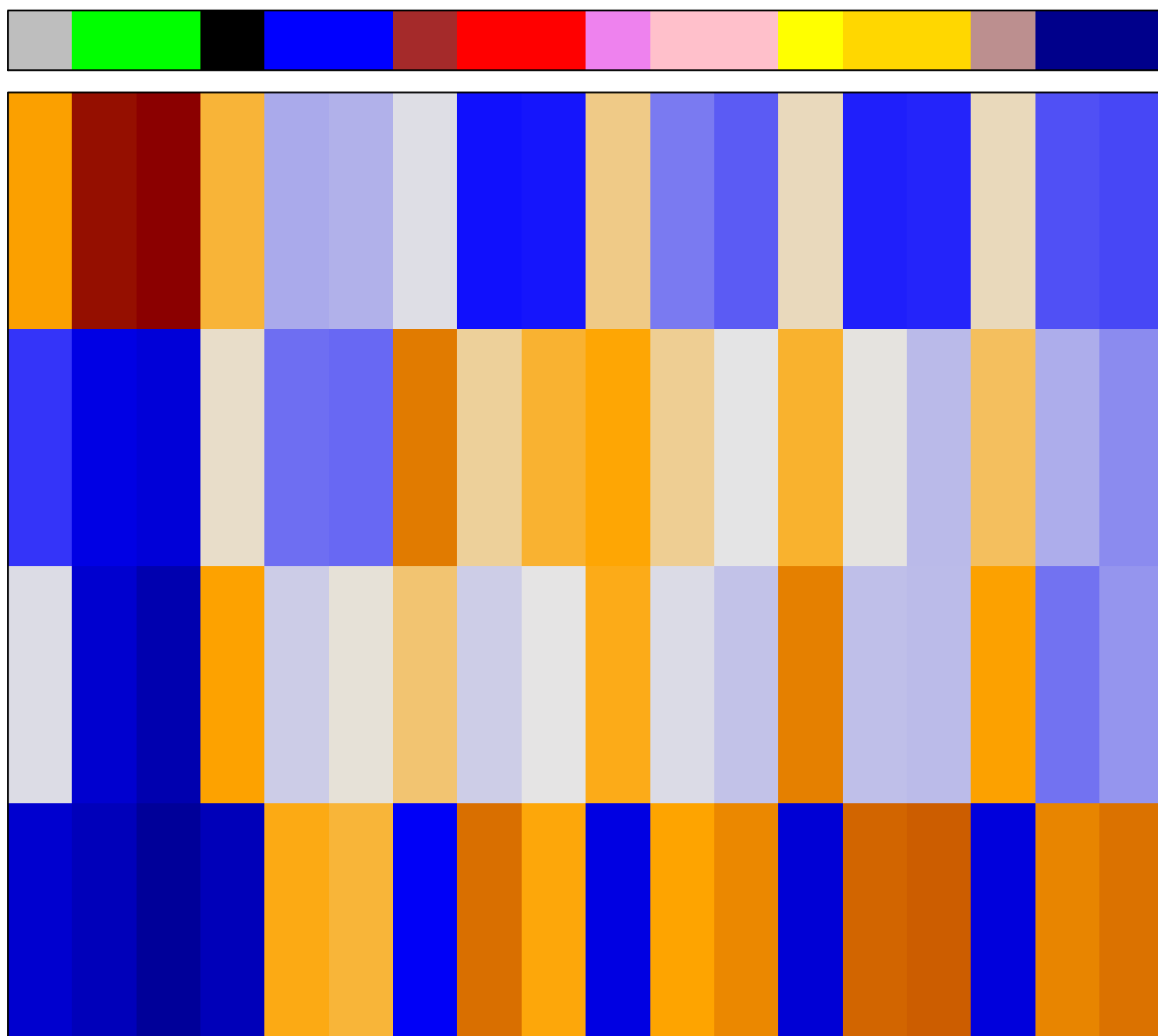
- A ■ hemoglobin complex
oxygen binding
oxygen transport
- B ■ visual perception
photoreceptor activity
phototransduction
- C ■ sequence-specific DNA binding
nervous system development
regulation of transcription, DNA-templated
- D ■ lipid transport
lipoprotein metabolic process
extracellular region

A

B

C

D



Overexpression Spots

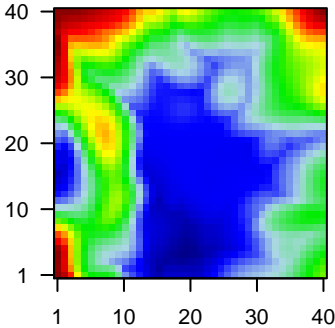
Spot Summary: A

metagenes = 5
genes = 125

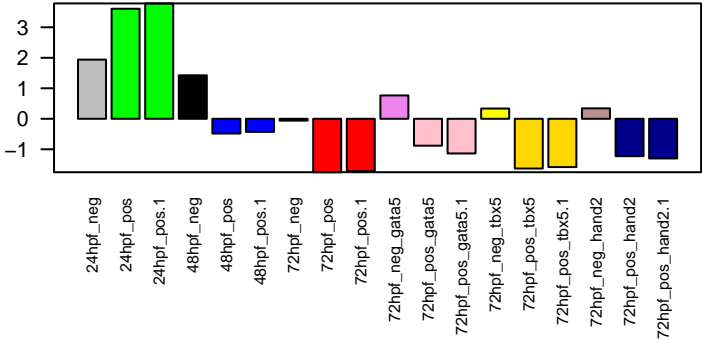
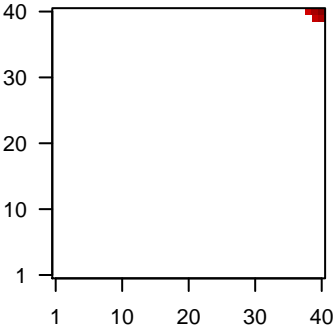
<r> metagenes = 1
<r> genes = 0.73
beta: r2= 28.87 / log p= -Inf

samples with spot = 3 (16.7 %)
24hpf_neg : 1 (100 %)
24hpf_pos : 2 (100 %)

Overview Map



Spot

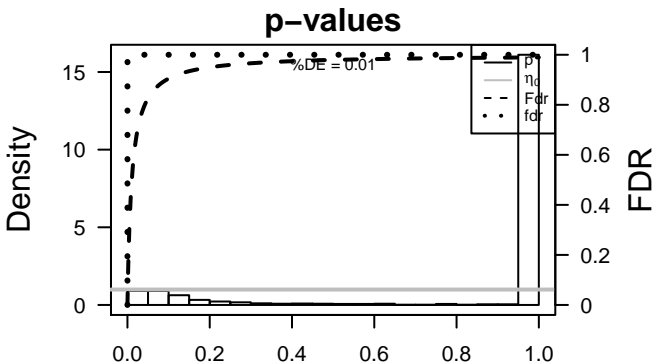


Spot Genelist

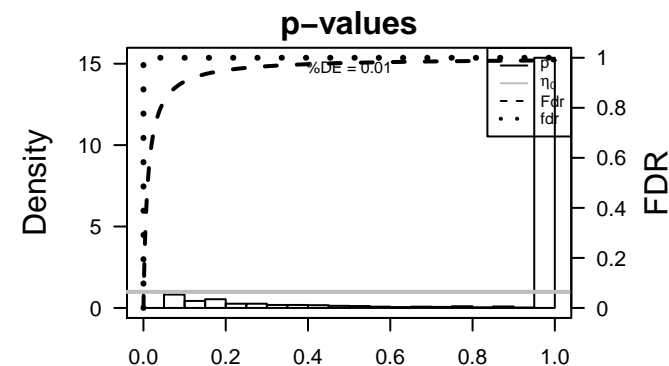
Rank	ID	max e	r	min e	Description	
					Symbol	
1	ENSDARG000	8.12	-6.4	0.89	hbbe3 hemoglobin beta embryonic-3 [Source:ZFIN;Acc:ZDB-GENE-991213-3]	hbbe3
2	ENSDARG000	7.83	-4.49	0.96	drl draculin [Source:ZFIN;Acc:ZDB-GENE-991213-3]	drl
3	ENSDARG000	7.36	-4.55	0.95	si:dkey-261k4.4 [Source:ZFIN;Acc:ZDB-GENE-060531-125]	si:dkey-261k4.4
4	ENSDARG000	7.35	-4.2	0.9	blf bloody fingers [Source:ZFIN;Acc:ZDB-GENE-050721-1]	blf
5	ENSDARG000	7.06	-5.06	0.95	si:dkey-261k4.3 [Source:ZFIN;Acc:ZDB-GENE-060531-124]	si:dkey-261k4.3
6	ENSDARG000	6.46	-4.6	0.75	protogenin homolog b (Gallus gallus) [Source:ZFIN;Acc:ZDB-GENE-041210-336]	protogenin homolog b (Gallus gallus)
7	ENSDARG000	6.43	-3.22	0.88	stab2 stabilin 2 [Source:ZFIN;Acc:ZDB-GENE-041210-336]	stab2
8	ENSDARG000	6.31	-1.79	0.87	ela2l elastase 2 like [Source:ZFIN;Acc:ZDB-GENE-040511-1]	ela2l
9	ENSDARG000	6.11	-4.16	0.95	tfr1a transferrin receptor 1a [Source:ZFIN;Acc:ZDB-GENE-04122	tfr1a
10	ENSDARG000	6	-2.33	0.92	si:ch73-299h12.2 [Source:ZFIN;Acc:ZDB-GENE-081031-7]	si:ch73-299h12.2
11	ENSDARG000	5.97	-3.89	0.91	kif17 Kruppel-like factor 17 [Source:ZFIN;Acc:ZDB-GENE-01012	kif17
12	ENSDARG000	5.69	-3.46	0.93	gata1a GATA binding protein 1a [Source:ZFIN;Acc:ZDB-GENE-980	gata1a
13	ENSDARG000	5.69	-3.04	0.91	gli1b growth factor independent 1B transcription repressor [Source	gli1b
14	ENSDARG000	5.53	-3.53	0.83	znfl2a zinc finger-like gene 2a [Source:ZFIN;Acc:ZDB-GENE-0308	znfl2a
15	ENSDARG000	5.51	-4.09	0.89	cpox coproporphyrinogen oxidase [Source:ZFIN;Acc:ZDB-GENE-	cpox
16	ENSDARG000	5.45	-1.91	0.76	hmsb hydroxymethylbilane synthase, b [Source:ZFIN;Acc:ZDB-GEI	hmsb
17	ENSDARG000	5.42	-2.18	0.8	hdr hematopoietic death receptor [Source:ZFIN;Acc:ZDB-GENE-	hdr
18	ENSDARG000	5.39	-4.85	0.92	tbx6l T-box 6, like [Source:ZFIN;Acc:ZDB-GENE-980526-171]	tbx6l
19	ENSDARG000	5.3	-2.88	0.84	susd1 sushi domain containing 1 [Source:ZFIN;Acc:ZDB-GENE-06	susd1
20	ENSDARG000	5.29	-4.07	0.89		

Geneset Overrepresentation

Rank	p-value	#in/all	Geneset
1	2e-21	10 / 14	CC 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 binding
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



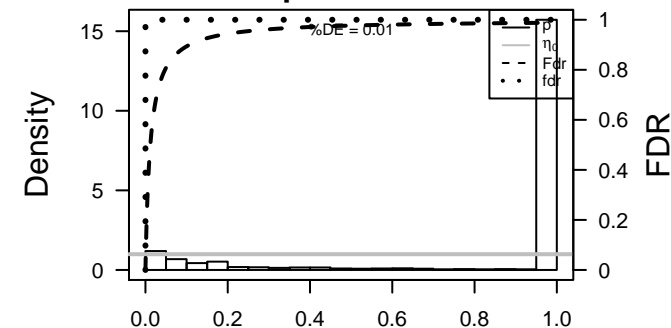
BP				CC				MF			
Rank	p-value	#in/all	Geneset	Rank	p-value	#in/all	Geneset	Rank	p-value	#in/all	Geneset
1	2e-19	10 / 19	oxygen transport	1	2e-21	10 / 14	hemoglobin complex	1	2e-19	10 / 19	oxygen binding
2	3e-17	10 / 28	embryonic hemopoiesis	2	2e-02	2 / 51	lysosomal membrane	2	2e-19	10 / 19	oxygen transporter 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 binding
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



BP				CC				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 acceptor
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



BP				CC				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 binding
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



BP				CC				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