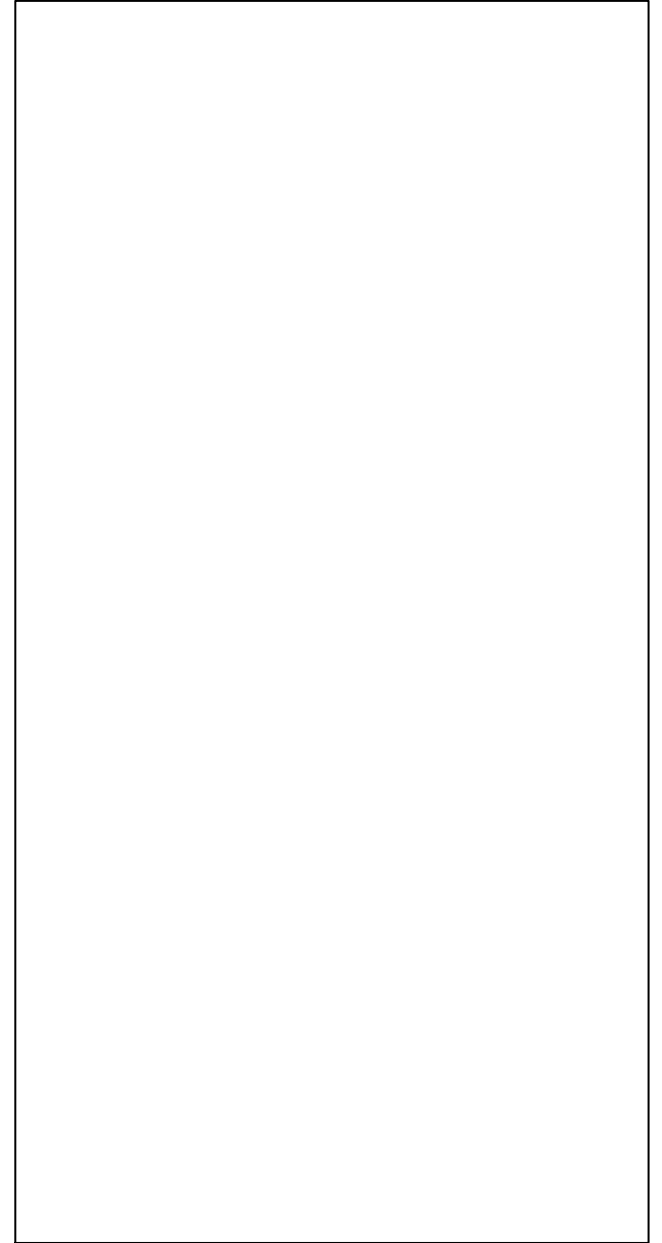
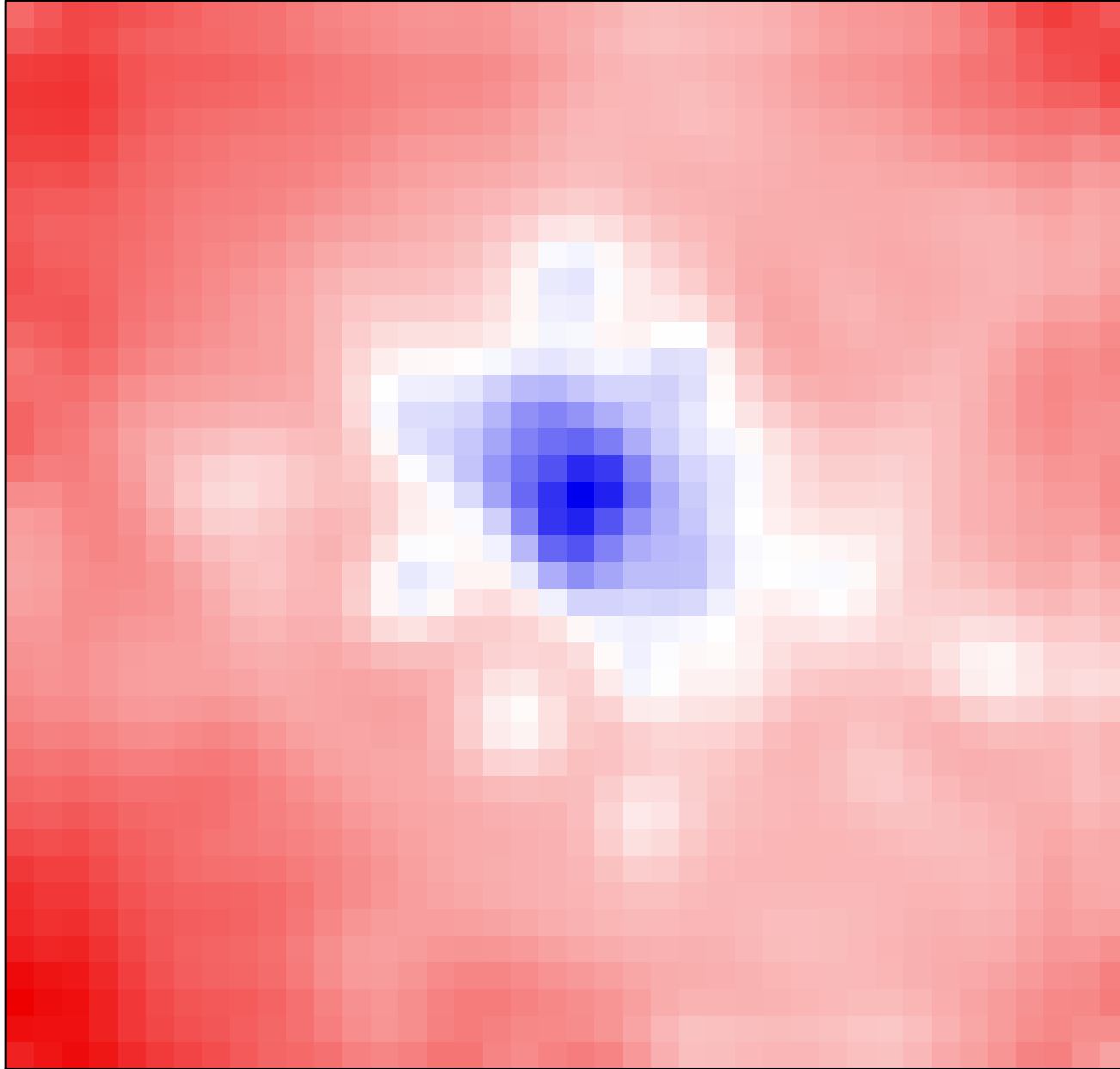


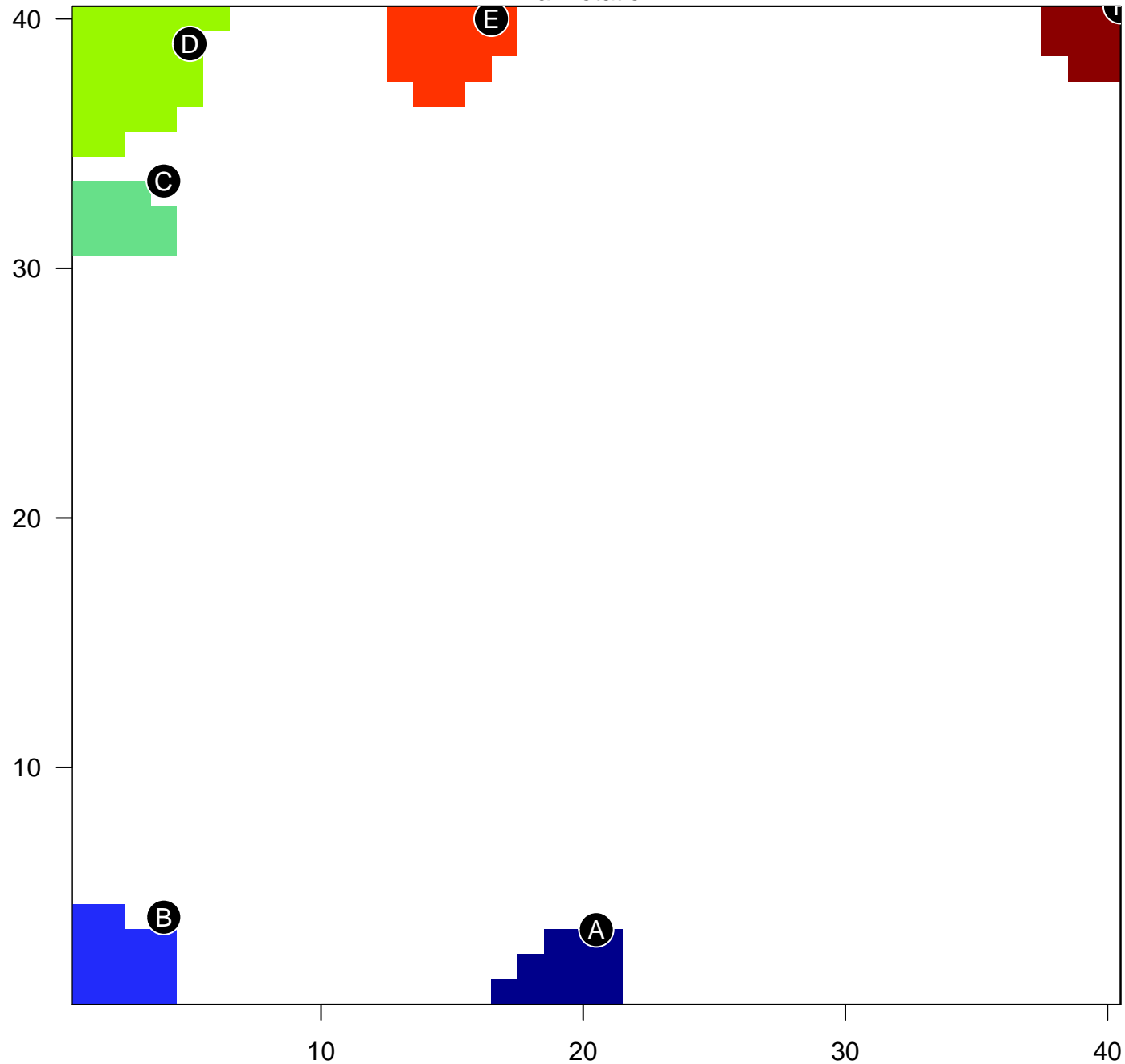
D-Cluster

landscape

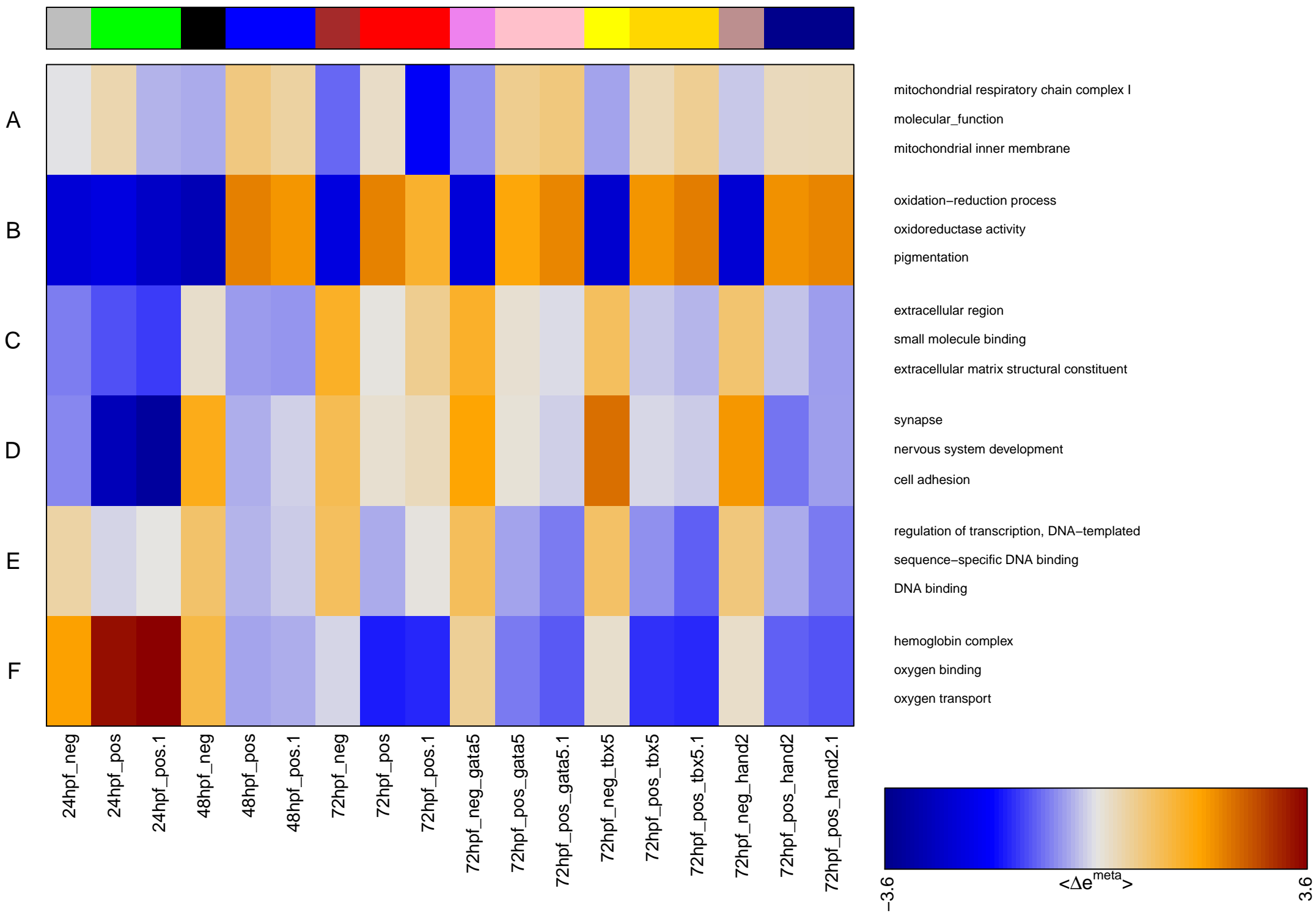


D-Cluster

annotation



- A ■ mitochondrial respiratory chain complex I
molecular_function
mitochondrial inner membrane
- B ■ oxidation-reduction process
oxidoreductase activity
pigmentation
- C ■ extracellular region
small molecule binding
extracellular matrix structural constituent
- D ■ synapse
nervous system development
cell adhesion
- E ■ regulation of transcription, DNA-templated
sequence-specific DNA binding
DNA binding
- F ■ hemoglobin complex
oxygen binding
oxygen transport



D-Cluster

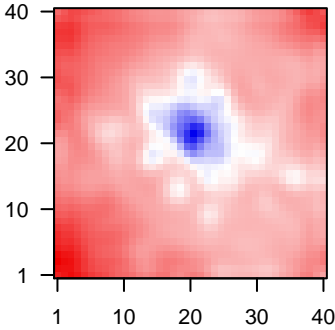
Spot Summary: A

metagenes = 12
genes = 213

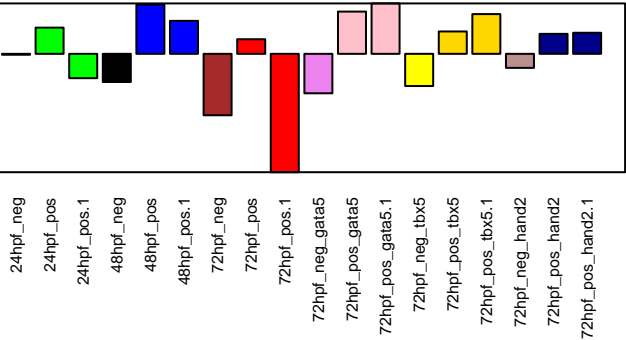
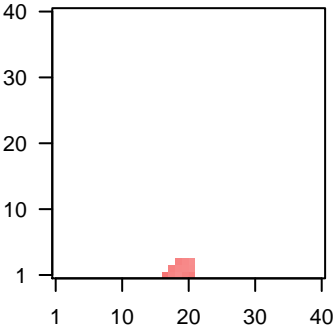
<r> metagenes = 0.98
<r> genes = 0.59
beta: r2= 5.29 / log p= -Inf

samples with spot = 0 (0 %)

Overview Map



Spot

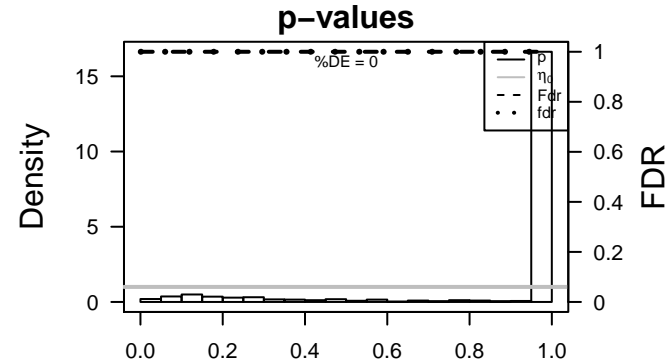


Spot Genelist

Rank	ID	max e	r	Description	
		min e		Symbol	
1	ENSDARG0000000001	2.94	-4.03	0.77	Metazoan signal recognition particle RNA [Source:RFAM;Acc:RF00001]
2	ENSDARG0000000002	2.85	-5.47	0.52	cbx7a chromobox homolog 7a [Source:ZFIN;Acc:ZDB-GENE-05042800]
3	ENSDARG0000000003	2.83	-1.77	0.52	sidkeyp-86h10.3 [Source:ZFIN;Acc:ZDB-GENE-100922-66]
4	ENSDARG0000000004	2.63	-3.12	0.77	Metazoan signal recognition particle RNA [Source:RFAM;Acc:RF00001]
5	ENSDARG0000000005	2.46	-5.71	0.87	Metazoan signal recognition particle RNA [Source:RFAM;Acc:RF00001]
6	ENSDARG0000000006	2.23	-3.57	0.76	Metazoan signal recognition particle RNA [Source:RFAM;Acc:RF00001]
7	ENSDARG0000000007	2.22	-4.69	0.9	zgc:165573.165573 [Source:ZFIN;Acc:ZDB-GENE-070615-27]
8	ENSDARG0000000008	2.18	-1.55	0.78	arl6ip5b ADP-ribosylation factor-like 6 interacting protein 5b [Source:ZFIN;Acc:ZDB-GENE-070705-284]
9	ENSDARG0000000009	2.12	-3.78	0.8	Metazoan signal recognition particle RNA [Source:RFAM;Acc:RF00001]
10	ENSDARG0000000010	2.1	-2.98	0.86	tpmt.1 thiopurine S-methyltransferase, tandem duplicate 1 [Source:ZFIN;Acc:ZDB-GENE-070705-284]
11	ENSDARG0000000011	2.09	-1.65	0.68	sidkeyp-160h10.2 [Source:ZFIN;Acc:ZDB-GENE-070705-284]
12	ENSDARG0000000012	2	-1.71	0.64	Metazoan signal recognition particle RNA [Source:RFAM;Acc:RF00001]
13	ENSDARG0000000013	2	-2.74	0.71	Metazoan signal recognition particle RNA [Source:RFAM;Acc:RF00001]
14	ENSDARG0000000014	1.98	-3.06	0.7	Small Cajal body specific RNA 6 [Source:RFAM;Acc:RF00471]
15	ENSDARG0000000015	1.97	-1.97	0.82	Metazoan signal recognition particle RNA [Source:RFAM;Acc:RF00001]
16	ENSDARG0000000016	1.93	-1.93	0.82	Metazoan signal recognition particle RNA [Source:RFAM;Acc:RF00001]
17	ENSDARG0000000017	1.87	-1.88	0.65	Metazoan signal recognition particle RNA [Source:RFAM;Acc:RF00001]
18	ENSDARG0000000018	1.85	-1.9	0.76	Metazoan signal recognition particle RNA [Source:RFAM;Acc:RF00001]
19	ENSDARG0000000019	1.85	-3.24	0.85	fam213b family with sequence similarity 213, member B [Source:ZFIN;Acc:ZDB-GENE-070705-284]
20	ENSDARG0000000020	1.85	-2.92	0.83	Metazoan signal recognition particle RNA [Source:RFAM;Acc:RF00001]

Geneset Overrepresentation

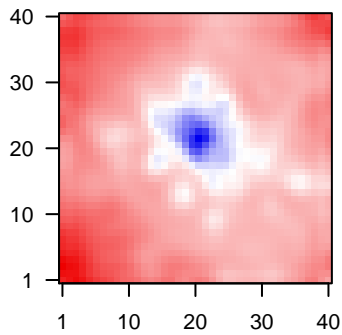
Rank	p-value	#in/all	Geneset
1	7e-04	3 / 23	CC mitochondrial respiratory chain complex I
2	1e-03	22 / 1437	MF molecular_function
3	1e-03	6 / 161	CC mitochondrial inner membrane
4	3e-03	2 / 11	BP lysosome organization
5	4e-03	2 / 12	BP positive regulation of NF-kappaB transcription factor activity
6	6e-03	20 / 1427	BP biological_process
7	1e-02	2 / 21	MF NADH dehydrogenase (ubiquinone) activity
8	1e-02	2 / 21	MF S-adenosylmethionine-dependent methyltransferase activity
9	1e-02	2 / 24	CC membrane raft
10	1e-02	2 / 24	CC respiratory chain
11	2e-02	2 / 27	BP defense response to virus
12	2e-02	4 / 144	BP methylation
13	3e-02	3 / 85	BP protein folding
14	3e-02	3 / 90	BP positive regulation of transcription, DNA-templated
15	3e-02	2 / 38	CC trans-Golgi network
16	5e-02	18 / 1580	CC cellular_component
17	6e-02	2 / 51	BP ER to Golgi vesicle-mediated transport
18	6e-02	2 / 52	BP positive regulation of apoptotic process
19	7e-02	2 / 58	BP RNA splicing
20	7e-02	1 / 10	CC anaphase-promoting complex
21	7e-02	1 / 10	MF cullin family protein binding
22	7e-02	1 / 10	CC mitochondrial envelope
23	7e-02	1 / 10	CC nuclear chromosome, telomeric region
24	7e-02	1 / 10	BP positive regulation of DNA repair
25	7e-02	1 / 10	BP protein secretion
26	8e-02	1 / 11	BP cholesterol homeostasis
27	8e-02	1 / 11	CC Cul4-RING E3 ubiquitin ligase complex
28	8e-02	1 / 11	MF enzyme regulator activity
29	8e-02	1 / 11	BP mitochondrial electron transport, NADH to ubiquinone
30	8e-02	1 / 11	BP mitotic spindle assembly checkpoint
31	8e-02	2 / 64	CC Cul3-RING ubiquitin ligase complex
32	9e-02	2 / 65	MF RNA polymerase II regulatory region sequence-specific DNA binding
33	9e-02	1 / 12	MF heat shock protein binding
34	9e-02	1 / 12	CC mitotic spindle
35	9e-02	1 / 12	BP regulation of angiogenesis
36	9e-02	1 / 12	MF transcription factor activity, RNA polymerase II transcription factor recruiting
37	9e-02	1 / 12	MF voltage-gated chloride channel activity
38	9e-02	2 / 67	MF unfolded protein binding
39	9e-02	1 / 13	BP acyl-CoA metabolic process
40	9e-02	1 / 13	MF antioxidant activity



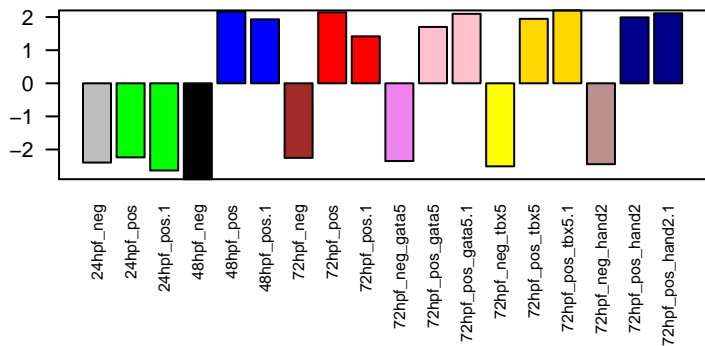
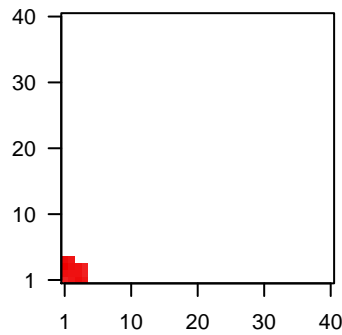
BP				CC				MF			
Rank	p-value	#in/all	Geneset	Rank	p-value	#in/all	Geneset	Rank	p-value	#in/all	Geneset
1	0.003	2 / 11	lysosome organization	1	7e-04	3 / 23	mitochondrial respiratory chain complex I	1	0.001	22 / 1437	molecular_function
2	0.004	2 / 12	positive regulation of NF-kappaB transcription factor activity	2	1e-03	6 / 161	mitochondrial inner membrane	2	0.011	2 / 21	NADH dehydrogenase (ubiquinone) activity
3	0.006	20 / 1427	biological_process	3	1e-02	2 / 24	membrane raft	3	0.011	2 / 21	S-adenosylmethionine-dependent methyltransferase activity
4	0.018	2 / 27	defense response to virus	4	1e-02	2 / 24	respiratory chain	4	0.073	1 / 10	cullin family protein binding
5	0.024	4 / 144	methylation	5	3e-02	2 / 38	trans-Golgi network	5	0.080	1 / 11	enzyme regulator activity
6	0.027	3 / 85	protein folding	6	5e-02	18 / 1580	cellular_component	6	0.087	2 / 65	RNA polymerase II regulatory region sequence-specific DNA binding
7	0.031	3 / 90	positive regulation of transcription, DNA-templated	7	7e-02	1 / 10	anaphase-promoting complex	7	0.087	1 / 12	heat shock protein binding
8	0.057	2 / 51	ER to Golgi vesicle-mediated transport	8	7e-02	1 / 10	mitochondrial envelope	8	0.087	1 / 12	transcription factor activity, RNA polymerase II transcription factor recruiting
9	0.059	2 / 52	positive regulation of apoptotic process	9	7e-02	1 / 10	nuclear chromosome, telomeric region	9	0.087	1 / 12	voltage-gated chloride channel activity
10	0.071	2 / 58	RNA splicing	10	8e-02	1 / 11	Cu4-RING E3 ubiquitin ligase complex	10	0.091	2 / 67	unfolded protein binding
11	0.073	1 / 10	positive regulation of DNA repair	11	8e-02	2 / 64	Cu3-RING ubiquitin ligase complex	11	0.094	1 / 13	antioxidant activity
12	0.073	1 / 10	protein secretion	12	9e-02	1 / 12	mitotic spindle	12	0.094	1 / 13	ATP-dependent microtubule motor activity, minus-end-directed
13	0.080	1 / 11	cholesterol homeostasis	13	1e-01	1 / 14	U12-type spliceosomal complex	13	0.101	1 / 14	chaperone binding
14	0.080	1 / 11	mitochondrial electron transport, NADH to ubiquinone	14	1e-01	1 / 15	cytoplasmic dynein complex	14	0.101	1 / 14	RNA polymerase II transcription factor binding
15	0.080	1 / 11	mitotic spindle assembly checkpoint	15	1e-01	1 / 15	mitochondrial small ribosomal subunit	15	0.107	1 / 15	exonuclease activity

```
# samples with spot = 10 ( 55.6 %)
48hpf_pos : 2 ( 100 %)
72hpf_pos : 2 ( 100 %)
72hpf_pos_gata5 : 2 ( 100 %)
72hpf_pos_tbx5 : 2 ( 100 %)
72hpf_pos_hand2 : 2 ( 100 %)
```

Overview Map



Spot

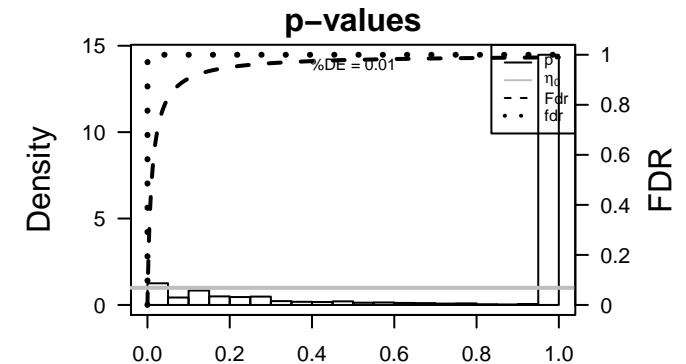


Spot Genelist

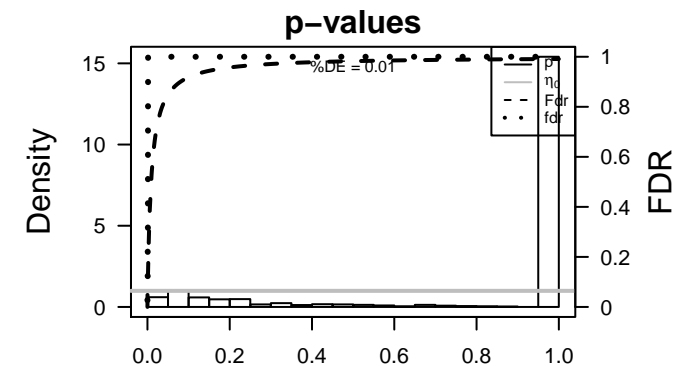
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1	ENSDARG00000000000	5.16	-6.13	0.98	oacyl	O-acyltransferase like [Source:ZFIN;Acc:ZDB-GENE-09071-1]
2	ENSDARG00000000000	4.98	-7.11	0.98	wu:fc46h12;fc46h12	[Source:ZFIN;Acc:ZDB-GENE-030131-3611]
3	ENSDARG00000000000	4.88	-6.93	0.98	slc:slc22a7a	[Source:ZFIN;Acc:ZDB-GENE-050506-10]
4	ENSDARG00000000000	4.72	-6.07	0.68	vmhcl	ventricular myosin heavy chain-like [Source:ZFIN;Acc:ZDB-GENE-030131-3611]
5	ENSDARG00000000000	4.71	-7.81	0.95	gch2	GTP cyclohydrolase 2 [Source:ZFIN;Acc:ZDB-GENE-00120-1]
6	ENSDARG00000000000	4.57	-5.01	0.77	serpina1	serpin peptidase inhibitor, clade A (alpha-1 antitrypsin), member 1 [Source:ZFIN;Acc:ZDB-GENE-030131-3611]
7	ENSDARG00000000000	4.53	-5.75	0.99	slc:slc22a7a	[Source:ZFIN;Acc:ZDB-GENE-141219-27]
8	ENSDARG00000000000	4.51	-4.97	0.97	zgc:113142	[Source:ZFIN;Acc:ZDB-GENE-050220-2]
9	ENSDARG00000000000	4.47	-7.23	0.98	xdh	xanthine dehydrogenase [Source:ZFIN;Acc:ZDB-GENE-070410-23]
10	ENSDARG00000000000	4.45	-2.24	0.77	plxdc1	plexin domain containing 1 [Source:ZFIN;Acc:ZDB-GENE-030131-3611]
11	ENSDARG00000000000	4.44	-6.92	0.98	zgc:162150	[Source:ZFIN;Acc:ZDB-GENE-070410-23]
12	ENSDARG00000000000	4.42	-4.7	0.66	tnnc1a	troponin C type 1a (slow) [Source:ZFIN;Acc:ZDB-GENE-030131-3611]
13	ENSDARG00000000000	4.4	-6.51	0.99	bscl2l	Bernardinelli-Seip congenital lipodystrophy 2, like [Source:ZFIN;Acc:ZDB-GENE-030131-3611]
14	ENSDARG00000000000	4.4	-5.48	0.97	uraha	urate (5-hydroxyiso-) hydrolase a [Source:ZFIN;Acc:ZDB-GENE-030131-3611]
15	ENSDARG00000000000	4.39	-5.45	0.97	sprb	sepiapterin reductase b [Source:ZFIN;Acc:ZDB-GENE-07071-1]
16	ENSDARG00000000000	4.38	-5.44	0.94	slc:slc22a7a	[Source:ZFIN;Acc:ZDB-GENE-030131-3611]
17	ENSDARG00000000000	4.34	-7.46	0.98	slc22a7a	solute carrier family 22 (organic anion transporter), member 7 [Source:ZFIN;Acc:ZDB-GENE-030131-3611]
18	ENSDARG00000000000	4.32	-6.44	0.73	cmlc1	cardiac myosin light chain-1 [Source:ZFIN;Acc:ZDB-GENE-030131-3611]
19	ENSDARG00000000000	4.31	-6.34	0.95	slc2a15a	solute carrier family 2 (facilitated glucose transporter), member 15 [Source:ZFIN;Acc:ZDB-GENE-030131-3611]
20	ENSDARG00000000000	4.3	-4.54	0.79	tnfb	tumor necrosis factor b (TNF superfamily, member 2) [Source:ZFIN;Acc:ZDB-GENE-030131-3611]

Geneset Overrepresentation

Rank	p-value	#in/all	GeneSet
1	2e-15	35 / 712	BP oxidation-reduction process
2	2e-14	29 / 522	MF oxidoreductase activity
3	3e-10	8 / 30	BP pigmentation
4	1e-09	7 / 23	BP lipoprotein metabolic process
5	2e-07	8 / 67	BP lipid transport
6	2e-06	4 / 10	CC melanosome
7	2e-06	16 / 414	BP metabolic process
8	2e-06	4 / 11	BP purine nucleotide biosynthetic process
9	3e-06	5 / 24	BP nucleoside metabolic process
10	1e-05	5 / 32	MF oxidoreductase activity, acting on the CH-OH group of donors, NAD or NADP
11	1e-05	5 / 33	MF NAD binding
12	2e-05	16 / 480	MF catalytic activity
13	6e-05	12 / 321	MF GTPase activity
14	1e-04	3 / 10	CC chylomicron
15	1e-04	3 / 10	CC high-density lipoprotein particle
16	1e-04	3 / 10	BP triglyceride catabolic process
17	1e-04	4 / 26	BP melanocyte differentiation
18	1e-04	5 / 50	BP lipid catabolic process
19	1e-04	3 / 11	BP cholesterol homeostasis
20	1e-04	3 / 11	BP melanosome organization
21	2e-04	4 / 29	BP cellular response to xenobiotic stimulus
22	2e-04	3 / 12	BP cholesterol biosynthetic process
23	2e-04	3 / 13	BP cholesterol efflux
24	2e-04	3 / 13	BP response to toxic substance
25	2e-04	30 / 1580	CC cellular_component
26	3e-04	15 / 561	MF GTP binding
27	4e-04	3 / 15	CC secretory granule
28	5e-04	6 / 105	MF lipid binding
29	5e-04	3 / 17	CC blood microparticle
30	5e-04	3 / 17	MF cholesterol binding
31	5e-04	3 / 17	MF cholesterol transporter activity
32	7e-04	4 / 43	MF iron-sulfur cluster binding
33	1e-03	3 / 21	MF substrate-specific transmembrane transporter activity
34	1e-03	20 / 969	MF hydrolase activity
35	1e-03	7 / 164	BP carbohydrate metabolic process
36	1e-03	15 / 634	CC extracellular region
37	1e-03	3 / 23	CC troponin complex
38	1e-03	5 / 85	CC cell
39	2e-03	3 / 25	MF glutathione transferase activity
40	2e-03	4 / 54	BP heart contraction



BP				CC				MF			
Rank	p-value	#in/all	Geneset	Rank	p-value	#in/all	Geneset	Rank	p-value	#in/all	Geneset
1	2e-15	35 / 712	oxidation-reduction process	1	2e-06	4 / 10	melanosome	1	2e-14	29 / 522	oxidoreductase activity
2	3e-10	8 / 30	pigmentation	2	1e-04	3 / 10	chylomicron	2	1e-05	5 / 32	oxidoreductase activity, acting on the CH-OH group of donors, NAD or NADP
3	1e-09	7 / 23	lipoprotein metabolic process	3	1e-04	3 / 10	high-density lipoprotein particle	3	1e-05	5 / 33	NAD binding
4	2e-07	8 / 67	lipid transport	4	2e-04	30 / 1580	cellular_component	4	2e-05	16 / 480	catalytic activity
5	2e-06	16 / 414	metabolic process	5	4e-04	3 / 15	secretory granule	5	6e-05	12 / 321	GTPase activity
6	2e-06	4 / 11	purine nucleotide biosynthetic process	6	5e-04	3 / 17	blood microparticle	6	3e-04	15 / 561	GTP binding
7	3e-06	5 / 24	nucleoside metabolic process	7	1e-03	15 / 634	extracellular region	7	5e-04	6 / 105	lipid binding
8	1e-04	3 / 10	triglyceride catabolic process	8	1e-03	3 / 23	troponin complex	8	5e-04	3 / 17	cholesterol binding
9	1e-04	4 / 26	melanocyte differentiation	9	1e-03	5 / 85	cell	9	5e-04	3 / 17	cholesterol transporter activity
10	1e-04	5 / 50	lipid catabolic process	10	2e-03	3 / 26	vesicle	10	7e-04	4 / 43	iron-sulfur cluster binding
11	1e-04	3 / 11	cholesterol homeostasis	11	4e-03	4 / 70	myosin complex	11	1e-03	3 / 21	substrate-specific transmembrane transporter activity
12	1e-04	3 / 11	melanosome organization	12	6e-03	3 / 38	trans-Golgi network	12	1e-03	20 / 969	hydrolase activity
13	2e-04	4 / 29	cellular response to xenobiotic stimulus	13	6e-03	77 / 6248	integral component of membrane	13	2e-03	3 / 25	glutathione transferase activity
14	2e-04	3 / 12	cholesterol biosynthetic process	14	7e-03	9 / 355	cytosol	14	2e-03	3 / 28	2 iron, 2 sulfur cluster binding
15	2e-04	3 / 13	cholesterol efflux	15	1e-02	4 / 96	lysosome	15	4e-03	3 / 33	photoreceptor activity



BP				CC				MF			
Rank	p-value	#in/all	Geneset	Rank	p-value	#in/all	Geneset	Rank	p-value	#in/all	Geneset
1	4e-04	3 / 27	axon extension	1	6e-08	17 / 634	extracellular region	1	2e-05	3 / 10	small molecule binding
2	5e-04	8 / 333	cell adhesion	2	2e-04	6 / 153	proteinaceous extracellular matrix	2	1e-04	4 / 49	extracellular matrix structural constituent
3	8e-04	4 / 76	cartilage development	3	5e-03	3 / 65	extracellular matrix	3	3e-04	3 / 25	integrin binding
4	1e-03	3 / 36	regulation of cell growth	4	1e-02	2 / 29	integrin complex	4	4e-04	4 / 64	serine-type endopeptidase inhibitor activity
5	1e-03	4 / 83	visual perception	5	2e-02	7 / 500	extracellular space	5	5e-04	12 / 717	calcium ion binding
6	2e-03	2 / 11	fructose 6-phosphate metabolic process	6	3e-02	2 / 46	collagen trimer	6	6e-04	3 / 30	insulin-like growth factor binding
7	2e-03	2 / 12	collagen fibril organization	7	4e-02	43 / 6248	integral component of membrane	7	6e-04	3 / 31	heparin binding
8	2e-03	2 / 12	positive regulation of sequence-specific DNA binding transcription factor activ	8	6e-02	1 / 11	membrane attack complex	8	2e-03	2 / 11	collagen binding
9	3e-03	2 / 15	negative regulation of cell death	9	6e-02	1 / 12	voltage-gated sodium channel complex	9	1e-02	2 / 29	3',5'-cyclic-nucleotide phosphodiesterase activity
10	3e-03	4 / 109	negative regulation of endopeptidase activity	10	6e-02	2 / 76	cilium	10	1e-02	2 / 29	dioxygenase activity
11	4e-03	2 / 18	pharyngeal system development	11	7e-02	1 / 14	peroxisomal membrane	11	2e-02	5 / 270	ion channel activity
12	6e-03	2 / 21	muscle contraction	12	8e-02	44 / 6723	membrane	12	2e-02	4 / 183	RNA polymerase II transcription factor activity, sequence-specific DNA bindin
13	6e-03	2 / 21	negative regulation of angiogenesis	13	9e-02	1 / 17	blood microparticle	13	2e-02	2 / 41	copper ion binding
14	6e-03	13 / 1084	transport	14	9e-02	1 / 17	external side of plasma membrane	14	2e-02	3 / 108	actin filament binding
15	1e-02	2 / 28	skeletal system development	15	9e-02	1 / 17	presynaptic active zone	15	3e-02	3 / 130	voltage-gated ion channel activity

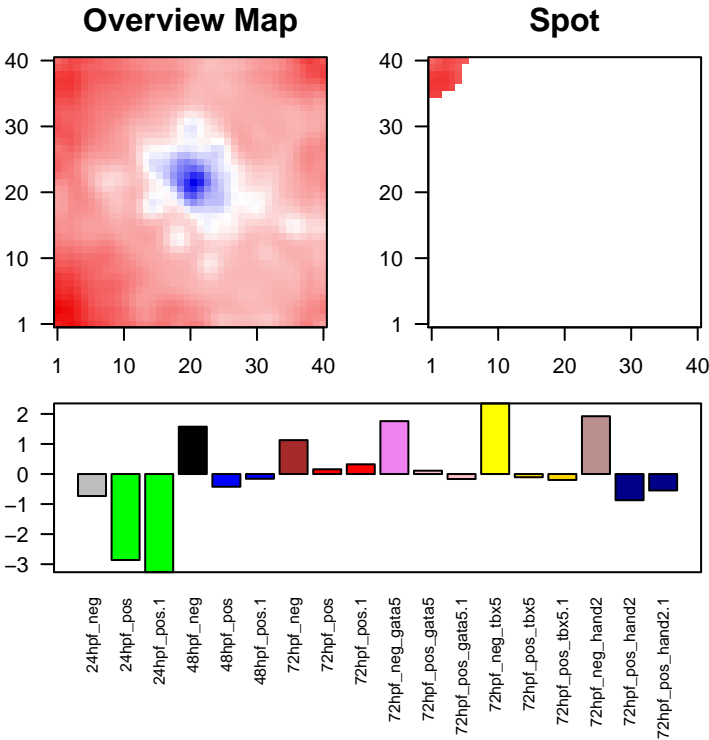
D-Cluster

Spot Summary: D

metagenes = 27
genes = 569

<r> metagenes = 0.97
<r> genes = 0.74
beta: r2= 31.93 / 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 %)

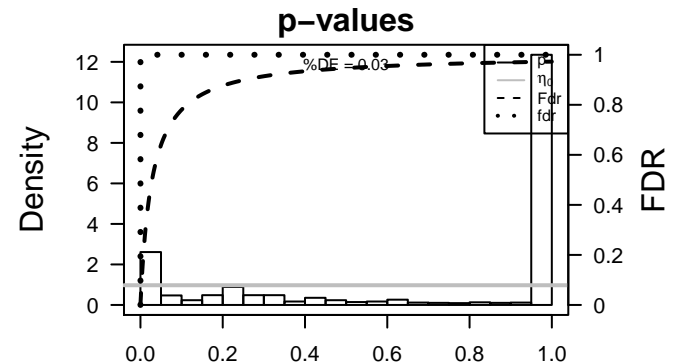


Spot Genelist

Rank	ID	max e	r	min e	Description
					Symbol
1	ENSDARG000	5.44	-2.17	0.58	opn1sw2 opsin 1 (cone pigments), short-wave-sensitive 2 [Source:ZFIN;Acc:ZDB-GENE-0050307-3]
2	ENSDARG000	5.4	-5.6	0.81	muc5.1 mucin 5.1, oligomeric mucus/gel-forming [Source:ZFIN;Acc:ZDB-GENE-0050307-3]
3	ENSDARG000	5.34	-6.98	0.79	matn1 matrilin 1 [Source:ZFIN;Acc:ZDB-GENE-0050307-3]
4	ENSDARG000	5.22	-3.71	0.57	opn1mw1 opsin 1 (cone pigments), medium-wave-sensitive, 1 [Source:ZFIN;Acc:ZDB-GENE-0050307-3]
5	ENSDARG000	5.19	-6.04	0.55	atp1a1a.2 ATPase, Na+/K+ transporting, alpha 1a polypeptide, tandem repeat domain [Source:ZFIN;Acc:ZDB-GENE-0050307-3]
6	ENSDARG000	5.16	-4.48	0.52	opn1sw1 opsin 1 (cone pigments), short-wave-sensitive 1 [Source:ZFIN;Acc:ZDB-GENE-0050307-3]
7	ENSDARG000	5.14	-4.55	0.77	rho rhodopsin [Source:ZFIN;Acc:ZDB-GENE-990415-271]
8	ENSDARG000	5.09	-5.91	0.76	and2 actinodin2 [Source:ZFIN;Acc:ZDB-GENE-041105-2]
9	ENSDARG000	5.01	-4.88	0.77	opn1lw2 opsin 1 (cone pigments), long-wave-sensitive, 2 [Source:ZFIN;Acc:ZDB-GENE-0050307-3]
10	ENSDARG000	4.9	-3.66	0.78	and1 actinodin1 [Source:ZFIN;Acc:ZDB-GENE-030131-9105]
11	ENSDARG000	4.85	-4.47	0.79	npas4a neuronal PAS domain protein 4a [Source:ZFIN;Acc:ZDB-GENE-0050307-3]
12	ENSDARG000	4.83	-5.45	0.78	arr3a arrestin 3a, retinal (X-arrestin) [Source:ZFIN;Acc:ZDB-GENE-0050307-3]
13	ENSDARG000	4.82	-3.89	0.65	gnb3b guanine nucleotide binding protein (G protein), beta polypeptide [Source:ZFIN;Acc:ZDB-GENE-0050307-3]
14	ENSDARG000	4.76	-5.55	0.82	col10a1a collagen, type X, alpha 1a [Source:ZFIN;Acc:ZDB-GENE-0050307-3]
15	ENSDARG000	4.72	-8.26	0.92	col11a2 collagen, type XI, alpha 2 [Source:ZFIN;Acc:ZDB-GENE-0050307-3]
16	ENSDARG000	4.71	-3.52	0.72	rcvrn3 recoverin 3 [Source:ZFIN;Acc:ZDB-GENE-040426-1661]
17	ENSDARG000	4.57	-3.71	0.67	pde6c phosphodiesterase 6C, cGMP-specific, cone, alpha prime [Source:ZFIN;Acc:ZDB-GENE-0050307-3]
18	ENSDARG000	4.55	-3.73	0.77	gnat2 guanine nucleotide binding protein (G protein), alpha transducin [Source:ZFIN;Acc:ZDB-GENE-0050307-3]
19	ENSDARG000	4.55	-4.06	0.68	gnat2 guanine nucleotide binding protein (G protein), alpha transducin [Source:ZFIN;Acc:ZDB-GENE-0050307-3]
20	ENSDARG000	4.49	-6.7	0.85	si:dkey-65b12.6 [Source:ZFIN;Acc:ZDB-GENE-060526-325]

Geneset Overrepresentation

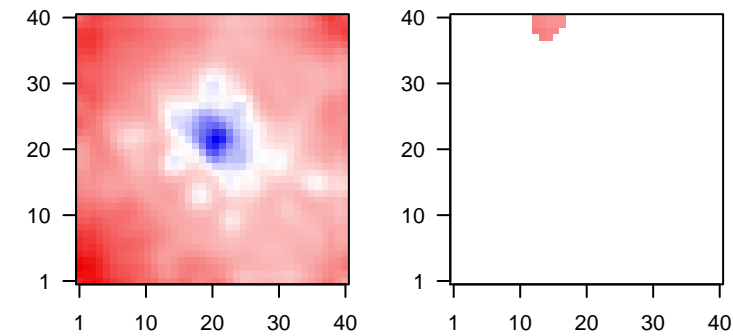
Rank	p-value	#in/all	Geneset
1	9e-19	28 / 155	CC synapse
2	3e-16	27 / 175	BP nervous system development
3	3e-16	36 / 333	BP cell adhesion
4	3e-16	44 / 499	BP ion transport
5	1e-13	24 / 172	BP homophilic cell adhesion via plasma membrane adhesion molecules
6	1e-13	49 / 717	MF calcium ion binding
7	1e-13	65 / 1162	CC plasma membrane
8	2e-13	23 / 158	MF microtubule binding
9	2e-12	28 / 270	MF ion channel activity
10	2e-11	11 / 32	MF extracellular-glutamate-gated ion channel activity
11	2e-11	11 / 32	MF ionotropic glutamate receptor activity
12	2e-11	11 / 32	BP ionotropic glutamate receptor signaling pathway
13	2e-11	15 / 74	CC neuron projection
14	6e-11	57 / 1084	BP transport
15	8e-11	204 / 6723	CC membrane
16	1e-10	37 / 537	MF sequence-specific DNA binding
17	1e-09	14 / 83	BP visual perception
18	3e-09	187 / 6248	CC integral component of membrane
19	3e-09	11 / 49	MF extracellular matrix structural constituent
20	4e-09	19 / 176	BP ion transmembrane transport
21	7e-09	13 / 79	BP excitatory postsynaptic potential
22	2e-08	20 / 219	CC cell junction
23	5e-07	11 / 78	BP axon guidance
24	5e-07	8 / 36	CC synaptic vesicle
25	6e-07	11 / 80	CC postsynaptic membrane
26	7e-07	6 / 17	CC presynaptic active zone
27	7e-07	10 / 65	BP sodium ion transport
28	8e-07	27 / 454	BP multicellular organism development
29	1e-06	6 / 18	MF tubulin binding
30	1e-06	13 / 124	MF receptor activity
31	2e-06	12 / 108	CC microtubule
32	2e-06	16 / 193	BP positive regulation of transcription from RNA polymerase II promoter
33	3e-06	12 / 113	BP transcription from RNA polymerase II promoter
34	4e-06	7 / 33	MF photoreceptor activity
35	4e-06	6 / 22	BP membrane depolarization during action potential
36	1e-05	10 / 86	BP chemical synaptic transmission
37	1e-05	7 / 39	BP neuron projection development
38	1e-05	8 / 55	BP central nervous system development
39	2e-05	13 / 153	CC proteinaceous extracellular matrix
40	2e-05	5 / 17	CC AMPA glutamate receptor complex



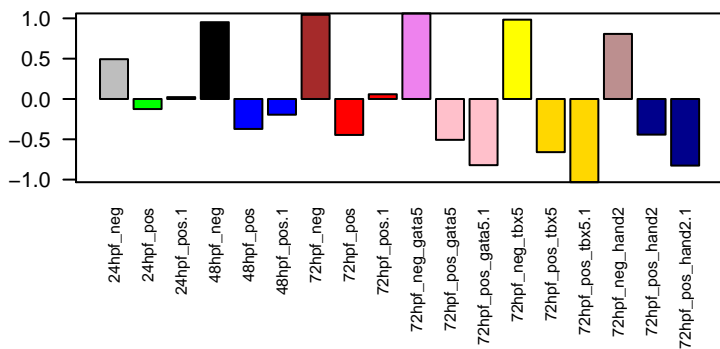
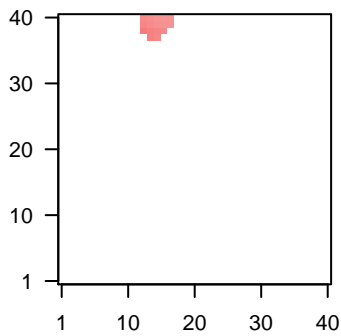
BP				CC				MF			
Rank	p-value	#in/all	Geneset	Rank	p-value	#in/all	Geneset	Rank	p-value	#in/all	Geneset
1	3e-16	27 / 175	nervous system development	1	9e-19	28 / 155	synapse	1	1e-13	49 / 717	calcium ion binding
2	3e-16	36 / 333	cell adhesion	2	1e-13	65 / 1162	plasma membrane	2	2e-13	23 / 158	microtubule binding
3	3e-16	44 / 499	ion transport	3	2e-11	15 / 74	neuron projection	3	2e-12	28 / 270	ion channel activity
4	1e-13	24 / 172	homophilic cell adhesion via plasma membrane adhesion molecules	4	8e-11	204 / 6723	membrane	4	2e-11	11 / 32	extracellular-glutamate-gated ion channel activity
5	2e-11	11 / 32	ionotropic glutamate receptor signaling pathway	5	3e-09	187 / 6248	integral component of membrane	5	2e-11	11 / 32	ionotropic glutamate receptor activity
6	6e-11	57 / 1084	transport	6	2e-08	20 / 219	cell junction	6	1e-10	37 / 537	sequence-specific DNA binding
7	1e-09	14 / 83	visual perception	7	5e-07	8 / 36	synaptic vesicle	7	3e-09	11 / 49	extracellular matrix structural constituent
8	4e-09	19 / 176	ion transmembrane transport	8	6e-07	11 / 80	postsynaptic membrane	8	1e-06	6 / 18	tubulin binding
9	7e-09	13 / 79	excitatory postsynaptic potential	9	7e-07	6 / 17	presynaptic active zone	9	1e-06	13 / 124	receptor activity
10	5e-07	11 / 78	axon guidance	10	2e-06	12 / 108	microtubule	10	4e-06	7 / 33	photoreceptor activity
11	7e-07	10 / 65	sodium ion transport	11	2e-05	13 / 153	proteinaceous extracellular matrix	11	3e-05	11 / 120	motor activity
12	8e-07	27 / 454	multicellular organism development	12	2e-05	5 / 17	AMPA glutamate receptor complex	12	5e-05	4 / 11	PDZ domain binding
13	2e-06	16 / 193	positive regulation of transcription from RNA polymerase II promoter	13	3e-05	6 / 31	photoreceptor outer segment	13	2e-04	4 / 15	calcium-transporting ATPase activity
14	3e-06	12 / 113	transcription from RNA polymerase II promoter	14	6e-05	34 / 809	integral component of plasma membrane	14	4e-04	5 / 31	G-protein coupled photoreceptor activity
15	4e-06	6 / 22	membrane depolarization during action potential	15	2e-04	4 / 15	protein phosphatase type 2A complex	15	4e-04	12 / 183	RNA polymerase II transcription factor activity, sequence-specific DNA binding

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# samples with spot = 0 ( 0 %)
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Overview Map



Spot

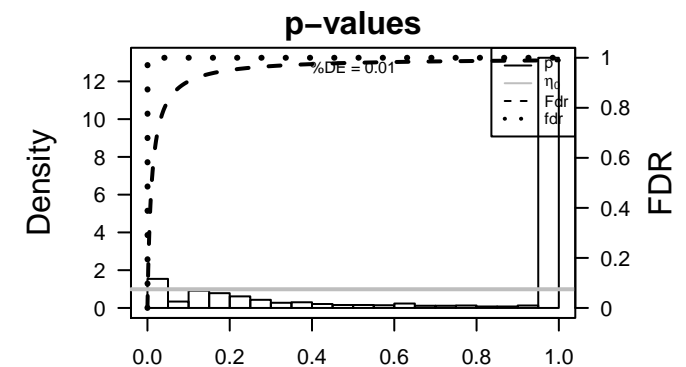


Spot Genelist

Rank	ID	max e			r	Description	
			min	e		Symbol	
1	ENSDARG00000000000	3.14	-2.31	0.89	frem2a	Fras1 related extracellular matrix protein 2a [Source:ZFIN;Acc:ZDB-GENE-140106-41]	
2	ENSDARG00000000000	2.97	-2.6	0.75	zmp:0000001081	[Source:ZFIN;Acc:ZDB-GENE-140106-41]	
3	ENSDARG00000000000	2.85	-1.86	0.88	vcnab	versican b [Source:ZFIN;Acc:ZDB-GENE-030131-2185]	
4	ENSDARG00000000000	2.79	-1.66	0.84	col4a6	collagen, type IV, alpha 6 [Source:ZFIN;Acc:ZDB-GENE-101121-7]	
5	ENSDARG00000000000	2.78	-1.46	0.62	abi3bpb	ABI family, member 3 (NESH) binding protein b [Source:ZFIN;Acc:ZDB-GENE-030131-8]	
6	ENSDARG00000000000	2.72	-4	0.79	mxra5b	matrix-remodelling associated 5b [Source:ZFIN;Acc:ZDB-GENE-030131-8]	
7	ENSDARG00000000000	2.66	-1.67	0.86	col4a5	collagen, type IV, alpha 5 (Alport syndrome) [Source:ZFIN;Acc:ZDB-GENE-030131-8]	
8	ENSDARG00000000000	2.62	-2.43	0.69	zgc:101810	zgc:101810 [Source:ZFIN;Acc:ZDB-GENE-041121-7]	
9	ENSDARG00000000000	2.48	-1.39	0.85	mxra5a	matrix-remodelling associated 5a [Source:ZFIN;Acc:ZDB-GENE-030131-8]	
10	ENSDARG00000000000	2.47	-2.65	0.86	ptx3a	pentraxin 3, long a [Source:ZFIN;Acc:ZDB-GENE-030131-8]	
11	ENSDARG00000000000	2.44	-1.52	0.78	zgc:158659	zgc:158659 [Source:ZFIN;Acc:ZDB-GENE-070112-492]	
12	ENSDARG00000000000	2.4	-2.57	0.75	barx1	BARX homeobox 1 [Source:ZFIN;Acc:ZDB-GENE-050522-7]	
13	ENSDARG00000000000	2.37	-1.88	0.84	igsf9b	immunoglobulin superfamily, member 9b [Source:ZFIN;Acc:ZDB-GENE-030131-8]	
14	ENSDARG00000000000	2.37	-1.66	0.97	col12a1b	collagen, type XII, alpha 1b [Source:ZFIN;Acc:ZDB-GENE-030131-8]	
15	ENSDARG00000000000	2.36	-2.98	0.73	adgrg6	adhesion G protein-coupled receptor G6 [Source:ZFIN;Acc:ZDB-GENE-030131-8]	
16	ENSDARG00000000000	2.32	-2.23	0.55	lamb4	laminin, beta 4 [Source:ZFIN;Acc:ZDB-GENE-021226-2]	
17	ENSDARG00000000000	2.31	-1.83	0.77	fibina	fin bud initiation factor a [Source:ZFIN;Acc:ZDB-GENE-111011-1]	
18	ENSDARG00000000000	2.29	-1.28	0.87	atp6ap1a	ATPase, H+ transporting, lysosomal accessory protein 1a [Source:ZFIN;Acc:ZDB-GENE-030131-8]	
19	ENSDARG00000000000	2.26	-1.33	0.9	col12a1a	collagen, type XII, alpha 1a [Source:ZFIN;Acc:ZDB-GENE-030131-8]	
20	ENSDARG00000000000	2.25	-2.92	0.83	hic1	hypermethylated in cancer 1 [Source:ZFIN;Acc:ZDB-GENE-030131-8]	

Geneset Overrepresentation

Rank	p-value	#in/all	GeneSet
1	2e-14	50 / 1239	BP regulation of transcription, DNA-templated
2	1e-11	29 / 537	MF sequence-specific DNA binding
3	6e-11	49 / 1484	MF DNA binding
4	2e-10	70 / 2716	CC nucleus
5	1e-08	27 / 633	MF transcription factor activity, sequence-specific DNA binding
6	8e-07	24 / 643	BP transcription, DNA-templated
7	2e-06	19 / 454	BP multicellular organism development
8	1e-05	15 / 333	BP cell adhesion
9	3e-05	6 / 52	MF transmembrane receptor protein tyrosine kinase activity
10	3e-05	5 / 32	BP retinal ganglion cell axon guidance
11	4e-05	7 / 78	BP axon guidance
12	9e-05	8 / 120	MF protein tyrosine phosphatase activity
13	9e-05	8 / 121	BP peptidyl-tyrosine dephosphorylation
14	1e-04	14 / 362	BP regulation of transcription from RNA polymerase II promoter
15	2e-04	5 / 44	BP neuron development
16	2e-04	5 / 45	BP embryonic cranial skeleton morphogenesis
17	2e-04	7 / 100	BP peptidyl-tyrosine phosphorylation
18	2e-04	4 / 25	BP negative chemotaxis
19	3e-04	11 / 257	BP cell differentiation
20	3e-04	7 / 106	MF phosphoprotein phosphatase activity
21	3e-04	9 / 180	BP dephosphorylation
22	3e-04	5 / 51	BP anatomical structure morphogenesis
23	3e-04	7 / 110	MF protein tyrosine kinase activity
24	4e-04	20 / 717	MF calcium ion binding
25	4e-04	5 / 54	BP fin regeneration
26	5e-04	8 / 153	CC proteinaceous extracellular matrix
27	7e-04	3 / 15	CC basement membrane
28	1e-03	8 / 172	BP homophilic cell adhesion via plasma membrane adhesion molecules
29	1e-03	6 / 98	CC transcription factor complex
30	1e-03	7 / 136	MF phosphatase activity
31	1e-03	8 / 176	BP protein dephosphorylation
32	1e-03	4 / 40	BP heart morphogenesis
33	1e-03	4 / 41	MF RNA polymerase II core promoter proximal region sequence-specific DNA
34	2e-03	3 / 20	BP fin development
35	2e-03	3 / 21	BP smoothened signaling pathway
36	2e-03	4 / 46	CC collagen trimer
37	2e-03	4 / 48	BP neural crest cell migration
38	3e-03	4 / 49	MF extracellular matrix structural constituent
39	3e-03	3 / 24	BP embryonic retina morphogenesis in camera-type eye
40	4e-03	3 / 28	BP skeletal system development



BP				CC				MF			
Rank	p-value	#in/all	Geneset	Rank	p-value	#in/all	Geneset	Rank	p-value	#in/all	Geneset
1	2e-14	50 / 1239	regulation of transcription, DNA-templated	1	2e-10	70 / 2716	nucleus	1	1e-11	29 / 537	sequence-specific DNA binding
2	8e-07	24 / 643	transcription, DNA-templated	2	5e-04	8 / 153	proteinaceous extracellular matrix	2	6e-11	49 / 1484	DNA binding
3	2e-06	19 / 454	multicellular organism development	3	7e-04	3 / 15	basement membrane	3	1e-08	27 / 633	transcription factor activity, sequence-specific DNA binding
4	1e-05	15 / 333	cell adhesion	4	1e-03	6 / 98	transcription factor complex	4	3e-05	6 / 52	transmembrane receptor protein tyrosine kinase activity
5	3e-05	5 / 32	retinal ganglion cell axon guidance	5	2e-03	4 / 46	collagen trimer	5	9e-05	8 / 120	protein tyrosine phosphatase activity
6	4e-05	7 / 78	axon guidance	6	6e-03	3 / 32	chromatin	6	3e-04	7 / 106	phosphoprotein phosphatase activity
7	9e-05	8 / 121	peptidyl-tyrosine dephosphorylation	7	7e-03	4 / 65	extracellular matrix	7	3e-04	7 / 110	protein tyrosine kinase activity
8	1e-04	14 / 362	regulation of transcription from RNA polymerase II promoter	8	1e-02	97 / 6723	membrane	8	4e-04	20 / 717	calcium ion binding
9	2e-04	5 / 44	neuron development	9	2e-02	22 / 1162	plasma membrane	9	1e-03	7 / 136	phosphatase activity
10	2e-04	5 / 45	embryonic cranial skeleton morphogenesis	10	3e-02	3 / 54	kinesin complex	10	1e-03	4 / 41	RNA polymerase II core promoter proximal region sequence-specific DNA binding
11	2e-04	7 / 100	peptidyl-tyrosine phosphorylation	11	3e-02	88 / 6248	integral component of membrane	11	3e-03	4 / 49	extracellular matrix structural constituent
12	2e-04	4 / 25	negative chemotaxis	12	3e-02	8 / 317	Golgi apparatus	12	5e-03	3 / 30	insulin-like growth factor binding
13	3e-04	11 / 257	cell differentiation	13	4e-02	11 / 500	extracellular space	13	6e-03	3 / 31	histone-lysine N-methyltransferase activity
14	3e-04	9 / 180	dephosphorylation	14	4e-02	13 / 634	extracellular region	14	6e-03	2 / 10	phosphatidylinositol 3-kinase binding
15	3e-04	5 / 51	anatomical structure morphogenesis	15	4e-02	7 / 268	cytoskeleton	15	6e-03	2 / 10	SMAD binding

D-Cluster

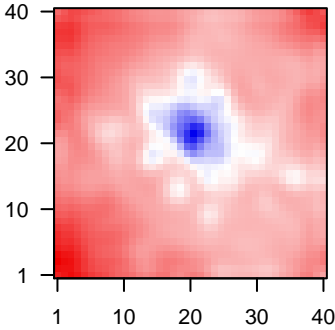
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genes = 163

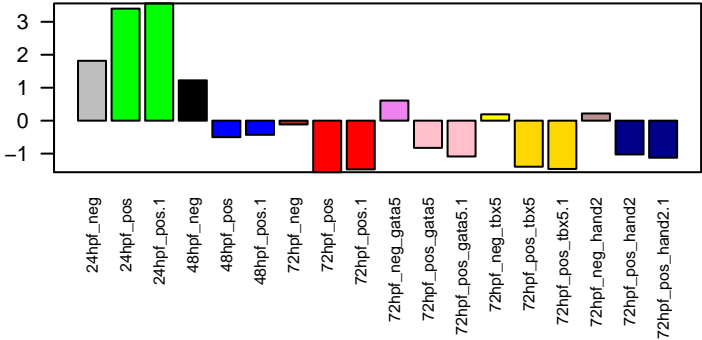
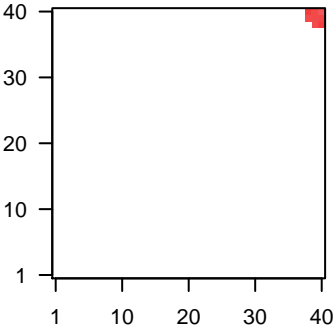
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<r> genes = 0.72
beta: r2= 26.66 / log p= -Inf

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

Overview Map



Spot

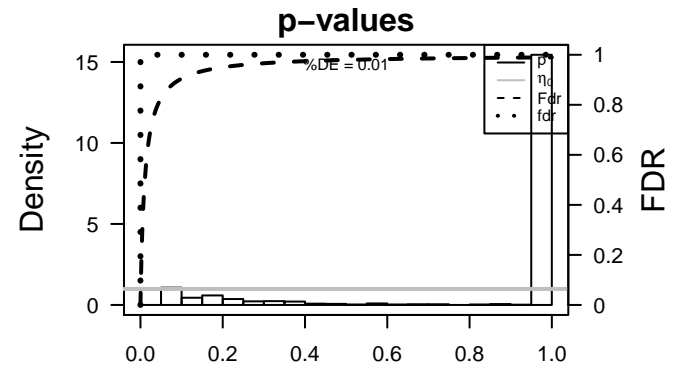


Spot Genelist

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]
2	ENSDARG000	7.83	-4.49	0.96	drl	draculin [Source:ZFIN;Acc:ZDB-GENE-991213-3]
3	ENSDARG000	7.36	-4.55	0.96	si:dkkey-26194-261j4.4	[Source:ZFIN;Acc:ZDB-GENE-060531-125]
4	ENSDARG000	7.35	-4.2	0.91	blf	bloody fingers [Source:ZFIN;Acc:ZDB-GENE-050721-1]
5	ENSDARG000	7.06	-5.06	0.95	si:dkkey-26194-261j4.3	[Source:ZFIN;Acc:ZDB-GENE-060531-124]
6	ENSDARG000	6.46	-4.6	0.75		protogenin homolog b (Gallus gallus) [Source:ZFIN;Acc:ZDB-GENE-041210-336]
7	ENSDARG000	6.43	-3.22	0.89	stab2	stabilin 2 [Source:ZFIN;Acc:ZDB-GENE-041210-336]
8	ENSDARG000	6.31	-1.79	0.88	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-041221-1]
10	ENSDARG000	6	-2.33	0.92	si:ch73-299h12.2	[Source:ZFIN;Acc:ZDB-GENE-081031-7]
11	ENSDARG000	5.97	-3.89	0.92	kif17	Kruppel-like factor 17 [Source:ZFIN;Acc:ZDB-GENE-010121-1]
12	ENSDARG000	5.69	-3.46	0.93	gata1a	GATA binding protein 1a [Source:ZFIN;Acc:ZDB-GENE-980526-171]
13	ENSDARG000	5.69	-3.04	0.91	gli1b	growth factor independent 1B transcription repressor [Source:ZFIN;Acc:ZDB-GENE-980526-171]
14	ENSDARG000	5.53	-3.53	0.83		zinc finger-like gene 2a [Source:ZFIN;Acc:ZDB-GENE-030801-1]
15	ENSDARG000	5.51	-4.09	0.88	znfl2a	zinc finger-like gene 2a [Source:ZFIN;Acc:ZDB-GENE-030801-1]
16	ENSDARG000	5.45	-1.91	0.79	cpox	coproporphyrinogen oxidase [Source:ZFIN;Acc:ZDB-GENE-030801-1]
17	ENSDARG000	5.42	-2.18	0.83	hmsb	hydroxymethylbilane synthase, b [Source:ZFIN;Acc:ZDB-GENE-030801-1]
18	ENSDARG000	5.39	-4.85	0.92	hdr	hematopoietic death receptor [Source:ZFIN;Acc:ZDB-GENE-030801-1]
19	ENSDARG000	5.3	-2.88	0.85	tbx6l	T-box 6, like [Source:ZFIN;Acc:ZDB-GENE-980526-171]
20	ENSDARG000	5.29	-4.07	0.9	susd1	sushi domain containing 1 [Source:ZFIN;Acc:ZDB-GENE-060531-125]

Geneset Overrepresentation

Rank	p-value	#in/all	Geneset
1	3e-20	10 / 14	CC hemoglobin complex
2	3e-18	10 / 19	MF oxygen binding
3	3e-18	10 / 19	BP oxygen transport
4	3e-18	10 / 19	MF oxygen transporter activity
5	4e-16	10 / 28	BP embryonic hemopoiesis
6	2e-14	10 / 40	BP erythrocyte differentiation
7	3e-12	13 / 145	MF heme binding
8	6e-10	12 / 178	MF iron ion binding
9	4e-09	6 / 24	BP myeloid cell differentiation
10	2e-08	5 / 15	BP heme biosynthetic process
11	2e-08	7 / 52	BP blood vessel development
12	3e-07	7 / 75	BP hemopoiesis
13	3e-06	13 / 454	BP multicellular organism development
14	4e-06	9 / 210	MF protein binding
15	6e-06	4 / 21	BP erythrocyte development
16	3e-05	25 / 1761	MF metal ion binding
17	4e-05	3 / 12	BP hemoglobin biosynthetic process
18	5e-05	3 / 13	BP gastrulation with mouth forming second
19	7e-05	4 / 38	BP vasculogenesis
20	2e-04	17 / 1084	BP transport
21	2e-04	4 / 50	BP vasculature development
22	4e-04	6 / 160	BP heart development
23	4e-04	3 / 24	BP primitive hemopoiesis
24	9e-04	3 / 33	BP blood vessel morphogenesis
25	1e-03	12 / 717	MF calcium ion binding
26	1e-03	10 / 537	MF sequence-specific DNA binding
27	1e-03	3 / 37	BP definitive hemopoiesis
28	1e-03	4 / 82	MF lyase activity
29	2e-03	2 / 12	BP cardiac muscle tissue development
30	3e-03	2 / 13	BP semicircular canal morphogenesis
31	3e-03	3 / 47	MF structural constituent of cytoskeleton
32	3e-03	4 / 104	BP transmembrane receptor protein tyrosine kinase signaling pathway
33	3e-03	3 / 52	MF transmembrane receptor protein tyrosine kinase activity
34	4e-03	2 / 16	BP defense response
35	4e-03	2 / 16	BP vascular endothelial growth factor receptor signaling pathway
36	4e-03	4 / 110	MF protein tyrosine kinase activity
37	4e-03	5 / 183	MF RNA polymerase II transcription factor activity, sequence-specific DNA binding
38	5e-03	4 / 116	MF metalloendopeptidase activity
39	5e-03	2 / 18	BP neutrophil differentiation
40	5e-03	2 / 19	BP embryonic heart tube morphogenesis



BP				CC				MF			
Rank	p-value	#in/all	Geneset	Rank	p-value	#in/all	Geneset	Rank	p-value	#in/all	Geneset
1	3e-18	10 / 19	oxygen transport	1	3e-20	10 / 14	hemoglobin complex	1	3e-18	10 / 19	oxygen binding
2	4e-16	10 / 28	embryonic hemopoiesis	2	2e-02	5 / 268	cytoskeleton	2	3e-18	10 / 19	oxygen transporter activity
3	2e-14	10 / 40	erythrocyte differentiation	3	4e-02	2 / 51	lysosomal membrane	3	3e-12	13 / 145	heme binding
4	4e-09	6 / 24	myeloid cell differentiation	4	4e-02	46 / 6248	integral component of membrane	4	6e-10	12 / 178	iron ion binding
5	2e-08	5 / 15	heme biosynthetic process	5	5e-02	9 / 809	integral component of plasma membrane	5	4e-06	9 / 210	protein binding
6	2e-08	7 / 52	blood vessel development	6	6e-02	48 / 6723	membrane	6	3e-05	25 / 1761	metal ion binding
7	3e-07	7 / 75	hemopoiesis	7	6e-02	1 / 11	exocytic vesicle	7	1e-03	12 / 717	calcium ion binding
8	3e-06	13 / 454	multicellular organism development	8	6e-02	2 / 71	endomembrane system	8	1e-03	10 / 537	sequence-specific DNA binding
9	6e-06	4 / 21	erythrocyte development	9	7e-02	1 / 12	mitotic spindle	9	1e-03	4 / 82	lyase activity
10	4e-05	3 / 12	hemoglobin biosynthetic process	10	7e-02	3 / 161	mitochondrial inner membrane	10	3e-03	3 / 47	structural constituent of cytoskeleton
11	5e-05	3 / 13	gastrulation with mouth forming second	11	7e-02	22 / 2716	nucleus	11	3e-03	3 / 52	transmembrane receptor protein tyrosine kinase activity
12	7e-05	4 / 38	vasculogenesis	12	8e-02	11 / 1162	plasma membrane	12	4e-03	4 / 110	protein tyrosine kinase activity
13	2e-04	17 / 1084	transport	13	9e-02	1 / 17	external side of plasma membrane	13	4e-03	5 / 183	RNA polymerase II transcription factor activity, sequence-specific DNA binding
14	2e-04	4 / 50	vasculature development	14	9e-02	1 / 17	integral component of nuclear inner membrane	14	5e-03	4 / 116	metalloendopeptidase activity
15	4e-04	6 / 160	heart development	15	1e-01	2 / 101	endosome	15	8e-03	2 / 23	hyaluronic acid binding