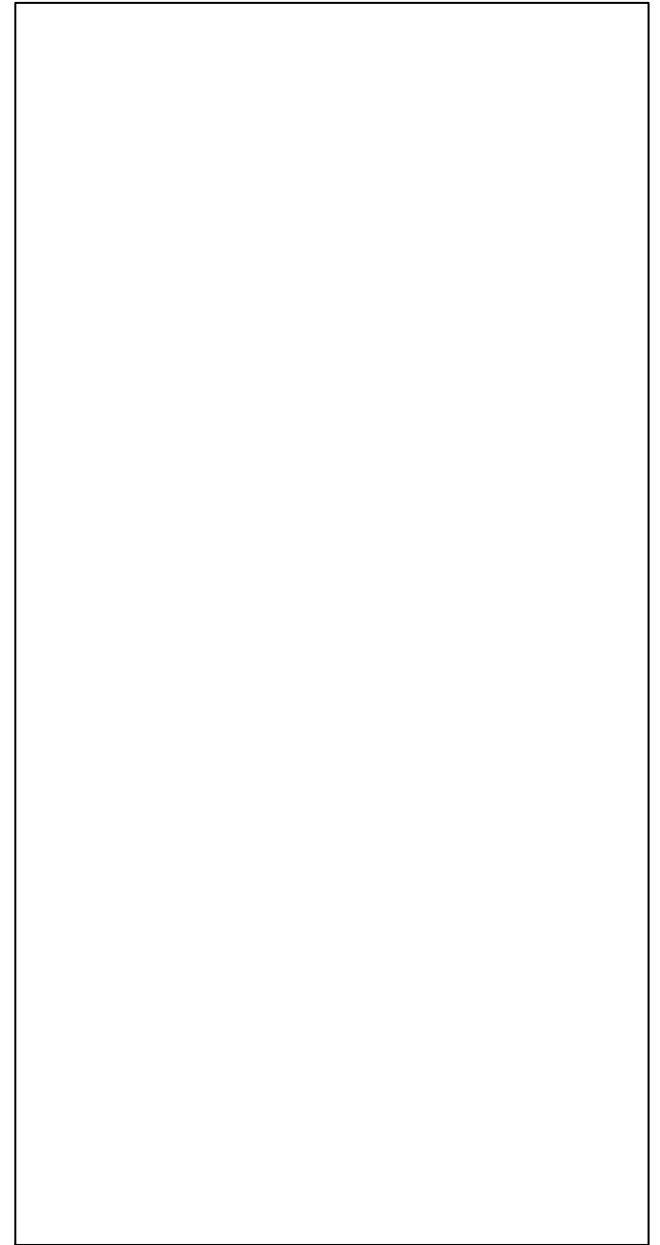
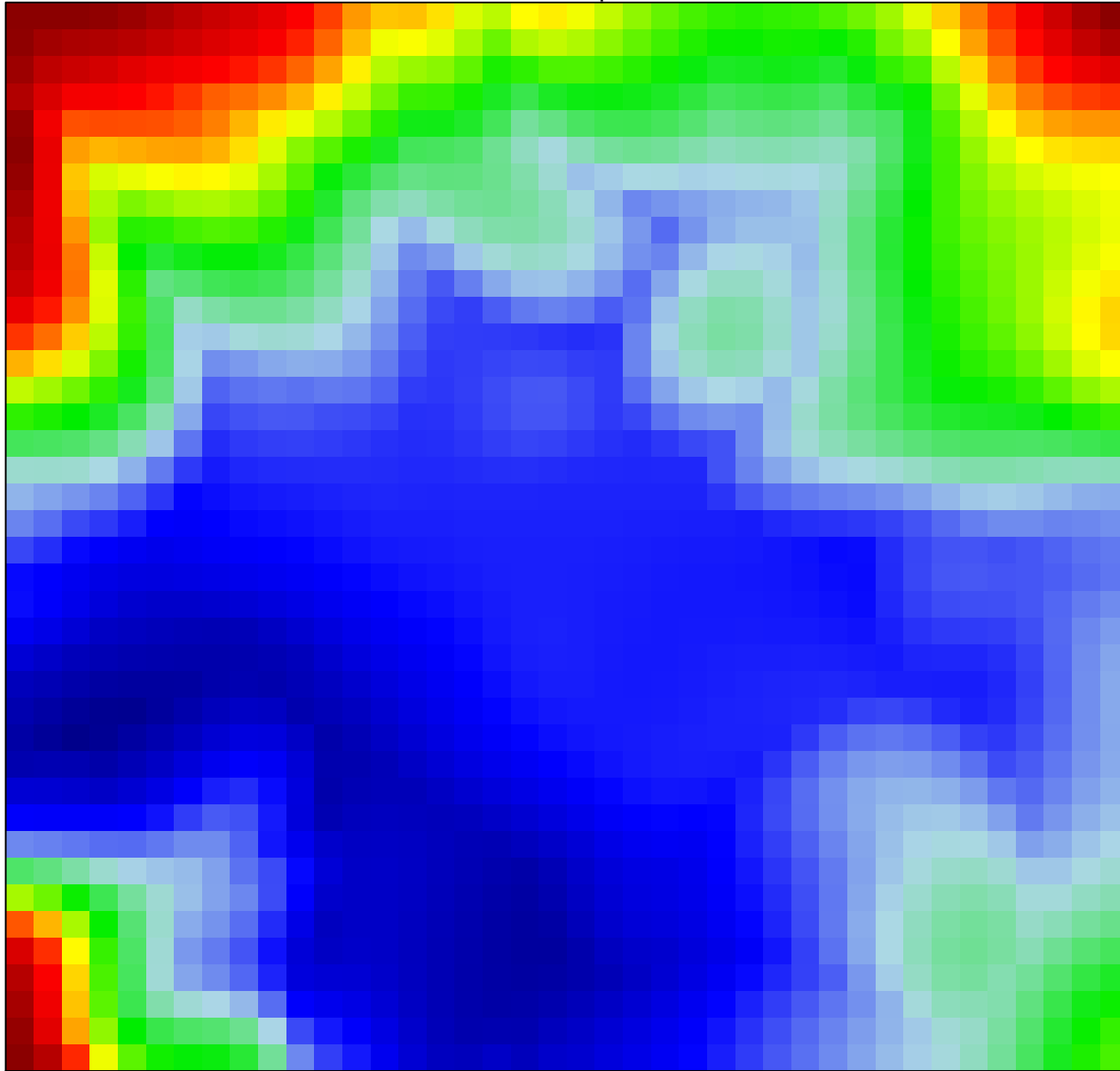
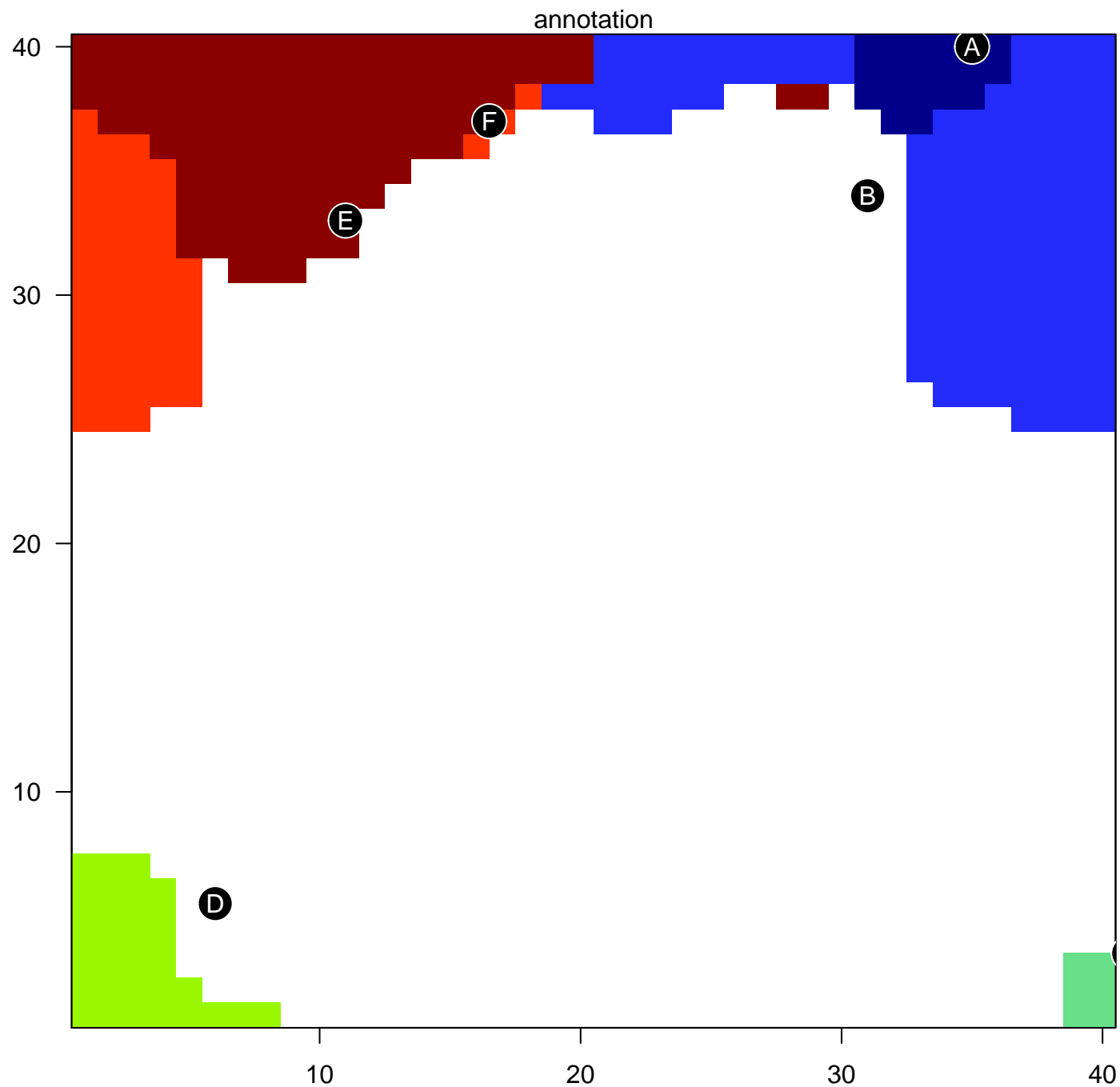


Group Overexpression Spots

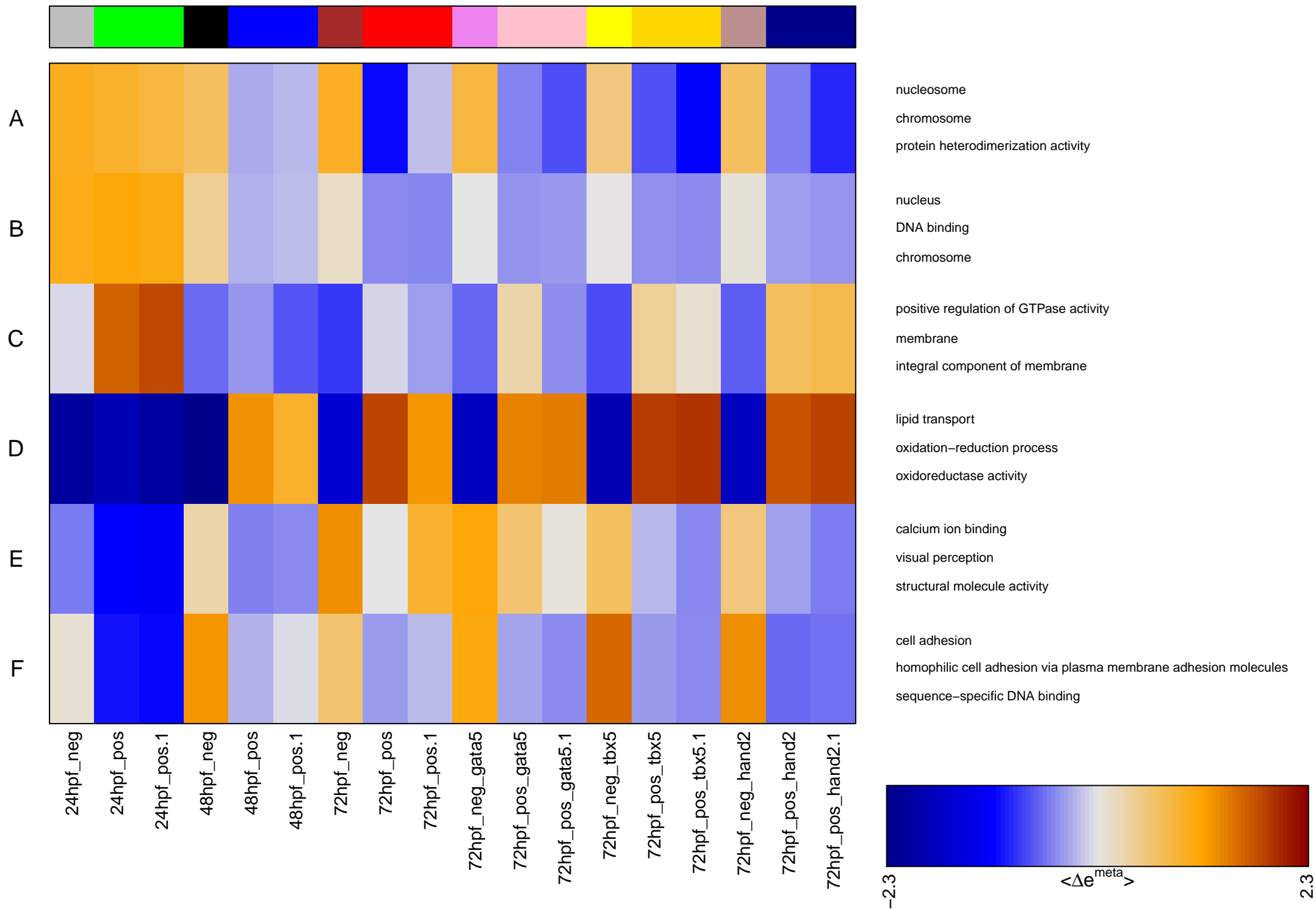
landscape

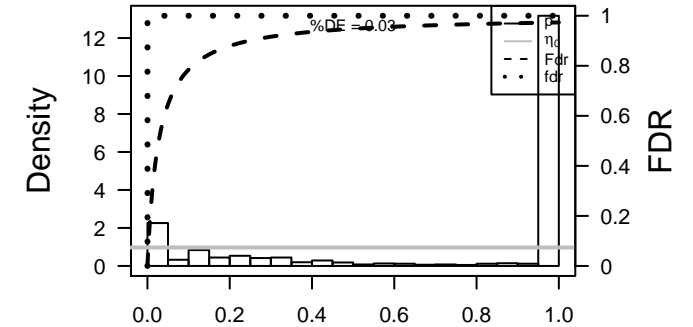


Group Overexpression Spots



- A nucleosome
chromosome
protein heterodimerization activity
- B nucleus
DNA binding
chromosome
- C positive regulation of GTPase activity
membrane
integral component of membrane
- D lipid transport
oxidation–reduction process
oxidoreductase activity
- E calcium ion binding
visual perception
structural molecule activity
- F cell adhesion
homophilic cell adhesion via plasma membrane adhesion m
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	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 activity
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

Group Overexpression Spot

Spot Summary: B

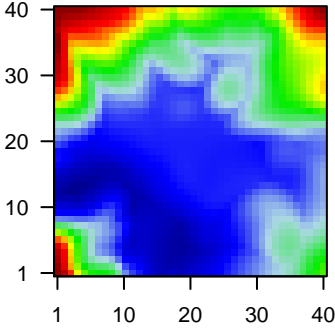
metagenes = 141
genes = 2477

<r> metagenes = 0.78

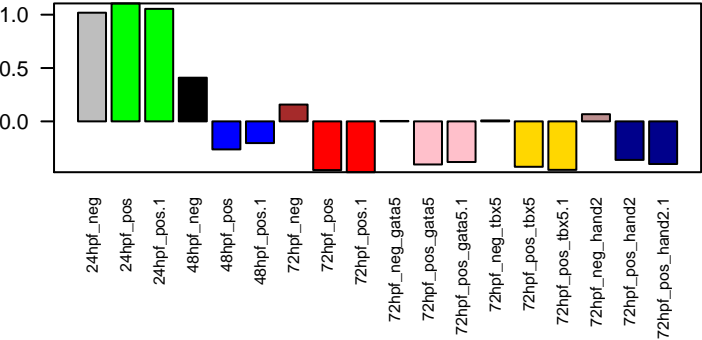
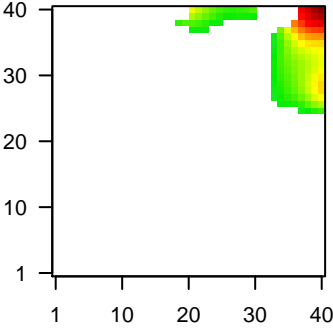
beta: r2= 5.85 / log p= -Inf

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

Overview Map



Spot

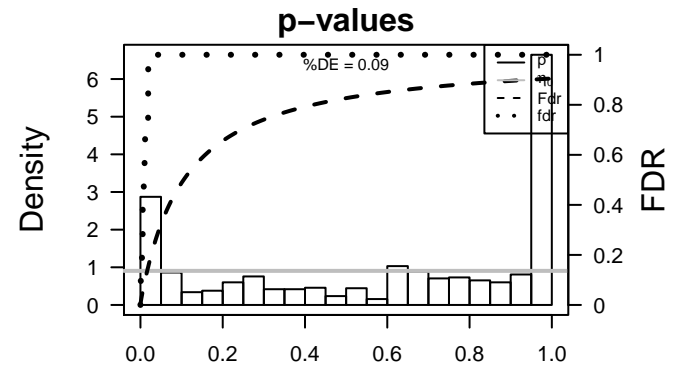


Spot Genelist

Rank	ID	max e	r	min e	Description
					Symbol
1	ENSDARG0001	8.23	-1.2	0.54	ednra endothelin receptor type A [Source:ZFIN;Acc:ZDB-GENE-0000000001]
2	ENSDARG0002	8.12	-6.4	0.84	hbbe3 hemoglobin beta embryonic-3 [Source:ZFIN;Acc:ZDB-GENE-0000000002]
3	ENSDARG0003	7.83	-4.49	0.94	drl draculin [Source:ZFIN;Acc:ZDB-GENE-991213-3]
4	ENSDARG0004	7.74	-1.79	0.54	LOC100506071 LOC100506071 [Source:ZFIN;Acc:ZDB-GENE-131121-8]
5	ENSDARG0005	7.36	-4.55	0.92	sidkey-261k4.4 sidkey-261k4.4 [Source:ZFIN;Acc:ZDB-GENE-060531-125]
6	ENSDARG0006	7.35	-4.2	0.9	bif bloody fingers [Source:ZFIN;Acc:ZDB-GENE-050721-1]
7	ENSDARG0007	7.06	-5.06	0.92	sidkey-261k4.3 sidkey-261k4.3 [Source:ZFIN;Acc:ZDB-GENE-060531-124]
8	ENSDARG0008	6.46	-4.6	0.78	protogenin homolog b (Gallus gallus) [Source:ZFIN;Acc:ZDB-GENE-0000000008]
9	ENSDARG0009	6.43	-3.22	0.88	stab2 stabilin 2 [Source:ZFIN;Acc:ZDB-GENE-041210-336]
10	ENSDARG0010	6.31	-1.79	0.87	ela2l elastase 2 like [Source:ZFIN;Acc:ZDB-GENE-040511-1]
11	ENSDARG0011	6.11	-4.16	0.93	tfr1a transferrin receptor 1a [Source:ZFIN;Acc:ZDB-GENE-041022-1]
12	ENSDARG0012	6	-2.33	0.87	si:ch73-299h12.2 [Source:ZFIN;Acc:ZDB-GENE-081031-7]
13	ENSDARG0013	5.97	-3.89	0.9	kif17 Kruppel-like factor 17 [Source:ZFIN;Acc:ZDB-GENE-010121-1]
14	ENSDARG0014	5.91	-1.27	0.64	sidkey-261k4.5 sidkey-261k4.5 [Source:ZFIN;Acc:ZDB-GENE-121214-19]
15	ENSDARG0015	5.89	-1.29	0.67	zgc:174855 zgc:174855 [Source:ZFIN;Acc:ZDB-GENE-071004-74]
16	ENSDARG0016	5.69	-3.46	0.93	gata1a GATA binding protein 1a [Source:ZFIN;Acc:ZDB-GENE-9800000016]
17	ENSDARG0017	5.69	-3.04	0.89	gfi1b growth factor independent 1B transcription repressor [Source:ZFIN;Acc:ZDB-GENE-0000000017]
18	ENSDARG0018	5.53	-3.53	0.87	
19	ENSDARG0019	5.51	-4.09	0.86	znf2a zinc finger-like gene 2a [Source:ZFIN;Acc:ZDB-GENE-0300000019]
20	ENSDARG0020	5.48	-1.21	0.59	zgc:174153 zgc:174153 [Source:ZFIN;Acc:ZDB-GENE-080215-7]

Geneset Overrepresentation

Rank	p-value	#in/all	Geneset
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
5	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 binding
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



BP				CC				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 binding
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

Group Overexpression Spot

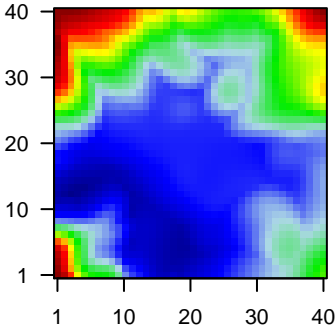
Spot Summary: C

metagenes = 6
genes = 180

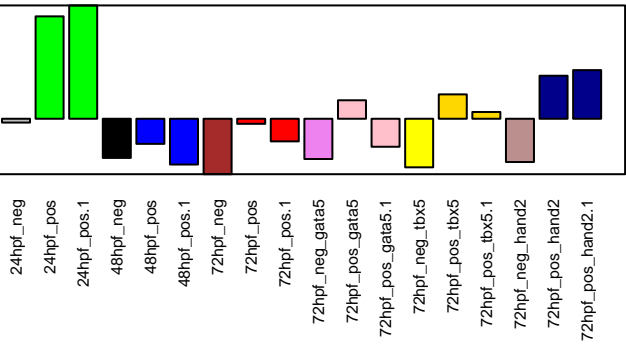
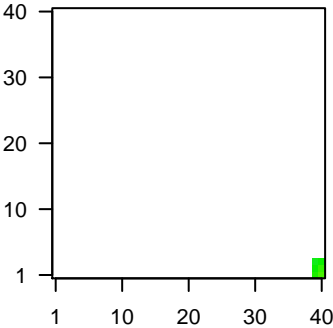
<r> metagenes = 0.99
<r> genes = 0.63
beta: r2= 7.43 / log p= -Inf

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

Overview Map



Spot

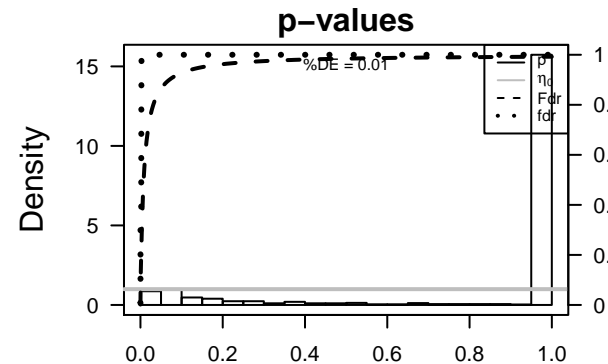


Spot Genelist

Rank	ID	max e	r	Description	
		min e		Symbol	
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	dnase1l4deoxyribonuclease 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	slc25a37solute carrier family 25 (mitochondrial iron transporter), memt
10	ENSDARG000	3.36	-1.95	0.84	slc29a1bolute carrier family 29 (equilibrative nucleoside transporter),
11	ENSDARG000	3.35	-2.16	0.86	LOC555354zfzf-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:ch73-24877248e21.7 [Source:ZFIN;Acc:ZDB-GENE-120215-2:
14	ENSDARG000	3.08	-2.4	0.8	fam117afamily 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:101663c:101663 [Source:ZFIN;Acc:ZDB-GENE-041114-149]
17	ENSDARG000	2.9	-3.03	0.88	ltk Bruton agammaglobulinemia tyrosine kinase [Source:ZFIN;Acc:
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	larf1b La ribonucleoprotein domain family, member 1B [Source:ZFIN
20	ENSDARG000	2.75	-1.6	0.84	si:ch1073-110421110a20.1 [Source:ZFIN;Acc:ZDB-GENE-121214-

Geneset Overrepresentation

Rank	p-value	#in/all	Geneset
1	1e-06	13 / 375	BP positive regulation of GTPase activity
2	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
7	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



BP				CC				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

BP				CC				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 NADP
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

Group Overexpression Spot

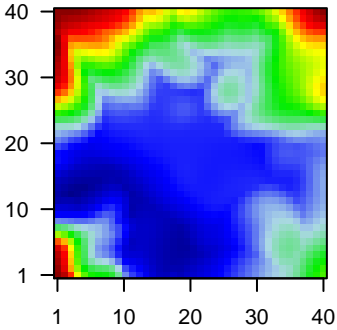
Spot Summary: E

metagenes = 56
genes = 868

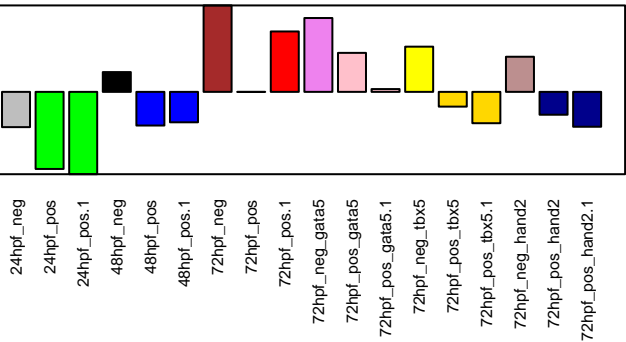
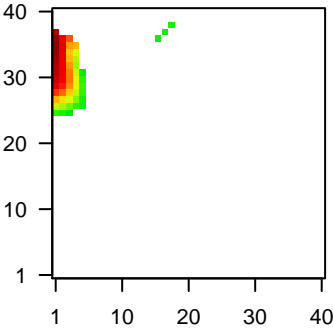
<r> metagenes = 0.82
<r> genes = 0.44
beta: r2= 9.33 / log p= -Inf

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

Overview Map



Spot

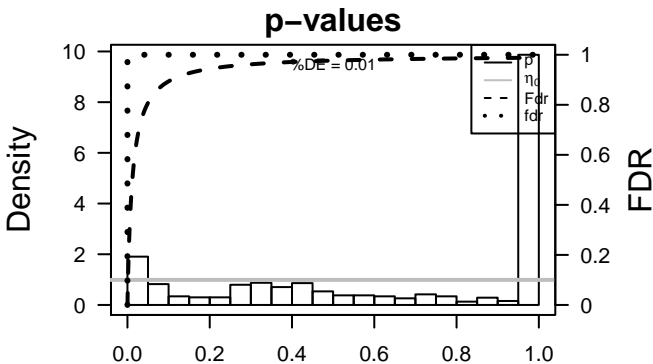


Spot Genelist

Rank	ID	max e	r	Description
		min e		Symbol
1	ENSDARG0000000001	11.88	-0.87	0.44
2	ENSDARG0000000002	7.94	-1.47	0.44
3	ENSDARG0000000003	5.44	-2.17	0.78
4	ENSDARG0000000004	5.34	-6.98	0.88
5	ENSDARG0000000005	5.22	-3.71	0.75
6	ENSDARG0000000006	5.16	-4.48	0.72
7	ENSDARG0000000007	5.14	-4.55	0.93
8	ENSDARG0000000008	5.13	-1.38	0.4
9	ENSDARG0000000009	5.09	-5.91	0.89
10	ENSDARG0000000010	5.01	-4.88	0.89
11	ENSDARG0000000011	4.9	-3.66	0.89
12	ENSDARG0000000012	4.83	-5.45	0.9
13	ENSDARG0000000013	4.82	-3.89	0.82
14	ENSDARG0000000014	4.71	-3.52	0.86
15	ENSDARG0000000015	4.62	-1.7	0.27
16	ENSDARG0000000016	4.57	-3.71	0.78
17	ENSDARG0000000017	4.55	-3.73	0.84
18	ENSDARG0000000018	4.55	-4.06	0.8
19	ENSDARG0000000019	4.25	-2.5	0.75
20	ENSDARG0000000020	4.23	-1.93	0.62

Geneset Overrepresentation

Rank	p-value	#in/all	Geneset
1	1e-18	72 / 717	MF calcium ion binding
2	3e-17	24 / 83	BP visual perception
3	1e-14	29 / 159	MF structural molecule activity
4	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	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
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
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 metalloproteinase activity



BP				CC				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



BP				CC				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	regulation 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