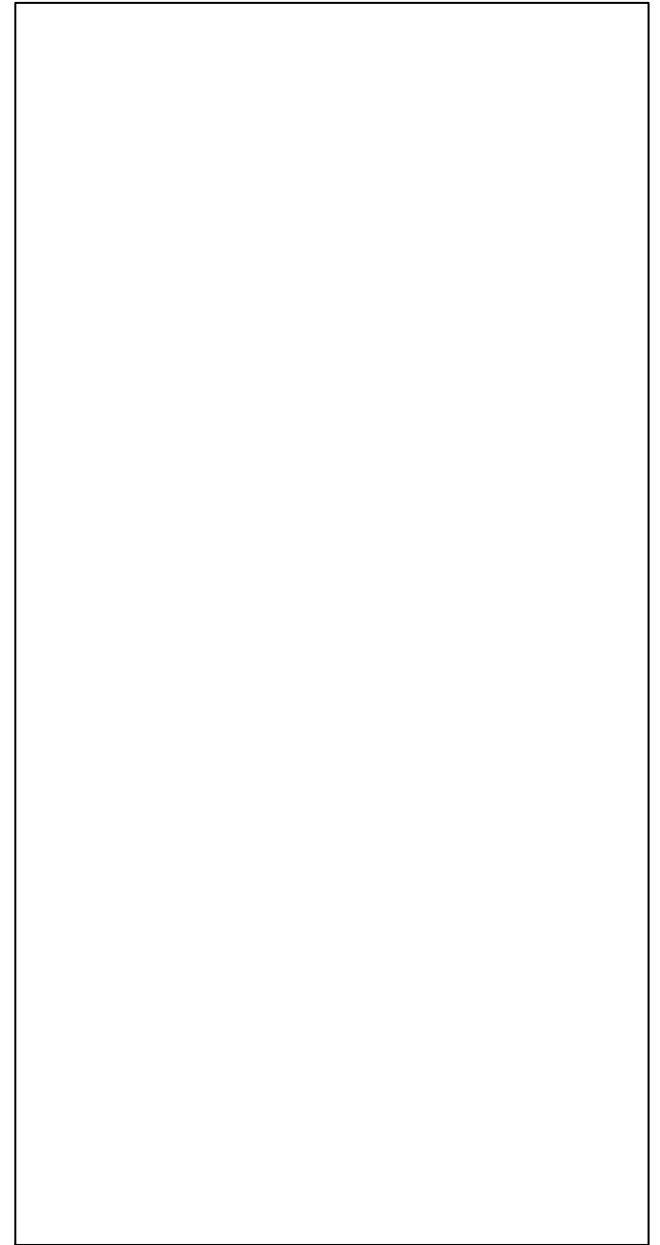
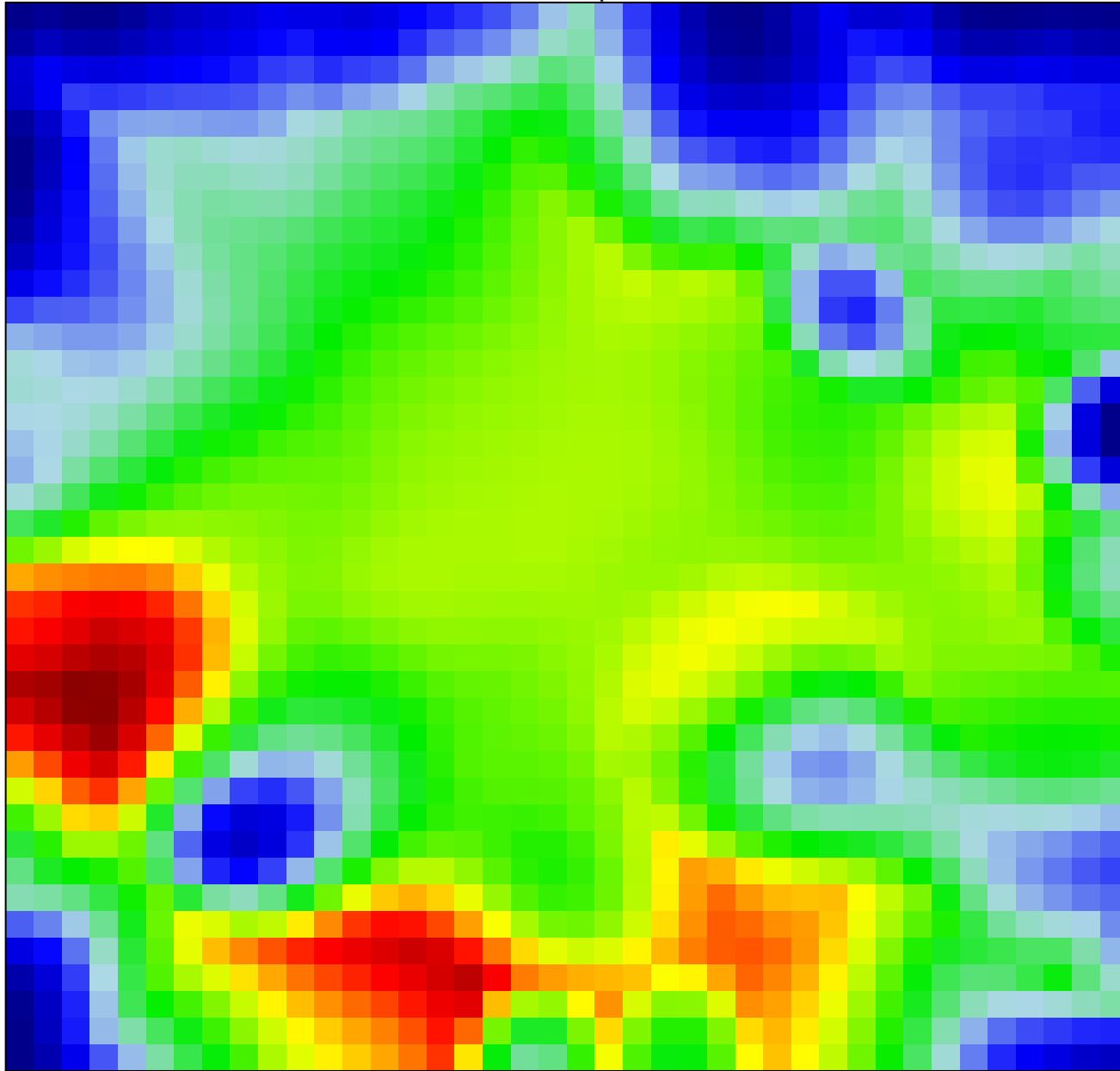


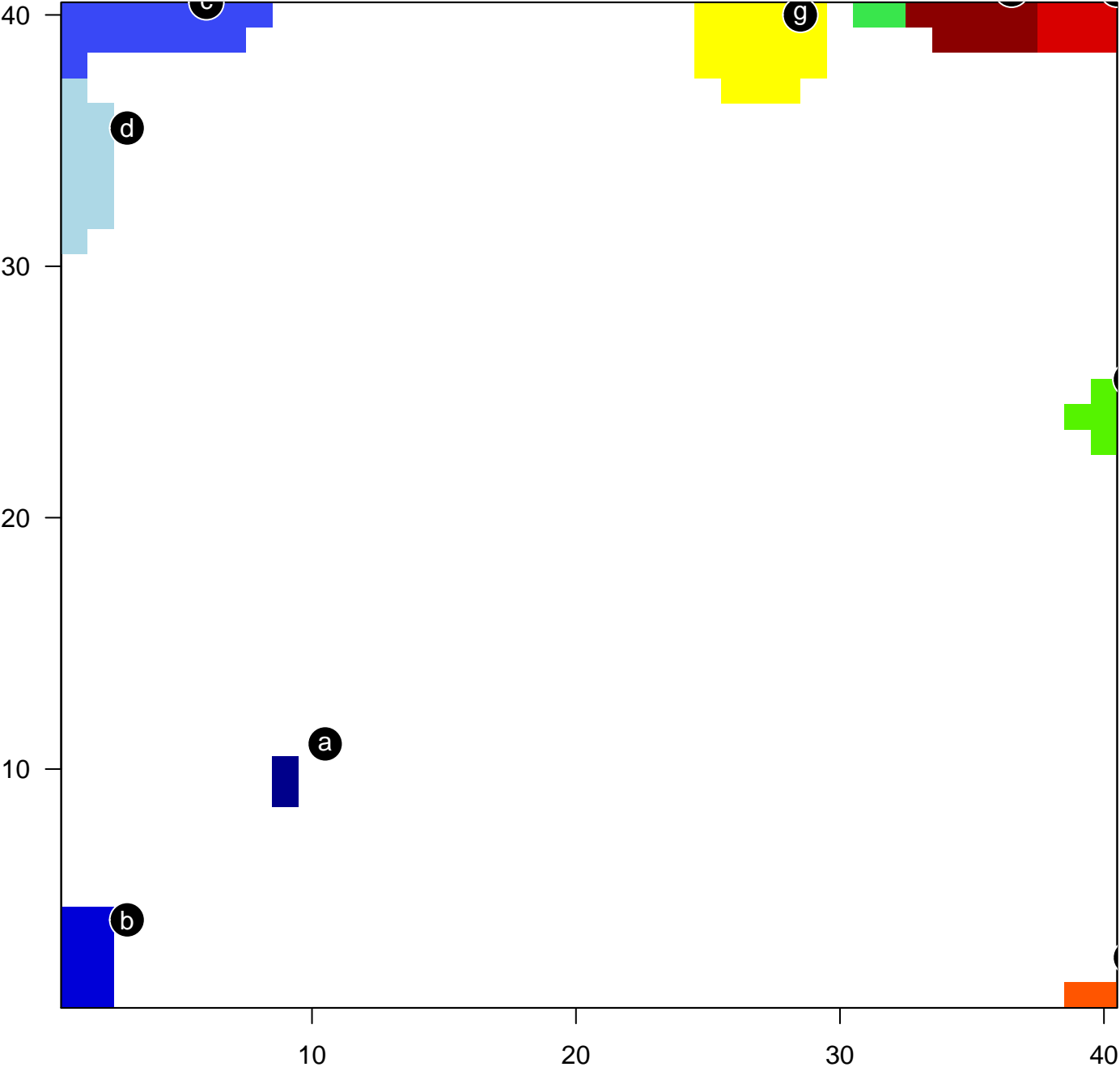
# Underexpression Spots

landscape

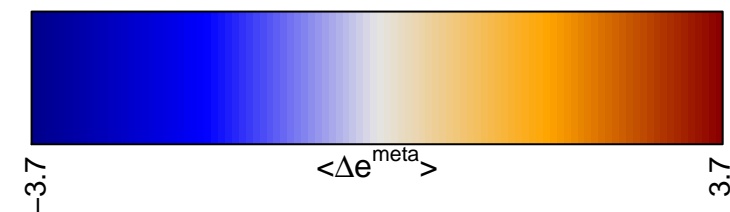
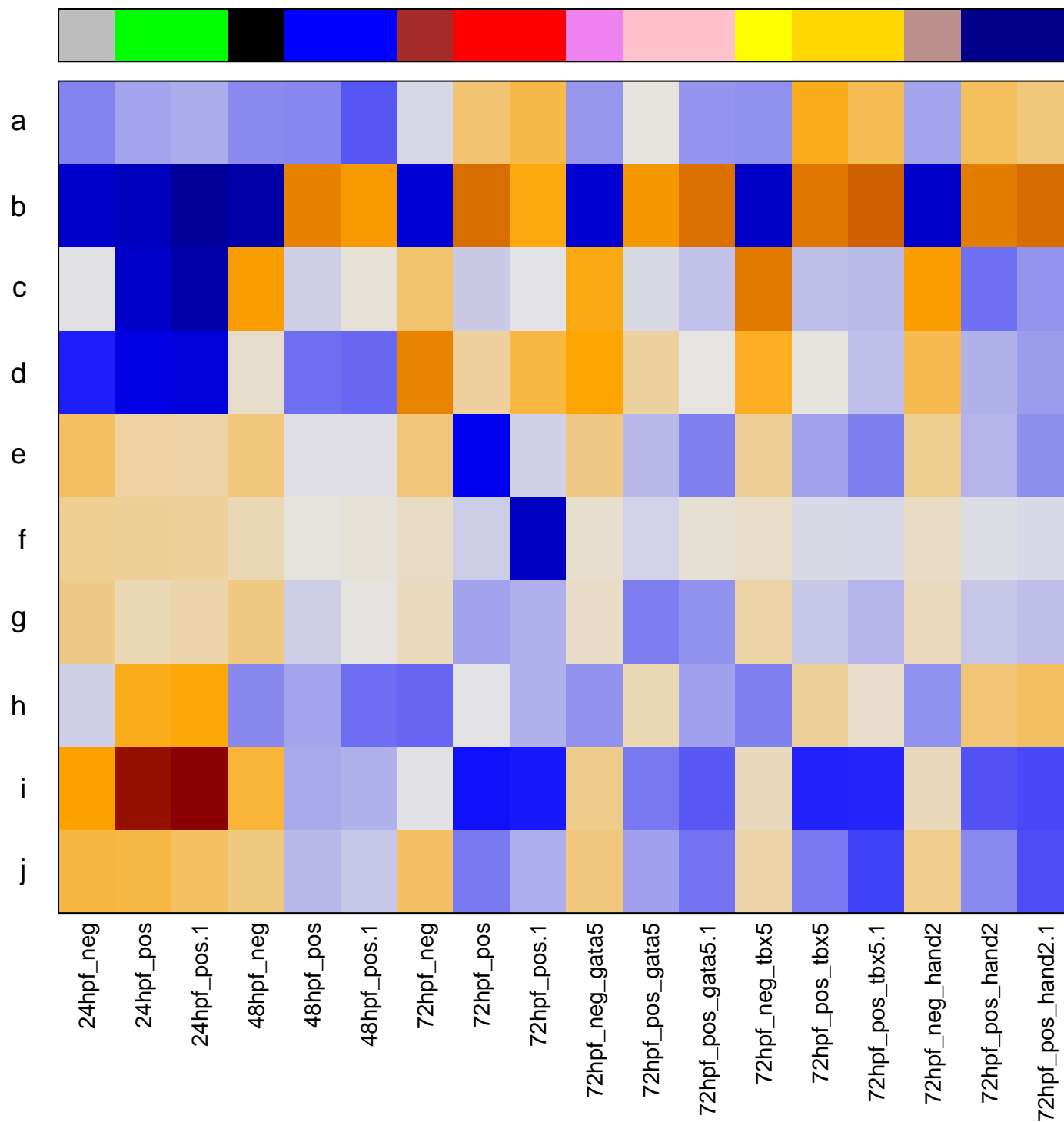


# Underexpression Spots

annotation



- a intracellular membrane-bounded organelle  
oxidoreductase activity, acting on paired donors, with incorporation of reduced sulfur
- b lipoprotein metabolic process  
lipid transport
- c sequence-specific DNA binding  
nervous system development  
regulation of transcription, DNA-templated
- d visual perception  
extracellular matrix structural constituent  
photoreceptor activity
- e hindbrain development  
DNA binding  
smoothed signaling pathway
- f chromosome  
nucleosome  
protein heterodimerization activity
- g nucleus  
nucleic acid binding  
RNA binding
- h positive regulation of GTPase activity  
intracellular signal transduction  
integrin-mediated signaling pathway
- i hemoglobin complex  
oxygen binding  
oxygen transport
- j nucleosome  
chromosome  
protein heterodimerization activity



# Underexpression Spots

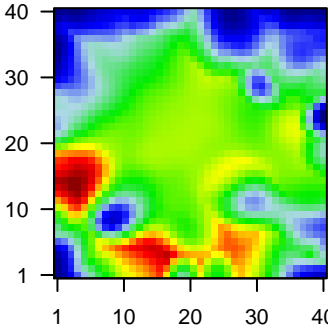
## Spot Summary: a

# metagenes = 2  
# genes = 32

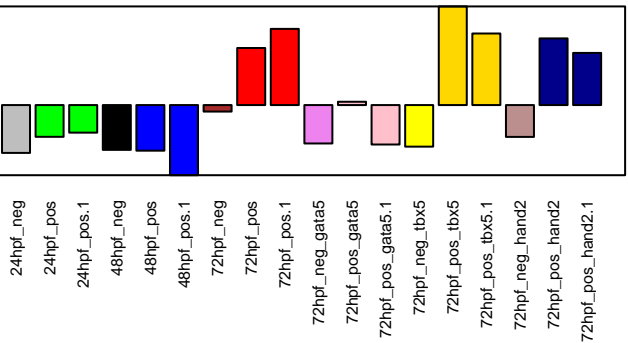
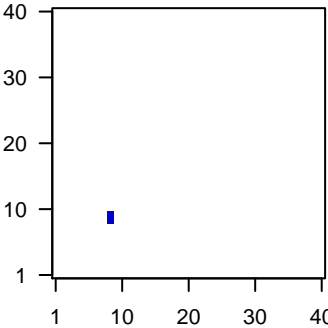
<r> metagenes = 1  
<r> genes = 0.71  
beta: r2= 7.04 / log p= -Inf

# samples with spot = 0 ( 0 %)

Overview Map



Spot

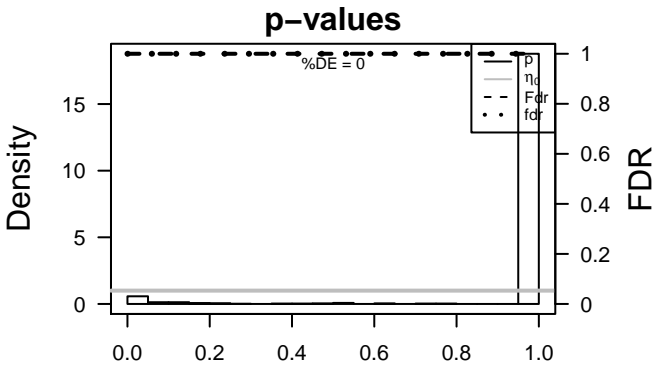


## Spot Genelist

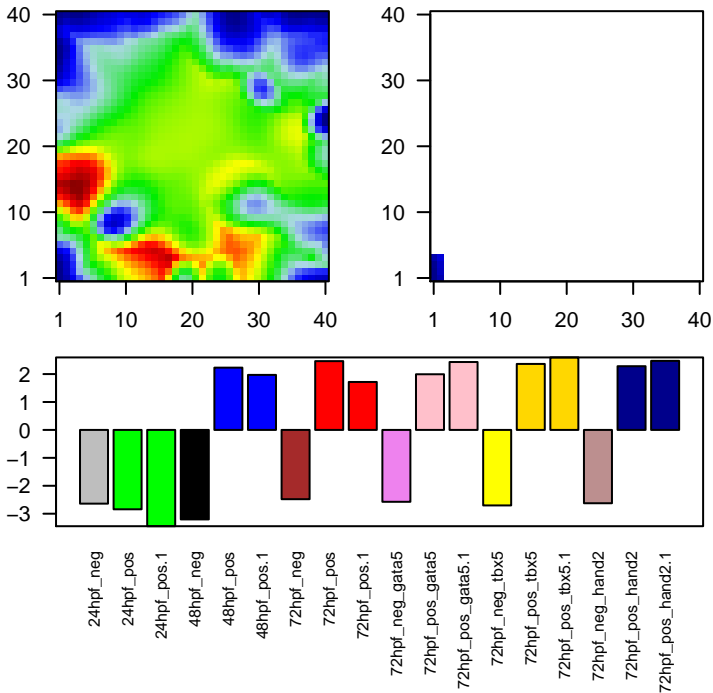
Rank	ID	max e	r	min e	Description
1	ENSDARG000	3.22	-3.48	0.91	cfh complement factor H [Source:ZFIN;Acc:ZDB-GENE-050208
2	ENSDARG000	2.84	-3.3	0.8	cyp24a1 cytochrome P450, family 24, subfamily A, polypeptide 1 [Sou
3	ENSDARG000	2.67	-2.47	0.88	cyp1a cytochrome P450, family 1, subfamily A [Source:ZFIN;Acc:ZC
4	ENSDARG000	3.14	-2.4	0.69	cyp1b1 cytochrome P450, family 1, subfamily B, polypeptide 1 [Sourc
5	ENSDARG000	2.12	-2.31	0.9	nfil3-6 nuclear factor, interleukin 3 regulated, member 6 [Source:ZFI
6	ENSDARG000	1.4	-1.84	0.86	ugt2a2 UDP glucuronosyltransferase 2 family, polypeptide A1 [Source
7	ENSDARG000	1.78	-1.81	0.88	si:ch211-93f2.1 [Source:ZFIN;Acc:ZDB-GENE-041014-96]
8	ENSDARG000	2.52	-1.7	0.89	abcc2 ATP-binding cassette, sub-family C (CFTR/MRP), member 2
9	ENSDARG000	2.2	-1.68	0.63	tnni2a.1 troponin I type 2a (skeletal, fast), tandem duplicate 1 [Source
10	ENSDARG000	1.18	-1.56	0.86	cxcr3.3 chemokine (C-X-C motif) receptor 3, tandem duplicate 3 [So
11	ENSDARG000	1.45	-1.4	0.83	rbm47 RNA binding motif protein 47 [Source:ZFIN;Acc:ZDB-GENE-
12	ENSDARG000	2.49	-1.39	0.85	adamts13 ADAM metalloproteinase with thrombospondin type 1 motif, 13
13	ENSDARG000	1.77	-1.39	0.87	si:dkay-194e6.1 [Source:ZFIN;Acc:ZDB-GENE-100922-43]
14	ENSDARG000	1.41	-1.37	0.88	enpp1 ectonucleotide pyrophosphatase/phosphodiesterase 1 [Sourc
15	ENSDARG000	1.57	-1.36	0.9	cx32.3 connexin 32.3 [Source:ZFIN;Acc:ZDB-GENE-030131-1337]
16	ENSDARG000	2.61	-1.31	0.77	zgc:92184:dkayp-52c3.2 [Source:ZFIN;Acc:ZDB-GENE-110411-46]
17	ENSDARG000	2.42	-1.3	0.87	serpind1 serpin peptidase inhibitor, clade D (heparin cofactor), membe
18	ENSDARG000	1.29	-1.24	0.86	suc1g2 succinate-CoA ligase, GDP-forming, beta subunit [Source:Zl
19	ENSDARG000	1.3	-1.22	0.81	dusp1 dual specificity phosphatase 1 [Source:ZFIN;Acc:ZDB-GENE-
20	ENSDARG000	1.98	-1.19	0.91	LOC100002960

## Geneset Overrepresentation

Rank	p-value	#in/all	Geneset
1	4e-05	3 / 59	CC intracellular membrane-bounded organelle
2	3e-04	3 / 110	MF oxidoreductase activity, acting on paired donors, with incorporation or reduc
3	3e-04	3 / 119	MF monooxygenase activity
4	4e-04	2 / 27	MF oxidoreductase activity, acting on paired donors, with incorporation or reduc
5	6e-04	3 / 145	MF heme binding
6	9e-04	2 / 39	CC connexin complex
7	1e-03	3 / 178	MF iron ion binding
8	1e-03	2 / 44	CC gap junction
9	2e-03	2 / 53	BP chemotaxis
10	2e-03	2 / 58	BP chemokine-mediated signaling pathway
11	2e-03	2 / 64	BP cell communication
12	3e-03	2 / 72	BP nucleic acid phosphodiester bond hydrolysis
13	3e-03	7 / 1761	MF metal ion binding
14	5e-03	3 / 297	BP immune response
15	9e-03	2 / 128	MF metalloproteinase activity
16	1e-02	1 / 10	BP circadian regulation of gene expression
17	1e-02	3 / 414	BP metabolic process
18	1e-02	1 / 12	BP head development
19	1e-02	1 / 12	BP response to xenobiotic stimulus
20	2e-02	1 / 15	BP cardiac muscle contraction
21	2e-02	1 / 15	MF MAP kinase tyrosine/serine/threonine phosphatase activity
22	2e-02	1 / 15	BP retinol metabolic process
23	2e-02	1 / 15	BP skeletal muscle contraction
24	2e-02	3 / 480	MF catalytic activity
25	2e-02	1 / 16	BP inactivation of MAPK activity
26	2e-02	1 / 16	MF polysaccharide binding
27	2e-02	1 / 17	MF organic anion transmembrane transporter activity
28	2e-02	1 / 17	MF transcriptional repressor activity, RNA polymerase II core promoter proxima
29	2e-02	1 / 18	MF steroid binding
30	2e-02	3 / 522	MF oxidoreductase activity
31	2e-02	1 / 19	BP organic anion transport
32	2e-02	1 / 20	BP steroid metabolic process
33	2e-02	4 / 969	MF hydrolase activity
34	2e-02	2 / 209	CC endoplasmic reticulum membrane
35	2e-02	1 / 22	MF chemokine receptor activity
36	3e-02	2 / 219	CC cell junction
37	3e-02	1 / 23	CC troponin complex
38	3e-02	1 / 25	BP tricarboxylic acid cycle
39	3e-02	1 / 29	BP cellular response to xenobiotic stimulus
40	3e-02	1 / 29	MF glucuronosyltransferase activity



BP				CC				MF			
Rank	p-value	#in/all	Geneset	Rank	p-value	#in/all	Geneset	Rank	p-value	#in/all	Geneset
1	0.002	2 / 53	chemotaxis	1	4e-05	3 / 59	intracellular membrane-bounded organelle	1	3e-04	3 / 110	oxidoreductase activity, acting on paired donors, with incorporation or reduction of molecular oxygen
2	0.002	2 / 58	chemokine-mediated signaling pathway	2	9e-04	2 / 39	connexin complex	2	3e-04	3 / 119	monooxygenase activity
3	0.002	2 / 64	cell communication	3	1e-03	2 / 44	gap junction	3	4e-04	2 / 27	oxidoreductase activity, acting on paired donors, with incorporation or reduction of molecular oxygen
4	0.003	2 / 72	nucleic acid phosphodiester bond hydrolysis	4	2e-02	2 / 209	endoplasmic reticulum membrane	4	6e-04	3 / 145	heme binding
5	0.005	3 / 297	immune response	5	3e-02	2 / 219	cell junction	5	1e-03	3 / 178	iron ion binding
6	0.011	1 / 10	circadian regulation of gene expression	6	3e-02	1 / 23	troponin complex	6	3e-03	7 / 1761	metal ion binding
7	0.011	3 / 414	metabolic process	7	4e-02	1 / 35	peroxisome	7	9e-03	2 / 128	metallopeptidase activity
8	0.014	1 / 12	head development	8	6e-02	2 / 337	endoplasmic reticulum	8	2e-02	1 / 15	MAP kinase tyrosine/serine/threonine phosphatase activity
9	0.014	1 / 12	response to xenobiotic stimulus	9	2e-01	10 / 6248	integral component of membrane	9	2e-02	3 / 480	catalytic activity
10	0.017	1 / 15	cardiac muscle contraction	10	2e-01	10 / 6723	membrane	10	2e-02	1 / 16	polysaccharide binding
11	0.017	1 / 15	retinol metabolic process	11	4e-01	1 / 410	mitochondrion	11	2e-02	1 / 17	organic anion transmembrane transporter activity
12	0.017	1 / 15	skeletal muscle contraction	12	4e-01	2 / 1162	plasma membrane	12	2e-02	1 / 17	transcriptional repressor activity, RNA polymerase II core promoter proximal region sequence-specific DNA binding
13	0.018	1 / 16	inactivation of MAPK activity	13	4e-01	1 / 500	extracellular space	13	2e-02	1 / 18	steroid binding
14	0.021	1 / 19	organic anion transport	14	5e-01	1 / 634	extracellular region	14	2e-02	3 / 522	oxidoreductase activity
15	0.023	1 / 20	steroid metabolic process	15	5e-01	2 / 1580	cellular_component	15	2e-02	4 / 969	hydrolase activity



BP

Rank

p-value

#in/all

Geneset

15e-117 / 23lipoprotein metabolic process

26e-098 / 67lipid transport

35e-0819 / 712oxidation-reduction process

42e-053 / 10triglyceride catabolic process

53e-053 / 11cholesterol homeostasis

63e-053 / 11melanosome organization

74e-053 / 12cholesterol biosynthetic process

86e-053 / 13cholesterol efflux

96e-053 / 13response to toxic substance

104e-043 / 24nucleoside metabolic process

115e-043 / 26melanosome transport

127e-043 / 30pigmentation

138e-043 / 31protein-chromophore linkage

149e-0411 / 591transmembrane transport

152e-032 / 12aromatic amino acid family metabolic process

CC

Rank

p-value

#in/all

Geneset

12e-074 / 10melanosome

22e-053 / 10chylomicron

32e-053 / 10high-density lipoprotein particle

49e-053 / 15secretory granule

51e-0413 / 634extracellular region

61e-043 / 17blood microparticle

75e-043 / 26vesicle

81e-033 / 38trans-Golgi network

92e-0354 / 6248integral component of membrane

103e-0356 / 6723membrane

118e-033 / 70myosin complex

124e-025 / 317Golgi apparatus

135e-0215 / 1580cellular\_component

146e-025 / 355cytosol

157e-022 / 71endomembrane system

MF

Rank

p-value

#in/all

Geneset

13e-0614 / 522oxidoreductase activity

22e-0510 / 321GTPase activity

34e-056 / 105lipid binding

41e-043 / 17cholesterol binding

51e-043 / 17cholesterol transporter activity

63e-043 / 21substrate-specific transmembrane transporter activity

76e-0411 / 561GTP binding

87e-044 / 67transmembrane transporter activity

91e-033 / 33photoreceptor activity

102e-033 / 43iron-sulfur cluster binding

113e-036 / 229transporter activity

124e-035 / 178iron ion binding

136e-033 / 60scavenger receptor activity

148e-032 / 23NADP binding

151e-022 / 25glutathione transferase activity

# Underexpression Spots

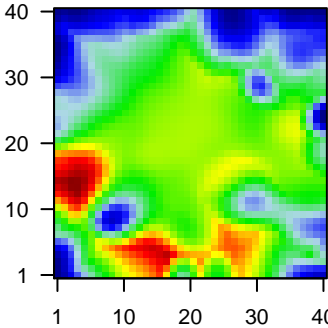
## Spot Summary: c

# metagenes = 16  
# genes = 457

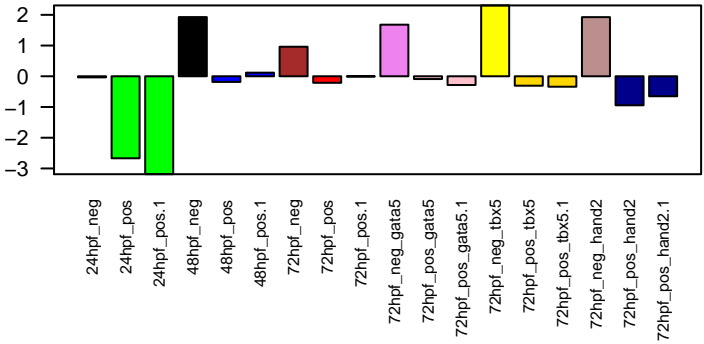
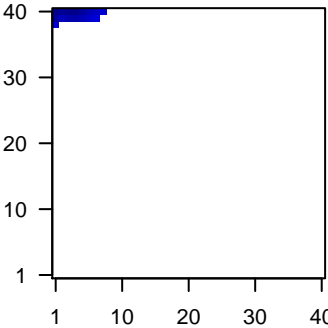
<r> metagenes = 0.97  
<r> genes = 0.77  
beta: r2= 31.01 / log p= -Inf

# samples with spot = 2 ( 11.1 %)  
24hpf\_pos : 2 ( 100 %)

Overview Map



Spot

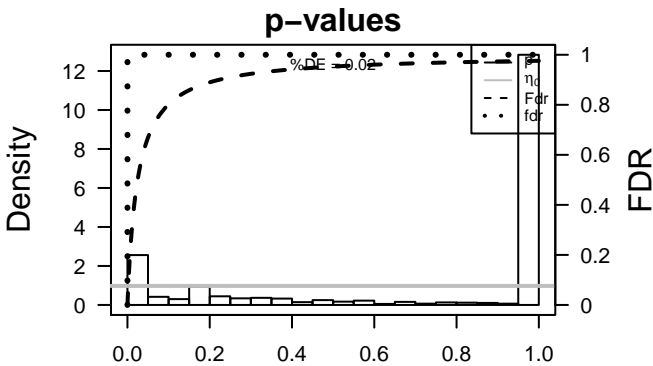


## Spot Genelist

Rank	ID	max e	r	Description	
		min e		Symbol	
1	ENSDARG000	2.06	-9.48	0.66	myhz1.1 myosin, heavy polypeptide 1.1, skeletal muscle [Source:ZFIN]
2	ENSDARG000	4.72	-8.26	0.86	col11a2 collagen, type XI, alpha 2 [Source:ZFIN;Acc:ZDB-GENE-000]
3	ENSDARG000	3.03	-7.84	0.76	kr191 keratin 17 [Source:ZFIN;Acc:ZDB-GENE-060503-86]
4	ENSDARG000	2.86	-7.73	0.92	stmn1b stathmin 1b [Source:ZFIN;Acc:ZDB-GENE-050417-397]
5	ENSDARG000	3.2	-7.21	0.96	gpm6aa glycoprotein M6Aa [Source:ZFIN;Acc:ZDB-GENE-030710-7]
6	ENSDARG000	2.35	-6.78	0.84	cpe carboxypeptidase E [Source:ZFIN;Acc:ZDB-GENE-090313-13]
7	ENSDARG000	4.49	-6.7	0.85	si:dkey-65b12.6 [Source:ZFIN;Acc:ZDB-GENE-060526-32]
8	ENSDARG000	2.15	-6.69	0.66	fkbp5 FK506 binding protein 5 [Source:ZFIN;Acc:ZDB-GENE-0306]
9	ENSDARG000	2.83	-6.67	0.93	neuronal differentiation 1 [Source:ZFIN;Acc:ZDB-GENE-990]
10	ENSDARG000	2.41	-6.61	0.87	atp1a1b ATPase, Na+/K+ transporting, alpha 1b polypeptide [Source:ZFIN]
11	ENSDARG000	1.97	-6.47	0.73	gfap glial fibrillary acidic protein [Source:ZFIN;Acc:ZDB-GENE-95]
12	ENSDARG000	3.37	-6.4	0.97	si:dkey-46c14.4-40m6.8 [Source:ZFIN;Acc:ZDB-GENE-100922-162]
13	ENSDARG000	4.01	-6.39	0.88	col9a3 collagen, type IX, alpha 3 [Source:ZFIN;Acc:ZDB-GENE-030]
14	ENSDARG000	3.14	-6.34	0.9	slc1a3b solute carrier family 1 (glial high affinity glutamate transporter)
15	ENSDARG000	3.23	-6.31	0.88	map1aa microtubule-associated protein 1Aa [Source:ZFIN;Acc:ZDB-GENE-030]
16	ENSDARG000	3.88	-6.3	0.95	pclob piccolo presynaptic cytomatrix protein b [Source:ZFIN;Acc:ZDB-GENE-030]
17	ENSDARG000	3.24	-6.26	0.96	Down syndrome cell adhesion molecule like 1 [Source:ZFIN;Acc:ZDB-GENE-030]
18	ENSDARG000	4	-6.25	0.81	epyc epiphycan [Source:ZFIN;Acc:ZDB-GENE-041008-9]
19	ENSDARG000	3.32	-6.25	0.96	kif5aa kinesin family member 5A, a [Source:ZFIN;Acc:ZDB-GENE-030]
20	ENSDARG000	3.36	-6.19	0.97	kif1ab kinesin family member 1Ab [Source:ZFIN;Acc:ZDB-GENE-030]

## Geneset Overrepresentation

Rank	p-value	#in/all	Geneset
1	2e-23	50 / 537	MF sequence-specific DNA binding
2	4e-23	31 / 175	BP nervous system development
3	1e-15	63 / 1239	BP regulation of transcription, DNA-templated
4	3e-14	35 / 454	BP multicellular organism development
5	2e-13	21 / 158	MF microtubule binding
6	1e-12	64 / 1484	MF DNA binding
7	8e-12	20 / 172	BP homophilic cell adhesion via plasma membrane adhesion molecules
8	1e-11	19 / 155	CC synapse
9	2e-11	91 / 2716	CC nucleus
10	3e-10	15 / 108	CC microtubule
11	5e-10	19 / 193	BP positive regulation of transcription from RNA polymerase II promoter
12	4e-09	48 / 1162	CC plasma membrane
13	5e-09	14 / 113	BP transcription from RNA polymerase II promoter
14	7e-09	23 / 333	BP cell adhesion
15	8e-09	33 / 643	BP transcription, DNA-templated
16	3e-08	8 / 32	MF extracellular-glutamate-gated ion channel activity
17	3e-08	8 / 32	MF ionotropic glutamate receptor activity
18	3e-08	8 / 32	BP ionotropic glutamate receptor signaling pathway
19	6e-08	27 / 499	BP ion transport
20	1e-07	33 / 717	MF calcium ion binding
21	3e-07	9 / 57	BP microtubule cytoskeleton organization
22	5e-07	10 / 78	BP axon guidance
23	7e-07	29 / 633	MF transcription factor activity, sequence-specific DNA binding
24	9e-07	13 / 147	BP brain development
25	1e-06	8 / 49	MF extracellular matrix structural constituent
26	2e-06	14 / 183	MF RNA polymerase II transcription factor activity, sequence-specific DNA binding
27	3e-06	7 / 39	BP neuron projection development
28	3e-06	9 / 74	CC neuron projection
29	3e-06	15 / 219	CC cell junction
30	5e-06	151 / 6723	CC membrane
31	6e-06	9 / 79	BP excitatory postsynaptic potential
32	6e-06	5 / 17	BP cytoskeleton-dependent intracellular transport
33	6e-06	5 / 17	CC presynaptic active zone
34	7e-06	7 / 44	BP neuron development
35	8e-06	5 / 18	MF tubulin binding
36	9e-06	7 / 46	BP eye development
37	1e-05	16 / 270	MF ion channel activity
38	1e-05	8 / 65	BP sodium ion transport
39	1e-05	6 / 33	BP hindbrain development
40	2e-05	4 / 11	MF spectrin binding





BP				CC				MF			
Rank	p-value	#in/all	Geneset	Rank	p-value	#in/all	Geneset	Rank	p-value	#in/all	Geneset
1	4e-23	31 / 175	nervous system development	1	1e-11	19 / 155	synapse	1	2e-23	50 / 537	sequence-specific DNA binding
2	1e-15	63 / 1239	regulation of transcription, DNA-templated	2	2e-11	91 / 2716	nucleus	2	2e-13	21 / 158	microtubule binding
3	3e-14	35 / 454	multicellular organism development	3	3e-10	15 / 108	microtubule	3	1e-12	64 / 1484	DNA binding
4	8e-12	20 / 172	homophilic cell adhesion via plasma membrane adhesion molecules	4	4e-09	48 / 1162	plasma membrane	4	3e-08	8 / 32	extracellular-glutamate-gated ion channel activity
5	5e-10	19 / 193	positive regulation of transcription from RNA polymerase II promoter	5	3e-06	9 / 74	neuron projection	5	3e-08	8 / 32	ionotropic glutamate receptor activity
6	5e-09	14 / 113	transcription from RNA polymerase II promoter	6	3e-06	15 / 219	cell junction	6	1e-07	33 / 717	calcium ion binding
7	7e-09	23 / 333	cell adhesion	7	5e-06	151 / 6723	membrane	7	7e-07	29 / 633	transcription factor activity, sequence-specific DNA binding
8	8e-09	33 / 643	transcription, DNA-templated	8	6e-06	5 / 17	presynaptic active zone	8	1e-06	8 / 49	extracellular matrix structural constituent
9	3e-08	8 / 32	ionotropic glutamate receptor signaling pathway	9	2e-05	6 / 36	synaptic vesicle	9	2e-06	14 / 183	RNA polymerase II transcription factor activity, sequence-specific DNA binding
10	6e-08	27 / 499	ion transport	10	5e-05	8 / 80	postsynaptic membrane	10	8e-06	5 / 18	tubulin binding
11	3e-07	9 / 57	microtubule cytoskeleton organization	11	1e-04	4 / 17	AMPA glutamate receptor complex	11	1e-05	16 / 270	ion channel activity
12	5e-07	10 / 78	axon guidance	12	1e-04	135 / 6248	integral component of membrane	12	2e-05	4 / 11	spectrin binding
13	9e-07	13 / 147	brain development	13	5e-04	3 / 10	clathrin-coated vesicle	13	3e-05	10 / 120	motor activity
14	3e-06	7 / 39	neuron projection development	14	5e-04	13 / 268	cytoskeleton	14	4e-05	10 / 124	receptor activity
15	6e-06	9 / 79	excitatory postsynaptic potential	15	8e-04	3 / 12	microtubule associated complex	15	1e-04	6 / 47	structural constituent of cytoskeleton

# Underexpression Spots

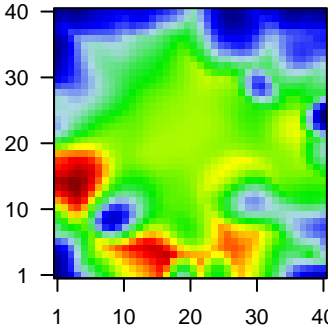
## Spot Summary: d

# metagenes = 12  
# genes = 204

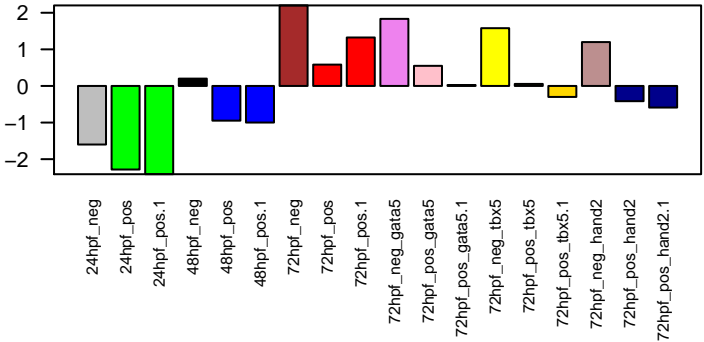
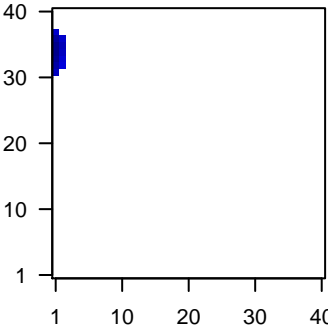
<r> metagenes = 0.98  
<r> genes = 0.69  
beta: r2= 21.54 / log p= -Inf

# samples with spot = 3 ( 16.7 %)  
24hpf\_neg : 1 ( 100 %)  
24hpf\_pos : 2 ( 100 %)

Overview Map



Spot

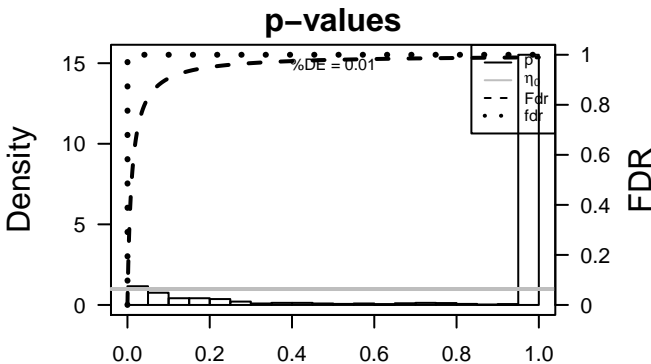


## Spot Genelist

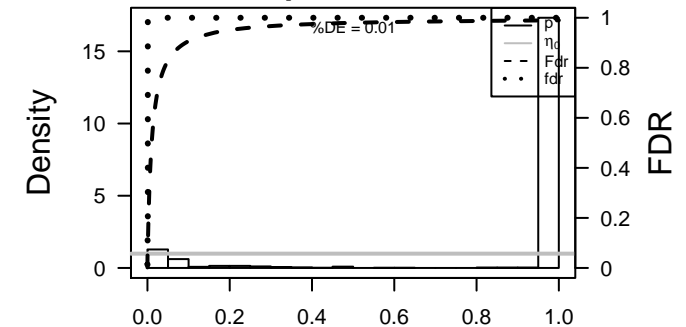
Rank	ID	max e	r	Description	
		min e		Symbol	
1	ENSDARG000	5.34	-6.98	0.94	matn1 matrilin 1 [Source:ZFIN;Acc:ZDB-GENE-050307-3]
2	ENSDARG000	3.36	-6.43	0.86	rbp4 retinol binding protein 4, plasma [Source:ZFIN;Acc:ZDB-GENE-050307-3]
3	ENSDARG000	5.09	-5.91	0.88	and2 actinodin2 [Source:ZFIN;Acc:ZDB-GENE-041105-2]
4	ENSDARG000	2.67	-5.74	0.89	lect1 leukocyte cell derived chemotaxin 1 [Source:ZFIN;Acc:ZDB-GENE-050307-3]
5	ENSDARG000	2.52	-5.65	0.88	chd3 chromodomain helicase DNA binding protein 3 [Source:ZFIN;Acc:ZDB-GENE-050307-3]
6	ENSDARG000	3.56	-5.56	0.75	krt1c19keratin type 1 c19e [Source:ZFIN;Acc:ZDB-GENE-050506-3]
7	ENSDARG000	3.82	-5.55	0.95	acana aggrecan a [Source:ZFIN;Acc:ZDB-GENE-050208-221]
8	ENSDARG000	1.93	-5.48	0.82	cdkn1d cyclin-dependent kinase inhibitor 1D [Source:ZFIN;Acc:ZDB-GENE-050307-3]
9	ENSDARG000	4.83	-5.45	0.97	arr3a arrestin 3a, retinal (X-arrestin) [Source:ZFIN;Acc:ZDB-GENE-050307-3]
10	ENSDARG000	2.41	-5.42	0.78	
11	ENSDARG000	3.69	-5.36	0.77	myhb myosin, heavy chain b [Source:ZFIN;Acc:ZDB-GENE-081112]
12	ENSDARG000	2.57	-5.36	0.86	prss35 protease, serine, 35 [Source:ZFIN;Acc:ZDB-GENE-040704-1]
13	ENSDARG000	2.64	-5.25	0.88	snap25b synaptosomal-associated protein, 25b [Source:ZFIN;Acc:ZDB-GENE-050307-3]
14	ENSDARG000	3.5	-5.21	0.94	tenascin XB a [Source:ZFIN;Acc:ZDB-GENE-070103-5]
15	ENSDARG000	2.33	-5.17	0.79	ngfra nerve growth factor receptor a (TNFR superfamily, member 1)
16	ENSDARG000	3.39	-5.13	0.82	col17a1collagen, type XVII, alpha 1a [Source:ZFIN;Acc:ZDB-GENE-050307-3]
17	ENSDARG000	3.77	-5.03	0.81	si:dkey-183b5-183i3.5 [Source:ZFIN;Acc:ZDB-GENE-030131-856]
18	ENSDARG000	3.59	-4.99	0.95	periostin, osteoblast specific factor a [Source:ZFIN;Acc:ZDB-GENE-050307-3]
19	ENSDARG000	2.32	-4.92	0.81	sgip1a SH3-domain GRB2-like (endophilin) interacting protein 1a [Source:ZFIN;Acc:ZDB-GENE-050307-3]
20	ENSDARG000	5.01	-4.88	0.95	opn1lw2 opsin 1 (cone pigments), long-wave-sensitive, 2 [Source:ZFIN;Acc:ZDB-GENE-050307-3]

## Geneset Overrepresentation

Rank	p-value	#in/all	Geneset
1	4e-17	15 / 83	BP visual perception
2	2e-09	8 / 49	MF extracellular matrix structural constituent
3	3e-09	7 / 33	MF photoreceptor activity
4	4e-08	6 / 28	BP phototransduction
5	9e-08	6 / 31	CC photoreceptor outer segment
6	9e-08	6 / 31	BP protein-chromophore linkage
7	1e-06	19 / 717	MF calcium ion binding
8	2e-06	9 / 153	CC proteinaceous extracellular matrix
9	3e-06	5 / 31	MF G-protein coupled photoreceptor activity
10	4e-06	17 / 634	CC extracellular region
11	1e-05	7 / 102	BP response to stimulus
12	4e-05	3 / 10	MF small molecule binding
13	6e-05	4 / 30	BP detection of visible light
14	8e-05	13 / 499	BP ion transport
15	9e-05	5 / 62	CC intermediate filament
16	1e-04	20 / 1084	BP transport
17	2e-04	5 / 76	BP cartilage development
18	3e-04	8 / 229	MF transporter activity
19	3e-04	7 / 176	BP ion transmembrane transport
20	4e-04	3 / 20	BP fin development
21	5e-04	3 / 21	BP negative regulation of angiogenesis
22	6e-04	3 / 23	MF hyaluronic acid binding
23	7e-04	4 / 55	BP central nervous system development
24	8e-04	8 / 270	MF ion channel activity
25	9e-04	65 / 6248	CC integral component of membrane
26	1e-03	5 / 106	BP calcium ion transmembrane transport
27	1e-03	3 / 28	BP skeletal system development
28	1e-03	3 / 29	MF 3',5'-cyclic-nucleotide phosphodiesterase activity
29	1e-03	4 / 64	MF serine-type endopeptidase inhibitor activity
30	1e-03	20 / 1295	BP signal transduction
31	1e-03	4 / 65	BP sodium ion transport
32	1e-03	68 / 6723	CC membrane
33	2e-03	4 / 70	BP sodium ion transmembrane transport
34	2e-03	3 / 35	BP cellular calcium ion homeostasis
35	2e-03	4 / 74	CC neuron projection
36	3e-03	4 / 79	MF calcium channel activity
37	3e-03	2 / 11	MF oxidoreductase activity, acting on the CH-NH2 group of donors, oxygen as
38	3e-03	8 / 333	BP cell adhesion
39	3e-03	3 / 41	MF copper ion binding
40	4e-03	2 / 13	BP synaptic vesicle endocytosis



BP				CC				MF			
Rank	p-value	#in/all	Geneset	Rank	p-value	#in/all	Geneset	Rank	p-value	#in/all	Geneset
1	4e-17	15 / 83	visual perception	1	9e-08	6 / 31	photoreceptor outer segment	1	2e-09	8 / 49	extracellular matrix structural constituent
2	4e-08	6 / 28	phototransduction	2	2e-06	9 / 153	proteinaceous extracellular matrix	2	3e-09	7 / 33	photoreceptor activity
3	9e-08	6 / 31	protein-chromophore linkage	3	4e-06	17 / 634	extracellular region	3	1e-06	19 / 717	calcium ion binding
4	1e-05	7 / 102	response to stimulus	4	9e-05	5 / 62	intermediate filament	4	3e-06	5 / 31	G-protein coupled photoreceptor activity
5	6e-05	4 / 30	detection of visible light	5	9e-04	65 / 6248	integral component of membrane	5	4e-05	3 / 10	small molecule binding
6	8e-05	13 / 499	ion transport	6	1e-03	68 / 6723	membrane	6	3e-04	8 / 229	transporter activity
7	1e-04	20 / 1084	transport	7	2e-03	4 / 74	neuron projection	7	6e-04	3 / 23	hyaluronic acid binding
8	2e-04	5 / 76	cartilage development	8	5e-03	3 / 48	heterotrimeric G-protein complex	8	8e-04	8 / 270	ion channel activity
9	3e-04	7 / 176	ion transmembrane transport	9	6e-03	5 / 155	synapse	9	1e-03	3 / 29	3',5'-cyclic-nucleotide phosphodiesterase activity
10	4e-04	3 / 20	fin development	10	1e-02	16 / 1162	plasma membrane	10	1e-03	4 / 64	serine-type endopeptidase inhibitor activity
11	5e-04	3 / 21	negative regulation of angiogenesis	11	1e-02	2 / 22	synaptic vesicle membrane	11	3e-03	4 / 79	calcium channel activity
12	7e-04	4 / 55	central nervous system development	12	2e-02	2 / 26	neuronal cell body	12	3e-03	2 / 11	oxidoreductase activity, acting on the CH-NH2 group of donors, oxygen as acceptor
13	1e-03	5 / 106	calcium ion transmembrane transport	13	3e-02	2 / 38	apical plasma membrane	13	3e-03	3 / 41	copper ion binding
14	1e-03	3 / 28	skeletal system development	14	3e-02	11 / 809	integral component of plasma membrane	14	5e-03	2 / 14	sodium:bicarbonate symporter activity
15	1e-03	20 / 1295	signal transduction	15	8e-02	4 / 219	cell junction	15	6e-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-06	4 / 33	hindbrain development	1	7e-04	3 / 70	cell projection	1	1e-05	14 / 1484	DNA binding
2	2e-05	3 / 21	smoothened signaling pathway	2	9e-04	16 / 2716	nucleus	2	3e-04	5 / 232	protein heterodimerization activity
3	7e-05	3 / 32	inner ear development	3	9e-04	3 / 76	cilium	3	4e-04	7 / 537	sequence-specific DNA binding
4	1e-04	4 / 104	transmembrane receptor protein tyrosine kinase signaling pathway	4	5e-03	4 / 268	cytoskeleton	4	8e-04	2 / 17	transmembrane receptor protein serine/threonine kinase activity
5	2e-04	11 / 1239	regulation of transcription, DNA-templated	5	7e-03	2 / 49	microtubule organizing center	5	1e-03	2 / 21	signal transducer, downstream of receptor, with serine/threonine kinase activity
6	3e-04	2 / 10	adenohypophysis development	6	9e-03	3 / 168	nucleosome	6	1e-03	6 / 491	kinase activity
7	4e-04	2 / 12	determination of liver left/right asymmetry	7	2e-02	2 / 80	centrosome	7	1e-03	2 / 23	dynein light intermediate chain binding
8	5e-04	2 / 14	inner ear morphogenesis	8	2e-02	3 / 229	chromosome	8	2e-03	8 / 914	protein kinase activity
9	7e-04	3 / 71	signal transduction by protein phosphorylation	9	3e-02	1 / 13	adherens junction	9	3e-03	3 / 110	protein tyrosine kinase activity
10	9e-04	3 / 76	cartilage development	10	4e-02	1 / 16	midbody	10	3e-03	3 / 116	metalloendopeptidase activity
11	1e-03	3 / 78	axon guidance	11	5e-02	1 / 19	axon	11	7e-03	2 / 52	transmembrane receptor protein tyrosine kinase activity
12	1e-03	2 / 19	positive regulation of BMP signaling pathway	12	5e-02	5 / 809	integral component of plasma membrane	12	1e-02	10 / 1787	ATP binding
13	1e-03	2 / 20	transmembrane receptor protein serine/threonine kinase signaling pathway	13	5e-02	1 / 22	dynein complex	13	2e-02	1 / 10	ion channel binding
14	1e-03	2 / 21	negative regulation of canonical Wnt signaling pathway	14	6e-02	1 / 26	microtubule cytoskeleton	14	3e-02	1 / 13	ATP-dependent microtubule motor activity, minus-end-directed
15	2e-03	3 / 91	heart looping	15	7e-02	1 / 30	ciliary basal body	15	3e-02	1 / 14	enzyme activator activity

# Underexpression Spots

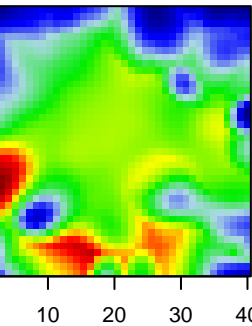
## Spot Summary: f

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# genes = 149

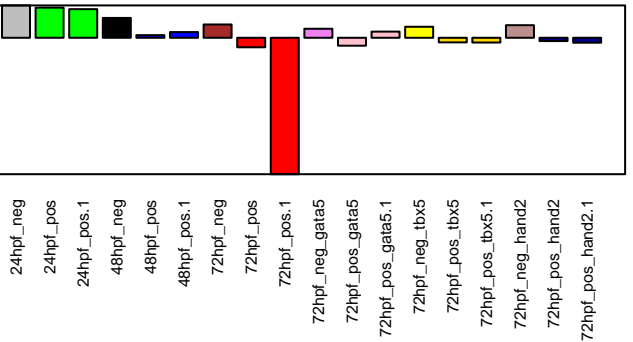
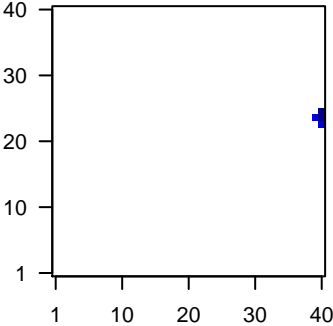
<r> metagenes = 0.99  
<r> genes = 0.67  
beta: r2= 5.43 / log p= -Inf

# samples with spot = 1 ( 5.6 %)  
72hpf\_pos : 1 ( 50 %)

Overview Map



Spot

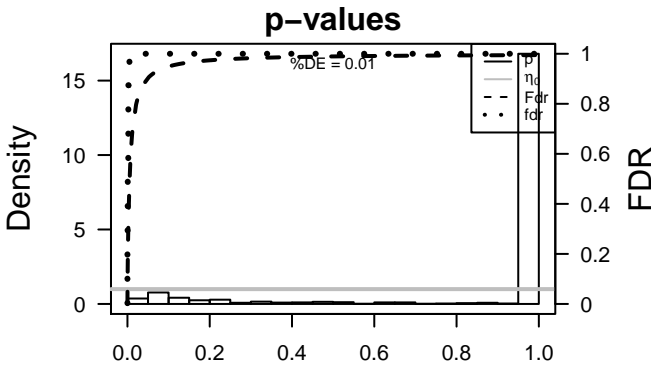


## Spot Genelist

Rank	ID	max e	r	min e	Description
					Symbol
1	ENSDARG0000000001	1.16	-5.89	0.87	ribosomal protein S26, like [Source:ZFIN;Acc:ZDB-GENE-0000000001]
2	ENSDARG0000000002	1.38	-5.67	0.95	zgc:112234c:112234 [Source:NCBI gene;Acc:554097]
3	ENSDARG0000000003	1.71	-5.65	0.78	Nuclear RNase P [Source:RFAM;Acc:RF00009]
4	ENSDARG0000000004	1.79	-4.69	0.92	si:dkey-261m9.6 [Source:ZFIN;Acc:ZDB-GENE-131127-10]
5	ENSDARG0000000005	1.84	-4.62	0.78	zgc:3h12b zinc finger CCCH-type containing 12B [Source:ZFIN;Acc:ZDB-GENE-0000000005]
6	ENSDARG0000000006	1.04	-4.56	0.91	lsm12a LSM12 homolog a [Source:ZFIN;Acc:ZDB-GENE-040516-1]
7	ENSDARG0000000007	1.23	-4.5	0.86	pigs phosphatidylinositol glycan anchor biosynthesis, class S [Source:ZFIN;Acc:ZDB-GENE-0000000007]
8	ENSDARG0000000008	1.8	-4.24	0.88	cd82b CD82 molecule b [Source:ZFIN;Acc:ZDB-GENE-030131-28]
9	ENSDARG0000000009	1.12	-4.19	0.93	traf2a Tnf receptor-associated factor 2a [Source:ZFIN;Acc:ZDB-GENE-0000000009]
10	ENSDARG0000000010	1.84	-4.19	0.6	Small nucleolar RNA SNORA53 [Source:RFAM;Acc:RF00565]
11	ENSDARG0000000011	1.51	-4.15	0.94	zgc:114046c:114046 [Source:ZFIN;Acc:ZDB-GENE-050320-24]
12	ENSDARG0000000012	0.87	-4.13	0.85	rwdd RWD domain containing 4 [Source:ZFIN;Acc:ZDB-GENE-0400000012]
13	ENSDARG0000000013	1.2	-4.1	0.92	dachc dachshund c [Source:ZFIN;Acc:ZDB-GENE-020402-5]
14	ENSDARG0000000014	1.92	-4.01	0.92	zgc:163046c:163046 [Source:ZFIN;Acc:ZDB-GENE-070927-10]
15	ENSDARG0000000015	1.23	-4.01	0.96	cdc23 CDC23 (cell division cycle 23, yeast, homolog) [Source:ZFIN;Acc:ZDB-GENE-0000000015]
16	ENSDARG0000000016	1.68	-3.95	0.82	egl2 egl-9 family hypoxia-inducible factor 2 [Source:ZFIN;Acc:ZDB-GENE-0000000016]
17	ENSDARG0000000017	1.49	-3.9	0.92	rab23 RAB23, member RAS oncogene family [Source:ZFIN;Acc:ZDB-GENE-0000000017]
18	ENSDARG0000000018	0.88	-3.84	0.97	tmem183a transmembrane protein 183A [Source:ZFIN;Acc:ZDB-GENE-0000000018]
19	ENSDARG0000000019	1.36	-3.83	0.94	wtip WT1 interacting protein [Source:ZFIN;Acc:ZDB-GENE-0504000019]
20	ENSDARG0000000020	1.37	-3.7	0.93	anapc2 anaphase promoting complex subunit 2 [Source:ZFIN;Acc:ZDB-GENE-0000000020]

## Geneset Overrepresentation

Rank	p-value	#in/all	Geneset
1	4e-07	10 / 229	CC chromosome
2	3e-06	8 / 168	CC nucleosome
3	4e-06	9 / 232	MF protein heterodimerization activity
4	3e-04	3 / 25	BP membrane disruption in other organism
5	5e-04	3 / 30	CC ciliary basal body
6	5e-04	3 / 30	BP defense response to Gram-positive bacterium
7	8e-04	3 / 34	BP chromatin silencing
8	1e-03	2 / 10	BP protein kinase C-activating G-protein coupled receptor signaling pathway
9	1e-03	2 / 11	MF diacylglycerol kinase activity
10	2e-03	3 / 47	CC integral component of endoplasmic reticulum membrane
11	2e-03	3 / 49	CC nuclear chromatin
12	3e-03	3 / 54	BP MAPK cascade
13	3e-03	3 / 57	MF mRNA binding
14	5e-03	2 / 19	BP determination of left/right asymmetry in lateral mesoderm
15	5e-03	2 / 20	MF MAP kinase activity
16	5e-03	2 / 20	MF NAD+ kinase activity
17	5e-03	2 / 21	CC axoneme
18	7e-03	4 / 140	CC nucleolus
19	7e-03	2 / 24	CC cell-cell junction
20	9e-03	24 / 2716	CC nucleus
21	1e-02	19 / 2030	MF nucleic acid binding
22	1e-02	2 / 31	BP autophagosome assembly
23	2e-02	2 / 42	BP determination of heart left/right asymmetry
24	2e-02	2 / 43	BP DNA-templated transcription, initiation
25	3e-02	14 / 1484	MF DNA binding
26	3e-02	11 / 1066	CC intracellular
27	3e-02	3 / 128	BP innate immune response
28	4e-02	3 / 138	BP cilium assembly
29	5e-02	1 / 10	BP activation of MAPK activity
30	5e-02	1 / 10	CC anaphase-promoting complex
31	5e-02	1 / 10	BP artery morphogenesis
32	5e-02	1 / 10	CC intracellular transport particle B
33	5e-02	1 / 10	BP muscle cell development
34	5e-02	1 / 10	BP protein O-linked mannosylation
35	5e-02	2 / 70	CC cell projection
36	5e-02	2 / 70	BP RNA processing
37	6e-02	1 / 11	MF 5'-nucleotidase activity
38	6e-02	1 / 11	BP establishment of mitotic spindle orientation
39	6e-02	1 / 11	BP fructose 6-phosphate metabolic process
40	6e-02	1 / 11	BP glutathione metabolic process



BP				CC				MF			
Rank	p-value	#in/all	Geneset	Rank	p-value	#in/all	Geneset	Rank	p-value	#in/all	Geneset
1	3e-04	3 / 25	membrane disruption in other organism	1	4e-07	10 / 229	chromosome	1	4e-06	9 / 232	protein heterodimerization activity
2	5e-04	3 / 30	defense response to Gram-positive bacterium	2	3e-06	8 / 168	nucleosome	2	1e-03	2 / 11	diacylglycerol kinase activity
3	8e-04	3 / 34	chromatin silencing	3	5e-04	3 / 30	ciliary basal body	3	3e-03	3 / 57	mRNA binding
4	1e-03	2 / 10	protein kinase C-activating G-protein coupled receptor signaling pathway	4	2e-03	3 / 47	integral component of endoplasmic reticulum membrane	4	5e-03	2 / 20	MAP kinase activity
5	3e-03	3 / 54	MAPK cascade	5	2e-03	3 / 49	nuclear chromatin	5	5e-03	2 / 20	NAD+ kinase activity
6	5e-03	2 / 19	determination of left/right asymmetry in lateral mesoderm	6	5e-03	2 / 21	axoneme	6	1e-02	19 / 2030	nucleic acid binding
7	1e-02	2 / 31	autophagosome assembly	7	7e-03	4 / 140	nucleolus	7	3e-02	14 / 1484	DNA binding
8	2e-02	2 / 42	determination of heart left/right asymmetry	8	7e-03	2 / 24	cell-cell junction	8	6e-02	1 / 11	5'-nucleotidase activity
9	2e-02	2 / 43	DNA-templated transcription, initiation	9	9e-03	24 / 2716	nucleus	9	6e-02	1 / 12	transcription factor activity, RNA polymerase II transcription factor recruiting
10	3e-02	3 / 128	innate immune response	10	3e-02	11 / 1066	intracellular	10	7e-02	1 / 13	SH3 domain binding
11	4e-02	3 / 138	cilium assembly	11	5e-02	1 / 10	anaphase-promoting complex	11	8e-02	1 / 15	alpha-(1->3)-fucosyltransferase activity
12	5e-02	1 / 10	activation of MAPK activity	12	5e-02	1 / 10	intraciliary transport particle B	12	8e-02	1 / 15	manganese ion binding
13	5e-02	1 / 10	artery morphogenesis	13	5e-02	2 / 70	cell projection	13	8e-02	12 / 1437	molecular_function
14	5e-02	1 / 10	muscle cell development	14	6e-02	2 / 76	cilium	14	9e-02	1 / 17	regulatory region DNA binding
15	5e-02	1 / 10	protein O-linked mannosylation	15	6e-02	1 / 12	pre-autophagosomal structure	15	1e-01	1 / 19	fucosyltransferase activity

# Underexpression Spots

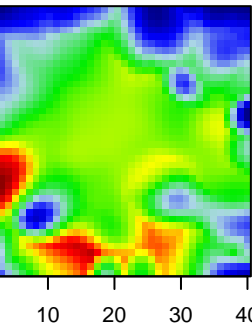
## Spot Summary: g

# metagenes = 18  
# genes = 327

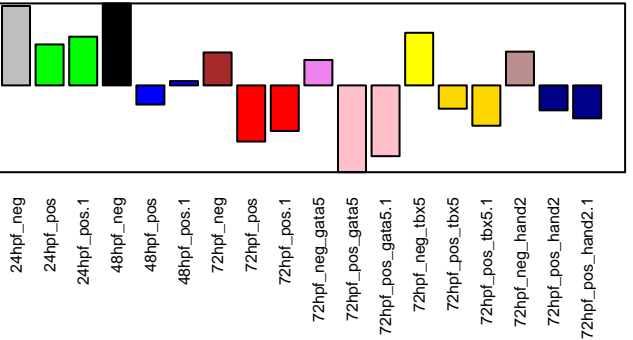
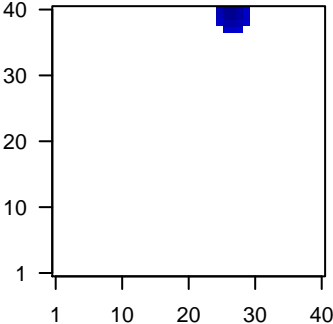
<r> metagenes = 0.97  
<r> genes = 0.61  
beta: r2= 3.63 / log p= -Inf

# samples with spot = 0 ( 0 %)

Overview Map



Spot

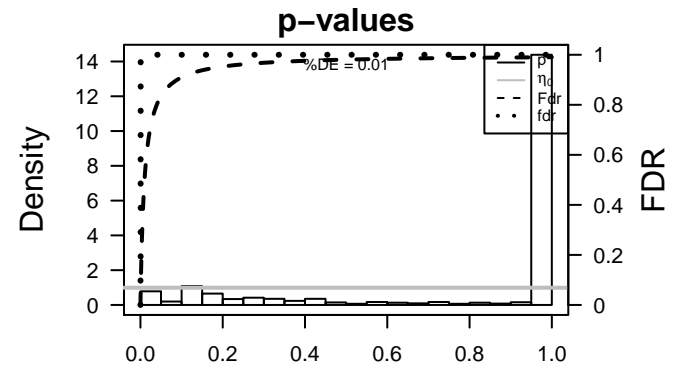


## Spot Genelist

Rank	ID	max e	r	min e	Description
					Symbol
1	ENSDARG00000000000	1.29	-3.05	0.62	LOC796000
2	ENSDARG00000000000	1.04	-2.7	0.61	abcg2c ATP-binding cassette, sub-family G (WHITE), member 2c [S
3	ENSDARG00000000000	1.69	-2.6	0.59	si:ch73-334d15.1 [Source:ZFIN;Acc:ZDB-GENE-091118-3]
4	ENSDARG00000000000	1.64	-2.42	0.74	enpp5 ectonucleotide pyrophosphatase/phosphodiesterase 5 [Sourc
5	ENSDARG00000000000	0.95	-2.39	0.6	LOC100306530 medin like 2A [Source:HGNC Symbol;Acc:HGNC:2727
6	ENSDARG00000000000	0.89	-2.37	0.69	znf438 zinc finger protein 438 [Source:ZFIN;Acc:ZDB-GENE-06092
7	ENSDARG00000000000	1.14	-2.33	0.81	fus FUS RNA binding protein [Source:ZFIN;Acc:ZDB-GENE-040
8	ENSDARG00000000000	0.7	-2.32	0.63	adnp2a ADNP homeobox 2a [Source:ZFIN;Acc:ZDB-GENE-040914-
9	ENSDARG00000000000	1.09	-2.32	0.52	sall3a spalt-like transcription factor 3a [Source:ZFIN;Acc:ZDB-GEN
10	ENSDARG00000000000	1.29	-2.26	0.52	fam117b family with sequence similarity 117, member Bb [Source:ZFI
11	ENSDARG00000000000	1.21	-2.2	0.81	tmtc2a transmembrane and tetratricopeptide repeat containing 2a [S
12	ENSDARG00000000000	1.39	-2.11	0.74	marcksa myristoylated alanine-rich protein kinase C substrate a [Sour
13	ENSDARG00000000000	1.62	-2.05	0.59	zgc:158689 [Source:ZFIN;Acc:ZDB-GENE-070112-1902]
14	ENSDARG00000000000	1.35	-2.04	0.86	usp49 ubiquitin specific peptidase 49 [Source:ZFIN;Acc:ZDB-GENE
15	ENSDARG00000000000	0.99	-2.02	0.6	alx4a ALX homeobox 4a [Source:ZFIN;Acc:ZDB-GENE-070728-3
16	ENSDARG00000000000	1.2	-2	0.83	si:ch73-251d73-211e3.1 [Source:ZFIN;Acc:ZDB-GENE-160728-51]
17	ENSDARG00000000000	0.9	-1.99	0.59	si:key-151d73-121j17.6 [Source:ZFIN;Acc:ZDB-GENE-121214-36
18	ENSDARG00000000000	0.95	-1.98	0.51	
19	ENSDARG00000000000	0.99	-1.98	0.78	round spermatid basic protein 1 [Source:HGNC Symbol;Acc:l
20	ENSDARG00000000000	1.25	-1.96	0.65	PAP associated domain containing 7 [Source:ZFIN;Acc:ZDB-

## Geneset Overrepresentation

Rank	p-value	#in/all	Geneset
1	3e-13	76 / 2716	CC nucleus
2	6e-11	59 / 2030	MF nucleic acid binding
3	9e-07	23 / 608	MF RNA binding
4	1e-06	6 / 30	MF transcription cofactor activity
5	4e-06	34 / 1239	BP regulation of transcription, DNA-templated
6	9e-06	6 / 42	MF histone binding
7	9e-06	5 / 25	MF histone acetyltransferase activity
8	1e-05	5 / 27	BP histone acetylation
9	2e-05	4 / 14	BP ATP-dependent chromatin remodeling
10	3e-05	36 / 1484	MF DNA binding
11	6e-05	8 / 115	MF chromatin binding
12	9e-05	39 / 1761	MF metal ion binding
13	2e-04	4 / 24	BP histone lysine methylation
14	4e-04	4 / 30	BP chromatin remodeling
15	4e-04	4 / 31	MF histone-lysine N-methyltransferase activity
16	5e-04	21 / 800	MF zinc ion binding
17	1e-03	5 / 65	MF transcription coactivator activity
18	1e-03	7 / 135	MF methyltransferase activity
19	1e-03	4 / 39	MF protein serine/threonine phosphatase activity
20	2e-03	7 / 144	BP methylation
21	2e-03	4 / 43	BP DNA-templated transcription, initiation
22	2e-03	3 / 21	CC nuclear membrane
23	2e-03	8 / 193	BP positive regulation of transcription from RNA polymerase II promoter
24	3e-03	3 / 25	BP regulation of nucleic acid-templated transcription
25	3e-03	23 / 1063	MF transferase activity
26	6e-03	6 / 138	BP cilium assembly
27	7e-03	4 / 65	MF RNA polymerase II regulatory region sequence-specific DNA binding
28	8e-03	2 / 12	BP left/right pattern formation
29	8e-03	2 / 12	CC transcription factor TFIID complex
30	9e-03	4 / 70	CC cell projection
31	1e-02	2 / 13	BP erythrocyte maturation
32	1e-02	2 / 13	MF p53 binding
33	1e-02	2 / 13	MF signal transducer activity, downstream of receptor
34	1e-02	4 / 72	MF helicase activity
35	1e-02	2 / 14	BP RNA polymerase II transcriptional preinitiation complex assembly
36	1e-02	2 / 15	BP dorsal convergence
37	1e-02	2 / 15	CC histone acetyltransferase complex
38	1e-02	3 / 43	BP canonical Wnt signaling pathway
39	1e-02	2 / 16	BP negative regulation of translation
40	2e-02	2 / 17	MF protein phosphatase inhibitor activity





BP

Rank	p-value	#in/all	Geneset
1	4e-06	34 / 1239	regulation of transcription, DNA-templated
2	1e-05	5 / 27	histone acetylation
3	2e-05	4 / 14	ATP-dependent chromatin remodeling
4	2e-04	4 / 24	histone lysine methylation
5	4e-04	4 / 30	chromatin remodeling
6	2e-03	7 / 144	methylation
7	2e-03	4 / 43	DNA-templated transcription, initiation
8	2e-03	8 / 193	positive regulation of transcription from RNA polymerase II promoter
9	3e-03	3 / 25	regulation of nucleic acid-templated transcription
10	6e-03	6 / 138	cilium assembly
11	8e-03	2 / 12	left/right pattern formation
12	1e-02	2 / 13	erythrocyte maturation
13	1e-02	2 / 14	RNA polymerase II transcriptional preinitiation complex assembly
14	1e-02	2 / 15	dorsal convergence
15	1e-02	3 / 43	canonical Wnt signaling pathway

CC

Rank	p-value	#in/all	Geneset
1	3e-13	76 / 2716	nucleus
2	2e-03	3 / 21	nuclear membrane
3	8e-03	2 / 12	transcription factor TFIID complex
4	9e-03	4 / 70	cell projection
5	1e-02	2 / 15	histone acetyltransferase complex
6	2e-02	2 / 19	axon
7	6e-02	3 / 76	cilium
8	7e-02	2 / 36	P-body
9	1e-01	1 / 10	chaperonin-containing T-complex
10	1e-01	2 / 51	lysosomal membrane
11	1e-01	1 / 11	clathrin-coated pit
12	1e-01	1 / 11	commitment complex
13	1e-01	5 / 229	chromosome
14	1e-01	1 / 12	histone deacetylase complex
15	1e-01	1 / 12	lamellipodium

MF

Rank	p-value	#in/all	Geneset
1	6e-11	59 / 2030	nucleic acid binding
2	9e-07	23 / 608	RNA binding
3	1e-06	6 / 30	transcription cofactor activity
4	9e-06	6 / 42	histone binding
5	9e-06	5 / 25	histone acetyltransferase activity
6	3e-05	36 / 1484	DNA binding
7	6e-05	8 / 115	chromatin binding
8	9e-05	39 / 1761	metal ion binding
9	4e-04	4 / 31	histone-lysine N-methyltransferase activity
10	5e-04	21 / 800	zinc ion binding
11	1e-03	5 / 65	transcription coactivator activity
12	1e-03	7 / 135	methyltransferase activity
13	1e-03	4 / 39	protein serine/threonine phosphatase activity
14	3e-03	23 / 1063	transferase activity
15	7e-03	4 / 65	RNA polymerase II regulatory region 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	5e-07	11 / 375	positive regulation of GTPase activity	1	5e-04	42 / 6248	integral component of membrane	1	4e-05	7 / 217	GTPase activator activity
2	1e-06	11 / 413	intracellular signal transduction	2	6e-04	44 / 6723	membrane	2	8e-04	2 / 10	GDP-dissociation inhibitor activity
3	2e-05	4 / 38	integrin-mediated signaling pathway	3	6e-03	2 / 29	integrin complex	3	8e-04	2 / 10	GTPase regulator activity
4	9e-05	16 / 1295	signal transduction	4	1e-02	2 / 43	extrinsic component of cytoplasmic side of plasma membrane	4	1e-03	3 / 49	non-membrane spanning protein tyrosine kinase activity
5	9e-04	2 / 11	spindle organization	5	3e-02	9 / 1066	intracellular	5	1e-03	2 / 13	signal transducer activity, downstream of receptor
6	1e-03	2 / 13	germ cell migration	6	4e-02	4 / 317	Golgi apparatus	6	4e-03	2 / 23	CCR chemokine receptor binding
7	2e-03	3 / 58	chemokine-mediated signaling pathway	7	5e-02	3 / 198	Golgi membrane	7	7e-03	4 / 178	iron ion binding
8	4e-03	2 / 23	cellular response to interferon-gamma	8	6e-02	1 / 15	intrinsic component of the cytoplasmic side of the plasma membrane	8	8e-03	3 / 96	Rho guanyl-nucleotide exchange factor activity
9	4e-03	2 / 23	lymphocyte chemotaxis	9	8e-02	1 / 20	exocyst	9	1e-02	3 / 110	oxidoreductase activity, acting on paired donors, with incorporation or reduction of simple inorganic group
10	4e-03	2 / 23	monocyte chemotaxis	10	8e-02	1 / 21	dendrite	10	1e-02	3 / 110	protein tyrosine kinase activity
11	4e-03	2 / 24	cellular response to interleukin-1	11	1e-01	1 / 27	guanylate cyclase complex, soluble	11	2e-02	2 / 47	chemokine activity
12	4e-03	2 / 24	cellular response to tumor necrosis factor	12	1e-01	1 / 27	integral component of Golgi membrane	12	2e-02	2 / 54	transferase activity, transferring hexosyl groups
13	7e-03	3 / 91	heart looping	13	2e-01	4 / 500	extracellular space	13	2e-02	3 / 145	heme binding
14	8e-03	2 / 33	positive regulation of ERK1 and ERK2 cascade	14	2e-01	1 / 47	integral component of endoplasmic reticulum membrane	14	3e-02	2 / 60	scavenger receptor activity
15	8e-03	3 / 100	peptidyl-tyrosine phosphorylation	15	2e-01	2 / 209	endoplasmic reticulum membrane	15	3e-02	3 / 158	microtubule binding

# Underexpression Spots

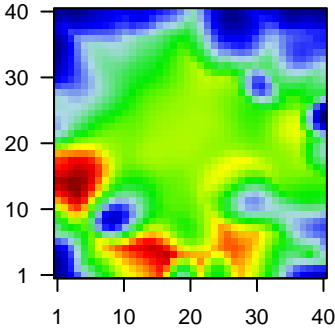
## Spot Summary: i

# metagenes = 6  
# genes = 134

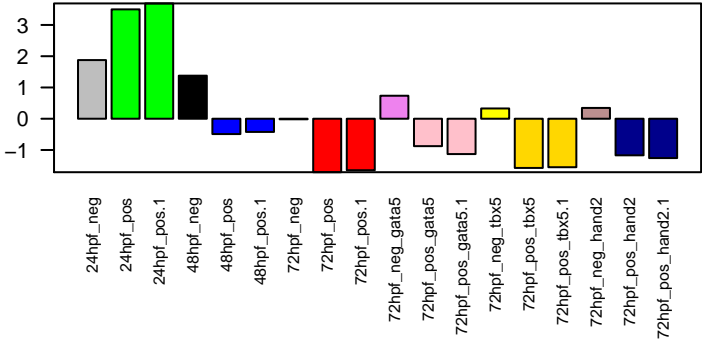
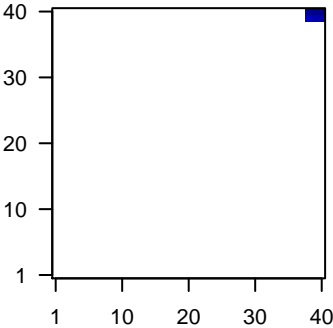
<r> metagenes = 1  
<r> genes = 0.73  
beta: r2= 28.11 / log p= -Inf

# samples with spot = 4 ( 22.2 % )  
72hpf\_pos : 2 ( 100 % )  
72hpf\_pos\_tbx5 : 2 ( 100 % )

Overview Map



Spot

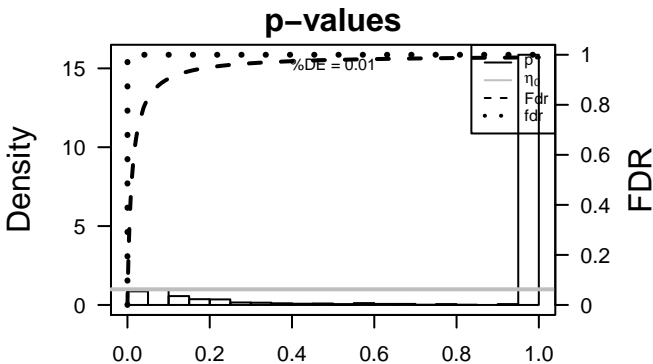


## Spot Genelist

Rank	ID	max e	r	min e	Description
1	ENSDARG000	8.12	-6.4	0.89	hbbe3 hemoglobin beta embryonic-3 [Source:ZFIN;Acc:ZDB-GENE-
2	ENSDARG000	4.82	-5.94	0.9	nmt1b N-myristoyltransferase 1b [Source:ZFIN;Acc:ZDB-GENE-08
3	ENSDARG000	3.63	-5.74	0.8	cxcl12b chemokine (C-X-C motif) ligand 12b (stromal cell-derived fa
4	ENSDARG000	7.06	-5.06	0.95	si:dkey-261k4.3 [Source:ZFIN;Acc:ZDB-GENE-060531-124
5	ENSDARG000	5.26	-4.98	0.9	tubb1 tubulin, beta 1 class VI [Source:ZFIN;Acc:ZDB-GENE-1104
6	ENSDARG000	5.39	-4.85	0.92	hdr hematopoietic death receptor [Source:ZFIN;Acc:ZDB-GENE-
7	ENSDARG000	4.79	-4.79	0.92	slc4a1a solute carrier family 4 (anion exchanger), member 1a (Diego I
8	ENSDARG000	6.46	-4.6	0.75	protogenin homolog b (Gallus gallus) [Source:ZFIN;Acc:ZDB-
9	ENSDARG000	2.43	-4.56	0.69	meis3 myeloid ecotropic viral integration site 3 [Source:ZFIN;Acc:ZC
10	ENSDARG000	7.36	-4.55	0.95	si:dkey-261k4.4 [Source:ZFIN;Acc:ZDB-GENE-060531-125
11	ENSDARG000	3.58	-4.55	0.79	hif1a2 hypoxia-inducible factor 1, alpha subunit, like 2 [Source:ZFIN
12	ENSDARG000	3.84	-4.5	0.83	mlt3 myeloid/lymphoid or mixed-lineage leukemia (trithorax homol
13	ENSDARG000	7.83	-4.49	0.96	drl draculin [Source:ZFIN;Acc:ZDB-GENE-991213-3]
14	ENSDARG000	2.88	-4.44	0.79	glcci1 glucocorticoid induced 1 [Source:ZFIN;Acc:ZDB-GENE-031
15	ENSDARG000	3.63	-4.42	0.85	egf7 EGF-like-domain, multiple 7 [Source:ZFIN;Acc:ZDB-GENE-
16	ENSDARG000	4.72	-4.38	0.89	epor erythropoietin receptor [Source:ZFIN;Acc:ZDB-GENE-07111
17	ENSDARG000	2.81	-4.37	0.75	gdf6a growth differentiation factor 6a [Source:ZFIN;Acc:ZDB-GENE
18	ENSDARG000	3.2	-4.37	0.82	nt5c2l1 5'-nucleotidase, cytosolic II, like 1 [Source:ZFIN;Acc:ZDB-GI
19	ENSDARG000	4.05	-4.36	0.78	LOC100537032
20	ENSDARG000	5.21	-4.29	0.89	rhesd Rieske (Fe-S) domain containing [Source:ZFIN;Acc:ZDB-GE

## Geneset Overrepresentation

Rank	p-value	#in/all	Geneset
1	4e-21	10 / 14	CC hemoglobin complex
2	4e-19	10 / 19	MF oxygen binding
3	4e-19	10 / 19	BP oxygen transport
4	4e-19	10 / 19	MF oxygen transporter activity
5	5e-17	10 / 28	BP embryonic hemopoiesis
6	2e-13	9 / 40	BP erythrocyte differentiation
7	2e-13	13 / 145	MF heme binding
8	6e-11	12 / 178	MF iron ion binding
9	1e-09	6 / 24	BP myeloid cell differentiation
10	5e-09	7 / 52	BP blood vessel development
11	6e-07	4 / 15	BP heme biosynthetic process
12	8e-07	9 / 210	MF protein binding
13	2e-06	6 / 75	BP hemopoiesis
14	3e-06	4 / 21	BP erythrocyte development
15	3e-06	24 / 1761	MF metal ion binding
16	1e-05	11 / 454	BP multicellular organism development
17	2e-05	3 / 12	BP hemoglobin biosynthetic process
18	3e-05	4 / 38	BP vasculogenesis
19	6e-05	16 / 1084	BP transport
20	1e-04	4 / 50	BP vasculature development
21	3e-04	10 / 537	MF sequence-specific DNA binding
22	7e-04	3 / 37	BP definitive hemopoiesis
23	9e-04	15 / 1239	BP regulation of transcription, DNA-templated
24	1e-03	3 / 47	MF structural constituent of cytoskeleton
25	2e-03	2 / 13	BP gastrulation with mouth forming second
26	2e-03	2 / 13	BP semicircular canal morphogenesis
27	2e-03	5 / 183	MF RNA polymerase II transcription factor activity, sequence-specific DNA binding
28	2e-03	4 / 116	MF metalloendopeptidase activity
29	3e-03	2 / 16	BP defense response
30	3e-03	2 / 16	BP vascular endothelial growth factor receptor signaling pathway
31	3e-03	2 / 18	BP neutrophil differentiation
32	4e-03	2 / 19	BP embryonic heart tube morphogenesis
33	4e-03	2 / 19	BP neuron migration
34	4e-03	2 / 20	BP positive regulation of gene expression
35	5e-03	2 / 23	MF hyaluronic acid binding
36	6e-03	2 / 24	BP primitive hemopoiesis
37	7e-03	4 / 160	BP heart development
38	9e-03	3 / 90	BP positive regulation of transcription, DNA-templated
39	1e-02	2 / 32	BP retinal ganglion cell axon guidance
40	1e-02	2 / 33	BP blood vessel morphogenesis



BP				CC				MF			
Rank	p-value	#in/all	Geneset	Rank	p-value	#in/all	Geneset	Rank	p-value	#in/all	Geneset
1	4e-19	10 / 19	oxygen transport	1	4e-21	10 / 14	hemoglobin complex	1	4e-19	10 / 19	oxygen binding
2	5e-17	10 / 28	embryonic hemopoiesis	2	2e-02	2 / 51	lysosomal membrane	2	4e-19	10 / 19	oxygen transporter activity
3	2e-13	9 / 40	erythrocyte differentiation	3	4e-02	4 / 268	cytoskeleton	3	2e-13	13 / 145	heme binding
4	1e-09	6 / 24	myeloid cell differentiation	4	4e-02	3 / 161	mitochondrial inner membrane	4	6e-11	12 / 178	iron ion binding
5	5e-09	7 / 52	blood vessel development	5	5e-02	1 / 11	exocytic vesicle	5	8e-07	9 / 210	protein binding
6	6e-07	4 / 15	heme biosynthetic process	6	6e-02	19 / 2716	nucleus	6	3e-06	24 / 1761	metal ion binding
7	2e-06	6 / 75	hemopoiesis	7	8e-02	1 / 17	external side of plasma membrane	7	3e-04	10 / 537	sequence-specific DNA binding
8	3e-06	4 / 21	erythrocyte development	8	8e-02	1 / 17	integral component of nuclear inner membrane	8	1e-03	3 / 47	structural constituent of cytoskeleton
9	1e-05	11 / 454	multicellular organism development	9	8e-02	2 / 101	endosome	9	2e-03	5 / 183	RNA polymerase II transcription factor activity, sequence-specific DNA binding
10	2e-05	3 / 12	hemoglobin biosynthetic process	10	9e-02	7 / 809	integral component of plasma membrane	10	2e-03	4 / 116	metalloendopeptidase activity
11	3e-05	4 / 38	vasculogenesis	11	1e-01	1 / 22	dynein complex	11	5e-03	2 / 23	hyaluronic acid binding
12	6e-05	16 / 1084	transport	12	1e-01	1 / 24	early endosome	12	1e-02	8 / 633	transcription factor activity, sequence-specific DNA binding
13	1e-04	4 / 50	vasculature development	13	1e-01	1 / 26	vesicle	13	1e-02	9 / 800	zinc ion binding
14	7e-04	3 / 37	definitive hemopoiesis	14	1e-01	36 / 6248	integral component of membrane	14	2e-02	3 / 115	chromatin binding
15	9e-04	15 / 1239	regulation of transcription, DNA-templated	15	1e-01	1 / 32	chromatin	15	2e-02	8 / 717	calcium ion binding

# Underexpression Spots

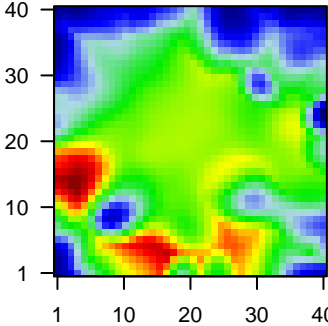
## Spot Summary: j

# metagenes = 9  
# genes = 190

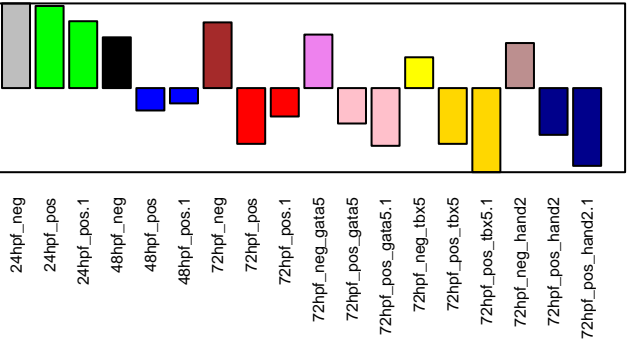
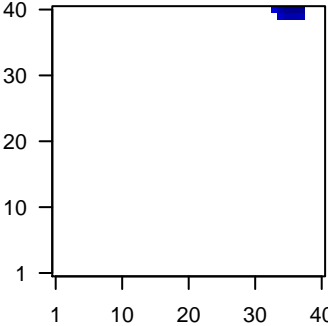
<r> metagenes = 0.98  
<r> genes = 0.72  
beta: r2= 12.14 / log p= -Inf

# samples with spot = 1 ( 5.6 %)  
72hpf\_pos\_tbx5 : 1 ( 50 %)

Overview Map



Spot

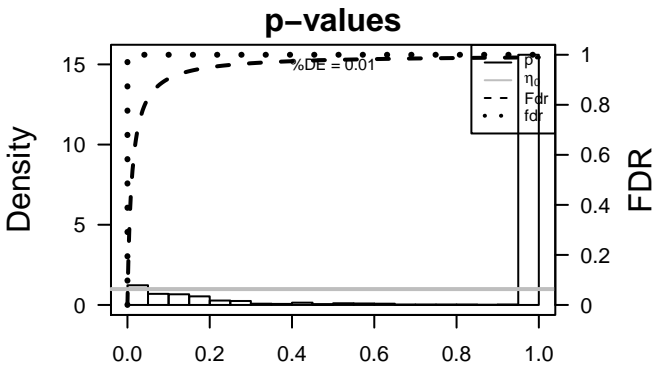


## Spot Genelist

Rank	ID	max e	r	Description	
		min e		Symbol	
1	ENSDARG0000000001	2.02	-4.77	0.57	slc12a11 solute carrier family 12 member 11 [Source:ZFIN;Acc:ZDB-GENE-081104-20]
2	ENSDARG0000000002	2.19	-4.71	0.8	reps2 RALBP1 associated Eps domain containing 2 [Source:ZFIN;Acc:ZDB-GENE-081104-20]
3	ENSDARG0000000003	1.53	-4.19	0.81	unc5b unc-5 netrin receptor B [Source:ZFIN;Acc:ZDB-GENE-0412-20]
4	ENSDARG0000000004	2.16	-4.13	0.72	plch1 phospholipase C, eta 1 [Source:ZFIN;Acc:ZDB-GENE-06051-20]
5	ENSDARG0000000005	2.8	-4.02	0.77	capn12 calpain 12 [Source:ZFIN;Acc:ZDB-GENE-050419-245]
6	ENSDARG0000000006	2.24	-3.74	0.79	emilin2b elastin microfibril interfacer 2b [Source:ZFIN;Acc:ZDB-GENE-081104-20]
7	ENSDARG0000000007	1.95	-3.56	0.74	depdc1a DEP domain containing 1a [Source:ZFIN;Acc:ZDB-GENE-081104-20]
8	ENSDARG0000000008	2.03	-3.47	0.8	tmem108transmembrane protein 108 [Source:ZFIN;Acc:ZDB-GENE-081104-20]
9	ENSDARG0000000009	1.71	-3.35	0.63	adamts6 ADAM metalloproteinase with thrombospondin type 1 motif, 6
10	ENSDARG0000000010	1.77	-3.26	0.71	isl2a ISL LIM homeobox 2a [Source:ZFIN;Acc:ZDB-GENE-98052-20]
11	ENSDARG0000000011	1.83	-3.24	0.87	bnc1 basonuclin 1 [Source:HGNC Symbol;Acc:HGNC:1081]
12	ENSDARG0000000012	2.38	-3.2	0.78	nr2f1b nuclear receptor subfamily 2, group F, member 1b [Source:ZFIN;Acc:ZDB-GENE-081104-20]
13	ENSDARG0000000013	1.55	-3.08	0.83	trabd2a TraB domain containing 2A [Source:ZFIN;Acc:ZDB-GENE-081104-20]
14	ENSDARG0000000014	1.79	-3.05	0.8	collagen type VII alpha 1-like [Source:ZFIN;Acc:ZDB-GENE-081104-20]
15	ENSDARG0000000015	1.55	-3.05	0.89	ephb4a eph receptor B4a [Source:ZFIN;Acc:ZDB-GENE-990415-62]
16	ENSDARG0000000016	2.69	-3.04	0.73	hbbe2 hemoglobin beta embryonic-2 [Source:ZFIN;Acc:ZDB-GENE-081104-20]
17	ENSDARG0000000017	1.48	-3.03	0.88	signal peptide, CUB domain, EGF-like 3 [Source:ZFIN;Acc:ZDB-GENE-081104-20]
18	ENSDARG0000000018	1.87	-2.92	0.73	foxf1 forkhead box F1 [Source:ZFIN;Acc:ZDB-GENE-050419-153]
19	ENSDARG0000000019	1.47	-2.87	0.85	fgfr1b fibroblast growth factor receptor 1b [Source:ZFIN;Acc:ZDB-GENE-081104-20]
20	ENSDARG0000000020	2.35	-2.81	0.71	esama endothelial cell adhesion molecule a [Source:ZFIN;Acc:ZDB-GENE-081104-20]

## Geneset Overrepresentation

Rank	p-value	#in/all	Geneset
1	1e-45	37 / 168	CC nucleosome
2	3e-40	37 / 229	CC chromosome
3	5e-40	37 / 232	MF protein heterodimerization activity
4	1e-35	28 / 117	BP nucleosome assembly
5	9e-28	17 / 37	MF nucleosomal DNA binding
6	6e-26	55 / 1484	MF DNA binding
7	8e-20	64 / 2716	CC nucleus
8	1e-12	9 / 34	BP ephrin receptor signaling pathway
9	8e-11	11 / 100	BP peptidyl-tyrosine phosphorylation
10	2e-10	11 / 110	MF protein tyrosine kinase activity
11	2e-09	6 / 19	MF ephrin receptor activity
12	2e-08	21 / 717	MF calcium ion binding
13	9e-08	16 / 454	BP multicellular organism development
14	6e-07	8 / 104	BP transmembrane receptor protein tyrosine kinase signaling pathway
15	1e-06	6 / 52	BP blood vessel development
16	3e-06	4 / 15	CC basement membrane
17	8e-06	5 / 41	BP positive regulation of cell proliferation
18	2e-05	7 / 117	BP Wnt signaling pathway
19	3e-05	5 / 52	MF transmembrane receptor protein tyrosine kinase activity
20	4e-05	3 / 10	BP adenylylation
21	1e-04	4 / 38	BP vasculogenesis
22	1e-04	3 / 15	MF ephrin receptor binding
23	1e-04	12 / 491	MF kinase activity
24	2e-04	5 / 78	BP axon guidance
25	2e-04	12 / 522	BP phosphorylation
26	3e-04	3 / 19	BP non-canonical Wnt signaling pathway
27	3e-04	20 / 1239	BP regulation of transcription, DNA-templated
28	4e-04	13 / 634	CC extracellular region
29	4e-04	15 / 809	CC integral component of plasma membrane
30	5e-04	3 / 23	MF Wnt-activated receptor activity
31	7e-04	3 / 26	MF Wnt-protein binding
32	1e-03	11 / 537	MF sequence-specific DNA binding
33	1e-03	12 / 633	MF transcription factor activity, sequence-specific DNA binding
34	1e-03	3 / 33	BP blood vessel morphogenesis
35	2e-03	3 / 36	BP fibroblast growth factor receptor signaling pathway
36	2e-03	5 / 130	MF growth factor activity
37	2e-03	2 / 10	BP muscle cell development
38	2e-03	8 / 333	BP cell adhesion
39	2e-03	10 / 500	CC extracellular space
40	3e-03	3 / 40	BP heart morphogenesis



BP

Rank	p-value	#in/all	Geneset
1	1e-35	28 / 117	nucleosome assembly
2	1e-12	9 / 34	ephrin receptor signaling pathway
3	8e-11	11 / 100	peptidyl-tyrosine phosphorylation
4	9e-08	16 / 454	multicellular organism development
5	6e-07	8 / 104	transmembrane receptor protein tyrosine kinase signaling pathway
6	1e-06	6 / 52	blood vessel development
7	8e-06	5 / 41	positive regulation of cell proliferation
8	2e-05	7 / 117	Wnt signaling pathway
9	4e-05	3 / 10	adenohypophysis development
10	1e-04	4 / 38	vasculogenesis
11	2e-04	5 / 78	axon guidance
12	2e-04	12 / 522	phosphorylation
13	3e-04	3 / 19	non-canonical Wnt signaling pathway
14	3e-04	20 / 1239	regulation of transcription, DNA-templated
15	1e-03	3 / 33	blood vessel morphogenesis

CC

Rank	p-value	#in/all	Geneset
1	1e-45	37 / 168	nucleosome
2	3e-40	37 / 229	chromosome
3	8e-20	64 / 2716	nucleus
4	3e-06	4 / 15	basement membrane
5	4e-04	13 / 634	extracellular region
6	4e-04	15 / 809	integral component of plasma membrane
7	2e-03	10 / 500	extracellular space
8	1e-02	3 / 65	extracellular matrix
9	2e-02	4 / 153	proteinaceous extracellular matrix
10	6e-02	52 / 6248	integral component of membrane
11	8e-02	1 / 13	transcriptional repressor complex
12	9e-02	1 / 14	hemoglobin complex
13	1e-01	1 / 16	midbody
14	1e-01	1 / 17	presynaptic active zone
15	1e-01	53 / 6723	membrane

MF

Rank	p-value	#in/all	Geneset
1	5e-40	37 / 232	protein heterodimerization activity
2	9e-28	17 / 37	nucleosomal DNA binding
3	6e-26	55 / 1484	DNA binding
4	2e-10	11 / 110	protein tyrosine kinase activity
5	2e-09	6 / 19	ephrin receptor activity
6	2e-08	21 / 717	calcium ion binding
7	3e-05	5 / 52	transmembrane receptor protein tyrosine kinase activity
8	1e-04	3 / 15	ephrin receptor binding
9	1e-04	12 / 491	kinase activity
10	5e-04	3 / 23	Wnt-activated receptor activity
11	7e-04	3 / 26	Wnt-protein binding
12	1e-03	11 / 537	sequence-specific DNA binding
13	1e-03	12 / 633	transcription factor activity, sequence-specific DNA binding
14	2e-03	5 / 130	growth factor activity
15	3e-03	6 / 210	protein binding