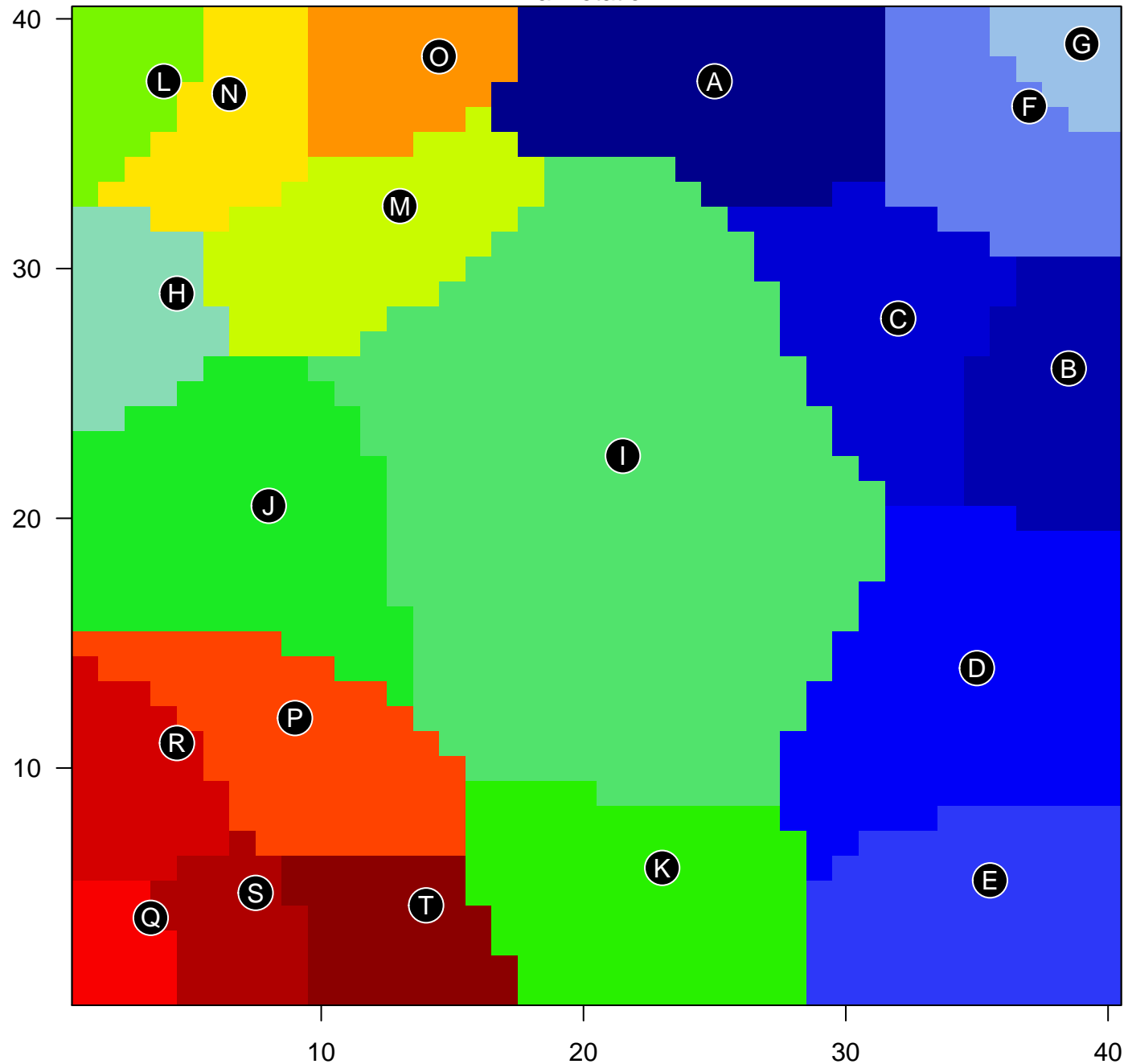
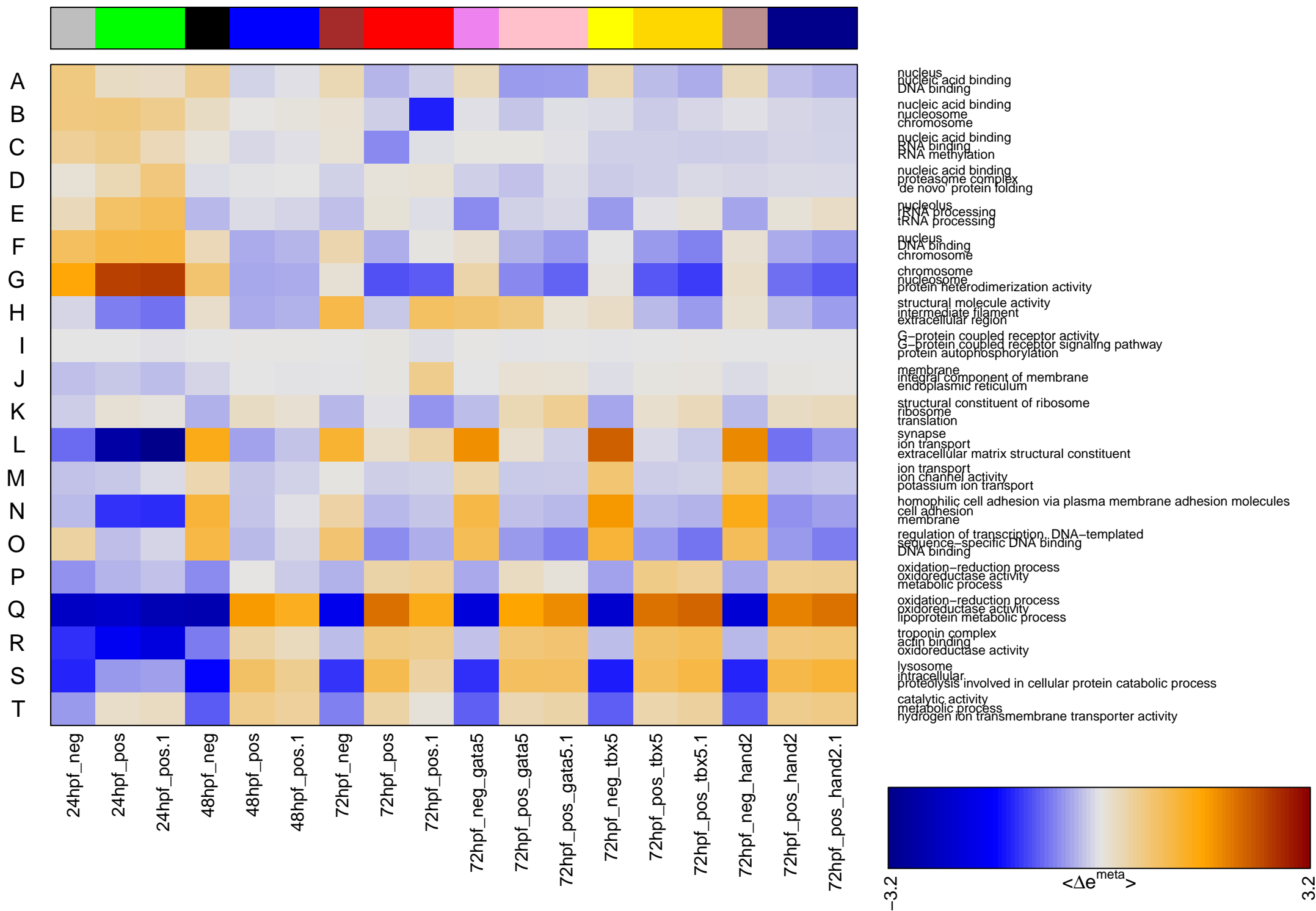


# K-Means Cluster

annotation



- A nucleus  
nucleic acid binding  
nucleosome
- B nucleic acid binding  
nucleosome
- C nucleic acid binding  
RNA binding
- D nucleic acid binding  
proteasome complex
- E nucleolus  
rRNA processing
- F nucleus  
DNA binding
- G chromosome  
nucleosome
- H structural molecule activity  
intermediate filament
- I G-protein coupled receptor activity  
G-protein coupled receptor signaling pathway
- J membrane  
integral component of membrane
- K structural constituent of ribosome  
ribosome
- L synapse  
ion transport
- M ion transport  
ion channel activity
- N homophilic cell adhesion via plasma membrane adhesion molecule  
cell adhesion
- O regulation of transcription, DNA-templated  
sequence-specific DNA binding
- P oxidation-reduction process  
oxidoreductase activity
- Q oxidation-reduction process  
oxidoreductase activity
- R troponin complex  
actin binding
- S lysosome  
intracellular
- T catalytic activity  
metabolic process



# K-Means Cluster

## Spot Summary: A

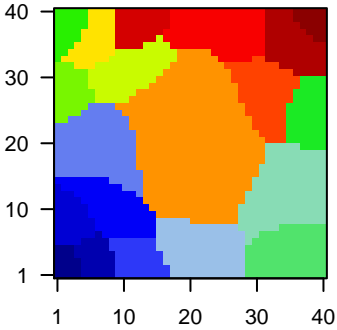
# metagenes = 99  
# genes = 1621

<r> metagenes = 0.83

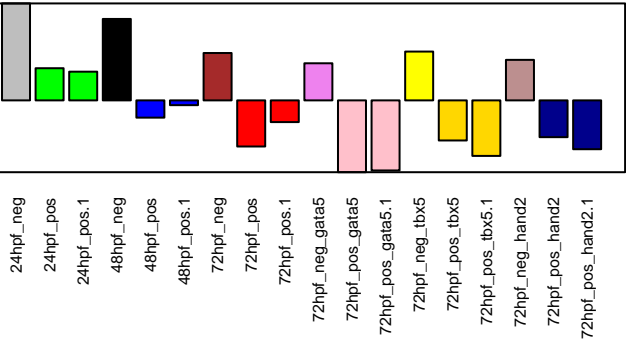
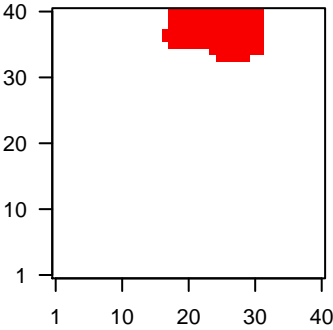
beta: r2= 2.76 / log p= -Inf

# samples with spot = 0 ( 0 %)

Overview Map



Spot

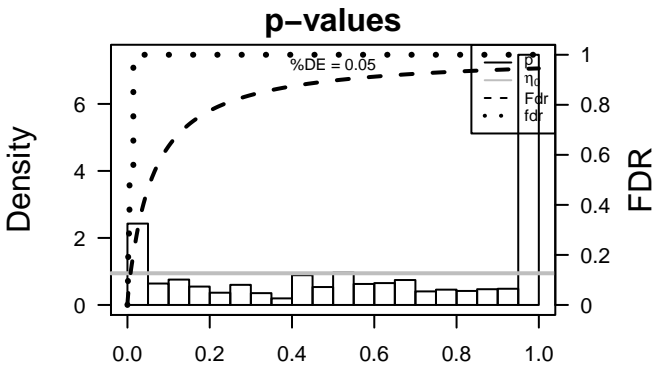


## Spot Genelist

Rank	ID	max e	r	Description	
		min e		Symbol	
1	ENSDARG000	4.38	-2.85	0.68	col28a2a collagen, type XXVIII, alpha 2a [Source:ZFIN;Acc:ZDB-GENE-
2	ENSDARG000	3.19	-3.3	0.52	plp1a proteolipid protein 1a [Source:ZFIN;Acc:ZDB-GENE-001202
3	ENSDARG000	3.06	-1.7	0.69	col7a1 collagen, type VII, alpha 1 [Source:ZFIN;Acc:ZDB-GENE-03
4	ENSDARG000	2.94	-1.72	0.75	sox19a SRY (sex determining region Y)-box 19a [Source:ZFIN;Acc:Z
5	ENSDARG000	2.94	-1.34	0.75	nes Nestin [Source:UniProtKB/Swiss-Prot;Acc:P86839]
6	ENSDARG000	2.91	-2.1	0.79	dld deltaD [Source:ZFIN;Acc:ZDB-GENE-990415-47]
7	ENSDARG000	2.85	-1.19	0.84	zic2b zic family member 2 (odd-paired homolog, Drosophila) b [Sou
8	ENSDARG000	2.75	-1.34	0.64	oligodendrocyte transcription factor 3 [Source:ZFIN;Acc:ZDB-
9	ENSDARG000	2.65	-1.55	0.48	
10	ENSDARG000	2.64	-1.85	0.6	sp8b sp8 transcription factor b [Source:ZFIN;Acc:ZDB-GENE-030
11	ENSDARG000	2.48	-1.49	0.5	
12	ENSDARG000	2.47	-1.28	0.76	igsf9a immunoglobulin superfamily, member 9a [Source:ZFIN;Acc:Zi
13	ENSDARG000	2.46	-1.7	0.58	si:ch211-193l2.3 [Source:ZFIN;Acc:ZDB-GENE-141216-14
14	ENSDARG000	2.38	-2.26	0.4	LOC100503499 and enhancer of split-related 15, tandem duplicate 1 [S
15	ENSDARG000	2.38	-1.82	0.6	her13 hairy-related 13 [Source:ZFIN;Acc:ZDB-GENE-050228-1]
16	ENSDARG000	2.37	-1.24	0.7	pax3a paired box 3a [Source:ZFIN;Acc:ZDB-GENE-980526-52]
17	ENSDARG000	2.36	-3.36	0.55	emilin2a elastin microfibril interfacer 2a [Source:ZFIN;Acc:ZDB-GENE
18	ENSDARG000	2.36	-1.06	0.91	notch3 notch 3 [Source:ZFIN;Acc:ZDB-GENE-000329-5]
19	ENSDARG000	2.3	-1.44	0.7	sox19b SRY (sex determining region Y)-box 19b [Source:ZFIN;Acc:Z
20	ENSDARG000	2.3	-1.78	0.62	tp63 tumor protein p63 [Source:ZFIN;Acc:ZDB-GENE-030819-1]

## Geneset Overrepresentation

Rank	p-value	#in/all	Geneset
1	5e-42	332 / 2716	CC nucleus
2	2e-38	266 / 2030	MF nucleic acid binding
3	5e-32	204 / 1484	MF DNA binding
4	1e-30	179 / 1239	BP regulation of transcription, DNA-templated
5	2e-18	94 / 608	MF RNA binding
6	1e-17	77 / 454	BP multicellular organism development
7	7e-14	32 / 117	BP Wnt signaling pathway
8	9e-10	68 / 537	MF sequence-specific DNA binding
9	1e-07	23 / 115	MF chromatin binding
10	6e-07	68 / 633	MF transcription factor activity, sequence-specific DNA binding
11	9e-07	13 / 45	BP Notch signaling pathway
12	1e-06	9 / 21	BP regulation of canonical Wnt signaling pathway
13	2e-06	14 / 55	BP neuron differentiation
14	2e-06	148 / 1761	MF metal ion binding
15	2e-06	79 / 800	MF zinc ion binding
16	3e-06	12 / 42	BP convergent extension
17	5e-06	7 / 14	BP regulation of Notch signaling pathway
18	6e-06	9 / 25	MF frizzled binding
19	8e-06	65 / 643	BP transcription, DNA-templated
20	1e-05	8 / 21	BP negative regulation of canonical Wnt signaling pathway
21	1e-05	22 / 138	BP cilium assembly
22	1e-05	42 / 362	BP regulation of transcription from RNA polymerase II promoter
23	1e-05	33 / 257	BP cell differentiation
24	2e-05	12 / 50	BP pronephros development
25	3e-05	9 / 30	MF transcription cofactor activity
26	4e-05	26 / 190	MF protein dimerization activity
27	4e-05	9 / 31	MF histone-lysine N-methyltransferase activity
28	4e-05	6 / 13	BP neural retina development
29	4e-05	6 / 13	BP ventral spinal cord interneuron differentiation
30	5e-05	8 / 25	BP cell fate commitment
31	7e-05	6 / 14	BP ATP-dependent chromatin remodeling
32	1e-04	28 / 229	CC chromosome
33	2e-04	9 / 37	MF nucleosomal DNA binding
34	2e-04	5 / 11	BP regulation of cell morphogenesis
35	3e-04	14 / 83	BP embryonic viscerocranium morphogenesis
36	3e-04	7 / 24	BP histone lysine methylation
37	3e-04	12 / 66	MF thiol-dependent ubiquitinyl hydrolase activity
38	4e-04	5 / 12	BP regulation of neurogenesis
39	4e-04	8 / 32	CC chromatin
40	4e-04	6 / 18	BP post-anal tail morphogenesis



BP

Rank

p-value

#in/all

Geneset

11e-30179 / 1239regulation of transcription, DNA-templated

21e-1777 / 454multicellular organism development

37e-1432 / 117Wnt signaling pathway

49e-0713 / 45Notch signaling pathway

51e-069 / 21regulation of canonical Wnt signaling pathway

62e-0614 / 55neuron differentiation

73e-0612 / 42convergent extension

85e-067 / 14regulation of Notch signaling pathway

98e-0665 / 643transcription, DNA-templated

101e-058 / 21negative regulation of canonical Wnt signaling pathway

111e-0522 / 138cilium assembly

121e-0542 / 362regulation of transcription from RNA polymerase II promoter

131e-0533 / 257cell differentiation

142e-0512 / 50pronephros development

154e-056 / 13neural retina development

CC

Rank

p-value

#in/all

Geneset

15e-42332 / 2716nucleus

21e-0428 / 229chromosome

34e-048 / 32chromatin

41e-036 / 22dynein complex

52e-0320 / 168nucleosome

62e-035 / 17U2-type prespliceosome

76e-0311 / 80centrosome

89e-034 / 15intrinsic component of the cytoplasmic side of the plasma membrane

91e-0210 / 76cilium

102e-0216 / 153proteinaceous extracellular matrix

112e-029 / 70cell projection

122e-024 / 19U1 snRNP

132e-027 / 49nucleoplasm

142e-025 / 29integrin complex

153e-024 / 21nuclear membrane

MF

Rank

p-value

#in/all

Geneset

12e-38266 / 2030nucleic acid binding

25e-32204 / 1484DNA binding

32e-1894 / 608RNA binding

49e-1068 / 537sequence-specific DNA binding

51e-0723 / 115chromatin binding

66e-0768 / 633transcription factor activity, sequence-specific DNA binding

72e-06148 / 1761metal ion binding

82e-0679 / 800zinc ion binding

96e-069 / 25frizzled binding

103e-059 / 30transcription cofactor activity

114e-0526 / 190protein dimerization activity

124e-059 / 31histone-lysine N-methyltransferase activity

132e-049 / 37nucleosomal DNA binding

143e-0412 / 66thiol-dependent ubiquitinyl hydrolase activity

155e-049 / 42histone binding

# K-Means Cluster

## Spot Summary: B

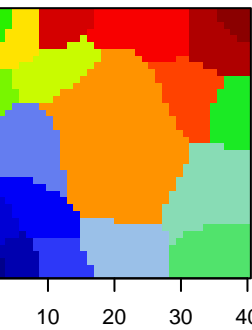
# metagenes = 58  
# genes = 1079

<r> metagenes = 0.88

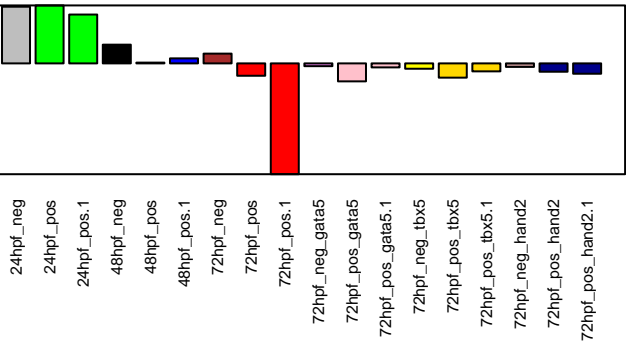
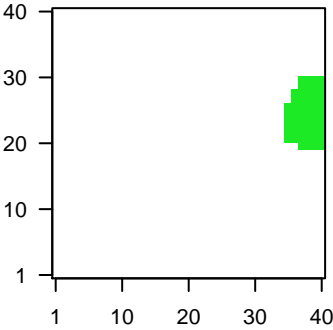
beta: r2= 3.46 / log p= -Inf

# samples with spot = 0 ( 0 %)

Overview Map



Spot

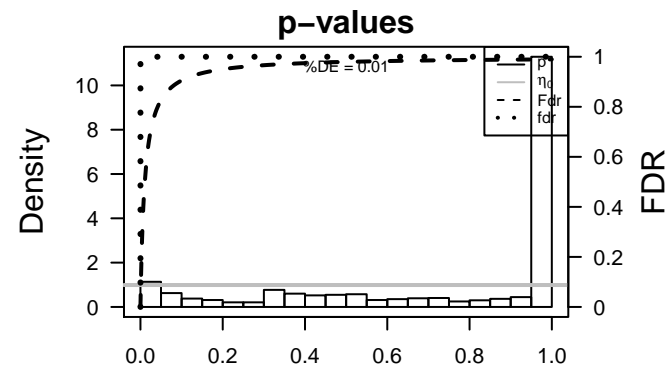


## Spot Genelist

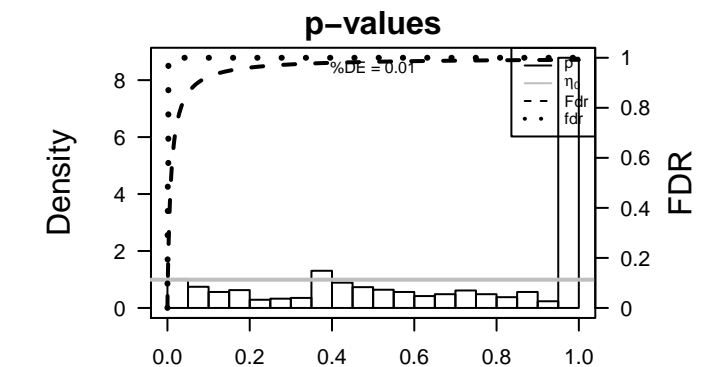
Rank	ID	max e	r	min e	Description
					Symbol
1	ENSDARG0000000001	8.23	-1.2	0.5	ednra endothelin receptor type A [Source:ZFIN;Acc:ZDB-GENE-121214-19]
2	ENSDARG0000000002	5.91	-1.27	0.58	si:dkey-26g8.5-26g8.5 [Source:ZFIN;Acc:ZDB-GENE-121214-19]
3	ENSDARG0000000003	5.48	-1.21	0.55	zgc:174153c:174153 [Source:ZFIN;Acc:ZDB-GENE-080215-7]
4	ENSDARG0000000004	5.31	-1.61	0.55	MGC174153 si:dkey-26g8.4 [Source:ZFIN;Acc:ZDB-GENE-121214-36]
5	ENSDARG0000000005	2.7	-1.67	0.65	ucp3 uncoupling protein 3 [Source:ZFIN;Acc:ZDB-GENE-040426-6]
6	ENSDARG0000000006	2.65	-1.35	0.65	si:ch73-364h19.1364h19.1 [Source:ZFIN;Acc:ZDB-GENE-031010-4]
7	ENSDARG0000000007	2.63	-0.64	0.6	si:dkey-26g8.5-239 [Source:ZFIN;Acc:ZDB-GENE-121214-52]
8	ENSDARG0000000008	2.52	-1.92	0.74	zgc:163040c:163040 [Source:ZFIN;Acc:ZDB-GENE-070927-1]
9	ENSDARG0000000009	2.5	-3.45	0.71	U2 spliceosomal RNA [Source:RFAM;Acc:RF00004]
10	ENSDARG0000000010	2.42	-4.01	0.91	ssbp3a single stranded DNA binding protein 3a [Source:ZFIN;Acc:ZDB-GENE-160113-7]
11	ENSDARG0000000011	2.4	-3.98	0.75	si:dkey-26g8.5-223a13.22 [Source:ZFIN;Acc:ZDB-GENE-160113-7]
12	ENSDARG0000000012	2.34	-2.31	0.91	tons1 tonsoku-like, DNA repair protein [Source:ZFIN;Acc:ZDB-GENE-110914-1]
13	ENSDARG0000000013	2.3	-1.26	0.39	si:dkey-240n22.8 [Source:ZFIN;Acc:ZDB-GENE-110914-1]
14	ENSDARG0000000014	2.27	-3.43	0.96	stil scl/tal1 interrupting locus [Source:ZFIN;Acc:ZDB-GENE-020416-5]
15	ENSDARG0000000015	2.26	-2.2	0.53	
16	ENSDARG0000000016	2.19	-0.96	0.61	tbx6 T-box 6 [Source:ZFIN;Acc:ZDB-GENE-020416-5]
17	ENSDARG0000000017	2.13	-1.76	0.73	zgc:165555c:165555 [Source:ZFIN;Acc:ZDB-GENE-070620-17]
18	ENSDARG0000000018	2.1	-2.66	0.75	LOC56277c:56277 [Source:ZFIN;Acc:ZDB-GENE-070927-1]
19	ENSDARG0000000019	2.09	-0.94	0.69	
20	ENSDARG0000000020	2.07	-2.01	0.87	cenpJ centromere protein J [Source:ZFIN;Acc:ZDB-GENE-030131-1]

## Geneset Overrepresentation

Rank	p-value	#in/all	Geneset
1	2e-67	254 / 2030	MF nucleic acid binding
2	6e-20	39 / 168	CC nucleosome
3	6e-19	44 / 229	CC chromosome
4	6e-18	43 / 232	MF protein heterodimerization activity
5	1e-15	15 / 25	BP membrane disruption in other organism
6	4e-14	15 / 30	BP defense response to Gram-positive bacterium
7	5e-14	181 / 2716	CC nucleus
8	4e-11	109 / 1484	MF DNA binding
9	2e-10	13 / 34	BP chromatin silencing
10	4e-10	14 / 43	BP DNA-templated transcription, initiation
11	3e-09	14 / 49	CC nuclear chromatin
12	9e-07	49 / 608	MF RNA binding
13	8e-06	17 / 128	BP innate immune response
14	1e-05	10 / 49	MF RNA-directed DNA polymerase activity
15	4e-05	15 / 117	BP nucleosome assembly
16	7e-05	9 / 48	BP RNA-dependent DNA biosynthetic process
17	1e-04	10 / 61	MF ubiquitin protein ligase binding
18	1e-04	5 / 14	CC U12-type spliceosomal complex
19	2e-04	12 / 91	BP cellular response to DNA damage stimulus
20	2e-04	16 / 148	BP DNA repair
21	2e-04	11 / 79	BP mRNA splicing, via spliceosome
22	3e-04	6 / 25	MF histone acetyltransferase activity
23	3e-04	5 / 17	CC U2-type prespliceosome
24	5e-04	5 / 18	CC U2 snRNP
25	6e-04	5 / 19	CC U1 snRNP
26	1e-03	5 / 21	CC spindle pole
27	1e-03	4 / 13	CC U5 snRNP
28	1e-03	9 / 70	BP RNA processing
29	2e-03	4 / 14	BP mitotic spindle assembly
30	2e-03	5 / 24	CC precatalytic spliceosome
31	2e-03	76 / 1427	BP biological_process
32	3e-03	4 / 16	BP mitochondrial translation
33	3e-03	4 / 17	MF DNA-directed DNA polymerase activity
34	3e-03	4 / 17	BP spliceosomal complex assembly
35	3e-03	9 / 80	CC centrosome
36	5e-03	5 / 30	MF damaged DNA binding
37	5e-03	5 / 30	MF N-acetyltransferase activity
38	5e-03	3 / 10	CC chromosome, telomeric region
39	5e-03	3 / 10	CC cullin-RING ubiquitin ligase complex
40	5e-03	3 / 10	CC intracellular transport particle B

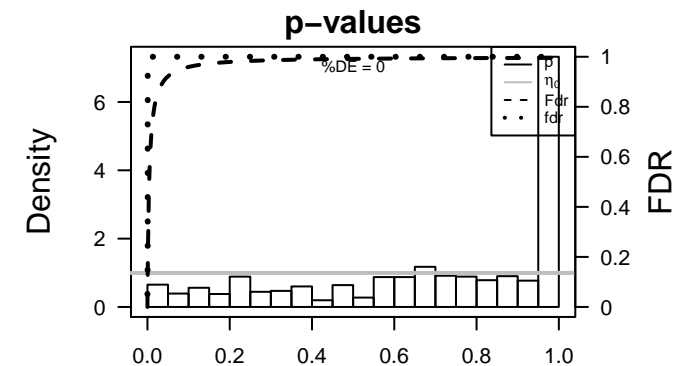


BP				CC				MF			
Rank	p-value	#in/all	Geneset	Rank	p-value	#in/all	Geneset	Rank	p-value	#in/all	Geneset
1	1e-15	15 / 25	membrane disruption in other organism	1	6e-20	39 / 168	nucleosome	1	2e-67	254 / 2030	nucleic acid binding
2	4e-14	15 / 30	defense response to Gram-positive bacterium	2	6e-19	44 / 229	chromosome	2	6e-18	43 / 232	protein heterodimerization activity
3	2e-10	13 / 34	chromatin silencing	3	5e-14	181 / 2716	nucleus	3	4e-11	109 / 1484	DNA binding
4	4e-10	14 / 43	DNA-templated transcription, initiation	4	3e-09	14 / 49	nuclear chromatin	4	9e-07	49 / 608	RNA binding
5	8e-06	17 / 128	innate immune response	5	1e-04	5 / 14	U12-type spliceosomal complex	5	1e-05	10 / 49	RNA-directed DNA polymerase activity
6	4e-05	15 / 117	nucleosome assembly	6	3e-04	5 / 17	U2-type prespliceosome	6	1e-04	10 / 61	ubiquitin protein ligase binding
7	7e-05	9 / 48	RNA-dependent DNA biosynthetic process	7	5e-04	5 / 18	U2 snRNP	7	3e-04	6 / 25	histone acetyltransferase activity
8	2e-04	12 / 91	cellular response to DNA damage stimulus	8	6e-04	5 / 19	U1 snRNP	8	3e-03	4 / 17	DNA-directed DNA polymerase activity
9	2e-04	16 / 148	DNA repair	9	1e-03	5 / 21	spindle pole	9	5e-03	5 / 30	damaged DNA binding
10	2e-04	11 / 79	mRNA splicing, via spliceosome	10	1e-03	4 / 13	U5 snRNP	10	5e-03	5 / 30	N-acetyltransferase activity
11	1e-03	9 / 70	RNA processing	11	2e-03	5 / 24	precatalytic spliceosome	11	6e-03	7 / 57	mRNA binding
12	2e-03	4 / 14	mitotic spindle assembly	12	3e-03	9 / 80	centrosome	12	9e-03	3 / 12	transcription factor activity, RNA polymerase II transcription factor recruiting
13	2e-03	76 / 1427	biological_process	13	5e-03	3 / 10	chromosome, telomeric region	13	1e-02	3 / 14	DNA-dependent ATPase activity
14	3e-03	4 / 16	mitochondrial translation	14	5e-03	3 / 10	cullin-RING ubiquitin ligase complex	14	2e-02	7 / 72	helicase activity
15	3e-03	4 / 17	spliceosomal complex assembly	15	5e-03	3 / 10	intraciliary transport particle B	15	2e-02	5 / 43	iron-sulfur cluster binding



BP				CC				MF			
Rank	p-value	#in/all	Geneset	Rank	p-value	#in/all	Geneset	Rank	p-value	#in/all	Geneset
1	3e-07	7 / 13	RNA methylation	1	3e-04	16 / 138	intracellular ribonucleoprotein complex	1	7e-30	200 / 2030	nucleic acid binding
2	1e-06	15 / 79	mRNA splicing, via spliceosome	2	8e-04	4 / 11	small ribosomal subunit	2	2e-10	62 / 608	RNA binding
3	5e-05	10 / 51	tRNA processing	3	2e-03	7 / 42	spliceosomal complex	3	1e-06	6 / 10	RNA methyltransferase activity
4	3e-04	12 / 88	mRNA processing	4	2e-03	4 / 14	U12-type spliceosomal complex	4	6e-05	17 / 135	methyltransferase activity
5	4e-04	16 / 144	methylation	5	3e-03	144 / 2716	nucleus	5	6e-03	5 / 28	double-stranded DNA binding
6	7e-04	10 / 70	RNA processing	6	4e-03	5 / 26	nuclear speck	6	9e-03	4 / 20	rRNA binding
7	2e-03	19 / 214	translation	7	8e-03	4 / 19	U1 snRNP	7	1e-02	4 / 22	tRNA binding
8	2e-03	4 / 14	mitotic spindle assembly	8	1e-02	13 / 147	ribosome	8	2e-02	11 / 123	cysteine-type peptidase activity
9	2e-03	5 / 23	cytoplasmic translation	9	1e-02	3 / 12	DNA-directed RNA polymerase II, core complex	9	2e-02	8 / 78	cysteine-type endopeptidase activity
10	3e-03	8 / 58	RNA splicing	10	1e-02	5 / 34	catalytic step 2 spliceosome	10	2e-02	12 / 144	structural constituent of ribosome
11	3e-03	4 / 15	mRNA polyadenylation	11	2e-02	3 / 13	cyclin-dependent protein kinase holoenzyme complex	11	2e-02	8 / 80	transcription regulatory region DNA binding
12	4e-03	27 / 362	regulation of transcription from RNA polymerase II promoter	12	2e-02	3 / 13	U5 snRNP	12	2e-02	4 / 26	RNA polymerase II transcription cofactor activity
13	4e-03	42 / 643	transcription, DNA-templated	13	2e-02	12 / 140	nucleolus	13	2e-02	3 / 15	exonuclease activity
14	6e-03	4 / 18	spliceosomal snRNP assembly	14	2e-02	6 / 49	nucleoplasm	14	2e-02	5 / 39	single-stranded DNA binding
15	7e-03	3 / 10	tRNA aminoacylation	15	2e-02	4 / 24	precatalytic spliceosome	15	2e-02	14 / 183	RNA polymerase II transcription factor activity, sequence-specific DNA binding





BP				CC				MF			
Rank	p-value	#in/all	Geneset	Rank	p-value	#in/all	Geneset	Rank	p-value	#in/all	Geneset
1	2e-04	6 / 12	'de novo' protein folding	1	3e-05	13 / 43	proteasome complex	1	1e-33	331 / 2030	nucleic acid binding
2	5e-04	11 / 42	cilium movement	2	4e-04	8 / 23	proteasome core complex	2	3e-04	8 / 22	threonine-type endopeptidase activity
3	1e-03	5 / 11	positive regulation of guanylate cyclase activity	3	7e-04	5 / 10	chaperonin-containing T-complex	3	4e-04	6 / 13	protein binding involved in protein folding
4	1e-03	6 / 16	DNA integration	4	7e-03	4 / 10	proteasome core complex, alpha-subunit complex	4	6e-04	10 / 36	endopeptidase activity
5	3e-03	8 / 31	chaperone-mediated protein folding	5	9e-03	8 / 36	P-body	5	7e-04	5 / 10	endodeoxyribonuclease activity
6	4e-03	5 / 14	transcription elongation from RNA polymerase II promoter	6	1e-02	4 / 11	P granule	6	7e-03	4 / 10	acetylglucosaminyltransferase activity
7	5e-03	6 / 20	nucleotide-excision repair	7	2e-02	8 / 42	spliceosomal complex	7	7e-03	7 / 28	hydrolase activity, acting on ester bonds
8	6e-03	5 / 15	mRNA polyadenylation	8	5e-02	5 / 24	precatalytic spliceosome	8	3e-02	4 / 15	adrenergic receptor activity
9	7e-03	14 / 80	liver development	9	6e-02	3 / 11	integral component of mitochondrial outer membrane	9	4e-02	5 / 23	fibroblast growth factor receptor binding
10	7e-03	4 / 10	nuclear-transcribed mRNA catabolic process	10	6e-02	6 / 34	catalytic step 2 spliceosome	10	4e-02	8 / 47	nucleotidyltransferase activity
11	8e-03	5 / 16	response to ionizing radiation	11	8e-02	7 / 45	ubiquitin ligase complex	11	4e-02	6 / 31	ubiquitin binding
12	1e-02	5 / 18	spliceosomal snRNP assembly	12	9e-02	3 / 13	proteasome regulatory particle, base subcomplex	12	5e-02	3 / 10	small protein activating enzyme activity
13	2e-02	8 / 40	erythrocyte differentiation	13	9e-02	3 / 13	viral nucleocapsid	13	5e-02	5 / 25	ATP-dependent microtubule motor activity, plus-end-directed
14	2e-02	8 / 40	regulation of translation	14	1e-01	10 / 76	cilium	14	6e-02	4 / 18	insulin receptor binding
15	2e-02	5 / 19	embryonic heart tube morphogenesis	15	1e-01	3 / 14	peroxisomal membrane	15	7e-02	3 / 12	secondary active sulfate transmembrane transporter activity

# K-Means Cluster

## Spot Summary: E

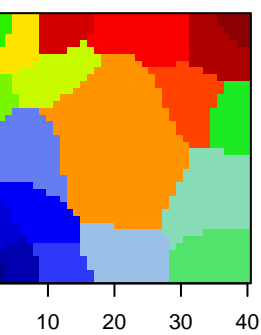
# metagenes = 88  
# genes = 1579

<r> metagenes = 0.83

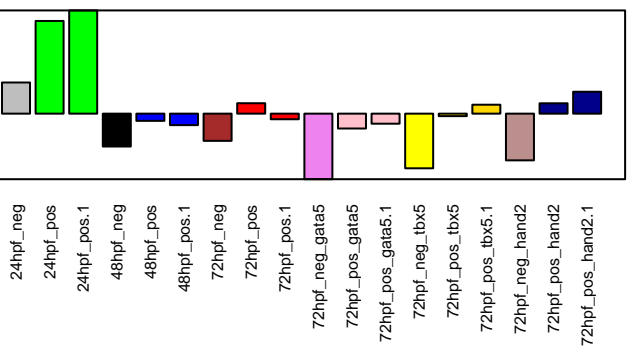
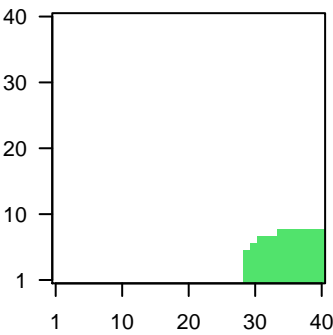
beta: r2= 3.36 / log p= -Inf

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

Overview Map



Spot

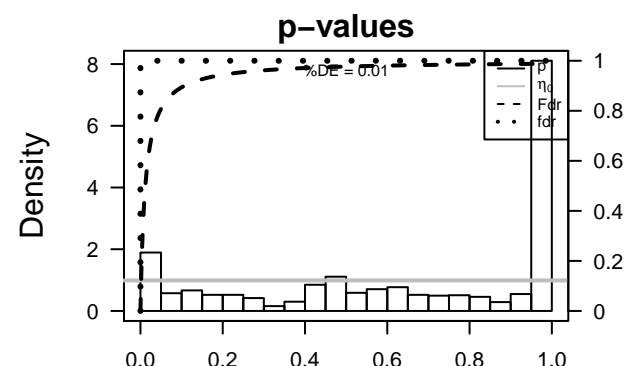


## Spot Genelist

Rank	ID	max e	r	Description			
		min e		Symbol			
1	ENSDARG000	8.47	-3.84	0.32			
2	ENSDARG000	8.19	-3.48	0.3			
3	ENSDARG000	8.13	-3.52	0.3			
4	ENSDARG000	8.08	-3.28	0.26			
5	ENSDARG000	6.87	-3.45	0.31			
6	ENSDARG000	6.62	-1.54	0.13			
7	ENSDARG000	5.93	-1.57	0.71	cyp7a1b		
8	ENSDARG000	5.27	-3.73	0.33			
9	ENSDARG000	5.15	-3.14	0.36			
10	ENSDARG000	5.09	-3.4	0.32			
11	ENSDARG000	5.06	-3.18	0.35			
12	ENSDARG000	4.97	-3.11	0.35			
13	ENSDARG000	4.93	-3.21	0.36			
14	ENSDARG000	4.13	-2.81	0.84	mrc1a	mannose receptor, C type 1a [Source:ZFIN;Acc:ZDB-GENE-	
15	ENSDARG000	4.07	-2.7	0.34			
16	ENSDARG000	3.95	-1.46	0.23			zgc:158463 [Source:ZFIN;Acc:ZDB-GENE-070410-9]
17	ENSDARG000	3.89	-1.94	0.8			nkx2.7
18	ENSDARG000	3.75	-3.16	0.75	dnase14d	deoxyribonuclease 1 like 4, tandem duplicate 1 [Source:ZFIN	
19	ENSDARG000	3.73	-2.69	0.09			
20	ENSDARG000	3.53	-3.11	0.83			ikzf1

## Geneset Overrepresentation

Rank	p-value	#in/all	Geneset
1	2e-22	45 / 140	CC nucleolus
2	7e-14	20 / 45	BP rRNA processing
3	1e-13	21 / 51	BP tRNA processing
4	5e-11	17 / 43	BP ribosome biogenesis
5	7e-10	10 / 15	BP pseudouridine synthesis
6	2e-09	28 / 135	MF methyltransferase activity
7	2e-09	29 / 144	BP methylation
8	2e-09	10 / 16	BP ribosomal large subunit biogenesis
9	7e-09	16 / 50	MF translation initiation factor activity
10	1e-08	174 / 2030	MF nucleic acid binding
11	1e-08	11 / 23	CC small-subunit processome
12	3e-08	16 / 55	BP translational initiation
13	4e-08	8 / 12	MF pseudouridine synthase activity
14	1e-07	8 / 13	BP RNA modification
15	1e-07	10 / 22	MF tRNA binding
16	2e-07	50 / 410	CC mitochondrion
17	4e-07	8 / 15	BP tRNA methylation
18	5e-07	7 / 11	BP maturation of SSU-rRNA
19	7e-07	25 / 148	BP DNA repair
20	1e-06	64 / 608	MF RNA binding
21	5e-06	6 / 10	MF snoRNA binding
22	7e-06	7 / 15	MF RNA polymerase III activity
23	1e-05	29 / 214	BP translation
24	1e-05	11 / 41	MF aminoacyl-tRNA ligase activity
25	1e-05	7 / 16	CC preribosome, large subunit precursor
26	1e-05	14 / 66	MF ligase activity
27	2e-05	6 / 12	CC eukaryotic 48S preinitiation complex
28	3e-05	7 / 18	CC DNA-directed RNA polymerase III complex
29	3e-05	7 / 18	CC eukaryotic translation initiation factor 3 complex
30	6e-05	6 / 14	BP formation of translation preinitiation complex
31	1e-04	7 / 21	MF S-adenosylmethionine-dependent methyltransferase activity
32	1e-04	5 / 10	CC eukaryotic 43S preinitiation complex
33	1e-04	7 / 22	MF metalloaminopeptidase activity
34	2e-04	9 / 37	MF DNA-directed 5'-3' RNA polymerase activity
35	2e-04	5 / 11	BP regulation of translational initiation
36	3e-04	9 / 40	BP tRNA aminoacylation for protein translation
37	3e-04	160 / 2189	CC cytoplasm
38	3e-04	5 / 12	BP tRNA modification
39	4e-04	86 / 1063	MF transferase activity
40	5e-04	5 / 13	BP NLS-bearing protein import into nucleus



BP				CC				MF			
Rank	p-value	#in/all	Geneset	Rank	p-value	#in/all	Geneset	Rank	p-value	#in/all	Geneset
1	7e-14	20 / 45	rRNA processing	1	2e-22	45 / 140	nucleolus	1	2e-09	28 / 135	methyltransferase activity
2	1e-13	21 / 51	tRNA processing	2	1e-08	11 / 23	small-subunit processome	2	7e-09	16 / 50	translation initiation factor activity
3	5e-11	17 / 43	ribosome biogenesis	3	2e-07	50 / 410	mitochondrion	3	1e-08	174 / 2030	nucleic acid binding
4	7e-10	10 / 15	pseudouridine synthesis	4	1e-05	7 / 16	preribosome, large subunit precursor	4	4e-08	8 / 12	pseudouridine synthase activity
5	2e-09	29 / 144	methylation	5	2e-05	6 / 12	eukaryotic 48S preinitiation complex	5	1e-07	10 / 22	tRNA binding
6	2e-09	10 / 16	ribosomal large subunit biogenesis	6	3e-05	7 / 18	DNA-directed RNA polymerase III complex	6	1e-06	64 / 608	RNA binding
7	3e-08	16 / 55	translational initiation	7	3e-05	7 / 18	eukaryotic translation initiation factor 3 complex	7	5e-06	6 / 10	snoRNA binding
8	1e-07	8 / 13	RNA modification	8	1e-04	5 / 10	eukaryotic 43S preinitiation complex	8	7e-06	7 / 15	RNA polymerase III activity
9	4e-07	8 / 15	tRNA methylation	9	3e-04	160 / 2189	cytoplasm	9	1e-05	11 / 41	aminoacyl-tRNA ligase activity
10	5e-07	7 / 11	maturation of SSU-rRNA	10	8e-04	6 / 21	nuclear membrane	10	1e-05	14 / 66	ligase activity
11	7e-07	25 / 148	DNA repair	11	3e-03	6 / 26	nuclear pore	11	1e-04	7 / 21	S-adenosylmethionine-dependent methyltransferase activity
12	1e-05	29 / 214	translation	12	5e-03	113 / 1580	cellular_component	12	1e-04	7 / 22	metalloaminopeptidase activity
13	6e-05	6 / 14	formation of translation preinitiation complex	13	5e-03	7 / 38	nuclear envelope	13	2e-04	9 / 37	DNA-directed 5'-3' RNA polymerase activity
14	2e-04	5 / 11	regulation of translational initiation	14	6e-03	4 / 14	M band	14	4e-04	86 / 1063	transferase activity
15	3e-04	9 / 40	tRNA aminoacylation for protein translation	15	7e-03	21 / 209	endoplasmic reticulum membrane	15	8e-04	6 / 21	Ran GTPase binding

# K-Means Cluster

## Spot Summary: F

# metagenes = 65  
# genes = 1082

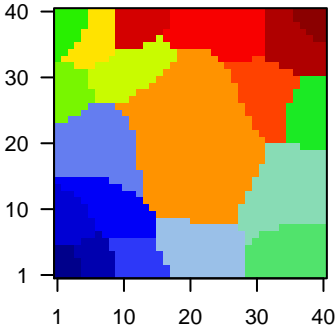
<r> metagenes = 0.9

beta: r2= 6.3 / log p= -Inf

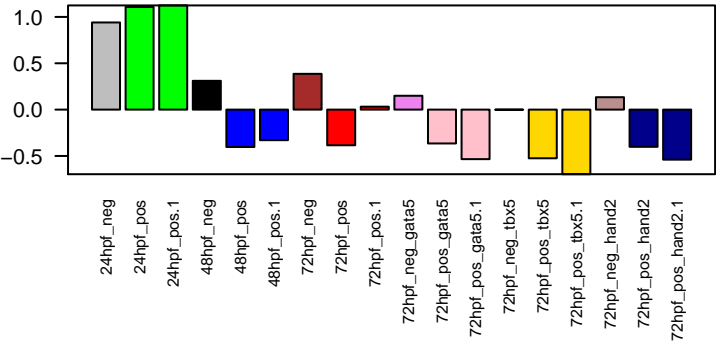
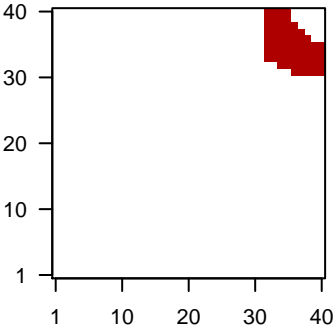
# samples with spot = 3 ( 16.7 %)

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

Overview Map



Spot

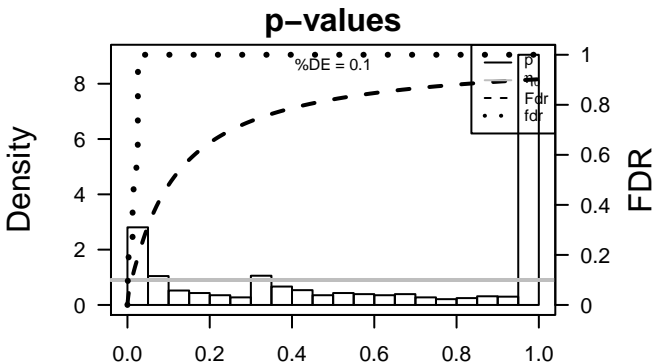


## Spot Genelist

Rank	ID	max e	r	min e	Description
					Symbol
1	ENSDARG000	3.53	-2.37	0.59	sele selectin E [Source:ZFIN;Acc:ZDB-GENE-041014-221]
2	ENSDARG000	3.22	-4.34	0.39	collagen, type XIV, alpha 1b [Source:ZFIN;Acc:ZDB-GENE-041014-221]
3	ENSDARG000	2.9	-2.63	0.61	
4	ENSDARG000	2.82	-0.76	0.54	
5	ENSDARG000	2.8	-4.02	0.63	capn12 calpain 12 [Source:ZFIN;Acc:ZDB-GENE-050419-245]
6	ENSDARG000	2.75	-1.65	0.66	gins1 GINS complex subunit 1 (Psf1 homolog) [Source:ZFIN;Acc:ZDB-GENE-050419-245]
7	ENSDARG000	2.69	-3.04	0.58	hbbe2 hemoglobin beta embryonic-2 [Source:ZFIN;Acc:ZDB-GENE-050419-245]
8	ENSDARG000	2.67	-2.02	0.7	f2r coagulation factor II (thrombin) receptor [Source:ZFIN;Acc:ZDB-GENE-050419-245]
9	ENSDARG000	2.66	-1.9	0.66	pdia2 protein disulfide isomerase family A, member 2 [Source:ZFIN;Acc:ZDB-GENE-050419-245]
10	ENSDARG000	2.65	-1.32	0.61	helb helicase (DNA) B [Source:ZFIN;Acc:ZDB-GENE-030729-16]
11	ENSDARG000	2.57	-1.21	0.59	
12	ENSDARG000	2.57	-2.05	0.49	crhbp corticotropin releasing hormone binding protein [Source:ZFIN;Acc:ZDB-GENE-030729-16]
13	ENSDARG000	2.56	-2.1	0.8	fibpb EGF containing fibulin-like extracellular matrix protein 2b [Source:ZFIN;Acc:ZDB-GENE-030729-16]
14	ENSDARG000	2.52	-2.36	0.68	slc22a13 solute carrier family 22 member 13.3 [Source:ZFIN;Acc:ZDB-GENE-141222-2]
15	ENSDARG000	2.51	-1.21	0.83	atp2b1a ATPase, Ca++ transporting, plasma membrane 1a [Source:ZFIN;Acc:ZDB-GENE-141222-2]
16	ENSDARG000	2.48	-1.83	0.81	scube2 signal peptide, CUB domain, EGF-like 2 [Source:ZFIN;Acc:ZDB-GENE-141222-2]
17	ENSDARG000	2.45	-2.43	0.7	
18	ENSDARG000	2.44	-1.1	0.82	slc22a13 solute carrier family 22 member 13.3 [Source:ZFIN;Acc:ZDB-GENE-141222-2]
19	ENSDARG000	2.41	-1.34	0.77	ell2 elongation factor, RNA polymerase II, 2 [Source:ZFIN;Acc:ZDB-GENE-141222-2]
20	ENSDARG000	2.39	-1.76	0.62	urb2 URB2 ribosome biogenesis 2 homolog (S. cerevisiae) [Source:ZFIN;Acc:ZDB-GENE-141222-2]

## Geneset Overrepresentation

Rank	p-value	#in/all	Geneset
1	4e-56	280 / 2716	CC nucleus
2	5e-38	169 / 1484	MF DNA binding
3	5e-34	61 / 229	CC chromosome
4	1e-29	49 / 168	CC nucleosome
5	2e-26	33 / 78	BP DNA replication
6	5e-24	37 / 117	BP nucleosome assembly
7	8e-18	43 / 232	MF protein heterodimerization activity
8	3e-15	14 / 22	BP DNA replication initiation
9	7e-15	16 / 32	BP DNA duplex unwinding
10	9e-15	31 / 148	BP DNA repair
11	2e-12	100 / 1239	BP regulation of transcription, DNA-templated
12	3e-10	48 / 454	BP multicellular organism development
13	7e-10	8 / 11	BP RNA export from nucleus
14	5e-09	12 / 36	BP protein import into nucleus
15	7e-09	20 / 110	BP cell cycle
16	1e-08	16 / 72	MF helicase activity
17	1e-08	12 / 39	MF single-stranded DNA binding
18	8e-08	54 / 643	BP transcription, DNA-templated
19	3e-07	16 / 91	BP cellular response to DNA damage stimulus
20	4e-07	46 / 537	MF sequence-specific DNA binding
21	4e-07	18 / 115	MF chromatin binding
22	9e-07	9 / 29	CC kinetochore
23	1e-06	6 / 11	MF DNA helicase activity
24	1e-06	6 / 11	MF structural constituent of nuclear pore
25	2e-06	7 / 17	MF DNA-directed DNA polymerase activity
26	3e-06	8 / 25	BP membrane disruption in other organism
27	1e-05	7 / 22	CC chromosome, centromeric region
28	1e-05	8 / 30	BP defense response to Gram-positive bacterium
29	1e-05	104 / 1787	MF ATP binding
30	2e-05	8 / 31	BP lymphangiogenesis
31	2e-05	12 / 72	BP nucleic acid phosphodiester bond hydrolysis
32	2e-05	5 / 10	BP adenohypophysis development
33	2e-05	6 / 16	BP G1/S transition of mitotic cell cycle
34	2e-05	9 / 41	BP positive regulation of cell proliferation
35	3e-05	14 / 100	BP peptidyl-tyrosine phosphorylation
36	3e-05	9 / 43	BP DNA-templated transcription, initiation
37	3e-05	5 / 11	BP mitotic spindle assembly checkpoint
38	5e-05	12 / 79	BP cell division
39	5e-05	44 / 608	MF RNA binding
40	6e-05	45 / 633	MF transcription factor activity, sequence-specific DNA binding



BP				CC				MF			
Rank	p-value	#in/all	Geneset	Rank	p-value	#in/all	Geneset	Rank	p-value	#in/all	Geneset
1	2e-26	33 / 78	DNA replication	1	4e-56	280 / 2716	nucleus	1	5e-38	169 / 1484	DNA binding
2	5e-24	37 / 117	nucleosome assembly	2	5e-34	61 / 229	chromosome	2	8e-18	43 / 232	protein heterodimerization activity
3	3e-15	14 / 22	DNA replication initiation	3	1e-29	49 / 168	nucleosome	3	1e-08	16 / 72	helicase activity
4	7e-15	16 / 32	DNA duplex unwinding	4	9e-07	9 / 29	kinetochore	4	1e-08	12 / 39	single-stranded DNA binding
5	9e-15	31 / 148	DNA repair	5	1e-05	7 / 22	chromosome, centromeric region	5	4e-07	46 / 537	sequence-specific DNA binding
6	2e-12	100 / 1239	regulation of transcription, DNA-templated	6	9e-05	9 / 49	nuclear chromatin	6	4e-07	18 / 115	chromatin binding
7	3e-10	48 / 454	multicellular organism development	7	1e-04	16 / 140	nucleolus	7	1e-06	6 / 11	DNA helicase activity
8	7e-10	8 / 11	RNA export from nucleus	8	1e-04	5 / 14	condensed chromosome kinetochore	8	1e-06	6 / 11	structural constituent of nuclear pore
9	5e-09	12 / 36	protein import into nucleus	9	2e-04	11 / 80	centrosome	9	2e-06	7 / 17	DNA-directed DNA polymerase activity
10	7e-09	20 / 110	cell cycle	10	4e-04	12 / 98	transcription factor complex	10	1e-05	104 / 1787	ATP binding
11	8e-08	54 / 643	transcription, DNA-templated	11	8e-04	5 / 20	centriole	11	5e-05	44 / 608	RNA binding
12	3e-07	16 / 91	cellular response to DNA damage stimulus	12	1e-03	7 / 42	spliceosomal complex	12	6e-05	45 / 633	transcription factor activity, sequence-specific DNA binding
13	3e-06	8 / 25	membrane disruption in other organism	13	2e-03	5 / 23	small-subunit processome	13	8e-05	9 / 48	transcription corepressor activity
14	1e-05	8 / 30	defense response to Gram-positive bacterium	14	2e-03	4 / 15	basement membrane	14	1e-04	5 / 14	ATP-dependent DNA helicase activity
15	2e-05	8 / 31	lymphangiogenesis	15	3e-03	5 / 26	nuclear pore	15	1e-04	9 / 52	transmembrane receptor protein tyrosine kinase activity

# K-Means Cluster

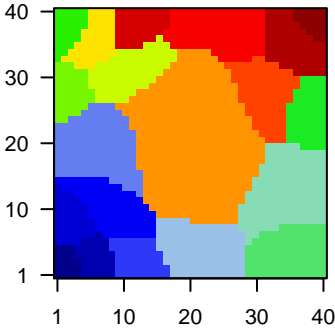
## Spot Summary: G

# metagenes = 19  
# genes = 366

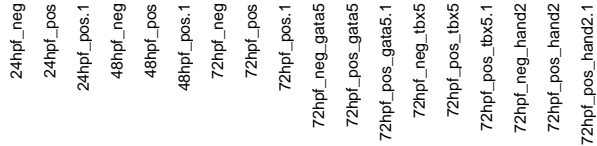
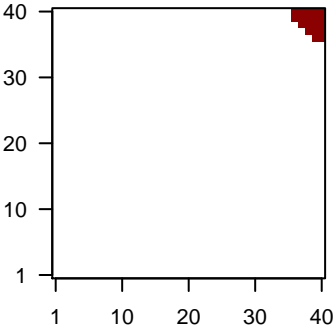
<r> metagenes = 0.98  
<r> genes = 0.7  
beta: r2= 19.09 / log p= -Inf

# samples with spot = 4 ( 22.2 % )  
24hpf\_neg : 1 ( 100 % )  
24hpf\_pos : 2 ( 100 % )  
48hpf\_neg : 1 ( 100 % )

Overview Map



Spot



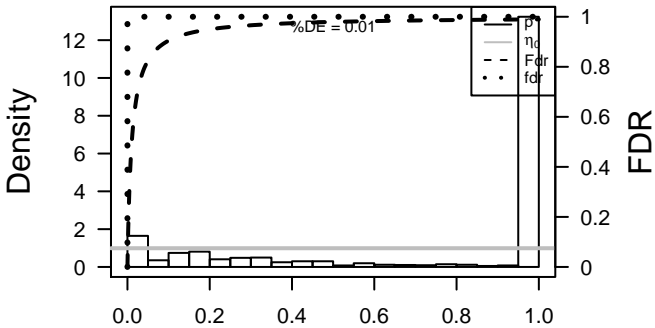
## Spot Genelist

Rank	ID	max e	r	min e	Description
					Symbol
1	ENSDARG000	8.12	-6.4	0.86	hbbe3 hemoglobin beta embryonic-3 [Source:ZFIN;Acc:ZDB-GENE-991213-3]
2	ENSDARG000	7.83	-4.49	0.95	drl draculin [Source:ZFIN;Acc:ZDB-GENE-991213-3]
3	ENSDARG000	7.74	-1.79	0.56	LOC100506671 LOC100506671-11n16.3 [Source:ZFIN;Acc:ZDB-GENE-131121-8]
4	ENSDARG000	7.36	-4.55	0.95	si:dkey-261k4.4-261j4.4 [Source:ZFIN;Acc:ZDB-GENE-060531-125]
5	ENSDARG000	7.35	-4.2	0.91	blf bloody fingers [Source:ZFIN;Acc:ZDB-GENE-050721-1]
6	ENSDARG000	7.06	-5.06	0.94	si:dkey-261k4.3-261j4.3 [Source:ZFIN;Acc:ZDB-GENE-060531-124]
7	ENSDARG000	6.46	-4.6	0.73	protogenin homolog b (Gallus gallus) [Source:ZFIN;Acc:ZDB-GENE-041210-336]
8	ENSDARG000	6.43	-3.22	0.91	stab2 stabilin 2 [Source:ZFIN;Acc:ZDB-GENE-041210-336]
9	ENSDARG000	6.31	-1.79	0.88	ela2l elastase 2 like [Source:ZFIN;Acc:ZDB-GENE-040511-1]
10	ENSDARG000	6.11	-4.16	0.95	tfr1a transferrin receptor 1a [Source:ZFIN;Acc:ZDB-GENE-04122]
11	ENSDARG000	6	-2.33	0.91	si:ch73-299h12.2 [Source:ZFIN;Acc:ZDB-GENE-081031-7]
12	ENSDARG000	5.97	-3.89	0.92	kif17 Kruppel-like factor 17 [Source:ZFIN;Acc:ZDB-GENE-01012]
13	ENSDARG000	5.89	-1.29	0.56	zgc:174855c:174855 [Source:ZFIN;Acc:ZDB-GENE-071004-74]
14	ENSDARG000	5.69	-3.46	0.93	gata1a GATA binding protein 1a [Source:ZFIN;Acc:ZDB-GENE-980]
15	ENSDARG000	5.69	-3.04	0.9	gfi1b growth factor independent 1B transcription repressor [Source:ZFIN;Acc:ZDB-GENE-071004-74]
16	ENSDARG000	5.53	-3.53	0.83	znf2a zinc finger-like gene 2a [Source:ZFIN;Acc:ZDB-GENE-0308]
17	ENSDARG000	5.51	-4.09	0.87	znf2a zinc finger-like gene 2a [Source:ZFIN;Acc:ZDB-GENE-0308]
18	ENSDARG000	5.45	-1.91	0.8	cpox coproporphyrinogen oxidase [Source:ZFIN;Acc:ZDB-GENE-071004-74]
19	ENSDARG000	5.42	-2.18	0.83	hmbsb hydroxymethylbilane synthase, b [Source:ZFIN;Acc:ZDB-GENE-071004-74]
20	ENSDARG000	5.39	-4.85	0.91	hdr hematopoietic death receptor [Source:ZFIN;Acc:ZDB-GENE-071004-74]

## Geneset Overrepresentation

Rank	p-value	#in/all	Geneset
1	4e-33	40 / 229	CC chromosome
2	7e-32	35 / 168	CC nucleosome
3	8e-27	35 / 232	MF protein heterodimerization activity
4	1e-26	19 / 37	MF nucleosomal DNA binding
5	1e-24	26 / 117	BP nucleosome assembly
6	3e-19	67 / 1484	MF DNA binding
7	1e-16	10 / 14	CC hemoglobin complex
8	1e-14	10 / 19	MF oxygen binding
9	1e-14	10 / 19	BP oxygen transport
10	1e-14	10 / 19	MF oxygen transporter activity
11	3e-13	82 / 2716	CC nucleus
12	1e-12	10 / 28	BP embryonic hemopoiesis
13	6e-11	11 / 52	BP blood vessel development
14	7e-11	10 / 40	BP erythrocyte differentiation
15	2e-08	7 / 24	BP myeloid cell differentiation
16	2e-08	6 / 15	BP heme biosynthetic process
17	6e-08	13 / 145	MF heme binding
18	1e-07	8 / 46	BP mitotic cell cycle
19	5e-07	7 / 38	BP vasculogenesis
20	2e-06	10 / 110	MF protein tyrosine kinase activity
21	4e-06	12 / 178	MF iron ion binding
22	6e-06	4 / 10	BP mitotic sister chromatid segregation
23	7e-06	9 / 100	BP peptidyl-tyrosine phosphorylation
24	9e-06	9 / 104	BP transmembrane receptor protein tyrosine kinase signaling pathway
25	2e-05	45 / 1787	MF ATP binding
26	3e-05	9 / 121	BP angiogenesis
27	6e-05	7 / 75	BP hemopoiesis
28	7e-05	5 / 34	BP ephrin receptor signaling pathway
29	7e-05	4 / 18	BP cell morphogenesis
30	8e-05	7 / 79	BP cell division
31	9e-05	18 / 491	MF kinase activity
32	1e-04	11 / 210	MF protein binding
33	1e-04	4 / 21	BP erythrocyte development
34	2e-04	18 / 522	BP phosphorylation
35	2e-04	6 / 66	BP sprouting angiogenesis
36	2e-04	4 / 24	BP primitive hemopoiesis
37	4e-04	36 / 1506	MF nucleotide binding
38	4e-04	5 / 47	MF nuclease activity
39	4e-04	3 / 12	BP hemoglobin biosynthetic process
40	4e-04	6 / 75	MF microtubule motor activity

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-24	26 / 117	nucleosome assembly	1	4e-33	40 / 229	chromosome	1	8e-27	35 / 232	protein heterodimerization activity
2	1e-14	10 / 19	oxygen transport	2	7e-32	35 / 168	nucleosome	2	1e-26	19 / 37	nucleosomal DNA binding
3	1e-12	10 / 28	embryonic hemopoiesis	3	1e-16	10 / 14	hemoglobin complex	3	3e-19	67 / 1484	DNA binding
4	6e-11	11 / 52	blood vessel development	4	3e-13	82 / 2716	nucleus	4	1e-14	10 / 19	oxygen binding
5	7e-11	10 / 40	erythrocyte differentiation	5	5e-04	4 / 29	kinetochore	5	1e-14	10 / 19	oxygen transporter activity
6	2e-08	7 / 24	myeloid cell differentiation	6	7e-04	5 / 54	kinesin complex	6	6e-08	13 / 145	heme binding
7	2e-08	6 / 15	heme biosynthetic process	7	1e-02	2 / 12	mitotic spindle	7	2e-06	10 / 110	protein tyrosine kinase activity
8	1e-07	8 / 46	mitotic cell cycle	8	1e-02	19 / 809	integral component of plasma membrane	8	4e-06	12 / 178	iron ion binding
9	5e-07	7 / 38	vasculogenesis	9	1e-02	2 / 13	transcriptional repressor complex	9	2e-05	45 / 1787	ATP binding
10	6e-06	4 / 10	mitotic sister chromatid segregation	10	2e-02	8 / 268	cytoskeleton	10	9e-05	18 / 491	kinase activity
11	7e-06	9 / 100	peptidyl-tyrosine phosphorylation	11	3e-02	2 / 22	cell cortex	11	1e-04	11 / 210	protein binding
12	9e-06	9 / 104	transmembrane receptor protein tyrosine kinase signaling pathway	12	3e-02	2 / 22	chromosome, centromeric region	12	4e-04	36 / 1506	nucleotide binding
13	3e-05	9 / 121	angiogenesis	13	4e-02	2 / 23	spindle	13	4e-04	5 / 47	nuclease activity
14	6e-05	7 / 75	hemopoiesis	14	4e-02	4 / 98	transcription factor complex	14	4e-04	6 / 75	microtubule motor activity
15	7e-05	5 / 34	ephrin receptor signaling pathway	15	5e-02	4 / 108	microtubule	15	6e-04	5 / 52	transmembrane receptor protein tyrosine kinase activity



# K-Means Cluster

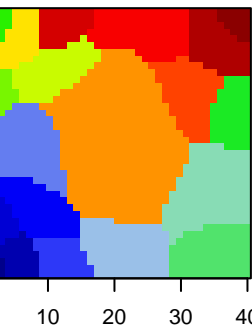
## Spot Summary: H

# metagenes = 41  
# genes = 628

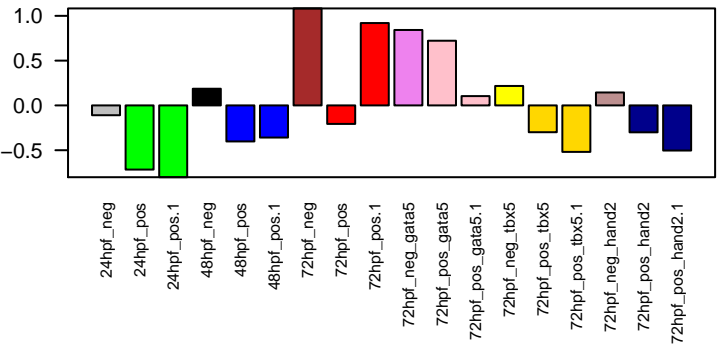
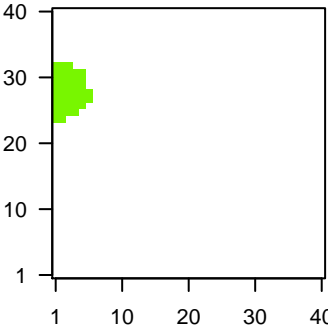
<r> metagenes = 0.87  
<r> genes = 0.41  
beta: r2= 5.38 / log p= -lnf

# samples with spot = 3 ( 16.7 %)  
72hpf\_neg : 1 ( 100 %)  
72hpf\_pos : 1 ( 50 %)  
72hpf\_neg\_gata5 : 1 ( 100 %)

Overview Map



Spot

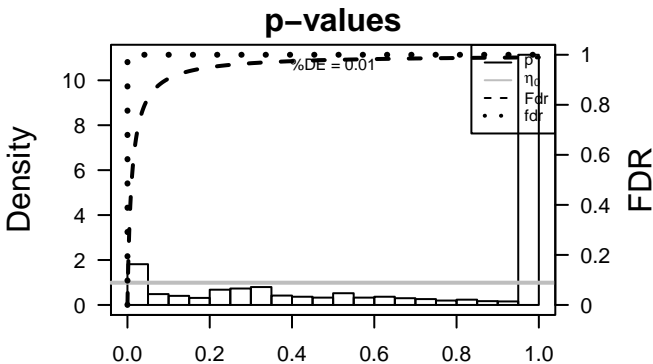


## Spot Genelist

Rank	ID	max e	r	Description
		min e		Symbol
1	ENSDARG0000000000	11.88	-0.87	0.47
2	ENSDARG0000000000	7.94	-1.47	0.51
3	ENSDARG0000000000	5.13	-1.38	0.48
4	ENSDARG0000000000	4.62	-1.7	0.36
5	ENSDARG0000000000	4.19	-2.48	0.81
6	ENSDARG0000000000	4.12	-3.12	0.9
7	ENSDARG0000000000	3.92	-3.3	0.68
8	ENSDARG0000000000	3.86	-2.03	0.39
9	ENSDARG0000000000	3.84	-1.98	0.32
10	ENSDARG0000000000	3.81	-3.87	0.7
11	ENSDARG0000000000	3.71	-3.28	0.64
12	ENSDARG0000000000	3.64	-2.02	0.42
13	ENSDARG0000000000	3.51	-3.12	0.69
14	ENSDARG0000000000	3.51	-2.68	0.6
15	ENSDARG0000000000	3.45	-2.19	0.62
16	ENSDARG0000000000	3.4	-3.43	0.74
17	ENSDARG0000000000	3.38	-4.07	0.78
18	ENSDARG0000000000	3.36	-3.38	0.65
19	ENSDARG0000000000	3.25	-3.18	0.46
20	ENSDARG0000000000	3.25	-1.91	0.4

## Geneset Overrepresentation

Rank	p-value	#in/all	Geneset
1	2e-13	24 / 159	MF structural molecule activity
2	7e-11	14 / 62	CC intermediate filament
3	5e-10	42 / 634	CC extracellular region
4	6e-10	45 / 717	MF calcium ion binding
5	4e-09	214 / 6723	CC membrane
6	3e-08	198 / 6248	CC integral component of membrane
7	5e-07	11 / 71	CC bicellular tight junction
8	6e-07	24 / 333	BP cell adhesion
9	7e-07	9 / 46	CC collagen trimer
10	6e-06	7 / 32	BP inner ear development
11	7e-06	23 / 358	MF peptidase activity
12	8e-06	32 / 609	BP proteolysis
13	1e-05	7 / 36	BP regulation of cell growth
14	3e-05	27 / 500	CC extracellular space
15	4e-05	13 / 153	CC proteinaceous extracellular matrix
16	5e-05	6 / 30	MF insulin-like growth factor binding
17	5e-05	4 / 10	MF small molecule binding
18	6e-05	45 / 1084	BP transport
19	7e-05	47 / 1162	CC plasma membrane
20	1e-04	9 / 83	BP visual perception
21	1e-04	4 / 13	MF ATP-activated inward rectifier potassium channel activity
22	2e-04	10 / 108	MF actin filament binding
23	2e-04	8 / 70	CC myosin complex
24	2e-04	13 / 176	BP ion transmembrane transport
25	3e-04	4 / 15	BP negative regulation of cell death
26	4e-04	13 / 191	MF serine-type endopeptidase activity
27	6e-04	5 / 31	MF inward rectifier potassium channel activity
28	9e-04	23 / 499	BP ion transport
29	1e-03	3 / 10	BP bicellular tight junction assembly
30	1e-03	13 / 219	CC cell junction
31	1e-03	9 / 119	MF serine-type peptidase activity
32	2e-03	9 / 120	MF motor activity
33	2e-03	7 / 76	BP cartilage development
34	2e-03	7 / 76	CC cilium
35	2e-03	3 / 12	MF acetylgalactosaminyltransferase activity
36	2e-03	5 / 41	MF copper ion binding
37	3e-03	9 / 130	BP regulation of ion transmembrane transport
38	3e-03	9 / 130	MF voltage-gated ion channel activity
39	3e-03	6 / 64	MF serine-type endopeptidase inhibitor activity
40	3e-03	14 / 270	MF ion channel activity



BP				CC				MF			
Rank	p-value	#in/all	Geneset	Rank	p-value	#in/all	Geneset	Rank	p-value	#in/all	Geneset
1	6e-07	24 / 333	cell adhesion	1	7e-11	14 / 62	intermediate filament	1	2e-13	24 / 159	structural molecule activity
2	6e-06	7 / 32	inner ear development	2	5e-10	42 / 634	extracellular region	2	6e-10	45 / 717	calcium ion binding
3	8e-06	32 / 609	proteolysis	3	4e-09	214 / 6723	membrane	3	7e-06	23 / 358	peptidase activity
4	1e-05	7 / 36	regulation of cell growth	4	3e-08	198 / 6248	integral component of membrane	4	5e-05	6 / 30	insulin-like growth factor binding
5	6e-05	45 / 1084	transport	5	5e-07	11 / 71	bicellular tight junction	5	5e-05	4 / 10	small molecule binding
6	1e-04	9 / 83	visual perception	6	7e-07	9 / 46	collagen trimer	6	1e-04	4 / 13	ATP-activated inward rectifier potassium channel activity
7	2e-04	13 / 176	ion transmembrane transport	7	3e-05	27 / 500	extracellular space	7	2e-04	10 / 108	actin filament binding
8	3e-04	4 / 15	negative regulation of cell death	8	4e-05	13 / 153	proteinaceous extracellular matrix	8	4e-04	13 / 191	serine-type endopeptidase activity
9	9e-04	23 / 499	ion transport	9	7e-05	47 / 1162	plasma membrane	9	6e-04	5 / 31	inward rectifier potassium channel activity
10	1e-03	3 / 10	bicellular tight junction assembly	10	2e-04	8 / 70	myosin complex	10	1e-03	9 / 119	serine-type peptidase activity
11	2e-03	7 / 76	cartilage development	11	1e-03	13 / 219	cell junction	11	2e-03	9 / 120	motor activity
12	3e-03	9 / 130	regulation of ion transmembrane transport	12	2e-03	7 / 76	cilium	12	2e-03	3 / 12	acetylgalactosaminyltransferase activity
13	3e-03	4 / 28	potassium ion import	13	4e-03	5 / 48	heterotrimeric G-protein complex	13	2e-03	5 / 41	copper ion binding
14	3e-03	3 / 14	glomerulus development	14	5e-03	30 / 809	integral component of plasma membrane	14	3e-03	9 / 130	voltage-gated ion channel activity
15	3e-03	3 / 14	posterior lateral line development	15	1e-02	5 / 65	extracellular matrix	15	3e-03	6 / 64	serine-type endopeptidase inhibitor activity

# K-Means Cluster

## Spot Summary: I

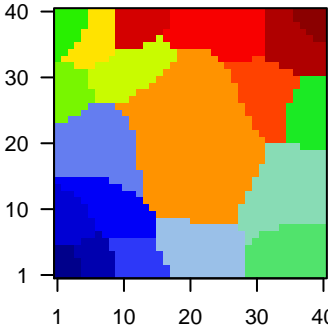
# metagenes = 380  
# genes = 7993

<r> metagenes = 0.02

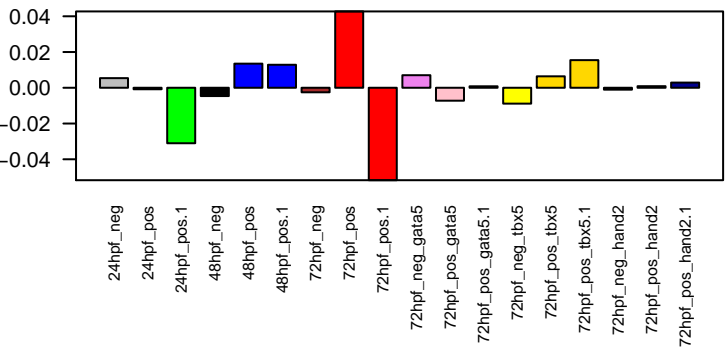
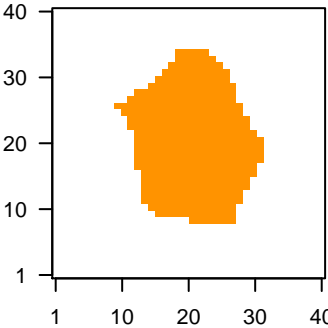
beta: r2= 0.15 / log p= -0.97

# samples with spot = 0 ( 0 %)

Overview Map

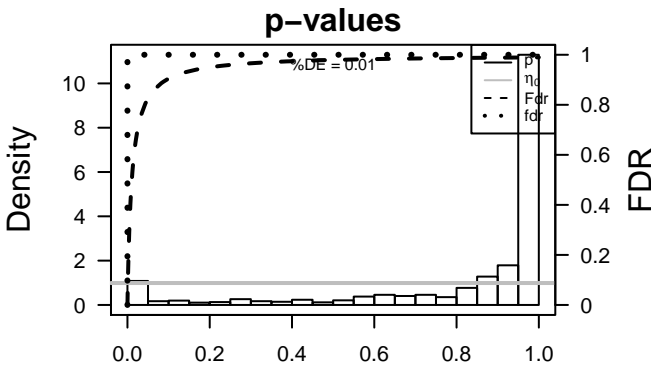


Spot

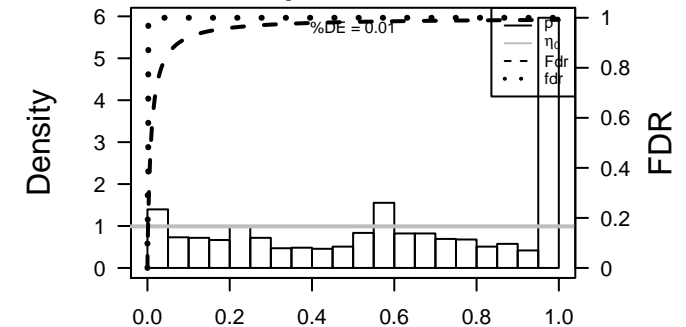


## Geneset Overrepresentation

Rank	p-value	#in/all	Geneset
1	1e-53	408 / 751	MF G-protein coupled receptor activity
2	5e-51	443 / 853	BP G-protein coupled receptor signaling pathway
3	1e-45	179 / 253	BP protein autophosphorylation
4	3e-44	213 / 329	BP negative regulation of apoptotic process
5	4e-40	191 / 294	BP regulation of mitotic cell cycle
6	2e-30	324 / 666	MF signal transducer activity
7	1e-27	56 / 59	BP detection of chemical stimulus involved in sensory perception of smell
8	1e-27	56 / 59	MF olfactory receptor activity
9	4e-24	45 / 46	MF trace-amine receptor activity
10	9e-24	57 / 65	BP sensory perception of smell
11	1e-18	39 / 42	BP detection of chemical stimulus involved in sensory perception
12	4e-17	109 / 192	MF transmembrane signaling receptor activity
13	4e-16	68 / 102	BP response to stimulus
14	2e-12	264 / 652	MF protein serine/threonine kinase activity
15	4e-11	467 / 1295	BP signal transduction
16	3e-10	133 / 297	BP immune response
17	1e-09	57 / 100	BP neuropeptide signaling pathway
18	6e-09	26 / 34	MF G-protein coupled serotonin receptor activity
19	4e-08	22 / 28	BP G-protein coupled serotonin receptor signaling pathway
20	4e-08	24 / 32	MF neurotransmitter receptor activity
21	7e-06	47 / 95	MF hormone activity
22	2e-05	27 / 47	MF chemokine activity
23	2e-05	311 / 914	MF protein kinase activity
24	4e-05	79 / 191	MF serine-type endopeptidase activity
25	8e-05	65 / 153	CC cell surface
26	1e-04	220 / 634	CC extracellular region
27	1e-04	10 / 12	MF neuropeptide receptor activity
28	1e-04	14 / 20	BP response to peptide
29	1e-04	11 / 14	MF neuropeptide Y receptor activity
30	2e-04	314 / 947	BP protein phosphorylation
31	3e-04	24 / 45	BP phospholipase C-activating G-protein coupled receptor signaling pathway
32	3e-04	9 / 11	BP immunoglobulin production
33	7e-04	50 / 119	MF carbohydrate binding
34	7e-04	20 / 37	MF peptide binding
35	9e-04	8 / 10	MF acrosin binding
36	9e-04	8 / 10	BP adenylyate cyclase-inhibiting serotonin receptor signaling pathway
37	9e-04	8 / 10	BP binding of sperm to zona pellucida
38	9e-04	8 / 10	BP egg coat formation
39	9e-04	8 / 10	BP positive regulation of acrosome reaction
40	9e-04	8 / 10	MF serotonin binding



BP				CC				MF			
Rank	p-value	#in/all	Geneset	Rank	p-value	#in/all	Geneset	Rank	p-value	#in/all	Geneset
1	5e-51	443 / 853	G-protein coupled receptor signaling pathway	1	8e-05	65 / 153	cell surface	1	1e-53	408 / 751	G-protein coupled receptor activity
2	1e-45	179 / 253	protein autophosphorylation	2	1e-04	220 / 634	extracellular region	2	2e-30	324 / 666	signal transducer activity
3	3e-44	213 / 329	negative regulation of apoptotic process	3	3e-02	9 / 17	integral component of nuclear inner membrane	3	1e-27	56 / 59	olfactory receptor activity
4	4e-40	191 / 294	regulation of mitotic cell cycle	4	1e-01	8 / 18	vacuole	4	4e-24	45 / 46	trace-amine receptor activity
5	1e-27	56 / 59	detection of chemical stimulus involved in sensory perception of smell	5	1e-01	12 / 31	photoreceptor outer segment	5	4e-17	109 / 192	transmembrane signaling receptor activity
6	9e-24	57 / 65	sensory perception of smell	6	1e-01	8 / 19	acetylcholine-gated channel complex	6	2e-12	264 / 652	protein serine/threonine kinase activity
7	1e-18	39 / 42	detection of chemical stimulus involved in sensory perception	7	2e-01	5 / 11	membrane attack complex	7	6e-09	26 / 34	G-protein coupled serotonin receptor activity
8	4e-16	68 / 102	response to stimulus	8	2e-01	22 / 65	extracellular matrix	8	4e-08	24 / 32	neurotransmitter receptor activity
9	4e-11	467 / 1295	signal transduction	9	2e-01	23 / 71	bicellular tight junction	9	7e-06	47 / 95	hormone activity
10	3e-10	133 / 297	immune response	10	3e-01	12 / 35	Golgi cisterna membrane	10	2e-05	27 / 47	chemokine activity
11	1e-09	57 / 100	neuropeptide signaling pathway	11	3e-01	4 / 10	integral component of peroxisomal membrane	11	2e-05	311 / 914	protein kinase activity
12	4e-08	22 / 28	G-protein coupled serotonin receptor signaling pathway	12	3e-01	233 / 809	integral component of plasma membrane	12	4e-05	79 / 191	serine-type endopeptidase activity
13	1e-04	14 / 20	response to peptide	13	3e-01	145 / 500	extracellular space	13	1e-04	10 / 12	neuropeptide receptor activity
14	2e-04	314 / 947	protein phosphorylation	14	3e-01	7 / 20	anchored component of membrane	14	1e-04	11 / 14	neuropeptide Y receptor activity
15	3e-04	24 / 45	phospholipase C-activating G-protein coupled receptor signaling pathway	15	3e-01	6 / 17	blood microparticle	15	7e-04	50 / 119	carbohydrate binding



BP				CC				MF			
Rank	p-value	#in/all	Geneset	Rank	p-value	#in/all	Geneset	Rank	p-value	#in/all	Geneset
1	3e-04	7 / 20	retrograde vesicle-mediated transport, Golgi to ER	1	5e-10	593 / 6723	membrane	1	0.002	157 / 1761	metal ion binding
2	4e-04	8 / 27	ubiquitin-dependent ERAD pathway	2	4e-08	543 / 6248	integral component of membrane	2	0.002	18 / 119	monooxygenase activity
3	6e-04	27 / 194	lipid metabolic process	3	3e-04	42 / 337	endoplasmic reticulum	3	0.002	55 / 522	oxidoreductase activity
4	7e-04	74 / 712	oxidation-reduction process	4	4e-04	28 / 198	Golgi membrane	4	0.003	7 / 28	protein domain specific binding
5	1e-03	7 / 25	steroid biosynthetic process	5	4e-04	29 / 209	endoplasmic reticulum membrane	5	0.004	14 / 88	guanyl-nucleotide exchange factor activity
6	2e-03	6 / 19	very long-chain fatty acid biosynthetic process	6	4e-04	8 / 27	recycling endosome	6	0.005	8 / 39	G-protein coupled receptor binding
7	2e-03	103 / 1084	transport	7	2e-03	37 / 317	Golgi apparatus	7	0.007	27 / 229	transporter activity
8	2e-03	61 / 591	transmembrane transport	8	2e-03	5 / 14	autophagosome	8	0.007	13 / 85	isomerase activity
9	3e-03	10 / 51	ER to Golgi vesicle-mediated transport	9	3e-03	45 / 410	mitochondrion	9	0.008	7 / 33	NAD binding
10	4e-03	4 / 10	receptor clustering	10	3e-03	189 / 2189	cytoplasm	10	0.008	126 / 1437	molecular_function
11	4e-03	41 / 375	positive regulation of GTPase activity	11	4e-03	140 / 1580	cellular_component	11	0.009	7 / 34	transcription regulatory region sequence-specific DNA binding
12	5e-03	7 / 31	one-carbon metabolic process	12	5e-03	8 / 38	trans-Golgi network	12	0.012	25 / 217	GTPase activator activity
13	7e-03	6 / 25	tricarboxylic acid cycle	13	5e-03	8 / 39	connexin complex	13	0.015	54 / 561	GTP binding
14	7e-03	5 / 18	phospholipase C-activating dopamine receptor signaling pathway	14	6e-03	9 / 48	heterotrimeric G-protein complex	14	0.015	6 / 29	G-protein beta/gamma-subunit complex binding
15	9e-03	6 / 26	mitophagy	15	7e-03	6 / 25	mitochondrial large ribosomal subunit	15	0.015	6 / 29	guanyl nucleotide binding

# K-Means Cluster

## Spot Summary: K

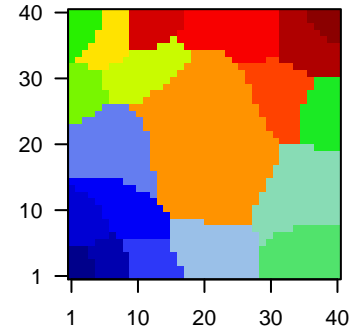
# metagenes = 102  
# genes = 1561

<r> metagenes = 0.74

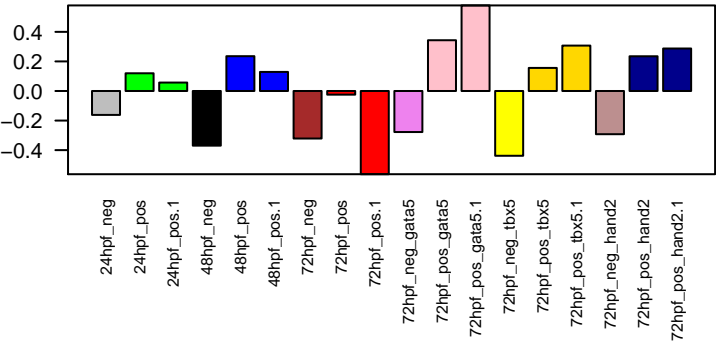
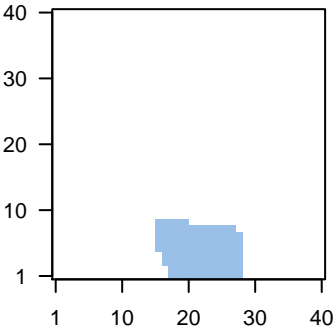
beta: r2= 2.13 / log p= -Inf

# samples with spot = 0 ( 0 %)

Overview Map



Spot



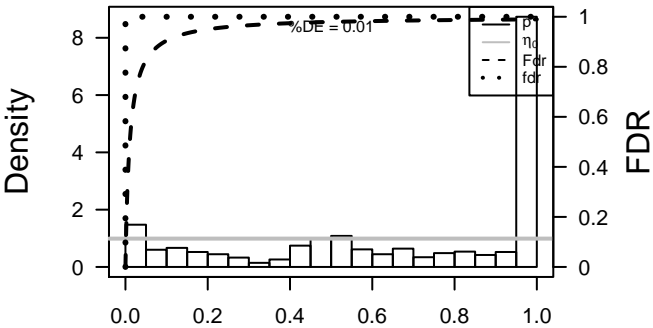
## Spot Genelist

Rank	ID	max e	r	Description	
		min e		Symbol	
1	ENSDARG000	2.94	-4.03	0.59	Metazoan signal recognition particle RNA [Source:RFAM;Acc:160493]
2	ENSDARG000	2.85	-5.47	0.46	cbx7a chromobox homolog 7a [Source:ZFIN;Acc:ZDB-GENE-050412-1]
3	ENSDARG000	2.83	-1.77	0.4	si:dkey-160k19.3-125i10.3 [Source:ZFIN;Acc:ZDB-GENE-100922-6f]
4	ENSDARG000	2.63	-3.12	0.55	Metazoan signal recognition particle RNA [Source:RFAM;Acc:160493]
5	ENSDARG000	2.62	-1.45	0.29	si:dkey-160k19.3-125i10.3 [Source:ZFIN;Acc:ZDB-GENE-060526-19]
6	ENSDARG000	2.59	-1.38	0.68	death associated protein 1b [Source:ZFIN;Acc:ZDB-GENE-070705-284]
7	ENSDARG000	2.46	-5.71	0.68	Metazoan signal recognition particle RNA [Source:RFAM;Acc:160493]
8	ENSDARG000	2.24	-1.13	0.44	si:dkey-160k19.3-102g19.3 [Source:ZFIN;Acc:ZDB-GENE-091204-2f]
9	ENSDARG000	2.23	-3.57	0.65	Metazoan signal recognition particle RNA [Source:RFAM;Acc:160493]
10	ENSDARG000	2.22	-4.69	0.93	zgc:165573c:165573 [Source:ZFIN;Acc:ZDB-GENE-070615-27]
11	ENSDARG000	2.12	-3.78	0.71	Metazoan signal recognition particle RNA [Source:RFAM;Acc:160493]
12	ENSDARG000	2.09	-1.65	0.74	si:dkey-160k19.3-10o6.2 [Source:ZFIN;Acc:ZDB-GENE-070705-284]
13	ENSDARG000	2.06	-0.5	0.51	si:ch211-165f21.7 [Source:ZFIN;Acc:ZDB-GENE-070912-1]
14	ENSDARG000	2.05	-0.89	0.29	zinc finger protein 70 [Source:HGNC Symbol;Acc:HGNC:131125-8]
15	ENSDARG000	2.02	-1.21	0.6	si:ch1073-190k2.1 [Source:ZFIN;Acc:ZDB-GENE-131127-4]
16	ENSDARG000	2	-1.71	0.5	Metazoan signal recognition particle RNA [Source:RFAM;Acc:160493]
17	ENSDARG000	1.98	-3.06	0.52	Small Cajal body specific RNA 6 [Source:RFAM;Acc:RF0047f]
18	ENSDARG000	1.97	-1.97	0.72	Metazoan signal recognition particle RNA [Source:RFAM;Acc:160493]
19	ENSDARG000	1.95	-1.69	0.62	si:dkey-250k12.2-234i14.2 [Source:ZFIN;Acc:ZDB-GENE-131127-59]
20	ENSDARG000	1.93	-0.98	0.47	si:ch211-194m7.4 [Source:ZFIN;Acc:ZDB-GENE-131125-8]

## Geneset Overrepresentation

Rank	p-value	#in/all	Geneset
1	2e-51	72 / 144	MF structural constituent of ribosome
2	1e-50	72 / 147	CC ribosome
3	5e-45	80 / 214	BP translation
4	2e-29	32 / 47	CC cytosolic large ribosomal subunit
5	4e-22	44 / 138	CC intracellular ribonucleoprotein complex
6	5e-16	19 / 33	CC cytosolic small ribosomal subunit
7	3e-15	124 / 1066	CC intracellular
8	2e-14	65 / 410	CC mitochondrion
9	4e-14	15 / 23	BP cytoplasmic translation
10	9e-09	15 / 45	BP hydrogen ion transmembrane transport
11	2e-07	126 / 1437	MF molecular_function
12	1e-06	10 / 28	MF cytochrome-c oxidase activity
13	2e-06	27 / 176	BP protein transport
14	2e-06	7 / 13	BP ribosomal small subunit assembly
15	3e-06	120 / 1427	BP biological_process
16	6e-06	8 / 20	MF rRNA binding
17	2e-05	8 / 23	CC mitochondrial respiratory chain complex I
18	3e-05	11 / 46	CC mitochondrial matrix
19	6e-05	65 / 712	BP oxidation-reduction process
20	6e-05	6 / 14	BP mitochondrial electron transport, cytochrome c to oxygen
21	8e-05	22 / 161	CC mitochondrial inner membrane
22	9e-05	11 / 51	BP ER to Golgi vesicle-mediated transport
23	1e-04	5 / 10	BP mitochondrial electron transport, ubiquinol to cytochrome c
24	1e-04	6 / 16	BP ribosomal large subunit assembly
25	2e-04	5 / 11	BP protein import into mitochondrial matrix
26	2e-04	11 / 55	BP translational initiation
27	2e-04	69 / 800	MF zinc ion binding
28	2e-04	6 / 17	CC mitochondrial respiratory chain complex IV
29	2e-04	25 / 209	CC endoplasmic reticulum membrane
30	3e-04	55 / 608	MF RNA binding
31	3e-04	9 / 40	BP erythrocyte differentiation
32	3e-04	7 / 25	CC mitochondrial large ribosomal subunit
33	3e-04	16 / 109	BP chordate embryonic development
34	4e-04	10 / 50	MF translation initiation factor activity
35	4e-04	31 / 293	BP protein ubiquitination
36	5e-04	11 / 61	BP protein polyubiquitination
37	6e-04	118 / 1580	CC cellular_component
38	8e-04	6 / 21	BP erythrocyte development
39	8e-04	7 / 29	MF ubiquitin conjugating enzyme binding
40	1e-03	5 / 15	BP aerobic respiration

p-values



BP				CC				MF			
Rank	p-value	#in/all	Geneset	Rank	p-value	#in/all	Geneset	Rank	p-value	#in/all	Geneset
1	5e-45	80 / 214	translation	1	1e-50	72 / 147	ribosome	1	2e-51	72 / 144	structural constituent of ribosome
2	4e-14	15 / 23	cytoplasmic translation	2	2e-29	32 / 47	cytosolic large ribosomal subunit	2	2e-07	126 / 1437	molecular_function
3	9e-09	15 / 45	hydrogen ion transmembrane transport	3	4e-22	44 / 138	intracellular ribonucleoprotein complex	3	1e-06	10 / 28	cytochrome-c oxidase activity
4	2e-06	27 / 176	protein transport	4	5e-16	19 / 33	cytosolic small ribosomal subunit	4	6e-06	8 / 20	rRNA binding
5	2e-06	7 / 13	ribosomal small subunit assembly	5	3e-15	124 / 1066	intracellular	5	2e-04	69 / 800	zinc ion binding
6	3e-06	120 / 1427	biological_process	6	2e-14	65 / 410	mitochondrion	6	3e-04	55 / 608	RNA binding
7	6e-05	65 / 712	oxidation-reduction process	7	2e-05	8 / 23	mitochondrial respiratory chain complex I	7	4e-04	10 / 50	translation initiation factor activity
8	6e-05	6 / 14	mitochondrial electron transport, cytochrome c to oxygen	8	3e-05	11 / 46	mitochondrial matrix	8	8e-04	7 / 29	ubiquitin conjugating enzyme binding
9	9e-05	11 / 51	ER to Golgi vesicle-mediated transport	9	8e-05	22 / 161	mitochondrial inner membrane	9	1e-03	6 / 22	metalloaminopeptidase activity
10	1e-04	5 / 10	mitochondrial electron transport, ubiquinol to cytochrome c	10	2e-04	6 / 17	mitochondrial respiratory chain complex IV	10	1e-03	6 / 22	threonine-type endopeptidase activity
11	1e-04	6 / 16	ribosomal large subunit assembly	11	2e-04	25 / 209	endoplasmic reticulum membrane	11	1e-03	19 / 156	ubiquitin protein ligase activity
12	2e-04	5 / 11	protein import into mitochondrial matrix	12	3e-04	7 / 25	mitochondrial large ribosomal subunit	12	1e-03	5 / 16	cysteine-type endopeptidase activity involved in execution phase of apoptosis
13	2e-04	11 / 55	translational initiation	13	6e-04	118 / 1580	cellular_component	13	2e-03	126 / 1761	metal ion binding
14	3e-04	9 / 40	erythrocyte differentiation	14	1e-03	6 / 23	proteasome core complex	14	3e-03	7 / 36	endopeptidase activity
15	3e-04	16 / 109	chordate embryonic development	15	2e-03	8 / 43	proteasome complex	15	6e-03	43 / 522	oxidoreductase activity



# K-Means Cluster

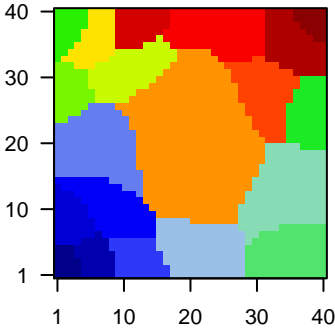
## Spot Summary: L

# metagenes = 29  
# genes = 578

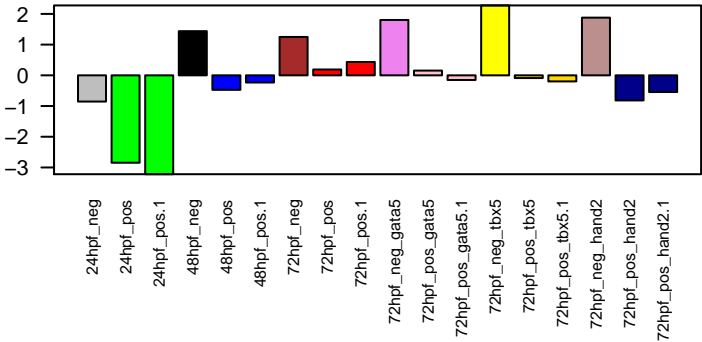
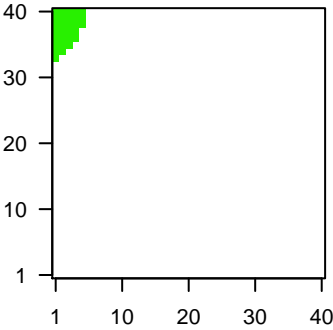
<r> metagenes = 0.96  
<r> genes = 0.72  
beta: r2= 31.47 / log p= -Inf

# 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

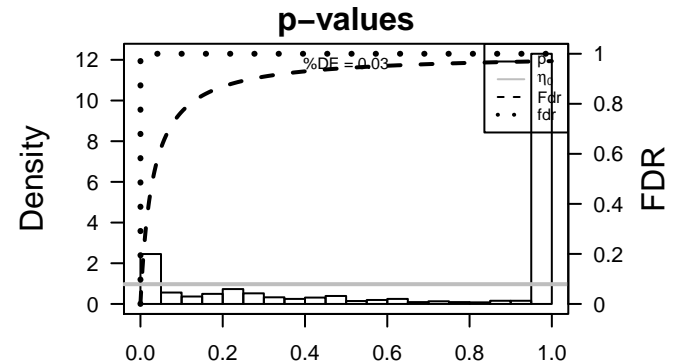


## Spot Genelist

Rank	ID	max e	r	Description	
		min e		Symbol	
1	ENSDARG000	5.44	-2.17	0.6	opn1sw2 opsin 1 (cone pigments), short-wave-sensitive 2 [Source:ZFIN]
2	ENSDARG000	5.4	-5.6	0.82	muc5.1 mucin 5.1, oligomeric mucus/gel-forming [Source:ZFIN;Acc:ZDB-GENE-050307-3]
3	ENSDARG000	5.34	-6.98	0.81	matn1 matrilin 1 [Source:ZFIN;Acc:ZDB-GENE-050307-3]
4	ENSDARG000	5.22	-3.71	0.6	opn1mw1 opsin 1 (cone pigments), medium-wave-sensitive, 1 [Source:ZFIN]
5	ENSDARG000	5.19	-6.04	0.55	atp1a1a.2 ATPase, Na+/K+ transporting, alpha 1a polypeptide, tandem c
6	ENSDARG000	5.16	-4.48	0.55	opn1sw1 opsin 1 (cone pigments), short-wave-sensitive 1 [Source:ZFIN]
7	ENSDARG000	5.14	-4.55	0.79	rho rhodopsin [Source:ZFIN;Acc:ZDB-GENE-990415-271]
8	ENSDARG000	5.09	-5.91	0.78	and2 actinodin2 [Source:ZFIN;Acc:ZDB-GENE-041105-2]
9	ENSDARG000	5.01	-4.88	0.79	opn1lw2 opsin 1 (cone pigments), long-wave-sensitive, 2 [Source:ZFIN]
10	ENSDARG000	4.9	-3.66	0.8	and1 actinodin1 [Source:ZFIN;Acc:ZDB-GENE-030131-9105]
11	ENSDARG000	4.85	-4.47	0.79	npas4a neuronal PAS domain protein 4a [Source:ZFIN;Acc:ZDB-GENE-040426-1661]
12	ENSDARG000	4.83	-5.45	0.81	arr3a arrestin 3a, retinal (X-arrestin) [Source:ZFIN;Acc:ZDB-GENE-040426-1661]
13	ENSDARG000	4.82	-3.89	0.68	gnb3b guanine nucleotide binding protein (G protein), beta polypeptide
14	ENSDARG000	4.76	-5.55	0.83	col10a1a collagen, type X, alpha 1a [Source:ZFIN;Acc:ZDB-GENE-030131-9105]
15	ENSDARG000	4.72	-8.26	0.94	col11a2 collagen, type XI, alpha 2 [Source:ZFIN;Acc:ZDB-GENE-000000-000000]
16	ENSDARG000	4.71	-3.52	0.74	rcvrn3 recoverin 3 [Source:ZFIN;Acc:ZDB-GENE-040426-1661]
17	ENSDARG000	4.57	-3.71	0.69	pde6c phosphodiesterase 6C, cGMP-specific, cone, alpha prime [Source:ZFIN]
18	ENSDARG000	4.55	-3.73	0.79	
19	ENSDARG000	4.55	-4.06	0.71	gnat2 guanine nucleotide binding protein (G protein), alpha transducin
20	ENSDARG000	4.49	-6.7	0.86	si:dkey-65b12.6 [Source:ZFIN;Acc:ZDB-GENE-060526-325]

## Geneset Overrepresentation

Rank	p-value	#in/all	Geneset
1	2e-17	27 / 155	CC synapse
2	1e-16	45 / 499	BP ion transport
3	1e-15	16 / 49	MF extracellular matrix structural constituent
4	7e-14	50 / 717	MF calcium ion binding
5	1e-13	33 / 333	BP cell adhesion
6	2e-13	23 / 158	MF microtubule binding
7	2e-13	24 / 175	BP nervous system development
8	3e-13	65 / 1162	CC plasma membrane
9	4e-12	60 / 1084	BP transport
10	1e-11	16 / 83	BP visual perception
11	2e-11	27 / 270	MF ion channel activity
12	2e-11	11 / 32	MF extracellular-glutamate-gated ion channel activity
13	2e-11	11 / 32	MF ionotropic glutamate receptor activity
14	2e-11	11 / 32	BP ionotropic glutamate receptor signaling pathway
15	2e-11	15 / 74	CC neuron projection
16	6e-11	207 / 6723	CC membrane
17	7e-11	21 / 172	BP homophilic cell adhesion via plasma membrane adhesion molecules
18	6e-10	192 / 6248	CC integral component of membrane
19	7e-10	20 / 176	BP ion transmembrane transport
20	8e-09	12 / 65	BP sodium ion transport
21	8e-09	13 / 79	BP excitatory postsynaptic potential
22	9e-09	34 / 537	MF sequence-specific DNA binding
23	3e-08	20 / 219	CC cell junction
24	6e-07	8 / 36	CC synaptic vesicle
25	7e-07	15 / 153	CC proteinaceous extracellular matrix
26	7e-07	11 / 80	CC postsynaptic membrane
27	8e-07	6 / 17	CC presynaptic active zone
28	1e-06	27 / 454	BP multicellular organism development
29	1e-06	6 / 18	MF tubulin binding
30	2e-06	12 / 108	CC microtubule
31	3e-06	10 / 75	BP calcium ion transport
32	4e-06	7 / 33	MF photoreceptor activity
33	4e-06	6 / 22	BP membrane depolarization during action potential
34	1e-05	10 / 86	BP chemical synaptic transmission
35	1e-05	15 / 193	BP positive regulation of transcription from RNA polymerase II promoter
36	1e-05	7 / 39	BP neuron projection development
37	1e-05	9 / 70	BP sodium ion transmembrane transport
38	2e-05	29 / 591	BP transmembrane transport
39	2e-05	5 / 17	BP cytoskeleton-dependent intracellular transport
40	2e-05	6 / 28	BP phototransduction



BP				CC				MF			
Rank	p-value	#in/all	Geneset	Rank	p-value	#in/all	Geneset	Rank	p-value	#in/all	Geneset
1	1e-16	45 / 499	ion transport	1	2e-17	27 / 155	synapse	1	1e-15	16 / 49	extracellular matrix structural constituent
2	1e-13	33 / 333	cell adhesion	2	3e-13	65 / 1162	plasma membrane	2	7e-14	50 / 717	calcium ion binding
3	2e-13	24 / 175	nervous system development	3	2e-11	15 / 74	neuron projection	3	2e-13	23 / 158	microtubule binding
4	4e-12	60 / 1084	transport	4	6e-11	207 / 6723	membrane	4	2e-11	27 / 270	ion channel activity
5	1e-11	16 / 83	visual perception	5	6e-10	192 / 6248	integral component of membrane	5	2e-11	11 / 32	extracellular-glutamate-gated ion channel activity
6	2e-11	11 / 32	ionotropic glutamate receptor signaling pathway	6	3e-08	20 / 219	cell junction	6	2e-11	11 / 32	ionotropic glutamate receptor activity
7	7e-11	21 / 172	homophilic cell adhesion via plasma membrane adhesion molecules	7	6e-07	8 / 36	synaptic vesicle	7	9e-09	34 / 537	sequence-specific DNA binding
8	7e-10	20 / 176	ion transmembrane transport	8	7e-07	15 / 153	proteinaceous extracellular matrix	8	1e-06	6 / 18	tubulin binding
9	8e-09	12 / 65	sodium ion transport	9	7e-07	11 / 80	postsynaptic membrane	9	4e-06	7 / 33	photoreceptor activity
10	8e-09	13 / 79	excitatory postsynaptic potential	10	8e-07	6 / 17	presynaptic active zone	10	5e-05	4 / 11	PDZ domain binding
11	1e-06	27 / 454	multicellular organism development	11	2e-06	12 / 108	microtubule	11	5e-05	11 / 124	receptor activity
12	3e-06	10 / 75	calcium ion transport	12	4e-05	6 / 31	photoreceptor outer segment	12	1e-04	13 / 183	RNA polymerase II transcription factor activity, sequence-specific DNA binding
13	4e-06	6 / 22	membrane depolarization during action potential	13	3e-04	4 / 17	AMPA glutamate receptor complex	13	2e-04	10 / 120	motor activity
14	1e-05	10 / 86	chemical synaptic transmission	14	4e-04	32 / 809	integral component of plasma membrane	14	2e-04	4 / 15	calcium-transporting ATPase activity
15	1e-05	15 / 193	positive regulation of transcription from RNA polymerase II promoter	15	8e-04	4 / 21	GABA-A receptor complex	15	4e-04	5 / 31	G-protein coupled photoreceptor activity

# K-Means Cluster

## Spot Summary: M

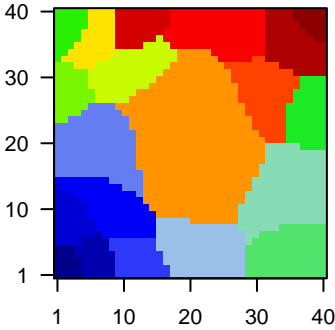
# metagenes = 76  
# genes = 1213

<r> metagenes = 0.8

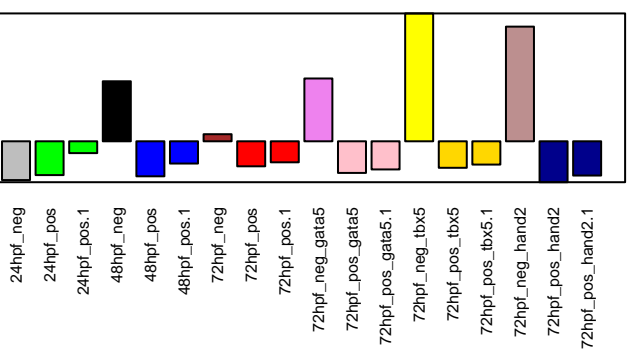
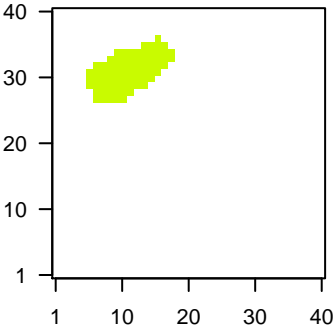
beta: r2= 2.25 / log p= -Inf

# samples with spot = 0 ( 0 %)

Overview Map



Spot

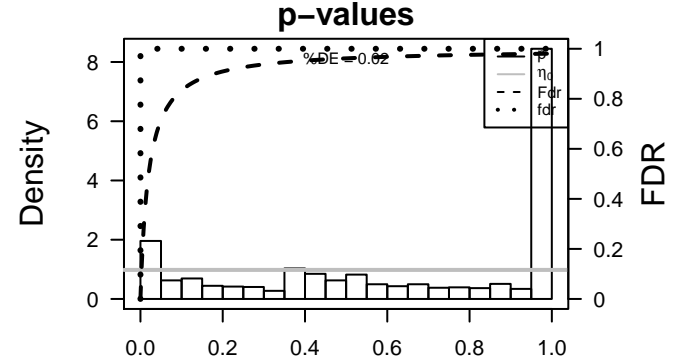


## Spot Genelist

Rank	ID	max e	r	min e	Description	
					Symbol	
1	ENSDARG000	2.78	-2.13	0.6	mmp9 matrix metalloproteinase 9 [Source:ZFIN;Acc:ZDB-GENE-04110425]	mmp9
2	ENSDARG000	2.71	-1.53	0.58	zgc:110425; zgc:110425 [Source:ZFIN;Acc:ZDB-GENE-050522-103]	zgc:110425
3	ENSDARG000	2.4	-1.48	0.67	zgc:65851; zgc:65851 [Source:ZFIN;Acc:ZDB-GENE-030131-9669]	zgc:65851
4	ENSDARG000	2.28	-1.17	0.28	si:ch211-166i24.1 [Source:ZFIN;Acc:ZDB-GENE-091204-3]	si:ch211-166i24.1
5	ENSDARG000	2.17	-1.56	0.7	ano3 anoctamin 3 [Source:ZFIN;Acc:ZDB-GENE-111031-3]	ano3
6	ENSDARG000	2.13	-2.08	0.73	rnf34b ring finger protein 34b [Source:ZFIN;Acc:ZDB-GENE-07100]	rnf34b
7	ENSDARG000	2.09	-1.28	0.66	panx2 pannexin 2 [Source:ZFIN;Acc:ZDB-GENE-050419-55]	panx2
8	ENSDARG000	2.08	-1.44	0.78	znf804a zinc finger protein 804A [Source:ZFIN;Acc:ZDB-GENE-0709]	znf804a
9	ENSDARG000	2.07	-1.79	0.71	lrfn5a leucine rich repeat and fibronectin type III domain containing	lrfn5a
10	ENSDARG000	2.06	-1.04	0.29	pcolce2a procollagen C-endopeptidase enhancer 2a [Source:ZFIN;Acc:ZDB-GENE-070206-3]	pcolce2a
11	ENSDARG000	2.01	-1.71	0.83	neuronal pentraxin receptor a [Source:ZFIN;Acc:ZDB-GENE-061110-1]	neuronal pentraxin receptor a
12	ENSDARG000	2.01	-1.43	0.79	nrxb1b neurexin 1b [Source:ZFIN;Acc:ZDB-GENE-070206-3]	nrxb1b
13	ENSDARG000	2	-1.12	0.88	si:ch211-166i24.1; si:ch211-166i24.1 [Source:ZFIN;Acc:ZDB-GENE-131127-4]	si:ch211-166i24.1
14	ENSDARG000	1.98	-0.96	0.27	crybb11 crystallin, beta B1, like 1 [Source:ZFIN;Acc:ZDB-GENE-100]	crybb11
15	ENSDARG000	1.97	-1.67	0.19	kcnk1a potassium voltage-gated channel, shaker-related subfamily,	kcnk1a
16	ENSDARG000	1.96	-1.18	0.67	prickle2a prickle homolog 2a [Source:ZFIN;Acc:ZDB-GENE-061110-1]	prickle2a
17	ENSDARG000	1.96	-1.64	0.73	grm4 glutamate receptor, metabotropic 4 [Source:ZFIN;Acc:ZDB-GENE-030131-9669]	grm4
18	ENSDARG000	1.96	-1.92	0.73	si:ch211-166i24.1; si:ch211-166i24.1 [Source:ZFIN;Acc:ZDB-GENE-030131-9669]	si:ch211-166i24.1
19	ENSDARG000	1.95	-1.19	0.37	Small nucleolar RNA SNORA73 family [Source:RFAM;Acc:RF000000]	Small nucleolar RNA SNORA73 family
20	ENSDARG000	1.94	-2.11	0.26		

## Geneset Overrepresentation

Rank	p-value	#in/all	Geneset
1	3e-21	75 / 499	BP ion transport
2	1e-17	49 / 270	MF ion channel activity
3	3e-14	31 / 138	BP potassium ion transport
4	8e-14	401 / 6723	CC membrane
5	1e-13	107 / 1162	CC plasma membrane
6	3e-13	375 / 6248	CC integral component of membrane
7	9e-13	30 / 147	BP potassium ion transmembrane transport
8	1e-12	23 / 86	MF voltage-gated potassium channel activity
9	1e-12	28 / 130	BP regulation of ion transmembrane transport
10	1e-12	28 / 130	MF voltage-gated ion channel activity
11	2e-11	22 / 90	MF potassium channel activity
12	8e-11	19 / 70	BP protein homooligomerization
13	6e-10	18 / 70	BP sodium ion transmembrane transport
14	2e-09	28 / 176	BP ion transmembrane transport
15	1e-08	20 / 103	BP cell-cell signaling
16	5e-08	24 / 155	CC synapse
17	6e-08	8 / 15	MF sodium channel activity
18	7e-08	14 / 56	CC voltage-gated potassium channel complex
19	8e-08	85 / 1084	BP transport
20	2e-07	15 / 69	MF extracellular ligand-gated ion channel activity
21	5e-07	9 / 25	MF GABA-A receptor activity
22	6e-07	66 / 809	CC integral component of plasma membrane
23	2e-06	92 / 1295	BP signal transduction
24	2e-06	51 / 591	BP transmembrane transport
25	9e-06	13 / 71	MF calmodulin binding
26	2e-05	7 / 21	CC GABA-A receptor complex
27	2e-05	21 / 175	BP nervous system development
28	2e-05	17 / 124	MF receptor activity
29	3e-05	55 / 717	MF calcium ion binding
30	4e-05	13 / 80	CC postsynaptic membrane
31	4e-05	11 / 59	MF syntaxin binding
32	5e-05	15 / 106	BP calcium ion transmembrane transport
33	5e-05	5 / 11	BP signaling
34	8e-05	23 / 219	CC cell junction
35	1e-04	11 / 65	BP sodium ion transport
36	1e-04	35 / 413	BP intracellular signal transduction
37	1e-04	12 / 79	MF calcium channel activity
38	1e-04	12 / 79	BP excitatory postsynaptic potential
39	2e-04	19 / 172	BP homophilic cell adhesion via plasma membrane adhesion molecules
40	2e-04	32 / 375	BP positive regulation of GTPase activity



BP

Rank

p-value

#in/all

Geneset

13e-2175 / 499ion transport

23e-1431 / 138potassium ion transport

39e-1330 / 147potassium ion transmembrane transport

41e-1228 / 130regulation of ion transmembrane transport

58e-1119 / 70protein homooligomerization

66e-1018 / 70sodium ion transmembrane transport

72e-0928 / 176ion transmembrane transport

81e-0820 / 103cell-cell signaling

98e-0885 / 1084transport

102e-0692 / 1295signal transduction

112e-0651 / 591transmembrane transport

122e-0521 / 175nervous system development

135e-0515 / 106calcium ion transmembrane transport

145e-055 / 11signaling

151e-0411 / 65sodium ion transport

CC

Rank

p-value

#in/all

Geneset

18e-14401 / 6723membrane

21e-13107 / 1162plasma membrane

33e-13375 / 6248integral component of membrane

45e-0824 / 155synapse

57e-0814 / 56voltage-gated potassium channel complex

66e-0766 / 809integral component of plasma membrane

72e-057 / 21GABA-A receptor complex

84e-0513 / 80postsynaptic membrane

98e-0523 / 219cell junction

103e-049 / 51presynapse

112e-034 / 13presynaptic membrane

123e-034 / 15cytoplasmic dynein complex

133e-034 / 15histone acetyltransferase complex

146e-034 / 18motile cilium

158e-034 / 19axon

MF

Rank

p-value

#in/all

Geneset

11e-1749 / 270ion channel activity

21e-1223 / 86voltage-gated potassium channel activity

31e-1228 / 130voltage-gated ion channel activity

42e-1122 / 90potassium channel activity

56e-088 / 15sodium channel activity

62e-0715 / 69extracellular ligand-gated ion channel activity

75e-079 / 25GABA-A receptor activity

89e-0613 / 71calmodulin binding

92e-0517 / 124receptor activity

103e-0555 / 717calcium ion binding

114e-0511 / 59syntaxin binding

121e-0412 / 79calcium channel activity

134e-048 / 42voltage-gated calcium channel activity

149e-046 / 27calmodulin-dependent protein kinase activity

151e-036 / 28protein domain specific binding

# K-Means Cluster

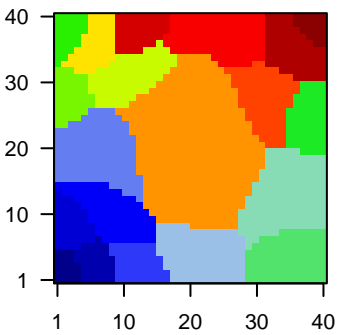
## Spot Summary: N

# metagenes = 45  
# genes = 810

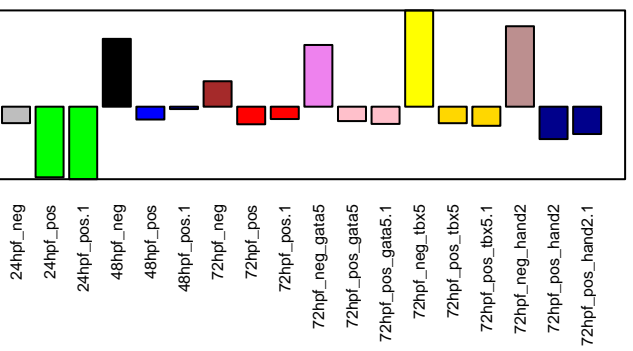
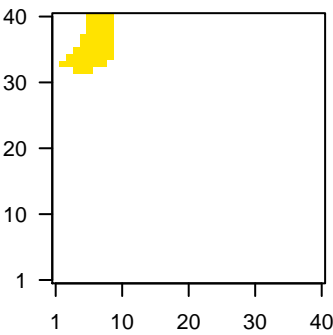
<r> metagenes = 0.93  
<r> genes = 0.62  
beta: r2= 12.85 / log p= -Inf

# samples with spot = 4 ( 22.2 % )  
48hpf\_neg : 1 ( 100 % )  
72hpf\_neg\_gata5 : 1 ( 100 % )  
72hpf\_neg\_tbx5 : 1 ( 100 % )  
72hpf\_neg\_hand2 : 1 ( 100 % )

Overview Map



Spot

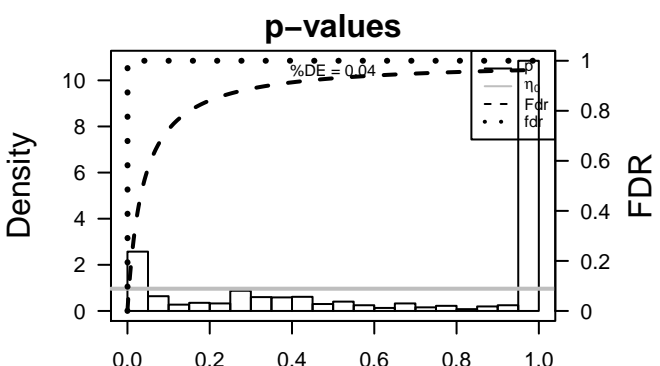


## Spot Genelist

Rank	ID	max e min e			Description Symbol
1	ENSDARG000	3.87	-1.49	0.84	slc6a17 solute carrier family 6 (neutral amino acid transporter), memb
2	ENSDARG000	3.35	-1.77	0.92	atp1a3a ATPase, Na+/K+ transporting, alpha 3a polypeptide [Source:2
3	ENSDARG000	3.22	-1.74	0.88	elavl3 ELAV like neuron-specific RNA binding protein 3 [Source:ZFI
4	ENSDARG000	3.21	-2.79	0.57	LOC100535713
5	ENSDARG000	3.18	-2.43	0.67	egr4 early growth response 4 [Source:ZFIN;Acc:ZDB-GENE-080
6	ENSDARG000	3.14	-1.84	0.86	slitrk1 SLIT and NTRK-like family, member 1 [Source:ZFIN;Acc:ZDB
7	ENSDARG000	3.13	-1.56	0.93	csmd2 CUB and Sushi multiple domains 2 [Source:ZFIN;Acc:ZDB-G
8	ENSDARG000	3.1	-3.27	0.91	cacna1a:calcium channel, voltage-dependent, P/Q type, alpha 1A sub
9	ENSDARG000	3.08	-2.8	0.75	syngap1synaptic Ras GTPase activating protein 1a [Source:ZFIN;Acc
10	ENSDARG000	3.08	-2.11	0.83	syn2b synapsin IIb [Source:ZFIN;Acc:ZDB-GENE-051127-49]
11	ENSDARG000	3.02	-2.23	0.74	evx2 even-skipped homeobox 2 [Source:ZFIN;Acc:ZDB-GENE-9
12	ENSDARG000	2.99	-1.76	0.73	dlx4a distal-less homeobox 4a [Source:ZFIN;Acc:ZDB-GENE-980
13	ENSDARG000	2.98	-2.28	0.73	pcsk1 proprotein convertase subtilisin/kexin type 1 [Source:ZFIN;Ac
14	ENSDARG000	2.97	-3.26	0.59	st8sia2 ST8 alpha-N-acetyl-neuraminide alpha-2,8-sialyltransferas
15	ENSDARG000	2.96	-1.66	0.85	sez6a seizure related 6 homolog a [Source:ZFIN;Acc:ZDB-GENE-(
16	ENSDARG000	2.94	-2.03	0.56	admb adrenomedullin b [Source:ZFIN;Acc:ZDB-GENE-120221-6]
17	ENSDARG000	2.9	-2.16	0.62	fat2 FAT atypical cadherin 2 [Source:ZFIN;Acc:ZDB-GENE-1110
18	ENSDARG000	2.88	-1.98	0.83	si:dkeyp-27e10.3 [Source:ZFIN;Acc:ZDB-GENE-041210-9
19	ENSDARG000	2.86	-1.72	0.8	syngap1synaptic Ras GTPase activating protein 1b [Source:ZFIN;Acc
20	ENSDARG000	2.84	-2.02	0.85	si:dkeyp-15e10.2-175g6.2 [Source:ZFIN;Acc:ZDB-GENE-030131-80

## Geneset Overrepresentation

Rank	p-value	#in/all	Geneset
1	6e-25	40 / 172	BP homophilic cell adhesion via plasma membrane adhesion molecules
2	9e-22	50 / 333	BP cell adhesion
3	5e-21	312 / 6723	CC membrane
4	4e-20	95 / 1162	CC plasma membrane
5	8e-20	292 / 6248	CC integral component of membrane
6	3e-17	67 / 717	MF calcium ion binding
7	3e-14	29 / 175	BP nervous system development
8	2e-11	32 / 270	MF ion channel activity
9	2e-11	45 / 499	BP ion transport
10	9e-11	78 / 1239	BP regulation of transcription, DNA-templated
11	1e-10	23 / 155	CC synapse
12	2e-10	21 / 130	BP regulation of ion transmembrane transport
13	2e-10	21 / 130	MF voltage-gated ion channel activity
14	2e-09	12 / 42	MF voltage-gated calcium channel activity
15	3e-09	84 / 1484	MF DNA binding
16	2e-08	10 / 33	CC voltage-gated calcium channel complex
17	2e-08	7 / 13	BP peripheral nervous system neuron axonogenesis
18	3e-08	11 / 44	BP neuron development
19	4e-08	16 / 103	BP cell-cell signaling
20	5e-08	40 / 537	MF sequence-specific DNA binding
21	2e-07	13 / 75	BP calcium ion transport
22	4e-07	43 / 643	BP transcription, DNA-templated
23	4e-07	6 / 12	MF glutamate receptor activity
24	8e-07	6 / 13	BP regulation of synaptic transmission, glutamatergic
25	8e-07	12 / 71	BP axonogenesis
26	8e-07	21 / 210	MF protein binding
27	1e-06	120 / 2716	CC nucleus
28	2e-06	10 / 51	CC presynapse
29	2e-06	17 / 153	CC proteinaceous extracellular matrix
30	2e-06	14 / 106	BP calcium ion transmembrane transport
31	3e-06	8 / 32	MF extracellular-glutamate-gated ion channel activity
32	3e-06	8 / 32	MF ionotropic glutamate receptor activity
33	3e-06	8 / 32	BP ionotropic glutamate receptor signaling pathway
34	3e-06	12 / 79	MF calcium channel activity
35	4e-06	10 / 56	CC voltage-gated potassium channel complex
36	6e-06	20 / 219	CC cell junction
37	7e-06	10 / 59	MF syntaxin binding
38	9e-06	7 / 27	BP axon extension
39	1e-05	46 / 809	CC integral component of plasma membrane
40	1e-05	5 / 12	BP neurotransmitter secretion



BP				CC				MF			
Rank	p-value	#in/all	Geneset	Rank	p-value	#in/all	Geneset	Rank	p-value	#in/all	Geneset
1	6e-25	40 / 172	homophilic cell adhesion via plasma membrane adhesion molecules	1	5e-21	312 / 6723	membrane	1	3e-17	67 / 717	calcium ion binding
2	9e-22	50 / 333	cell adhesion	2	4e-20	95 / 1162	plasma membrane	2	2e-11	32 / 270	ion channel activity
3	3e-14	29 / 175	nervous system development	3	8e-20	292 / 6248	integral component of membrane	3	2e-10	21 / 130	voltage-gated ion channel activity
4	2e-11	45 / 499	ion transport	4	1e-10	23 / 155	synapse	4	2e-09	12 / 42	voltage-gated calcium channel activity
5	9e-11	78 / 1239	regulation of transcription, DNA-templated	5	2e-08	10 / 33	voltage-gated calcium channel complex	5	3e-09	84 / 1484	DNA binding
6	2e-10	21 / 130	regulation of ion transmembrane transport	6	1e-06	120 / 2716	nucleus	6	5e-08	40 / 537	sequence-specific DNA binding
7	2e-08	7 / 13	peripheral nervous system neuron axonogenesis	7	2e-06	10 / 51	presynapse	7	4e-07	6 / 12	glutamate receptor activity
8	3e-08	11 / 44	neuron development	8	2e-06	17 / 153	proteinaceous extracellular matrix	8	8e-07	21 / 210	protein binding
9	4e-08	16 / 103	cell-cell signaling	9	4e-06	10 / 56	voltage-gated potassium channel complex	9	3e-06	8 / 32	extracellular-glutamate-gated ion channel activity
10	2e-07	13 / 75	calcium ion transport	10	6e-06	20 / 219	cell junction	10	3e-06	8 / 32	ionotropic glutamate receptor activity
11	4e-07	43 / 643	transcription, DNA-templated	11	1e-05	46 / 809	integral component of plasma membrane	11	3e-06	12 / 79	calcium channel activity
12	8e-07	6 / 13	regulation of synaptic transmission, glutamatergic	12	1e-05	13 / 108	microtubule	12	7e-06	10 / 59	syntaxin binding
13	8e-07	12 / 71	axonogenesis	13	2e-05	5 / 13	presynaptic membrane	13	1e-05	14 / 124	receptor activity
14	2e-06	14 / 106	calcium ion transmembrane transport	14	3e-05	5 / 14	postsynaptic density	14	6e-05	11 / 90	potassium channel activity
15	3e-06	8 / 32	ionotropic glutamate receptor signaling pathway	15	1e-04	10 / 80	postsynaptic membrane	15	9e-05	5 / 17	transcriptional repressor activity, RNA polymerase II core promoter proximal region sequence-specific DNA binding

# K-Means Cluster

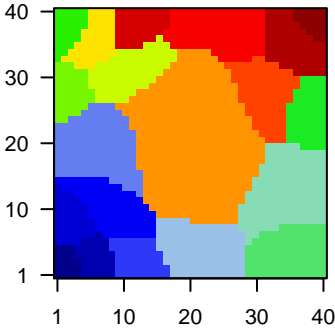
## Spot Summary: O

# metagenes = 41  
# genes = 757

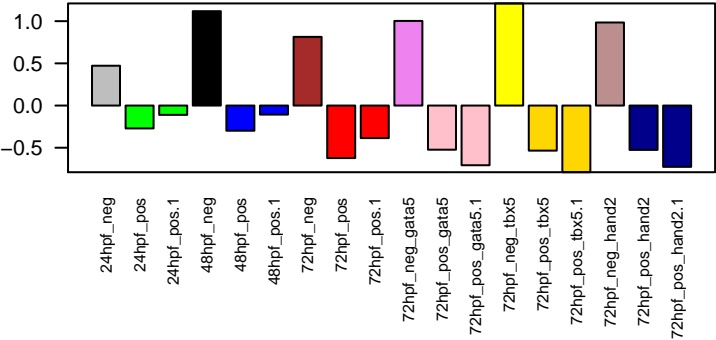
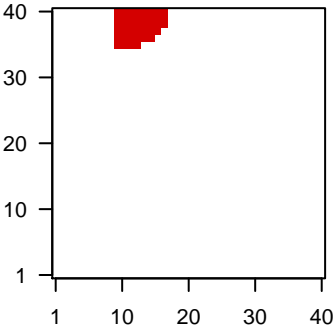
<r> metagenes = 0.94  
<r> genes = 0.63  
beta: r2= 8.12 / log p= -Inf

# 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

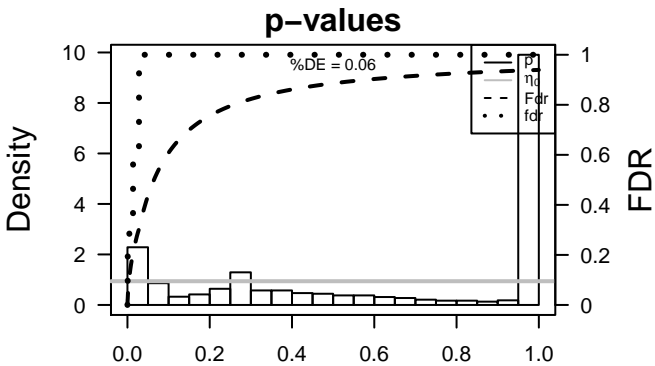


## Spot Genelist

Rank	ID	max e	r	min e	Description
1	ENSDARG000	3.14	-2.31	0.84	frem2a Fras1 related extracellular matrix protein 2a [Source:ZFIN;Acc:ZDB-GENE-130530-1]
2	ENSDARG000	3.08	-2.37	0.64	tubby like protein 4b [Source:ZFIN;Acc:ZDB-GENE-130530-1]
3	ENSDARG000	2.97	-2.6	0.69	zmp:0000001081 [Source:ZFIN;Acc:ZDB-GENE-140106-41]
4	ENSDARG000	2.87	-3.42	0.75	si:dkeyp-37844p-77h1.4 [Source:ZFIN;Acc:ZDB-GENE-050208-18]
5	ENSDARG000	2.85	-1.86	0.77	vcanb versican b [Source:ZFIN;Acc:ZDB-GENE-030131-2185]
6	ENSDARG000	2.81	-1.92	0.83	lrm1 leucine rich repeat neuronal 1 [Source:ZFIN;Acc:ZDB-GENE-030131-2185]
7	ENSDARG000	2.79	-1.66	0.73	col4a6 collagen, type IV, alpha 6 [Source:ZFIN;Acc:ZDB-GENE-101]
8	ENSDARG000	2.78	-1.46	0.53	abi3bpb ABI family, member 3 (NESH) binding protein b [Source:ZFIN;Acc:ZDB-GENE-030131-2185]
9	ENSDARG000	2.72	-4	0.72	mxra5b matrix-remodelling associated 5b [Source:ZFIN;Acc:ZDB-GENE-030131-2185]
10	ENSDARG000	2.69	-2.29	0.72	lrfn5b leucine rich repeat and fibronectin type III domain containing: ryanodine receptor 2 [Source:HGNC Symbol;Acc:HGNC:104]
11	ENSDARG000	2.67	-1.51	0.76	ryanodine receptor 2 [Source:HGNC Symbol;Acc:HGNC:104]
12	ENSDARG000	2.66	-1.67	0.76	col4a5 collagen, type IV, alpha 5 (Alport syndrome) [Source:ZFIN;Acc:ZDB-GENE-030131-2185]
13	ENSDARG000	2.65	-2.02	0.59	aspn asporin (LRR class 1) [Source:ZFIN;Acc:ZDB-GENE-041101-7]
14	ENSDARG000	2.65	-2.8	0.87	thsd7aa thrombospondin, type I, domain containing 7Aa [Source:ZFIN;Acc:ZDB-GENE-030131-2185]
15	ENSDARG000	2.63	-1.69	0.97	nova2 neuro-oncological ventral antigen 2 [Source:ZFIN;Acc:ZDB-GENE-030131-2185]
16	ENSDARG000	2.62	-2.43	0.6	zgc:101810c:101810 [Source:ZFIN;Acc:ZDB-GENE-041121-7]
17	ENSDARG000	2.54	-3.15	0.8	stmn2a stathmin 2a [Source:ZFIN;Acc:ZDB-GENE-041010-85]
18	ENSDARG000	2.53	-1.54	0.81	entpd5a ectonucleoside triphosphate diphosphohydrolase 5a [Source:ZFIN;Acc:ZDB-GENE-030131-2185]
19	ENSDARG000	2.52	-1.6	0.71	entpd5a ectonucleoside triphosphate diphosphohydrolase 5a [Source:ZFIN;Acc:ZDB-GENE-030131-2185]
20	ENSDARG000	2.52	-1.65	0.93	dclk1b doublecortin-like kinase 1b [Source:ZFIN;Acc:ZDB-GENE-030131-2185]

## Geneset Overrepresentation

Rank	p-value	#in/all	Geneset
1	2e-27	108 / 1239	BP regulation of transcription, DNA-templated
2	3e-24	65 / 537	MF sequence-specific DNA binding
3	1e-20	107 / 1484	MF DNA binding
4	2e-16	146 / 2716	CC nucleus
5	7e-14	38 / 333	BP cell adhesion
6	1e-13	54 / 633	MF transcription factor activity, sequence-specific DNA binding
7	5e-11	24 / 172	BP homophilic cell adhesion via plasma membrane adhesion molecules
8	2e-10	16 / 78	BP axon guidance
9	3e-09	37 / 454	BP multicellular organism development
10	7e-09	10 / 32	BP retinal ganglion cell axon guidance
11	9e-09	48 / 717	MF calcium ion binding
12	2e-08	44 / 643	BP transcription, DNA-templated
13	9e-08	18 / 147	BP brain development
14	5e-06	9 / 48	BP neural crest cell migration
15	7e-06	7 / 28	BP retina morphogenesis in camera-type eye
16	2e-05	12 / 100	BP peptidyl-tyrosine phosphorylation
17	2e-05	56 / 1162	CC plasma membrane
18	2e-05	16 / 175	BP nervous system development
19	4e-05	12 / 110	MF protein tyrosine kinase activity
20	6e-05	26 / 413	BP intracellular signal transduction
21	8e-05	226 / 6723	CC membrane
22	8e-05	6 / 28	BP skeletal system development
23	1e-04	7 / 41	MF RNA polymerase II core promoter proximal region sequence-specific DNA binding
24	1e-04	211 / 6248	CC integral component of membrane
25	2e-04	7 / 44	BP neuron development
26	2e-04	28 / 491	MF kinase activity
27	2e-04	7 / 45	BP embryonic cranial skeleton morphogenesis
28	2e-04	9 / 76	BP actin cytoskeleton organization
29	2e-04	13 / 149	BP cell surface receptor signaling pathway
30	3e-04	7 / 49	MF extracellular matrix structural constituent
31	5e-04	7 / 52	MF transmembrane receptor protein tyrosine kinase activity
32	5e-04	5 / 25	BP negative chemotaxis
33	5e-04	28 / 522	BP phosphorylation
34	6e-04	7 / 54	BP fin regeneration
35	6e-04	22 / 375	BP positive regulation of GTPase activity
36	6e-04	15 / 210	MF protein binding
37	7e-04	4 / 16	BP primitive erythrocyte differentiation
38	9e-04	12 / 153	CC proteinaceous extracellular matrix
39	1e-03	10 / 115	MF chromatin binding
40	2e-03	10 / 120	MF protein tyrosine phosphatase activity



BP				CC				MF			
Rank	p-value	#in/all	Geneset	Rank	p-value	#in/all	Geneset	Rank	p-value	#in/all	Geneset
1	2e-27	108 / 1239	regulation of transcription, DNA-templated	1	2e-16	146 / 2716	nucleus	1	3e-24	65 / 537	sequence-specific DNA binding
2	7e-14	38 / 333	cell adhesion	2	2e-05	56 / 1162	plasma membrane	2	1e-20	107 / 1484	DNA binding
3	5e-11	24 / 172	homophilic cell adhesion via plasma membrane adhesion molecules	3	8e-05	226 / 6723	membrane	3	1e-13	54 / 633	transcription factor activity, sequence-specific DNA binding
4	2e-10	16 / 78	axon guidance	4	1e-04	211 / 6248	integral component of membrane	4	9e-09	48 / 717	calcium ion binding
5	3e-09	37 / 454	multicellular organism development	5	9e-04	12 / 153	proteinaceous extracellular matrix	5	4e-05	12 / 110	protein tyrosine kinase activity
6	7e-09	10 / 32	retinal ganglion cell axon guidance	6	2e-03	5 / 32	chromatin	6	1e-04	7 / 41	RNA polymerase II core promoter proximal region sequence-specific DNA binding
7	2e-08	44 / 643	transcription, DNA-templated	7	4e-03	44 / 1066	intracellular	7	2e-04	28 / 491	kinase activity
8	9e-08	18 / 147	brain development	8	4e-03	35 / 809	integral component of plasma membrane	8	3e-04	7 / 49	extracellular matrix structural constituent
9	5e-06	9 / 48	neural crest cell migration	9	5e-03	8 / 98	transcription factor complex	9	5e-04	7 / 52	transmembrane receptor protein tyrosine kinase activity
10	7e-06	7 / 28	retina morphogenesis in camera-type eye	10	6e-03	4 / 27	guanylate cyclase complex, soluble	10	6e-04	15 / 210	protein binding
11	2e-05	12 / 100	peptidyl-tyrosine phosphorylation	11	7e-03	3 / 15	basement membrane	11	1e-03	10 / 115	chromatin binding
12	2e-05	16 / 175	nervous system development	12	8e-03	6 / 65	extracellular matrix	12	2e-03	10 / 120	protein tyrosine phosphatase activity
13	6e-05	26 / 413	intracellular signal transduction	13	1e-02	16 / 317	Golgi apparatus	13	3e-03	3 / 11	collagen binding
14	8e-05	6 / 28	skeletal system development	14	2e-02	6 / 80	postsynaptic membrane	14	4e-03	4 / 24	ARF guanyl-nucleotide exchange factor activity
15	2e-04	7 / 44	neuron development	15	3e-02	2 / 10	clathrin-coated vesicle	15	4e-03	14 / 231	actin binding



# K-Means Cluster

## Spot Summary: P

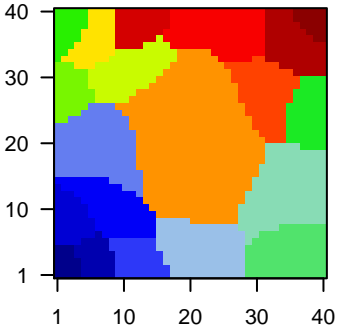
# metagenes = 80  
# genes = 1254

<r> metagenes = 0.82

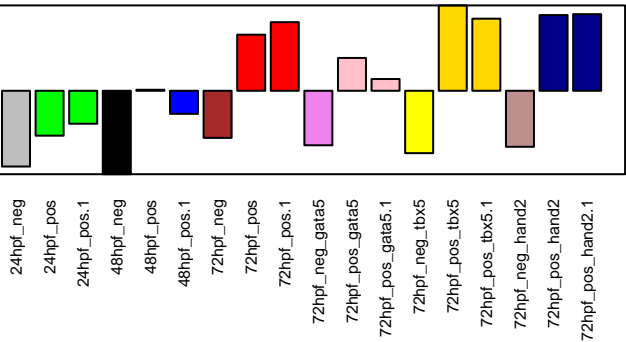
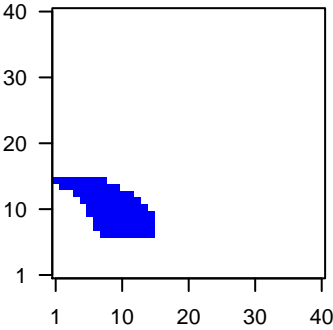
beta: r2= 4.04 / log p= -Inf

# samples with spot = 0 ( 0 %)

Overview Map



Spot

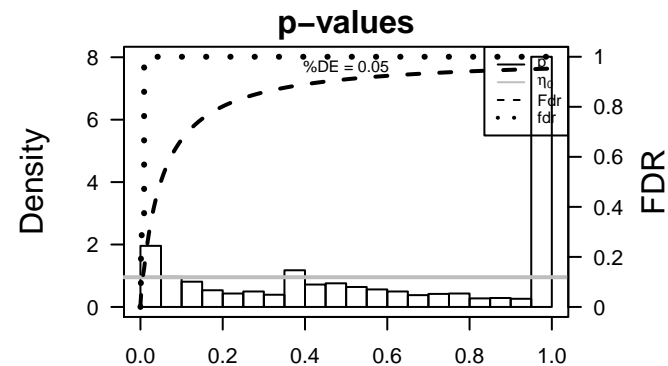


## Spot Genelist

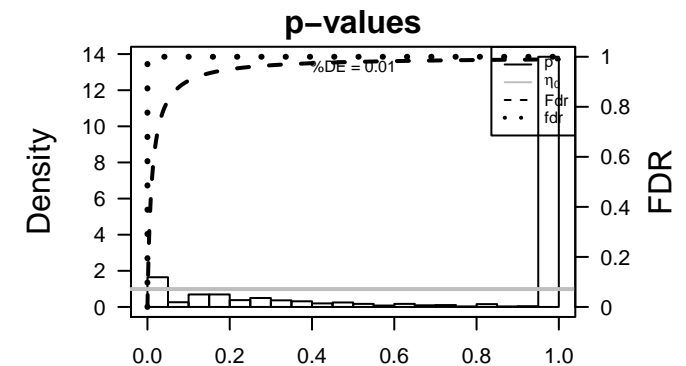
Rank	ID	max e	r	min e	Description
					Symbol
1	ENSDARG0000000001	6.21	-1.42	0.4	scpp5 secretory calcium-binding phosphoprotein 5 [Source:ZFIN;Acc:ZDB-GENE-050208]
2	ENSDARG0000000002	3.42	-1.9	0.41	pcyt11b phosphate cytidylyltransferase 1, choline, beta b [Source:ZFIN;Acc:ZDB-GENE-050208]
3	ENSDARG0000000003	3.22	-3.48	0.69	ctf complement factor H [Source:ZFIN;Acc:ZDB-GENE-050208]
4	ENSDARG0000000004	3.14	-2.4	0.49	cyp1b1 cytochrome P450, family 1, subfamily B, polypeptide 1 [Source:ZFIN;Acc:ZDB-GENE-050208]
5	ENSDARG0000000005	2.92	-1.62	0.78	sepp1b selenoprotein P, plasma, 1b [Source:ZFIN;Acc:ZDB-GENE-050208]
6	ENSDARG0000000006	2.92	-2.18	0.9	tagapa T-cell activation RhoGTPase activating protein a [Source:ZFIN;Acc:ZDB-GENE-050208]
7	ENSDARG0000000007	2.91	-3.06	0.83	agt angiotensinogen [Source:ZFIN;Acc:ZDB-GENE-030131-12]
8	ENSDARG0000000008	2.88	-1.91	0.81	dpydb dihydropyrimidine dehydrogenase b [Source:ZFIN;Acc:ZDB-GENE-050208]
9	ENSDARG0000000009	2.86	-1.8	0.83	abcb11b ATP-binding cassette, sub-family B (MDR/TAP), member 11b [Source:ZFIN;Acc:ZDB-GENE-050208]
10	ENSDARG0000000010	2.85	-2.98	0.57	hsp70l heat shock cognate 70-kd protein, like [Source:ZFIN;Acc:ZDB-GENE-050208]
11	ENSDARG0000000011	2.84	-3.3	0.67	cyp24a1 cytochrome P450, family 24, subfamily A, polypeptide 1 [Source:ZFIN;Acc:ZDB-GENE-050208]
12	ENSDARG0000000012	2.82	-2.28	0.69	si:ch211-256a19-264f5.2 [Source:ZFIN;Acc:ZDB-GENE-080303-2]
13	ENSDARG0000000013	2.78	-1.4	0.87	ch25h cholesterol 25-hydroxylase [Source:ZFIN;Acc:ZDB-GENE-050208]
14	ENSDARG0000000014	2.78	-1.92	0.81	SEC14-like lipid binding 7 [Source:ZFIN;Acc:ZDB-GENE-050208]
15	ENSDARG0000000015	2.76	-2.97	0.51	hsp70.1 heat shock cognate 70-kd protein, tandem duplicate 2 [Source:ZFIN;Acc:ZDB-GENE-050208]
16	ENSDARG0000000016	2.75	-3.08	0.49	si:ch211-256a19-256m1.8 [Source:ZFIN;Acc:ZDB-GENE-131127-4]
17	ENSDARG0000000017	2.73	-1.98	0.85	serpinc1 serpin peptidase inhibitor, clade C (antithrombin), member 1 [Source:ZFIN;Acc:ZDB-GENE-050208]
18	ENSDARG0000000018	2.71	-1.4	0.19	tbx18 T-box 18 [Source:ZFIN;Acc:ZDB-GENE-020529-2]
19	ENSDARG0000000019	2.69	-4.1	0.81	RAB44, member RAS oncogene family [Source:ZFIN;Acc:ZDB-GENE-050208]
20	ENSDARG0000000020	2.67	-2.47	0.72	cyp1a cytochrome P450, family 1, subfamily A [Source:ZFIN;Acc:ZDB-GENE-050208]

## Geneset Overrepresentation

Rank	p-value	#in/all	Geneset
1	3e-21	94 / 712	BP oxidation-reduction process
2	8e-20	76 / 522	MF oxidoreductase activity
3	2e-10	50 / 414	BP metabolic process
4	2e-09	389 / 6723	CC membrane
5	1e-08	46 / 410	CC mitochondrion
6	1e-08	51 / 480	MF catalytic activity
7	2e-08	361 / 6248	CC integral component of membrane
8	2e-08	8 / 13	BP response to cadmium ion
9	3e-08	24 / 145	MF heme binding
10	3e-08	10 / 24	CC respiratory chain
11	6e-08	21 / 119	MF monooxygenase activity
12	8e-08	20 / 110	MF oxidoreductase activity, acting on paired donors, with incorporation or reduction of molecular oxygen
13	1e-07	26 / 178	MF iron ion binding
14	1e-07	9 / 21	MF NADH dehydrogenase (ubiquinone) activity
15	2e-06	9 / 27	MF oxidoreductase activity, acting on paired donors, with incorporation or reduction of molecular oxygen
16	4e-06	27 / 229	MF transporter activity
17	6e-06	51 / 591	BP transmembrane transport
18	1e-05	9 / 33	MF oxidoreductase activity, acting on the CH-CH group of donors
19	4e-05	6 / 16	MF acyl-CoA dehydrogenase activity
20	4e-05	7 / 23	CC mitochondrial respiratory chain complex I
21	6e-05	5 / 11	MF oxidoreductase activity, acting on NAD(P)H
22	8e-05	7 / 25	BP ATP synthesis coupled proton transport
23	1e-04	5 / 12	MF FMN binding
24	1e-04	5 / 12	CC mitochondrial proton-transporting ATP synthase complex, coupling factor F1
25	2e-04	68 / 969	MF hydrolase activity
26	2e-04	10 / 57	MF flavin adenine dinucleotide binding
27	2e-04	8 / 38	CC apical plasma membrane
28	3e-04	18 / 161	CC mitochondrial inner membrane
29	4e-04	14 / 109	BP apoptotic process
30	4e-04	7 / 31	MF hydrogen ion transmembrane transporter activity
31	4e-04	15 / 122	BP inflammatory response
32	5e-04	108 / 1761	MF metal ion binding
33	7e-04	6 / 25	MF tumor necrosis factor-activated receptor activity
34	7e-04	4 / 10	BP response to methylmercury
35	7e-04	5 / 17	MF hydrolase activity, acting on carbon-nitrogen (but not peptide) bonds
36	7e-04	5 / 17	BP regulation of actin filament polymerization
37	8e-04	7 / 35	CC peroxisome
38	8e-04	70 / 1066	CC intracellular
39	1e-03	4 / 11	BP mitochondrial electron transport, NADH to ubiquinone
40	1e-03	4 / 11	BP nitrogen compound metabolic process



BP				CC				MF			
Rank	p-value	#in/all	Geneset	Rank	p-value	#in/all	Geneset	Rank	p-value	#in/all	Geneset
1	3e-21	94 / 712	oxidation-reduction process	1	2e-09	389 / 6723	membrane	1	8e-20	76 / 522	oxidoreductase activity
2	2e-10	50 / 414	metabolic process	2	1e-08	46 / 410	mitochondrion	2	1e-08	51 / 480	catalytic activity
3	2e-08	8 / 13	response to cadmium ion	3	2e-08	361 / 6248	integral component of membrane	3	3e-08	24 / 145	heme binding
4	6e-06	51 / 591	transmembrane transport	4	3e-08	10 / 24	respiratory chain	4	6e-08	21 / 119	monooxygenase activity
5	8e-05	7 / 25	ATP synthesis coupled proton transport	5	4e-05	7 / 23	mitochondrial respiratory chain complex I	5	8e-08	20 / 110	oxidoreductase activity, acting on paired donors, with incorporation or reduction of molecular oxygen
6	4e-04	14 / 109	apoptotic process	6	1e-04	5 / 12	mitochondrial proton-transporting ATP synthase complex, coupling factor F(0)	6	1e-07	26 / 178	iron ion binding
7	4e-04	15 / 122	inflammatory response	7	2e-04	8 / 38	apical plasma membrane	7	1e-07	9 / 21	NADH dehydrogenase (ubiquinone) activity
8	7e-04	4 / 10	response to methylmercury	8	3e-04	18 / 161	mitochondrial inner membrane	8	2e-06	9 / 27	oxidoreductase activity, acting on paired donors, with incorporation or reduction of molecular oxygen
9	7e-04	5 / 17	regulation of actin filament polymerization	9	8e-04	7 / 35	peroxisome	9	4e-06	27 / 229	transporter activity
10	1e-03	4 / 11	mitochondrial electron transport, NADH to ubiquinone	10	8e-04	70 / 1066	intracellular	10	1e-05	9 / 33	oxidoreductase activity, acting on the CH-CH group of donors
11	1e-03	4 / 11	nitrogen compound metabolic process	11	2e-03	7 / 39	Z disc	11	4e-05	6 / 16	acyl-CoA dehydrogenase activity
12	1e-03	8 / 47	proton transport	12	6e-03	4 / 17	Arp2/3 protein complex	12	6e-05	5 / 11	oxidoreductase activity, acting on NAD(P)H
13	1e-03	8 / 47	response to lipopolysaccharide	13	6e-03	122 / 2189	cytoplasm	13	1e-04	5 / 12	FMN binding
14	1e-03	19 / 194	lipid metabolic process	14	9e-03	25 / 337	endoplasmic reticulum	14	2e-04	68 / 969	hydrolase activity
15	1e-03	5 / 19	vacuolar transport	15	1e-02	7 / 54	actin cytoskeleton	15	2e-04	10 / 57	flavin adenine dinucleotide binding



BP				CC				MF			
Rank	p-value	#in/all	Geneset	Rank	p-value	#in/all	Geneset	Rank	p-value	#in/all	Geneset
1	2e-18	43 / 712	oxidation-reduction process	1	4e-12	7 / 10	chylomicron	1	3e-17	36 / 522	oxidoreductase activity
2	5e-14	10 / 23	lipoprotein metabolic process	2	6e-10	6 / 10	high-density lipoprotein particle	2	3e-08	6 / 17	cholesterol binding
3	2e-11	12 / 67	lipid transport	3	6e-10	7 / 17	blood microparticle	3	3e-08	6 / 17	cholesterol transporter activity
4	5e-11	9 / 30	pigmentation	4	3e-09	28 / 634	extracellular region	4	1e-07	7 / 33	endopeptidase inhibitor activity
5	6e-10	6 / 10	triglyceride catabolic process	5	4e-06	4 / 10	melanosome	5	4e-05	5 / 32	oxidoreductase activity, acting on the CH-OH group of donors, NAD or NADP
6	1e-09	6 / 11	cholesterol homeostasis	6	1e-04	17 / 500	extracellular space	6	4e-05	8 / 105	lipid binding
7	2e-09	6 / 12	cholesterol biosynthetic process	7	5e-04	6 / 85	cell	7	4e-05	5 / 33	NAD binding
8	4e-09	6 / 13	cholesterol efflux	8	7e-04	3 / 15	secretory granule	8	7e-05	17 / 480	catalytic activity
9	8e-08	11 / 109	negative regulation of endopeptidase activity	9	8e-04	4 / 35	peroxisome	9	1e-04	13 / 321	GTPase activity
10	7e-07	19 / 414	metabolic process	10	1e-03	33 / 1580	cellular_component	10	2e-04	3 / 10	protein binding, bridging
11	6e-06	4 / 11	purine nucleotide biosynthetic process	11	2e-03	3 / 23	troponin complex	11	5e-04	17 / 561	GTP binding
12	8e-06	5 / 24	nucleoside metabolic process	12	4e-03	3 / 26	vesicle	12	1e-03	23 / 969	hydrolase activity
13	1e-05	5 / 25	cellular response to estrogen stimulus	13	6e-03	5 / 96	lysosome	13	2e-03	4 / 43	iron-sulfur cluster binding
14	1e-05	5 / 26	melanocyte differentiation	14	1e-02	4 / 70	myosin complex	14	2e-03	3 / 21	substrate-specific transmembrane transporter activity
15	2e-05	5 / 29	cellular response to xenobiotic stimulus	15	1e-02	3 / 38	trans-Golgi network	15	3e-03	6 / 119	monooxygenase activity

# K-Means Cluster

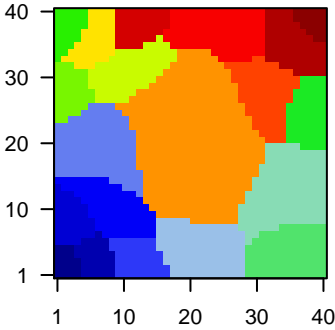
## Spot Summary: R

# metagenes = 40  
# genes = 621

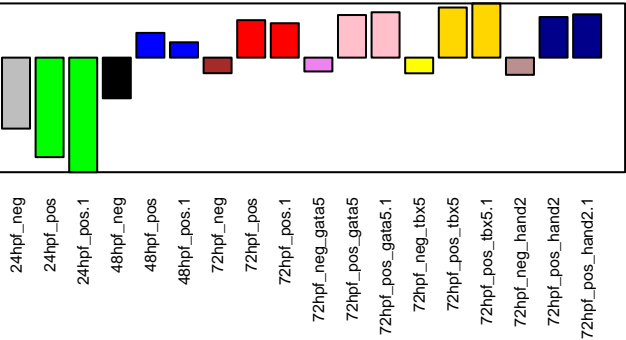
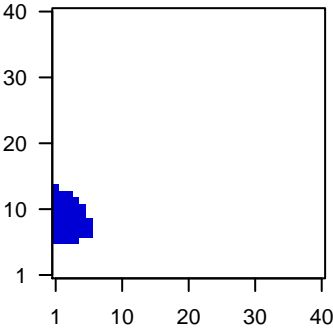
<r> metagenes = 0.95  
<r> genes = 0.63  
beta: r2= 14.06 / log p= -Inf

# samples with spot = 3 ( 16.7 %)  
72hpf\_pos\_gata5 : 1 ( 50 %)  
72hpf\_pos\_tbx5 : 2 ( 100 %)

Overview Map



Spot

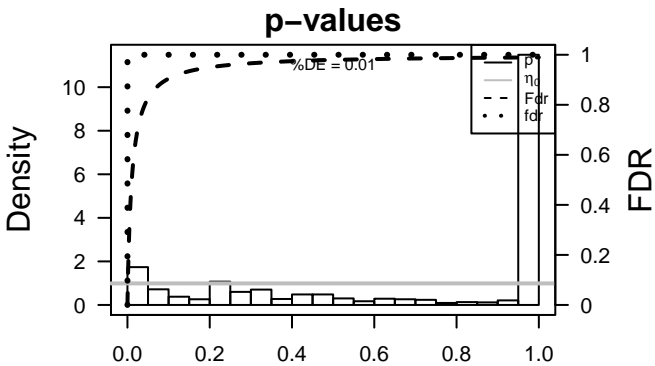


## Spot Genelist

Rank	ID	max e	r	Description	
		min e		Symbol	
1	ENSDARG000	5.99	-1.86	0.39	si:ch211-220f21.2 [Source:ZFIN;Acc:ZDB-GENE-160113-1]
2	ENSDARG000	4.89	-6.08	0.63	si:dkcy-9l20.3 [Source:ZFIN;Acc:ZDB-GENE-090313-369]
3	ENSDARG000	4.72	-2.88	0.52	si:ch211-117a21.5 17m20.5 [Source:ZFIN;Acc:ZDB-GENE-030131-1]
4	ENSDARG000	4.58	-2.18	0.63	zgc:111983c:111983 [Source:ZFIN;Acc:ZDB-GENE-050417-335]
5	ENSDARG000	4.25	-3.15	0.44	si:ch211-308a21-239b22.1 [Source:ZFIN;Acc:ZDB-GENE-131119-12]
6	ENSDARG000	4.19	-1.87	0.68	hal histidine ammonia-lyase [Source:ZFIN;Acc:ZDB-GENE-070]
7	ENSDARG000	4.15	-2.21	0.64	oxct1b 3-oxoacid CoA transferase 1b [Source:ZFIN;Acc:ZDB-GENE-060503-86]
8	ENSDARG000	4.09	-6.65	0.6	krt17 keratin 17 [Source:ZFIN;Acc:ZDB-GENE-060503-86]
9	ENSDARG000	3.79	-2.85	0.68	si:ch211-195b21.3 195b11.3 [Source:ZFIN;Acc:ZDB-GENE-141222-4]
10	ENSDARG000	3.79	-2.06	0.52	icn2 ictacalcin 2 [Source:ZFIN;Acc:ZDB-GENE-070822-9]
11	ENSDARG000	3.78	-3.48	0.7	mtp microsomal triglyceride transfer protein [Source:ZFIN;Acc:ZDB-GENE-070822-9]
12	ENSDARG000	3.73	-2.36	0.7	phosphorylase, glycogen, liver [Source:ZFIN;Acc:ZDB-GENE-070822-9]
13	ENSDARG000	3.72	-2.88	0.62	fabp10a fatty acid binding protein 10a, liver basic [Source:ZFIN;Acc:ZDB-GENE-061207-4]
14	ENSDARG000	3.72	-3.24	0.59	si:ch211-217k17.9 [Source:ZFIN;Acc:ZDB-GENE-061207-4]
15	ENSDARG000	3.63	-2.04	0.68	zgc:172051c:172051 [Source:ZFIN;Acc:ZDB-GENE-080219-23]
16	ENSDARG000	3.62	-2.04	0.66	gc group-specific component (vitamin D binding protein) [Source:ZFIN;Acc:ZDB-GENE-080219-23]
17	ENSDARG000	3.61	-2.02	0.74	LOC108190221:11-212c13.8 [Source:ZFIN;Acc:ZDB-GENE-131118-4]
18	ENSDARG000	3.56	-1.31	0.54	jacalin 10 [Source:ZFIN;Acc:ZDB-GENE-071004-126]
19	ENSDARG000	3.53	-3.48	0.64	g6pca.2 glucose-6-phosphatase a, catalytic subunit, tandem duplicat
20	ENSDARG000	3.52	-2.88	0.85	uroc1 urocanate hydratase 1 [Source:ZFIN;Acc:ZDB-GENE-08102]

## Geneset Overrepresentation

Rank	p-value	#in/all	Geneset
1	7e-10	9 / 23	CC troponin complex
2	2e-09	23 / 231	MF actin binding
3	8e-09	35 / 522	MF oxidoreductase activity
4	3e-08	41 / 712	BP oxidation-reduction process
5	1e-07	40 / 717	MF calcium ion binding
6	2e-07	6 / 13	BP regulation of muscle contraction
7	4e-07	11 / 70	CC myosin complex
8	9e-07	13 / 109	BP negative regulation of endopeptidase activity
9	1e-06	7 / 26	BP mitophagy
10	2e-06	5 / 11	BP cellular response to nitrogen starvation
11	2e-06	5 / 11	MF ferric iron binding
12	2e-06	6 / 19	BP gluconeogenesis
13	6e-06	5 / 13	BP iron ion transport
14	7e-06	25 / 414	BP metabolic process
15	1e-05	67 / 1761	MF metal ion binding
16	1e-05	27 / 480	MF catalytic activity
17	1e-05	6 / 24	BP cellular iron ion homeostasis
18	1e-05	5 / 15	BP response to mechanical stimulus
19	1e-05	6 / 25	MF glutathione transferase activity
20	1e-05	12 / 120	MF motor activity
21	5e-05	6 / 31	BP autophagosome assembly
22	6e-05	9 / 79	MF steroid hormone receptor activity
23	8e-05	9 / 81	BP steroid hormone mediated signaling pathway
24	8e-05	6 / 33	MF endopeptidase inhibitor activity
25	9e-05	6 / 34	BP glycolytic process
26	1e-04	4 / 12	BP response to activity
27	2e-04	7 / 53	BP autophagy
28	2e-04	13 / 178	MF iron ion binding
29	2e-04	6 / 40	BP intracellular receptor signaling pathway
30	3e-04	4 / 15	BP cardiac muscle contraction
31	3e-04	4 / 15	MF nucleoside diphosphate kinase activity
32	3e-04	4 / 15	BP nucleoside diphosphate phosphorylation
33	3e-04	4 / 15	BP skeletal muscle contraction
34	6e-04	55 / 1580	CC cellular_component
35	7e-04	6 / 49	BP cell-matrix adhesion
36	1e-03	5 / 35	BP sarcomere organization
37	1e-03	3 / 10	BP glycogen biosynthetic process
38	1e-03	9 / 119	BP regulation of cell proliferation
39	2e-03	3 / 11	BP photoperiodism
40	2e-03	4 / 25	BP tricarboxylic acid cycle



BP				CC				MF			
Rank	p-value	#in/all	Geneset	Rank	p-value	#in/all	Geneset	Rank	p-value	#in/all	Geneset
1	3e-08	41 / 712	oxidation-reduction process	1	7e-10	9 / 23	troponin complex	1	2e-09	23 / 231	actin binding
2	2e-07	6 / 13	regulation of muscle contraction	2	4e-07	11 / 70	myosin complex	2	8e-09	35 / 522	oxidoreductase activity
3	9e-07	13 / 109	negative regulation of endopeptidase activity	3	6e-04	55 / 1580	cellular_component	3	1e-07	40 / 717	calcium ion binding
4	1e-06	7 / 26	mitophagy	4	3e-03	17 / 355	cytosol	4	2e-06	5 / 11	ferric iron binding
5	2e-06	5 / 11	cellular response to nitrogen starvation	5	3e-03	3 / 14	autophagosome	5	1e-05	67 / 1761	metal ion binding
6	2e-06	6 / 19	gluconeogenesis	6	9e-03	15 / 337	endoplasmic reticulum	6	1e-05	27 / 480	catalytic activity
7	6e-06	5 / 13	iron ion transport	7	1e-02	6 / 85	cell	7	1e-05	6 / 25	glutathione transferase activity
8	7e-06	25 / 414	metabolic process	8	1e-02	5 / 62	intermediate filament	8	1e-05	12 / 120	motor activity
9	1e-05	6 / 24	cellular iron ion homeostasis	9	2e-02	3 / 24	respiratory chain	9	6e-05	9 / 79	steroid hormone receptor activity
10	1e-05	5 / 15	response to mechanical stimulus	10	2e-02	10 / 209	endoplasmic reticulum membrane	10	8e-05	6 / 33	endopeptidase inhibitor activity
11	5e-05	6 / 31	autophagosome assembly	11	3e-02	4 / 54	actin cytoskeleton	11	2e-04	13 / 178	iron ion binding
12	8e-05	9 / 81	steroid hormone mediated signaling pathway	12	4e-02	4 / 56	mitochondrial outer membrane	12	3e-04	4 / 15	nucleoside diphosphate kinase activity
13	9e-05	6 / 34	glycolytic process	13	5e-02	3 / 39	Z disc	13	2e-03	8 / 105	lipid binding
14	1e-04	4 / 12	response to activity	14	6e-02	3 / 40	perinuclear region of cytoplasm	14	3e-03	3 / 13	sodium channel regulator activity
15	2e-04	7 / 53	autophagy	15	6e-02	5 / 96	lysosome	15	3e-03	4 / 27	cytokine receptor activity

# K-Means Cluster

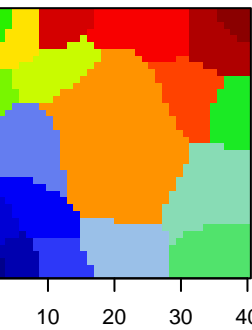
## Spot Summary: S

# metagenes = 31  
# genes = 520

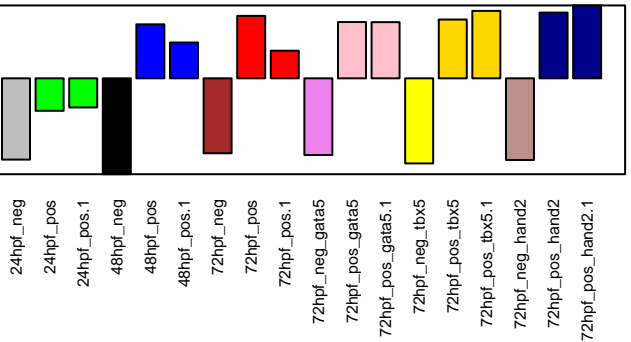
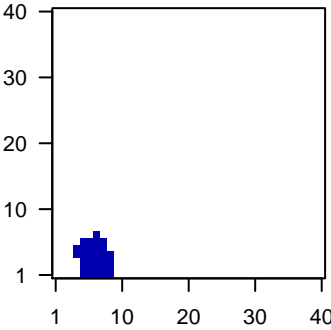
<r> metagenes = 0.97  
<r> genes = 0.75  
beta: r2= 20.77 / log p= -Inf

# samples with spot = 8 ( 44.4 % )  
48hpf\_pos : 1 ( 50 % )  
72hpf\_pos : 1 ( 50 % )  
72hpf\_pos\_gata5 : 2 ( 100 % )  
72hpf\_pos\_tbx5 : 2 ( 100 % )  
72hpf\_pos\_hand2 : 2 ( 100 % )

Overview Map



Spot

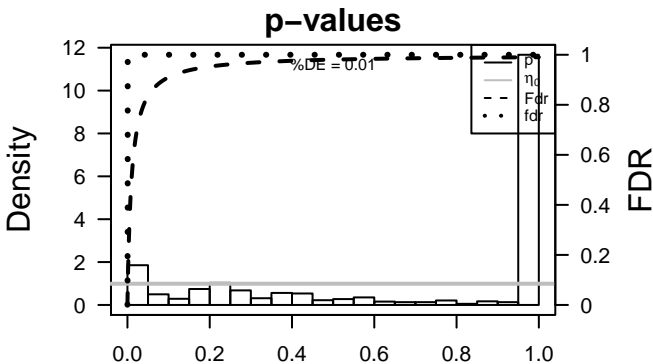


## Spot Genelist

Rank	ID	max e	r	Description	
		min e		Symbol	
1	ENSDARG000	4.01	-2.52	0.6	
2	ENSDARG000	3.99	-4.09	0.77	myl7 myosin, light chain 7, regulatory [Source:ZFIN;Acc:ZDB-GENE-131121-1]
3	ENSDARG000	3.62	-3.18	0.71	plaua plasminogen activator, urokinase a [Source:ZFIN;Acc:ZDB-GENE-131121-1]
4	ENSDARG000	3.51	-4.07	0.77	hsbp7 heat shock protein family, member 7 (cardiovascular) [Source:ZFIN;Acc:ZDB-GENE-131121-1]
5	ENSDARG000	3.42	-2.94	0.67	lrrc10 leucine rich repeat containing 10 [Source:ZFIN;Acc:ZDB-GENE-131121-1]
6	ENSDARG000	3.41	-3.37	0.76	mybpc3 myosin binding protein C, cardiac [Source:ZFIN;Acc:ZDB-GENE-131121-1]
7	ENSDARG000	3.33	-5.73	0.71	slc8a1a solute carrier family 8 (sodium/calcium exchanger), member 1 [Source:ZFIN;Acc:ZDB-GENE-131121-1]
8	ENSDARG000	3.24	-3.98	0.76	ryanodine receptor 2b (cardiac) [Source:ZFIN;Acc:ZDB-GENE-131121-1]
9	ENSDARG000	3.24	-2.94	0.8	
10	ENSDARG000	3.15	-3.12	0.64	lmod2b leiomodulin 2 (cardiac) b [Source:ZFIN;Acc:ZDB-GENE-131121-1]
11	ENSDARG000	3.14	-3.74	0.69	qdpra quinoid dihydropteridine reductase a [Source:ZFIN;Acc:ZDB-GENE-131121-1]
12	ENSDARG000	3.1	-3	0.6	LOC100150682 polymerization promoting protein [Source:ZFIN;Acc:ZDB-GENE-131121-1]
13	ENSDARG000	2.98	-3.59	0.88	mrc1b mannose receptor, C type 1b [Source:ZFIN;Acc:ZDB-GENE-131121-1]
14	ENSDARG000	2.97	-3	0.88	si:ch211-194m7.3 [Source:ZFIN;Acc:ZDB-GENE-131121-1]
15	ENSDARG000	2.81	-2.52	0.86	si:ch211-209f23.6 [Source:ZFIN;Acc:ZDB-GENE-141211-7]
16	ENSDARG000	2.78	-4.04	0.9	ctss2.1 cathepsin S, ortholog2, tandem duplicate 1 [Source:ZFIN;Acc:ZDB-GENE-131121-1]
17	ENSDARG000	2.77	-2.86	0.73	myh7bb myosin, heavy chain 7B, cardiac muscle, beta b [Source:ZFIN;Acc:ZDB-GENE-131121-1]
18	ENSDARG000	2.75	-2.5	0.94	hmox1a heme oxygenase 1a [Source:ZFIN;Acc:ZDB-GENE-030131-1]
19	ENSDARG000	2.73	-2.21	0.75	adhesion G protein-coupled receptor G3 [Source:ZFIN;Acc:ZDB-GENE-131121-1]
20	ENSDARG000	2.72	-3.38	0.9	il10ra interleukin 10 receptor, alpha [Source:ZFIN;Acc:ZDB-GENE-131121-1]

## Geneset Overrepresentation

Rank	p-value	#in/all	Geneset
1	6e-17	21 / 96	CC lysosome
2	6e-07	44 / 1066	CC intracellular
3	2e-06	9 / 62	BP proteolysis involved in cellular protein catabolic process
4	5e-06	39 / 969	MF hydrolase activity
5	2e-05	10 / 101	CC endosome
6	4e-05	7 / 51	CC lysosomal membrane
7	4e-05	19 / 358	MF peptidase activity
8	8e-05	26 / 609	BP proteolysis
9	8e-05	5 / 25	MF proton-transporting ATPase activity, rotational mechanism
10	1e-04	8 / 78	MF cysteine-type endopeptidase activity
11	1e-04	4 / 15	BP macrophage differentiation
12	2e-04	6 / 47	BP activation of GTPase activity
13	2e-04	5 / 31	BP ATP hydrolysis coupled proton transport
14	3e-04	158 / 6723	CC membrane
15	5e-04	9 / 123	MF cysteine-type peptidase activity
16	6e-04	7 / 79	MF phosphatidylinositol binding
17	7e-04	3 / 10	MF bicarbonate transmembrane transporter activity
18	7e-04	3 / 10	MF oxalate transmembrane transporter activity
19	7e-04	3 / 10	BP oxalate transport
20	7e-04	44 / 1437	MF molecular_function
21	8e-04	18 / 414	BP metabolic process
22	8e-04	4 / 23	BP bicarbonate transport
23	8e-04	21 / 522	MF oxidoreductase activity
24	8e-04	7 / 82	MF lyase activity
25	8e-04	5 / 40	BP regulation of vesicle fusion
26	9e-04	3 / 11	MF serine-type carboxypeptidase activity
27	1e-03	11 / 194	BP lipid metabolic process
28	1e-03	35 / 1084	BP transport
29	1e-03	3 / 12	MF secondary active sulfate transmembrane transporter activity
30	1e-03	60 / 2189	CC cytoplasm
31	2e-03	3 / 13	BP response to cytokine
32	2e-03	4 / 29	CC integrin complex
33	2e-03	3 / 14	MF anion:anion antiporter activity
34	2e-03	3 / 14	MF aspartic-type endopeptidase activity
35	2e-03	3 / 14	BP sulfate transmembrane transport
36	2e-03	3 / 14	MF sulfate transmembrane transporter activity
37	2e-03	6 / 71	CC endomembrane system
38	2e-03	5 / 49	MF calcium-dependent phospholipid binding
39	2e-03	4 / 30	MF chloride channel activity
40	2e-03	4 / 30	BP pigmentation



BP				CC				MF			
Rank	p-value	#in/all	Geneset	Rank	p-value	#in/all	Geneset	Rank	p-value	#in/all	Geneset
1	2e-06	9 / 62	proteolysis involved in cellular protein catabolic process	1	6e-17	21 / 96	lysosome	1	5e-06	39 / 969	hydrolase activity
2	8e-05	26 / 609	proteolysis	2	6e-07	44 / 1066	intracellular	2	4e-05	19 / 358	peptidase activity
3	1e-04	4 / 15	macrophage differentiation	3	2e-05	10 / 101	endosome	3	8e-05	5 / 25	proton-transporting ATPase activity, rotational mechanism
4	2e-04	6 / 47	activation of GTPase activity	4	4e-05	7 / 51	lysosomal membrane	4	1e-04	8 / 78	cysteine-type endopeptidase activity
5	2e-04	5 / 31	ATP hydrolysis coupled proton transport	5	3e-04	158 / 6723	membrane	5	5e-04	9 / 123	cysteine-type peptidase activity
6	7e-04	3 / 10	oxalate transport	6	1e-03	60 / 2189	cytoplasm	6	6e-04	7 / 79	phosphatidylinositol binding
7	8e-04	18 / 414	metabolic process	7	2e-03	4 / 29	integrin complex	7	7e-04	3 / 10	bicarbonate transmembrane transporter activity
8	8e-04	4 / 23	bicarbonate transport	8	2e-03	6 / 71	endomembrane system	8	7e-04	3 / 10	oxalate transmembrane transporter activity
9	8e-04	5 / 40	regulation of vesicle fusion	9	2e-03	143 / 6248	integral component of membrane	9	7e-04	44 / 1437	molecular_function
10	1e-03	11 / 194	lipid metabolic process	10	7e-03	43 / 1580	cellular_component	10	8e-04	21 / 522	oxidoreductase activity
11	1e-03	35 / 1084	transport	11	7e-03	3 / 22	cytoplasmic vesicle membrane	11	8e-04	7 / 82	lyase activity
12	2e-03	3 / 13	response to cytokine	12	9e-03	3 / 24	membrane raft	12	9e-04	3 / 11	serine-type carboxypeptidase activity
13	2e-03	3 / 14	sulfate transmembrane transport	13	1e-02	3 / 26	vesicle	13	1e-03	3 / 12	secondary active sulfate transmembrane transporter activity
14	2e-03	4 / 30	pigmentation	14	2e-02	13 / 355	cytosol	14	2e-03	3 / 14	anion:anion antiporter activity
15	2e-03	3 / 15	negative regulation of cell migration	15	2e-02	2 / 11	BLOC-1 complex	15	2e-03	3 / 14	aspartic-type endopeptidase activity



# K–Means Cluster

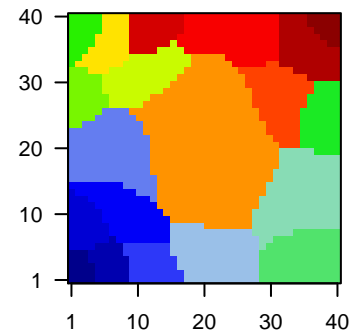
## Spot Summary: T

# metagenes = 44  
# genes = 722

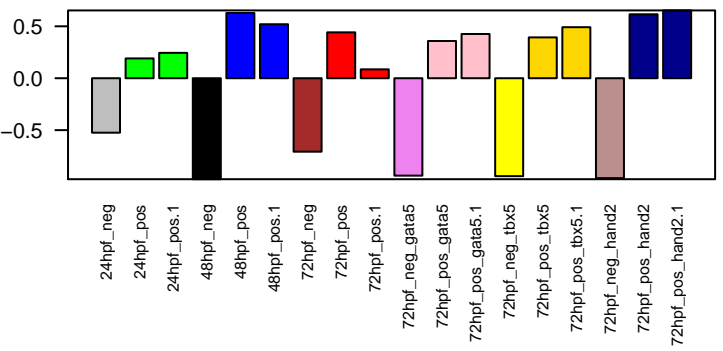
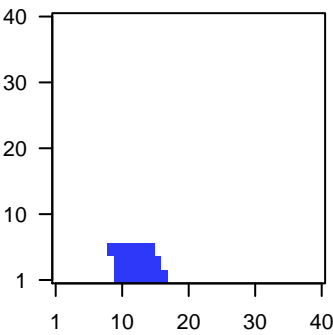
<r> metagenes = 0.94  
<r> genes = 0.6  
beta: r2= 7.01 / log p= -Inf

# samples with spot = 0 ( 0 %)

Overview Map



Spot

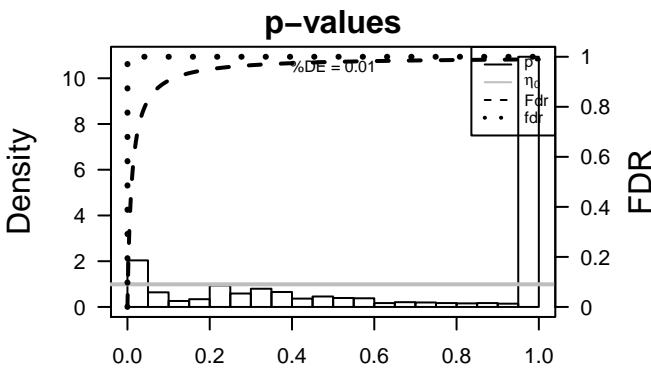


## Spot Genelist

Rank	ID	max e	r	min e	Description
1	ENSDARG0000000000	3.59	-3.41	0.69	vmhc ventricular myosin heavy chain [Source:ZFIN;Acc:ZDB-GENE-0000000000]
2	ENSDARG0000000000	3.21	-3.58	0.62	clec19a C-type lectin domain containing 19A [Source:ZFIN;Acc:ZDB-GENE-0000000000]
3	ENSDARG0000000000	2.88	-2.32	0.56	nkx2.5 NK2 homeobox 5 [Source:ZFIN;Acc:ZDB-GENE-0000000000]
4	ENSDARG0000000000	2.82	-1.8	0.75	synpo2lb synaptopodin 2-like b [Source:ZFIN;Acc:ZDB-GENE-0000000000]
5	ENSDARG0000000000	2.81	-2.63	0.65	myosin, heavy chain 7B, cardiac muscle, beta a [Source:ZFIN;Acc:ZDB-GENE-0000000000]
6	ENSDARG0000000000	2.73	-1.88	0.66	hebp2 heme binding protein 2 [Source:ZFIN;Acc:ZDB-GENE-0000000000]
7	ENSDARG0000000000	2.7	-3.16	0.66	mylk2 myosin light chain kinase 2 [Source:ZFIN;Acc:ZDB-GENE-0000000000]
8	ENSDARG0000000000	2.64	-2.08	0.78	mibp muscle-specific beta 1 integrin binding protein [Source:ZFIN;Acc:ZDB-GENE-0000000000]
9	ENSDARG0000000000	2.64	-3.7	0.53	LOC565195ch211-233h19.2 [Source:ZFIN;Acc:ZDB-GENE-0000000000]
10	ENSDARG0000000000	2.51	-1.81	0.67	csrp3 cysteine and glycine-rich protein 3 (cardiac LIM protein) [Source:ZFIN;Acc:ZDB-GENE-0000000000]
11	ENSDARG0000000000	2.46	-1.35	0.65	nppb natriuretic peptide B [Source:ZFIN;Acc:ZDB-GENE-0000000000]
12	ENSDARG0000000000	2.44	-2.75	0.7	mylk3 myosin light chain kinase 3 [Source:ZFIN;Acc:ZDB-GENE-0000000000]
13	ENSDARG0000000000	2.43	-3.39	0.76	gata4 GATA binding protein 4 [Source:ZFIN;Acc:ZDB-GENE-0000000000]
14	ENSDARG0000000000	2.4	-3.18	0.56	si:ch73-248e21.5 [Source:ZFIN;Acc:ZDB-GENE-0000000000]
15	ENSDARG0000000000	2.39	-2.43	0.74	popdc2 popeye domain containing 2 [Source:ZFIN;Acc:ZDB-GENE-0000000000]
16	ENSDARG0000000000	2.37	-1.55	0.74	
17	ENSDARG0000000000	2.36	-4.29	0.52	obs1a obscurin-like 1a [Source:ZFIN;Acc:ZDB-GENE-0000000000]
18	ENSDARG0000000000	2.33	-2.97	0.77	gata5 GATA binding protein 5 [Source:ZFIN;Acc:ZDB-GENE-0000000000]
19	ENSDARG0000000000	2.32	-2.15	0.64	alp3a alpha-kinase 3a [Source:ZFIN;Acc:ZDB-GENE-0000000000]
20	ENSDARG0000000000	2.32	-2.72	0.5	crestin crestin [Source:ZFIN;Acc:ZDB-GENE-0000000000]

## Geneset Overrepresentation

Rank	p-value	#in/all	Geneset
1	9e-11	40 / 480	MF catalytic activity
2	1e-08	33 / 414	BP metabolic process
3	6e-08	9 / 31	MF hydrogen ion transmembrane transporter activity
4	3e-07	14 / 101	CC endosome
5	9e-07	8 / 31	BP ATP hydrolysis coupled proton transport
6	1e-06	17 / 164	BP carbohydrate metabolic process
7	1e-06	16 / 147	BP vesicle-mediated transport
8	2e-06	7 / 25	MF proton-transporting ATPase activity, rotational mechanism
9	2e-06	19 / 210	BP intracellular protein transport
10	7e-06	9 / 53	MF pyridoxal phosphate binding
11	1e-05	5 / 13	CC proton-transporting V-type ATPase, V0 domain
12	2e-05	6 / 23	BP retrograde transport, endosome to Golgi
13	2e-05	8 / 47	BP proton transport
14	3e-05	22 / 321	MF GTPase activity
15	4e-05	50 / 1066	CC intracellular
16	4e-05	9 / 64	MF hydrolase activity, acting on glycosyl bonds
17	5e-05	14 / 156	BP small GTPase mediated signal transduction
18	6e-05	31 / 561	MF GTP binding
19	7e-05	5 / 18	CC endosome membrane
20	8e-05	9 / 71	CC endomembrane system
21	1e-04	17 / 231	MF actin binding
22	1e-04	8 / 59	BP actin filament organization
23	2e-04	5 / 21	BP muscle contraction
24	2e-04	48 / 1084	BP transport
25	2e-04	83 / 2189	CC cytoplasm
26	3e-04	4 / 13	BP cellular response to oxidative stress
27	3e-04	4 / 13	BP vesicle organization
28	3e-04	7 / 51	CC lysosomal membrane
29	3e-04	5 / 24	BP metal ion transport
30	3e-04	6 / 37	BP myofibril assembly
31	4e-04	5 / 25	BP phosphatidylinositol dephosphorylation
32	4e-04	212 / 6723	CC membrane
33	4e-04	43 / 969	MF hydrolase activity
34	4e-04	6 / 39	CC Z disc
35	6e-04	4 / 16	MF FAD binding
36	7e-04	6 / 42	MF SNAP receptor activity
37	8e-04	4 / 17	CC Arp2/3 protein complex
38	1e-03	8 / 79	MF phosphatidylinositol binding
39	1e-03	20 / 355	CC cytosol
40	1e-03	12 / 161	CC mitochondrial inner membrane



BP				CC				MF			
Rank	p-value	#in/all	Geneset	Rank	p-value	#in/all	Geneset	Rank	p-value	#in/all	Geneset
1	1e-08	33 / 414	metabolic process	1	3e-07	14 / 101	endosome	1	9e-11	40 / 480	catalytic activity
2	9e-07	8 / 31	ATP hydrolysis coupled proton transport	2	1e-05	5 / 13	proton-transporting V-type ATPase, V0 domain	2	6e-08	9 / 31	hydrogen ion transmembrane transporter activity
3	1e-06	17 / 164	carbohydrate metabolic process	3	4e-05	50 / 1066	intracellular	3	2e-06	7 / 25	proton-transporting ATPase activity, rotational mechanism
4	1e-06	16 / 147	vesicle-mediated transport	4	7e-05	5 / 18	endosome membrane	4	7e-06	9 / 53	pyridoxal phosphate binding
5	2e-06	19 / 210	intracellular protein transport	5	8e-05	9 / 71	endomembrane system	5	3e-05	22 / 321	GTPase activity
6	2e-05	6 / 23	retrograde transport, endosome to Golgi	6	2e-04	83 / 2189	cytoplasm	6	4e-05	9 / 64	hydrolase activity, acting on glycosyl bonds
7	2e-05	8 / 47	proton transport	7	3e-04	7 / 51	lysosomal membrane	7	6e-05	31 / 561	GTP binding
8	5e-05	14 / 156	small GTPase mediated signal transduction	8	4e-04	212 / 6723	membrane	8	1e-04	17 / 231	actin binding
9	1e-04	8 / 59	actin filament organization	9	4e-04	6 / 39	Z disc	9	4e-04	43 / 969	hydrolase activity
10	2e-04	5 / 21	muscle contraction	10	8e-04	4 / 17	Arp2/3 protein complex	10	6e-04	4 / 16	FAD binding
11	2e-04	48 / 1084	transport	11	1e-03	20 / 355	cytosol	11	7e-04	6 / 42	SNAP receptor activity
12	3e-04	4 / 13	cellular response to oxidative stress	12	1e-03	12 / 161	mitochondrial inner membrane	12	1e-03	8 / 79	phosphatidylinositol binding
13	3e-04	4 / 13	vesicle organization	13	1e-03	4 / 18	late endosome membrane	13	1e-03	8 / 82	lyase activity
14	3e-04	5 / 24	metal ion transport	14	1e-03	4 / 18	vacuole	14	2e-03	3 / 11	coenzyme binding
15	3e-04	6 / 37	myofibril assembly	15	1e-03	4 / 19	extrinsic component of membrane	15	3e-03	4 / 24	SH3/SH2 adaptor activity