

#### Spot Summary: A

# metagenes = 32 # genes = 600

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

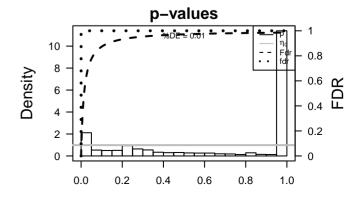
# samples with spot = 2 ( 11.1 %)

24hpf\_neg: 1 (100%) 48hpf\_neg: 1 (100%)

#### **Overview Map Spot** 30 20 20 10 10 10 20 30 30 10 20 0.8 0.6 0.4 0.2 0.0 -0.2 -0.4 72hpf\_neg\_gata5 72hpf\_pos\_gata5 48hpf\_pos.1 72hpf\_neg 48hpf\_pos 72hpf\_pos 72hpf\_pos.1 72hpf\_neg\_tbx5 72hpf\_pos\_hand2 72hpf\_pos\_gata5.1

# **Spot Genelist**

Rai	nk ID	max	e min e	r e	Syml	Description pol	Rank	p-value	#in/all	Ge	neset
1	ENSDARG000	4.38	-2.85	0.81	col28a2	acollagen, type XXVIII, alpha 2a [Source:ZFIN;Acc:ZDB-GENI	1	1e-31	101 / 1239	BP	regulation of transcription, DNA-templated
_							2	6e-30	153 / 2716		nucleus
2	ENSDARG000	3.19	-3.3	0.71	plp1a	proteolipid protein 1a [Source:ZFIN;Acc:ZDB-GENE-001202	3	3e-27	104 / 1484		DNA binding
_							4	5e-23	52 / 454	BP	multicellular organism development
3	ENSDARG000	3.06	-1.7	8.0	col7a1	collagen, type VII, alpha 1 [Source:ZFIN;Acc:ZDB-GENE-03	5	3e-14	44 / 537	MF	sequence-specific DNA binding
							6	4e-09	16 / 117	BP	Wnt signaling pathway
4	ENSDARG000	2.94	-1.72	0.92	sox19a	SRY (sex determining region Y)-box 19a [Source:ZFIN;Acc:Z	/	8e-09	83 / 2030	MF	nucleic acid binding
							8	4e-08	37 / 633	MF	transcription factor activity, sequence–specific DNA binding
5	ENSDARG000	2.94	-1.34	0.75	nes	Nestin [Source:UniProtKB/Swiss-Prot;Acc:P86839]	9	6e-08	9 / 37	MF	nucleosomal DNA binding
							10	2e-07	10 / 55	BP	neuron differentiation
6	ENSDARG000	2.91	-2.1	0.89	dld	deltaD [Source:ZFIN;Acc:ZDB-GENE-990415-47]	11	5e-07	35 / 643	BP	transcription, DNA-templated
							12	3e-06	6 / 20	MF	L-ascorbic acid binding
7	ENSDARG000	2.79	-1.66	0.79	col4a6	collagen, type IV, alpha 6 [Source:ZFIN;Acc:ZDB-GENE-101	13	3e-06	5/12	BP	regulation of neurogenesis
							14	3e-06	14 / 147	BP	brain development
8	ENSDARG000	2.75	-1.34	0.71		oligodendrocyte transcription factor 3 [Source:ZFIN;Acc:ZDB-	15	4e-06	16 / 190	MF	protein dimerization activity
							16	4e-06	7 / 32	CC	chromatin
9	ENSDARG000	2.66	-1.67	0.83	col4a5	collagen, type IV, alpha 5 (Alport syndrome) [Source:ZFIN;Ac	17	4e-06	8 / 45	BP	Notch signaling pathway
							18	5e-06	14 / 153	CC	proteinaceous extracellular matrix
10	ENSDARG000	2.64	-1.85	0.83	sp8b	sp8 transcription factor b [Source:ZFIN;Acc:ZDB-GENE-030	19	8e-06	31 / 608	MF	RNA binding
							20	1e-05	10 / 83	BP	embryonic viscerocranium morphogenesis
11	ENSDARG000	2.62	-2.43	0.76	zgc:101	829c:101810 [Source:ZFIN;Acc:ZDB-GENE-041121-7]	21	2e-05	14 / 168	CC	nucleosome
							22	2e-05	5 / 17	BP	photoreceptor cell outer segment organization
12	ENSDARG000	2.48	-1.49	0.56			23 24	3e-05	5 / 18	BP	otic placode formation
								4e-05	17 / 257	BP	cell differentiation
13	ENSDARG000	2.47	-1.28	0.81	igsf9a	immunoglobulin superfamily, member 9a [Source:ZFIN;Acc:Zl	25	4e-05	11 / 117	BP	nucleosome assembly hindbrain development
							26 27	6e-05	6/33	BP BP	
14	ENSDARG00	2.46	-1.7	0.75		si:ch211-193l2.3 [Source:ZFIN;Acc:ZDB-GENE-141216-14	27 28	7e-05	5 / 21	BP	midbrain-hindbrain boundary development
							26 29	7e-05 1e-04	7 / 48		neural crest cell migration floor plate formation
15	ENSDARG00	2.38	-2.26	0.55	LOC100	053aig0and enhancer of split-related 15, tandem duplicate 1 [S	30	1e-04 1e-04	4 / 13 4 / 13	BP BP	sensory epithelium regeneration
							31	1e-04 1e-04	4/13	BP	ventral spinal cord interneuron differentiation
16	ENSDARG00	2.38	-1.82	0.71	her13	hairy-related 13 [Source:ZFIN;Acc:ZDB-GENE-050228-1]	32	1e-04 1e-04	15 / 229	CC	chromosome
10						, , , , , , , , , , , , , , , , , , , ,	33	2e-04	5 / 25	BP	cell fate commitment
17	ENSDARG00	2 37	-1.24	0.77	рах3а	paired box 3a [Source:ZFIN;Acc:ZDB-GENE-980526-52]	34	2e-04 2e-04	5 / 25	MF	frizzled binding
.,	2.102/11000			****		,	35	2e-04 2e-04	9/93	BP	dorsal/ventral pattern formation
18	ENSDARG000	2 36	-1.06	0.9	notch3	notch 3 [Source:ZFIN;Acc:ZDB-GENE-000329-5]	36	2e-04 2e-04	4/14	BP	oligodendrocyte differentiation
10	2.102/110001	2.00	-1.00	0.0	.1010110		36 37	2e-04 2e-04	4/14	BP	regulation of Notch signaling pathway
19	ENSDARG000	2 32	-2.23	0.59	lamb4	laminin, beta 4 [Source:ZFIN;Acc:ZDB-GENE-021226-2]	38	2e-04 2e-04	11 / 138	BP	cilium assembly
19	LINSDANGOON	2.02	-2.23	0.55	iaiiib4		36 39	2e-04 2e-04	5/26	MF	Wnt-protein binding
20	ENSDARG000	2.3	-1.44	0.82	sox19b	SRY (sex determining region Y)-box 19b [Source:ZFIN;Acc:2	39 40	2e-04 2e-04	8/77	BP	determination of left/right symmetry



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

# Spot Summary: B

# metagenes = 28 # genes = 472

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

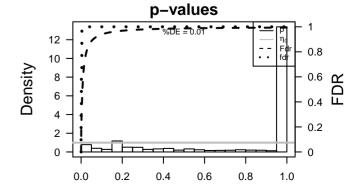
# samples with spot = 2 ( 11.1 %) 24hpf\_neg : 1 ( 100 %)

48hpf\_neg: 1 (100%)

#### **Overview Map Spot** 30 20 20 10 10 10 20 30 20 30 10 0.6 0.4 0.2 0.0 -0.2 -0.4 -0.6 72hpf\_neg\_gata5 72hpf\_pos\_gata5 48hpf\_pos.1 72hpf\_neg 48hpf\_pos 72hpf\_pos 72hpf\_pos.1 72hpf\_pos\_gata5.1 72hpf\_neg\_tbx5 72hpf\_pos\_hand2

# **Spot Genelist**

Ra	nk	max	е	r		Description	Rank	p-value	#in/all	Ge	neset
	ID		min (	е	Syml	bol					
					•						
1	ENSDARG000	1 04	-0.89	0.63		subcommissural organ spondin [Source:ZFIN;Acc:ZDB-GEN	1	7e-32	115 / 2030	MF	nucleic acid binding
1	LINSDANGOO	1.54	-0.03	0.03		oubscriming and organis operating (course.E.i.m.), too.EBB CEN	2	2e-13	40 / 608	MF	RNA binding
2	ENSDARG000	1 70	-1.16	0.61	1.0079/	4549tone 1, H4, like [Source:ZFIN;Acc:ZDB-GENE-070927-10	3	4e-07	80 / 2716	CC	nucleus
_	LINODAIRCOOK	1.75	-1.10	0.01	L00/3-	75-5-6-16 1, 111, 1110 [55-6155-12] 111, 155-255 52-12 51-5527 11	4	5e-04	5/39	MF	protein serine/threonine phosphatase activity
3	ENSDARG000	1 77	-0.93	0.62	susd4	sushi domain containing 4 [Source:ZFIN;Acc:ZDB-GENE-11	5	7e-04	3 / 11	BP	establishment or maintenance of cell polarity
9	LINODAIRCOOK		0.00	0.02	odod i		6	8e-04	6 / 66	MF	thiol-dependent ubiquitinyl hydrolase activity
4	ENSDARG000	1 68	-0.56	0.72		si:ch211-106f21.1 [Source:ZFIN;Acc:ZDB-GENE-141216-3	7	1e-03	6/70	BP	protein deubiquitination
4	LINSDAIRGOON	1.00	-0.50	0.72		3.01211-100121.1 [000100.21 IIV,700.2DB-0EIVE-141210-0	8	1e-03	3 / 13	MF	signal transducer activity, downstream of receptor
5	ENSDARG000	1 69	-1.23	0.41	irx4b	iroquois homeobox 4b [Source:ZFIN;Acc:ZDB-GENE-04071	9	1e-03	6 / 72	MF	helicase activity
3	LINODAIRCOOK	1.00	-1.20	0.41	IIA-ID	TO GOOD TO TO TO SO TO TO TO THE SOURCE OF T	10	1e-03	3 / 14	BP	transcription elongation from RNA polymerase II promoter
6	ENSDARG000	1 67	-1.19	0.56	apr37l1:	a G protein-coupled receptor 37 like 1a [Source:ZFIN;Acc:ZDB	11	2e-03	8 / 138	BP	cilium assembly
O	ENSDARGOO	1.07	-1.13	0.50	gpioriti	a o protein-coupled receptor or line 1a [course.21 in, no.255	12	3e-03	3 / 17	CC	U2-type prespliceosome
7	ENSDARG000	1 67	-1.13	0.65		si:dkey-250i3.3 [Source:ZFIN;Acc:ZDB-GENE-110131-5]	13	3e-03	45 / 1761	MF	metal ion binding
1	ENSDARGOO	1.07	-1.13	0.03		Silukey-2000.0 [Source.21 IIV,Acc.2DD-GEIVE-110101-0]	14	3e-03	14 / 362	BP	regulation of transcription from RNA polymerase II promoter
8	ENSDARG000	1 64	-1.01	0.71	gbx1	gastrulation brain homeobox 1 [Source:ZFIN;Acc:ZDB-GENE	15	4e-03	34 / 1239	BP	regulation of transcription, DNA-templated
0	ENSDARGOO	1.04	-1.01	0.71	gbxi	gasti diation brain nomeobox 1 [Source.21 III,Acc.2DB=GENE	16	4e-03	3 / 19	CC	U1 snRNP
0	ENCDARCOO!	1 64	-1.59	0.78	jag2b	jagged 2b [Source:ZFIN;Acc:ZDB-GENE-011128-3]	17	5e-03	5 / 65	BP	covalent chromatin modification
9	ENSDARG000	1.04	-1.59	0.76	Jagzu	Jagged 2D [Godice.21 III,Acc.2DD-GEIVE-011120-3]	18	5e-03	3 / 21	MF	dynein light chain binding
40	ENCDARCOO!	4.00	2.05	0.70		zgc:158689 [Source:ZFIN;Acc:ZDB-GENE-070112-1902]	19	6e-03	5 / 70	BP	RNA processing
10	ENSDARG000	1.02	-2.05	0.73		2gc. 130009 [3001ce.2Filv,Acc.2DB-GENE-070112-1902]	20	7e-03	3 / 24	MF	cation binding
4.4	ENODA DOSS	4.57	4.05	0.07	-:	26-412 20-0 2 [C75]N: A7DD	21	8e-03	4 / 47	BP	regulation of GTPase activity
11	ENSDARG000	1.57	-1.95	0.67	si:ukey-	-29ipskay-29p9.3 [Source:ZFIN;Acc:ZDB-GENE-141216-161]	22	9e-03	4 / 49	BP	regulation of cell shape
40	=======================================					shareshare harmalas Ch (Carress ZEIN) A an ZDD (CENIE 440C	23	1e-02	4 / 51	BP	anatomical structure morphogenesis
12	ENSDARG000	1.54	-1.41	0.82		chromobox homolog 6b [Source:ZFIN;Acc:ZDB-GENE-1106	24	1e-02	5/79	BP	mRNA splicing, via spliceosome
40	=======================================						25	1e-02	37 / 1484	MF	DNA binding
13	ENSDARG000	1.51	-0.95	0.73			26	1e-02	5 / 80	MF	transcription regulatory region DNA binding
							27	1e-02	4 / 53	BP	convergent extension involved in gastrulation
14	ENSDARG000	1.49	-1.52	0.92	ankrd10	)aankyrin repeat domain 10a [Source:ZFIN;Acc:ZDB-GENE-0	28	1e-02	2/11	CC	commitment complex
4.5							29	1e-02	5 / 85	BP	protein folding
15	ENSDARG000	1.48	-1.1	0.88	znf281b	zinc finger protein 281b [Source:ZFIN;Acc:ZDB-GENE-0502	30	2e-02	35 / 1427	BP	biological_process
4.0							31	2e-02	2 / 12	MF	acetylgalactosaminyltransferase activity
16	ENSDARG000	1.45	-1	0.65	tmem13	88transmembrane protein 138 [Source:ZFIN;Acc:ZDB-GENE-1	32	2e-02	2 / 12	BP	neural tube formation
4-							33	2e-02	2 / 13	BP	cilium organization
17	ENSDARG000	1.44	-1.44	0.61		adhesion G protein-coupled receptor A3 [Source:ZFIN;Acc:Z	34	2e-02	2 / 13	MF	dynein heavy chain binding
4.0							35	2e-02	2 / 13	BP	mitotic sister chromatid cohesion
18	ENSDARG000	1.43	-0.73	0.81	plxnb1b	plexin b1b [Source:ZFIN;Acc:ZDB-GENE-090812-4]	36	2e-02	2 / 13	MF	TBP-class protein binding
4.0							37	2e-02	3 / 35	BP	cell projection organization
19	ENSDARG000	1.43	-1.31	0.57		si:ch211-196c10.11 [Source:ZFIN;Acc:ZDB-GENE-081104-	38	2e-02	2/14	BP	ATP-dependent chromatin remodeling
0.0							39	2e-02	2/14	BP	chromatin organization
20	ENSDARG000	1.43	-1.83	0.77		si:ch211-246m6.5 [Source:ZFIN;Acc:ZDB-GENE-050208-5	40	2e-02	2/14	BP	response to heat



BP				СС				MF			
Rank	p-value	#in/all	Geneset	Rank	p-value	#in/all	Geneset	Rank	p-value	#in/all	Geneset
1	7e-04	3/11	establishment or maintenance of cell polarity	1	4e-07	80 / 2716	nucleus	1	7e-32	115 / 2030	nucleic acid binding
2	1e-03	6 / 70	protein deubiquitination	2	3e-03	3 / 17	U2-type prespliceosome	2	2e-13	40 / 608	RNA binding
3	1e-03	3 / 14	transcription elongation from RNA polymerase II promoter	3	4e-03	3 / 19	U1 snRNP	3	5e-04	5 / 39	protein serine/threonine phosphatase activity
4	2e-03	8 / 138	cilium assembly	4	1e-02	2/11	commitment complex	4	8e-04	6 / 66	thiol-dependent ubiquitinyl hydrolase activity
5	3e-03	14 / 362	regulation of transcription from RNA polymerase II promoter	5	3e-02	2 / 15	intrinsic component of the cytoplasmic side of the plasma membrane	5	1e-03	3 / 13	signal transducer activity, downstream of receptor
6	4e-03	34 / 1239	regulation of transcription, DNA-templated	6	4e-02	4/76	cilium	6	1e-03	6 / 72	helicase activity
7	5e-03	5 / 65	covalent chromatin modification	7	5e-02	2/21	nuclear membrane	7	3e-03	45 / 1761	metal ion binding
8	6e-03	5 / 70	RNA processing	8	5e-02	2 / 22	dynein complex	8	5e-03	3 / 21	dynein light chain binding
9	8e-03	4 / 47	regulation of GTPase activity	9	8e-02	34 / 1580	cellular_component	9	7e-03	3 / 24	cation binding
10	9e-03	4 / 49	regulation of cell shape	10	8e-02	8 / 268	cytoskeleton	10	1e-02	37 / 1484	DNA binding
11	1e-02	4 / 51	anatomical structure morphogenesis	11	9e-02	2/30	ciliary basal body	11	1e-02	5 / 80	transcription regulatory region DNA binding
12	1e-02	5 / 79	mRNA splicing, via spliceosome	12	1e-01	2/34	catalytic step 2 spliceosome	12	2e-02	2 / 12	acetylgalactosaminyltransferase activity
13	1e-02	4 / 53	convergent extension involved in gastrulation	13	1e-01	3/70	cell projection	13	2e-02	2/13	dynein heavy chain binding
14	1e-02	5 / 85	protein folding	14	1e-01	2 / 35	Golgi cisterna membrane	14	2e-02	2/13	TBP-class protein binding
15	2e-02	35 / 1427	biological_process	15	1e-01	2/38	apical plasma membrane	15	3e-02	4 / 67	unfolded protein binding

# Spot Summary: C

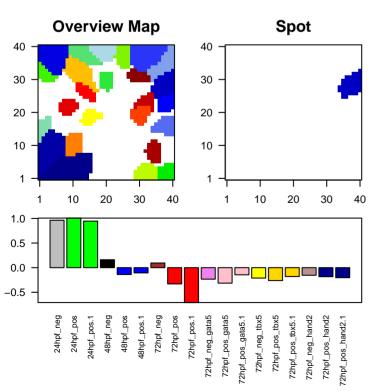
# metagenes = 42 # genes = 731

<r> metagenes = 0.92</r> <r> genes = 0.56

 beta: r2= 3.93 / log p= -Inf

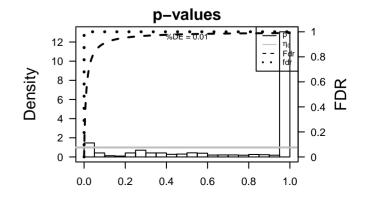
# samples with spot = 3 (16.7 %)

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



# **Spot Genelist**

Rank		max e r			Description		Rank	p-value	#in/all	/all Geneset			
	ID		min e	е	Sym	bol							
1	ENSDARG000	8 23	-1.2	0.6	odnrah	endothelin recentor type A	b [Source:ZFIN;Acc:ZDB-GENE-0	1	9e-46	173 / 2030	ME	nucleic acid binding	
•	LINSDANGOO	0.23	-1.2	0.0	eumab	ondomonin rocopion typo 7	5 (000100.E. 111,100.E.5.5 OE11E C	2	2e-18	148 / 2716		nucleus	
2	ENSDARG000	5 91	-1.27	0.71	si:dkev	-26inflkfev-26a8 5 [Source:7]	FIN;Acc:ZDB-GENE-121214-19]	3	2e-13	89 / 1484	MF	DNA binding	
_	LINODAIRCOOK	0.01	-1.27	0.71	onanoy	Lugaro, Luguro (Couroc.L.	, 100.233 02.12 12.2.1 10]	4	1e-11	11 / 25	BP	membrane disruption in other organism	
3	ENSDARG000	5.48	-1.21	0.65	zac:17	4158c:174153 [Source:ZEIN:	Acc:ZDB-GENE-080215-7]	5	1e-11	17 / 78	BP	DNA replication	
5	LINSDAIRGOON	0.40	-1.21	0.00	_go	rrago.rr rroo [couroc.zr m,	7.00.255 02.12 0002.0 1,	6	4e-11	22 / 148	BP	DNA repair	
4	ENSDARG000	5 31	-1.61	0.62	MGC17	7.4 sk#kev=26a8 4 [Source:7]	FIN;Acc:ZDB-GENE-121214-36]	7	9e-11	23 / 168	CC	nucleosome	
7	LINODAIRCOOK	0.01	-1.01	0.02	WICOTA	14400 No. 2090: 1 [000100:2.	, 100.255 02.12 12.2.1 00]	8	1e-10	11 / 30	BP	defense response to Gram-positive bacterium	
5	ENSDARG000	27	-1.67	0.73	ucp3	uncoupling protein 3 [Sour	ce:ZFIN;Acc:ZDB-GENE-040426-	9	3e-10	26 / 229	CC	chromosome	
J	2110271110001	2	1.01	0.70				10	4e-09	8 / 17	MF	DNA-directed DNA polymerase activity	
6	ENSDARG000	2 65	-1.35	0.74	si:ch73	–3≰iath/784364h19.1 [Source	:ZFIN;Acc:ZDB-GENE-031010-4	11	1e-08	24 / 232	MF	protein heterodimerization activity	
U	LINODAIRCOOK	2.00	1.00	0	0			12	2e-08	8 / 20	BP	DNA biosynthetic process	
7	ENSDARG000	2 63	-0.64	0.7	si:dkev	-269ifk@v-239i18.2 [Source:	ZFIN;Acc:ZDB-GENE-121214-52	13	1e-07	40 / 608	MF	RNA binding	
'	2110271110001	2.00	0.01	0.,	,			14	5e-06	5/11	BP	DNA-dependent DNA replication	
8	ENSDARG00	2 52	-1.92	0.7	zac:163	3040stone 1. H4. like [Source	:ZFIN;Acc:ZDB-GENE-070927-10	15	6e-06	8 / 39	MF	single-stranded DNA binding	
U	2.102/110001	2.02	1.02	0.,	-5	, ,		16	9e-06	7 / 30	MF	damaged DNA binding	
9	ENSDARG000	2.34	-2.31	0.94	tonsl	tonsoku-like. DNA repair r	protein [Source:ZFIN;Acc:ZDB-GEI	17	9e-06	7 / 30	BP	DNA recombination	
J	2110271110001				101101		,	18	1e-05	8 / 43	BP	DNA-templated transcription, initiation	
10	ENSDARG00	2.3	-1.05	0.68				19	2e-05	8 / 45	BP	rRNA processing	
10	2.102/110001	2.0	1.00	0.00				20	2e-05	7 / 34	BP	chromatin silencing	
11	ENSDARG00	2.27	-1.35	0.7		Fanconi anemia, complem	entation group B [Source:ZFIN;Acc	21	3e-05	13 / 128	BP	innate immune response	
				***			3 11, (111111111111111111111111111111111	22	4e-05	8 / 49	CC	nuclear chromatin	
12	ENSDARG00	2 26	-1.06	0.8	st3gal3	b ST3 beta-galactoside alph	na-2,3-sialyltransferase 3b [Source	23	1e-04	7 / 43	MF	iron-sulfur cluster binding	
12	2110271110001	E.EO	1.00	0.0		J	,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,	24	1e-04	10 / 91	BP	cellular response to DNA damage stimulus	
13	ENSDARG00	2.21	-1.65	0.71	LOC56	90% anscription elongation fac	ctor B (SIII), polypeptide 2 [Source:	25	1e-04	4/11	BP	telomere maintenance	
10				•			(- )// - )/ - (	26	2e-04	6/32	BP	DNA duplex unwinding	
14	ENSDARG00	2.21	-1.03	0.78	zgc:174	48@2c:174862 [Source:ZFIN;	Acc:ZDB-GENE-080303-29]	27	3e-04	7 / 49	MF	RNA-directed DNA polymerase activity	
• •							•	28 29	3e-04 3e-04	12 / 140	CC BP	nucleolus tRNA processing	
15	ENSDARG00	2.19	-0.96	0.74	tbx6	T-box 6 [Source:ZFIN;Acc	::ZDB-GENE-020416-5]	29 30	5e-04	7 / 51 5 / 26	MF	4 iron, 4 sulfur cluster binding	
						, , ,	•	30 31		8/72	MF	helicase activity	
16	ENSDARG00	2.13	-1.72	0.73	fancq	Fanconi anemia, complem	entation group G [Source:ZFIN;Acc	32	6e-04 1e-03	10 / 117	BP	nucleosome assembly	
					•			33	1e-03	8 / 80	MF	transcription regulatory region DNA binding	
17	ENSDARG000	2.09	-0.94	0.83				34	1e-03	20 / 362	BP	regulation of transcription from RNA polymerase II promoter	
• •								35	1e-03	6 / 48	BP	RNA-dependent DNA biosynthetic process	
18	ENSDARG00	2.07	-2.01	0.9	cenpi	centromere protein J [Sou	rce:ZFIN;Acc:ZDB-GENE-030131	36	2e-03	6 / 49	CC	nucleoplasm	
					.,			37	2e-03	5/36	BP	protein import into nucleus	
19	ENSDARG000	2.07	-0.42	0.79	zgc:173	34 <b>25</b> c:173425 [Source:ZFIN;	Acc:ZDB-GENE-071004-51]	38	2e-03	4 / 22	BP	DNA replication initiation	
					-		•	39	2e-03	4 / 22	BP	double-strand break repair via homologous recombination	
20	ENSDARG000	2.06	-0.5	0.87	si:dkey	p- <b>siesk@</b> yp-2e4.2 [Source:ZF	FIN;Acc:ZDB-GENE-030131-9307	40	3e-03	7 / 72	BP	nucleic acid phosphodiester bond hydrolysis	



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

# Spot Summary: D

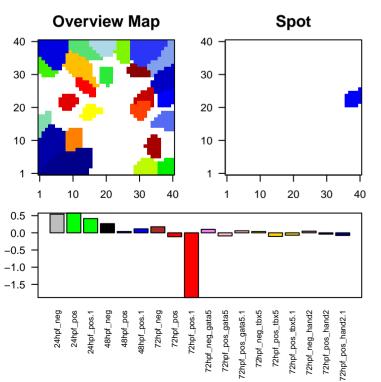
```
# genes = 480

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

# samples with spot = 2 ( 11.1 %)
```

24hpf\_neg : 1 ( 100 %) 24hpf\_pos : 1 ( 50 %)

# metagenes = 24



### **Spot Genelist**

max e

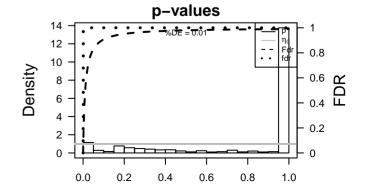
Rank

rtai	ÏD		min e		Symbol
1	ENSDARG000	2.5	-3.45	0.65	U2 spliceosomal RNA [Source:RFAM;Acc:RF00004]
2	ENSDARG000	2.42	-4.01	0.88	ssbp3a single stranded DNA binding protein 3a [Source:ZFIN;Acc:ZD
3	ENSDARG000	2.4	-3.98	0.73	si:dkey-28iadkeg223a13.22 [Source:ZFIN;Acc:ZDB-GENE-160113-78
4	ENSDARG000	2.27	-3.43	0.89	stil scl/tal1 interrupting locus [Source:ZFIN;Acc:ZDB-GENE-020
5	ENSDARG000	2.26	-2.2	0.53	
6	ENSDARG000	2.13	-1.76	0.7	zgc:1655 <b>55</b> jc:165555 [Source:ZFIN;Acc:ZDB-GENE-070620-17]
7	ENSDARG000	2.1	-2.66	0.75	LOC56277/6stone 1, H4, like [Source:ZFIN;Acc:ZDB-GENE-070927-10
8	ENSDARG000	2.07	-3.17	0.8	haus3 HAUS augmin-like complex, subunit 3 [Source:ZFIN;Acc:ZDE
9	ENSDARG000	2.02	-2.24	0.77	zgc:1630 <b>4g</b> c:163040 [Source:ZFIN;Acc:ZDB-GENE-070424-79]
10	ENSDARG000	2	-2.93	0.83	tspan2a tetraspanin 2a [Source:ZFIN;Acc:ZDB-GENE-050522-511]
11	ENSDARG000	2	-1.89	0.72	rhbdl3 rhomboid, veinlet-like 3 (Drosophila) [Source:ZFIN;Acc:ZDB-
12	ENSDARG000	1.94	-2.76	0.68	rpe65b retinal pigment epithelium-specific protein 65b [Source:ZFIN;
13	ENSDARG000	1.92	-4.01	0.92	zgc:1630#@stone 1, H4, like [Source:ZFIN;Acc:ZDB-GENE-070927-10
14	ENSDARG000	1.84	-2.41	0.39	calcium channel, voltage-dependent, T type, alpha 1G subun
15	ENSDARG000	1.84	-4.62	0.76	zc3h12b zinc finger CCCH-type containing 12B [Source:ZFIN;Acc:ZDI
16	ENSDARG000	1.84	-4.19	0.58	Small nucleolar RNA SNORA53 [Source:RFAM;Acc:RF00562
17	ENSDARG000	1.82	-2.83	0.7	si:dkey-112g5.12 [Source:ZFIN;Acc:ZDB-GENE-081028-32
18	ENSDARG000	1.8	-4.24	0.84	cd82b CD82 molecule b [Source:ZFIN;Acc:ZDB-GENE-030131-28
19	ENSDARG000	1.79	-4.69	0.91	si:dkey-26/1dh@y6-261m9.6 [Source:ZFIN;Acc:ZDB-GENE-131127-10
20	ENSDARG000	1.78	-2.04	0.75	LOC1001H866histone family member X [Source:HGNC Symbol;Acc:HC

Description

# **Geneset Overrepresentation**

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



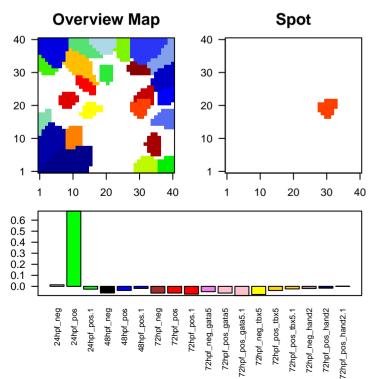
BP				CC				MF			
Rank	p-value	#in/all	Geneset	Rank	p-value	#in/all	Geneset	Rank	p-value	#in/all	Geneset
1	7e-06	7 / 43	DNA-templated transcription, initiation	1	1e-11	23 / 229	chromosome	1	3e-18	92 / 2030	nucleic acid binding
2	2e-05	6 / 34	chromatin silencing	2	8e-11	19 / 168	nucleosome	2	9e-11	22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

# Spot Summary: E

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

# metagenes = 27 # genes = 521

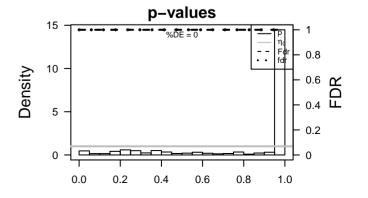
# samples with spot = 1 (5.6 %) 24hpf\_pos: 1 (50 %)



# **Spot Genelist**

Ra	nk ID	max	e min	r e	Symi	Description pol		Rank	p-value	#in/all	Ge	neset
1	ENSDARG00	1.85	-0.54	0.83	si:ch73-	-3xi3th78-343l4.8 [Source:ZFIN;Acc:ZDB	-GENE-090313-159	1	8e-05	15 / 253	BP	protein aut
_	=							2	1e-04	16 / 294	BP	regulation
2	ENSDARG000	1.79	-0.47	0.87				3 4	2e-04 6e-04	29 / 751 30 / 853	MF BP	G-protein G-protein
2	ENODADOSS.	4.70	0.40	0.00		airah211 14p21 4 [Courae:7EIN: Ace:7E	D CENE 070012 0	5	1e-03	15 / 329	BP	negative re
3	ENSDARG000	1.72	-0.43	0.86		si:ch211-14p21.4 [Source:ZFIN;Acc:ZE	D-GENE-0/0912-9:	6	2e-03	3 / 13	BP	RNA meth
4	ENSDARG000	1 71	-0.32	0.91				7	2e-03	5/51	BP	tRNA proc
4	ENSDARGOO	1.71	-0.32	0.91				8	3e-03	4/32	BP	positive re
5	ENSDARG000	1 66	-0.37	0.81	tmom4/	transmembrane protein 44 [Source:ZFII	N-Acc-7DB_GENE_0f	9	3e-03	4/32	BP	positive re
5	ENSDARGOO	1.00	-0.37	0.61	unem44	transmembrane protein 44 [300rce.21 ii	N,ACC.ZDD-GENE-OC	10	7e-03	22 / 666	MF	signal tran
6	ENSDARG000	1.64	-0.82	0.72	sirch21	I-sli9xh28l.12194p6.12 [Source:ZFIN;Acc:Z	DR_GENE_160728_0	11	8e-03	3 / 23	BP	meiotic cel
O	ENSDARGOO	1.04	-0.02	0.72	31.0112.1	1-3134px.12134po.12 [000100.21114,700.2	DD OLINE 100720 .	12	1e-02	36 / 1295	BP	signal tran
7	ENSDARG000	1 61	-0.55	0.78	zac:114	0 <b>±</b> ኒc:114041 [Source:ZFIN;Acc:ZDB-GE	NE 050706 1221	13	1e-02	2/10	MF	RNA meth
1	ENSDARGOO	1.01	-0.55	0.76	2g0.114	0±gc.114041 [30tilde.21114,Acc.2DB=GL	INL-030700-122j	14	2e-02	3 / 29	BP	inorganic a
8	ENSDARG000	1.57	-0.29	0.85	ryfn3 2s	relaxin/insulin-like family peptide recep	tor 3.2a [Source:7FIN	15	2e-02	2/11	CC	DNA-direc
O	LINSDARGOON	1.57	-0.23	0.00	12100.20	relaxiii/iiisuiiii-iike lairiiiy pepilae recep	101 0.24 [OOGICC.21 114	16	2e-02	2/11	MF	RNA polyn
9	ENSDARG000	1 55	-0.56	0.81		si:dkey-163m14.6 [Source:ZFIN;Acc:ZI	OB-GENE-120215-5	17	2e-02	2/11	MF	thrombin-
9	LINSDARGOON	1.00	-0.50	0.01		S. a.	55 02.12 1202.0 0	18	2e-02	2/11	BP	thrombin-
10	ENSDARG000	1.54	-0.6	0.73	arem2a	gremlin 2, DAN family BMP antagonist	Source:7FIN:Acc:71	19	2e-02	2 / 12	MF	extracellula
10	LINSDARGOON	1.54	-0.0	0.73	gicinza	gremmi 2, Draviamily Divir anagomst	2 [OOGIOC.21 114,7100.21	20	2e-02	2 / 12	MF	purinergic
11	ENSDARG000	1.52	-0.61	0.84	clc25a3	5 solute carrier family 25, member 35 [So	urce: ZEIN: Acc: ZDR_(	21	2e-02	2 / 12	BP	purinergic
11	LINSDARGOON	1.02	-0.01	0.04	3102040	330idic carrier farmiy 23, member 33 [00	urcc.21 114,7400.200-4	22	2e-02	2 / 12	BP	response t
12	ENSDARG000	1.52	-0.67	0.74				23	2e-02	3 / 33	BP	blood coag
12	ENSDARGOO	1.52	-0.67	0.74				24	3e-02	2/14	BP	regulation
13	ENSDARG000	1 /19	-0.76	0.69	dph1	diphthamide biosynthesis 1 [Source:ZF	N-Acc-7DB_GENE_0	25	3e-02	2 / 14	MF	sodium-in
13	LINSDARGOON	1.40	-0.70	0.03	арпт	dipitalamide biosynthesis i [Godice.21	111,7100.2DD-OE11E-0	26	3e-02	2 / 14	BP	sodium-in
14	ENSDARG000	1 45	-0.34	0.88	mafa	v-maf avian musculoaponeurotic fibros	arcoma oncodene hor	27	3e-02	2 / 15	BP	positive re
14	LINSDARGOON	1.40	-0.04	0.00	maia	Timal avial maccalcapencare incree	arooma onoogono noi	28	3e-02	3 / 37	MF	DNA-direc
15	ENSDARG000	1.45	-0.3	0.85	sirch21	I- <b>al8thgti3</b> I- <b>5</b> 281g13.5 [Source:ZFIN;Acc:Z	DR_GENE_090311_:	29	3e-02	19 / 652	MF	protein ser
13	LINSDARGOON	1.40	-0.5	0.00	01.01121	. <b>3.6.19.10.10</b> [Oddicc.21 114,7400.2	DD OLINE 030311-1	30	4e-02	4 / 67	MF	transmemi
16	ENSDARG000	1 44	-0.35	0.77	usp18	ubiquitin specific peptidase 18 [Source:	ZEIN:Acc:ZDB_GENE	31	4e-02	2 / 17	CC	integral co
10	LINSDARGOON	1.44	-0.55	0.77	азрто	abiquian specific peptidase to toource.	EI IIV,7000.ZDD-OEIVE	32	4e-02	5 / 102	BP	response t
17	ENSDARG000	1 43	-0.34	0.9				33	4e-02	3 / 42	BP	detection of DNA-direction
17	LINSDARGOON	1.40	-0.04	0.5				34	4e-02	2/18	CC	acetylcholi
18	ENSDARG000	1.43	-0.33	0.85		si:ch211-14p21.3 [Source:ZFIN;Acc:ZE	B_GENE_070912_9	35	5e-02 5e-02	2 / 19 3 / 45	CC BP	phospholip
10	LINSDARGOON	1.43	-0.55	0.00		31.01211-14p21.0 [000100.21 114,700.22	D-0EIVE-070312-3	36		6/144	BP	methylatio
19	ENSDARG000	1 42	-0.3	0.81	anr55a	G protein-coupled receptor 55a [Source	e-ZEIN-Acc:ZDB_GEN	37 38	5e-02 6e-02	3/47	BP BP	regulation
19	LINODANGOO	1.42	-0.5	0.01	gpiooa	o protesti doupled receptor da [doute	J.L, 1,100.200-3LI	36 39	6e-02	2/21	MF	inorganic a
20	ENSDARG000	1 /11	-0.3	0.92		si:ch73-129a22.11 [Source:ZFIN;Acc:Z	DB_GENE_100921 4	39 40	6e-02	4/79	BP	excitatory
20	ENSDARGUU	1.41	-0.3	0.32		51.017.5-12.5422.11 [50010e.2FIN,ACC.2	DD-GLINE-100921-0	40	06-02	4/19	БР	CAGRAROTY

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



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

#### Spot Summary: F

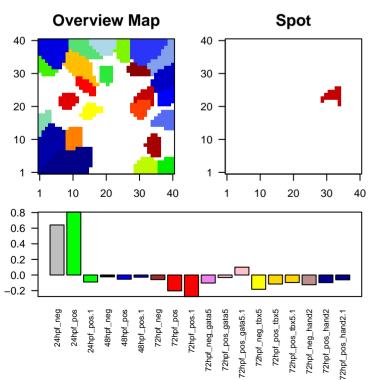
# metagenes = 20

# genes = 291

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

# samples with spot = 2 ( 11.1 %)

24hpf\_neg : 1 ( 100 %) 24hpf\_pos : 1 ( 50 %)

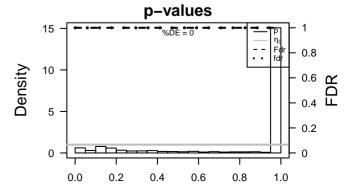


### **Spot Genelist**

Rai	nk ID	max	e min e	r e	Description Symbol
1	ENSDARG000	2.68	-0.85	0.89	si:dkey-28g8:174855 [Source:ZFIN;Acc:ZDB-GENE-071004-74]
2	ENSDARG000	2.35	-0.89	0.87	wu:fa26c@athepsin Lb [Source:ZFIN;Acc:ZDB-GENE-980526-285]
3	ENSDARG000	2.27	-0.8	0.88	si:dkey-269thely-269i1.4 [Source:ZFIN;Acc:ZDB-GENE-121214-37]
4	ENSDARG000	2.13	-0.58	0.88	si:dkey-2 <b>si9jtke</b> y3-239j18.3 [Source:ZFIN;Acc:ZDB-GENE-121214-39]
5	ENSDARG000	2.08	-0.57	0.87	ctslb cathepsin Lb [Source:ZFIN;Acc:ZDB-GENE-980526-285]
6	ENSDARG000	2.01	-0.68	0.91	LOC1005960699-26911.4 [Source:ZFIN;Acc:ZDB-GENE-121214-37]
7	ENSDARG000	1.96	-0.76	0.86	fgf8a fibroblast growth factor 8a [Source:ZFIN;Acc:ZDB-GENE-99
8	ENSDARG000	1.93	-0.76	0.73	ece2a endothelin converting enzyme 2a [Source:ZFIN;Acc:ZDB-GE
9	ENSDARG000	1.63	-1.36	0.56	zgc:1534@gc:153409 [Source:ZFIN;Acc:ZDB-GENE-060929-224]
10	ENSDARG000	1.61	-0.56	0.81	U2 spliceosomal RNA [Source:RFAM;Acc:RF00004]
11	ENSDARG000	1.59	-1.36	0.74	gmnn geminin, DNA replication inhibitor [Source:ZFIN;Acc:ZDB-GE
12	ENSDARG000	1.58	-0.46	0.81	si:ch211-57f7.7 [Source:ZFIN;Acc:ZDB-GENE-090313-119
13	ENSDARG000	1.57	-0.53	0.71	
14	ENSDARG000	1.54	-1.04	0.64	fam212b family with sequence similarity 212, member B [Source:ZFIN;
15	ENSDARG000	1.52	-0.43	0.84	si:ch211- <b>sluh2</b> 3:3-74m13.1 [Source:ZFIN;Acc:ZDB-GENE-081104-1
16	ENSDARG000	1.52	-2.24	0.43	hvcn1 hydrogen voltage–gated channel 1 [Source:ZFIN;Acc:ZDB–G
17	ENSDARG000	1.51	-1.29	0.78	ngdn neuroguidin, EIF4E binding protein [Source:ZFIN;Acc:ZDB-G
18	ENSDARG000	1.5	-0.83	0.51	zbtb43 zinc finger and BTB domain containing 43 [Source:ZFIN;Acc:
19	ENSDARG000	1.48	-1.22	0.79	ppih peptidylprolyl isomerase H (cyclophilin H) [Source:ZFIN;Acc:2
20	ENSDARG000	1.45	-1.01	0.69	zgc:163046stone 1, H4, like [Source:ZFIN;Acc:ZDB-GENE-070927-10

# Geneset Overrepresentation

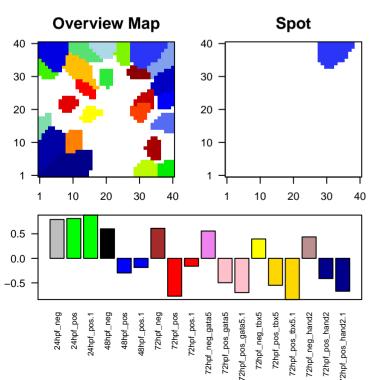
1	3e-11	55 / 2030	MF	nucleic acid binding
2 3 4 5 6 7 8 9	2e-07	11 / 138	CC	intracellular ribonucleoprotein complex
3	2e-06	12 / 214	BP	translation
4	4e-05	8 / 123	MF	cysteine-type peptidase activity
5	8e-05	4 / 23	BP	cytoplasmic translation
6	1e-04	5 / 47	CC	cytosolic large ribosomal subunit
7	1e-04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



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

# Spot Summary: G

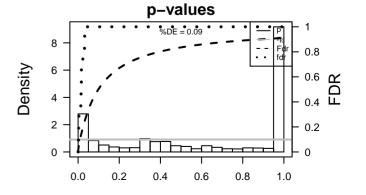
# metagenes = 66 # genes = 1025 <r> metagenes = 0.94 beta: r2= 6.48 / log p= -Inf # samples with spot = 6 ( 33.3 %) 24hpf\_neg: 1 (100 %) 24hpf\_pos : 2 ( 100 %) 48hpf\_neg: 1 (100%) 72hpf\_neg: 1 (100%) 72hpf\_neg\_gata5 : 1 ( 100 %)



### **Spot Genelist**

Raı	nk ID	max	e min e	r ∋	Symb	Description ool	Rank	p-value	#in/all	Gei	neset
1	ENSDARG000	3.45	-2.09	0.85	si:ch211	- <b>ฆ่าฆ่า</b> ชีเ5212k18.5 [Source:ZFIN;Acc:ZDB-GENE-030131-(	1	2e-59	73 / 168	СС	nucleoso
2	ENSDARG000	3.26	-3.26	0.58	mmp13a	a matrix metallopeptidase 13a [Source:ZFIN;Acc:ZDB-GENE-	2	8e-54 3e-50	78 / 229 184 / 1484	CC MF	DNA bin
3	ENSDARG000	3.22	-4.34	0.54		collagen, type XIV, alpha 1b [Source:ZFIN;Acc:ZDB-GENE-(	4 5	5e-50 6e-46	260 / 2716 54 / 117	CC BP	nucleoso
4	ENSDARG000	3.19	-3.27	0.83	si:ch211	-នា់រងរាំលាស្រី -14k19.8 [Source:ZFIN;Acc:ZDB-GENE-051214-4]	6 7	4e-41 1e-22	67 / 232 22 / 37	MF MF	nucleoso
5	ENSDARG000	3.15	-3.55	0.89	aplnrb	apelin receptor b [Source:ZFIN;Acc:ZDB-GENE-050913-90]	8	6e-19 1e-18	112 / 1239 61 / 454	BP BP	regulatio multicelli
6	ENSDARG000	2.85	-2.82	0.82	si:dkey-	25iall6e9-25o16.2 [Source:ZFIN;Acc:ZDB-GENE-121214-307	10 11	2e-13 2e-10	15 / 34 22 / 117	BP BP	ephrin re Wnt sign
7	ENSDARG000	2.85	-1.19	0.72	zic2b	zic family member 2 (odd-paired homolog, Drosophila) b [Soi	12 13	2e-09 2e-09	50 / 537 13 / 43	MF BP	DNA-ter
8	ENSDARG000	2.84	-1.51	0.94	aspm	abnormal spindle microtubule assembly [Source:ZFIN;Acc:ZE	14 15	6e-09 8e-09	11 / 31 54 / 633	MF MF	histone- transcrip
9	ENSDARG000	2.8	-4.02	0.74	capn12	calpain 12 [Source:ZFIN;Acc:ZDB-GENE-050419-245]	16 17	1e-08 2e-08	54 / 643 19 / 110	BP MF	protein ty
10	ENSDARG000	2.76	-2.68	0.87	fam65c	family with sequence similarity 65, member C [Source:ZFIN;A	18 19	2e-08 2e-07	18 / 100 8 / 19	BP MF	peptidyl- ephrin re
11	ENSDARG000	2.71	-3.94	0.59	kel	Kell blood group, metallo-endopeptidase [Source:ZFIN;Acc:Z	20 21	3e-07 4e-07	15 / 83 18 / 121	BP BP	embryon
12	ENSDARG000	2.71	-2.42	0.8	adrb3a	adrenoceptor beta 3a [Source:ZFIN;Acc:ZDB-GENE-080917	22 23	4e-07 6e-07	7/15	MF BP	ephrin re sprouting
13	ENSDARG000		-2.77	0.89		DEP domain containing 1B [Source:HGNC Symbol;Acc:HGN	24 25	8e-07 1e-06	14 / 78 8 / 24	BP BP	axon gui
14	ENSDARG00		-3.04	0.7	hbbe2	hemoglobin beta embryonic-2 [Source:ZFIN;Acc:ZDB-GENE	26 27	3e-06 3e-06	10 / 43 69 / 1063	BP MF	canonica transfera
15	ENSDARG00	2.69	-1.89	0.86	add2	adducin 2 (beta) [Source:ZFIN;Acc:ZDB-GENE-080718-4]	28 29	4e-06 5e-06	7 / 20 39 / 491	BP MF	transmer kinase a
					auuz	adducin 2 (beta) [Source.21 IN,Acc.2DB-GENE-0007 10-4]	30 31	6e-06 6e-06	15 / 104 7 / 21	BP BP	regulatio
16	ENSDARG00		-1.55	0.43		KN seek and adjustic assess described 4 (Course 7FIN) Ann 7D	32 33	6e-06 7e-06	7 / 21 10 / 48	MF BP	signal tra
17	ENSDARG00		-1.72	0.82	kank4	KN motif and ankyrin repeat domains 4 [Source:ZFIN;Acc:ZD	34 35	1e-05 1e-05	40 / 522 5 / 10	BP BP	phospho adenohy
18	ENSDARG00		-1.9	0.74	her8a	hairy-related 8a [Source:ZFIN;Acc:ZDB-GENE-030131-237	36 37	2e-05 2e-05	10 / 52 15 / 115	MF MF	transmer chromati
19	ENSDARG00	2.6	-1.22	0.8		nuclear receptor subfamily 6, group A, member 1a [Source:Zf	38 39	2e-05 3e-05	6 / 17 9 / 45	MF BP	transmer Notch sig
20	ENSDARG000	2.59	-1.88	0.71	zgc:112	234c:112234 [Source:NCBI gene;Acc:554097]	40	3e-05	7 / 26	MF	Wnt-pro

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



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

# Spot Summary: H

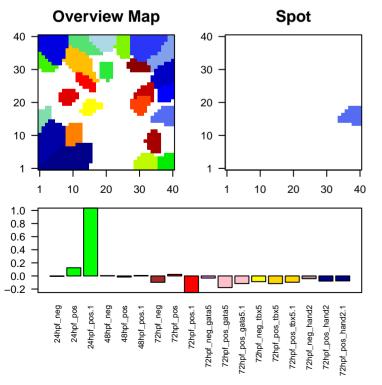
```
# genes = 849

<r> metagenes = 0.93
<r> genes = 0.53
beta: r2= 1.23 / log p= -Inf

# samples with spot = 1 ( 5.6 %)
```

24hpf\_pos: 1 (50 %)

# metagenes = 32



### **Spot Genelist**

Rar	nk ID	max	e min e	r e	Description Symbol	Rank	p-value	#in/all	Ge	neset
1	ENSDARG000	2.63	-1.3	0.68	ampd2a adenosine monophosphate deaminase 2a [Source:ZFIN;Acc:	1	6e-05	24 / 329	BP	negative regulation of apoptotic process
						2	2e-04	19 / 253	BP	protein autophosphorylation
2	ENSDARG000	2.29	-0.81	0.83		3	1e-03	6 / 42	BP	cilium movement
						4	2e-03	19 / 294	BP	regulation of mitotic cell cycle
3	ENSDARG000	2.23	-0.61	0.69	pm20d1.1peptidase M20 domain containing 1, tandem duplicate 1 [Sou	5	2e-03	19 / 297	BP	immune response
						<u>6</u>	2e-03	12 / 153	CC	cell surface
4	ENSDARG000	2.18	-0.75	0.82		7	3e-03	83 / 2030	MF	nucleic acid binding
						8	3e-03	16 / 244	MF	receptor binding
5	ENSDARG000	2.09	-0.6	0.81	zgc:10992gc:109913 [Source:ZFIN;Acc:ZDB-GENE-050522-72]	9	7e-03	35 / 751	MF	G-protein coupled receptor activity
						10	1e-02	5 / 47	BP	response to lipopolysaccharide
6	ENSDARG000	2.09	-0.73	0.85	mhc1ubamajor histocompatibility complex class I UBA [Source:ZFIN;A	11	1e-02	4/31	BP	protein-chromophore linkage
						12	2e-02	4/33	MF	photoreceptor activity
7	ENSDARG000	2.09	-0.52	0.74	LOC571488	13	3e-02	36 / 853	BP	G-protein coupled receptor signaling pathway
						14	3e-02	4 / 40	BP	regulation of translation
8	ENSDARG000	2.07	-0.92	0.69		15	3e-02	3 / 24	BP	cerebellum development
_						16	3e-02	2/10	BP	chondrocyte differentiation
9	ENSDARG000	2.05	-0.32	0.87	si:ch211-163c2.2 [Source:ZFIN;Acc:ZDB-GENE-160114-56	17	3e-02	2/10	BP	tachykinin receptor signaling pathway
Ū					•	18	4e-02	2/11	BP	induction of positive chemotaxis
10	ENSDARG000	2.01	-1.15	0.68	zgc:1585 <b>2g</b> c:173517 [Source:ZFIN;Acc:ZDB-GENE-071004-104]	19	4e-02	2/11	BP	positive regulation of guanylate cyclase activity
10					3 3 (	20	4e-02	2/11	BP	regulation of pH
11	ENSDARG000	2	-0.43	0.87		21	4e-02	2/11	MF	solute:proton antiporter activity
	2.1027.110001	_	0.10	0.01		22	4e-02	3 / 26	MF	oxidoreductase activity, acting on single donors with incorporation of molec
12	ENSDARG000	2	-0.6	0.82	cd28 si:ch211-67e16.2 [Source:ZFIN;Acc:ZDB-GENE-070912-3(	23	4e-02	10 / 178	MF	iron ion binding
12	ENSDARGOO	2	-0.0	0.02	51.01211-07e10.2 [Source.211N,Acc.2DB-GENE-070312-5]	24	5e-02	3 / 27	CC	recycling endosome
40	ENSDARG000	4.07	-0.54	0.00	si;ch211-si3dh223-3 30m23.3 [Source:ZFIN;Acc:ZDB-GENE-060531-	25	5e-02	2 / 12	MF	FMN binding
13	ENSDARGUU	1.97	-0.54	0.82	SI:Ch211-Si3uir23-3 SUI125.3 [Sudice.2FIN,ACC.2DB-GENE-000551-	26	5e-02	2 / 12	BP	smooth muscle contraction
4.4	=	4.07	0.75	0.70		27	5e-02	3 / 28	BP	phototransduction
14	ENSDARG000	1.97	-0.75	0.79	zmp:000000000000000001316 [Source:ZFIN;Acc:ZDB-GENE-140106-27	28	6e-02	3 / 29	MF	dioxygenase activity
4.5	=				FO The second DNA IO DEAM A DECOCOM	29	6e-02	3 / 29	BP	heart jogging
15	ENSDARG000	1.96	-0.38	0.93	5S ribosomal RNA [Source:RFAM;Acc:RF00001]	30	6e-02	4 / 48	BP	RNA-dependent DNA biosynthetic process
4.0						31	6e-02	2 / 13	BP	cilium organization
16	ENSDARG000	1.95	-1.37	0.66		32	6e-02	2 / 13	CC	viral nucleocapsid
						33	6e-02	4 / 49	MF	RNA-directed DNA polymerase activity
17	ENSDARG000	1.93	-0.41	0.77	zgc:162239 [Source:ZFIN;Acc:ZDB-GENE-070424-28]	34	6e-02	2 / 14	BP	transcription elongation from RNA polymerase II promoter
						35	7e-02	4 / 51	BP	mitochondrial transport
18	ENSDARG000	1.92	-0.4	0.9	si:dkey-18/3#kef0183p4.10 [Source:ZFIN;Acc:ZDB-GENE-081104-33	36	7e-02	27 / 666	MF	signal transducer activity
						37	7e-02	2 / 15	MF	adrenergic receptor activity
19	ENSDARG000	1.92	-0.41	0.82		38	7e-02	2 / 15	BP	positive regulation of vasoconstriction
						39	7e-02	2/15	BP	response to mechanical stimulus
20	ENSDARG000	1.9	-0.45	0.81	asb15b ankyrin repeat and SOCS box containing 15b [Source:ZFIN;A	40	7e-02	4 / 53	BP	cation transport

				1					
á	7e-02	2 / 15	BP.	response to	mechanical s	timulus			
<b>`</b>	7e-02	4 / 53		cation trans					
,	76-02	4/53	в вр	CallOII trails	port				
				n_vs	ılues				
				P-46	liucs				
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						-	– Fdr	- 0.8	
	10 -	1				١.	<ul> <li>fdr</li> </ul>	- 0.0	
>							$\perp$		
₽,	8 -	4						0.6	
Density	·							0.6	$\simeq$
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	2 -							0.2	
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		0.0	0.2	0.4	0.6	8.0	1.0		

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

#### Spot Summary: I

# metagenes = 42
# genes = 779

<r> metagenes = 0.97</r> <r> genes = 0.64

 beta: r2= 9.35 / log p= -Inf

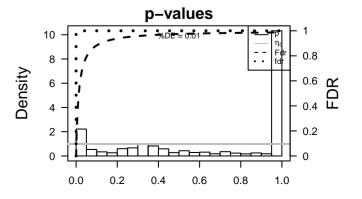
# samples with spot = 3 ( 16.7 %)

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

#### **Overview Map** Spot 30 20 20 10 10 20 30 30 10 10 20 1.5 1.0 0.5 0.0 -0.5 72hpf\_neg\_gata5 72hpf\_pos\_gata5 48hpf\_pos.1 72hpf\_neg 48hpf\_pos 72hpf\_pos 72hpf\_pos.1 72hpf\_neg\_tbx5 72hpf\_pos\_hand2 72hpf\_pos\_gata5.1

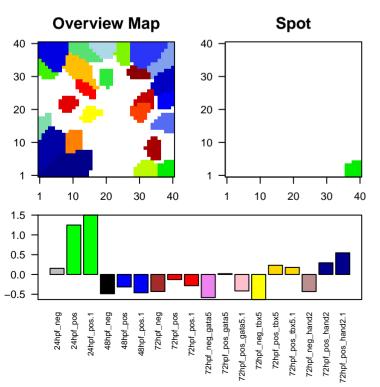
# **Spot Genelist**

Rai	nk ID	max	e min e	r e	Symi	Description bol	Rank	p-value	#in/all	Ge	neset
1	ENSDARG000	8.12	-6.4	0.79	hbbe3	hemoglobin beta embryonic-3 [Source:ZFIN;Acc:ZDB-GENE	1	4e-28	31 / 78	ВР	DNA replication
							2	8e-25	170 / 2716	CC	nucleus
2	ENSDARG000	7.83	-4.49	0.92	drl	draculin [Source:ZFIN;Acc:ZDB-GENE-991213-3]	3	4e-17	14 / 22	BP	DNA replication initiation
							4	4e-14	14 / 32	BP	DNA duplex unwinding
3	ENSDARG000	7.74	-1.79	0.61	LOC100	)59jggg/11-11n16.3 [Source:ZFIN;Acc:ZDB-GENE-131121-86	5	5e-14	94 / 1484	MF	DNA binding
							<u>6</u>	2e-13	10 / 14	CC	hemoglobin complex
4	ENSDARG000	7.36	-4.55	0.91	si:dkey-	-26/1/4/4/2-261j4.4 [Source:ZFIN;Acc:ZDB-GENE-060531-125]	7	4e-13	25 / 148	BP	DNA repair
							8	3e-12	21 / 110	BP	cell cycle
5	ENSDARG000	7.35	-4.2	0.92	blf	bloody fingers [Source:ZFIN;Acc:ZDB-GENE-050721-1]	9	1e-11	29 / 229	CC	chromosome
							10	1e-11	8/10	BP	mitotic sister chromatid segregation
6	ENSDARG000	7.06	-5.06	0.89	si:dkey-	-261j4.3 [Source:ZFIN;Acc:ZDB-GENE-060531-124]	11	2e-11	10 / 19	MF	oxygen binding
							12	2e-11	10 / 19	BP	oxygen transport
7	ENSDARG000	6.46	-4.6	0.68		protogenin homolog b (Gallus gallus) [Source:ZFIN;Acc:ZDB-	13	2e-11	10 / 19	MF	oxygen transporter activity
							14	9e-11	11 / 28	BP	embryonic hemopoiesis mitotic cell cycle
8	ENSDARG000	6.43	-3.22	0.95	stab2	stabilin 2 [Source:ZFIN;Acc:ZDB-GENE-041210-336]	15 16	2e-10	13 / 46 95 / 1787	BP	ATP binding
								7e-10	13 / 52	MF BP	•
9	ENSDARG000	6.31	-1.79	0.9	ela2l	elastase 2 like [Source:ZFIN;Acc:ZDB-GENE-040511-1]	17 18	1e-09 3e-09			blood vessel development
									10 / 29 16 / 91	CC BP	kinetochore cellular response to DNA damage stimulus
10	ENSDARG000	6.11	-4.16	0.94	tfr1a	transferrin receptor 1a [Source:ZFIN;Acc:ZDB-GENE-04122	19 20	4e-09 3e-08	14 / 79	BP	cell division
							21	3e-08 1e-07	10 / 40	BP BP	erythrocyte differentiation
11	ENSDARG000	6	-2.33	0.88		si:ch73-299h12.2 [Source:ZFIN;Acc:ZDB-GENE-081031-7]	22	2e-07	77 / 1506	MF	nucleotide binding
							23	2e-07 2e-07	6/11	MF	DNA helicase activity
12	ENSDARG000	5.97	-3.89	0.88	klf17	Kruppel-like factor 17 [Source:ZFIN;Acc:ZDB-GENE-01012!	24	5e-07	8 / 27	BP	chromosome segregation
							25	6e-07	12 / 72	MF	helicase activity
13	ENSDARG000	5.89	-1.29	0.58	zgc:174	855c:174855 [Source:ZFIN;Acc:ZDB-GENE-071004-74]	26	7e-07	9/38	BP	vasculogenesis
							27	1e-06	7 / 22	CC	chromosome, centromeric region
14	ENSDARG000	5.69	-3.46	0.88	gata1a	GATA binding protein 1a [Source:ZFIN;Acc:ZDB-GENE-9808	28	2e-06	6 / 15	BP	heme biosynthetic process
							29	2e-06	10 / 54	CC	kinesin complex
15	ENSDARG000	5.69	-3.04	0.86	gfi1b	growth factor independent 1B transcription repressor [Source	30	3e-06	7/24	BP	myeloid cell differentiation
							31	4e-06	14 / 115	MF	chromatin binding
16	ENSDARG000	5.53	-3.53	0.79			32	4e-06	11 / 72	BP	nucleic acid phosphodiester bond hydrolysis
							33	6e-06	5 / 11	MF	structural constituent of nuclear pore
17	ENSDARG000	5.51	-4.09	0.83	znfl2a	zinc finger-like gene 2a [Source:ZFIN;Acc:ZDB-GENE-0308	34	6e-06	5 / 11	BP	thymus development
							35	1e-05	17 / 178	MF	iron ion binding
18	ENSDARG000	5.45	-1.91	0.88	cpox	coproporphyrinogen oxidase [Source:ZFIN;Acc:ZDB-GENE-	36	1e-05	54 / 1063	MF	transferase activity
							37	2e-05	8 / 42	MF	histone binding
19	ENSDARG000	5.42	-2.18	0.89	hmbsb	hydroxymethylbilane synthase, b [Source:ZFIN;Acc:ZDB-GEI	38	2e-05	13 / 117	BP	nucleosome assembly
							39	2e-05	9 / 57	BP	microtubule cytoskeleton organization
20	ENSDARG000	5.39	-4.85	0.84	hdr	hematopoietic death receptor [Source:ZFIN;Acc:ZDB-GENE-	40	3e-05	5 / 14	СС	condensed chromosome kinetochore



#### Spot Summary: J

# metagenes = 23 # genes = 445 <r> metagenes = 0.95 <r> genes = 0.56 beta: r2= 5.48 / log p= -Inf # samples with spot = 3 ( 16.7 %) 24hpf\_pos : 2 ( 100 %) 72hpf\_pos\_hand2 : 1 ( 50 %)

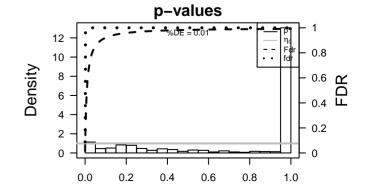


### **Spot Genelist**

Raı	nk ID	max e r min e			Syml	Description pol
1	ENSDARG000	8.47	-3.84	0.36		
2	ENSDARG000	8.19	-3.48	0.33		
3	ENSDARG000	8.13	-3.52	0.32		
4	ENSDARG000	8.08	-3.28	0.28		
5	ENSDARG000	6.87	-3.45	0.32		
6	ENSDARG000	5.93	-1.57	0.79	cyp7a1b	
7	ENSDARG000	5.27	-3.73	0.37		
8	ENSDARG000	5.09	-3.4	0.37		
9	ENSDARG000	4.13	-2.81	0.91	mrc1a	mannose receptor, C type 1a [Source:ZFIN;Acc:ZDB-GENE-
10	ENSDARG000	4.07	-2.7	0.43		
11	ENSDARG000	3.95	-1.46	0.32		zgc:158463 [Source:ZFIN;Acc:ZDB-GENE-070410-9]
12	ENSDARG000	3.89	-1.94	0.78	nkx2.7	NK2 transcription factor related 7 [Source:ZFIN;Acc:ZDB-GE
13	ENSDARG000	3.75	-3.16	0.84	dnase1l	4.deoxyribonuclease 1 like 4, tandem duplicate 1 [Source:ZFIN
14	ENSDARG000	3.73	-2.69	0.21		
15	ENSDARG000	3.53	-3.11	0.86	ikzf1	IKAROS family zinc finger 1 (Ikaros) [Source:ZFIN;Acc:ZDB-
16	ENSDARG000	3.47	-3.88	0.77	il6r	interleukin 6 receptor [Source:ZFIN;Acc:ZDB-GENE-080107
17	ENSDARG000	3.44	-2.62	0.83		
18	ENSDARG000	3.38	-2.19	0.85	ampd3b	adenosine monophosphate deaminase 3b [Source:ZFIN;Acc:
19	ENSDARG000	3.36	-3.58	0.73	slc25a3	7 solute carrier family 25 (mitochondrial iron transporter), memt
20	ENSDARG000	3.36	-1.95	0.83	slc29a1	b solute carrier family 29 (equilibrative nucleoside transporter),

# **Geneset Overrepresentation**

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



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

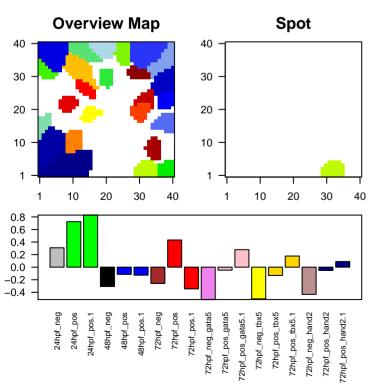
#### Spot Summary: K

# genes = 541

<r> metagenes = 0.93
<r> genes = 0.51
beta: r2= 2.55 / log p= -Inf

# metagenes = 31

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

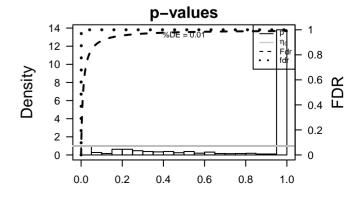


# **Spot Genelist**

Ra	nk ID	max	e min e	r e	Syml	Description pol
					•	
1	ENSDARG000	6.62	-1.54	0.14		
2	ENSDARG000	5.15	-3.14	0.47		
3	ENSDARG000	5.06	-3.18	0.47		
4	ENSDARG000	4.97	-3.11	0.45		
5	ENSDARG000	4.93	-3.21	0.46		
6	ENSDARG000	2.52	-2.14	0.6	il13ra2	interleukin 13 receptor, alpha 2 [Source:ZFIN;Acc:ZDB-GENI
7	ENSDARG000	1.92	-1.52	0.67		peptidyl-tRNA hydrolase 1 homolog [Source:ZFIN;Acc:ZDB-
8	ENSDARG000	1.78	-0.66	0.79	adcy6a	adenylate cyclase 6a [Source:ZFIN;Acc:ZDB-GENE-060221
9	ENSDARG000	1.78	-0.84	0.71		
10	ENSDARG000	1.76	-0.61	0.67		
11	ENSDARG000	1.73	-0.48	0.81	pou5f3	POU domain, class 5, transcription factor 3 [Source:ZFIN;Acc
12	ENSDARG000	1.7	-0.89	0.74	dip2ca	disco-interacting protein 2 homolog Ca [Source:ZFIN;Acc:ZD
13	ENSDARG000	1.67	-0.97	0.83	stra13	stimulated by retinoic acid 13 homolog (mouse) [Source:ZFIN
14	ENSDARG000	1.67	-0.87	0.58	si:cabz0	01054394.6
15	ENSDARG000	1.66	-1.16	0.81	armc6	armadillo repeat containing 6 [Source:HGNC Symbol;Acc:HG
16	ENSDARG000	1.65	-1.15	0.72	cyb5d2	cytochrome b5 domain containing 2 [Source:ZFIN;Acc:ZDB-(
17	ENSDARG000	1.62	-1.07	0.82	zgc:162	89gc:162895 [Source:ZFIN;Acc:ZDB-GENE-070410-106]
18	ENSDARG000	1.62	-0.58	0.78	cdnf	cerebral dopamine neurotrophic factor [Source:ZFIN;Acc:ZDE
19	ENSDARG000	1.62	-1.01	0.8	siva1	SIVA1, apoptosis-inducing factor [Source:ZFIN;Acc:ZDB-GE
20	ENSDARG000	1.61	-1.11	0.7		

# Geneset Overrepresentation

	0. 40	04 / 440	00	and all a
1	3e-13 9e-09	21 / 140 7 / 16	CC BP	nucleolus ribosomal large subunit biogenesis
2	9e-09 2e-07	9 / 45	BP	rRNA processing
3 4	2e-07 1e-06		BP	maturation of SSU-rRNA
5	3e-06	5 / 11 69 / 2030	MF	nucleic acid binding
5	2e-05	7 / 43	BP	ribosome biogenesis
6 7	2e-05 2e-05	7 / 43 15 / 214	BP	translation
8	4e-05	8/66	MF	ligase activity
9	4e-05 5e-05	7/50	MF	translation initiation factor activity
10	5e-05	7 / 30 5 / 22	MF	tRNA binding
11	5e-05	7/51	BP	tRNA processing
12	8e-05	7 / 55	BP	translational initiation
13	1e-04	6 / 41	MF	aminoacyl-tRNA ligase activity
14	2e-04	4 / 15	BP	pseudouridine synthesis
15	8e-04	3 / 10	MF	snoRNA binding
16	9e-04	4 / 23	CC	small-subunit processome
17	1e-03	18 / 410	CC	mitochondrion
18	1e-03	3 / 12	MF	pseudouridine synthase activity
19	1e-03	3 / 12	BP	ubiquinone biosynthetic process
20	2e-03	3 / 13	BP	RNA modification
21	2e-03	9 / 144	BP	methylation
22	2e-03	4/30	MF	damaged DNA binding
23	3e-03	34 / 1063	MF	transferase activity
24	3e-03	3 / 16	CC	preribosome, large subunit precursor
25	5e-03	3 / 18	CC	eukaryotic translation initiation factor 3 complex
26	5e-03	8 / 135	MF	methyltransferase activity
27	5e-03	4/36	MF	endonuclease activity
28	5e-03	3 / 19	MF	phosphotransferase activity, alcohol group as acceptor
29	6e-03	18 / 480	MF	catalytic activity
30	7e-03	43 / 1506	MF	nucleotide binding
31	7e-03	4 / 40	BP	tRNA aminoacylation for protein translation
32	8e-03	8 / 148	BP	DNA repair
33	8e-03	3 / 22	BP	protein N-linked glycosylation
34	9e-03	6/92	MF	magnesium ion binding
35	9e-03	44 / 1580	CC	cellular_component
36	1e-02	40 / 1437	MF	molecular_function
37	1e-02	8 / 161	CC	mitochondrial inner membrane
38	1e-02	4 / 49	CC	nucleoplasm
39	1e-02	20 / 608	MF	RNA binding
40	1e-02	2/10	CC	nuclear chromosome, telomeric region



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

# Spot Summary: L

```
# metagenes = 26

# genes = 383

<r> metagenes = 0.93

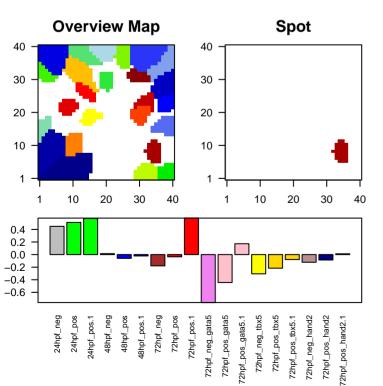
<r> genes = 0.47

beta: r2= 1.9 / log p= -Inf

# samples with spot = 2 ( 11.1 %)

24hpf_pos : 1 ( 50 %)

72hpf_pos : 1 ( 50 %)
```

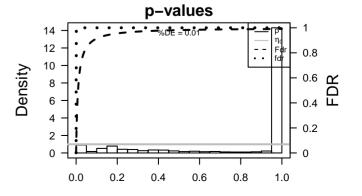


# **Spot Genelist**

Rar	nk ID	max	e min e	r <del>)</del>	Symb	Description pol	
1	ENSDARG000	1.71	-1.55	0.8		protein O-glucosyltransferase 1 [Source:ZFIN;Acc:ZDB-GEN	
2	ENSDARG000	1.63	-0.7	0.83	ccm2l	cerebral cavernous malformation 2-like [Source:ZFIN;Acc:ZC	
3	ENSDARG000	1.61	-1.64	0.73		si:dkeyp-11g8.3 [Source:ZFIN;Acc:ZDB-GENE-110131-2]	
4	ENSDARG000	1.56	-0.73	0.5	si:dkey-	25/3dla3y42/53d23.12 [Source:ZFIN;Acc:ZDB-GENE-070912-4	
5	ENSDARG000	1.54	-1.14	0.83			
6	ENSDARG000	1.52	-3.06	0.95	rfc2	replication factor C (activator 1) 2 [Source:ZFIN;Acc:ZDB-GE	
7	ENSDARG000	1.5	-0.57	0.49	endou2	endonuclease, polyU-specific 2 [Source:ZFIN;Acc:ZDB-GEN	
8	ENSDARG000	1.48	-1.15	0.55	tnnt2c	troponin T2c, cardiac [Source:ZFIN;Acc:ZDB-GENE-030520	
9	ENSDARG000	1.45	-0.33	0.53		si:ch211-261i17.2 [Source:ZFIN;Acc:ZDB-GENE-160113-1	
10	ENSDARG000	1.44	-0.71	0.74			
11	ENSDARG000	1.44	-1.1	0.78	ogmb	oligodendrocyte myelin glycoprotein b [Source:ZFIN;Acc:ZDB	
12	ENSDARG000	1.44	-1.6	0.62	trmt10c	tRNA methyltransferase 10C, mitochondrial RNase P subunit	
13	ENSDARG000	1.44	-1.59	0.62	bcl7bb	B-cell CLL/lymphoma 7B, b [Source:ZFIN;Acc:ZDB-GENE-(	
14	ENSDARG000	1.43	-0.77	0.52	si:ch211	-si2shg*161.4126g16.11 [Source:ZFIN;Acc:ZDB-GENE-081105-	
15	ENSDARG000	1.42	-0.69	0.72	capn3a	calpain 3a, (p94) [Source:ZFIN;Acc:ZDB-GENE-040912-97]	
16	ENSDARG000	1.41	-1.27	0.84	ddx24	DEAD (Asp-Glu-Ala-Asp) box helicase 24 [Source:ZFIN;Acc	
17	ENSDARG000	1.41	-1.02	0.7	nprl3	NPR3-like, GATOR1 complex subunit [Source:ZFIN;Acc:ZDB	
18	ENSDARG000	1.4	-1.23	0.5	si:dkey-	557kdfrety-57k17.1 [Source:ZFIN;Acc:ZDB-GENE-110913-105	
19	ENSDARG000	1.39	-1.24	0.79	fastkd5	FAST kinase domains 5 [Source:ZFIN;Acc:ZDB-GENE-1110	
20	ENSDARG000	1.38	-0.99	0.56		si:ch211-245n8.4 [Source:ZFIN;Acc:ZDB-GENE-110914-56	

# Geneset Overrepresentation

4				analata asta bisaltas
1	3e-12	68 / 2030	MF	nucleic acid binding
2 3 4 5 6 7 8 9	9e-07 3e-06	12 / 148	BP CC	DNA repair
3	3e-06 8e-06	11 / 140	CC	
4	3e-05	64 / 2716 30 / 969	MF	nucleus hydrolase activity
5		22 / 608	MF	RNA binding
9	3e-05 4e-05		BP	tRNA methylation
/	4e-05 5e-05	4 / 15 7 / 70	BP	RNA processing
0	5e-05		CC	preribosome, large subunit precursor
10	6e-05	4 / 16	BP	tRNA processing
11	9e-05	6 / 51 7 / 78	BP	DNA replication
12	9e-05 1e-04	5/37	MF	thiol-dependent ubiquitin-specific protease activity
13	1e-04 2e-04	7/88	BP	mRNA processing
14	2e-04 3e-04	5 / 43	CC	proteasome complex
15	3e-04 7e-04	6/79	BP	mRNA splicing, via spliceosome
16	7e-04 1e-03	4/34	CC	catalytic step 2 spliceosome
17	1e-03	13 / 355	CC	cytosol
18	1e-03	3 / 16	BP	protein sumoylation
19	1e-03	3/16	BP	ribosomal large subunit biogenesis
20	1e-03	4/36	MF	endopeptidase activity
20 21	2e-03	4 / 36 14 / 410	CC	mitochondrion
22	2e-03	3/18	BP	base-excision repair
23	2e-03	4/42	CC	spliceosomal complex
23	2e-03 3e-03	3/21	CC	nuclear membrane
25	3e-03	5/72	MF	helicase activity
26 26	3e-03	21 / 800	MF	zinc ion binding
20 27	3e-03	4 / 46	MF	ATP-dependent RNA helicase activity
28	4e-03	3/24	CC	precatalytic spliceosome
29	6e-03	3/28	MF	hydrolase activity, acting on ester bonds
30	8e-03	2/10	BP	nuclear-transcribed mRNA catabolic process
31	8e-03	4/58	BP	RNA splicing
32	8e-03	3/31	MF	ubiquitin binding
33	9e-03	2/11	BP	cellular metabolic process
34	9e-03	2/11	CC	commitment complex
35	9e-03	2/11	BP	DNA-dependent DNA replication
36	9e-03	2/11	BP	positive regulation of protein ubiquitination
37	1e-02	6 / 135	MF	methyltransferase activity
38	1e-02	4/64	CC	Cul3–RING ubiquitin ligase complex
39	1e-02	2/13	BP	NLS-bearing protein import into nucleus
40	1e-02	2/13	CC	U5 snRNP
40	10-02	2/13	CC	OO SHIMI



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

# Spot Summary: M

# metagenes = 21 # genes = 291

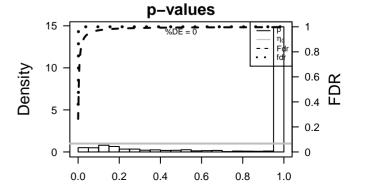
<r> metagenes = 0.92 <r> genes = 0.45 beta: r2= 1.77 / log p= -Inf

# samples with spot = 0 ( 0 %)

#### **Overview Map** Spot 30 20 20 10 10 20 30 30 10 10 20 0.4 0.2 0.0 -0.2 -0.4 -0.6 -0.8 72hpf\_neg\_gata5 72hpf\_pos\_gata5 48hpf\_pos.1 72hpf\_neg 72hpf\_pos.1 48hpf\_pos 72hpf\_pos 72hpf\_neg\_tbx5 72hpf\_pos\_hand2 72hpf\_pos\_gata5.1

# **Spot Genelist**

Rank ID		max	e min	r e	Sym	Description bol	Rank	p-value	#in/all	Ge	neset
						7500	D ( 4				DM - Francisco
1	ENSDARG000	1.73	-1.59	0.62	slc16a6	Sa solute carrier family 16, member 6a [Source:ZFIN;Acc:ZD	•	2e-04 1e-03	6 / 79 36 / 2030	BP MF	mRNA splicing, via spliceosome nucleic acid binding
2	ENCDARCOO!	4.70	-0.78	0.50			2 3	1e-03	4 / 45	BP	Notch signaling pathway
2	ENSDARG00	1.73	-0.78	0.53			4	1e-03	3 / 21	BP	smoothened signaling pathway
2	ENODA DOSS	4.7	4.0	0.04	L-40L7	hydroxy-delta-5-steroid dehydrogenase, 3 beta- and ste		1e-03	11 / 362	BP	regulation of transcription from RNA polymerase II promoter
3	ENSDARG00	1.7	-1.8	0.64	nsu3D7	nydroxy-delta-5-steroid denydrogenase, 5 beta- and ste	6	2e-03	4 / 48	BP	RNA-dependent DNA biosynthetic process
4	ENSDARG00	1 64	-1.65	0.57		si:dkey-7i4.7 [Source:ZFIN;Acc:ZDB-GENE-131119-71	_	2e-03	4 / 49	MF	RNA-directed DNA polymerase activity
4	ENSDARGOO	1.04	-1.05	0.57		31.dkey=714.7 [30dice.21 IIV,Acc.2DD=GEIVE=131113=71]	8	3e-03	15 / 633	MF	transcription factor activity, sequence-specific DNA binding
5	ENSDARG00	1 60	-1.5	0.87		solute carrier family 34 (type II sodium/phosphate cotrans	õ	3e-03	7 / 183	MF	RNA polymerase II transcription factor activity, sequence–specific DNA b
5	ENSDARGOO	1.02	-1.5	0.07		Solute carrier larning 54 (type if Souldingphosphate cottans	10	4e-03	4 / 64	CC	Cul3–RING ubiquitin ligase complex
6	ENSDARG000	1 57	-1.17	0.48		HERV-H LTR-associating 2a, tandem duplicate 2 [Source	4.4	5e-03	2/10	BP	tRNA aminoacylation
O	ENSDARGOO	1.57	-1.17	0.40		TIETV-IT ETT-associating 2a, tandem deplicate 2 [could	12	5e-03	23 / 1239	BP	regulation of transcription, DNA-templated
7	ENSDARG00	1 56	-1.07	0.66	notchl	notch homolog, like [Source:ZFIN;Acc:ZDB-GENE-0702	40	6e-03	3 / 35	BP	positive regulation of proteasomal ubiquitin-dependent protein catabolic
,	LINSDANGOO	1.50	-1.07	0.00	HOLCHI	noter nomolog, like [Godico.21 IIV, Acc. 255 GENE - 0702	14	6e-03	3 / 36	CC	P-body
8	ENSDARG000	1 53	-1.67	0.54	myh9a	myosin, heavy chain 9a, non-muscle [Source:ZFIN;Acc:Z	<sub>DB.</sub> 15	7e-03	2 / 12	MF	acetylgalactosaminyltransferase activity
O	LINODAIRCOOL	1.55	-1.07	0.54	mynoa	myoon, noary onam oa, non maooro (coarco.e. m, roo.e.	16	8e-03	14 / 643	BP	transcription, DNA-templated
9	ENSDARG000	1 53	-2.2	0.77			17	8e-03	3 / 39	MF	hydrolase activity, hydrolyzing O-glycosyl compounds
9	LINSDANGOO	1.55	-2.2	0.77			18	8e-03	2 / 13	BP	RNA methylation
10	ENSDARG000	1.52	-1.02	0.59	foxa1	forkhead box A1 [Source:ZFIN;Acc:ZDB-GENE-990415-	<sub>781</sub> 19	1e-02	4 / 80	MF	transcription regulatory region DNA binding
10	LINSDANGOO	1.52	-1.02	0.55	IOAAT	IOMICAA BOX / (I [OUIICC.21 III,/ICC.255-GENE-350+15	20	1e-02	2 / 15	BP	RNA phosphodiester bond hydrolysis, exonucleolytic
11	ENSDARG000	1.45	-1.7	0.73	nik3c2c	phosphatidylinositol-4-phosphate 3-kinase catalytic sub-	<sub>ınit</sub> 21	1e-02	2 / 16	BP	negative regulation of translation
	LINODAIRCOOL	1.40	-1.7	0.70	piiloozg	g proopriately incolor i proopriate o initade datalytic data	22	1e-02	2 / 16	BP	regulation of small GTPase mediated signal transduction
12	ENSDARG000	1 45	-1.02	0.82			23	1e-02	3 / 48	MF	transcription factor binding
12	LINSDANGOO	1.45	-1.02	0.02			24	2e-02	9 / 375	BP	positive regulation of GTPase activity
13	ENSDARG000	1 44	-0.78	0.44	znfl1	zinc finger-like gene 1 [Source:ZFIN;Acc:ZDB-GENE-03	082 25	2e-02	7 / 257	BP	cell differentiation
13	LINSDANGOO	1.44	-0.76	0.44	211111	Zine iniger-ince gene 1 [course.27 int,766.25B-GENE-66	20	2e-02	2/22	BP	transcription from RNA polymerase III promoter
14	ENSDARG000	1 43	-1.47	0.79	col4a4	collagen, type IV, alpha 4 [Source:ZFIN;Acc:ZDB-GENE-	101 27	2e-02	2 / 22	MF	tRNA binding
17	LINSDANGOON	1.40	-1.47	0.73	COITAT	oonagon, typo 11, apria 1 (ooaroo.e. 111, too.e.b.b. Oe112	20	3e-02	6 / 217	MF	GTPase activator activity
15	ENSDARG000	1 42	-2.3	0.82	elk3	ELK3, ETS-domain protein [Source:ZFIN;Acc:ZDB-GEN	29	3e-02	3 / 64	MF	hydrolase activity, acting on glycosyl bonds
10	LINODAIRCOOL	1.72	-2.0	0.02	CINO	ELIO, ETO domain protoin (courso.Et int,) too.EBB GEN	30	3e-02	18 / 1063	MF	transferase activity
16	ENSDARG000	1 30	-1.27	0.72	neu4	sialidase 4 [Source:ZFIN;Acc:ZDB-GENE-050522-125]	31	3e-02	2 / 26	MF	RNA polymerase II transcription cofactor activity
10	LINODAIRCOOL	1.00	-1.27	0.72	11CU-4	Standard T (Coursella III, Nov.EBB CENE GOODE 120)	32	3e-02	3 / 65	BP	covalent chromatin modification
17	ENSDARG000	1.38	-0.93	0.78	nav2b	neuron navigator 2b [Source:ZFIN;Acc:ZDB-GENE-0612	33 <sup>07-</sup> 34	3e-02 3e-02	2 / 27	CC MF	mediator complex actin binding
	LINODAIRCOOL	1.00	0.00	00	Havzb		35	3e-02 3e-02	6 / 231 38 / 2716	CC	nucleus
18	ENSDARG000	1 37	-1.29	0.7	ccdc58	coiled-coil domain containing 58 [Source:ZFIN;Acc:ZDB-		4e-02	2/29	MF	3',5'-cyclic-nucleotide phosphodiesterase activity
10	LINODAIRCOOL	1.07	-1.25	0.7	codooo	conce con containing of feeding. Entry, too. ESS	37	4e-02 4e-02	2/29	MF	ubiquitin conjugating enzyme binding
19	ENSDARG000	1.37	-1.42	0.65	ssbp2	single-stranded DNA binding protein 2 [Source:ZFIN;Acc		4e-02 4e-02	3/70	CC	myosin complex
13	21402/11/3001	1.07	-1.72	0.00	OODPE	[250 270 5 many protein 2 [250 00:21 114,700	39	4e-02 4e-02	2/32	BP	regulation of signal transduction
20	ENSDARG000	1.36	-1.59	0.78		GATS protein-like 3 [Source:ZFIN;Acc:ZDB-GENE-0503		5e-02	2/35	BP	cell projection organization
20	21102/11/3001			00		of the same of the	70		2700	Di	



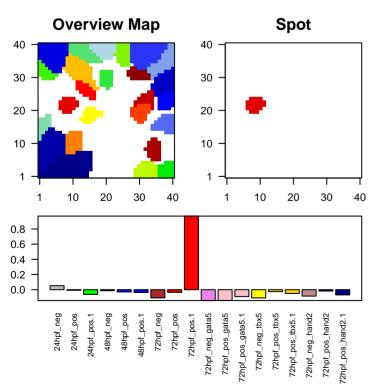
ВР				СС				MF			
Rank	p-value	#in/all	Geneset	Rank	p-value	#in/all	Geneset	Rank	p-value	#in/all	Geneset
1	2e-04	6 / 79	mRNA splicing, via spliceosome	1	0.004	4 / 64	Cul3–RING ubiquitin ligase complex	1	0.001	36 / 2030	nucleic acid binding
2	1e-03	4 / 45	Notch signaling pathway	2	0.006	3 / 36	P-body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

# Spot Summary: N

# metagenes = 24 # genes = 452

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

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



# Spot Genelist

18 ENSDARGOO 1.58

19 ENSDARG00( 1.5720 ENSDARG00( 1.57

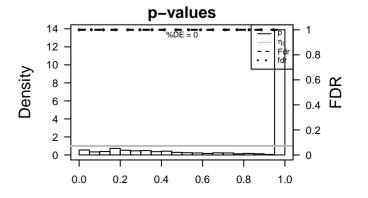
-0.39

Rank ID			max	e min e	r ∋	Symb	Description ool	Rank	p-value	#in/all	Gei	neset
	1	ENSDARG000	5.69	-0.44	0.98	slc28a1	solute carrier family 28 (concentrative nucleoside transporter)	1	3e-05	145 / 6723	СС	membra
	2	ENSDARG000	2.21	-0.29	0.91		si:ch211-167j6.4 [Source:ZFIN;Acc:ZDB-GENE-070912-14	2	2e-04 2e-03	133 / 6248 5 / 53	CC BP	chemota
	3	ENSDARG000	1.98	-2.35	0.42	pmela	premelanosome protein a [Source:ZFIN;Acc:ZDB-GENE-03]	4 5	3e-03 4e-03	4/39 3/20	MF BP	hydrolas regulatio
	4	ENSDARG000	1.92	-0.81	0.72	si:ch73-	1 <b>ទទេ២%2</b> 185c24.2 [Source:ZFIN;Acc:ZDB-GENE-131121-18	6 7	7e-03 9e-03	18 / 591 3 / 27	BP BP	transmer developr
	5	ENSDARG000	1.84	-1.26	0.65	ryr1b	ryanodine receptor 1b (skeletal) [Source:ZFIN;Acc:ZDB-GEN	8 9	1e-02 1e-02	7 / 147 2 / 10	BP CC	potassiu melanos
	6	ENSDARG000	1.82	-1.3	0.58		dopachrome tautomerase [Source:ZFIN;Acc:ZDB-GENE-00]	10 11	1e-02 1e-02	2 / 10 22 / 809	BP CC	outer dy integral
	7	ENSDARG000		-0.7	0.74	ankrd1h	ankyrin repeat domain 1b (cardiac muscle) [Source:ZFIN:Acc	12 13	1e-02 1e-02	6 / 119 2 / 11	MF BP	serine-ty melanos
	8	ENSDARG00		-0.6	0.77		si:ch211-2408.4  Source:ZFIN;Acc:ZDB-GENE-141212-25(	14 15	1e-02 2e-02	4 / 58 2 / 12	BP MF	chemoki calcium-
	9	ENSDARG00		-0.9	0.78	pex2	peroxisomal biogenesis factor 2 [Source:ZFIN:Acc:ZDB-GEN	16 17	2e-02 2e-02	2 / 12 15 / 499	BP BP	skeletal i
						pexz		18 19	2e-02 2e-02	2 / 13 2 / 13	BP BP	cellular r glycolipid
	10	ENSDARG000		-0.89	0.76		si:dkey-62k3.5 [Source:ZFIN;Acc:ZDB-GENE-160727-7]	20 21	2e-02 2e-02	2 / 14 3 / 39	BP CC	posterior
	11	ENSDARG000	1.64	-0.69	0.65	pdx1	pancreatic and duodenal homeobox 1 [Source:ZFIN;Acc:ZDB	22 23	3e-02 3e-02	3 / 42	BP BP	cilium me
	12	ENSDARG000	1.62	-0.77	0.62	hoxd9a	homeobox D9a [Source:ZFIN;Acc:ZDB-GENE-990415-121]	24 25	3e-02 3e-02	3 / 43 8 / 229	BP MF	notochor
	13	ENSDARG000	1.61	-0.53	0.79	si:ch73-	1ន់ប្រវាត្រ3-15b2.5 [Source:ZFIN;Acc:ZDB-GENE-030131-540(	26 27	3e-02 3e-02	4 / 75 2 / 18	BP BP	calcium i
	14	ENSDARG000	1.61	-0.65	0.76	tgm2a	transglutaminase 2, C polypeptide A [Source:ZFIN;Acc:ZDB-	28 29	3e-02 3e-02 3e-02	2/18	MF CC	steroid b
	15	ENSDARG000	1.6	-0.46	0.87		si:ch211-218k8.1 [Source:ZFIN;Acc:ZDB-GENE-141215-9]	30 31	3e-02	3 / 44	BP	regulatio
	16	ENSDARG000	1.6	-0.44	0.68	gdpd3b	glycerophosphodiester phosphodiesterase domain containing	32	3e-02 3e-02	20 / 800	MF MF	serine-ty
	17	ENSDARG000	1.58	-0.47	0.85			33 34	4e-02 4e-02	2/19 2/20	BP BP	G-prote

pmelb premelanosome protein b [Source:ZFIN;Acc:ZDB-GENE-05

tripartite motif containing 35-13 [Source:ZFIN;Acc:ZDB-GEN

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



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

# Spot Summary: O

# metagenes = 21 # genes = 477

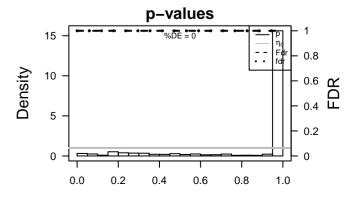
<r> metagenes = 0.94 <r> genes = 0.57 beta: r2= 0.24 / log p= -1.41

# samples with spot = 0 ( 0 %)

#### **Overview Map** Spot 30 20 20 10 10 10 20 30 30 10 20 40 0.5 0.4 0.3 0.2 0.1 0.0 72hpf\_neg\_gata5 72hpf\_pos\_gata5 48hpf\_pos.1 72hpf\_neg 72hpf\_pos 48hpf\_pos 72hpf\_pos.1 72hpf\_pos\_hand2 72hpf\_neg\_tbx5 72hpf\_pos\_gata5.1

# **Spot Genelist**

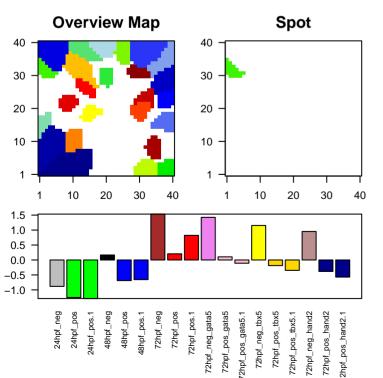
Ra	nk	max	е	r	Description	Rank	p-value	#in/all	Ge	neset
ID			min (	е	Symbol					
1	ENSDARG000	1.45	-1.13	0.53	complement component 6 [Source:ZFIN;Acc:ZDB-GENE-04	1	5e-05	31 / 853	BP	G-protein coupled receptor signaling pathway
_						2	2e-04	27 / 751	MF	G-protein coupled receptor activity
2	ENSDARG000	1.27	-0.8	0.62		3	1e-03	7 / 100	BP	neuropeptide signaling pathway
_						4	2e-03	5 / 53	BP	chemotaxis
3	ENSDARG000	1.24	-0.39	0.63		5	3e-03	5 / 58	BP	chemokine-mediated signaling pathway
						6	4e-03	21 / 666	MF	signal transducer activity
4	ENSDARG000	1.2	-1.31	0.53	zgc:13679tgc:136791 [Source:ZFIN;Acc:ZDB-GENE-060421-8264]	/	4e-03	12 / 297	BP	immune response
						8	6e-03	3 / 22	MF	chemokine receptor activity
5	ENSDARG000	1.13	-0.78	0.59	ak7a adenylate kinase 7a [Source:ZFIN;Acc:ZDB-GENE-040724-	9	7e-03	4 / 45	BP	phospholipase C-activating G-protein coupled receptor signaling pathway
						10	1e-02	3 / 28	BP	G-protein coupled serotonin receptor signaling pathway
6	ENSDARG000	1.07	-0.58	0.67		11	1e-02	2/10	BP	cellular glucose homeostasis
						12	1e-02	2/11	BP	detection of mechanical stimulus
7	ENSDARG000	1.07	-0.33	0.64	si:ch211-si43h220.4149e23.4 [Source:ZFIN;Acc:ZDB-GENE-131121-(	13	1e-02	2/11	BP	multicellular organismal response to stress
						14	1e-02	7 / 153	CC	cell surface
8	ENSDARG000	1.07	-0.75	0.52	atoh7 atonal bHLH transcription factor 7 [Source:ZFIN;Acc:ZDB-GE	15	2e-02	2 / 12	BP	smooth muscle contraction
						16	2e-02	3 / 34	MF	G-protein coupled serotonin receptor activity
9	ENSDARG000	1.06	-0.63	0.56	Ipl lipoprotein lipase [Source:ZFIN;Acc:ZDB-GENE-990415-13	17	2e-02	9 / 244	MF	receptor binding
						18	2e-02	2/14	BP	positive regulation of cytosolic calcium ion concentration
10	ENSDARG000	1.04	-0.32	0.64	UDP glucuronosyltransferase 1 family, pseudogene B6 [Source	19	2e-02	2 / 14	BP	spermatid development
						20	3e-02	4 / 69	MF	extracellular ligand–gated ion channel activity
11	ENSDARG000	1.04	-0.33	0.57	si:dkey-92i15.4 [Source:ZFIN;Acc:ZDB-GENE-030131-842.	21	4e-02	17 / 634	CC	extracellular region
						22	4e-02	7 / 191	MF	serine-type endopeptidase activity
12	ENSDARG000	1.02	-0.5	0.65	fpr1 formyl peptide receptor 1 [Source:ZFIN;Acc:ZDB-GENE-121	23	4e-02	30 / 1295	BP	signal transduction
12	LINODAIRCOOK	1.02	-0.0	0.00	· · · · · · · · · · · · · · · · · · ·	24	5e-02	5 / 119	MF	serine-type peptidase activity
13	ENSDARG000	1.01	-0.22	0.8	zgc:110188c:110183 [Source:ZFIN;Acc:ZDB-GENE-050417-380]	25	6e-02	2/23	MF	CCR chemokine receptor binding
13	LINSDARGOON	1.01	-0.22	0.0	2go.1101@go.110100 [00d100.21114,700.2DD-02142-000417-000]	26	6e-02	2 / 23	BP	cellular response to interferon–gamma
11	ENCDAD COO	1.01	-0.47	0.69	si:dkey-29988-4-239i20.4 [Source:ZFIN:Acc:ZDB-GENE-030131-26	27	6e-02	2/23	BP	lymphocyte chemotaxis
14	ENSDARG000	1.01	-0.47	0.09	51.ukey-23130000y-233120.4 [30010e.21 111,Acc.200-30140-30131-20	28	6e-02	2 / 23	BP	monocyte chemotaxis
4.5	=======================================				1/-0 - 1 1-1/1	29	6e-02	2/24	BP	cell recognition
15	ENSDARG000	0.98	-0.26	0.7	bfsp2 beaded filament structural protein 2, phakinin [Source:ZFIN;A	30	6e-02	2/24	BP	cellular response to interleukin–1
4.0						31	6e-02	2/24	BP	cellular response to tumor necrosis factor
16	ENSDARG000	0.97	-0.36	0.72	si:ch211-271d10.2 [Source:ZFIN;Acc:ZDB-GENE-141212-;	32	6e-02	2 / 25	MF	acetylcholine-gated cation-selective channel activity
						33	6e-02	2 / 25	BP	activation of MAPKK activity
17	ENSDARG000	0.96	-0.15	0.88		34	6e-02	2 / 25	BP	cell fate commitment
						35	7e-02	5 / 134	BP	protein glycosylation
18	ENSDARG000	0.96	-0.14	0.89	zgc:5662&gc:56628 [Source:ZFIN;Acc:ZDB-GENE-040426-1099]	36	7e-02	4 / 95	MF	hormone activity
						37	8e-02	7 / 223	MF	transferase activity, transferring glycosyl groups
19	ENSDARG000	0.95	-0.43	0.72		38	8e-02	2/29	MF	glucuronosyltransferase activity
						39	9e-02	2/30	MF	cell adhesion molecule binding
20	ENSDARG000	0.95	-0.31	0.42	si:dkey-2sicdk@y-21c1.6 [Source:ZFIN;Acc:ZDB-GENE-031118-158]	40	9e-02	2/30	BP	heterophilic cell-cell adhesion via plasma membrane cell adhesion molecu



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

#### Spot Summary: P

# metagenes = 20 # genes = 292 <r> metagenes = 0.97 <r> genes = 0.61 beta: r2= 11.26 / log p= -Inf # samples with spot = 5 ( 27.8 %) 72hpf\_neg: 1 (100 %) 72hpf\_pos: 1 (50 %) 72hpf\_neg\_gata5 : 1 ( 100 %) 72hpf\_neg\_hand2:1(100%)



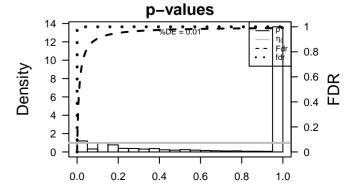
### **Spot Genelist**

Rank ID		max	e min e	r e	Symb	Description ool
1	ENSDARG000	5.44	-2.17	0.82	opn1sw2	2 opsin 1 (cone pigments), short-wave-sensitive 2 [Source:ZFI
2	ENSDARG000	5.22	-3.71	0.78	opn1mw	1opsin 1 (cone pigments), medium-wave-sensitive, 1 [Source:
3	ENSDARG000	5.16	-4.48	0.78	opn1sw	opsin 1 (cone pigments), short-wave-sensitive 1 [Source:ZFI
4	ENSDARG000	4.25	-2.5	0.84	opn1lw1	opsin 1 (cone pigments), long-wave-sensitive, 1 [Source:ZFI
5	ENSDARG000	4.23	-1.93	0.65	fbp2	fructose-1,6-bisphosphatase 2 [Source:ZFIN;Acc:ZDB-GEN
6	ENSDARG000	4.19	-2.48	0.75	and3	actinodin3 [Source:ZFIN;Acc:ZDB-GENE-040724-185]
7	ENSDARG000	4.16	-2.83	0.73	pde6h	phosphodiesterase 6H, cGMP-specific, cone, gamma [Sourc
8	ENSDARG000	4.11	-2.9	0.82	grk7a	G protein-coupled receptor kinase 7a [Source:ZFIN;Acc:ZDB
9	ENSDARG000	4.05	-2.29	0.86	prph2b	peripherin 2b (retinal degeneration, slow) [Source:ZFIN;Acc:Z
10	ENSDARG000	3.64	-2.02	0.59	prph2a	peripherin 2a (retinal degeneration, slow) [Source:ZFIN;Acc:Z
11	ENSDARG000	3.63	-1.95	0.78	gngt2b	guanine nucleotide binding protein (G protein), gamma transc
12	ENSDARG000	3.58	-2.81	0.8	mbpa	myelin basic protein a [Source:ZFIN;Acc:ZDB-GENE-03012I
13	ENSDARG000	3.36	-3.38	0.6	col8a2	collagen, type VIII, alpha 2 [Source:ZFIN;Acc:ZDB-GENE-06
14	ENSDARG000	3.33	-2.55	0.85	si:dkey-	29ii thteay-22i16.3 [Source:ZFIN;Acc:ZDB-GENE-071005-4]
15	ENSDARG000	3.26	-2.37	0.86	gc3	guanylyl cyclase 3 [Source:ZFIN;Acc:ZDB-GENE-011128-9
16	ENSDARG000	3.26	-1.88	0.78	clcn2c	chloride channel 2c [Source:ZFIN;Acc:ZDB-GENE-050506-
17	ENSDARG000	3.25	-2.13	0.88	col6a2	collagen, type VI, alpha 2 [Source:ZFIN;Acc:ZDB-GENE-07(
18	ENSDARG000	3.23	-2.34	0.93	irbp	interphotoreceptor retinoid-binding protein [Source:ZFIN;Acc
19	ENSDARG000	3.19	-2.16	0.82	slc24a2	solute carrier family 24 (sodium/potassium/calcium exchange

20 ENSDARG00i 3.17 -1.92 0.88 col6a1 collagen, type VI, alpha 1 [Source:ZFIN;Acc:ZDB-GENE-070]

#### **Geneset Overrepresentation**

4	2e-13	14 / 83	BP	visual perception
1 2 3 4 5 6 7 8 9	Ze-13 7e-10	27 / 634	CC	extracellular region
2	8e-09	13 / 153	CC	proteinaceous extracellular matrix
<u>ح</u>	1e-05	6/49	MF	extracellular matrix structural constituent
5	2e-05	5/31	MF	heparin binding
5	2e-05 2e-05	5/33	MF	photoreceptor activity
9	2e-05 2e-05	21 / 717	MF	calcium ion binding
0	2e-05 3e-05	5/36	BP	regulation of cell growth
0	5e-05	6 / 64	MF	serine-type endopeptidase inhibitor activity
10	7e-05	26 / 1084	BP	transport
11	1e-03	9 / 176	BP	ion transmembrane transport
12	1e-04	4/25	MF	integrin binding
13	1e-04 1e-04	3/10	MF	small molecule binding
14	2e-04	3/10	MF	collagen binding
15	2e-04 2e-04	4/28	BP	phototransduction
16	2e-04	12 / 333	BP	cell adhesion
17	2e-04 2e-04	4/29	MF	3',5'-cyclic-nucleotide phosphodiesterase activity
18	2e-04 2e-04	3/12	BP	collagen fibril organization
19	3e-04	4/30	MF	insulin-like growth factor binding
20	3e-04	15 / 499	BP	ion transport
21	3e-04	4/31	BP	protein-chromophore linkage
22	6e-04	10 / 270	MF	ion channel activity
23	6e-04	5/65	CC	extracellular matrix
24	6e-04	89 / 6248	CC	integral component of membrane
25	1e-03	6 / 109	BP	negative regulation of endopeptidase activity
26	1e-03	5/76	BP	cartilage development
27	1e-03	3/21	BP	negative regulation of angiogenesis
28	1e-03	3 / 21	BP	response to light stimulus
29	1e-03	4 / 46	CC	collagen trimer
30	1e-03	6/116	MF	metalloendopeptidase activity
31	2e-03	92 / 6723	CC	membrane
32	2e-03	6 / 128	MF	metallopeptidase activity
33	3e-03	3 / 27	BP	axon extension
34	3e-03	8 / 229	MF	transporter activity
35	4e-03	3 / 30	BP	detection of visible light
36	4e-03	3/31	MF	G-protein coupled photoreceptor activity
37	4e-03	3 / 31	CC	photoreceptor outer segment
38	4e-03	5 / 102	BP	response to stimulus
39	4e-03	3 / 32	BP	muscle organ development
40	5e-03	22 / 1162	CC	plasma membrane



BP				СС				MF			
Rank	p-value	#in/all	Geneset	Rank	p-value	#in/all	Geneset	Rank	p-value	#in/all	Geneset
1	2e-13	14 / 83	visual perception	1	7e-10	27 / 634	extracellular region	1	1e-05	6 / 49	extracellular matrix structural constituent
2	3e-05	5 / 36	regulation of cell growth	2	8e-09	13 / 153	proteinaceous extracellular matrix	2	2e-05	5 / 31	heparin binding
3	7e-05	26 / 1084	transport	3	6e-04	5 / 65	extracellular matrix	3	2e-05	5 / 33	photoreceptor activity
4	1e-04	9 / 176	ion transmembrane transport	4	6e-04	89 / 6248	integral component of membrane	4	2e-05	21 / 717	calcium ion binding
5	2e-04	4/28	phototransduction	5	1e-03	4 / 46	collagen trimer	5	5e-05	6 / 64	serine-type endopeptidase inhibitor activity
6	2e-04	12 / 333	cell adhesion	6	2e-03	92 / 6723	membrane	6	1e-04	4 / 25	integrin binding
7	2e-04	3 / 12	collagen fibril organization	7	4e-03	3 / 31	photoreceptor outer segment	7	1e-04	3/10	small molecule binding
8	3e-04	15 / 499	ion transport	8	5e-03	22 / 1162	plasma membrane	8	2e-04	3/11	collagen binding
9	3e-04	4/31	protein-chromophore linkage	9	1e-02	16 / 809	integral component of plasma membrane	9	2e-04	4 / 29	3',5'-cyclic-nucleotide phosphodiesterase activity
10	1e-03	6 / 109	negative regulation of endopeptidase activity	10	1e-02	3 / 48	heterotrimeric G-protein complex	10	3e-04	4/30	insulin-like growth factor binding
11	1e-03	5/76	cartilage development	11	2e-02	11 / 500	extracellular space	11	6e-04	10 / 270	ion channel activity
12	1e-03	3 / 21	negative regulation of angiogenesis	12	2e-02	4/98	transcription factor complex	12	1e-03	6/116	metalloendopeptidase activity
13	1e-03	3 / 21	response to light stimulus	13	2e-02	2/22	synaptic vesicle membrane	13	2e-03	6 / 128	metallopeptidase activity
14	3e-03	3 / 27	axon extension	14	3e-02	2 / 27	guanylate cyclase complex, soluble	14	3e-03	8 / 229	transporter activity
15	4e-03	3 / 30	detection of visible light	15	3e-02	2 / 27	postsynapse	15	4e-03	3 / 31	G-protein coupled photoreceptor activity

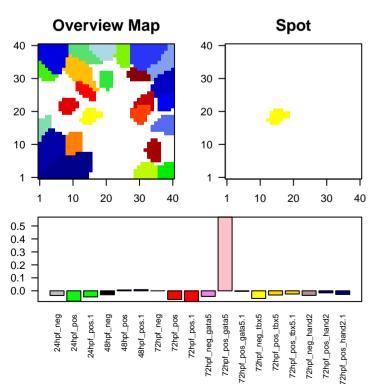
# Spot Summary: Q

# metagenes = 23 # genes = 560

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

# samples with spot = 1 (5.6 %)

72hpf\_pos\_gata5 : 1 ( 50 %



### **Spot Genelist**

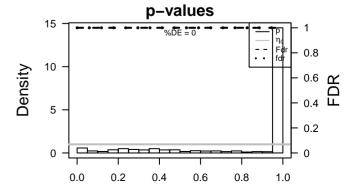
20 ENSDARG00 1.21

Rar	nk ID	max	e min e	r	Symb	Description pol
1	ENSDARG000	1.71	-0.89	0.69		adhesion G protein-coupled receptor F6 [Source:ZFIN;Acc:Z
2	ENSDARG000	1.68	-0.51	0.81	card14	caspase recruitment domain family, member 14 [Source:ZFIN
3	ENSDARG000	1.66	-1.26	0.55	si:ch211	-si2sh22h1+129c21.1 [Source:ZFIN;Acc:ZDB-GENE-030131-{
4	ENSDARG000	1.65	-1	0.61	abch1	ATP-binding cassette, sub-family H, member 1 [Source:ZFIN
5	ENSDARG000	1.62	-1.08	0.65	dnaaf2	dynein, axonemal, assembly factor 2 [Source:ZFIN;Acc:ZDB-
6	ENSDARG000	1.6	-0.89	0.65		U5 spliceosomal RNA [Source:RFAM;Acc:RF00020]
7	ENSDARG000	1.56	-0.79	0.63	styk1	serine/threonine/tyrosine kinase 1 [Source:ZFIN;Acc:ZDB-Gt
8	ENSDARG000	1.53	-0.52	0.69	klf6b	Kruppel-like factor 6b [Source:ZFIN;Acc:ZDB-GENE-07091:
9	ENSDARG000	1.46	-0.65	0.69		si:ch73-23l24.1 [Source:ZFIN;Acc:ZDB-GENE-131127-400
10	ENSDARG000	1.42	-0.48	0.66	zgc:112	28gc:112285 [Source:ZFIN;Acc:ZDB-GENE-050913-132]
11	ENSDARG000	1.41	-0.59	0.77	rab25b	RAB25, member RAS oncogene family b [Source:ZFIN;Acc:Z
12	ENSDARG000	1.37	-0.35	0.88	LOC108	araga:ሰុ\$3932 [Source:ZFIN;Acc:ZDB-GENE-070209-223]
13	ENSDARG000	1.34	-0.55	0.65	zgc:194	838c:194839 [Source:ZFIN;Acc:ZDB-GENE-081022-153]
14	ENSDARG000	1.33	-0.55	0.68	zgc:163	12gc:163121 [Source:ZFIN;Acc:ZDB-GENE-070424-80]
15	ENSDARG000	1.29	-0.53	0.68	s100w	S100 calcium binding protein W [Source:ZFIN;Acc:ZDB–GEN
16	ENSDARG000	1.29	-0.91	0.66	herc3	HECT and RLD domain containing E3 ubiquitin protein ligase
17	ENSDARG000	1.28	-0.31	0.81		si:ch211-250e5.2 [Source:ZFIN;Acc:ZDB-GENE-030131-8(
18	ENSDARG000	1.23	-0.29	0.76	trim110	tripartite motif containing 110 [Source:ZFIN;Acc:ZDB-GENE-
19	ENSDARG000	1.23	-0.37	0.76	psma6l	proteasome subunit alpha 6, like [Source:ZFIN;Acc:ZDB-GEI

si:ch73-1910h73-1181m17.1 [Source:ZFIN;Acc:ZDB-GENE-131122-4

#### **Geneset Overrepresentation**

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



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

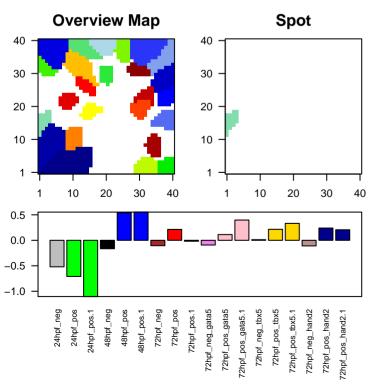
### Spot Summary: R

```
# genes = 373

<r> metagenes = 0.95
<r> genes = 0.47
beta: r2= 3.1 / log p= -Inf
```

# samples with spot = 1 ( 5.6 %) 48hpf\_pos : 1 ( 50 %)

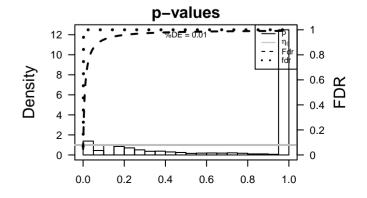
# metagenes = 21



#### **Spot Genelist**

Rank ID		max	e min e	r e	Sym	Description bol	Rank	p-value	#in/all	Ge	neset
1	ENSDARG000	3.79	-2.06	0.55	icn2	ictacalcin 2 [Source:ZFIN;Acc:ZDB-GENE-070822-9]	1	3e-05	5 / 28	MF	protein o
2	ENSDARG000	3.15	-2.71	0.52	si:dkey-	-26/21/12/20-202122.6 [Source:ZFIN;Acc:ZDB-GENE-131121-18	2 3 4	1e-04 1e-04 2e-04	50 / 2189 7 / 85 15 / 375	CC MF BP	cytoplas isomera: positive
3	ENSDARG000	2.71	-1.4	0.48	tbx18	T-box 18 [Source:ZFIN;Acc:ZDB-GENE-020529-2]	5	3e-04	5 / 44 5 / 44	MF BP	peptidyl- protein p
4	ENSDARG000	2.61	-1.29	0.27	tg	thyroglobulin [Source:ZFIN;Acc:ZDB-GENE-030519-1]	6 7	3e-04 4e-04	13 / 321	MF CC	GTPase
5	ENSDARG00	2.32	-2.56	0.57	fhl1a	four and a half LIM domains 1a [Source:ZFIN;Acc:ZDB-GEN	8 9	4e-04 7e-04	7 / 101 11 / 257	BP	endoson cell diffe
6	ENSDARG000	2.27	-2.26	0.71	wt1a	wilms tumor 1a [Source:ZFIN;Acc:ZDB-GENE-980526-558]	10 11	8e-04 9e-04	8 / 147 5 / 56	BP CC	wesicle-
7	ENSDARG000	2.17	-1.36	0.55	si:dkey-	-164f24;2-164f24.2 [Source:ZFIN;Acc:ZDB-GENE-030131-70	12 13	9e-04 1e-03	3 / 15 6 / 88	MF MF	FK506 b guanyl-i
8	ENSDARG000	2.13	-0.99	0.59	si:dkey-	-2 <b>%能版</b> 公-238i5.2 [Source:ZFIN;Acc:ZDB-GENE-030131-971	14 15	1e-03 2e-03	3 / 16 5 / 65	BP BP	regulatio
9	ENSDARG000	2.02	-2.17	0.71		fumarylacetoacetate hydrolase (fumarylacetoacetase) [Sourc	16 17	2e-03 2e-03	12 / 337 9 / 209	CC	endopla:
10	ENSDARG000	2	-2.87	0.69	phlda1	pleckstrin homology-like domain, family A, member 1 [Source	18 19	2e-03 3e-03	9/210 3/21	BP BP	vesicle o
11	ENSDARG000	1.99	-2.84	0.82	stx12l	syntaxin 12, like [Source:ZFIN;Acc:ZDB-GENE-110715-1]	20 21	3e-03 4e-03	5 / 74 16 / 561	BP MF	negative GTP bin
12	ENSDARG000		-1.07	0.6		heat shock protein, alpha–crystallin–related, b11 [Source:ZFI	22 23	4e-03 5e-03	5 / 78 4 / 51	BP BP	protein u ER to Ge
13	ENSDARG00		-1.88	0.61		cholinergic receptor, muscarinic 2a [Source:ZFIN;Acc:ZDB-G	24 25	5e-03 5e-03	3 / 26 7 / 156	BP BP	mitopha
							26 27	5e-03 5e-03	3 / 27 3 / 27	CC BP	recycling ubiquitin
14	ENSDARG000		-1.45	0.57	2gc:918	16&gc:91968 [Source:ZFIN;Acc:ZDB-GENE-040704-1]	28 29	5e-03 6e-03	4 / 53 5 / 85	BP BP	converge protein fe
15	ENSDARG00		-3.45	0.62			30 31	6e-03 7e-03	3 / 28 8 / 210	MF BP	protein k regulatio
16	ENSDARG000	1.86	-1.77	0.76	rbp4l	retinol binding protein 4, like [Source:ZFIN;Acc:ZDB-GENE-(	32 33	7e-03 7e-03	2 / 10 2 / 10	BP BP	cellular I glycoger
17	ENSDARG000	1.86	-1.39	0.51	lyve1a	lymphatic vessel endothelial hyaluronic receptor 1a [Source:Z	34 35	8e-03 8e-03	3 / 31 3 / 31	BP BP	autopha chapero
18	ENSDARG000	1.84	-2.14	0.61	msmo1	methylsterol monooxygenase 1 [Source:ZFIN;Acc:ZDB-GEN	36 37	9e-03 9e-03	3 / 32 3 / 33	BP MF	muscle o
19	ENSDARG000	1.77	-2	0.58	si:ch21	1-3696211(2269c21.2 [Source:ZFIN;Acc:ZDB-GENE-090313-	38 39	1e-02 1e-02	10 / 317 2 / 12	CC BP	Golgi ap
20	ENSDARG00	1.73	-1.54	0.54	si:ch21	1-3436201.3243a20.3 [Source:ZFIN;Acc:ZDB-GENE-061207-;	40	1e-02	2/12	CC	microtub

1	3e-05	5 / 28	MF	protein domain specific binding
	1e-04	50 / 2189	CC	cytoplasm
3	1e-04	7 / 85	MF	isomerase activity
4	2e-04	15 / 375	BP	positive regulation of GTPase activity
2 3 4 5 6 7	3e-04	5 / 44	MF	peptidyl-prolyl cis-trans isomerase activity
6	3e-04	5 / 44	BP	protein peptidyl-prolyl isomerization
7	4e-04	13 / 321	MF	GTPase activity
8	4e-04	7 / 101	CC	endosome
9	7e-04	11 / 257	BP	cell differentiation
10	8e-04	8 / 147	BP	vesicle-mediated transport
11	9e-04	5 / 56	CC	mitochondrial outer membrane
12	9e-04	3 / 15	MF	FK506 binding
13	1e-03	6 / 88	MF	guanyl-nucleotide exchange factor activity
14	1e-03	3 / 16	BP	regulation of protein kinase activity
15	2e-03	5 / 65	BP	endocytosis
16	2e-03	12 / 337	CC	endoplasmic reticulum
17	2e-03	9 / 209	CC	endoplasmic reticulum membrane
18	2e-03	9 / 210	BP	intracellular protein transport
19	3e-03	3 / 21	BP	vesicle docking
20	3e-03	5 / 74	BP	negative regulation of transcription, DNA-templated
21	4e-03	16 / 561	MF	GTP binding
22	4e-03	5 / 78	BP	protein ubiquitination involved in ubiquitin-dependent protein catabo
23	5e-03	4 / 51	BP	ER to Golgi vesicle-mediated transport
24	5e-03	3 / 26	BP	mitophagy
25	5e-03	7 / 156	BP	small GTPase mediated signal transduction
26	5e-03	3 / 27	CC	recycling endosome
27	5e-03	3 / 27	BP	ubiquitin-dependent ERAD pathway
28	5e-03	4 / 53	BP	convergent extension involved in gastrulation
29	6e-03	5 / 85	BP	protein folding
30	6e-03	3 / 28	MF	protein kinase binding
31	7e-03	8 / 210	BP	regulation of apoptotic process
32	7e-03	2/10	BP	cellular lipid metabolic process
33	7e-03	2/10	BP	glycogen biosynthetic process
34	8e-03	3 / 31	BP	autophagosome assembly
35	8e-03	3 / 31	BP	chaperone-mediated protein folding
36	9e-03	3 / 32	BP	muscle organ development
37	9e-03	3 / 33	MF	oxidoreductase activity, acting on the CH-CH group of donors
38	1e-02	10 / 317	CC	Golgi apparatus
39	1e-02	2 / 12	BP	aromatic amino acid family metabolic process
40	1e-02	2/12	CC	microtubule associated complex



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

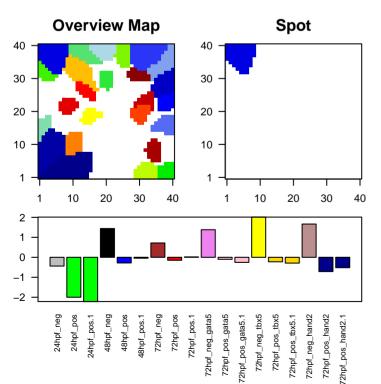
#### Spot Summary: S

# metagenes = 64
# genes = 1209

<r> metagenes = 0.94

beta: r2= 20.51 / log p= -Inf

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



#### **Spot Genelist**

max e

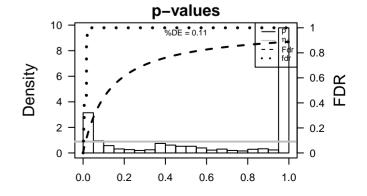
Rank

INai	ID .	max	min e	;	Symb	pol
1	ENSDARG000	5.4	-5.6	0.78	muc5.1	mucin 5.1, oligomeric mucus/gel-forming [Source:ZFIN;Acc:Z
2	ENSDARG000	5.34	-6.98	0.71	matn1	matrilin 1 [Source:ZFIN;Acc:ZDB-GENE-050307-3]
3	ENSDARG000	5.19	-6.04	0.49	atp1a1a	.2ATPase, Na+/K+ transporting, alpha 1a polypeptide, tandem o
4	ENSDARG000	5.14	-4.55	0.71	rho	rhodopsin [Source:ZFIN;Acc:ZDB-GENE-990415-271]
5	ENSDARG000	5.09	-5.91	0.72	and2	actinodin2 [Source:ZFIN;Acc:ZDB-GENE-041105-2]
6	ENSDARG000	5.01	-4.88	0.69	opn1lw2	opsin 1 (cone pigments), long-wave-sensitive, 2 [Source:ZFI
7	ENSDARG000	4.9	-3.66	0.74	and1	actinodin1 [Source:ZFIN;Acc:ZDB-GENE-030131-9105]
8	ENSDARG000	4.85	-4.47	0.76	npas4a	neuronal PAS domain protein 4a [Source:ZFIN;Acc:ZDB-GEI
9	ENSDARG000	4.83	-5.45	0.69	arr3a	arrestin 3a, retinal (X-arrestin) [Source:ZFIN;Acc:ZDB-GENE
10	ENSDARG000	4.82	-3.89	0.56	gnb3b	guanine nucleotide binding protein (G protein), beta polypepti
11	ENSDARG000	4.76	-5.55	0.79	col10a1a	acollagen, type X, alpha 1a [Source:ZFIN;Acc:ZDB-GENE-03
12	ENSDARG000	4.72	-8.26	0.88	col11a2	collagen, type XI, alpha 2 [Source:ZFIN;Acc:ZDB-GENE-000
13	ENSDARG000	4.71	-3.52	0.64	rcvrn3	recoverin 3 [Source:ZFIN;Acc:ZDB-GENE-040426-1661]
14	ENSDARG000	4.57	-3.71	0.6	pde6c	phosphodiesterase 6C, cGMP-specific, cone, alpha prime [Si
15	ENSDARG000	4.55	-3.73	0.75		
16	ENSDARG000	4.55	-4.06	0.6	gnat2	guanine nucleotide binding protein (G protein), alpha transdu
17	ENSDARG000	4.49	-6.7	0.83		si:dkey-65b12.6 [Source:ZFIN;Acc:ZDB-GENE-060526-32\$
18	ENSDARG000	4.19	-3.55	0.73	scn4ab	sodium channel, voltage-gated, type IV, alpha, b [Source:ZFI
19	ENSDARG000	4.03	-3.48	0.68	slc12a10	0.20lute carrier family 12 (sodium/potassium/chloride transporte
20	ENSDARG000	4.01	-3.22	0.96	sv2a	synaptic vesicle glycoprotein 2A [Source:ZFIN;Acc:ZDB-GEN

Description

#### **Geneset Overrepresentation**

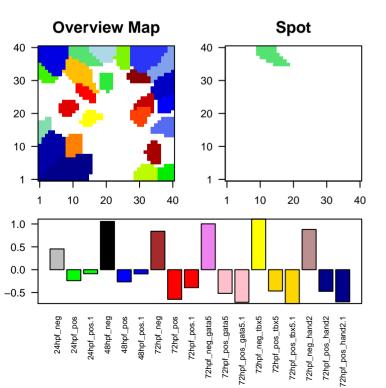
1	7e-34	56 / 172	BP	homophilic cell adhesion via plasma membrane adhesion molecule
	7e-33	75 / 333	BP	cell adhesion
3	2e-30	143 / 1162	CC	plasma membrane
4	2e-27	50 / 175	BP	nervous system development
5	3e-27	103 / 717	MF	calcium ion binding
2 3 4 5 6 7	4e-27	47 / 155	CC	synapse
7	2e-25	447 / 6723	CC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



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

### Spot Summary: T

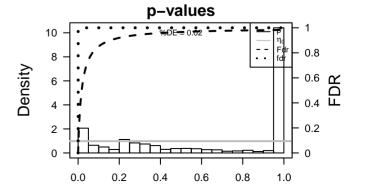
# metagenes = 37 # genes = 666 <r> metagenes = 0.96 <r> genes = 0.64 beta: r2= 7.21 / log p= -Inf # samples with spot = 5 ( 27.8 %) 48hpf\_neg : 1 ( 100 %) 72hpf\_neg : 1 ( 100 %) 72hpf\_neg\_gata5 : 1 ( 100 %) 72hpf\_neg\_hand2 : 1 ( 100 %)



#### **Spot Genelist**

Rank max e ID min		r €	Symb	Description ool	Rank	p-value	#in/all	Ge	neset		
1	ENSDARG00	3.14	-2.31	0.85	frem2a	Fras1 related extracellular matrix protein 2a [Source:ZFIN;Ac	1	3e-27	100 / 1239	BP	regulatio
2	ENSDARG000	2 97	-2.6	0.68		zmp:0000001081 [Source:ZFIN;Acc:ZDB-GENE-140106-41	2	2e-20 7e-20	98 / 1484 55 / 537	MF MF	DNA bin sequence
_	2.102/11000	2.07	2.0	0.00			4	1e-16	134 / 2716	CC	nucleus
3	ENSDARG000	2.87	-3.42	0.75	si:dkeyp	-sīrtikle∳p-77h1.4 [Source:ZFIN;Acc:ZDB-GENE-050208-18]	5	2e-12	48 / 633	MF	transcrip
•							6	2e-11	32 / 333	BP	cell adhe
4	ENSDARG000	2.85	-1.86	0.77	vcanb	versican b [Source:ZFIN;Acc:ZDB-GENE-030131-2185]	7	1e-09	46 / 717	MF	calcium
•							8	5e-09	20 / 172	BP	homophi
5	ENSDARG000	2.81	-1.92	0.82	Irrn1	leucine rich repeat neuronal 1 [Source:ZFIN;Acc:ZDB-GENE	9	1e-08	41 / 643	BP	transcrip
-							10	3e-08	13 / 78	BP	axon gui
6	ENSDARG000	2.78	-1.46	0.55	abi3bpb	ABI family, member 3 (NESH) binding protein b [Source:ZFIN	11	3e-06	7 / 28	BP	retina me
							12	5e-06	28 / 454	BP	multicell
7	ENSDARG000	2.72	-4	0.71	mxra5b	matrix-remodelling associated 5b [Source:ZFIN;Acc:ZDB-GI	13	8e-06	7 / 32	BP	retinal ga
							14	2e-05	28 / 491	MF	kinase a
8	ENSDARG000	2.65	-2.02	0.61	aspn	asporin (LRR class 1) [Source:ZFIN;Acc:ZDB-GENE-04110!	15	4e-05	7 / 41	MF	RNA pol
							16	6e-05	24 / 413	BP	intracellu
9	ENSDARG000	2.65	-2.8	0.87	thsd7aa	thrombospondin, type I, domain containing 7Aa [Source:ZFIN	17	6e-05	28 / 522	BP	phospho
							18	8e-05	49 / 1162	CC	plasma r
10	ENSDARG000	2.63	-1.69	0.97	nova2	neuro-oncological ventral antigen 2 [Source:ZFIN;Acc:ZDB-0	19	9e-05	67 / 1761	MF	metal ior
-							20	1e-04	7 / 48	BP	neural cr
11	ENSDARG000	2.54	-3.15	0.81			21	1e-04	10 / 100	BP	peptidyl-
							22	2e-04	21 / 362	BP	regulatio
12	ENSDARG000	2.52	-1.6	0.72	entpd5a	ectonucleoside triphosphate diphosphohydrolase 5a [Source:	23	2e-04	12 / 147	BP	brain de
							24 25	3e-04	5 / 25 10 / 110	BP MF	negative protein to
13	ENSDARG000	2.52	-1.65	0.92	dclk1b	doublecortin-like kinase 1b [Source:ZFIN;Acc:ZDB-GENE-0	25 26	3e-04 5e-04	4/16	BP	primitive
							27	5e-04 5e-04	5/28	BP	skeletal
14	ENSDARG000	2.5	-2.64	0.73	nlgn2b	neuroligin 2b [Source:ZFIN;Acc:ZDB-GENE-090918-3]	28	6e-04	6/44	BP	neuron o
							29	6e-04	4 / 17	BP	lymph ve
15	ENSDARG000	2.5	-1.63	0.74	fhdc1	FH2 domain containing 1 [Source:ZFIN;Acc:ZDB-GENE-040	30	6e-04	5/30	MF	transcrip
							31	7e-04	183 / 6248	CC	integral
16	ENSDARG000	2.49	-2.15	0.82	prdm12b	PR domain containing 12b [Source:ZFIN;Acc:ZDB-GENE-04	32	7e-04	10 / 124	MF	receptor
							33	8e-04	34 / 800	MF	zinc ion
17	ENSDARG000	2.48	-1.39	0.81	mxra5a	matrix-remodelling associated 5a [Source:ZFIN;Acc:ZDB-GI	34	9e-04	4/19	BP	semapho
							35	9e-04	4/19	MF	semapho
18	ENSDARG000	2.47	-3.39	0.75	kirrelb	kin of IRRE like b [Source:ZFIN;Acc:ZDB-GENE-070912-17	36	1e-03	12 / 180	BP	dephosp
							37	1e-03	193 / 6723	CC	membra
19	ENSDARG000	2.47	-2.65	0.77	ptx3a	pentraxin 3, long a [Source:ZFIN;Acc:ZDB-GENE-030131-8	38	1e-03	15 / 257	BP	cell differ
							39	1e-03	3 / 10	BP	optic ner
20	ENSDARG000	2.46	-3.93	0.79	tmem17	ggansmembrane protein 178B [Source:ZFIN;Acc:ZDB-GENE-	40	2e-03	9 / 115	MF	chromati

1	3e-27	100 / 1239	BP	regulation of transcription, DNA-templated
	2e-20	98 / 1484	MF	DNA binding
2	7e-20	55 / 537	MF	sequence-specific DNA binding
4	1e-16	134 / 2716	СС	nucleus
4 5	2e-12	48 / 633	MF	transcription factor activity, sequence-specific DNA binding
6	2e-11	32 / 333	BP	cell adhesion
7	1e-09	46 / 717	MF	calcium ion binding
8	5e-09	20 / 172	BP	homophilic cell adhesion via plasma membrane adhesion molecules
9	1e-08	41 / 643	BP	transcription, DNA-templated
10	3e-08	13 / 78	BP	axon guidance
11	3e-06	7 / 28	BP	retina morphogenesis in camera-type eye
12	5e-06	28 / 454	BP	multicellular organism development
13	8e-06	7 / 32	BP	retinal ganglion cell axon guidance
14	2e-05	28 / 491	MF	kinase activity
15	4e-05	7 / 41	MF	RNA polymerase II core promoter proximal region sequence-specific
16	6e-05	24 / 413	BP	intracellular signal transduction
17	6e-05	28 / 522	BP	phosphorylation
18	8e-05	49 / 1162	CC	plasma membrane
19	9e-05	67 / 1761	MF	metal ion binding
20	1e-04	7 / 48	BP	neural crest cell migration
21	1e-04	10 / 100	BP	peptidyl-tyrosine phosphorylation
22	2e-04	21 / 362	BP	regulation of transcription from RNA polymerase II promoter
23	2e-04	12 / 147	BP	brain development
24	3e-04	5 / 25	BP	negative chemotaxis
25	3e-04	10 / 110	MF	protein tyrosine kinase activity
26	5e-04	4 / 16	BP	primitive erythrocyte differentiation
27	5e-04	5 / 28	BP	skeletal system development
28	6e-04	6 / 44	BP	neuron development
29	6e-04	4 / 17	BP	lymph vessel development
30	6e-04	5/30	MF	transcription cofactor activity
31	7e-04	183 / 6248	CC	integral component of membrane
32	7e-04	10 / 124	MF	receptor activity
33	8e-04	34 / 800	MF	zinc ion binding
34	9e-04	4 / 19	BP	semaphorin-plexin signaling pathway
35	9e-04	4 / 19	MF	semaphorin receptor activity
36	1e-03	12 / 180	BP	dephosphorylation
37	1e-03	193 / 6723	CC	membrane
38	1e-03	15 / 257	BP	cell differentiation
39	1e-03	3 / 10	BP	optic nerve development
40	2e-03	9 / 115	MF	chromatin binding



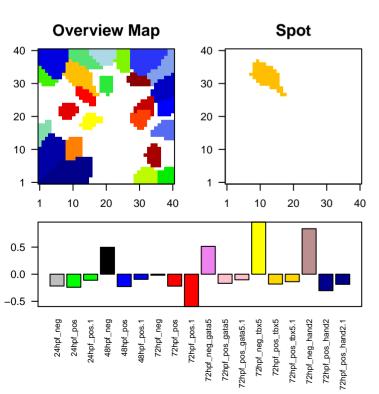
BP				СС				MF			
Rank	p-value	#in/all	Geneset	Rank	p-value	#in/all	Geneset	Rank	p-value	#in/all	Geneset
1	3e-27	100 / 1239	regulation of transcription, DNA-templated	1	1e-16	134 / 2716	nucleus	1	2e-20	98 / 1484	DNA binding
2	2e-11	32 / 333	cell adhesion	2	8e-05	49 / 1162	plasma membrane	2	7e-20	55 / 537	sequence–specific DNA binding
3	5e-09	20 / 172	homophilic cell adhesion via plasma membrane adhesion molecules	3	7e-04	183 / 6248	integral component of membrane	3	2e-12	48 / 633	transcription factor activity, sequence–specific DNA binding
4	1e-08	41 / 643	transcription, DNA-templated	4	1e-03	193 / 6723	membrane	4	1e-09	46 / 717	calcium ion binding
5	3e-08	13 / 78	axon guidance	5	2e-03	41 / 1066	intracellular	5	2e-05	28 / 491	kinase activity
6	3e-06	7 / 28	retina morphogenesis in camera-type eye	6	5e-03	3 / 15	histone acetyltransferase complex	6	4e-05	7 / 41	RNA polymerase II core promoter proximal region sequence-specific DNA bit
7	5e-06	28 / 454	multicellular organism development	7	7e-03	4/32	chromatin	7	9e-05	67 / 1761	metal ion binding
8	8e-06	7 / 32	retinal ganglion cell axon guidance	8	1e-02	9 / 153	proteinaceous extracellular matrix	8	3e-04	10 / 110	protein tyrosine kinase activity
9	6e-05	24 / 413	intracellular signal transduction	9	2e-02	29 / 809	integral component of plasma membrane	9	6e-04	5/30	transcription cofactor activity
10	6e-05	28 / 522	phosphorylation	10	2e-02	5 / 65	extracellular matrix	10	7e-04	10 / 124	receptor activity
11	1e-04	7 / 48	neural crest cell migration	11	2e-02	14/317	Golgi apparatus	11	8e-04	34 / 800	zinc ion binding
12	1e-04	10 / 100	peptidyl-tyrosine phosphorylation	12	3e-02	2/11	clathrin-coated pit	12	9e-04	4 / 19	semaphorin receptor activity
13	2e-04	21 / 362	regulation of transcription from RNA polymerase II promoter	13	3e-02	6 / 98	transcription factor complex	13	2e-03	9 / 115	chromatin binding
14	2e-04	12 / 147	brain development	14	3e-02	2/12	microtubule associated complex	14	2e-03	3/11	collagen binding
15	3e-04	5 / 25	negative chemotaxis	15	4e-02	5 / 80	postsynaptic membrane	15	2e-03	8 / 96	Rho guanyl–nucleotide exchange factor activity

#### Spot Summary: U

# metagenes = 56 # genes = 857

<r> metagenes = 0.93 <r> genes = 0.46 beta: r2= 2.85 / log p= -Inf

# samples with spot = 2 ( 11.1 %)
72hpf\_neg\_tbx5 : 1 ( 100 %)
72hpf\_neg\_hand2 : 1 ( 100 %)



#### **Spot Genelist**

19 ENSDARG000 2.2620 ENSDARG000 2.25

Rai	nk ID	max	e min e	r <del>)</del>	Syml	Description pol
1	ENSDARG000	3.21	-2.79	0.82	LOC100	)535713
2	ENSDARG000		-2.37	0.77		tubby like protein 4b [Source:ZFIN;Acc:ZDB-GENE-130530-
3	ENSDARG000	2.78	-2.13	0.59	mmp9	matrix metallopeptidase 9 [Source:ZFIN;Acc:ZDB-GENE-04
4	ENSDARG000	2.69	-2.29	0.72	Irfn5b	leucine rich repeat and fibronectin type III domain containing
5	ENSDARG000	2.67	-1.51	0.81		ryanodine receptor 2 [Source:HGNC Symbol;Acc:HGNC:104
6	ENSDARG000	2.59	-1.69	0.76	gabrd	gamma-aminobutyric acid (GABA) A receptor, delta [Source:
7	ENSDARG000	2.57	-2.36	0.91	cntnap5	bcontactin associated protein-like 5b [Source:ZFIN;Acc:ZDB-I
8	ENSDARG000	2.56	-1.87	0.89	srgap1b	SLIT-ROBO Rho GTPase activating protein 1b [Source:ZFIN
9	ENSDARG000	2.54	-4.07	0.79	gap43	growth associated protein 43 [Source:ZFIN;Acc:ZDB-GENE-
10	ENSDARG000	2.53	-1.54	0.9	stmn2a	stathmin 2a [Source:ZFIN;Acc:ZDB-GENE-041010-85]
11	ENSDARG000	2.53	-2.54	0.87	si:ch211	-នាំ <u>ទង់ខ្លាំ 3</u> -15e22.3 [Source:ZFIN;Acc:ZDB-GENE-090312-1
12	ENSDARG000	2.41	-1.7	0.85	kiaa154	9klIAA1549-like a [Source:ZFIN;Acc:ZDB-GENE-061207-55]
13	ENSDARG000	2.34	-3.11	0.87		contactin 5 [Source:ZFIN;Acc:ZDB-GENE-030131-5640]
14	ENSDARG000	2.33	-1.61	0.92	wscd1b	WSC domain containing 1b [Source:ZFIN;Acc:ZDB-GENE-0
15	ENSDARG000	2.32	-1.75	0.78		low density lipoprotein receptor-related protein 1Ba [Source:2
16	ENSDARG000	2.31	-1.37	0.83	cdh8	cadherin 8 [Source:ZFIN;Acc:ZDB-GENE-130530-597]
17	ENSDARG000	2.31	-1.42	0.72	slitrk3a	SLIT and NTRK-like family, member 3a [Source:ZFIN;Acc:ZE

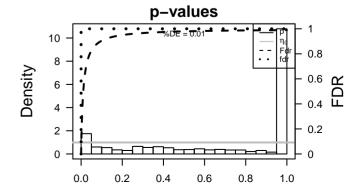
dclk1a doublecortin-like kinase 1a [Source:ZFIN;Acc:ZDB-GENE-0

si:ch211-si8t6i2.t8I-186i3.6 [Source:ZFIN:Acc:ZDB-GENE-130530-84

ptprnb protein tyrosine phosphatase, receptor type, Nb [Source:ZFIN

#### **Geneset Overrepresentation**

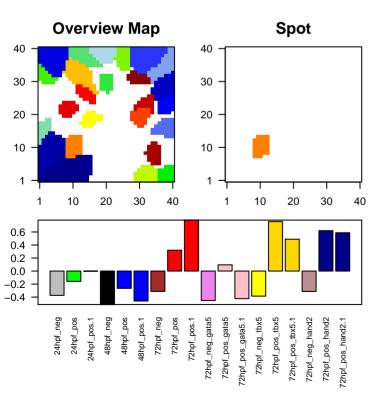
1	2e-18	317 / 6723	СС	membrane
2	3e-18	300 / 6248	CC	integral component of membrane
3	1e-16	40 / 270	MF	ion channel activity
4	2e-16	55 / 499	BP	ion transport
2 3 4 5 6 7	2e-13	84 / 1162	CC	plasma membrane
6	8e-10	17 / 86	MF	voltage-gated potassium channel activity
7	8e-10	24 / 175	BP	nervous system development
8	2e-09	16 / 79	MF	calcium channel activity
9	3e-09	20 / 130	BP	regulation of ion transmembrane transport
10	3e-09	20 / 130	MF	voltage-gated ion channel activity
11	3e-09	23 / 172	BP	homophilic cell adhesion via plasma membrane adhesion molecu
12	3e-09	18 / 106	BP	calcium ion transmembrane transport
13	8e-09	20 / 138	BP	potassium ion transport
14	1e-08	21 / 155	CC	synapse
15	1e-08	56 / 809	CC	integral component of plasma membrane
16	1e-08	17 / 103	BP	cell-cell signaling
17	2e-08	14 / 70	BP	protein homooligomerization
18	2e-08	20 / 147	BP	potassium ion transmembrane transport
19	8e-08	66 / 1084	BP	transport
20	1e-07	12/56	CC	voltage-gated potassium channel complex
21	2e-07	43 / 591	BP	transmembrane transport
22	6e-07	14/90	MF	potassium channel activity
23	3e-06	70 / 1295	BP	signal transduction
24	5e-06	27 / 333	BP	cell adhesion
25	6e-06	5/10	MF	store-operated calcium channel activity
26	8e-06	8 / 35	BP	calcium ion-regulated exocytosis of neurotransmitter
27	8e-06	11 / 70	BP	sodium ion transmembrane transport
28	1e-05	44 / 717	MF	calcium ion binding
29	1e-05	7 / 27	MF	calmodulin-dependent protein kinase activity
30	1e-05	11 / 74	CC	neuron projection
31	3e-05	5 / 13	CC	presynaptic membrane
32	3e-05	5 / 13	BP	regulation of synaptic transmission, glutamatergic
33	3e-05	17 / 176	BP	ion transmembrane transport
34	3e-05	11 / 80	CC	postsynaptic membrane
35	4e-05	27 / 375	BP	positive regulation of GTPase activity
36	4e-05	6/22	BP	regulation of ARF protein signal transduction
37	4e-05	5 / 14	BP	regulation of cytosolic calcium ion concentration
38	5e-05	19/219	CC	cell junction
39	7e-05	6 / 24	MF	ARF guanyl-nucleotide exchange factor activity
40	7e-05	9/59	MF	syntaxin binding



BP				CC				MF			
Rank	p-value	#in/all	Geneset	Rank	p-value	#in/all	Geneset	Rank	p-value	#in/all	Geneset
1	2e-16	55 / 499	ion transport	1	2e-18	317 / 6723	membrane	1	1e-16	40 / 270	ion channel activity
2	8e-10	24 / 175	nervous system development	2	3e-18	300 / 6248	integral component of membrane	2	8e-10	17 / 86	voltage-gated potassium channel activity
3	3e-09	20 / 130	regulation of ion transmembrane transport	3	2e-13	84 / 1162	plasma membrane	3	2e-09	16 / 79	calcium channel activity
4	3e-09	23 / 172	homophilic cell adhesion via plasma membrane adhesion molecules	4	1e-08	21 / 155	synapse	4	3e-09	20 / 130	voltage-gated ion channel activity
5	3e-09	18 / 106	calcium ion transmembrane transport	5	1e-08	56 / 809	integral component of plasma membrane	5	6e-07	14 / 90	potassium channel activity
6	8e-09	20 / 138	potassium ion transport	6	1e-07	12 / 56	voltage-gated potassium channel complex	6	6e-06	5/10	store-operated calcium channel activity
7	1e-08	17 / 103	cell-cell signaling	7	1e-05	11 / 74	neuron projection	7	1e-05	44 / 717	calcium ion binding
8	2e-08	14 / 70	protein homooligomerization	8	3e-05	5 / 13	presynaptic membrane	8	1e-05	7 / 27	calmodulin-dependent protein kinase activity
9	2e-08	20 / 147	potassium ion transmembrane transport	9	3e-05	11 / 80	postsynaptic membrane	9	7e-05	6 / 24	ARF guanyl-nucleotide exchange factor activity
10	8e-08	66 / 1084	transport	10	5e-05	19 / 219	cell junction	10	7e-05	9 / 59	syntaxin binding
11	2e-07	43 / 591	transmembrane transport	11	7e-04	4 / 14	postsynaptic density	11	3e-04	7 / 42	voltage-gated calcium channel activity
12	3e-06	70 / 1295	signal transduction	12	9e-04	7 / 51	presynapse	12	3e-04	9/71	calmodulin binding
13	5e-06	27 / 333	cell adhesion	13	3e-03	4/21	GABA-A receptor complex	13	3e-04	4 / 12	glutamate receptor activity
14	8e-06	8 / 35	calcium ion-regulated exocytosis of neurotransmitter	14	1e-02	3 / 15	cytoplasmic dynein complex	14	4e-04	6 / 32	extracellular-glutamate-gated ion channel activity
15	8e-06	11 / 70	sodium ion transmembrane transport	15	1e-02	3 / 17	AMPA glutamate receptor complex	15	4e-04	6 / 32	ionotropic glutamate receptor activity

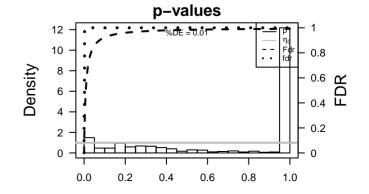
#### Spot Summary: V

```
# metagenes = 32
# genes = 474
<r> metagenes = 0.95
< r > genes = 0.46
beta: r2=3.16 / log p = -lnf
# samples with spot = 4 ( 22.2 %)
   72hpf_pos: 1 (50 %)
   72hpf_pos_hand2: 2 (100%)
```



#### **Spot Genelist**

Rar	nk ID	max	e min e	r e	Symb	Description pol	Rank	p-value	#in/all	Gei	neset
1	ENSDARG000	6.21	-1.42	0.55	scpp5	secretory calcium-binding phosphoprotein 5 [Source:ZFIN;Ac	1	6e-10	28 / 414	ВР	metabolic process
_							2	1e-06	26 / 522	MF	oxidoreductase activity
2	ENSDARG000	3.42	-1.9	0.45	pcyt1bb	phosphate cytidylyltransferase 1, choline, beta b [Source:ZFII	3	2e-06	31 / 712	BP	oxidation–reduction process
_					_		4	5e-06	156 / 6723		membrane
3	ENSDARG000	3.22	-3.48	0.83	cfh	complement factor H [Source:ZFIN;Acc:ZDB-GENE-050208	5 6	1e-05	145 / 6248 25 / 591	CC BP	integral component of membrane transmembrane transport
	=					A STATE OF THE STA	7	3e-05 2e-04	13 / 229	MF	transporter activity
4	ENSDARG000	3.14	-2.4	0.59	cyp1b1	cytochrome P450, family 1, subfamily B, polypeptide 1 [Sourc	8	6e-04	19 / 480	MF	catalytic activity
_	ENODA DOSS	0.04		0.74		natarbarra DAFO family 24 subfamily A salaratida 4 (Caus	9	8e-04	5 / 43	BP	fatty acid metabolic process
5	ENSDARG00	2.84	-3.3	0.74	сур24а і	cytochrome P450, family 24, subfamily A, polypeptide 1 [Sour	10	8e-04	9 / 145	MF	heme binding
6	ENCDARCOO!	2 02	-2.28	0.8	-:	-sight812 -264f5.2 [Source:ZFIN;Acc:ZDB-GENE-080303-2]	11	9e-04	10 / 178	MF	iron ion binding
6	ENSDARG000	2.82	-2.28	0.8	si:cn211	-26418.2-20413.2 [Source.2FIN,Acc.2DB-GENE-000303-2]	12	1e-03	3 / 13	BP	antigen processing and presentation
7	ENSDARG00	2.75	-3.08	0.6	oirob211	-প্রক্রাপ্র118-256m1.8 [Source:ZFIN;Acc:ZDB-GENE-131127-4	13	2e-03	3 / 15	BP	cardiac muscle contraction
,	ENSDARGOO	2.75	-3.00	0.6	SI.CHZ I I	-233014136-230111.0 [30010e.211N,A00.2DB-GENE-131121-4	14	2e-03	3 / 15	BP	sphingolipid biosynthetic process
8	ENSDARG000	2.67	-2.47	0.84	cyp1a	cytochrome P450, family 1, subfamily A [Source:ZFIN;Acc:ZC	15	2e-03	5 / 53	BP	chemotaxis
O	LINSDARGOON	2.07	-2.41	0.04	сурта	cytodilone i 450, lanny i, sublanny ii joodioo.21 ht,/too.22	16	2e-03	6/79	BP	cation transmembrane transport
9	ENSDARG000	2 62	-3.11	0.39	rrad	Ras-related associated with diabetes [Source:ZFIN;Acc:ZDB	17	2e-03	29 / 969	MF	hydrolase activity
9	LINSDARGOON	2.02	-0.11	0.00	IIau	rtas-related associated with diabetes [Oddroc.21 II4,7100.2DD	18	2e-03	3 / 16	MF	cation channel activity
10	ENSDARG000	2.61	-1.31	0.75	zac:921	84i:dkeyp-52c3.2 [Source:ZFIN;Acc:ZDB-GENE-110411-46]	19	2e-03	4 / 34	BP	fatty acid biosynthetic process
10	LINODAIRCOOK	2.01	-1.01	0.70	Lgo.oL	56.dats)p 5255.2 [55da55.21 http://doi.255/5/2112 http://doi.255/5/212 ht	20	3e-03	7 / 110	MF	oxidoreductase activity, acting on paired donors, with incorporation or reduc
11	ENSDARG000	2 52	-1.7	0.92	abcc2	ATP-binding cassette, sub-family C (CFTR/MRP), member 2	21	3e-03	5 / 58	BP	chemokine-mediated signaling pathway
	2110271110001	2.02	•••	0.02	abooz	· · · · · · · · · · · · · · · · · · ·	22	3e-03	5 / 59	CC	intracellular membrane-bounded organelle
12	ENSDARG00	2 49	-1.39	0.81	adamts1	3ADAM metallopeptidase with thrombospondin type 1 motif, 13	23	3e-03	5 / 60	MF	scavenger receptor activity
12	2110271110001	2.10	1.00	0.01	adamito		24	4e-03	3 / 19	BP	very long-chain fatty acid biosynthetic process
13	ENSDARG000	2.46	-2.88	0.81	fybb	FYN binding protein b [Source:ZFIN;Acc:ZDB-GENE-09120	25	4e-03	7 / 119	MF	monooxygenase activity
10					,		26	4e-03	4/39	CC	Z disc
14	ENSDARG000	2.45	-2.95	0.58	zac:172	325c:172315 [Source:ZFIN;Acc:ZDB-GENE-080220-7]	27	5e-03	5 / 65	BP	sodium ion transport
1-7	2110271110001				3.	,	28	5e-03	12 / 297	BP	immune response
15	ENSDARG000	2.42	-1.3	0.84	serpind1	serpin peptidase inhibitor, clade D (heparin cofactor), membe	29 30	6e-03	3 / 22 9 / 194	MF	chemokine receptor activity lipid metabolic process
					·	( ), , , , , , , , , , , , , , , , , , ,	30 31	6e-03 6e-03	4 / 44	BP BP	skeletal muscle tissue development
16	ENSDARG000	2.34	-1.1	0.4		si:cabz01036006.1 [Source:ZFIN;Acc:ZDB-GENE-160113-1	32	7e-03	5/70	BP	receptor-mediated endocytosis
. •							33	8e-03	4 / 47	CC	integral component of endoplasmic reticulum membrane
17	ENSDARG000	2.29	-3.57	0.33	hivep2b	human immunodeficiency virus type I enhancer binding protein	34	1e-02	3/27	MF	oxidoreductase activity, acting on paired donors, with incorporation or reduc
							35	1e-02	6 / 109	BP	apoptotic process
18	ENSDARG000	2.26	-1.47	0.79	mybpc1	myosin binding protein C, slow type [Source:ZFIN;Acc:ZDB-C	36	1e-02	3 / 28	BP	anion transmembrane transport
							37	1e-02	2/10	MF	hydrolase activity, acting on carbon-nitrogen (but not peptide) bonds, in line
19	ENSDARG000	2.23	-1.09	0.84	agxta	alanine-glyoxylate aminotransferase a [Source:ZFIN;Acc:ZDI	38	1e-02	2/10	CC	phosphatidylinositol 3-kinase complex
							39	1e-02	2/10	BP	receptor clustering
20	ENSDARG000	2.21	-1.17	0.58	rltgr	RAMP-like triterpene glycoside receptor [Source:ZFIN;Acc:Z	40	1e-02	2/10	BP	response to methylmercury



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

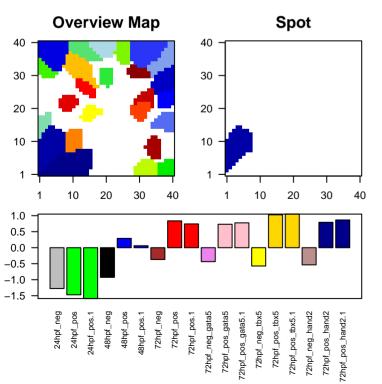
### Spot Summary: W

# metagenes = 74
# genes = 1173

<r> metagenes = 0.93

beta: r2= 13.28 / log p= -Inf

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

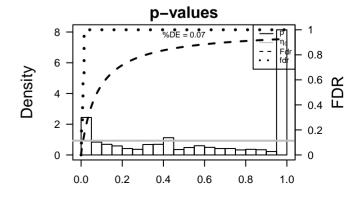


#### **Spot Genelist**

Rar	nk ID	max	e min e	r e	Symb	Description pol	
1	ENSDARG000	5.99	-1.86	0.39		si:ch211-220f21.2 [Source:ZFIN;Acc:ZDB-GENE-160113-1	
2	ENSDARG000	4.9	-4.2	0.85	zgc:112	265c:112265 [Source:ZFIN;Acc:ZDB-GENE-050626-133]	
3	ENSDARG000	4.89	-6.08	0.53		si:dkey-9l20.3 [Source:ZFIN;Acc:ZDB-GENE-090313-369]	
4	ENSDARG000	4.84	-5.75	0.92	serpina1	Ilserine (or cysteine) proteinase inhibitor, clade A (alpha-1 anti	
5	ENSDARG000	4.78	-3.37	0.89	c3a.3	complement component c3a, duplicate 3 [Source:ZFIN;Acc:Z	
6	ENSDARG000	4.72	-2.88	0.48	si:ch211	-នាំ <b>រវាក់និវិច.</b> ៩ 17m20.5 [Source:ZFIN;Acc:ZDB-GENE-030131-	
7	ENSDARG000	4.69	-4.69	0.8	agxtb	alanine-glyoxylate aminotransferase b [Source:ZFIN;Acc:ZDI	
8	ENSDARG000	4.67	-4.1	0.88	plg	plasminogen [Source:ZFIN;Acc:ZDB-GENE-030131-1411]	
9	ENSDARG000	4.58	-3.93	0.85	fga	fibrinogen alpha chain [Source:ZFIN;Acc:ZDB-GENE-03101	
10	ENSDARG000	4.58	-2.18	0.63	zgc:111	98gc:111983 [Source:ZFIN;Acc:ZDB-GENE-050417-335]	
11	ENSDARG000	4.57	-5.01	0.92	serpina1	I serpin peptidase inhibitor, clade A (alpha-1 antiproteinase, ar	
12	ENSDARG000	4.53	-4.41	0.92	fgb	fibrinogen beta chain [Source:ZFIN;Acc:ZDB-GENE-030131	
13	ENSDARG000	4.36	-3.88	0.92	pck1	phosphoenolpyruvate carboxykinase 1 (soluble) [Source:ZFIN	
14	ENSDARG000	4.3	-4.54	0.83	tnfb	tumor necrosis factor b (TNF superfamily, member 2) [Source	
15	ENSDARG000	4.29	-6.23	0.94	apoa1b	apolipoprotein A-lb [Source:ZFIN;Acc:ZDB-GENE-050302-	
16	ENSDARG000	4.28	-3.75	0.88	cfb	complement factor B [Source:ZFIN;Acc:ZDB-GENE-980526-	
17	ENSDARG000	4.27	-3.95	0.78	itih2	inter-alpha-trypsin inhibitor heavy chain 2 [Source:ZFIN;Acc:	
18	ENSDARG000	4.27	-3.36	0.77	c3a.2	complement component c3a, duplicate 2 [Source:ZFIN;Acc:Z	
19	ENSDARG000	4.25	-3.15	0.43	si:ch211	-রাপ্তাপ্তর্যু –239b22.1 [Source:ZFIN;Acc:ZDB-GENE-131119-12	
20	ENSDARG000	4.22	-4.69	0.96	fgg	fibrinogen gamma chain [Source:ZFIN;Acc:ZDB-GENE-0404	

#### **Geneset Overrepresentation**

1	6e-25	97 / 712	BP	oxidation-reduction process
2	5e-24	80 / 522	MF	oxidoreductase activity
2 3 4 5	7e-16	29 / 109	BP	negative regulation of endopeptidase activity
4	2e-11	14/33	MF	endopeptidase inhibitor activity
5	4e-10	8 / 10	CC	chylomicron
6	1e-09	10 / 19	BP	gluconeogenesis
6 7	3e-09	32 / 231	MF	actin binding
8	1e-08	10 / 23	CC	troponin complex
9	2e-08	7 / 10	CC	high-density lipoprotein particle
10	2e-08	7 / 10	BP	triglyceride catabolic process
11	6e-08	7 / 11	BP	cholesterol homeostasis
12	1e-07	25 / 178	MF	iron ion binding
13	1e-07	42 / 414	BP	metabolic process
14	1e-07	61 / 717	MF	calcium ion binding
15	1e-07	7 / 12	BP	cholesterol biosynthetic process
16	2e-07	8 / 17	CC	blood microparticle
17	2e-07	46 / 480	MF	catalytic activity
18	2e-07	9 / 23	BP	lipoprotein metabolic process
19	3e-07	7 / 13	BP	cholesterol efflux
20	3e-07	7 / 13	BP	regulation of muscle contraction
21	4e-07	9 / 25	BP	cellular response to estrogen stimulus
22	7e-07	40 / 410	CC	mitochondrion
23	1e-06	14 / 70	CC	myosin complex
24	2e-06	7 / 16	MF	acyl-CoA dehydrogenase activity
25	2e-06	6/11	BP	cellular response to nitrogen starvation
26	3e-06	7 / 17	MF	cholesterol binding
27	3e-06	7 / 17	MF	cholesterol transporter activity
28	4e-06	8 / 24	CC	respiratory chain
29	6e-06	9 / 33	MF	oxidoreductase activity, acting on the CH-CH group of donors
30	7e-06	6 / 13	BP	iron ion transport
31	7e-06	7 / 19	BP	vacuolar transport
32	7e-06	16 / 105	MF	lipid binding
33	2e-05	7 / 21	MF	NADH dehydrogenase (ubiquinone) activity
34	2e-05	11 / 57	MF	flavin adenine dinucleotide binding
35	2e-05	109 / 1761	MF	metal ion binding
36	3e-05	41 / 500	CC	extracellular space
37	4e-05	7 / 24	BP	cellular iron ion homeostasis
38	5e-05	19 / 161	CC	mitochondrial inner membrane
39	5e-05	5 / 11	MF	ferric iron binding
40	6e-05	8 / 34	BP	glycolytic process



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

### Spot Summary: X

# metagenes = 22 # genes = 526

<r> metagenes = 0.94 <r> genes = 0.45 beta: r2= 0.24 / log p= -1.4

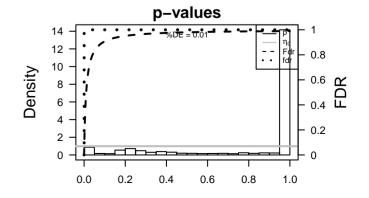
# samples with spot = 0 ( 0 %)

#### **Overview Map** Spot 30 20 20 10 10 30 10 20 20 30 10 0.4 0.3 0.2 0.1 0.0 -0.1 48hpf\_pos.1 72hpf\_neg 72hpf\_neg\_gata5 72hpf\_pos\_gata5 48hpf\_pos 72hpf\_pos 72hpf\_pos.1 72hpf\_neg\_tbx5 72hpf\_pos\_hand2 72hpf\_pos\_gata5.1

# **Spot Genelist**

Ra	nk ID	max	e min e	r e	Symb	Description ool	Rank	p-value	#in/all	Ge	neset
1	ENSDARG00	1.94	-2.11	0.53		Small nucleolar RNA SNORA73 family [Source:RFAM;Acc:RF	1	7e-11	43 / 751	MF	G-protei
2	ENSDARG000	1.76	-1.78	0.56		Small nucleolar RNA SNORA73 family [Source:RFAM;Acc:RF	2	3e-10 3e-10	39 / 666 45 / 853	MF BP	signal tra G-protei
_						,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,	4	2e-06	49 / 1295	BP	signal tra
3	ENSDARG000	1.54	-1.51	0.44		Small nucleolar RNA SNORA81 [Source:RFAM;Acc:RF01241	5	2e-06	11 / 100	BP	neuroper
U	21102/1110001					,	6	5e-06	12 / 130	BP	regulation
4	ENSDARG000	1.49	-1	0.43	drd1b	dopamine receptor D1b [Source:ZFIN;Acc:ZDB-GENE-0705	7	5e-06	12 / 130	MF	voltage-
7	2.102/110001		·	0.10	GIG ID		8	2e-05	5 / 19	BP	feeding b
5	ENSDARG000	1.3	-0.84	0.75	rac3b	ras-related C3 botulinum toxin substrate 3b (rho family, small	9	4e-05	9 / 90	MF	potassiur
J	LINODAIRCOOK	1.5	-0.04	0.70	14000	Tab Totalog de Betamam toxim cabellate eb (me lamin), emain	10	6e-05	23 / 499	BP	ion trans
6	ENSDARG000	1 28	-1.54	0.57		Small Cajal body specific RNA 13 [Source:RFAM;Acc:RF002:	11	7e-05	9 / 95	MF	hormone
O	ENSDARGOO	1.20	-1.54	0.57		Official Oujal body Specific NAV 10 [Obdite: N. 7400. N. 602.	12	9e-05	11 / 147	BP	potassiu
7	ENCDARCOO	4.40	-1.06	0.57	-:	3si3392627334392o20.1 [Source:ZFIN;Acc:ZDB-GENE-091204-	13	1e-04	4 / 14	BP	carbohyo
7	ENSDARG000	1.10	-1.00	0.57	SI.CITIO7	3939202017392020.1 [3001ce.21 IIV,Acc.2DD-GEIVE-091204-	14	2e-04	8 / 86	BP	chemical
0	ENODA DOSS		4.00	0.04	-II 4h-	diana lana (Barandila) baranta arranistad arranis Ab (Car	15	3e-04	10 / 138	BP	potassiur
8	ENSDARG000	1.14	-1.33	0.61	uiyap4b	discs, large (Drosophila) homolog-associated protein 4b [Sou	16	3e-04	4 / 18	BP	stabilizat
^	=======================================		0.00	0.05	at all ac	060445-0 060445-0 [C75]N.A7DD, CENE 004405-67	17	4e-04	4 / 19	MF	potassiu
9	ENSDARG000	1.14	-0.68	0.65	si:ukey-	2633ft6y2-263f15.2 [Source:ZFIN;Acc:ZDB-GENE-081105-67	18	4e-04	5 / 34	MF	G-protei
							19	4e-04	4 / 20	BP	response
10	ENSDARG000	1.14	-0.49	0.74		gamma-aminobutyric acid (GABA) A receptor, alpha 3 [Source	20	7e-04	3 / 10	BP	tachykini
							21	8e-04	24 / 634	CC	extracellu
11	ENSDARG000	1.12	-1.01	0.5		Small nucleolar RNA SNORA23 [Source:RFAM;Acc:RF00319	22	1e-03	28 / 809	CC	integral o
							23	1e-03	3 / 12	MF	neuroper
12	ENSDARG00	1.12	-0.51	0.67		si:dkey-192j17.1 [Source:ZFIN;Acc:ZDB-GENE-091113-38]	24	2e-03	6 / 68	MF	sulfotrans
							25	2e-03	4 / 28	BP	cellular re
13	ENSDARG000	1.11	-0.3	0.84		RIMS binding protein 2 [Source:ZFIN;Acc:ZDB-GENE-0407;	26	2e-03	4 / 28	BP	G-protei
							27	2e-03	4/31	MF	inward re
14	ENSDARG000	1.08	-1.07	0.54	pvalb7	parvalbumin 7 [Source:ZFIN;Acc:ZDB-GENE-040718-285]	28	3e-03	4/32	MF	neurotrai
							29	3e-03	3 / 17	CC	AMPA gli
15	ENSDARG000	1.05	-0.89	0.53	ybx1	Y box binding protein 1 [Source:ZFIN;Acc:ZDB-GENE-0006;	30	5e-03	4 / 37	MF	peptide b
							31	5e-03	3 / 19	BP	transmis
16	ENSDARG000	1.05	-1.36	0.47	palm2	paralemmin 2 [Source:ZFIN;Acc:ZDB-GENE-050208-62]	32	5e-03	6 / 86	MF	voltage-
							33	5e-03	140 / 6248	CC	integral o
17	ENSDARG000	1.05	-0.76	0.61	bach2a	BTB and CNC homology 1, basic leucine zipper transcription	34	6e-03	32 / 1084	BP	transport
							35	6e-03	3 / 21	MF	substrate
18	ENSDARG000	1.04	-1.7	0.41	b4galt5	UDP-Gal:betaGlcNAc beta 1,4- galactosyltransferase, polyp	36	7e-03	3 / 22	MF	neuroper
							37	1e-02	4 / 46	MF	trace-an
19	ENSDARG000	1.03	-0.87	0.44	bbc3	BCL2 binding component 3 [Source:ZFIN;Acc:ZDB-GENE-0	38	1e-02	3 / 25	MF	GABA-A
							39	1e-02	8 / 164	BP	carbohyo
20	ENSDARG000	1.02	-0.37	0.79			40	1e-02	11 / 270	MF	ion chan

1	7e-11	43 / 751	MF	G-protein coupled receptor activity
2	3e-10	39 / 666	MF	signal transducer activity
3	3e-10	45 / 853	BP	G-protein coupled receptor signaling pathway
4	2e-06	49 / 1295	BP	signal transduction
5	2e-06	11 / 100	BP	neuropeptide signaling pathway
6	5e-06	12 / 130	BP	regulation of ion transmembrane transport
<del>7</del>	5e-06	12 / 130	MF	voltage-gated ion channel activity
8	2e-05	5 / 19	BP	feeding behavior
9	4e-05	9 / 90	MF	potassium channel activity
10	6e-05	23 / 499	BP	ion transport
11	7e-05	9 / 95	MF	hormone activity
12	9e-05	11 / 147	BP	potassium ion transmembrane transport
13	1e-04	4 / 14	BP	carbohydrate biosynthetic process
14	2e-04	8 / 86	BP	chemical synaptic transmission
15	3e-04	10 / 138	BP	potassium ion transport
16	3e-04	4 / 18	BP	stabilization of membrane potential
17	4e-04	4 / 19	MF	potassium ion leak channel activity
18	4e-04	5 / 34	MF	G-protein coupled serotonin receptor activity
19	4e-04	4 / 20	BP	response to peptide
20	7e-04	3 / 10	BP	tachykinin receptor signaling pathway
21	8e-04	24 / 634	CC	extracellular region
22	1e-03	28 / 809	CC	integral component of plasma membrane
23	1e-03	3 / 12	MF	neuropeptide receptor activity
24	2e-03	6 / 68	MF	sulfotransferase activity
25	2e-03	4 / 28	BP	cellular response to hormone stimulus
26	2e-03	4 / 28	BP	G-protein coupled serotonin receptor signaling pathway
27	2e-03	4 / 31	MF	inward rectifier potassium channel activity
28	3e-03	4 / 32	MF	neurotransmitter receptor activity
29	3e-03	3 / 17	CC	AMPA glutamate receptor complex
30	5e-03	4 / 37	MF	peptide binding
31	5e-03	3 / 19	BP	transmission of nerve impulse
32	5e-03	6 / 86	MF	voltage-gated potassium channel activity
33	5e-03	140 / 6248	CC	integral component of membrane
34	6e-03	32 / 1084	BP	transport
35	6e-03	3 / 21	MF	substrate-specific transmembrane transporter activity
36	7e-03	3 / 22	MF	neuropeptide hormone activity
37	1e-02	4 / 46	MF	trace-amine receptor activity
38	1e-02	3 / 25	MF	GABA-A receptor activity
39	1e-02	8 / 164	BP	carbohydrate metabolic process
40	1e-02	11 / 270	MF	ion channel activity



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

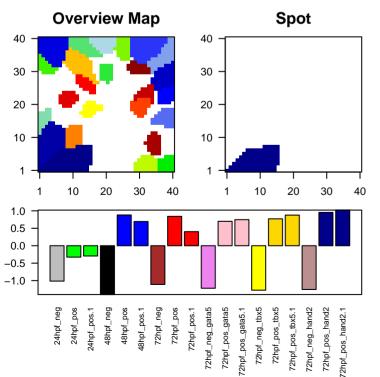
### Spot Summary: Y

# metagenes = 94
# genes = 1577

<r> metagenes = 0.93

beta: r2= 14.91 / log p= -Inf

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



#### **Spot Genelist**

Rar	nk ID	max	e min e	r <del>)</del>	Symbo	Description ol
1	ENSDARG000	5.16	-6.13	0.91	oacyl	O-acyltransferase like [Source:ZFIN;Acc:ZDB-GENE-09071
2	ENSDARG000	4.98	-7.11	0.97	wu:fc46h1	wgu:fc46h12 [Source:ZFIN;Acc:ZDB-GENE-030131-3611]
3	ENSDARG000	4.88	-6.93	0.97	si:dkey-2	stidke:2-251i10.2 [Source:ZFIN;Acc:ZDB-GENE-050506-10:
4	ENSDARG000	4.72	-6.07	0.81	vmhcl	ventricular myosin heavy chain-like [Source:ZFIN;Acc:ZDB-C
5	ENSDARG000	4.71	-7.81	0.97	gch2	GTP cyclohydrolase 2 [Source:ZFIN;Acc:ZDB-GENE-00120
6	ENSDARG000	4.53	-5.75	0.92	:	si:dkey-73n8.3 [Source:ZFIN;Acc:ZDB-GENE-141219-27]
7	ENSDARG000	4.51	-4.97	0.91	zgc:11314	<b>1g</b> c:113142 [Source:ZFIN;Acc:ZDB–GENE–050220–2]
8	ENSDARG000	4.47	-7.23	0.92	xdh :	xanthine dehydrogenase [Source:ZFIN;Acc:ZDB-GENE-070
9	ENSDARG000	4.45	-2.24	0.71	plxdc1	plexin domain containing 1 [Source:ZFIN;Acc:ZDB-GENE-08
10	ENSDARG000	4.44	-6.92	0.98	zgc:1621	āģc:162150 [Source:ZFIN;Acc:ZDB-GENE-070410-23]
11	ENSDARG000	4.42	-4.7	0.8	tnnc1a	troponin C type 1a (slow) [Source:ZFIN;Acc:ZDB-GENE-030
12	ENSDARG000	4.4	-6.51	0.94	bscl2l	Bernardinelli-Seip congenital lipodystrophy 2, like [Source:ZF
13	ENSDARG000	4.4	-5.48	0.95	uraha	urate (5-hydroxyiso-) hydrolase a [Source:ZFIN;Acc:ZDB-G
14	ENSDARG000	4.39	-5.45	0.91	sprb :	sepiapterin reductase b [Source:ZFIN;Acc:ZDB-GENE-0707
15	ENSDARG000	4.38	-5.44	0.96		6-pyruvoyltetrahydropterin synthase [Source:ZFIN;Acc:ZDB-
16	ENSDARG000	4.34	-7.46	0.95	slc22a7a	solute carrier family 22 (organic anion transporter), member 7
17	ENSDARG000	4.32	-6.44	0.88	cmlc1	cardiac myosin light chain-1 [Source:ZFIN;Acc:ZDB-GENE-
18	ENSDARG000	4.31	-6.34	0.97	slc2a15a	solute carrier family 2 (facilitated glucose transporter), member
19	ENSDARG000	4.29	-4.58	0.93	cyb561a3	tbytochrome b561 family, member A3b [Source:ZFIN;Acc:ZDB
20	ENSDARG000	4.29	-5.32	0.89	zgc:15303	agc:153031 [Source:ZFIN;Acc:ZDB-GENE-060929-1190]

Description

#### **Geneset Overrepresentation**

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

