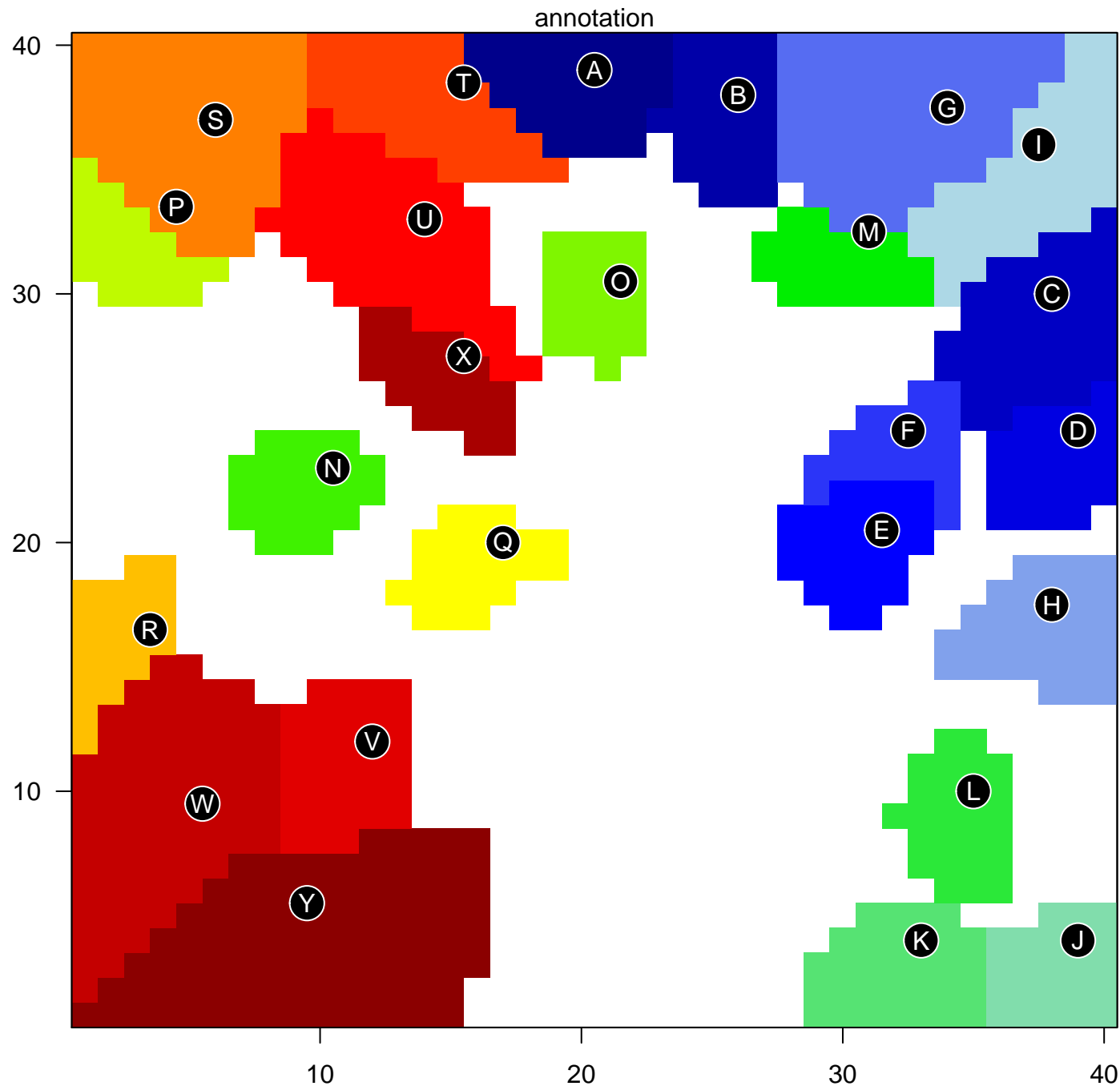
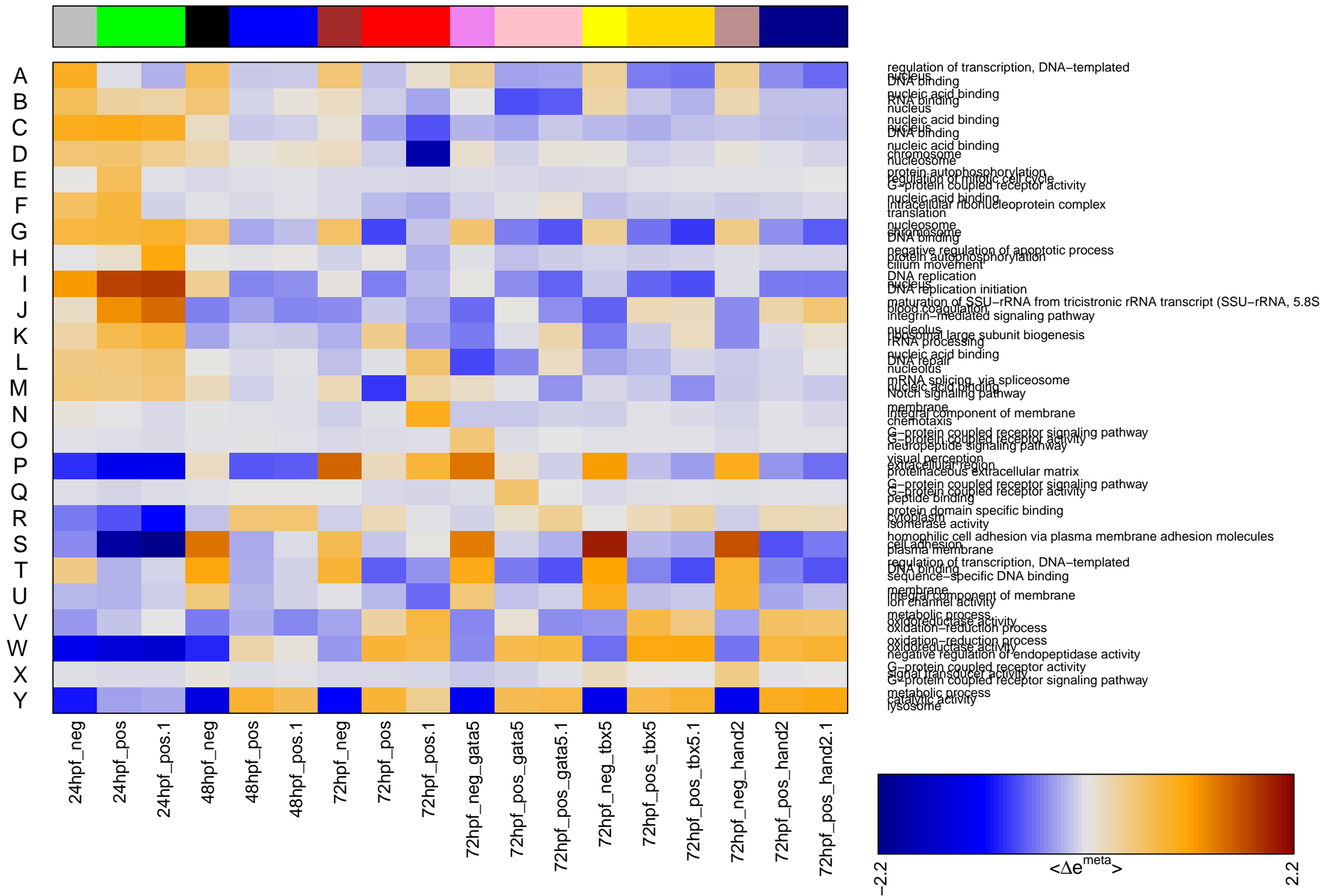


# Correlation Cluster



- A regulation of transcription, DNA-templated nucleus
- B nucleic acid binding RNA binding
- C nucleic acid binding nucleus
- D nucleic acid binding chromosome
- E protein autophosphorylation regulation of mitotic cell cycle
- F nucleic acid binding intracellular ribonucleoprotein complex
- G nucleosome chromosome
- H negative regulation of apoptotic process protein autophosphorylation
- I DNA replication nucleus
- J maturation of SSU-rRNA from tricistronic rRNA transcript (S)
- K nucleolus ribosomal large subunit biogenesis
- L nucleic acid binding DNA repair
- M mRNA splicing, via spliceosome nucleic acid binding
- N membrane integral component of membrane
- O G-protein coupled receptor signaling pathway G-protein coupled receptor activity
- P visual perception extracellular region
- Q G-protein coupled receptor signaling pathway G-protein coupled receptor activity
- R protein domain specific binding cytoplasm
- S homophilic cell adhesion via plasma membrane adhesion m
- T regulation of transcription, DNA-templated DNA binding
- U membrane integral component of membrane
- V metabolic process oxidoreductase activity
- W oxidation-reduction process oxidoreductase activity



# Correlation Cluster

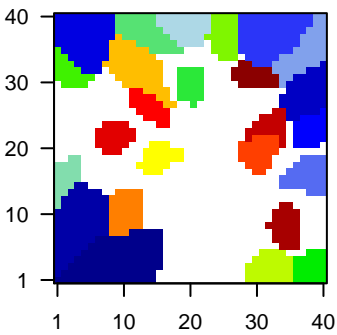
## Spot Summary: A

# metagenes = 32  
# genes = 600

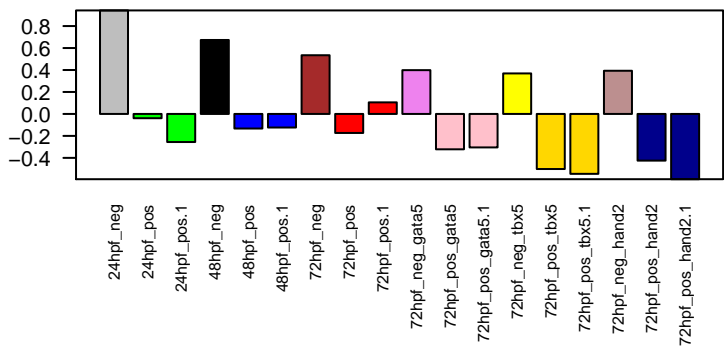
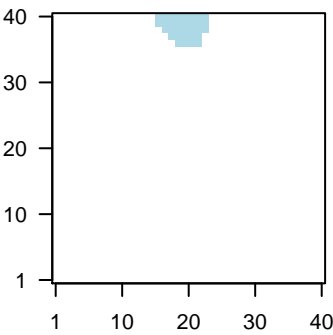
<r> metagenes = 0.94  
<r> genes = 0.51  
beta: r2= 3.22 / log p= -Inf

# samples with spot = 2 ( 11.1 %)  
24hpf\_neg : 1 ( 100 %)  
48hpf\_neg : 1 ( 100 %)

Overview Map



Spot

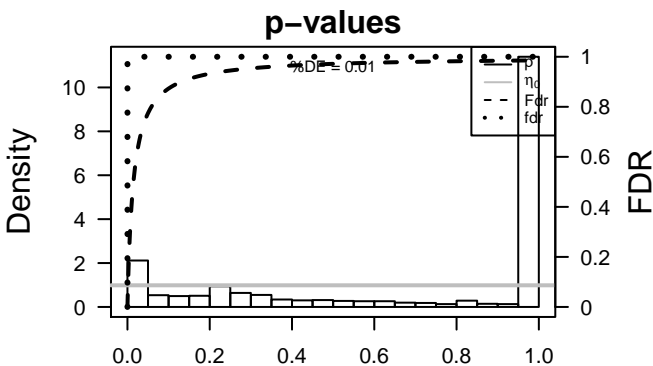


## Spot Genelist

Rank	ID	max e	r	Description	
			min e	Symbol	
1	ENSDARG000	4.38	-2.85	0.81	col28a2a collagen, type XXVIII, alpha 2a [Source:ZFIN;Acc:ZDB-GENE-001202]
2	ENSDARG000	3.19	-3.3	0.71	plp1a proteolipid protein 1a [Source:ZFIN;Acc:ZDB-GENE-001202]
3	ENSDARG000	3.06	-1.7	0.8	col7a1 collagen, type VII, alpha 1 [Source:ZFIN;Acc:ZDB-GENE-001202]
4	ENSDARG000	2.94	-1.72	0.92	sox19a SRY (sex determining region Y)-box 19a [Source:ZFIN;Acc:ZDB-GENE-001202]
5	ENSDARG000	2.94	-1.34	0.75	nes Nestin [Source:UniProtKB/Swiss-Prot;Acc:P6839]
6	ENSDARG000	2.91	-2.1	0.89	did deltaD [Source:ZFIN;Acc:ZDB-GENE-990415-47]
7	ENSDARG000	2.79	-1.66	0.79	col4a6 collagen, type IV, alpha 6 [Source:ZFIN;Acc:ZDB-GENE-101202]
8	ENSDARG000	2.75	-1.34	0.71	oligodendrocyte transcription factor 3 [Source:ZFIN;Acc:ZDB-GENE-001202]
9	ENSDARG000	2.66	-1.67	0.83	col4a5 collagen, type IV, alpha 5 (Alport syndrome) [Source:ZFIN;Acc:ZDB-GENE-001202]
10	ENSDARG000	2.64	-1.85	0.83	sp8b sp8 transcription factor b [Source:ZFIN;Acc:ZDB-GENE-001202]
11	ENSDARG000	2.62	-2.43	0.76	zgc:101810 zgc:101810 [Source:ZFIN;Acc:ZDB-GENE-041121-7]
12	ENSDARG000	2.48	-1.49	0.56	
13	ENSDARG000	2.47	-1.28	0.81	igsf9a immunoglobulin superfamily, member 9a [Source:ZFIN;Acc:ZDB-GENE-001202]
14	ENSDARG000	2.46	-1.7	0.75	si:ch211-193l2.3 [Source:ZFIN;Acc:ZDB-GENE-141216-14]
15	ENSDARG000	2.38	-2.26	0.55	LOC100506000 and enhancer of split-related 15, tandem duplicate 1 [Source:ZFIN;Acc:ZDB-GENE-001202]
16	ENSDARG000	2.38	-1.82	0.71	her13 hairy-related 13 [Source:ZFIN;Acc:ZDB-GENE-050228-1]
17	ENSDARG000	2.37	-1.24	0.77	pax3a paired box 3a [Source:ZFIN;Acc:ZDB-GENE-980526-52]
18	ENSDARG000	2.36	-1.06	0.9	notch3 notch 3 [Source:ZFIN;Acc:ZDB-GENE-000329-5]
19	ENSDARG000	2.32	-2.23	0.59	lamb4 laminin, beta 4 [Source:ZFIN;Acc:ZDB-GENE-021226-2]
20	ENSDARG000	2.3	-1.44	0.82	sox19b SRY (sex determining region Y)-box 19b [Source:ZFIN;Acc:ZDB-GENE-001202]

## Geneset Overrepresentation

Rank	p-value	#in/all	Geneset
1	1e-31	101 / 1239	BP regulation of transcription, DNA-templated
2	6e-30	153 / 2716	CC nucleus
3	3e-27	104 / 1484	MF DNA binding
4	5e-23	52 / 454	BP multicellular organism development
5	3e-14	44 / 537	MF sequence-specific DNA binding
6	4e-09	16 / 117	BP Wnt signaling pathway
7	8e-09	83 / 2030	MF nucleic acid binding
8	4e-08	37 / 633	MF transcription factor activity, sequence-specific DNA binding
9	6e-08	9 / 37	MF nucleosomal DNA binding
10	2e-07	10 / 55	BP neuron differentiation
11	5e-07	35 / 643	BP transcription, DNA-templated
12	3e-06	6 / 20	MF L-ascorbic acid binding
13	3e-06	5 / 12	BP regulation of neurogenesis
14	3e-06	14 / 147	BP brain development
15	4e-06	16 / 190	MF protein dimerization activity
16	4e-06	7 / 32	CC chromatin
17	4e-06	8 / 45	BP Notch signaling pathway
18	5e-06	14 / 153	CC proteinaceous extracellular matrix
19	8e-06	31 / 608	MF RNA binding
20	1e-05	10 / 83	BP embryonic viscerocranium morphogenesis
21	2e-05	14 / 168	CC nucleosome
22	2e-05	5 / 17	BP photoreceptor cell outer segment organization
23	3e-05	5 / 18	BP otic placode formation
24	4e-05	17 / 257	BP cell differentiation
25	4e-05	11 / 117	BP nucleosome assembly
26	6e-05	6 / 33	BP hindbrain development
27	7e-05	5 / 21	BP midbrain-hindbrain boundary development
28	7e-05	7 / 48	BP neural crest cell migration
29	1e-04	4 / 13	BP floor plate formation
30	1e-04	4 / 13	BP sensory epithelium regeneration
31	1e-04	4 / 13	BP ventral spinal cord interneuron differentiation
32	1e-04	15 / 229	CC chromosome
33	2e-04	5 / 25	BP cell fate commitment
34	2e-04	5 / 25	MF frizzled binding
35	2e-04	9 / 93	BP dorsal/ventral pattern formation
36	2e-04	4 / 14	BP oligodendrocyte differentiation
37	2e-04	4 / 14	BP regulation of Notch signaling pathway
38	2e-04	11 / 138	BP cilium assembly
39	2e-04	5 / 26	MF Wnt-protein binding
40	2e-04	8 / 77	BP determination of left/right symmetry



BP				CC				MF			
Rank	p-value	#in/all	Geneset	Rank	p-value	#in/all	Geneset	Rank	p-value	#in/all	Geneset
1	1e-31	101 / 1239	regulation of transcription, DNA-templated	1	6e-30	153 / 2716	nucleus	1	3e-27	104 / 1484	DNA binding
2	5e-23	52 / 454	multicellular organism development	2	4e-06	7 / 32	chromatin	2	3e-14	44 / 537	sequence-specific DNA binding
3	4e-09	16 / 117	Wnt signaling pathway	3	5e-06	14 / 153	proteinaceous extracellular matrix	3	8e-09	83 / 2030	nucleic acid binding
4	2e-07	10 / 55	neuron differentiation	4	2e-05	14 / 168	nucleosome	4	4e-08	37 / 633	transcription factor activity, sequence-specific DNA binding
5	5e-07	35 / 643	transcription, DNA-templated	5	1e-04	15 / 229	chromosome	5	6e-08	9 / 37	nucleosomal DNA binding
6	3e-06	5 / 12	regulation of neurogenesis	6	3e-04	5 / 29	integrin complex	6	3e-06	6 / 20	L-ascorbic acid binding
7	3e-06	14 / 147	brain development	7	1e-03	8 / 98	transcription factor complex	7	4e-06	16 / 190	protein dimerization activity
8	4e-06	8 / 45	Notch signaling pathway	8	2e-03	3 / 13	viral nucleocapsid	8	8e-06	31 / 608	RNA binding
9	1e-05	10 / 83	embryonic viscerocranium morphogenesis	9	3e-03	5 / 46	collagen trimer	9	2e-04	5 / 25	frizzled binding
10	2e-05	5 / 17	photoreceptor cell outer segment organization	10	4e-03	3 / 15	basement membrane	10	2e-04	5 / 26	Wnt-protein binding
11	3e-05	5 / 18	otic placode formation	11	4e-03	5 / 49	nucleoplasm	11	5e-04	14 / 232	protein heterodimerization activity
12	4e-05	17 / 257	cell differentiation	12	1e-02	3 / 22	dynein complex	12	6e-04	6 / 49	extracellular matrix structural constituent
13	4e-05	11 / 117	nucleosome assembly	13	1e-02	14 / 337	endoplasmic reticulum	13	8e-04	9 / 115	chromatin binding
14	6e-05	6 / 33	hindbrain development	14	2e-02	3 / 27	integral component of Golgi membrane	14	1e-03	4 / 23	Wnt-activated receptor activity
15	7e-05	5 / 21	midbrain-hindbrain boundary development	15	2e-02	5 / 76	cilium	15	2e-03	4 / 26	oxidoreductase activity, acting on single donors with incorporation of molecular oxygen

# Correlation Cluster

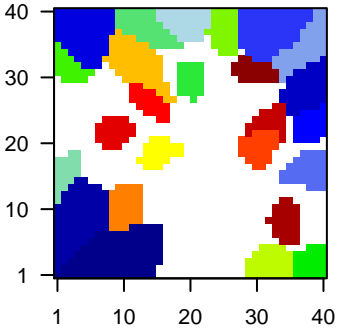
## Spot Summary: B

# metagenes = 28  
# genes = 472

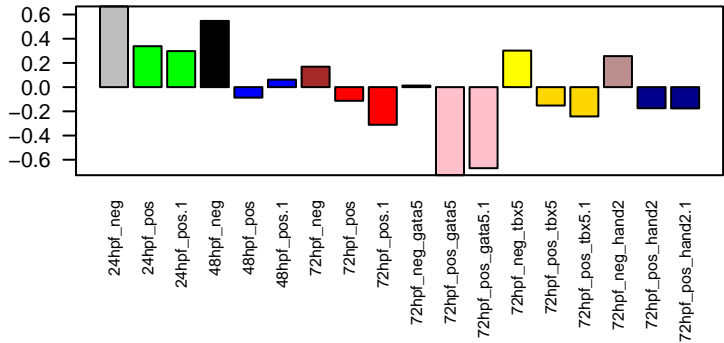
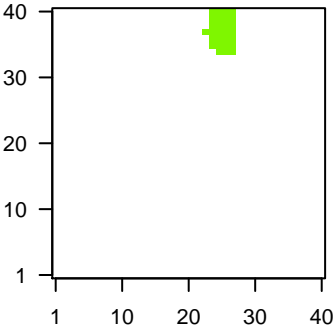
<r> metagenes = 0.95  
<r> genes = 0.49  
beta: r2= 2.23 / log p= -Inf

# samples with spot = 2 ( 11.1 %)  
24hpf\_neg : 1 ( 100 %)  
48hpf\_neg : 1 ( 100 %)

Overview Map



Spot

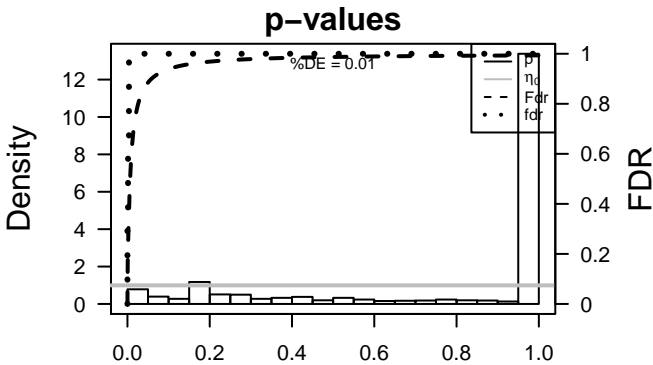


## Spot Genelist

Rank	ID	max e	r	Description	
		min e		Symbol	
1	ENSDARG0000000000	1.94	-0.89	0.63	subcommissural organ spondin [Source:ZFIN;Acc:ZDB-GENE-070927-10]
2	ENSDARG0000000000	1.79	-1.16	0.61	LOC794540 stone 1, H4, like [Source:ZFIN;Acc:ZDB-GENE-070927-10]
3	ENSDARG0000000000	1.77	-0.93	0.62	susd4 sushi domain containing 4 [Source:ZFIN;Acc:ZDB-GENE-110131-5]
4	ENSDARG0000000000	1.68	-0.56	0.72	si:ch211-106f21.1 [Source:ZFIN;Acc:ZDB-GENE-141216-3]
5	ENSDARG0000000000	1.68	-1.23	0.41	irx4b iroquois homeobox 4b [Source:ZFIN;Acc:ZDB-GENE-040719-1]
6	ENSDARG0000000000	1.67	-1.19	0.56	gpr371a G protein-coupled receptor 37 like 1a [Source:ZFIN;Acc:ZDB-GENE-040719-1]
7	ENSDARG0000000000	1.67	-1.13	0.65	si:dkey-250i3.3 [Source:ZFIN;Acc:ZDB-GENE-110131-5]
8	ENSDARG0000000000	1.64	-1.01	0.71	gbx1 gastrulation brain homeobox 1 [Source:ZFIN;Acc:ZDB-GENE-040719-1]
9	ENSDARG0000000000	1.64	-1.59	0.78	jag2b jagged 2b [Source:ZFIN;Acc:ZDB-GENE-011128-3]
10	ENSDARG0000000000	1.62	-2.05	0.73	zgc:158689 [Source:ZFIN;Acc:ZDB-GENE-070112-1902]
11	ENSDARG0000000000	1.57	-1.95	0.67	si:dkey-250i3.3 [Source:ZFIN;Acc:ZDB-GENE-141216-161]
12	ENSDARG0000000000	1.54	-1.41	0.82	chromobox homolog 6b [Source:ZFIN;Acc:ZDB-GENE-110610-1]
13	ENSDARG0000000000	1.51	-0.95	0.73	ankrd10ankyrin repeat domain 10a [Source:ZFIN;Acc:ZDB-GENE-040719-1]
14	ENSDARG0000000000	1.49	-1.52	0.92	ankrd10ankyrin repeat domain 10a [Source:ZFIN;Acc:ZDB-GENE-040719-1]
15	ENSDARG0000000000	1.48	-1.1	0.88	znf281b zinc finger protein 281b [Source:ZFIN;Acc:ZDB-GENE-050208-5]
16	ENSDARG0000000000	1.45	-1	0.65	tmem138transmembrane protein 138 [Source:ZFIN;Acc:ZDB-GENE-110610-1]
17	ENSDARG0000000000	1.44	-1.44	0.61	adhesion G protein-coupled receptor A3 [Source:ZFIN;Acc:ZDB-GENE-040719-1]
18	ENSDARG0000000000	1.43	-0.73	0.81	plxbn1b plexin b1b [Source:ZFIN;Acc:ZDB-GENE-090812-4]
19	ENSDARG0000000000	1.43	-1.31	0.57	si:ch211-196c10.11 [Source:ZFIN;Acc:ZDB-GENE-081104-1]
20	ENSDARG0000000000	1.43	-1.83	0.77	si:ch211-246m6.5 [Source:ZFIN;Acc:ZDB-GENE-050208-5]

## Geneset Overrepresentation

Rank	p-value	#in/all	Geneset
1	7e-32	115 / 2030	MF nucleic acid binding
2	2e-13	40 / 608	MF RNA binding
3	4e-07	80 / 2716	CC nucleus
4	5e-04	5 / 39	MF protein serine/threonine phosphatase activity
5	7e-04	3 / 11	BP establishment or maintenance of cell polarity
6	8e-04	6 / 66	MF thiol-dependent ubiquitinyl hydrolase activity
7	1e-03	6 / 70	BP protein deubiquitination
8	1e-03	3 / 13	MF signal transducer activity, downstream of receptor
9	1e-03	6 / 72	MF helicase activity
10	1e-03	3 / 14	BP transcription elongation from RNA polymerase II promoter
11	2e-03	8 / 138	BP cilium assembly
12	3e-03	3 / 17	CC U2-type prespliceosome
13	3e-03	45 / 1761	MF metal ion binding
14	3e-03	14 / 362	BP regulation of transcription from RNA polymerase II promoter
15	4e-03	34 / 1239	BP regulation of transcription, DNA-templated
16	4e-03	3 / 19	CC U1 snRNP
17	5e-03	5 / 65	BP covalent chromatin modification
18	5e-03	3 / 21	MF dynein light chain binding
19	6e-03	5 / 70	BP RNA processing
20	7e-03	3 / 24	MF cation binding
21	8e-03	4 / 47	BP regulation of GTPase activity
22	9e-03	4 / 49	BP regulation of cell shape
23	1e-02	4 / 51	BP anatomical structure morphogenesis
24	1e-02	5 / 79	BP mRNA splicing, via spliceosome
25	1e-02	37 / 1484	MF DNA binding
26	1e-02	5 / 80	MF transcription regulatory region DNA binding
27	1e-02	4 / 53	BP convergent extension involved in gastrulation
28	1e-02	2 / 11	CC commitment complex
29	1e-02	5 / 85	BP protein folding
30	2e-02	35 / 1427	BP biological_process
31	2e-02	2 / 12	MF acetylglucosaminyltransferase activity
32	2e-02	2 / 12	BP neural tube formation
33	2e-02	2 / 13	BP cilium organization
34	2e-02	2 / 13	MF dynein heavy chain binding
35	2e-02	2 / 13	BP mitotic sister chromatid cohesion
36	2e-02	2 / 13	MF TBP-class protein binding
37	2e-02	3 / 35	BP cell projection organization
38	2e-02	2 / 14	BP ATP-dependent chromatin remodeling
39	2e-02	2 / 14	BP chromatin organization
40	2e-02	2 / 14	BP response to heat



BP

Rank

p-value

#in/all

Geneset

1	7e-04	3 / 11	establishment or maintenance of cell polarity
2	1e-03	6 / 70	protein deubiquitination
3	1e-03	3 / 14	transcription elongation from RNA polymerase II promoter
4	2e-03	8 / 138	cilium assembly
5	3e-03	14 / 362	regulation of transcription from RNA polymerase II promoter
6	4e-03	34 / 1239	regulation of transcription, DNA-templated
7	5e-03	5 / 65	covalent chromatin modification
8	6e-03	5 / 70	RNA processing
9	8e-03	4 / 47	regulation of GTPase activity
10	9e-03	4 / 49	regulation of cell shape
11	1e-02	4 / 51	anatomical structure morphogenesis
12	1e-02	5 / 79	mRNA splicing, via spliceosome
13	1e-02	4 / 53	convergent extension involved in gastrulation
14	1e-02	5 / 85	protein folding
15	2e-02	35 / 1427	biological_process

CC

Rank

p-value

#in/all

Geneset

1	4e-07	80 / 2716	nucleus
2	3e-03	3 / 17	U2-type prespliceosome
3	4e-03	3 / 19	U1 snRNP
4	1e-02	2 / 11	commitment complex
5	3e-02	2 / 15	intrinsic component of the cytoplasmic side of the plasma membrane
6	4e-02	4 / 76	cilium
7	5e-02	2 / 21	nuclear membrane
8	5e-02	2 / 22	dynein complex
9	8e-02	34 / 1580	cellular_component
10	8e-02	8 / 268	cytoskeleton
11	9e-02	2 / 30	ciliary basal body
12	1e-01	2 / 34	catalytic step 2 spliceosome
13	1e-01	3 / 70	cell projection
14	1e-01	2 / 35	Golgi cisterna membrane
15	1e-01	2 / 38	apical plasma membrane

MF

Rank

p-value

#in/all

Geneset

1	7e-32	115 / 2030	nucleic acid binding
2	2e-13	40 / 608	RNA binding
3	5e-04	5 / 39	protein serine/threonine phosphatase activity
4	8e-04	6 / 66	thiol-dependent ubiquitinyl hydrolase activity
5	1e-03	3 / 13	signal transducer activity, downstream of receptor
6	1e-03	6 / 72	helicase activity
7	3e-03	45 / 1761	metal ion binding
8	5e-03	3 / 21	dynein light chain binding
9	7e-03	3 / 24	cation binding
10	1e-02	37 / 1484	DNA binding
11	1e-02	5 / 80	transcription regulatory region DNA binding
12	2e-02	2 / 12	acetylgalactosaminyltransferase activity
13	2e-02	2 / 13	dynein heavy chain binding
14	2e-02	2 / 13	TBP-class protein binding
15	3e-02	4 / 67	unfolded protein binding

# Correlation Cluster

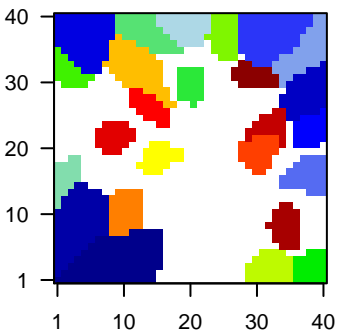
## Spot Summary: C

# metagenes = 42  
# genes = 731

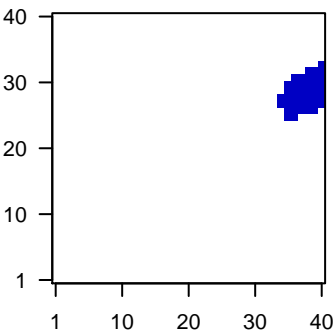
<r> metagenes = 0.92  
<r> genes = 0.56  
beta: r2= 3.93 / log p= -Inf

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

Overview Map



Spot



24hpf\_neg  
24hpf\_pos  
24hpf\_pos.1  
48hpf\_neg  
48hpf\_pos  
48hpf\_pos.1  
72hpf\_neg  
72hpf\_pos  
72hpf\_pos.1  
72hpf\_neg\_gata5  
72hpf\_pos\_gata5  
72hpf\_pos\_gata5.1  
72hpf\_neg\_tbx5  
72hpf\_pos\_tbx5  
72hpf\_pos\_tbx5.1  
72hpf\_neg\_hand2  
72hpf\_pos\_hand2  
72hpf\_pos\_hand2.1

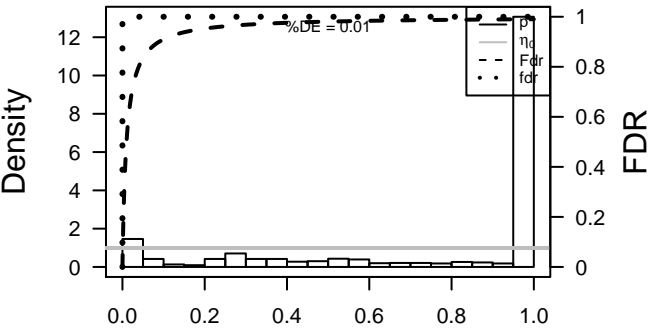
## Spot Genelist

Rank	ID	max e	r	min e	Description	
					Symbol	
1	ENSDARG000	8.23	-1.2	0.6	ednra endothelin receptor type Ab [Source:ZFIN;Acc:ZDB-GENE-121214-19]	ednra
2	ENSDARG000	5.91	-1.27	0.71	sidkey-26g8.5-26g8.5 [Source:ZFIN;Acc:ZDB-GENE-121214-19]	sidkey-26g8.5
3	ENSDARG000	5.48	-1.21	0.65	zgc:174153c:174153 [Source:ZFIN;Acc:ZDB-GENE-080215-7]	zgc:174153c
4	ENSDARG000	5.31	-1.61	0.62	MGC174153c:174153 [Source:ZFIN;Acc:ZDB-GENE-121214-36]	MGC174153c
5	ENSDARG000	2.7	-1.67	0.73	ucp3 uncoupling protein 3 [Source:ZFIN;Acc:ZDB-GENE-040426-6]	ucp3
6	ENSDARG000	2.65	-1.35	0.74	si:ch73-364h19.1-364h19.1 [Source:ZFIN;Acc:ZDB-GENE-031010-4]	si:ch73-364h19.1
7	ENSDARG000	2.63	-0.64	0.7	sidkey-26g8.4-23918.2 [Source:ZFIN;Acc:ZDB-GENE-121214-52]	sidkey-26g8.4
8	ENSDARG000	2.52	-1.92	0.7	zgc:163046c:163046 [Source:ZFIN;Acc:ZDB-GENE-070927-1]	zgc:163046c
9	ENSDARG000	2.34	-2.31	0.94	tons1 tonsoku-like, DNA repair protein [Source:ZFIN;Acc:ZDB-GENE-040426-6]	tons1
10	ENSDARG000	2.3	-1.05	0.68		
11	ENSDARG000	2.27	-1.35	0.7	Fanconi anemia, complementation group B [Source:ZFIN;Acc:ZDB-GENE-020416-5]	Fanconi anemia, complementation group B
12	ENSDARG000	2.26	-1.06	0.8	st3gal3b ST3 beta-galactoside alpha-2,3-sialyltransferase 3b [Source:ZFIN;Acc:ZDB-GENE-020416-5]	st3gal3b
13	ENSDARG000	2.21	-1.65	0.71	LOC56909 transcription elongation factor B (SIII), polypeptide 2 [Source:ZFIN;Acc:ZDB-GENE-080303-29]	LOC56909
14	ENSDARG000	2.21	-1.03	0.78	zgc:174862c:174862 [Source:ZFIN;Acc:ZDB-GENE-080303-29]	zgc:174862c
15	ENSDARG000	2.19	-0.96	0.74	tbx6 T-box 6 [Source:ZFIN;Acc:ZDB-GENE-020416-5]	tbx6
16	ENSDARG000	2.13	-1.72	0.73	fancg Fanconi anemia, complementation group G [Source:ZFIN;Acc:ZDB-GENE-020416-5]	fancg
17	ENSDARG000	2.09	-0.94	0.83		
18	ENSDARG000	2.07	-2.01	0.9	cenpj centromere protein J [Source:ZFIN;Acc:ZDB-GENE-030131-3]	cenpj
19	ENSDARG000	2.07	-0.42	0.79	zgc:173425c:173425 [Source:ZFIN;Acc:ZDB-GENE-071004-51]	zgc:173425c
20	ENSDARG000	2.06	-0.5	0.87	sidkey-26g8.4-2e4.2 [Source:ZFIN;Acc:ZDB-GENE-030131-9307]	sidkey-26g8.4

## Geneset Overrepresentation

Rank	p-value	#in/all	Geneset
1	9e-46	173 / 2030	MF nucleic acid binding
2	2e-18	148 / 2716	CC nucleus
3	2e-13	89 / 1484	MF DNA binding
4	1e-11	11 / 25	BP membrane disruption in other organism
5	1e-11	17 / 78	BP DNA replication
6	4e-11	22 / 148	BP DNA repair
7	9e-11	23 / 168	CC nucleosome
8	1e-10	11 / 30	BP defense response to Gram-positive bacterium
9	3e-10	26 / 229	CC chromosome
10	4e-09	8 / 17	MF DNA-directed DNA polymerase activity
11	1e-08	24 / 232	MF protein heterodimerization activity
12	2e-08	8 / 20	BP DNA biosynthetic process
13	1e-07	40 / 608	MF RNA binding
14	5e-06	5 / 11	BP DNA-dependent DNA replication
15	6e-06	8 / 39	MF single-stranded DNA binding
16	9e-06	7 / 30	MF damaged DNA binding
17	9e-06	7 / 30	BP DNA recombination
18	1e-05	8 / 43	BP DNA-templated transcription, initiation
19	2e-05	8 / 45	BP rRNA processing
20	2e-05	7 / 34	BP chromatin silencing
21	3e-05	13 / 128	BP innate immune response
22	4e-05	8 / 49	CC nuclear chromatin
23	1e-04	7 / 43	MF iron-sulfur cluster binding
24	1e-04	10 / 91	BP cellular response to DNA damage stimulus
25	1e-04	4 / 11	BP telomere maintenance
26	2e-04	6 / 32	BP DNA duplex unwinding
27	3e-04	7 / 49	MF RNA-directed DNA polymerase activity
28	3e-04	12 / 140	CC nucleolus
29	3e-04	7 / 51	BP tRNA processing
30	5e-04	5 / 26	MF 4 iron, 4 sulfur cluster binding
31	6e-04	8 / 72	MF helicase activity
32	1e-03	10 / 117	BP nucleosome assembly
33	1e-03	8 / 80	MF transcription regulatory region DNA binding
34	1e-03	20 / 362	BP regulation of transcription from RNA polymerase II promoter
35	1e-03	6 / 48	BP RNA-dependent DNA biosynthetic process
36	2e-03	6 / 49	CC nucleoplasm
37	2e-03	5 / 36	BP protein import into nucleus
38	2e-03	4 / 22	BP DNA replication initiation
39	2e-03	4 / 22	BP double-strand break repair via homologous recombination
40	3e-03	7 / 72	BP nucleic acid phosphodiester bond hydrolysis

p-values



BP				CC				MF			
Rank	p-value	#in/all	Geneset	Rank	p-value	#in/all	Geneset	Rank	p-value	#in/all	Geneset
1	1e-11	11 / 25	membrane disruption in other organism	1	2e-18	148 / 2716	nucleus	1	9e-46	173 / 2030	nucleic acid binding
2	1e-11	17 / 78	DNA replication	2	9e-11	23 / 168	nucleosome	2	2e-13	89 / 1484	DNA binding
3	4e-11	22 / 148	DNA repair	3	3e-10	26 / 229	chromosome	3	4e-09	8 / 17	DNA-directed DNA polymerase activity
4	1e-10	11 / 30	defense response to Gram-positive bacterium	4	4e-05	8 / 49	nuclear chromatin	4	1e-08	24 / 232	protein heterodimerization activity
5	2e-08	8 / 20	DNA biosynthetic process	5	3e-04	12 / 140	nucleolus	5	1e-07	40 / 608	RNA binding
6	5e-06	5 / 11	DNA-dependent DNA replication	6	2e-03	6 / 49	nucleoplasm	6	6e-06	8 / 39	single-stranded DNA binding
7	9e-06	7 / 30	DNA recombination	7	3e-03	4 / 24	precatalytic spliceosome	7	9e-06	7 / 30	damaged DNA binding
8	1e-05	8 / 43	DNA-templated transcription, initiation	8	4e-03	4 / 26	nuclear pore	8	1e-04	7 / 43	iron-sulfur cluster binding
9	2e-05	8 / 45	rRNA processing	9	8e-03	3 / 16	preribosome, large subunit precursor	9	3e-04	7 / 49	RNA-directed DNA polymerase activity
10	2e-05	7 / 34	chromatin silencing	10	1e-02	3 / 18	eukaryotic translation initiation factor 3 complex	10	5e-04	5 / 26	4 iron, 4 sulfur cluster binding
11	3e-05	13 / 128	innate immune response	11	1e-02	3 / 18	U4/U6 x U5 tri-snRNP complex	11	6e-04	8 / 72	helicase activity
12	1e-04	10 / 91	cellular response to DNA damage stimulus	12	1e-02	4 / 34	catalytic step 2 spliceosome	12	1e-03	8 / 80	transcription regulatory region DNA binding
13	1e-04	4 / 11	telomere maintenance	13	1e-02	3 / 20	centriole	13	4e-03	5 / 41	aminoacyl-tRNA ligase activity
14	2e-04	6 / 32	DNA duplex unwinding	14	2e-02	3 / 21	spindle pole	14	5e-03	3 / 14	ATP-dependent DNA helicase activity
15	3e-04	7 / 51	tRNA processing	15	2e-02	3 / 22	chromosome, centromeric region	15	5e-03	3 / 14	DNA-dependent ATPase activity



# Correlation Cluster

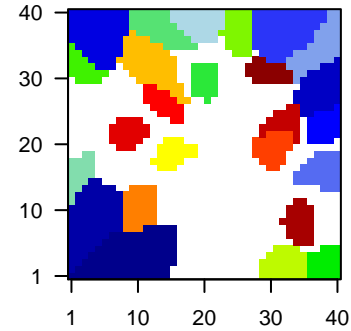
## Spot Summary: D

# metagenes = 24  
# genes = 480

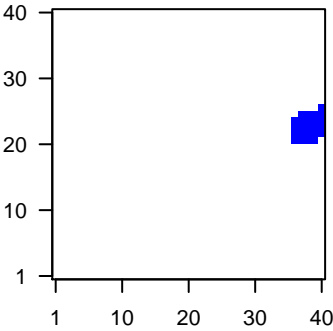
<r> metagenes = 0.96  
<r> genes = 0.52  
beta: r2= 3.56 / log p= -Inf

# samples with spot = 2 ( 11.1 % )  
24hpf\_neg : 1 ( 100 % )  
24hpf\_pos : 1 ( 50 % )

Overview Map



Spot



24hpf\_neg  
24hpf\_pos  
24hpf\_pos.1  
48hpf\_neg  
48hpf\_pos  
48hpf\_pos.1  
72hpf\_neg  
72hpf\_pos  
72hpf\_pos.1  
72hpf\_neg\_gata5  
72hpf\_pos\_gata5  
72hpf\_pos\_gata5.1  
72hpf\_neg\_tbx5  
72hpf\_pos\_tbx5  
72hpf\_pos\_tbx5.1  
72hpf\_neg\_hand2  
72hpf\_pos\_hand2  
72hpf\_pos\_hand2.1

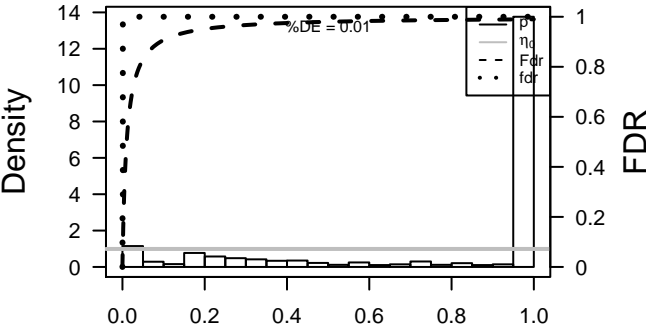
## Spot Genelist

Rank	ID	max e	r	Description	
		min e		Symbol	
1	ENSDARG0000000001	2.5	-3.45	0.65	U2 spliceosomal RNA [Source:RFAM;Acc:RF00004]
2	ENSDARG0000000002	2.42	-4.01	0.88	ssbp3a single stranded DNA binding protein 3a [Source:ZFIN;Acc:ZD
3	ENSDARG0000000003	2.4	-3.98	0.73	si:dkey-281k223a13.22 [Source:ZFIN;Acc:ZDB-GENE-160113-7f
4	ENSDARG0000000004	2.27	-3.43	0.89	stil scl/tal1 interrupting locus [Source:ZFIN;Acc:ZDB-GENE-020
5	ENSDARG0000000005	2.26	-2.2	0.53	
6	ENSDARG0000000006	2.13	-1.76	0.7	zgc:165555c:165555 [Source:ZFIN;Acc:ZDB-GENE-070620-17]
7	ENSDARG0000000007	2.1	-2.66	0.75	LOC562776 histone 1, H4, like [Source:ZFIN;Acc:ZDB-GENE-070927-1f
8	ENSDARG0000000008	2.07	-3.17	0.8	haus3 HAUS augmin-like complex, subunit 3 [Source:ZFIN;Acc:ZD
9	ENSDARG0000000009	2.02	-2.24	0.77	zgc:163040c:163040 [Source:ZFIN;Acc:ZDB-GENE-070424-79]
10	ENSDARG0000000010	2	-2.93	0.83	tspan2a tetraspanin 2a [Source:ZFIN;Acc:ZDB-GENE-050522-511]
11	ENSDARG0000000011	2	-1.89	0.72	rhubd3 rhomboid, veinlet-like 3 (Drosophila) [Source:ZFIN;Acc:ZDB-
12	ENSDARG0000000012	1.94	-2.76	0.68	rpe65b retinal pigment epithelium-specific protein 65b [Source:ZFIN;
13	ENSDARG0000000013	1.92	-4.01	0.92	zgc:163040c:163040 histone 1, H4, like [Source:ZFIN;Acc:ZDB-GENE-070927-1f
14	ENSDARG0000000014	1.84	-2.41	0.39	calcium channel, voltage-dependent, T type, alpha 1G subun
15	ENSDARG0000000015	1.84	-4.62	0.76	zc3h12b zinc finger CCCH-type containing 12B [Source:ZFIN;Acc:ZDI
16	ENSDARG0000000016	1.84	-4.19	0.58	Small nucleolar RNA SNORA53 [Source:RFAM;Acc:RF00565
17	ENSDARG0000000017	1.82	-2.83	0.7	si:dkey-112g5.12 [Source:ZFIN;Acc:ZDB-GENE-081028-3f
18	ENSDARG0000000018	1.8	-4.24	0.84	cd82b CD82 molecule b [Source:ZFIN;Acc:ZDB-GENE-030131-28
19	ENSDARG0000000019	1.79	-4.69	0.91	si:dkey-261m9.6 [Source:ZFIN;Acc:ZDB-GENE-131127-10
20	ENSDARG0000000020	1.78	-2.04	0.75	LOC100148601 histone family member X [Source:HGNC Symbol;Acc:HC

## Geneset Overrepresentation

Rank	p-value	#in/all	Geneset
1	3e-18	92 / 2030	MF nucleic acid binding
2	1e-11	23 / 229	CC chromosome
3	8e-11	19 / 168	CC nucleosome
4	9e-11	22 / 232	MF protein heterodimerization activity
5	7e-06	7 / 43	BP DNA-templated transcription, initiation
6	9e-06	76 / 2716	CC nucleus
7	2e-05	6 / 34	BP chromatin silencing
8	3e-05	47 / 1484	MF DNA binding
9	5e-05	5 / 25	BP membrane disruption in other organism
10	1e-04	5 / 30	BP defense response to Gram-positive bacterium
11	2e-04	6 / 49	CC nuclear chromatin
12	5e-04	3 / 10	CC intracellular transport particle B
13	6e-04	6 / 61	MF ubiquitin protein ligase binding
14	8e-04	4 / 25	MF histone acetyltransferase activity
15	9e-04	8 / 117	BP nucleosome assembly
16	9e-04	3 / 12	BP intracellular transport
17	9e-04	3 / 12	BP spindle assembly
18	1e-03	6 / 70	BP RNA processing
19	2e-03	4 / 30	CC ciliary basal body
20	2e-03	21 / 608	MF RNA binding
21	2e-03	3 / 15	CC mitochondrial small ribosomal subunit
22	2e-03	6 / 79	BP mRNA splicing, via spliceosome
23	2e-03	3 / 16	BP mitochondrial translation
24	2e-03	3 / 16	BP nuclear-transcribed mRNA catabolic process, nonsense-mediated decay
25	2e-03	6 / 80	CC centrosome
26	3e-03	3 / 17	BP mRNA transport
27	3e-03	3 / 17	CC U2-type prespliceosome
28	3e-03	5 / 57	MF mRNA binding
29	4e-03	3 / 19	CC U1 snRNP
30	4e-03	3 / 20	MF NAD+ kinase activity
31	4e-03	3 / 20	BP regulation of autophagy
32	6e-03	9 / 192	MF ubiquitin-protein transferase activity
33	6e-03	4 / 44	MF peptidyl-prolyl cis-trans isomerase activity
34	6e-03	4 / 44	BP protein peptidyl-prolyl isomerization
35	8e-03	4 / 47	MF nucleotidyltransferase activity
36	9e-03	7 / 138	BP cilium assembly
37	9e-03	3 / 26	BP mitophagy
38	9e-03	3 / 26	CC SCF ubiquitin ligase complex
39	9e-03	5 / 76	CC cilium
40	1e-02	9 / 214	BP translation

p-values



BP				CC				MF			
Rank	p-value	#in/all	Geneset	Rank	p-value	#in/all	Geneset	Rank	p-value	#in/all	Geneset
1	7e-06	7 / 43	DNA-templated transcription, initiation	1	1e-11	23 / 229	chromosome	1	3e-18	92 / 2030	nucleic acid binding
2	2e-05	6 / 34	chromatin silencing	2	8e-11	19 / 168	nucleosome	2	9e-11	22 / 232	protein heterodimerization activity
3	5e-05	5 / 25	membrane disruption in other organism	3	9e-06	76 / 2716	nucleus	3	3e-05	47 / 1484	DNA binding
4	1e-04	5 / 30	defense response to Gram-positive bacterium	4	2e-04	6 / 49	nuclear chromatin	4	6e-04	6 / 61	ubiquitin protein ligase binding
5	9e-04	8 / 117	nucleosome assembly	5	5e-04	3 / 10	intraciliary transport particle B	5	8e-04	4 / 25	histone acetyltransferase activity
6	9e-04	3 / 12	intraciliary transport	6	2e-03	4 / 30	ciliary basal body	6	2e-03	21 / 608	RNA binding
7	9e-04	3 / 12	spindle assembly	7	2e-03	3 / 15	mitochondrial small ribosomal subunit	7	3e-03	5 / 57	mRNA binding
8	1e-03	6 / 70	RNA processing	8	2e-03	6 / 80	centrosome	8	4e-03	3 / 20	NAD+ kinase activity
9	2e-03	6 / 79	mRNA splicing, via spliceosome	9	3e-03	3 / 17	U2-type prespliceosome	9	6e-03	9 / 192	ubiquitin-protein transferase activity
10	2e-03	3 / 16	mitochondrial translation	10	4e-03	3 / 19	U1 snRNP	10	6e-03	4 / 44	peptidyl-prolyl cis-trans isomerase activity
11	2e-03	3 / 16	nuclear-transcribed mRNA catabolic process, nonsense-mediated decay	11	9e-03	3 / 26	SCF ubiquitin ligase complex	11	8e-03	4 / 47	nucleotidyltransferase activity
12	3e-03	3 / 17	mRNA transport	12	9e-03	5 / 76	cilium	12	1e-02	3 / 30	N-acetyltransferase activity
13	4e-03	3 / 20	regulation of autophagy	13	1e-02	2 / 10	cullin-RING ubiquitin ligase complex	13	1e-02	2 / 11	diacylglycerol kinase activity
14	6e-03	4 / 44	protein peptidyl-prolyl isomerization	14	2e-02	2 / 12	mitotic spindle	14	2e-02	7 / 156	ubiquitin protein ligase activity
15	9e-03	7 / 138	cilium assembly	15	2e-02	2 / 14	U12-type spliceosomal complex	15	4e-02	6 / 144	structural constituent of ribosome

Correlation Cluster

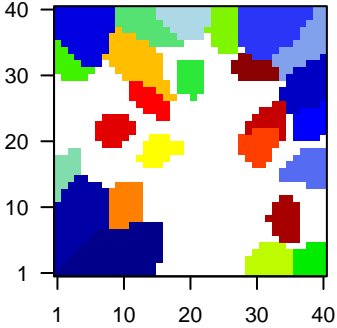
Spot Summary: E

# metagenes = 27  
# genes = 521

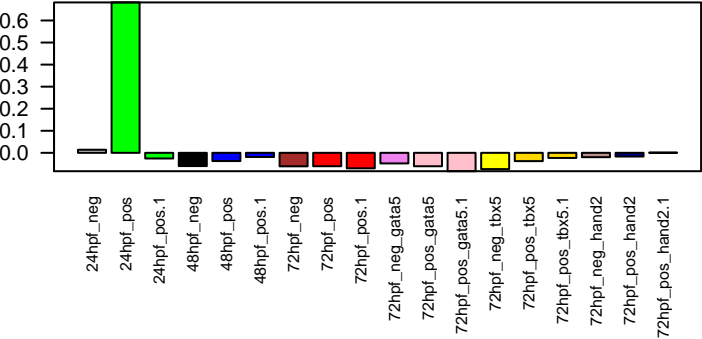
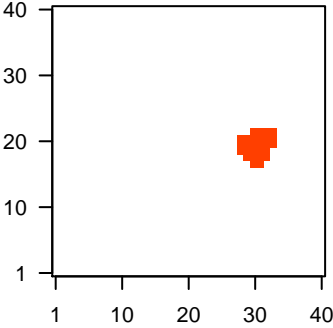
<r> metagenes = 0.92  
<r> genes = 0.53  
beta: r2= 0.39 / log p= -2.25

# samples with spot = 1 ( 5.6 %)  
24hpf\_pos : 1 ( 50 %)

Overview Map



Spot

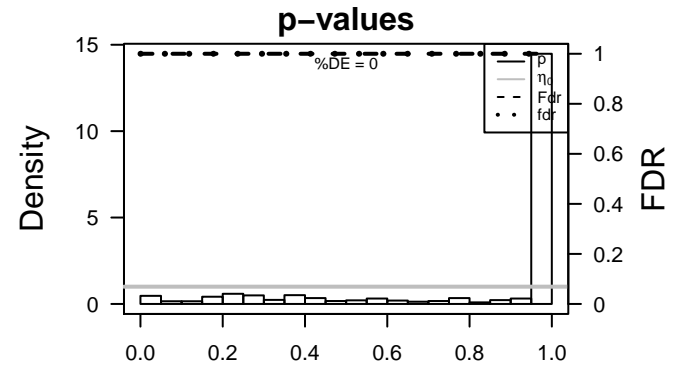


Spot Genelist

Rank	ID	max e	r	Description	
		min e		Symbol	
1	ENSDARG0001	1.85	-0.54	0.83	si:ch73-343m12-343i4.8 [Source:ZFIN;Acc:ZDB-GENE-090313-159]
2	ENSDARG0001	1.79	-0.47	0.87	
3	ENSDARG0001	1.72	-0.43	0.86	si:ch211-14p21.4 [Source:ZFIN;Acc:ZDB-GENE-070912-9]
4	ENSDARG0001	1.71	-0.32	0.91	
5	ENSDARG0001	1.66	-0.37	0.81	tmem44 transmembrane protein 44 [Source:ZFIN;Acc:ZDB-GENE-060313-12]
6	ENSDARG0001	1.64	-0.82	0.72	si:ch211-14p21.4 [Source:ZFIN;Acc:ZDB-GENE-160728-1]
7	ENSDARG0001	1.61	-0.55	0.78	zgc:114041c:114041 [Source:ZFIN;Acc:ZDB-GENE-050706-122]
8	ENSDARG0001	1.57	-0.29	0.85	rxfp3.2a relaxin/insulin-like family peptide receptor 3.2a [Source:ZFIN;Acc:ZDB-GENE-070912-9]
9	ENSDARG0001	1.55	-0.56	0.81	si:key-163m14.6 [Source:ZFIN;Acc:ZDB-GENE-120215-5]
10	ENSDARG0001	1.54	-0.6	0.73	grem2a gremlin 2, DAN family BMP antagonist a [Source:ZFIN;Acc:ZDB-GENE-070912-9]
11	ENSDARG0001	1.52	-0.61	0.84	slc25a35 solute carrier family 25, member 35 [Source:ZFIN;Acc:ZDB-GENE-070912-9]
12	ENSDARG0001	1.52	-0.67	0.74	
13	ENSDARG0001	1.48	-0.76	0.69	dph1 diphthamide biosynthesis 1 [Source:ZFIN;Acc:ZDB-GENE-070912-9]
14	ENSDARG0001	1.45	-0.34	0.88	mafa v-maf avian musculoaponeurotic fibrosarcoma oncogene homolog 1 [Source:ZFIN;Acc:ZDB-GENE-070912-9]
15	ENSDARG0001	1.45	-0.3	0.85	si:ch211-14p21.4 [Source:ZFIN;Acc:ZDB-GENE-090313-159]
16	ENSDARG0001	1.44	-0.35	0.77	usp18 ubiquitin specific peptidase 18 [Source:ZFIN;Acc:ZDB-GENE-070912-9]
17	ENSDARG0001	1.43	-0.34	0.9	
18	ENSDARG0001	1.43	-0.33	0.85	si:ch211-14p21.3 [Source:ZFIN;Acc:ZDB-GENE-070912-9]
19	ENSDARG0001	1.42	-0.3	0.81	gpr55a G protein-coupled receptor 55a [Source:ZFIN;Acc:ZDB-GENE-070912-9]
20	ENSDARG0001	1.41	-0.3	0.92	si:ch73-129a22.11 [Source:ZFIN;Acc:ZDB-GENE-100921-4]

Geneset Overrepresentation

Rank	p-value	#in/all	Geneset
1	8e-05	15 / 253	BP protein autophosphorylation
2	1e-04	16 / 294	BP regulation of mitotic cell cycle
3	2e-04	29 / 751	MF G-protein coupled receptor activity
4	6e-04	30 / 853	BP G-protein coupled receptor signaling pathway
5	1e-03	15 / 329	BP negative regulation of apoptotic process
6	2e-03	3 / 13	BP RNA methylation
7	2e-03	5 / 51	BP tRNA processing
8	3e-03	4 / 32	BP positive regulation of cytosolic calcium ion concentration involved in phosphatidylinositol 3-kinase/Akt signaling pathway
9	3e-03	4 / 32	BP positive regulation of Rho protein signal transduction
10	7e-03	22 / 666	MF signal transducer activity
11	8e-03	3 / 23	BP meiotic cell cycle
12	1e-02	36 / 1295	BP signal transduction
13	1e-02	2 / 10	MF RNA methyltransferase activity
14	2e-02	3 / 29	BP inorganic anion transport
15	2e-02	2 / 11	CC DNA-directed RNA polymerase I complex
16	2e-02	2 / 11	MF RNA polymerase I activity
17	2e-02	2 / 11	MF thrombin-activated receptor activity
18	2e-02	2 / 11	BP thrombin-activated receptor signaling pathway
19	2e-02	2 / 12	MF extracellular ATP-gated cation channel activity
20	2e-02	2 / 12	MF purinergic nucleotide receptor activity
21	2e-02	2 / 12	BP purinergic nucleotide receptor signaling pathway
22	2e-02	2 / 12	BP response to ATP
23	2e-02	3 / 33	BP blood coagulation
24	3e-02	2 / 14	BP regulation of cell adhesion
25	3e-02	2 / 14	MF sodium-independent organic anion transmembrane transporter activity
26	3e-02	2 / 14	BP sodium-independent organic anion transport
27	3e-02	2 / 15	BP positive regulation of vasoconstriction
28	3e-02	3 / 37	MF DNA-directed 5'-3' RNA polymerase activity
29	3e-02	19 / 652	MF protein serine/threonine kinase activity
30	4e-02	4 / 67	MF transmembrane transporter activity
31	4e-02	2 / 17	CC integral component of nuclear inner membrane
32	4e-02	5 / 102	BP response to stimulus
33	4e-02	3 / 42	BP detection of chemical stimulus involved in sensory perception
34	4e-02	2 / 18	CC DNA-directed RNA polymerase III complex
35	5e-02	2 / 19	CC acetylcholine-gated channel complex
36	5e-02	3 / 45	BP phospholipase C-activating G-protein coupled receptor signaling pathway
37	5e-02	6 / 144	BP methylation
38	6e-02	3 / 47	BP regulation of MAPK cascade
39	6e-02	2 / 21	MF inorganic anion exchanger activity
40	6e-02	4 / 79	BP excitatory postsynaptic potential



BP				CC				MF			
Rank	p-value	#in/all	Geneset	Rank	p-value	#in/all	Geneset	Rank	p-value	#in/all	Geneset
1	8e-05	15 / 253	protein autophosphorylation	1	0.02	2 / 11	DNA-directed RNA polymerase I complex	1	2e-04	29 / 751	G-protein coupled receptor activity
2	1e-04	16 / 294	regulation of mitotic cell cycle	2	0.04	2 / 17	integral component of nuclear inner membrane	2	7e-03	22 / 666	signal transducer activity
3	6e-04	30 / 853	G-protein coupled receptor signaling pathway	3	0.04	2 / 18	DNA-directed RNA polymerase III complex	3	1e-02	2 / 10	RNA methyltransferase activity
4	1e-03	15 / 329	negative regulation of apoptotic process	4	0.05	2 / 19	acetylcholine-gated channel complex	4	2e-02	2 / 11	RNA polymerase I activity
5	2e-03	3 / 13	RNA methylation	5	0.09	2 / 27	postsynapse	5	2e-02	2 / 11	thrombin-activated receptor activity
6	2e-03	5 / 51	tRNA processing	6	0.14	2 / 35	Golgi cisterna membrane	6	2e-02	2 / 12	extracellular ATP-gated cation channel activity
7	3e-03	4 / 32	positive regulation of cytosolic calcium ion concentration involved in phospholi	7	0.17	19 / 809	integral component of plasma membrane	7	2e-02	2 / 12	purinergic nucleotide receptor activity
8	3e-03	4 / 32	positive regulation of Rho protein signal transduction	8	0.17	1 / 10	high-density lipoprotein particle	8	3e-02	2 / 14	sodium-independent organic anion transmembrane transporter activity
9	8e-03	3 / 23	meiotic cell cycle	9	0.18	3 / 80	postsynaptic membrane	9	3e-02	3 / 37	DNA-directed 5'-3' RNA polymerase activity
10	1e-02	36 / 1295	signal transduction	10	0.19	1 / 11	P granule	10	3e-02	19 / 652	protein serine/threonine kinase activity
11	2e-02	3 / 29	inorganic anion transport	11	0.19	1 / 11	small ribosomal subunit	11	4e-02	4 / 67	transmembrane transporter activity
12	2e-02	2 / 11	thrombin-activated receptor signaling pathway	12	0.20	1 / 12	DNA-directed RNA polymerase II, core complex	12	6e-02	2 / 21	inorganic anion exchanger activity
13	2e-02	2 / 12	purinergic nucleotide receptor signaling pathway	13	0.21	1 / 13	cyclin-dependent protein kinase holoenzyme complex	13	8e-02	2 / 25	acetylcholine-gated cation-selective channel activity
14	2e-02	2 / 12	response to ATP	14	0.22	6 / 219	cell junction	14	1e-01	3 / 59	olfactory receptor activity
15	2e-02	3 / 33	blood coagulation	15	0.23	1 / 14	hemoglobin complex	15	1e-01	5 / 135	methyltransferase activity

# Correlation Cluster

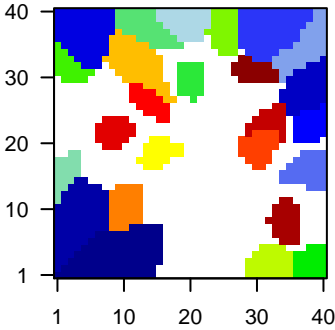
## Spot Summary: F

# metagenes = 20  
# genes = 291

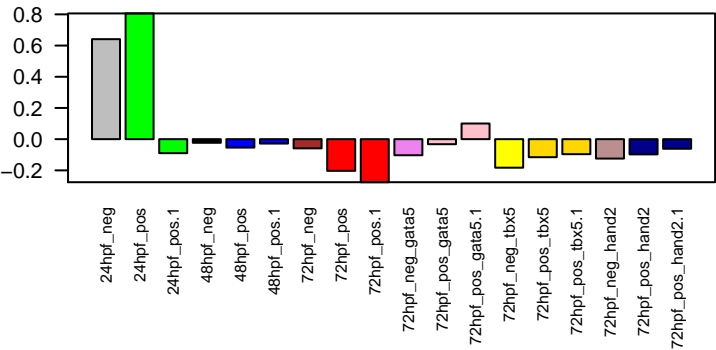
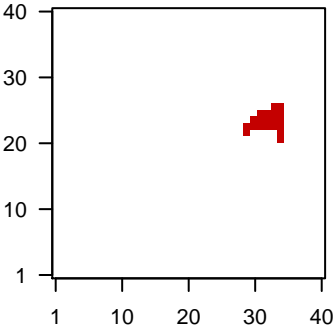
<r> metagenes = 0.93  
<r> genes = 0.44  
beta: r2= 0.96 / log p= -11.93

# samples with spot = 2 ( 11.1 %)  
24hpf\_neg : 1 ( 100 %)  
24hpf\_pos : 1 ( 50 %)

Overview Map



Spot

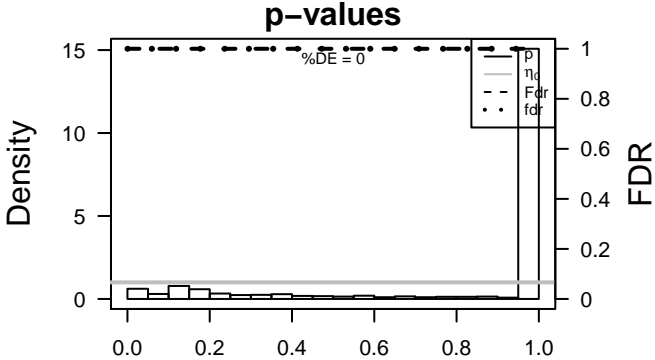


## Spot Genelist

Rank	ID	max e	r	Description	
		min e		Symbol	
1	ENSDARG000	2.68	-0.85	0.89	si:dkey-269k1.4 [Source:ZFIN;Acc:ZDB-GENE-071004-74]
2	ENSDARG000	2.35	-0.89	0.87	wu:fa26c03 cathepsin Lb [Source:ZFIN;Acc:ZDB-GENE-980526-285]
3	ENSDARG000	2.27	-0.8	0.88	si:dkey-269k1.4 [Source:ZFIN;Acc:ZDB-GENE-121214-37]
4	ENSDARG000	2.13	-0.58	0.88	si:dkey-269k1.4 [Source:ZFIN;Acc:ZDB-GENE-121214-39]
5	ENSDARG000	2.08	-0.57	0.87	ctslb cathepsin Lb [Source:ZFIN;Acc:ZDB-GENE-980526-285]
6	ENSDARG000	2.01	-0.68	0.91	LOC100506013 si:dkey-269k1.4 [Source:ZFIN;Acc:ZDB-GENE-121214-37]
7	ENSDARG000	1.96	-0.76	0.86	fgf8a fibroblast growth factor 8a [Source:ZFIN;Acc:ZDB-GENE-99
8	ENSDARG000	1.93	-0.76	0.73	ece2a endothelin converting enzyme 2a [Source:ZFIN;Acc:ZDB-GE
9	ENSDARG000	1.63	-1.36	0.56	zgc:153409 cc:153409 [Source:ZFIN;Acc:ZDB-GENE-060929-224]
10	ENSDARG000	1.61	-0.56	0.81	U2 spliceosomal RNA [Source:RFAM;Acc:RF00004]
11	ENSDARG000	1.59	-1.36	0.74	gmn geminin, DNA replication inhibitor [Source:ZFIN;Acc:ZDB-GE
12	ENSDARG000	1.58	-0.46	0.81	si:ch211-5717.7 [Source:ZFIN;Acc:ZDB-GENE-090313-119]
13	ENSDARG000	1.57	-0.53	0.71	
14	ENSDARG000	1.54	-1.04	0.64	fam212b family with sequence similarity 212, member B [Source:ZFIN;
15	ENSDARG000	1.52	-0.43	0.84	si:ch211-5717.7 [Source:ZFIN;Acc:ZDB-GENE-081104-1
16	ENSDARG000	1.52	-2.24	0.43	hvcn1 hydrogen voltage-gated channel 1 [Source:ZFIN;Acc:ZDB-G
17	ENSDARG000	1.51	-1.29	0.78	ngdn neuroguidin, EIF4E binding protein [Source:ZFIN;Acc:ZDB-G
18	ENSDARG000	1.5	-0.83	0.51	zbtb43 zinc finger and BTB domain containing 43 [Source:ZFIN;Acc:
19	ENSDARG000	1.48	-1.22	0.79	ppih peptidylprolyl isomerase H (cyclophilin H) [Source:ZFIN;Acc:Z
20	ENSDARG000	1.45	-1.01	0.69	zgc:163046 stone 1, H4, like [Source:ZFIN;Acc:ZDB-GENE-070927-1(

## Geneset Overrepresentation

Rank	p-value	#in/all	Geneset
1	3e-11	55 / 2030	MF nucleic acid binding
2	2e-07	11 / 138	CC intracellular ribonucleoprotein complex
3	2e-06	12 / 214	BP translation
4	4e-05	8 / 123	MF cysteine-type peptidase activity
5	8e-05	4 / 23	BP cytoplasmic translation
6	1e-04	5 / 47	CC cytosolic large ribosomal subunit
7	1e-04	8 / 147	CC ribosome
8	2e-04	17 / 608	MF RNA binding
9	6e-04	5 / 65	BP somitogenesis
10	7e-04	7 / 144	MF structural constituent of ribosome
11	1e-03	5 / 78	MF cysteine-type endopeptidase activity
12	3e-03	5 / 96	CC lysosome
13	4e-03	4 / 62	BP proteolysis involved in cellular protein catabolic process
14	6e-03	2 / 12	BP tRNA modification
15	8e-03	3 / 40	BP erythrocyte differentiation
16	1e-02	3 / 45	BP rRNA processing
17	1e-02	2 / 16	BP mesoderm development
18	1e-02	9 / 358	MF peptidase activity
19	1e-02	2 / 17	BP positive regulation of cell migration
20	1e-02	2 / 18	MF acetylcholine binding
21	1e-02	2 / 18	BP embryonic neurocranium morphogenesis
22	1e-02	2 / 18	BP response to nicotine
23	1e-02	2 / 18	BP spliceosomal snRNP assembly
24	2e-02	2 / 19	CC acetylcholine-gated channel complex
25	2e-02	2 / 19	BP neuromuscular synaptic transmission
26	2e-02	2 / 19	CC U1 snRNP
27	2e-02	2 / 20	BP embryonic pattern specification
28	2e-02	3 / 54	BP Kupffer's vesicle development
29	2e-02	3 / 55	BP neuron differentiation
30	2e-02	2 / 22	MF tRNA binding
31	2e-02	3 / 58	BP RNA splicing
32	3e-02	2 / 24	BP peripheral nervous system development
33	3e-02	2 / 25	MF acetylcholine-gated cation-selective channel activity
34	3e-02	5 / 164	BP carbohydrate metabolic process
35	3e-02	2 / 27	BP synaptic transmission, cholinergic
36	3e-02	3 / 68	MF sulfotransferase activity
37	4e-02	2 / 29	MF dioxygenase activity
38	4e-02	4 / 121	BP angiogenesis
39	4e-02	22 / 1427	BP biological_process
40	4e-02	2 / 31	BP autophagosome assembly



BP				CC				MF			
Rank	p-value	#in/all	Geneset	Rank	p-value	#in/all	Geneset	Rank	p-value	#in/all	Geneset
1	2e-06	12 / 214	translation	1	2e-07	11 / 138	intracellular ribonucleoprotein complex	1	3e-11	55 / 2030	nucleic acid binding
2	8e-05	4 / 23	cytoplasmic translation	2	1e-04	5 / 47	cytosolic large ribosomal subunit	2	4e-05	8 / 123	cysteine-type peptidase activity
3	6e-04	5 / 65	somitogenesis	3	1e-04	8 / 147	ribosome	3	2e-04	17 / 608	RNA binding
4	4e-03	4 / 62	proteolysis involved in cellular protein catabolic process	4	3e-03	5 / 96	lysosome	4	7e-04	7 / 144	structural constituent of ribosome
5	6e-03	2 / 12	tRNA modification	5	2e-02	2 / 19	acetylcholine-gated channel complex	5	1e-03	5 / 78	cysteine-type endopeptidase activity
6	8e-03	3 / 40	erythrocyte differentiation	6	2e-02	2 / 19	U1 snRNP	6	1e-02	9 / 358	peptidase activity
7	1e-02	3 / 45	rRNA processing	7	5e-02	2 / 33	cytosolic small ribosomal subunit	7	1e-02	2 / 18	acetylcholine binding
8	1e-02	2 / 16	mesoderm development	8	5e-02	3 / 80	postsynaptic membrane	8	2e-02	2 / 22	tRNA binding
9	1e-02	2 / 17	positive regulation of cell migration	9	1e-01	1 / 10	anaphase-promoting complex	9	3e-02	2 / 25	acetylcholine-gated cation-selective channel activity
10	1e-02	2 / 18	embryonic neurocranium morphogenesis	10	1e-01	1 / 10	sarcoplasmic reticulum	10	3e-02	3 / 68	sulfotransferase activity
11	1e-02	2 / 18	response to nicotine	11	1e-01	1 / 11	commitment complex	11	4e-02	2 / 29	dioxygenase activity
12	1e-02	2 / 18	spliceosomal snRNP assembly	12	1e-01	1 / 11	DNA-directed RNA polymerase I complex	12	4e-02	2 / 32	oxidoreductase activity, acting on the CH-OH group of donors, NAD or NADP
13	2e-02	2 / 19	neuromuscular synaptic transmission	13	1e-01	1 / 11	small ribosomal subunit	13	7e-02	2 / 41	aminoacyl-tRNA ligase activity
14	2e-02	2 / 20	embryonic pattern specification	14	1e-01	2 / 56	mitochondrial outer membrane	14	1e-01	1 / 10	hydrolase activity, acting on carbon-nitrogen (but not peptide) bonds, in linear
15	2e-02	3 / 54	Kupffer's vesicle development	15	1e-01	1 / 12	DNA-directed RNA polymerase II, core complex	15	1e-01	1 / 10	NAD-dependent histone deacetylase activity (H3-K14 specific)

# Correlation Cluster

## Spot Summary: G

# metagenes = 66  
# genes = 1025

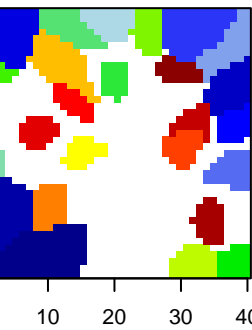
<r> metagenes = 0.94

beta: r2= 6.48 / log p= -Inf

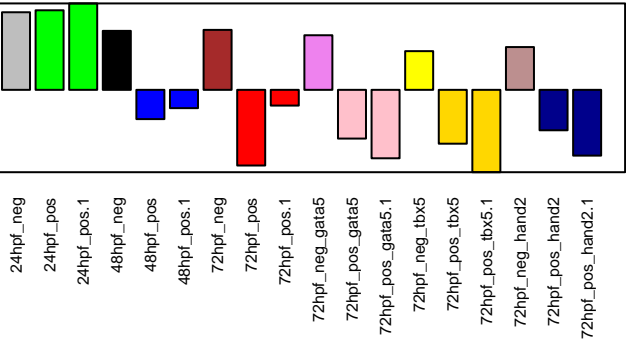
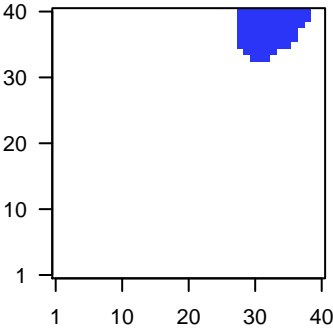
# samples with spot = 6 ( 33.3 %)

24hpf\_neg : 1 ( 100 %)  
24hpf\_pos : 2 ( 100 %)  
48hpf\_neg : 1 ( 100 %)  
72hpf\_neg : 1 ( 100 %)  
72hpf\_neg\_gata5 : 1 ( 100 %)

### Overview Map



### Spot

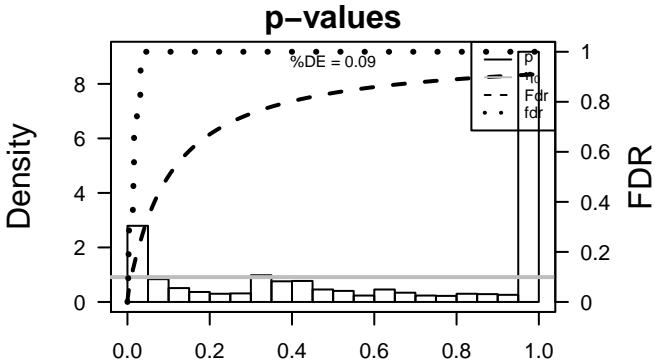


## Spot Genelist

Rank	ID	max e	r	Description	
		min e		Symbol	
1	ENSDARG0000000001	3.45	-2.09	0.85	sl:ch211-521k18.5 [Source:ZFIN;Acc:ZDB-GENE-030131-4]
2	ENSDARG0000000002	3.26	-3.26	0.58	mmp13a matrix metalloproteinase 13a [Source:ZFIN;Acc:ZDB-GENE-030131-4]
3	ENSDARG0000000003	3.22	-4.34	0.54	collagen, type XIV, alpha 1b [Source:ZFIN;Acc:ZDB-GENE-030131-4]
4	ENSDARG0000000004	3.19	-3.27	0.83	sl:ch211-521k18.5-14k19.8 [Source:ZFIN;Acc:ZDB-GENE-051214-4]
5	ENSDARG0000000005	3.15	-3.55	0.89	aplnrb apelin receptor b [Source:ZFIN;Acc:ZDB-GENE-050913-90]
6	ENSDARG0000000006	2.85	-2.82	0.82	sl:dky-250k16.2 [Source:ZFIN;Acc:ZDB-GENE-121214-30]
7	ENSDARG0000000007	2.85	-1.19	0.72	zic2b zic family member 2 (odd-paired homolog, Drosophila) b [Source:ZFIN;Acc:ZDB-GENE-030131-4]
8	ENSDARG0000000008	2.84	-1.51	0.94	aspm abnormal spindle microtubule assembly [Source:ZFIN;Acc:ZDB-GENE-030131-4]
9	ENSDARG0000000009	2.8	-4.02	0.74	capn12 calpain 12 [Source:ZFIN;Acc:ZDB-GENE-050419-245]
10	ENSDARG0000000010	2.76	-2.68	0.87	fam65c family with sequence similarity 65, member C [Source:ZFIN;Acc:ZDB-GENE-030131-4]
11	ENSDARG0000000011	2.71	-3.94	0.59	kel Kell blood group, metallo-endopeptidase [Source:ZFIN;Acc:ZDB-GENE-030131-4]
12	ENSDARG0000000012	2.71	-2.42	0.8	adrb3a adrenoceptor beta 3a [Source:ZFIN;Acc:ZDB-GENE-080917-4]
13	ENSDARG0000000013	2.71	-2.77	0.89	DEP domain containing 1B [Source:HGNC Symbol;Acc:HGNC:10000]
14	ENSDARG0000000014	2.69	-3.04	0.7	hbbe2 hemoglobin beta embryonic-2 [Source:ZFIN;Acc:ZDB-GENE-030131-4]
15	ENSDARG0000000015	2.69	-1.89	0.86	add2 adducin 2 (beta) [Source:ZFIN;Acc:ZDB-GENE-080718-4]
16	ENSDARG0000000016	2.65	-1.55	0.43	
17	ENSDARG0000000017	2.62	-1.72	0.82	kank4 KN motif and ankyrin repeat domains 4 [Source:ZFIN;Acc:ZDB-GENE-030131-4]
18	ENSDARG0000000018	2.61	-1.9	0.74	her8a hairy-related 8a [Source:ZFIN;Acc:ZDB-GENE-030131-237]
19	ENSDARG0000000019	2.6	-1.22	0.8	nr6a1a nuclear receptor subfamily 6, group A, member 1a [Source:ZFIN;Acc:ZDB-GENE-030131-4]
20	ENSDARG0000000020	2.59	-1.88	0.71	zgc:112234 zgc:112234 [Source:NCBI gene;Acc:554097]

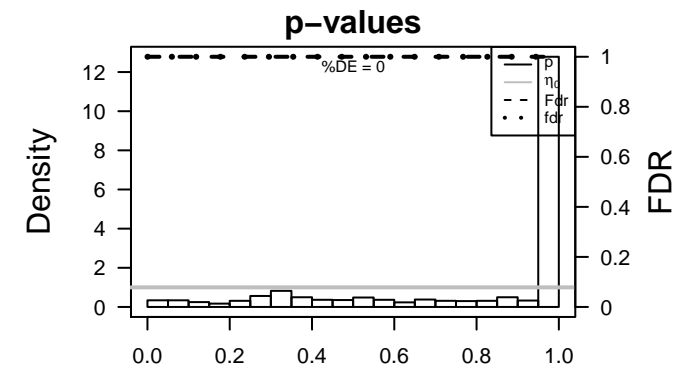
## Geneset Overrepresentation

Rank	p-value	#in/all	Geneset
1	2e-59	73 / 168	CC nucleosome
2	8e-54	78 / 229	CC chromosome
3	3e-50	184 / 1484	MF DNA binding
4	5e-50	260 / 2716	CC nucleus
5	6e-46	54 / 117	BP nucleosome assembly
6	4e-41	67 / 232	MF protein heterodimerization activity
7	1e-22	22 / 37	MF nucleosomal DNA binding
8	6e-19	112 / 1239	BP regulation of transcription, DNA-templated
9	1e-18	61 / 454	BP multicellular organism development
10	2e-13	15 / 34	BP ephrin receptor signaling pathway
11	2e-10	22 / 117	BP Wnt signaling pathway
12	2e-09	50 / 537	MF sequence-specific DNA binding
13	2e-09	13 / 43	BP DNA-templated transcription, initiation
14	6e-09	11 / 31	MF histone-lysine N-methyltransferase activity
15	8e-09	54 / 633	MF transcription factor activity, sequence-specific DNA binding
16	1e-08	54 / 643	BP transcription, DNA-templated
17	2e-08	19 / 110	MF protein tyrosine kinase activity
18	2e-08	18 / 100	BP peptidyl-tyrosine phosphorylation
19	2e-07	8 / 19	MF ephrin receptor activity
20	3e-07	15 / 83	BP embryonic viscerocranium morphogenesis
21	4e-07	18 / 121	BP angiogenesis
22	4e-07	7 / 15	MF ephrin receptor binding
23	6e-07	13 / 66	BP sprouting angiogenesis
24	8e-07	14 / 78	BP axon guidance
25	1e-06	8 / 24	BP histone lysine methylation
26	3e-06	10 / 43	BP canonical Wnt signaling pathway
27	3e-06	69 / 1063	MF transferase activity
28	4e-06	7 / 20	BP transmembrane receptor protein serine/threonine kinase signaling pathway
29	5e-06	39 / 491	MF kinase activity
30	6e-06	15 / 104	BP transmembrane receptor protein tyrosine kinase signaling pathway
31	6e-06	7 / 21	BP regulation of canonical Wnt signaling pathway
32	6e-06	7 / 21	MF signal transducer, downstream of receptor, with serine/threonine kinase activity
33	7e-06	10 / 48	BP neural crest cell migration
34	1e-05	40 / 522	BP phosphorylation
35	1e-05	5 / 10	BP adenohypophysis development
36	2e-05	10 / 52	MF transmembrane receptor protein tyrosine kinase activity
37	2e-05	15 / 115	MF chromatin binding
38	2e-05	6 / 17	MF transmembrane receptor protein serine/threonine kinase activity
39	3e-05	9 / 45	BP Notch signaling pathway
40	3e-05	7 / 26	MF Wnt-protein binding



BP				CC				MF			
Rank	p-value	#in/all	Geneset	Rank	p-value	#in/all	Geneset	Rank	p-value	#in/all	Geneset
1	6e-46	54 / 117	nucleosome assembly	1	2e-59	73 / 168	nucleosome	1	3e-50	184 / 1484	DNA binding
2	6e-19	112 / 1239	regulation of transcription, DNA-templated	2	8e-54	78 / 229	chromosome	2	4e-41	67 / 232	protein heterodimerization activity
3	1e-18	61 / 454	multicellular organism development	3	5e-50	260 / 2716	nucleus	3	1e-22	22 / 37	nucleosomal DNA binding
4	2e-13	15 / 34	ephrin receptor signaling pathway	4	1e-04	5 / 15	basement membrane	4	2e-09	50 / 537	sequence-specific DNA binding
5	2e-10	22 / 117	Wnt signaling pathway	5	9e-04	11 / 98	transcription factor complex	5	6e-09	11 / 31	histone-lysine N-methyltransferase activity
6	2e-09	13 / 43	DNA-templated transcription, initiation	6	2e-03	8 / 65	extracellular matrix	6	8e-09	54 / 633	transcription factor activity, sequence-specific DNA binding
7	1e-08	54 / 643	transcription, DNA-templated	7	3e-03	9 / 80	centrosome	7	2e-08	19 / 110	protein tyrosine kinase activity
8	2e-08	18 / 100	peptidyl-tyrosine phosphorylation	8	1e-02	18 / 268	cytoskeleton	8	2e-07	8 / 19	ephrin receptor activity
9	3e-07	15 / 83	embryonic viscerocranium morphogenesis	9	1e-02	29 / 500	extracellular space	9	4e-07	7 / 15	ephrin receptor binding
10	4e-07	18 / 121	angiogenesis	10	1e-02	7 / 70	cell projection	10	3e-06	69 / 1063	transferase activity
11	6e-07	13 / 66	sprouting angiogenesis	11	2e-02	3 / 15	histone acetyltransferase complex	11	5e-06	39 / 491	kinase activity
12	8e-07	14 / 78	axon guidance	12	2e-02	34 / 634	extracellular region	12	6e-06	7 / 21	signal transducer, downstream of receptor, with serine/threonine kinase activity
13	1e-06	8 / 24	histone lysine methylation	13	2e-02	7 / 76	cilium	13	2e-05	10 / 52	transmembrane receptor protein tyrosine kinase activity
14	3e-06	10 / 43	canonical Wnt signaling pathway	14	3e-02	3 / 19	axon	14	2e-05	15 / 115	chromatin binding
15	4e-06	7 / 20	transmembrane receptor protein serine/threonine kinase signaling pathway	15	3e-02	5 / 49	microtubule organizing center	15	2e-05	6 / 17	transmembrane receptor protein serine/threonine kinase activity





BP				CC				MF			
Rank	p-value	#in/all	Geneset	Rank	p-value	#in/all	Geneset	Rank	p-value	#in/all	Geneset
1	6e-05	24 / 329	negative regulation of apoptotic process	1	0.002	12 / 153	cell surface	1	0.003	83 / 2030	nucleic acid binding
2	2e-04	19 / 253	protein autophosphorylation	2	0.046	3 / 27	recycling endosome	2	0.003	16 / 244	receptor binding
3	1e-03	6 / 42	cilium movement	3	0.056	2 / 13	viral nucleocapsid	3	0.007	35 / 751	G-protein coupled receptor activity
4	2e-03	19 / 294	regulation of mitotic cell cycle	4	0.078	5 / 76	cilium	4	0.016	4 / 33	photoreceptor activity
5	2e-03	19 / 297	immune response	5	0.100	2 / 18	motile cilium	5	0.041	2 / 11	solute:proton antiporter activity
6	1e-02	5 / 47	response to lipopolysaccharide	6	0.110	2 / 19	axon	6	0.042	3 / 26	oxidoreductase activity, acting on single donors with incorporation of molecules
7	1e-02	4 / 31	protein-chromophore linkage	7	0.130	2 / 21	axoneme	7	0.043	10 / 178	iron ion binding
8	3e-02	36 / 853	G-protein coupled receptor signaling pathway	8	0.130	2 / 21	dendrite	8	0.049	2 / 12	FMN binding
9	3e-02	4 / 40	regulation of translation	9	0.140	2 / 22	cytoplasmic vesicle membrane	9	0.055	3 / 29	dioxygenase activity
10	3e-02	3 / 24	cerebellum development	10	0.159	3 / 46	collagen trimer	10	0.059	4 / 49	RNA-directed DNA polymerase activity
11	3e-02	2 / 10	chondrocyte differentiation	11	0.161	2 / 24	early endosome	11	0.072	27 / 666	signal transducer activity
12	3e-02	2 / 10	tachykinin receptor signaling pathway	12	0.183	2 / 26	neuronal cell body	12	0.073	2 / 15	adrenergic receptor activity
13	4e-02	2 / 11	induction of positive chemotaxis	13	0.194	2 / 27	postsynapse	13	0.082	2 / 16	tumor necrosis factor receptor binding
14	4e-02	2 / 11	positive regulation of guanylate cyclase activity	14	0.238	2 / 31	photoreceptor outer segment	14	0.088	26 / 652	protein serine/threonine kinase activity
15	4e-02	2 / 11	regulation of pH	15	0.249	2 / 32	cell-cell adherens junction	15	0.097	7 / 130	growth factor activity

# Correlation Cluster

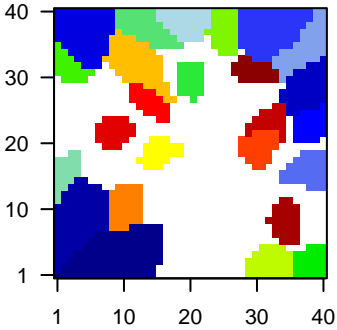
## Spot Summary: I

# metagenes = 42  
# genes = 779

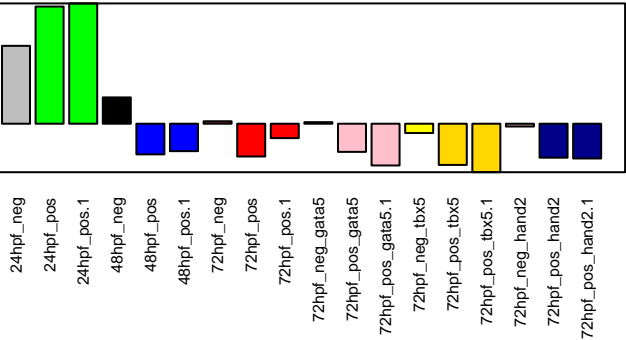
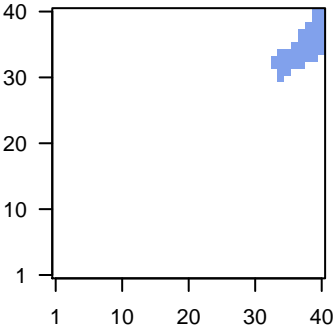
<r> metagenes = 0.97  
<r> genes = 0.64  
beta: r2= 9.35 / log p= -Inf

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

Overview Map



Spot

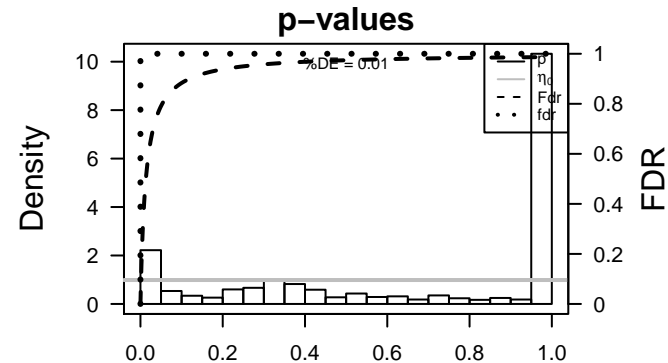


## Spot Genelist

Rank	ID	max e	r	min e	Description	
					Symbol	
1	ENSDARG000	8.12	-6.4	0.79	hbbe3 hemoglobin beta embryonic-3 [Source:ZFIN;Acc:ZDB-GENE-991213-3]	hbbe3
2	ENSDARG000	7.83	-4.49	0.92	drl draculin [Source:ZFIN;Acc:ZDB-GENE-991213-3]	drl
3	ENSDARG000	7.74	-1.79	0.61	LOC100506871-11n16.3 [Source:ZFIN;Acc:ZDB-GENE-131121-8]	LOC100506871-11n16.3
4	ENSDARG000	7.36	-4.55	0.91	si:dkey-261k4.4 [Source:ZFIN;Acc:ZDB-GENE-060531-125]	si:dkey-261k4.4
5	ENSDARG000	7.35	-4.2	0.92	blf bloody fingers [Source:ZFIN;Acc:ZDB-GENE-050721-1]	blf
6	ENSDARG000	7.06	-5.06	0.89	si:dkey-261k4.3 [Source:ZFIN;Acc:ZDB-GENE-060531-124]	si:dkey-261k4.3
7	ENSDARG000	6.46	-4.6	0.68	protogenin homolog b (Gallus gallus) [Source:ZFIN;Acc:ZDB-GENE-041210-336]	protogenin homolog b (Gallus gallus)
8	ENSDARG000	6.43	-3.22	0.95	stab2 stabilin 2 [Source:ZFIN;Acc:ZDB-GENE-041210-336]	stab2
9	ENSDARG000	6.31	-1.79	0.9	ela2l elastase 2 like [Source:ZFIN;Acc:ZDB-GENE-040511-1]	ela2l
10	ENSDARG000	6.11	-4.16	0.94	tfr1a transferrin receptor 1a [Source:ZFIN;Acc:ZDB-GENE-04122	tfr1a
11	ENSDARG000	6	-2.33	0.88	si:ch73-299h12.2 [Source:ZFIN;Acc:ZDB-GENE-081031-7]	si:ch73-299h12.2
12	ENSDARG000	5.97	-3.89	0.88	kif17 Kruppel-like factor 17 [Source:ZFIN;Acc:ZDB-GENE-01012	kif17
13	ENSDARG000	5.89	-1.29	0.58	zgc:174855c:174855 [Source:ZFIN;Acc:ZDB-GENE-071004-74]	zgc:174855c:174855
14	ENSDARG000	5.69	-3.46	0.88	gata1a GATA binding protein 1a [Source:ZFIN;Acc:ZDB-GENE-980	gata1a
15	ENSDARG000	5.69	-3.04	0.86	gfi1b growth factor independent 1B transcription repressor [Source	gfi1b
16	ENSDARG000	5.53	-3.53	0.79		
17	ENSDARG000	5.51	-4.09	0.83	znfl2a zinc finger-like gene 2a [Source:ZFIN;Acc:ZDB-GENE-0308	znfl2a
18	ENSDARG000	5.45	-1.91	0.88	cpox coproporphyrinogen oxidase [Source:ZFIN;Acc:ZDB-GENE-	cpox
19	ENSDARG000	5.42	-2.18	0.89	hmbsb hydroxymethylbilane synthase, b [Source:ZFIN;Acc:ZDB-GEI	hmbsb
20	ENSDARG000	5.39	-4.85	0.84	hdr hematopoietic death receptor [Source:ZFIN;Acc:ZDB-GENE-	hdr

## Geneset Overrepresentation

Rank	p-value	#in/all	Geneset
1	4e-28	31 / 78	BP DNA replication
2	8e-25	170 / 2716	CC nucleus
3	4e-17	14 / 22	BP DNA replication initiation
4	4e-14	14 / 32	BP DNA duplex unwinding
5	5e-14	94 / 1484	MF DNA binding
6	2e-13	10 / 14	CC hemoglobin complex
7	4e-13	25 / 148	BP DNA repair
8	3e-12	21 / 110	BP cell cycle
9	1e-11	29 / 229	CC chromosome
10	1e-11	8 / 10	BP mitotic sister chromatid segregation
11	2e-11	10 / 19	MF oxygen binding
12	2e-11	10 / 19	BP oxygen transport
13	2e-11	10 / 19	MF oxygen transporter activity
14	9e-11	11 / 28	BP embryonic hemopoiesis
15	2e-10	13 / 46	BP mitotic cell cycle
16	7e-10	95 / 1787	MF ATP binding
17	1e-09	13 / 52	BP blood vessel development
18	3e-09	10 / 29	CC kinetochore
19	4e-09	16 / 91	BP cellular response to DNA damage stimulus
20	3e-08	14 / 79	BP cell division
21	1e-07	10 / 40	BP erythrocyte differentiation
22	2e-07	77 / 1506	MF nucleotide binding
23	2e-07	6 / 11	MF DNA helicase activity
24	5e-07	8 / 27	BP chromosome segregation
25	6e-07	12 / 72	MF helicase activity
26	7e-07	9 / 38	BP vasculogenesis
27	1e-06	7 / 22	CC chromosome, centromeric region
28	2e-06	6 / 15	BP heme biosynthetic process
29	2e-06	10 / 54	CC kinesin complex
30	3e-06	7 / 24	BP myeloid cell differentiation
31	4e-06	14 / 115	MF chromatin binding
32	4e-06	11 / 72	BP nucleic acid phosphodiester bond hydrolysis
33	6e-06	5 / 11	MF structural constituent of nuclear pore
34	6e-06	5 / 11	BP thymus development
35	1e-05	17 / 178	MF iron ion binding
36	1e-05	54 / 1063	MF transferase activity
37	2e-05	8 / 42	MF histone binding
38	2e-05	13 / 117	BP nucleosome assembly
39	2e-05	9 / 57	BP microtubule cytoskeleton organization
40	3e-05	5 / 14	CC condensed chromosome kinetochore



BP

Rank

p-value

#in/all

Geneset

1

4e-28

31 / 78

DNA replication

2

4e-17

14 / 22

DNA replication initiation

3

4e-14

14 / 32

DNA duplex unwinding

4

4e-13

25 / 148

DNA repair

5

3e-12

21 / 110

cell cycle

6

1e-11

8 / 10

mitotic sister chromatid segregation

7

2e-11

10 / 19

oxygen transport

8

9e-11

11 / 28

embryonic hemopoiesis

9

2e-10

13 / 46

mitotic cell cycle

10

1e-09

13 / 52

blood vessel development

11

4e-09

16 / 91

cellular response to DNA damage stimulus

12

3e-08

14 / 79

cell division

13

1e-07

10 / 40

erythrocyte differentiation

14

5e-07

8 / 27

chromosome segregation

15

7e-07

9 / 38

vasculogenesis

CC

Rank

p-value

#in/all

Geneset

1

8e-25

170 / 2716

nucleus

2

2e-13

10 / 14

hemoglobin complex

3

1e-11

29 / 229

chromosome

4

3e-09

10 / 29

kinetochore

5

1e-06

7 / 22

chromosome, centromeric region

6

2e-06

10 / 54

kinesin complex

7

3e-05

5 / 14

condensed chromosome kinetochore

8

5e-05

12 / 108

microtubule

9

6e-05

6 / 26

nuclear pore

10

7e-05

15 / 168

nucleosome

11

2e-04

19 / 268

cytoskeleton

12

2e-04

4 / 12

mitotic spindle

13

4e-04

9 / 80

centrosome

14

2e-03

3 / 10

anaphase-promoting complex

15

3e-03

4 / 23

small-subunit processome

MF

Rank

p-value

#in/all

Geneset

1

5e-14

94 / 1484

DNA binding

2

2e-11

10 / 19

oxygen binding

3

2e-11

10 / 19

oxygen transporter activity

4

7e-10

95 / 1787

ATP binding

5

2e-07

77 / 1506

nucleotide binding

6

2e-07

6 / 11

DNA helicase activity

7

6e-07

12 / 72

helicase activity

8

4e-06

14 / 115

chromatin binding

9

6e-06

5 / 11

structural constituent of nuclear pore

10

1e-05

17 / 178

iron ion binding

11

1e-05

54 / 1063

transferase activity

12

2e-05

8 / 42

histone binding

13

3e-05

13 / 120

motor activity

14

3e-05

15 / 158

microtubule binding

15

4e-05

8 / 47

structural constituent of cytoskeleton

# Correlation Cluster

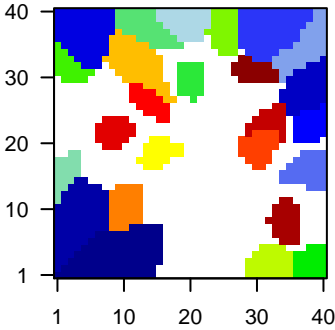
## Spot Summary: J

# metagenes = 23  
# genes = 445

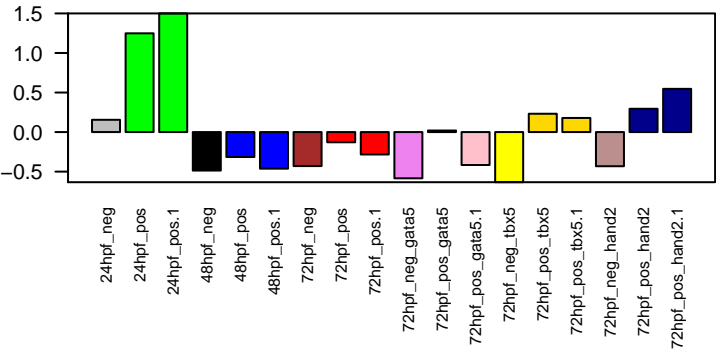
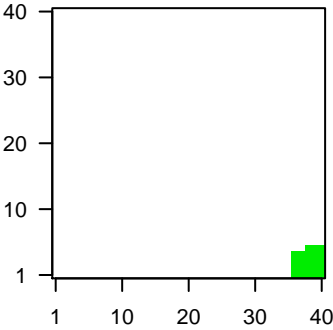
<r> metagenes = 0.95  
<r> genes = 0.56  
beta: r2= 5.48 / log p= -Inf

# samples with spot = 3 ( 16.7 %)  
24hpf\_pos : 2 ( 100 %)  
72hpf\_pos\_hand2 : 1 ( 50 %)

Overview Map



Spot

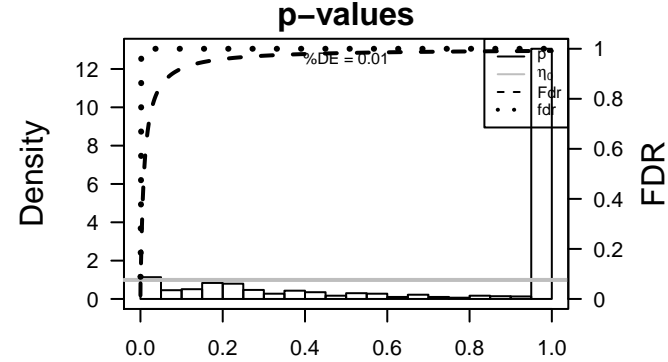


## Spot Genelist

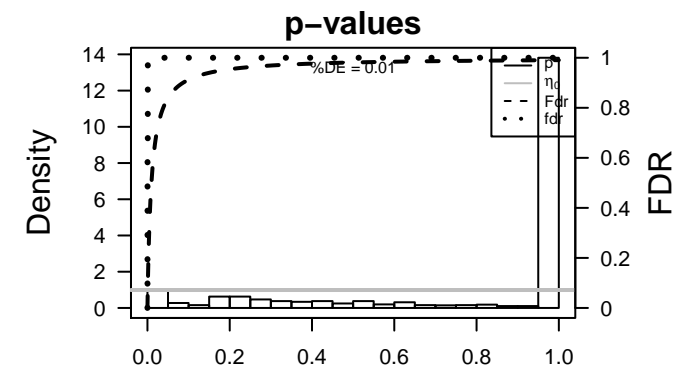
Rank	ID	max e	r	min e	Description
					Symbol
1	ENSDARG000	8.47	-3.84	0.36	
2	ENSDARG000	8.19	-3.48	0.33	
3	ENSDARG000	8.13	-3.52	0.32	
4	ENSDARG000	8.08	-3.28	0.28	
5	ENSDARG000	6.87	-3.45	0.32	
6	ENSDARG000	5.93	-1.57	0.79	cyp7a1b
7	ENSDARG000	5.27	-3.73	0.37	
8	ENSDARG000	5.09	-3.4	0.37	
9	ENSDARG000	4.13	-2.81	0.91	mrc1a mannose receptor, C type 1a [Source:ZFIN;Acc:ZDB-GENE-
10	ENSDARG000	4.07	-2.7	0.43	
11	ENSDARG000	3.95	-1.46	0.32	zgc:158463 [Source:ZFIN;Acc:ZDB-GENE-070410-9]
12	ENSDARG000	3.89	-1.94	0.78	nkx2.7 NK2 transcription factor related 7 [Source:ZFIN;Acc:ZDB-GE
13	ENSDARG000	3.75	-3.16	0.84	dnase1l4deoxyribonuclease 1 like 4, tandem duplicate 1 [Source:ZFIN
14	ENSDARG000	3.73	-2.69	0.21	
15	ENSDARG000	3.53	-3.11	0.86	ikzf1 IKAROS family zinc finger 1 (Ikaros) [Source:ZFIN;Acc:ZDB-
16	ENSDARG000	3.47	-3.88	0.77	il6r interleukin 6 receptor [Source:ZFIN;Acc:ZDB-GENE-080107
17	ENSDARG000	3.44	-2.62	0.83	
18	ENSDARG000	3.38	-2.19	0.85	ampd3b adenosine monophosphate deaminase 3b [Source:ZFIN;Acc:
19	ENSDARG000	3.36	-3.58	0.73	slc25a37 solute carrier family 25 (mitochondrial iron transporter), memt
20	ENSDARG000	3.36	-1.95	0.83	slc29a1b solute carrier family 29 (equilibrative nucleoside transporter),

## Geneset Overrepresentation

Rank	p-value	#in/all	Geneset
1	9e-06	5 / 19	BP maturation of SSU-rRNA from tricistronic rRNA transcript (SSU-rRNA, 5.8
2	2e-04	5 / 33	BP blood coagulation
3	3e-04	5 / 38	BP integrin-mediated signaling pathway
4	4e-04	16 / 375	BP positive regulation of GTPase activity
5	4e-04	4 / 22	BP transcription from RNA polymerase III promoter
6	4e-04	4 / 22	MF tRNA binding
7	4e-04	9 / 140	CC nucleolus
8	5e-04	4 / 24	BP cerebellum development
9	6e-04	5 / 43	BP ribosome biogenesis
10	6e-04	6 / 65	BP endocytosis
11	6e-04	3 / 11	BP spindle organization
12	1e-03	23 / 712	BP oxidation-reduction process
13	1e-03	5 / 51	BP camera-type eye development
14	1e-03	3 / 14	BP formation of translation preinitiation complex
15	2e-03	3 / 15	MF RNA polymerase III activity
16	2e-03	3 / 16	BP iron-sulfur cluster assembly
17	2e-03	6 / 83	BP embryonic viscerocranium morphogenesis
18	3e-03	10 / 217	MF GTPase activator activity
19	3e-03	3 / 18	CC DNA-directed RNA polymerase III complex
20	3e-03	4 / 37	MF DNA-directed 5'-3' RNA polymerase activity
21	5e-03	3 / 22	MF metalloaminopeptidase activity
22	6e-03	3 / 23	CC small-subunit processome
23	6e-03	7 / 135	MF methyltransferase activity
24	7e-03	14 / 413	BP intracellular signal transduction
25	8e-03	3 / 26	BP positive regulation of catalytic activity
26	8e-03	4 / 50	MF translation initiation factor activity
27	8e-03	7 / 144	BP methylation
28	9e-03	4 / 51	BP tRNA processing
29	9e-03	3 / 27	MF cytokine receptor activity
30	1e-02	3 / 28	BP embryonic hemopoiesis
31	1e-02	2 / 10	CC eukaryotic 43S preinitiation complex
32	1e-02	2 / 10	MF GDP-dissociation inhibitor activity
33	1e-02	2 / 10	MF GTPase regulator activity
34	1e-02	3 / 29	CC integrin complex
35	1e-02	4 / 55	BP translational initiation
36	1e-02	9 / 231	MF actin binding
37	1e-02	6 / 120	MF protein tyrosine phosphatase activity
38	1e-02	2 / 11	BP actin polymerization or depolymerization
39	1e-02	2 / 11	MF deaminase activity
40	1e-02	2 / 11	BP regulation of translational initiation



BP				CC				MF			
Rank	p-value	#in/all	Geneset	Rank	p-value	#in/all	Geneset	Rank	p-value	#in/all	Geneset
1	9e-06	5 / 19	maturation of SSU-rRNA from tricistronic rRNA transcript (SSU-rRNA, 5.8S r	1	4e-04	9 / 140	nucleolus	1	4e-04	4 / 22	tRNA binding
2	2e-04	5 / 33	blood coagulation	2	3e-03	3 / 18	DNA-directed RNA polymerase III complex	2	2e-03	3 / 15	RNA polymerase III activity
3	3e-04	5 / 38	integrin-mediated signaling pathway	3	6e-03	3 / 23	small-subunit processome	3	3e-03	10 / 217	GTPase activator activity
4	4e-04	16 / 375	positive regulation of GTPase activity	4	1e-02	2 / 10	eukaryotic 43S preinitiation complex	4	3e-03	4 / 37	DNA-directed 5'-3' RNA polymerase activity
5	4e-04	4 / 22	transcription from RNA polymerase III promoter	5	1e-02	3 / 29	integrin complex	5	5e-03	3 / 22	metalloaminopeptidase activity
6	5e-04	4 / 24	cerebellum development	6	1e-02	2 / 12	eukaryotic 48S preinitiation complex	6	6e-03	7 / 135	methyltransferase activity
7	6e-04	5 / 43	ribosome biogenesis	7	3e-02	2 / 18	eukaryotic translation initiation factor 3 complex	7	8e-03	4 / 50	translation initiation factor activity
8	6e-04	6 / 65	endocytosis	8	4e-02	2 / 19	extrinsic component of membrane	8	9e-03	3 / 27	cytokine receptor activity
9	6e-04	3 / 11	spindle organization	9	4e-02	3 / 46	mitochondrial matrix	9	1e-02	2 / 10	GDP-dissociation inhibitor activity
10	1e-03	23 / 712	oxidation-reduction process	10	4e-02	7 / 198	Golgi membrane	10	1e-02	2 / 10	GTPase regulator activity
11	1e-03	5 / 51	camera-type eye development	11	5e-02	122 / 6723	membrane	11	1e-02	9 / 231	actin binding
12	1e-03	3 / 14	formation of translation preinitiation complex	12	6e-02	113 / 6248	integral component of membrane	12	1e-02	6 / 120	protein tyrosine phosphatase activity
13	2e-03	3 / 16	iron-sulfur cluster assembly	13	7e-02	9 / 317	Golgi apparatus	13	1e-02	2 / 11	deaminase activity
14	2e-03	6 / 83	embryonic viscerocranium morphogenesis	14	8e-02	4 / 101	endosome	14	1e-02	2 / 11	thrombin-activated receptor activity
15	7e-03	14 / 413	intracellular signal transduction	15	1e-01	5 / 153	cell surface	15	2e-02	2 / 13	signal transducer activity, downstream of receptor



BP				CC				MF			
Rank	p-value	#in/all	Geneset	Rank	p-value	#in/all	Geneset	Rank	p-value	#in/all	Geneset
1	9e-09	7 / 16	ribosomal large subunit biogenesis	1	3e-13	21 / 140	nucleolus	1	3e-06	69 / 2030	nucleic acid binding
2	2e-07	9 / 45	rRNA processing	2	9e-04	4 / 23	small-subunit processome	2	4e-05	8 / 66	ligase activity
3	1e-06	5 / 11	maturation of SSU-rRNA	3	1e-03	18 / 410	mitochondrion	3	5e-05	7 / 50	translation initiation factor activity
4	2e-05	7 / 43	ribosome biogenesis	4	3e-03	3 / 16	preribosome, large subunit precursor	4	5e-05	5 / 22	tRNA binding
5	2e-05	15 / 214	translation	5	5e-03	3 / 18	eukaryotic translation initiation factor 3 complex	5	1e-04	6 / 41	aminoacyl-tRNA ligase activity
6	5e-05	7 / 51	tRNA processing	6	9e-03	44 / 1580	cellular_component	6	8e-04	3 / 10	snoRNA binding
7	8e-05	7 / 55	translational initiation	7	1e-02	8 / 161	mitochondrial inner membrane	7	1e-03	3 / 12	pseudouridine synthase activity
8	2e-04	4 / 15	pseudouridine synthesis	8	1e-02	4 / 49	nucleoplasm	8	2e-03	4 / 30	damaged DNA binding
9	1e-03	3 / 12	ubiquinone biosynthetic process	9	1e-02	2 / 10	nuclear chromosome, telomeric region	9	3e-03	34 / 1063	transferase activity
10	2e-03	3 / 13	RNA modification	10	2e-02	2 / 12	eukaryotic 48S preinitiation complex	10	5e-03	8 / 135	methyltransferase activity
11	2e-03	9 / 144	methylation	11	2e-02	2 / 13	proteasome regulatory particle, base subcomplex	11	5e-03	4 / 36	endonuclease activity
12	7e-03	4 / 40	tRNA aminoacylation for protein translation	12	4e-02	54 / 2189	cytoplasm	12	5e-03	3 / 19	phosphotransferase activity, alcohol group as acceptor
13	8e-03	8 / 148	DNA repair	13	5e-02	2 / 18	DNA-directed RNA polymerase III complex	13	6e-03	18 / 480	catalytic activity
14	8e-03	3 / 22	protein N-linked glycosylation	14	5e-02	4 / 71	endomembrane system	14	7e-03	43 / 1506	nucleotide binding
15	1e-02	2 / 10	otolith morphogenesis	15	6e-02	3 / 46	mitochondrial matrix	15	9e-03	6 / 92	magnesium ion binding



# Correlation Cluster

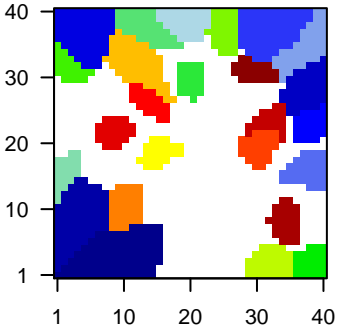
## Spot Summary: L

# metagenes = 26  
# genes = 383

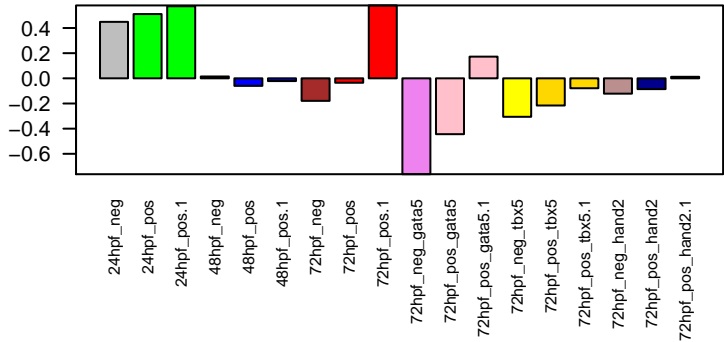
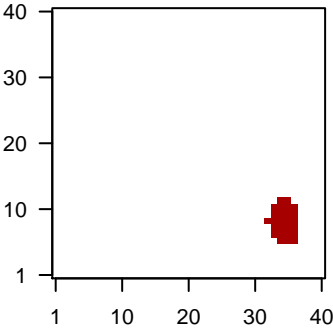
<r> metagenes = 0.93  
<r> genes = 0.47  
beta: r2= 1.9 / log p= -Inf

# samples with spot = 2 ( 11.1 %)  
24hpf\_pos : 1 ( 50 %)  
72hpf\_pos : 1 ( 50 %)

Overview Map



Spot

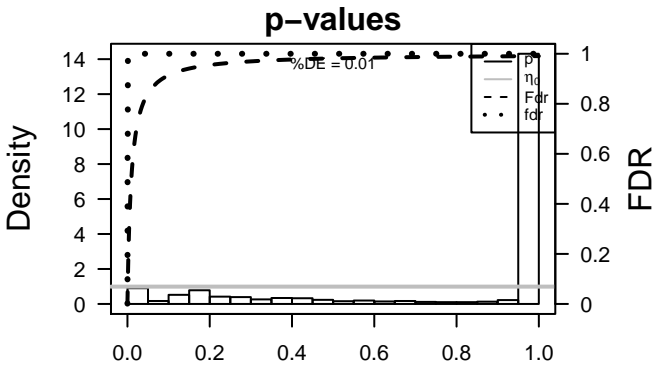


## Spot Genelist

Rank	ID	max e	r	Description	
		min e		Symbol	
1	ENSDARG000	1.71	-1.55	0.8	protein O-glucosyltransferase 1 [Source:ZFIN;Acc:ZDB-GENE-110131-2]
2	ENSDARG000	1.63	-0.7	0.83	ccm2l cerebral cavernous malformation 2-like [Source:ZFIN;Acc:ZDB-GENE-110131-2]
3	ENSDARG000	1.61	-1.64	0.73	si:dkey-11g8.3 [Source:ZFIN;Acc:ZDB-GENE-110131-2]
4	ENSDARG000	1.56	-0.73	0.5	si:dkey-253d23.12 [Source:ZFIN;Acc:ZDB-GENE-070912-4]
5	ENSDARG000	1.54	-1.14	0.83	si:dkey-55d23.12 [Source:ZFIN;Acc:ZDB-GENE-070912-4]
6	ENSDARG000	1.52	-3.06	0.95	rfc2 replication factor C (activator 1) 2 [Source:ZFIN;Acc:ZDB-GENE-110131-2]
7	ENSDARG000	1.5	-0.57	0.49	endou2 endonuclease, polyU-specific 2 [Source:ZFIN;Acc:ZDB-GENE-110131-2]
8	ENSDARG000	1.48	-1.15	0.55	tnnt2c troponin T2c, cardiac [Source:ZFIN;Acc:ZDB-GENE-030520]
9	ENSDARG000	1.45	-0.33	0.53	si:ch211-261i17.2 [Source:ZFIN;Acc:ZDB-GENE-160113-1]
10	ENSDARG000	1.44	-0.71	0.74	si:dkey-55d23.12 [Source:ZFIN;Acc:ZDB-GENE-070912-4]
11	ENSDARG000	1.44	-1.1	0.78	ogmb oligodendrocyte myelin glycoprotein b [Source:ZFIN;Acc:ZDB-GENE-110131-2]
12	ENSDARG000	1.44	-1.6	0.62	trmt10c tRNA methyltransferase 10C, mitochondrial RNase P subunit [Source:ZFIN;Acc:ZDB-GENE-110131-2]
13	ENSDARG000	1.44	-1.59	0.62	bcl7bb B-cell CLL/lymphoma 7B, b [Source:ZFIN;Acc:ZDB-GENE-110131-2]
14	ENSDARG000	1.43	-0.77	0.52	si:ch211-52g16.11 [Source:ZFIN;Acc:ZDB-GENE-081105-1]
15	ENSDARG000	1.42	-0.69	0.72	capn3a calpain 3a, (p94) [Source:ZFIN;Acc:ZDB-GENE-040912-97]
16	ENSDARG000	1.41	-1.27	0.84	ddx24 DEAD (Asp-Glu-Ala-Asp) box helicase 24 [Source:ZFIN;Acc:ZDB-GENE-110131-2]
17	ENSDARG000	1.41	-1.02	0.7	npri3 NPR3-like, GATOR1 complex subunit [Source:ZFIN;Acc:ZDB-GENE-110131-2]
18	ENSDARG000	1.4	-1.23	0.5	si:dkey-55d23.12 [Source:ZFIN;Acc:ZDB-GENE-070912-4]
19	ENSDARG000	1.39	-1.24	0.79	fastkd5 FAST kinase domains 5 [Source:ZFIN;Acc:ZDB-GENE-111105-1]
20	ENSDARG000	1.38	-0.99	0.56	si:ch211-245n8.4 [Source:ZFIN;Acc:ZDB-GENE-110914-5]

## Geneset Overrepresentation

Rank	p-value	#in/all	Geneset
1	3e-12	68 / 2030	MF nucleic acid binding
2	9e-07	12 / 148	BP DNA repair
3	3e-06	11 / 140	CC nucleolus
4	8e-06	64 / 2716	CC nucleus
5	3e-05	30 / 969	MF hydrolase activity
6	3e-05	22 / 608	MF RNA binding
7	4e-05	4 / 15	BP tRNA methylation
8	5e-05	7 / 70	BP RNA processing
9	5e-05	4 / 16	CC preribosome, large subunit precursor
10	6e-05	6 / 51	BP tRNA processing
11	9e-05	7 / 78	BP DNA replication
12	1e-04	5 / 37	MF thiol-dependent ubiquitin-specific protease activity
13	2e-04	7 / 88	BP mRNA processing
14	3e-04	5 / 43	CC proteasome complex
15	7e-04	6 / 79	BP mRNA splicing, via spliceosome
16	1e-03	4 / 34	CC catalytic step 2 spliceosome
17	1e-03	13 / 355	CC cytosol
18	1e-03	3 / 16	BP protein sumoylation
19	1e-03	3 / 16	BP ribosomal large subunit biogenesis
20	1e-03	4 / 36	MF endopeptidase activity
21	2e-03	14 / 410	CC mitochondrion
22	2e-03	3 / 18	BP base-excision repair
23	2e-03	4 / 42	CC spliceosomal complex
24	3e-03	3 / 21	CC nuclear membrane
25	3e-03	5 / 72	MF helicase activity
26	3e-03	21 / 800	MF zinc ion binding
27	3e-03	4 / 46	MF ATP-dependent RNA helicase activity
28	4e-03	3 / 24	CC precatlytic spliceosome
29	6e-03	3 / 28	MF hydrolase activity, acting on ester bonds
30	8e-03	2 / 10	BP nuclear-transcribed mRNA catabolic process
31	8e-03	4 / 58	BP RNA splicing
32	8e-03	3 / 31	MF ubiquitin binding
33	9e-03	2 / 11	BP cellular metabolic process
34	9e-03	2 / 11	CC commitment complex
35	9e-03	2 / 11	BP DNA-dependent DNA replication
36	9e-03	2 / 11	BP positive regulation of protein ubiquitination
37	1e-02	6 / 135	MF methyltransferase activity
38	1e-02	4 / 64	CC Cul3-RING ubiquitin ligase complex
39	1e-02	2 / 13	BP NLS-bearing protein import into nucleus
40	1e-02	2 / 13	CC U5 snRNP



BP				CC				MF			
Rank	p-value	#in/all	Geneset	Rank	p-value	#in/all	Geneset	Rank	p-value	#in/all	Geneset
1	9e-07	12 / 148	DNA repair	1	3e-06	11 / 140	nucleolus	1	3e-12	68 / 2030	nucleic acid binding
2	4e-05	4 / 15	tRNA methylation	2	8e-06	64 / 2716	nucleus	2	3e-05	30 / 969	hydrolase activity
3	5e-05	7 / 70	RNA processing	3	5e-05	4 / 16	preribosome, large subunit precursor	3	3e-05	22 / 608	RNA binding
4	6e-05	6 / 51	tRNA processing	4	3e-04	5 / 43	proteasome complex	4	1e-04	5 / 37	thiol-dependent ubiquitin-specific protease activity
5	9e-05	7 / 78	DNA replication	5	1e-03	4 / 34	catalytic step 2 spliceosome	5	1e-03	4 / 36	endopeptidase activity
6	2e-04	7 / 88	mRNA processing	6	1e-03	13 / 355	cytosol	6	3e-03	5 / 72	helicase activity
7	7e-04	6 / 79	mRNA splicing, via spliceosome	7	2e-03	14 / 410	mitochondrion	7	3e-03	21 / 800	zinc ion binding
8	1e-03	3 / 16	protein sumoylation	8	2e-03	4 / 42	spliceosomal complex	8	3e-03	4 / 46	ATP-dependent RNA helicase activity
9	1e-03	3 / 16	ribosomal large subunit biogenesis	9	3e-03	3 / 21	nuclear membrane	9	6e-03	3 / 28	hydrolase activity, acting on ester bonds
10	2e-03	3 / 18	base-excision repair	10	4e-03	3 / 24	precatalytic spliceosome	10	8e-03	3 / 31	ubiquitin binding
11	8e-03	2 / 10	nuclear-transcribed mRNA catabolic process	11	9e-03	2 / 11	commitment complex	11	1e-02	6 / 135	methyltransferase activity
12	8e-03	4 / 58	RNA splicing	12	1e-02	4 / 64	Cul3-RING ubiquitin ligase complex	12	1e-02	2 / 14	single-stranded RNA binding
13	9e-03	2 / 11	cellular metabolic process	13	1e-02	2 / 13	U5 snRNP	13	2e-02	3 / 39	single-stranded DNA binding
14	9e-03	2 / 11	DNA-dependent DNA replication	14	1e-02	2 / 14	U12-type spliceosomal complex	14	2e-02	2 / 15	cyclin-dependent protein serine/threonine kinase activity
15	9e-03	2 / 11	positive regulation of protein ubiquitination	15	2e-02	2 / 18	U4/U6 x U5 tri-snRNP complex	15	2e-02	5 / 115	chromatin binding



BP				CC				MF			
Rank	p-value	#in/all	Geneset	Rank	p-value	#in/all	Geneset	Rank	p-value	#in/all	Geneset
1	2e-04	6 / 79	mRNA splicing, via spliceosome	1	0.004	4 / 64	Cul3-RING ubiquitin ligase complex	1	0.001	36 / 2030	nucleic acid binding
2	1e-03	4 / 45	Notch signaling pathway	2	0.006	3 / 36	P-body	2	0.002	4 / 49	RNA-directed DNA polymerase activity
3	1e-03	3 / 21	smoothened signaling pathway	3	0.032	2 / 27	mediator complex	3	0.003	15 / 633	transcription factor activity, sequence-specific DNA binding
4	1e-03	11 / 362	regulation of transcription from RNA polymerase II promoter	4	0.035	38 / 2716	nucleus	4	0.003	7 / 183	RNA polymerase II transcription factor activity, sequence-specific DNA binding
5	2e-03	4 / 48	RNA-dependent DNA biosynthetic process	5	0.036	3 / 70	myosin complex	5	0.007	2 / 12	acetylgalactosaminyltransferase activity
6	5e-03	2 / 10	tRNA aminoacylation	6	0.051	2 / 35	Golgi cisterna membrane	6	0.008	3 / 39	hydrolase activity, hydrolyzing O-glycosyl compounds
7	5e-03	23 / 1239	regulation of transcription, DNA-templated	7	0.061	6 / 268	cytoskeleton	7	0.010	4 / 80	transcription regulatory region DNA binding
8	6e-03	3 / 35	positive regulation of proteasomal ubiquitin-dependent protein catabolic process	8	0.070	2 / 42	spliceosomal complex	8	0.013	3 / 48	transcription factor binding
9	8e-03	14 / 643	transcription, DNA-templated	9	0.071	30 / 2189	cytoplasm	9	0.022	2 / 22	tRNA binding
10	8e-03	2 / 13	RNA methylation	10	0.079	2 / 45	ubiquitin ligase complex	10	0.026	6 / 217	GTPase activator activity
11	1e-02	2 / 15	RNA phosphodiester bond hydrolysis, exonucleolytic	11	0.099	1 / 10	ER membrane protein complex	11	0.029	3 / 64	hydrolase activity, acting on glycosyl bonds
12	1e-02	2 / 16	negative regulation of translation	12	0.099	1 / 10	nuclear chromosome, telomeric region	12	0.029	18 / 1063	transferase activity
13	1e-02	2 / 16	regulation of small GTPase mediated signal transduction	13	0.099	1 / 10	phosphatidylinositol 3-kinase complex	13	0.029	2 / 26	RNA polymerase II transcription cofactor activity
14	2e-02	9 / 375	positive regulation of GTPase activity	14	0.108	1 / 11	membrane attack complex	14	0.034	6 / 231	actin binding
15	2e-02	7 / 257	cell differentiation	15	0.117	1 / 12	transcription factor TFIID complex	15	0.036	2 / 29	3',5'-cyclic-nucleotide phosphodiesterase activity

# Correlation Cluster

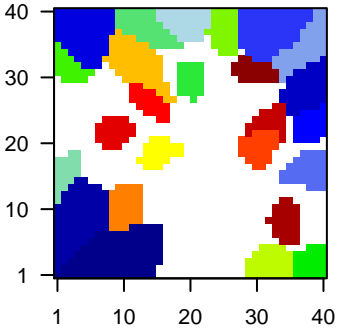
## Spot Summary: N

# metagenes = 24  
# genes = 452

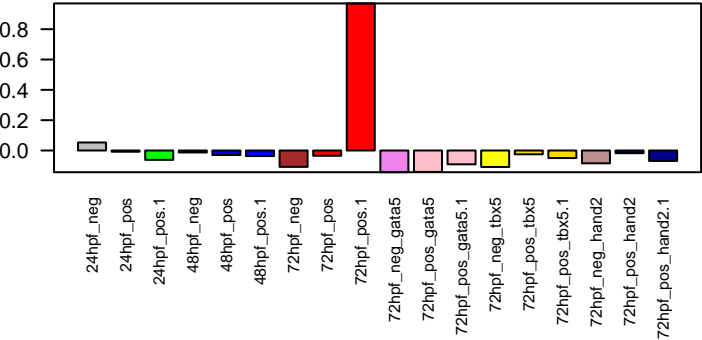
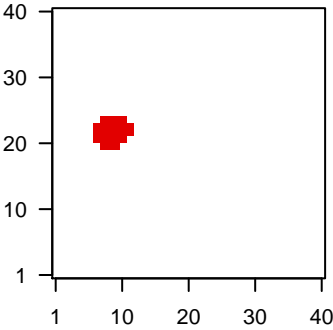
<r> metagenes = 0.92  
<r> genes = 0.53  
beta: r2= 0.85 / log p= -7.23

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

Overview Map



Spot

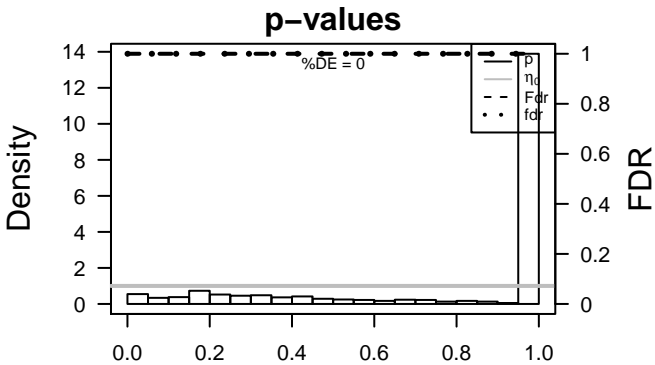


## Spot Genelist

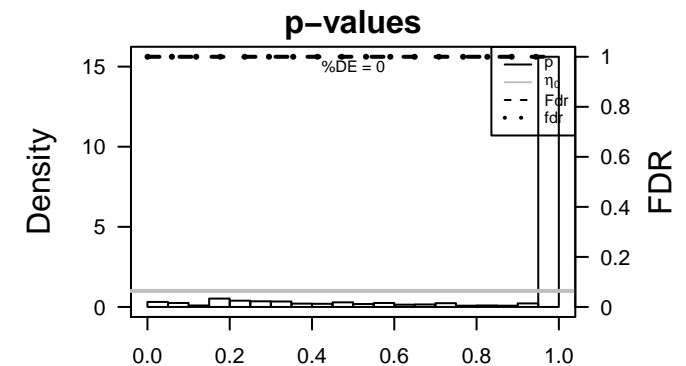
Rank	ID	max e	r	min e	Description
1	ENSDARG0000000001	5.69	-0.44	0.98	slc28a1 solute carrier family 28 (concentrative nucleoside transporter)
2	ENSDARG0000000002	2.21	-0.29	0.91	si:ch211-167j6.4 [Source:ZFIN;Acc:ZDB-GENE-070912-14]
3	ENSDARG0000000003	1.98	-2.35	0.42	pmela premelanosome protein a [Source:ZFIN;Acc:ZDB-GENE-031121-11]
4	ENSDARG0000000004	1.92	-0.81	0.72	si:ch73-15b2185c24.2 [Source:ZFIN;Acc:ZDB-GENE-131121-11]
5	ENSDARG0000000005	1.84	-1.26	0.65	ryr1b ryanodine receptor 1b (skeletal) [Source:ZFIN;Acc:ZDB-GENE-031121-11]
6	ENSDARG0000000006	1.82	-1.3	0.58	dopachrome tautomerase [Source:ZFIN;Acc:ZDB-GENE-0000000006]
7	ENSDARG0000000007	1.72	-0.7	0.74	ankrd1b ankyrin repeat domain 1b (cardiac muscle) [Source:ZFIN;Acc:ZDB-GENE-031121-11]
8	ENSDARG0000000008	1.67	-0.6	0.77	si:ch211-24o8.4 [Source:ZFIN;Acc:ZDB-GENE-141212-25]
9	ENSDARG0000000009	1.66	-0.9	0.78	pex2 peroxisomal biogenesis factor 2 [Source:ZFIN;Acc:ZDB-GENE-031121-11]
10	ENSDARG0000000010	1.66	-0.89	0.76	si:key-62k3.5 [Source:ZFIN;Acc:ZDB-GENE-160727-7]
11	ENSDARG0000000011	1.64	-0.69	0.65	pdx1 pancreatic and duodenal homeobox 1 [Source:ZFIN;Acc:ZDB-GENE-031121-11]
12	ENSDARG0000000012	1.62	-0.77	0.62	hoxd9a homeobox D9a [Source:ZFIN;Acc:ZDB-GENE-990415-121]
13	ENSDARG0000000013	1.61	-0.53	0.79	si:ch73-15b2185c24.2 [Source:ZFIN;Acc:ZDB-GENE-030131-540]
14	ENSDARG0000000014	1.61	-0.65	0.76	tgm2a transglutaminase 2, C polypeptide A [Source:ZFIN;Acc:ZDB-GENE-031121-11]
15	ENSDARG0000000015	1.6	-0.46	0.87	si:ch211-218k8.1 [Source:ZFIN;Acc:ZDB-GENE-141215-9]
16	ENSDARG0000000016	1.6	-0.44	0.68	gdpd3b glycerophosphodiester phosphodiesterase domain containing
17	ENSDARG0000000017	1.58	-0.47	0.85	
18	ENSDARG0000000018	1.58	-1.29	0.58	pmelb premelanosome protein b [Source:ZFIN;Acc:ZDB-GENE-051121-11]
19	ENSDARG0000000019	1.57	-0.46	0.78	
20	ENSDARG0000000020	1.57	-0.39	0.8	tripartite motif containing 35-13 [Source:ZFIN;Acc:ZDB-GENE-031121-11]

## Geneset Overrepresentation

Rank	p-value	#in/all	Geneset
1	3e-05	145 / 6723	CC membrane
2	2e-04	133 / 6248	CC integral component of membrane
3	2e-03	5 / 53	BP chemotaxis
4	3e-03	4 / 39	MF hydrolase activity, hydrolyzing O-glycosyl compounds
5	4e-03	3 / 20	BP regulation of molecular function
6	7e-03	18 / 591	BP transmembrane transport
7	9e-03	3 / 27	BP developmental pigmentation
8	1e-02	7 / 147	BP potassium ion transmembrane transport
9	1e-02	2 / 10	CC melanosome
10	1e-02	2 / 10	BP outer dynein arm assembly
11	1e-02	22 / 809	CC integral component of plasma membrane
12	1e-02	6 / 119	MF serine-type peptidase activity
13	1e-02	2 / 11	BP melanosome organization
14	1e-02	4 / 58	BP chemokine-mediated signaling pathway
15	2e-02	2 / 12	MF calcium-activated potassium channel activity
16	2e-02	2 / 12	BP skeletal muscle cell differentiation
17	2e-02	15 / 499	BP ion transport
18	2e-02	2 / 13	BP cellular response to oxidative stress
19	2e-02	2 / 13	BP glycolipid biosynthetic process
20	2e-02	2 / 14	BP posterior lateral line neuromast development
21	2e-02	3 / 39	CC connexin complex
22	3e-02	3 / 42	BP cilium movement
23	3e-02	3 / 43	BP negative regulation of cell proliferation
24	3e-02	3 / 43	BP notochord development
25	3e-02	8 / 229	MF transporter activity
26	3e-02	4 / 75	BP calcium ion transport
27	3e-02	2 / 18	BP intra-Golgi vesicle-mediated transport
28	3e-02	2 / 18	MF steroid binding
29	3e-02	3 / 44	CC gap junction
30	3e-02	3 / 44	BP regulation of membrane potential
31	3e-02	20 / 800	MF zinc ion binding
32	3e-02	7 / 191	MF serine-type endopeptidase activity
33	4e-02	2 / 19	BP release of sequestered calcium ion into cytosol
34	4e-02	2 / 20	BP G-protein coupled receptor signaling pathway, coupled to cyclic nucleotide
35	4e-02	2 / 20	BP retrograde vesicle-mediated transport, Golgi to ER
36	4e-02	6 / 159	MF structural molecule activity
37	4e-02	2 / 21	MF dynein light chain binding
38	4e-02	2 / 21	CC membrane coat
39	4e-02	25 / 1084	BP transport
40	5e-02	5 / 122	BP inflammatory response



BP				CC				MF			
Rank	p-value	#in/all	Geneset	Rank	p-value	#in/all	Geneset	Rank	p-value	#in/all	Geneset
1	0.002	5 / 53	chemotaxis	1	3e-05	145 / 6723	membrane	1	0.003	4 / 39	hydrolase activity, hydrolyzing O-glycosyl compounds
2	0.004	3 / 20	regulation of molecular function	2	2e-04	133 / 6248	integral component of membrane	2	0.012	6 / 119	serine-type peptidase activity
3	0.007	18 / 591	transmembrane transport	3	1e-02	2 / 10	melanosome	3	0.015	2 / 12	calcium-activated potassium channel activity
4	0.009	3 / 27	developmental pigmentation	4	1e-02	22 / 809	integral component of plasma membrane	4	0.032	8 / 229	transporter activity
5	0.010	7 / 147	potassium ion transmembrane transport	5	2e-02	3 / 39	connexin complex	5	0.033	2 / 18	steroid binding
6	0.011	2 / 10	outer dynein arm assembly	6	3e-02	3 / 44	gap junction	6	0.034	20 / 800	zinc ion binding
7	0.013	2 / 11	melanosome organization	7	4e-02	2 / 21	membrane coat	7	0.035	7 / 191	serine-type endopeptidase activity
8	0.014	4 / 58	chemokine-mediated signaling pathway	8	6e-02	7 / 219	cell junction	8	0.043	6 / 159	structural molecule activity
9	0.015	2 / 12	skeletal muscle cell differentiation	9	7e-02	3 / 59	intracellular membrane-bounded organelle	9	0.044	2 / 21	dynein light chain binding
10	0.015	15 / 499	ion transport	10	9e-02	2 / 31	photoreceptor outer segment	10	0.048	4 / 85	cytokine activity
11	0.018	2 / 13	cellular response to oxidative stress	11	1e-01	2 / 33	voltage-gated calcium channel complex	11	0.048	2 / 22	chemokine receptor activity
12	0.018	2 / 13	glycolipid biosynthetic process	12	1e-01	3 / 71	bicellular tight junction	12	0.056	3 / 54	transferase activity, transferring hexosyl groups
13	0.020	2 / 14	posterior lateral line neuromast development	13	1e-01	2 / 39	Z disc	13	0.058	5 / 130	growth factor activity
14	0.030	3 / 42	cilium movement	14	1e-01	1 / 10	sarcoplasmic reticulum	14	0.061	3 / 56	symporter activity
15	0.031	3 / 43	negative regulation of cell proliferation	15	2e-01	1 / 11	exocytic vesicle	15	0.065	2 / 26	neuropeptide binding



BP				CC				MF			
Rank	p-value	#in/all	Geneset	Rank	p-value	#in/all	Geneset	Rank	p-value	#in/all	Geneset
1	5e-05	31 / 853	G-protein coupled receptor signaling pathway	1	0.01	7 / 153	cell surface	1	2e-04	27 / 751	G-protein coupled receptor activity
2	1e-03	7 / 100	neuropeptide signaling pathway	2	0.04	17 / 634	extracellular region	2	4e-03	21 / 666	signal transducer activity
3	2e-03	5 / 53	chemotaxis	3	0.10	2 / 32	cell-cell adherens junction	3	6e-03	3 / 22	chemokine receptor activity
4	3e-03	5 / 58	chemokine-mediated signaling pathway	4	0.15	1 / 10	chylomicron	4	2e-02	3 / 34	G-protein coupled serotonin receptor activity
5	4e-03	12 / 297	immune response	5	0.15	1 / 10	sarcoplasmic reticulum	5	2e-02	9 / 244	receptor binding
6	7e-03	4 / 45	phospholipase C-activating G-protein coupled receptor signaling pathway	6	0.16	6 / 219	cell junction	6	3e-02	4 / 69	extracellular ligand-gated ion channel activity
7	1e-02	3 / 28	G-protein coupled serotonin receptor signaling pathway	7	0.17	1 / 11	membrane attack complex	7	4e-02	7 / 191	serine-type endopeptidase activity
8	1e-02	2 / 10	cellular glucose homeostasis	8	0.18	1 / 12	endoplasmic reticulum lumen	8	5e-02	5 / 119	serine-type peptidase activity
9	1e-02	2 / 11	detection of mechanical stimulus	9	0.20	1 / 13	transcriptional repressor complex	9	6e-02	2 / 23	CCR chemokine receptor binding
10	1e-02	2 / 11	multicellular organismal response to stress	10	0.22	11 / 500	extracellular space	10	6e-02	2 / 25	acetylcholine-gated cation-selective channel activity
11	2e-02	2 / 12	smooth muscle contraction	11	0.22	1 / 15	secretory granule	11	7e-02	4 / 95	hormone activity
12	2e-02	2 / 14	positive regulation of cytosolic calcium ion concentration	12	0.24	1 / 16	midbody	12	8e-02	7 / 223	transferase activity, transferring glycosyl groups
13	2e-02	2 / 14	spermatid development	13	0.26	2 / 59	intracellular membrane-bounded organelle	13	8e-02	2 / 29	glucuronosyltransferase activity
14	4e-02	30 / 1295	signal transduction	14	0.26	4 / 155	synapse	14	9e-02	2 / 30	cell adhesion molecule binding
15	6e-02	2 / 23	cellular response to interferon-gamma	15	0.27	1 / 19	extrinsic component of membrane	15	9e-02	2 / 31	heparin binding



# Correlation Cluster

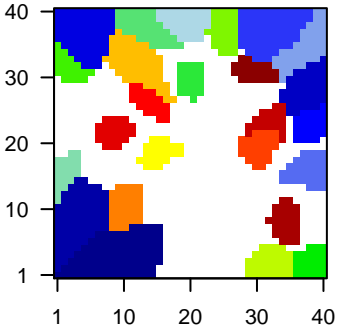
## Spot Summary: P

# metagenes = 20  
# genes = 292

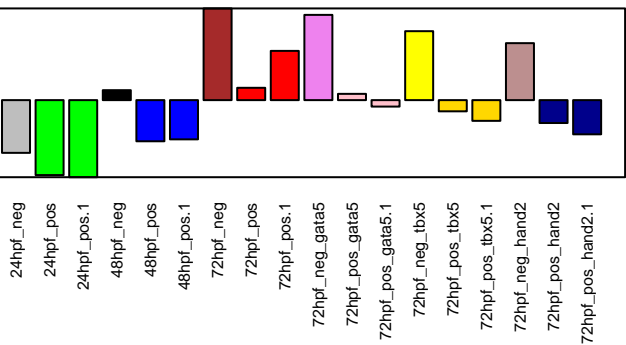
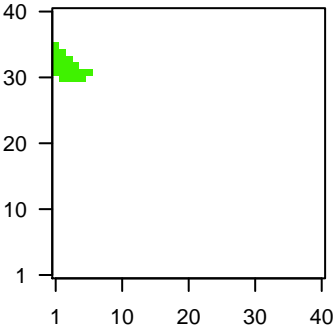
<r> metagenes = 0.97  
<r> genes = 0.61  
beta: r2= 11.26 / log p= -Inf

# samples with spot = 5 ( 27.8 % )  
72hpf\_neg : 1 ( 100 % )  
72hpf\_pos : 1 ( 50 % )  
72hpf\_neg\_gata5 : 1 ( 100 % )  
72hpf\_neg\_tbx5 : 1 ( 100 % )  
72hpf\_neg\_hand2 : 1 ( 100 % )

Overview Map



Spot

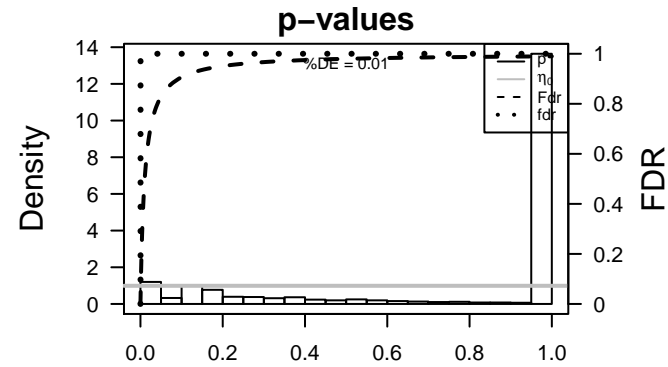


## Spot Genelist

Rank	ID	max e	r	min e	Description	
					Symbol	
1	ENSDARG000	5.44	-2.17	0.82	opn1sw2 opsin 1 (cone pigments), short-wave-sensitive 2 [Source:ZFIN]	OPN1SW2
2	ENSDARG000	5.22	-3.71	0.78	opn1mw1 opsin 1 (cone pigments), medium-wave-sensitive, 1 [Source:ZFIN]	OPN1MW1
3	ENSDARG000	5.16	-4.48	0.78	opn1sw1 opsin 1 (cone pigments), short-wave-sensitive 1 [Source:ZFIN]	OPN1SW1
4	ENSDARG000	4.25	-2.5	0.84	opn1lw1 opsin 1 (cone pigments), long-wave-sensitive, 1 [Source:ZFIN]	OPN1LW1
5	ENSDARG000	4.23	-1.93	0.65	fbp2 fructose-1,6-bisphosphatase 2 [Source:ZFIN;Acc:ZDB-GENE-040724-185]	FBP2
6	ENSDARG000	4.19	-2.48	0.75	and3 actinodin3 [Source:ZFIN;Acc:ZDB-GENE-040724-185]	AND3
7	ENSDARG000	4.16	-2.83	0.73	pde6h phosphodiesterase 6H, cGMP-specific, cone, gamma [Source:ZFIN]	PDE6H
8	ENSDARG000	4.11	-2.9	0.82	grk7a G protein-coupled receptor kinase 7a [Source:ZFIN;Acc:ZDB-GENE-040724-185]	GRK7A
9	ENSDARG000	4.05	-2.29	0.86	prph2b peripherin 2b (retinal degeneration, slow) [Source:ZFIN;Acc:ZDB-GENE-040724-185]	PRPH2B
10	ENSDARG000	3.64	-2.02	0.59	prph2a peripherin 2a (retinal degeneration, slow) [Source:ZFIN;Acc:ZDB-GENE-040724-185]	PRPH2A
11	ENSDARG000	3.63	-1.95	0.78	gngt2b guanine nucleotide binding protein (G protein), gamma transducin [Source:ZFIN]	GNGT2B
12	ENSDARG000	3.58	-2.81	0.8	mbpa myelin basic protein a [Source:ZFIN;Acc:ZDB-GENE-030121-185]	MBPA
13	ENSDARG000	3.36	-3.38	0.6	col8a2 collagen, type VIII, alpha 2 [Source:ZFIN;Acc:ZDB-GENE-040724-185]	COL8A2
14	ENSDARG000	3.33	-2.55	0.85	slc24a2 solute carrier family 24 (sodium/potassium/calcium exchange) [Source:ZFIN]	SLC24A2
15	ENSDARG000	3.26	-2.37	0.86	gc3 guanylyl cyclase 3 [Source:ZFIN;Acc:ZDB-GENE-011128-9]	GC3
16	ENSDARG000	3.26	-1.88	0.78	clcn2c chloride channel 2c [Source:ZFIN;Acc:ZDB-GENE-050506-185]	CLCN2C
17	ENSDARG000	3.25	-2.13	0.88	col6a2 collagen, type VI, alpha 2 [Source:ZFIN;Acc:ZDB-GENE-040724-185]	COL6A2
18	ENSDARG000	3.23	-2.34	0.93	irbp interphotoreceptor retinoid-binding protein [Source:ZFIN;Acc:ZDB-GENE-040724-185]	IRBP
19	ENSDARG000	3.19	-2.16	0.82	slc24a2 solute carrier family 24 (sodium/potassium/calcium exchange) [Source:ZFIN]	SLC24A2
20	ENSDARG000	3.17	-1.92	0.88	col6a1 collagen, type VI, alpha 1 [Source:ZFIN;Acc:ZDB-GENE-040724-185]	COL6A1

## Geneset Overrepresentation

Rank	p-value	#in/all	Geneset
1	2e-13	14 / 83	BP visual perception
2	7e-10	27 / 634	CC extracellular region
3	8e-09	13 / 153	CC proteinaceous extracellular matrix
4	1e-05	6 / 49	MF extracellular matrix structural constituent
5	2e-05	5 / 31	MF heparin binding
6	2e-05	5 / 33	MF photoreceptor activity
7	2e-05	21 / 717	MF calcium ion binding
8	3e-05	5 / 36	BP regulation of cell growth
9	5e-05	6 / 64	MF serine-type endopeptidase inhibitor activity
10	7e-05	26 / 1084	BP transport
11	1e-04	9 / 176	BP ion transmembrane transport
12	1e-04	4 / 25	MF integrin binding
13	1e-04	3 / 10	MF small molecule binding
14	2e-04	3 / 11	MF collagen binding
15	2e-04	4 / 28	BP phototransduction
16	2e-04	12 / 333	BP cell adhesion
17	2e-04	4 / 29	MF 3',5'-cyclic-nucleotide phosphodiesterase activity
18	2e-04	3 / 12	BP collagen fibril organization
19	3e-04	4 / 30	MF insulin-like growth factor binding
20	3e-04	15 / 499	BP ion transport
21	3e-04	4 / 31	BP protein-chromophore linkage
22	6e-04	10 / 270	MF ion channel activity
23	6e-04	5 / 65	CC extracellular matrix
24	6e-04	89 / 6248	CC integral component of membrane
25	1e-03	6 / 109	BP negative regulation of endopeptidase activity
26	1e-03	5 / 76	BP cartilage development
27	1e-03	3 / 21	BP negative regulation of angiogenesis
28	1e-03	3 / 21	BP response to light stimulus
29	1e-03	4 / 46	CC collagen trimer
30	1e-03	6 / 116	MF metalloendopeptidase activity
31	2e-03	92 / 6723	CC membrane
32	2e-03	6 / 128	MF metalloproteinase activity
33	3e-03	3 / 27	BP axon extension
34	3e-03	8 / 229	MF transporter activity
35	4e-03	3 / 30	BP detection of visible light
36	4e-03	3 / 31	MF G-protein coupled photoreceptor activity
37	4e-03	3 / 31	CC photoreceptor outer segment
38	4e-03	5 / 102	BP response to stimulus
39	4e-03	3 / 32	BP muscle organ development
40	5e-03	22 / 1162	CC plasma membrane



BP

Rank

p-value

#in/all

Geneset

1

2e-13

14 / 83

visual perception

2

3e-05

5 / 36

regulation of cell growth

3

7e-05

26 / 1084

transport

4

1e-04

9 / 176

ion transmembrane transport

5

2e-04

4 / 28

phototransduction

6

2e-04

12 / 333

cell adhesion

7

2e-04

3 / 12

collagen fibril organization

8

3e-04

15 / 499

ion transport

9

3e-04

4 / 31

protein-chromophore linkage

10

1e-03

6 / 109

negative regulation of endopeptidase activity

11

1e-03

5 / 76

cartilage development

12

1e-03

3 / 21

negative regulation of angiogenesis

13

1e-03

3 / 21

response to light stimulus

14

3e-03

3 / 27

axon extension

15

4e-03

3 / 30

detection of visible light

CC

Rank

p-value

#in/all

Geneset

1

7e-10

27 / 634

extracellular region

2

8e-09

13 / 153

proteinaceous extracellular matrix

3

6e-04

5 / 65

extracellular matrix

4

6e-04

89 / 6248

integral component of membrane

5

1e-03

4 / 46

collagen trimer

6

2e-03

92 / 6723

membrane

7

4e-03

3 / 31

photoreceptor outer segment

8

5e-03

22 / 1162

plasma membrane

9

1e-02

16 / 809

integral component of plasma membrane

10

1e-02

3 / 48

heterotrimeric G-protein complex

11

2e-02

11 / 500

extracellular space

12

2e-02

4 / 98

transcription factor complex

13

2e-02

2 / 22

synaptic vesicle membrane

14

3e-02

2 / 27

guanylate cyclase complex, soluble

15

3e-02

2 / 27

postsynapse

MF

Rank

p-value

#in/all

Geneset

1

1e-05

6 / 49

extracellular matrix structural constituent

2

2e-05

5 / 31

heparin binding

3

2e-05

5 / 33

photoreceptor activity

4

2e-05

21 / 717

calcium ion binding

5

5e-05

6 / 64

serine-type endopeptidase inhibitor activity

6

1e-04

4 / 25

integrin binding

7

1e-04

3 / 10

small molecule binding

8

2e-04

3 / 11

collagen binding

9

2e-04

4 / 29

3',5'-cyclic-nucleotide phosphodiesterase activity

10

3e-04

4 / 30

insulin-like growth factor binding

11

6e-04

10 / 270

ion channel activity

12

1e-03

6 / 116

metalloendopeptidase activity

13

2e-03

6 / 128

metallopeptidase activity

14

3e-03

8 / 229

transporter activity

15

4e-03

3 / 31

G-protein coupled photoreceptor activity

Correlation Cluster

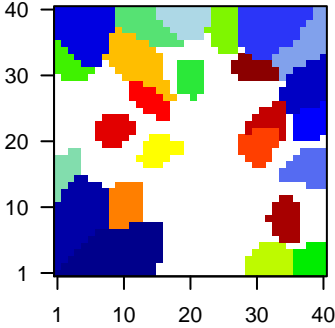
Spot Summary: Q

# metagenes = 23  
# genes = 560

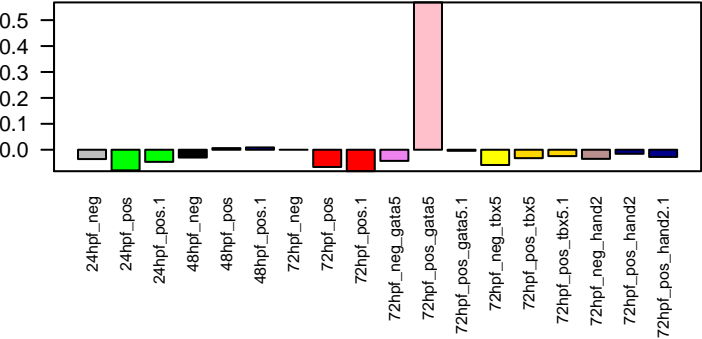
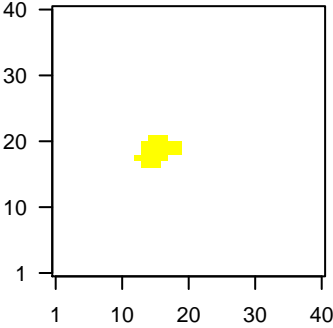
<r> metagenes = 0.94  
<r> genes = 0.51  
beta: r2= 0.25 / log p= -1.45

# samples with spot = 1 ( 5.6 %)  
72hpf\_pos\_gata5 : 1 ( 50 %)

Overview Map



Spot

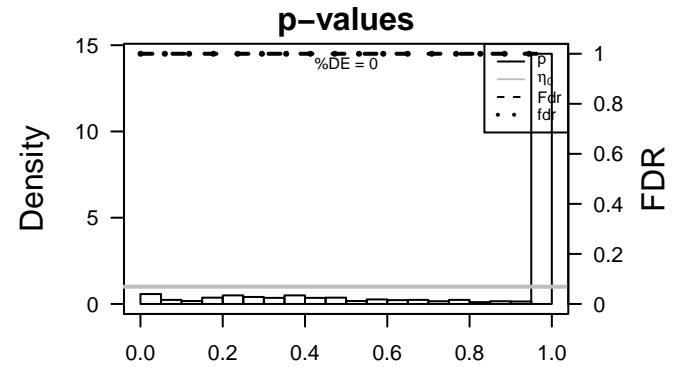


Spot Genelist

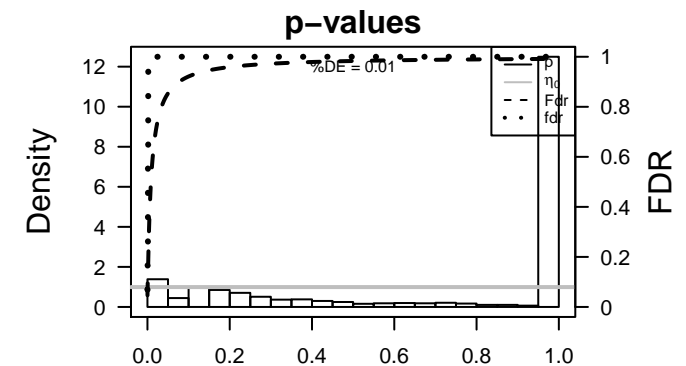
Rank	ID	max e	r	min e	Description
1	ENSDARG000	1.71	-0.89	0.69	adhesion G protein-coupled receptor F6 [Source:ZFIN;Acc:Z
2	ENSDARG000	1.68	-0.51	0.81	card14 caspase recruitment domain family, member 14 [Source:ZFIN
3	ENSDARG000	1.66	-1.26	0.55	si:ch211-129c21.1 [Source:ZFIN;Acc:ZDB-GENE-030131-8
4	ENSDARG000	1.65	-1	0.61	abch1 ATP-binding cassette, sub-family H, member 1 [Source:ZFIN
5	ENSDARG000	1.62	-1.08	0.65	dnaaf2 dynein, axonemal, assembly factor 2 [Source:ZFIN;Acc:ZDB-
6	ENSDARG000	1.6	-0.89	0.65	U5 spliceosomal RNA [Source:RFAM;Acc:RF00020]
7	ENSDARG000	1.56	-0.79	0.63	styk1 serine/threonine/tyrosine kinase 1 [Source:ZFIN;Acc:ZDB-Gt
8	ENSDARG000	1.53	-0.52	0.69	klf6b Kruppel-like factor 6b [Source:ZFIN;Acc:ZDB-GENE-07091
9	ENSDARG000	1.46	-0.65	0.69	si:ch73-23l24.1 [Source:ZFIN;Acc:ZDB-GENE-131127-400
10	ENSDARG000	1.42	-0.48	0.66	zgc:112285c:112285 [Source:ZFIN;Acc:ZDB-GENE-050913-132]
11	ENSDARG000	1.41	-0.59	0.77	rab25b RAB25, member RAS oncogene family b [Source:ZFIN;Acc:Z
12	ENSDARG000	1.37	-0.35	0.88	LOC1081731053932 [Source:ZFIN;Acc:ZDB-GENE-070209-223]
13	ENSDARG000	1.34	-0.55	0.65	zgc:194839c:194839 [Source:ZFIN;Acc:ZDB-GENE-081022-153]
14	ENSDARG000	1.33	-0.55	0.68	zgc:163125c:163121 [Source:ZFIN;Acc:ZDB-GENE-070424-80]
15	ENSDARG000	1.29	-0.53	0.68	s100w S100 calcium binding protein W [Source:ZFIN;Acc:ZDB-GEN
16	ENSDARG000	1.29	-0.91	0.66	herc3 HECT and RLD domain containing E3 ubiquitin protein ligase
17	ENSDARG000	1.28	-0.31	0.81	si:ch211-250e5.2 [Source:ZFIN;Acc:ZDB-GENE-030131-8
18	ENSDARG000	1.23	-0.29	0.76	trim110 tripartite motif containing 110 [Source:ZFIN;Acc:ZDB-GENE-
19	ENSDARG000	1.23	-0.37	0.76	psma6l proteasome subunit alpha 6, like [Source:ZFIN;Acc:ZDB-GEI
20	ENSDARG000	1.21	-0.38	0.73	si:ch73-181m17.1 [Source:ZFIN;Acc:ZDB-GENE-131122-4

Geneset Overrepresentation

Rank	p-value	#in/all	Geneset
1	5e-07	40 / 853	BP G-protein coupled receptor signaling pathway
2	1e-06	36 / 751	MF G-protein coupled receptor activity
3	8e-04	5 / 37	MF peptide binding
4	9e-04	26 / 666	MF signal transducer activity
5	2e-03	3 / 13	BP antigen processing and presentation
6	2e-03	22 / 561	MF GTP binding
7	3e-03	14 / 297	BP immune response
8	5e-03	10 / 192	MF transmembrane signaling receptor activity
9	7e-03	3 / 20	BP response to peptide
10	7e-03	4 / 39	CC connexin complex
11	9e-03	4 / 41	BP peptidyl-tyrosine autophosphorylation
12	1e-02	4 / 43	CC extrinsic component of cytoplasmic side of plasma membrane
13	1e-02	4 / 44	CC gap junction
14	1e-02	4 / 46	MF trace-amine receptor activity
15	2e-02	2 / 10	BP cellular glucose homeostasis
16	2e-02	4 / 49	MF non-membrane spanning protein tyrosine kinase activity
17	2e-02	21 / 634	CC extracellular region
18	2e-02	3 / 28	BP cellular response to hormone stimulus
19	2e-02	2 / 11	BP positive regulation of cysteine-type endopeptidase activity involved in apop
20	2e-02	2 / 12	MF neuropeptide receptor activity
21	2e-02	2 / 12	BP peptide catabolic process
22	2e-02	3 / 31	BP one-carbon metabolic process
23	3e-02	2 / 13	MF dopamine neurotransmitter receptor activity
24	3e-02	2 / 13	BP somite specification
25	3e-02	36 / 1295	BP signal transduction
26	3e-02	3 / 33	BP cell chemotaxis
27	3e-02	143 / 6248	CC integral component of membrane
28	3e-02	7 / 149	BP cell surface receptor signaling pathway
29	3e-02	4 / 59	BP detection of chemical stimulus involved in sensory perception of smell
30	3e-02	4 / 59	MF olfactory receptor activity
31	3e-02	2 / 14	BP carbohydrate biosynthetic process
32	3e-02	6 / 119	BP regulation of cell proliferation
33	3e-02	2 / 15	BP cAMP biosynthetic process
34	3e-02	2 / 15	BP type B pancreatic cell development
35	4e-02	4 / 64	BP cell communication
36	4e-02	2 / 16	CC midbody
37	4e-02	2 / 16	BP protein sumoylation
38	4e-02	4 / 65	BP sensory perception of smell
39	4e-02	2 / 17	BP ceramide biosynthetic process
40	5e-02	7 / 164	BP carbohydrate metabolic process



BP				CC				MF			
Rank	p-value	#in/all	Geneset	Rank	p-value	#in/all	Geneset	Rank	p-value	#in/all	Geneset
1	5e-07	40 / 853	G-protein coupled receptor signaling pathway	1	0.007	4 / 39	connexin complex	1	1e-06	36 / 751	G-protein coupled receptor activity
2	2e-03	3 / 13	antigen processing and presentation	2	0.010	4 / 43	extrinsic component of cytoplasmic side of plasma membrane	2	8e-04	5 / 37	peptide binding
3	3e-03	14 / 297	immune response	3	0.011	4 / 44	gap junction	3	9e-04	26 / 666	signal transducer activity
4	7e-03	3 / 20	response to peptide	4	0.016	21 / 634	extracellular region	4	2e-03	22 / 561	GTP binding
5	9e-03	4 / 41	peptidyl-tyrosine autophosphorylation	5	0.029	143 / 6248	integral component of membrane	5	5e-03	10 / 192	transmembrane signaling receptor activity
6	2e-02	2 / 10	cellular glucose homeostasis	6	0.039	2 / 16	midbody	6	1e-02	4 / 46	trace-amine receptor activity
7	2e-02	3 / 28	cellular response to hormone stimulus	7	0.064	149 / 6723	membrane	7	2e-02	4 / 49	non-membrane spanning protein tyrosine kinase activity
8	2e-02	2 / 11	positive regulation of cysteine-type endopeptidase activity involved in apoptot	8	0.085	6 / 153	cell surface	8	2e-02	2 / 12	neuropeptide receptor activity
9	2e-02	2 / 12	peptide catabolic process	9	0.146	7 / 219	cell junction	9	3e-02	2 / 13	dopamine neurotransmitter receptor activity
10	2e-02	3 / 31	one-carbon metabolic process	10	0.181	1 / 10	proteasome core complex, alpha-subunit complex	10	3e-02	4 / 59	olfactory receptor activity
11	3e-02	2 / 13	somite specification	11	0.214	1 / 12	histone deacetylase complex	11	5e-02	4 / 68	sulfotransferase activity
12	3e-02	36 / 1295	signal transduction	12	0.214	1 / 12	voltage-gated sodium channel complex	12	5e-02	3 / 41	cytoskeletal protein binding
13	3e-02	3 / 33	cell chemotaxis	13	0.254	2 / 49	microtubule organizing center	13	5e-02	2 / 18	carbonate dehydratase activity
14	3e-02	7 / 149	cell surface receptor signaling pathway	14	0.259	1 / 15	cytoplasmic dynein complex	14	6e-02	9 / 244	receptor binding
15	3e-02	4 / 59	detection of chemical stimulus involved in sensory perception of smell	15	0.271	35 / 1580	cellular_component	15	7e-02	3 / 47	chemokine activity



BP				CC				MF			
Rank	p-value	#in/all	Geneset	Rank	p-value	#in/all	Geneset	Rank	p-value	#in/all	Geneset
1	2e-04	15 / 375	positive regulation of GTPase activity	1	1e-04	50 / 2189	cytoplasm	1	3e-05	5 / 28	protein domain specific binding
2	3e-04	5 / 44	protein peptidyl-prolyl isomerization	2	4e-04	7 / 101	endosome	2	1e-04	7 / 85	isomerase activity
3	7e-04	11 / 257	cell differentiation	3	9e-04	5 / 56	mitochondrial outer membrane	3	3e-04	5 / 44	peptidyl-prolyl cis-trans isomerase activity
4	8e-04	8 / 147	vesicle-mediated transport	4	2e-03	12 / 337	endoplasmic reticulum	4	4e-04	13 / 321	GTPase activity
5	1e-03	3 / 16	regulation of protein kinase activity	5	2e-03	9 / 209	endoplasmic reticulum membrane	5	9e-04	3 / 15	FK506 binding
6	2e-03	5 / 65	endocytosis	6	5e-03	3 / 27	recycling endosome	6	1e-03	6 / 88	guanyl-nucleotide exchange factor activity
7	2e-03	9 / 210	intracellular protein transport	7	1e-02	10 / 317	Golgi apparatus	7	4e-03	16 / 561	GTP binding
8	3e-03	3 / 21	vesicle docking	8	1e-02	2 / 12	microtubule associated complex	8	6e-03	3 / 28	protein kinase binding
9	3e-03	5 / 74	negative regulation of transcription, DNA-templated	9	1e-02	3 / 35	peroxisome	9	9e-03	3 / 33	oxidoreductase activity, acting on the CH-CH group of donors
10	4e-03	5 / 78	protein ubiquitination involved in ubiquitin-dependent protein catabolic proces	10	1e-02	2 / 14	autophagosome	10	1e-02	35 / 1761	metal ion binding
11	5e-03	4 / 51	ER to Golgi vesicle-mediated transport	11	2e-02	23 / 1066	intracellular	11	1e-02	2 / 13	SH3 domain binding
12	5e-03	3 / 26	mitophagy	12	2e-02	2 / 15	cytoplasmic dynein complex	12	1e-02	13 / 491	kinase activity
13	5e-03	7 / 156	small GTPase mediated signal transduction	13	2e-02	3 / 43	extrinsic component of cytoplasmic side of plasma membrane	13	2e-02	4 / 75	microtubule motor activity
14	5e-03	3 / 27	ubiquitin-dependent ERAD pathway	14	2e-02	3 / 45	SNARE complex	14	2e-02	6 / 156	ubiquitin protein ligase activity
15	5e-03	4 / 53	convergent extension involved in gastrulation	15	3e-02	2 / 19	extrinsic component of membrane	15	2e-02	3 / 42	SNAP receptor activity

# Correlation Cluster

## Spot Summary: S

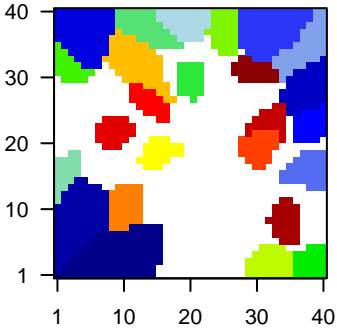
# metagenes = 64  
# genes = 1209

<r> metagenes = 0.94

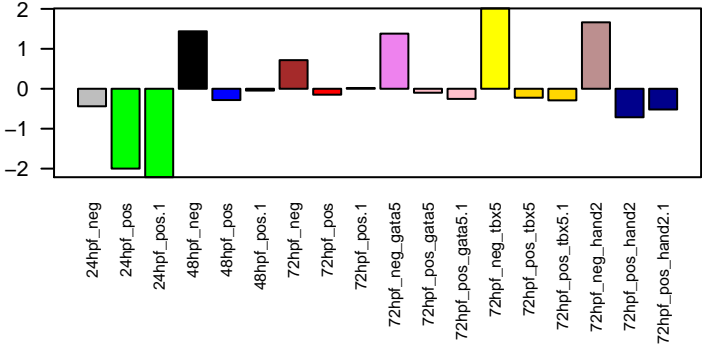
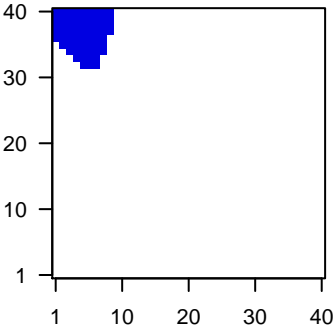
beta: r2= 20.51 / log p= -Inf

# samples with spot = 5 ( 27.8 % )  
48hpf\_neg : 1 ( 100 % )  
72hpf\_neg : 1 ( 100 % )  
72hpf\_neg\_gata5 : 1 ( 100 % )  
72hpf\_neg\_tbx5 : 1 ( 100 % )  
72hpf\_neg\_hand2 : 1 ( 100 % )

Overview Map



Spot

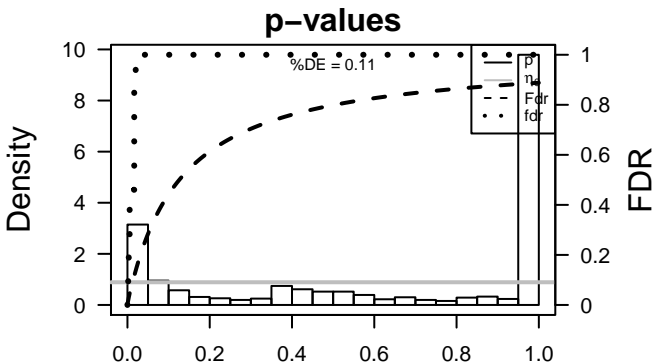


## Spot Genelist

Rank	ID	max e	r	Description	
		min e		Symbol	
1	ENSDARG000	5.4	-5.6	0.78	muc5.1 mucin 5.1, oligomeric mucus/gel-forming [Source:ZFIN;Acc:Z
2	ENSDARG000	5.34	-6.98	0.71	matn1 matrilin 1 [Source:ZFIN;Acc:ZDB-GENE-050307-3]
3	ENSDARG000	5.19	-6.04	0.49	atp1a1a.2ATPase, Na+/K+ transporting, alpha 1a polypeptide, tandem c
4	ENSDARG000	5.14	-4.55	0.71	rho rhodopsin [Source:ZFIN;Acc:ZDB-GENE-990415-271]
5	ENSDARG000	5.09	-5.91	0.72	and2 actinodin2 [Source:ZFIN;Acc:ZDB-GENE-041105-2]
6	ENSDARG000	5.01	-4.88	0.69	opn1lw2 opsin 1 (cone pigments), long-wave-sensitive, 2 [Source:ZFI
7	ENSDARG000	4.9	-3.66	0.74	and1 actinodin1 [Source:ZFIN;Acc:ZDB-GENE-030131-9105]
8	ENSDARG000	4.85	-4.47	0.76	npas4a neuronal PAS domain protein 4a [Source:ZFIN;Acc:ZDB-GENE-
9	ENSDARG000	4.83	-5.45	0.69	arr3a arrestin 3a, retinal (X-arrestin) [Source:ZFIN;Acc:ZDB-GENE-
10	ENSDARG000	4.82	-3.89	0.56	gnb3b guanine nucleotide binding protein (G protein), beta polypepti
11	ENSDARG000	4.76	-5.55	0.79	col10a1acollagen, type X, alpha 1a [Source:ZFIN;Acc:ZDB-GENE-03
12	ENSDARG000	4.72	-8.26	0.88	col11a2 collagen, type XI, alpha 2 [Source:ZFIN;Acc:ZDB-GENE-000
13	ENSDARG000	4.71	-3.52	0.64	rcvrn3 recoverin 3 [Source:ZFIN;Acc:ZDB-GENE-040426-1661]
14	ENSDARG000	4.57	-3.71	0.6	pde6c phosphodiesterase 6C, cGMP-specific, cone, alpha prime [Si
15	ENSDARG000	4.55	-3.73	0.75	
16	ENSDARG000	4.55	-4.06	0.6	gnat2 guanine nucleotide binding protein (G protein), alpha transdu
17	ENSDARG000	4.49	-6.7	0.83	si:dkey-65b12.6 [Source:ZFIN;Acc:ZDB-GENE-060526-325]
18	ENSDARG000	4.19	-3.55	0.73	scn4ab sodium channel, voltage-gated, type IV, alpha, b [Source:ZFI
19	ENSDARG000	4.03	-3.48	0.68	slc12a10solute carrier family 12 (sodium/potassium/chloride transport
20	ENSDARG000	4.01	-3.22	0.96	sv2a synaptic vesicle glycoprotein 2A [Source:ZFIN;Acc:ZDB-GENE-

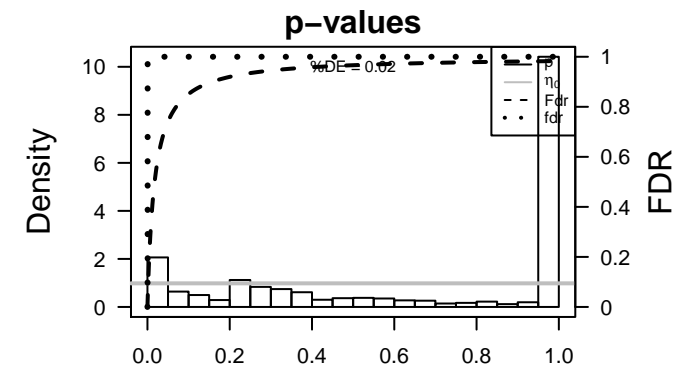
## Geneset Overrepresentation

Rank	p-value	#in/all	Geneset
1	7e-34	56 / 172	BP homophilic cell adhesion via plasma membrane adhesion molecules
2	7e-33	75 / 333	BP cell adhesion
3	2e-30	143 / 1162	CC plasma membrane
4	2e-27	50 / 175	BP nervous system development
5	3e-27	103 / 717	MF calcium ion binding
6	4e-27	47 / 155	CC synapse
7	2e-25	447 / 6723	CC membrane
8	3e-23	78 / 499	BP ion transport
9	5e-23	415 / 6248	CC integral component of membrane
10	2e-18	50 / 270	MF ion channel activity
11	4e-17	71 / 537	MF sequence-specific DNA binding
12	2e-15	17 / 32	MF extracellular-glutamate-gated ion channel activity
13	2e-15	17 / 32	MF ionotropic glutamate receptor activity
14	2e-15	17 / 32	BP ionotropic glutamate receptor signaling pathway
15	5e-15	34 / 158	MF microtubule binding
16	1e-14	114 / 1239	BP regulation of transcription, DNA-templated
17	4e-13	22 / 75	BP calcium ion transport
18	6e-13	100 / 1084	BP transport
19	3e-11	20 / 74	CC neuron projection
20	3e-11	24 / 108	CC microtubule
21	4e-11	119 / 1484	MF DNA binding
22	8e-11	28 / 153	CC proteinaceous extracellular matrix
23	9e-11	34 / 219	CC cell junction
24	1e-10	20 / 79	BP excitatory postsynaptic potential
25	1e-10	9 / 12	BP neurotransmitter secretion
26	1e-10	15 / 42	MF voltage-gated calcium channel activity
27	2e-10	52 / 454	BP multicellular organism development
28	2e-10	15 / 44	BP neuron development
29	3e-10	25 / 130	BP regulation of ion transmembrane transport
30	3e-10	25 / 130	MF voltage-gated ion channel activity
31	3e-10	10 / 17	CC presynaptic active zone
32	4e-10	11 / 22	BP membrane depolarization during action potential
33	4e-10	13 / 33	CC voltage-gated calcium channel complex
34	5e-10	29 / 176	BP ion transmembrane transport
35	9e-10	19 / 80	CC postsynaptic membrane
36	1e-09	15 / 49	MF extracellular matrix structural constituent
37	3e-09	23 / 124	MF receptor activity
38	4e-09	179 / 2716	CC nucleus
39	4e-09	21 / 106	BP calcium ion transmembrane transport
40	2e-08	12 / 36	CC synaptic vesicle

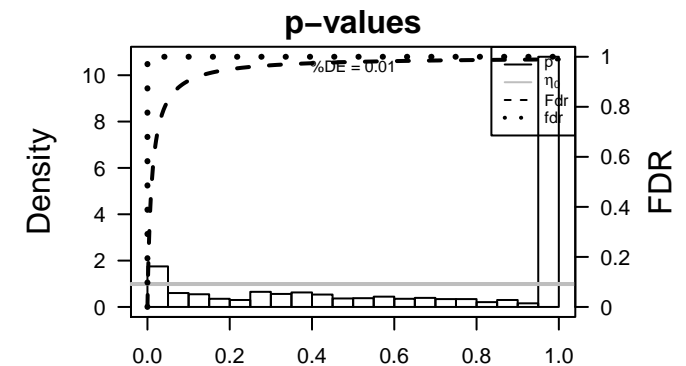


BP				CC				MF			
Rank	p-value	#in/all	Geneset	Rank	p-value	#in/all	Geneset	Rank	p-value	#in/all	Geneset
1	7e-34	56 / 172	homophilic cell adhesion via plasma membrane adhesion molecules	1	2e-30	143 / 1162	plasma membrane	1	3e-27	103 / 717	calcium ion binding
2	7e-33	75 / 333	cell adhesion	2	4e-27	47 / 155	synapse	2	2e-18	50 / 270	ion channel activity
3	2e-27	50 / 175	nervous system development	3	2e-25	447 / 6723	membrane	3	4e-17	71 / 537	sequence-specific DNA binding
4	3e-23	78 / 499	ion transport	4	5e-23	415 / 6248	integral component of membrane	4	2e-15	17 / 32	extracellular-glutamate-gated ion channel activity
5	2e-15	17 / 32	ionotropic glutamate receptor signaling pathway	5	3e-11	20 / 74	neuron projection	5	2e-15	17 / 32	ionotropic glutamate receptor activity
6	1e-14	114 / 1239	regulation of transcription, DNA-templated	6	3e-11	24 / 108	microtubule	6	5e-15	34 / 158	microtubule binding
7	4e-13	22 / 75	calcium ion transport	7	8e-11	28 / 153	proteinaceous extracellular matrix	7	4e-11	119 / 1484	DNA binding
8	6e-13	100 / 1084	transport	8	9e-11	34 / 219	cell junction	8	1e-10	15 / 42	voltage-gated calcium channel activity
9	1e-10	20 / 79	excitatory postsynaptic potential	9	3e-10	10 / 17	presynaptic active zone	9	3e-10	25 / 130	voltage-gated ion channel activity
10	1e-10	9 / 12	neurotransmitter secretion	10	4e-10	13 / 33	voltage-gated calcium channel complex	10	1e-09	15 / 49	extracellular matrix structural constituent
11	2e-10	52 / 454	multicellular organism development	11	9e-10	19 / 80	postsynaptic membrane	11	3e-09	23 / 124	receptor activity
12	2e-10	15 / 44	neuron development	12	4e-09	179 / 2716	nucleus	12	1e-06	15 / 79	calcium channel activity
13	3e-10	25 / 130	regulation of ion transmembrane transport	13	2e-08	12 / 36	synaptic vesicle	13	2e-06	54 / 633	transcription factor activity, sequence-specific DNA binding
14	4e-10	11 / 22	membrane depolarization during action potential	14	2e-08	14 / 51	presynapse	14	4e-06	7 / 17	transcriptional repressor activity, RNA polymerase II core promoter proximal region sequence-specific DNA binding
15	5e-10	29 / 176	ion transmembrane transport	15	3e-08	70 / 809	integral component of plasma membrane	15	6e-06	7 / 18	tubulin binding





BP				CC				MF			
Rank	p-value	#in/all	Geneset	Rank	p-value	#in/all	Geneset	Rank	p-value	#in/all	Geneset
1	3e-27	100 / 1239	regulation of transcription, DNA-templated	1	1e-16	134 / 2716	nucleus	1	2e-20	98 / 1484	DNA binding
2	2e-11	32 / 333	cell adhesion	2	8e-05	49 / 1162	plasma membrane	2	7e-20	55 / 537	sequence-specific DNA binding
3	5e-09	20 / 172	homophilic cell adhesion via plasma membrane adhesion molecules	3	7e-04	183 / 6248	integral component of membrane	3	2e-12	48 / 633	transcription factor activity, sequence-specific DNA binding
4	1e-08	41 / 643	transcription, DNA-templated	4	1e-03	193 / 6723	membrane	4	1e-09	46 / 717	calcium ion binding
5	3e-08	13 / 78	axon guidance	5	2e-03	41 / 1066	intracellular	5	2e-05	28 / 491	kinase activity
6	3e-06	7 / 28	retina morphogenesis in camera-type eye	6	5e-03	3 / 15	histone acetyltransferase complex	6	4e-05	7 / 41	RNA polymerase II core promoter proximal region sequence-specific DNA binding
7	5e-06	28 / 454	multicellular organism development	7	7e-03	4 / 32	chromatin	7	9e-05	67 / 1761	metal ion binding
8	8e-06	7 / 32	retinal ganglion cell axon guidance	8	1e-02	9 / 153	proteinaceous extracellular matrix	8	3e-04	10 / 110	protein tyrosine kinase activity
9	6e-05	24 / 413	intracellular signal transduction	9	2e-02	29 / 809	integral component of plasma membrane	9	6e-04	5 / 30	transcription cofactor activity
10	6e-05	28 / 522	phosphorylation	10	2e-02	5 / 65	extracellular matrix	10	7e-04	10 / 124	receptor activity
11	1e-04	7 / 48	neural crest cell migration	11	2e-02	14 / 317	Golgi apparatus	11	8e-04	34 / 800	zinc ion binding
12	1e-04	10 / 100	peptidyl-tyrosine phosphorylation	12	3e-02	2 / 11	clathrin-coated pit	12	9e-04	4 / 19	semaphorin receptor activity
13	2e-04	21 / 362	regulation of transcription from RNA polymerase II promoter	13	3e-02	6 / 98	transcription factor complex	13	2e-03	9 / 115	chromatin binding
14	2e-04	12 / 147	brain development	14	3e-02	2 / 12	microtubule associated complex	14	2e-03	3 / 11	collagen binding
15	3e-04	5 / 25	negative chemotaxis	15	4e-02	5 / 80	postsynaptic membrane	15	2e-03	8 / 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-16	55 / 499	ion transport	1	2e-18	317 / 6723	membrane	1	1e-16	40 / 270	ion channel activity
2	8e-10	24 / 175	nervous system development	2	3e-18	300 / 6248	integral component of membrane	2	8e-10	17 / 86	voltage-gated potassium channel activity
3	3e-09	20 / 130	regulation of ion transmembrane transport	3	2e-13	84 / 1162	plasma membrane	3	2e-09	16 / 79	calcium channel activity
4	3e-09	23 / 172	homophilic cell adhesion via plasma membrane adhesion molecules	4	1e-08	21 / 155	synapse	4	3e-09	20 / 130	voltage-gated ion channel activity
5	3e-09	18 / 106	calcium ion transmembrane transport	5	1e-08	56 / 809	integral component of plasma membrane	5	6e-07	14 / 90	potassium channel activity
6	8e-09	20 / 138	potassium ion transport	6	1e-07	12 / 56	voltage-gated potassium channel complex	6	6e-06	5 / 10	store-operated calcium channel activity
7	1e-08	17 / 103	cell-cell signaling	7	1e-05	11 / 74	neuron projection	7	1e-05	44 / 717	calcium ion binding
8	2e-08	14 / 70	protein homooligomerization	8	3e-05	5 / 13	presynaptic membrane	8	1e-05	7 / 27	calmodulin-dependent protein kinase activity
9	2e-08	20 / 147	potassium ion transmembrane transport	9	3e-05	11 / 80	postsynaptic membrane	9	7e-05	6 / 24	ARF guanyl-nucleotide exchange factor activity
10	8e-08	66 / 1084	transport	10	5e-05	19 / 219	cell junction	10	7e-05	9 / 59	syntaxin binding
11	2e-07	43 / 591	transmembrane transport	11	7e-04	4 / 14	postsynaptic density	11	3e-04	7 / 42	voltage-gated calcium channel activity
12	3e-06	70 / 1295	signal transduction	12	9e-04	7 / 51	presynapse	12	3e-04	9 / 71	calmodulin binding
13	5e-06	27 / 333	cell adhesion	13	3e-03	4 / 21	GABA-A receptor complex	13	3e-04	4 / 12	glutamate receptor activity
14	8e-06	8 / 35	calcium ion-regulated exocytosis of neurotransmitter	14	1e-02	3 / 15	cytoplasmic dynein complex	14	4e-04	6 / 32	extracellular-glutamate-gated ion channel activity
15	8e-06	11 / 70	sodium ion transmembrane transport	15	1e-02	3 / 17	AMPA glutamate receptor complex	15	4e-04	6 / 32	ionotropic glutamate receptor activity

# Correlation Cluster

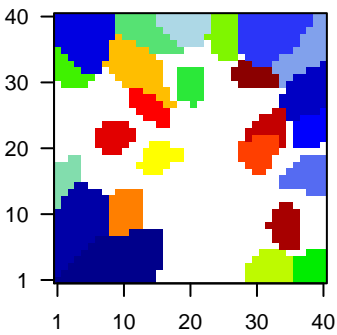
## Spot Summary: V

# metagenes = 32  
# genes = 474

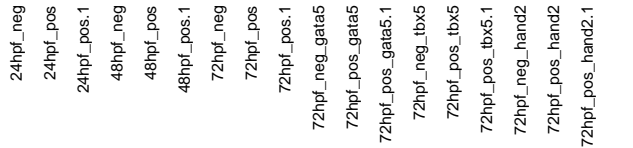
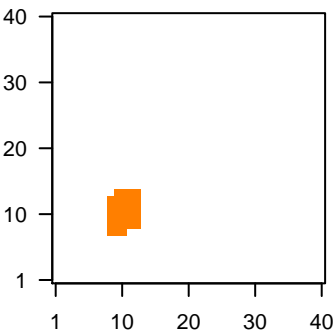
<r> metagenes = 0.95  
<r> genes = 0.46  
beta: r2= 3.16 / log p= -Inf

# samples with spot = 4 ( 22.2 %)  
72hpf\_pos : 1 ( 50 %)  
72hpf\_pos\_tbx5 : 1 ( 50 %)  
72hpf\_pos\_hand2 : 2 ( 100 %)

Overview Map



Spot

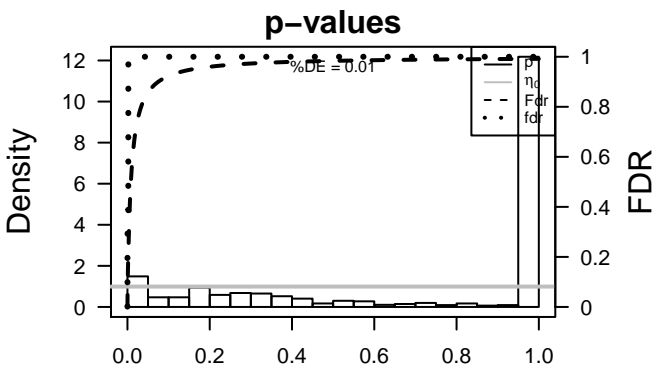


## Spot Genelist

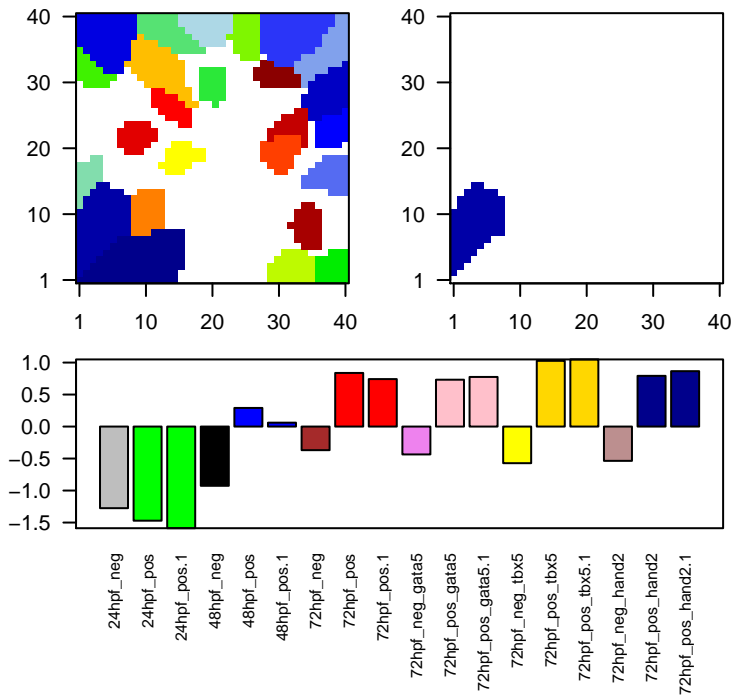
Rank	ID	max e	r	min e	Description
					Symbol
1	ENSDARG000	6.21	-1.42	0.55	scpp5 secretory calcium-binding phosphoprotein 5 [Source:ZFIN;Ac
2	ENSDARG000	3.42	-1.9	0.45	pcyt11b phosphate cytidylyltransferase 1, choline, beta b [Source:ZFI
3	ENSDARG000	3.22	-3.48	0.83	ctf complement factor H [Source:ZFIN;Acc:ZDB-GENE-050208
4	ENSDARG000	3.14	-2.4	0.59	cyp1b1 cytochrome P450, family 1, subfamily B, polypeptide 1 [Sourc
5	ENSDARG000	2.84	-3.3	0.74	cyp24a1 cytochrome P450, family 24, subfamily A, polypeptide 1 [Sou
6	ENSDARG000	2.82	-2.28	0.8	si:ch211-264f5.2-264f5.2 [Source:ZFIN;Acc:ZDB-GENE-080303-2]
7	ENSDARG000	2.75	-3.08	0.6	si:ch211-256m1.8-256m1.8 [Source:ZFIN;Acc:ZDB-GENE-131127-4]
8	ENSDARG000	2.67	-2.47	0.84	cyp1a cytochrome P450, family 1, subfamily A [Source:ZFIN;Acc:ZC
9	ENSDARG000	2.62	-3.11	0.39	rrad Ras-related associated with diabetes [Source:ZFIN;Acc:ZDB
10	ENSDARG000	2.61	-1.31	0.75	zgc:92184i:dkcyp-52c3.2 [Source:ZFIN;Acc:ZDB-GENE-110411-46]
11	ENSDARG000	2.52	-1.7	0.92	abcc2 ATP-binding cassette, sub-family C (CFTR/MRP), member 2
12	ENSDARG000	2.49	-1.39	0.81	adamts1 ADAM metalloproteinase with thrombospondin type 1 motif, 1
13	ENSDARG000	2.46	-2.88	0.81	fybb FYN binding protein b [Source:ZFIN;Acc:ZDB-GENE-09120-
14	ENSDARG000	2.45	-2.95	0.58	zgc:172315c:172315 [Source:ZFIN;Acc:ZDB-GENE-080220-7]
15	ENSDARG000	2.42	-1.3	0.84	serpind1 serpin peptidase inhibitor, clade D (heparin cofactor), membe
16	ENSDARG000	2.34	-1.1	0.4	si:cabz01036006.1 [Source:ZFIN;Acc:ZDB-GENE-160113-1]
17	ENSDARG000	2.29	-3.57	0.33	hivp2b human immunodeficiency virus type I enhancer binding prote
18	ENSDARG000	2.26	-1.47	0.79	mybpc1 myosin binding protein C, slow type [Source:ZFIN;Acc:ZDB-C
19	ENSDARG000	2.23	-1.09	0.84	agxta alanine-glyoxylate aminotransferase a [Source:ZFIN;Acc:ZDI
20	ENSDARG000	2.21	-1.17	0.58	rtgr RAMP-like triterpene glycoside receptor [Source:ZFIN;Acc:Z

## Geneset Overrepresentation

Rank	p-value	#in/all	Geneset
1	6e-10	28 / 414	BP metabolic process
2	1e-06	26 / 522	MF oxidoreductase activity
3	2e-06	31 / 712	BP oxidation-reduction process
4	5e-06	156 / 6723	CC membrane
5	1e-05	145 / 6248	CC integral component of membrane
6	3e-05	25 / 591	BP transmembrane transport
7	2e-04	13 / 229	MF transporter activity
8	6e-04	19 / 480	MF catalytic activity
9	8e-04	5 / 43	BP fatty acid metabolic process
10	8e-04	9 / 145	MF heme binding
11	9e-04	10 / 178	MF iron ion binding
12	1e-03	3 / 13	BP antigen processing and presentation
13	2e-03	3 / 15	BP cardiac muscle contraction
14	2e-03	3 / 15	BP sphingolipid biosynthetic process
15	2e-03	5 / 53	BP chemotaxis
16	2e-03	6 / 79	BP cation transmembrane transport
17	2e-03	29 / 969	MF hydrolase activity
18	2e-03	3 / 16	MF cation channel activity
19	2e-03	4 / 34	BP fatty acid biosynthetic process
20	3e-03	7 / 110	MF oxidoreductase activity, acting on paired donors, with incorporation or reduc
21	3e-03	5 / 58	BP chemokine-mediated signaling pathway
22	3e-03	5 / 59	CC intracellular membrane-bounded organelle
23	3e-03	5 / 60	MF scavenger receptor activity
24	4e-03	3 / 19	BP very long-chain fatty acid biosynthetic process
25	4e-03	7 / 119	MF monooxygenase activity
26	4e-03	4 / 39	CC Z disc
27	5e-03	5 / 65	BP sodium ion transport
28	5e-03	12 / 297	BP immune response
29	6e-03	3 / 22	MF chemokine receptor activity
30	6e-03	9 / 194	BP lipid metabolic process
31	6e-03	4 / 44	BP skeletal muscle tissue development
32	7e-03	5 / 70	BP receptor-mediated endocytosis
33	8e-03	4 / 47	CC integral component of endoplasmic reticulum membrane
34	1e-02	3 / 27	MF oxidoreductase activity, acting on paired donors, with incorporation or reduc
35	1e-02	6 / 109	BP apoptotic process
36	1e-02	3 / 28	BP anion transmembrane transport
37	1e-02	2 / 10	MF hydrolase activity, acting on carbon-nitrogen (but not peptide) bonds, in line
38	1e-02	2 / 10	CC phosphatidylinositol 3-kinase complex
39	1e-02	2 / 10	BP receptor clustering
40	1e-02	2 / 10	BP response to methylmercury

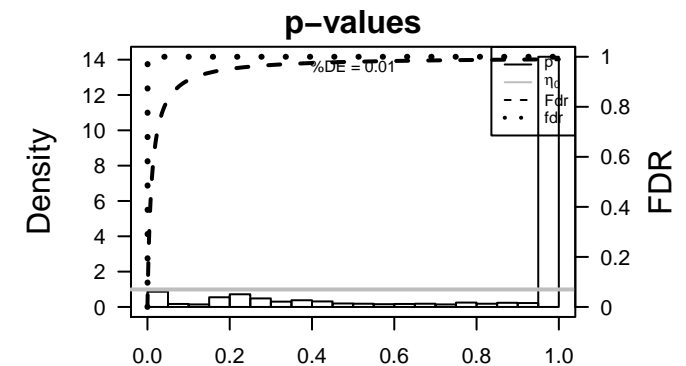


BP				CC				MF			
Rank	p-value	#in/all	Geneset	Rank	p-value	#in/all	Geneset	Rank	p-value	#in/all	Geneset
1	6e-10	28 / 414	metabolic process	1	5e-06	156 / 6723	membrane	1	1e-06	26 / 522	oxidoreductase activity
2	2e-06	31 / 712	oxidation-reduction process	2	1e-05	145 / 6248	integral component of membrane	2	2e-04	13 / 229	transporter activity
3	3e-05	25 / 591	transmembrane transport	3	3e-03	5 / 59	intracellular membrane-bounded organelle	3	6e-04	19 / 480	catalytic activity
4	8e-04	5 / 43	fatty acid metabolic process	4	4e-03	4 / 39	Z disc	4	8e-04	9 / 145	heme binding
5	1e-03	3 / 13	antigen processing and presentation	5	8e-03	4 / 47	integral component of endoplasmic reticulum membrane	5	9e-04	10 / 178	iron ion binding
6	2e-03	3 / 15	cardiac muscle contraction	6	1e-02	2 / 10	phosphatidylinositol 3-kinase complex	6	2e-03	29 / 969	hydrolase activity
7	2e-03	3 / 15	sphingolipid biosynthetic process	7	2e-02	13 / 410	mitochondrion	7	2e-03	3 / 16	cation channel activity
8	2e-03	5 / 53	chemotaxis	8	3e-02	8 / 209	endoplasmic reticulum membrane	8	3e-03	7 / 110	oxidoreductase activity, acting on paired donors, with incorporation or reduction of molecular oxygen
9	2e-03	6 / 79	cation transmembrane transport	9	3e-02	3 / 39	connexin complex	9	3e-03	5 / 60	scavenger receptor activity
10	2e-03	4 / 34	fatty acid biosynthetic process	10	3e-02	11 / 337	endoplasmic reticulum	10	4e-03	7 / 119	monooxygenase activity
11	3e-03	5 / 58	chemokine-mediated signaling pathway	11	3e-02	2 / 16	midbody	11	6e-03	3 / 22	chemokine receptor activity
12	4e-03	3 / 19	very long-chain fatty acid biosynthetic process	12	3e-02	8 / 219	cell junction	12	1e-02	3 / 27	oxidoreductase activity, acting on paired donors, with incorporation or reduction of molecular oxygen
13	5e-03	5 / 65	sodium ion transport	13	4e-02	3 / 44	gap junction	13	1e-02	2 / 10	hydrolase activity, acting on carbon-nitrogen (but not peptide) bonds, in linear tetrapeptides
14	5e-03	12 / 297	immune response	14	4e-02	2 / 19	acetylcholine-gated channel complex	14	1e-02	3 / 29	glucuronosyltransferase activity
15	6e-03	9 / 194	lipid metabolic process	15	4e-02	3 / 46	mitochondrial matrix	15	1e-02	28 / 1063	transferase activity



BP				CC				MF			
Rank	p-value	#in/all	Geneset	Rank	p-value	#in/all	Geneset	Rank	p-value	#in/all	Geneset
1	6e-25	97 / 712	oxidation-reduction process	1	4e-10	8 / 10	chylomicron	1	5e-24	80 / 522	oxidoreductase activity
2	7e-16	29 / 109	negative regulation of endopeptidase activity	2	1e-08	10 / 23	troponin complex	2	2e-11	14 / 33	endopeptidase inhibitor activity
3	1e-09	10 / 19	gluconeogenesis	3	2e-08	7 / 10	high-density lipoprotein particle	3	3e-09	32 / 231	actin binding
4	2e-08	7 / 10	triglyceride catabolic process	4	2e-07	8 / 17	blood microparticle	4	1e-07	25 / 178	iron ion binding
5	6e-08	7 / 11	cholesterol homeostasis	5	7e-07	40 / 410	mitochondrion	5	1e-07	61 / 717	calcium ion binding
6	1e-07	42 / 414	metabolic process	6	1e-06	14 / 70	myosin complex	6	2e-07	46 / 480	catalytic activity
7	1e-07	7 / 12	cholesterol biosynthetic process	7	4e-06	8 / 24	respiratory chain	7	2e-06	7 / 16	acyl-CoA dehydrogenase activity
8	2e-07	9 / 23	lipoprotein metabolic process	8	3e-05	41 / 500	extracellular space	8	3e-06	7 / 17	cholesterol binding
9	3e-07	7 / 13	cholesterol efflux	9	5e-05	19 / 161	mitochondrial inner membrane	9	3e-06	7 / 17	cholesterol transporter activity
10	3e-07	7 / 13	regulation of muscle contraction	10	2e-04	46 / 634	extracellular region	10	6e-06	9 / 33	oxidoreductase activity, acting on the CH-CH group of donors
11	4e-07	9 / 25	cellular response to estrogen stimulus	11	4e-04	9 / 54	actin cytoskeleton	11	7e-06	16 / 105	lipid binding
12	2e-06	6 / 11	cellular response to nitrogen starvation	12	9e-04	23 / 268	cytoskeleton	12	2e-05	7 / 21	NADH dehydrogenase (ubiquinone) activity
13	7e-06	6 / 13	iron ion transport	13	2e-03	7 / 42	mitochondrial membrane	13	2e-05	11 / 57	flavin adenine dinucleotide binding
14	7e-06	7 / 19	vacuolar transport	14	2e-03	119 / 2189	cytoplasm	14	2e-05	109 / 1761	metal ion binding
15	4e-05	7 / 24	cellular iron ion homeostasis	15	3e-03	10 / 85	cell	15	5e-05	5 / 11	ferric iron binding





BP				CC				MF			
Rank	p-value	#in/all	Geneset	Rank	p-value	#in/all	Geneset	Rank	p-value	#in/all	Geneset
1	3e-10	45 / 853	G-protein coupled receptor signaling pathway	1	8e-04	24 / 634	extracellular region	1	7e-11	43 / 751	G-protein coupled receptor activity
2	2e-06	49 / 1295	signal transduction	2	1e-03	28 / 809	integral component of plasma membrane	2	3e-10	39 / 666	signal transducer activity
3	2e-06	11 / 100	neuropeptide signaling pathway	3	3e-03	3 / 17	AMPA glutamate receptor complex	3	5e-06	12 / 130	voltage-gated ion channel activity
4	5e-06	12 / 130	regulation of ion transmembrane transport	4	5e-03	140 / 6248	integral component of membrane	4	4e-05	9 / 90	potassium channel activity
5	2e-05	5 / 19	feeding behavior	5	2e-02	2 / 11	P granule	5	7e-05	9 / 95	hormone activity
6	6e-05	23 / 499	ion transport	6	2e-02	4 / 56	voltage-gated potassium channel complex	6	4e-04	4 / 19	potassium ion leak channel activity
7	9e-05	11 / 147	potassium ion transmembrane transport	7	2e-02	144 / 6723	membrane	7	4e-04	5 / 34	G-protein coupled serotonin receptor activity
8	1e-04	4 / 14	carbohydrate biosynthetic process	8	8e-02	3 / 54	kinesin complex	8	1e-03	3 / 12	neuropeptide receptor activity
9	2e-04	8 / 86	chemical synaptic transmission	9	8e-02	2 / 26	neuronal cell body	9	2e-03	6 / 68	sulfotransferase activity
10	3e-04	10 / 138	potassium ion transport	10	1e-01	2 / 31	photoreceptor outer segment	10	2e-03	4 / 31	inward rectifier potassium channel activity
11	3e-04	4 / 18	stabilization of membrane potential	11	2e-01	5 / 155	synapse	11	3e-03	4 / 32	neurotransmitter receptor activity
12	4e-04	4 / 20	response to peptide	12	2e-01	2 / 39	Z disc	12	5e-03	4 / 37	peptide binding
13	7e-04	3 / 10	tachykinin receptor signaling pathway	13	2e-01	1 / 10	mitochondrial envelope	13	5e-03	6 / 86	voltage-gated potassium channel activity
14	2e-03	4 / 28	cellular response to hormone stimulus	14	2e-01	1 / 11	integral component of mitochondrial inner membrane	14	6e-03	3 / 21	substrate-specific transmembrane transporter activity
15	2e-03	4 / 28	G-protein coupled serotonin receptor signaling pathway	15	2e-01	1 / 11	membrane attack complex	15	7e-03	3 / 22	neuropeptide hormone activity

# Correlation Cluster

## Spot Summary: Y

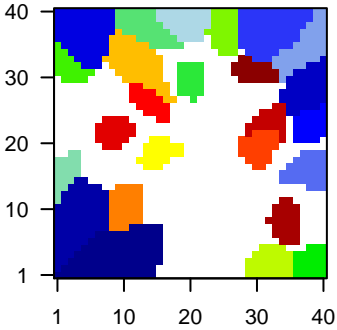
# metagenes = 94  
# genes = 1577

<r> metagenes = 0.93

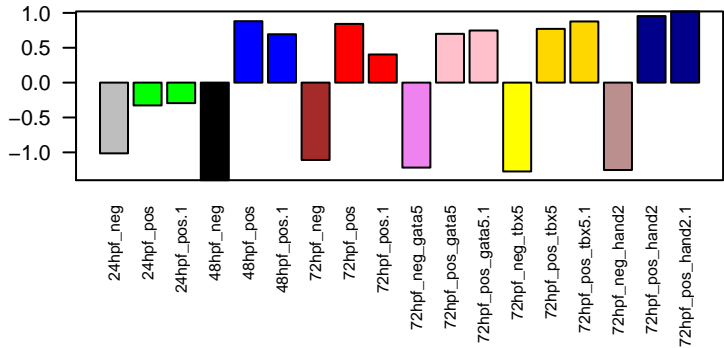
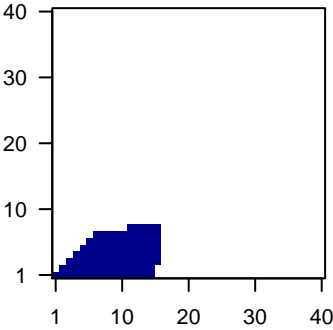
beta: r2= 14.91 / log p= -Inf

# samples with spot = 9 ( 50 %)  
48hpf\_pos : 2 ( 100 %)  
72hpf\_pos : 1 ( 50 %)  
72hpf\_pos\_gata5 : 2 ( 100 %)  
72hpf\_pos\_tbx5 : 2 ( 100 %)  
72hpf\_pos\_hand2 : 2 ( 100 %)

Overview Map



Spot

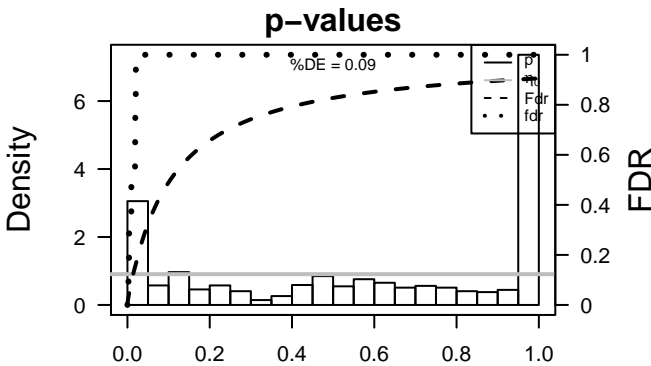


## Spot Genelist

Rank	ID	max e	r	Description	
		min e		Symbol	
1	ENSDARG000	5.16	-6.13	0.91	oacyl O-acyltransferase like [Source:ZFIN;Acc:ZDB-GENE-09071
2	ENSDARG000	4.98	-7.11	0.97	wu.fc46h12:fc46h12 [Source:ZFIN;Acc:ZDB-GENE-030131-3611]
3	ENSDARG000	4.88	-6.93	0.97	si:dkkey-25110.2:251110.2 [Source:ZFIN;Acc:ZDB-GENE-050506-10
4	ENSDARG000	4.72	-6.07	0.81	vmhcl ventricular myosin heavy chain-like [Source:ZFIN;Acc:ZDB-G
5	ENSDARG000	4.71	-7.81	0.97	gch2 GTP cyclohydrolase 2 [Source:ZFIN;Acc:ZDB-GENE-00120
6	ENSDARG000	4.53	-5.75	0.92	si:dkkey-73n8.3 [Source:ZFIN;Acc:ZDB-GENE-141219-27]
7	ENSDARG000	4.51	-4.97	0.91	zgc:113142:113142 [Source:ZFIN;Acc:ZDB-GENE-050220-2]
8	ENSDARG000	4.47	-7.23	0.92	xdh xanthine dehydrogenase [Source:ZFIN;Acc:ZDB-GENE-070
9	ENSDARG000	4.45	-2.24	0.71	plxdc1 plexin domain containing 1 [Source:ZFIN;Acc:ZDB-GENE-0
10	ENSDARG000	4.44	-6.92	0.98	zgc:162150:162150 [Source:ZFIN;Acc:ZDB-GENE-070410-23]
11	ENSDARG000	4.42	-4.7	0.8	tnnc1a troponin C type 1a (slow) [Source:ZFIN;Acc:ZDB-GENE-030
12	ENSDARG000	4.4	-6.51	0.94	bscl2l Bernardinelli-Seip congenital lipodystrophy 2, like [Source:ZF
13	ENSDARG000	4.4	-5.48	0.95	uraha urate (5-hydroxyiso-) hydrolase a [Source:ZFIN;Acc:ZDB-GI
14	ENSDARG000	4.39	-5.45	0.91	sprb sepiapterin reductase b [Source:ZFIN;Acc:ZDB-GENE-0707
15	ENSDARG000	4.38	-5.44	0.96	6-pyruvoyltetrahydropterin synthase [Source:ZFIN;Acc:ZDB-
16	ENSDARG000	4.34	-7.46	0.95	slc22a7a solute carrier family 22 (organic anion transporter), member 7
17	ENSDARG000	4.32	-6.44	0.88	cmlc1 cardiac myosin light chain-1 [Source:ZFIN;Acc:ZDB-GENE-
18	ENSDARG000	4.31	-6.34	0.97	slc2a15a solute carrier family 2 (facilitated glucose transporter), membr
19	ENSDARG000	4.29	-4.58	0.93	cyb561a3 cytochrome b561 family, member A3b [Source:ZFIN;Acc:ZDB
20	ENSDARG000	4.29	-5.32	0.89	zgc:153031:153031 [Source:ZFIN;Acc:ZDB-GENE-060929-1190]

## Geneset Overrepresentation

Rank	p-value	#in/all	Geneset
1	3e-17	71 / 414	BP metabolic process
2	7e-16	75 / 480	MF catalytic activity
3	4e-15	30 / 96	CC lysosome
4	1e-12	89 / 712	BP oxidation-reduction process
5	2e-12	72 / 522	MF oxidoreductase activity
6	1e-11	15 / 30	BP pigmentation
7	1e-10	104 / 969	MF hydrolase activity
8	1e-09	24 / 101	CC endosome
9	2e-09	12 / 25	MF proton-transporting ATPase activity, rotational mechanism
10	4e-09	13 / 31	BP ATP hydrolysis coupled proton transport
11	5e-09	46 / 321	MF GTPase activity
12	9e-09	30 / 164	BP carbohydrate metabolic process
13	1e-08	16 / 51	CC lysosomal membrane
14	2e-08	16 / 54	BP heart contraction
15	4e-08	467 / 6723	CC membrane
16	5e-08	103 / 1066	CC intracellular
17	5e-08	18 / 71	CC endomembrane system
18	2e-07	26 / 147	BP vesicle-mediated transport
19	3e-07	10 / 24	BP nucleoside metabolic process
20	5e-07	11 / 31	MF hydrogen ion transmembrane transporter activity
21	5e-07	18 / 82	MF lyase activity
22	6e-07	61 / 561	MF GTP binding
23	8e-07	31 / 210	BP intracellular protein transport
24	9e-07	14 / 53	MF pyridoxal phosphate binding
25	9e-07	134 / 1580	CC cellular_component
26	1e-06	99 / 1084	BP transport
27	1e-06	174 / 2189	CC cytoplasm
28	1e-06	17 / 79	MF phosphatidylinositol binding
29	3e-06	61 / 591	BP transmembrane transport
30	3e-06	15 / 67	BP lipid transport
31	6e-06	31 / 231	MF actin binding
32	8e-06	12 / 47	BP proton transport
33	1e-05	14 / 64	MF hydrolase activity, acting on glycosyl bonds
34	1e-05	41 / 355	CC cytosol
35	1e-05	6 / 11	BP purine nucleotide biosynthetic process
36	1e-05	30 / 229	MF transporter activity
37	1e-05	10 / 35	BP sarcomere organization
38	2e-05	418 / 6248	CC integral component of membrane
39	2e-05	12 / 52	BP biosynthetic process
40	3e-05	7 / 18	CC endosome membrane



BP				CC				MF			
Rank	p-value	#in/all	Geneset	Rank	p-value	#in/all	Geneset	Rank	p-value	#in/all	Geneset
1	3e-17	71 / 414	metabolic process	1	4e-15	30 / 96	lysosome	1	7e-16	75 / 480	catalytic activity
2	1e-12	89 / 712	oxidation-reduction process	2	1e-09	24 / 101	endosome	2	2e-12	72 / 522	oxidoreductase activity
3	1e-11	15 / 30	pigmentation	3	1e-08	16 / 51	lysosomal membrane	3	1e-10	104 / 969	hydrolase activity
4	4e-09	13 / 31	ATP hydrolysis coupled proton transport	4	4e-08	467 / 6723	membrane	4	2e-09	12 / 25	proton-transporting ATPase activity, rotational mechanism
5	9e-09	30 / 164	carbohydrate metabolic process	5	5e-08	103 / 1066	intracellular	5	5e-09	46 / 321	GTPase activity
6	2e-08	16 / 54	heart contraction	6	5e-08	18 / 71	endomembrane system	6	5e-07	11 / 31	hydrogen ion transmembrane transporter activity
7	2e-07	26 / 147	vesicle-mediated transport	7	9e-07	134 / 1580	cellular_component	7	5e-07	18 / 82	lyase activity
8	3e-07	10 / 24	nucleoside metabolic process	8	1e-06	174 / 2189	cytoplasm	8	6e-07	61 / 561	GTP binding
9	8e-07	31 / 210	intracellular protein transport	9	1e-05	41 / 355	cytosol	9	9e-07	14 / 53	pyridoxal phosphate binding
10	1e-06	99 / 1084	transport	10	2e-05	418 / 6248	integral component of membrane	10	1e-06	17 / 79	phosphatidylinositol binding
11	3e-06	61 / 591	transmembrane transport	11	3e-05	7 / 18	endosome membrane	11	6e-06	31 / 231	actin binding
12	3e-06	15 / 67	lipid transport	12	3e-05	10 / 38	trans-Golgi network	12	1e-05	14 / 64	hydrolase activity, acting on glycosyl bonds
13	8e-06	12 / 47	proton transport	13	4e-05	6 / 13	proton-transporting V-type ATPase, V0 domain	13	1e-05	30 / 229	transporter activity
14	1e-05	6 / 11	purine nucleotide biosynthetic process	14	4e-05	10 / 39	Z disc	14	5e-04	110 / 1437	molecular_function
15	1e-05	10 / 35	sarcomere organization	15	3e-04	5 / 12	proton-transporting V-type ATPase, V1 domain	15	6e-04	13 / 82	Rab GTPase binding