

#### Spot Summary: A

# metagenes = 99 # genes = 1621

<r> metagenes = 0.83

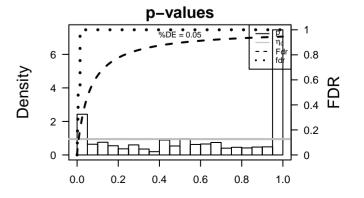
beta: r2= 2.76 / log p= -Inf

# samples with spot = 0 ( 0 %)

#### **Overview Map** Spot 30 30 20 20 10 -10 20 30 40 20 30 10 0.6 0.4 0.0 -0.2 -0.4 72hpf\_neg\_gata5 72hpf\_pos\_gata5 48hpf\_pos.1 72hpf\_neg 72hpf\_pos.1 48hpf\_pos 72hpf\_pos 72hpf\_pos\_gata5.1 72hpf\_neg\_tbx5 72hpf\_pos\_hand2

## **Spot Genelist**

Rai	nk ID	max	e min e	r e	Symi	Description pol	Rank	p-value	#in/all	Ge	neset
1	ENSDARG000	4.38	-2.85	0.68	col28a2	acollagen, type XXVIII, alpha 2a [Source:ZFIN;Acc:ZDB-GENI	1	5e-42	332 / 2716	СС	nucleus
							2	2e-38	266 / 2030	MF	nucleic acid binding
2	ENSDARG000	3.19	-3.3	0.52	plp1a	proteolipid protein 1a [Source:ZFIN;Acc:ZDB-GENE-001202	3	5e-32	204 / 1484	MF	DNA binding
							4	1e-30	179 / 1239	BP	regulation of transcription, DNA-templated
3	ENSDARG000	3.06	-1.7	0.69	col7a1	collagen, type VII, alpha 1 [Source:ZFIN;Acc:ZDB-GENE-03	5	2e-18	94 / 608	MF	RNA binding
							6	1e-17	77 / 454	BP	multicellular organism development
4	ENSDARG000	2.94	-1.72	0.75	sox19a	SRY (sex determining region Y)-box 19a [Source:ZFIN;Acc:Z	7	7e-14	32 / 117	BP	Wnt signaling pathway
							8	9e-10	68 / 537	MF	sequence–specific DNA binding
5	ENSDARG000	2.94	-1.34	0.75	nes	Nestin [Source:UniProtKB/Swiss-Prot;Acc:P86839]	9	1e-07	23 / 115	MF	chromatin binding
-							10	6e-07	68 / 633	MF	transcription factor activity, sequence-specific DNA binding
6	ENSDARG000	2.91	-2.1	0.79	dld	deltaD [Source:ZFIN;Acc:ZDB-GENE-990415-47]	11	9e-07	13 / 45	BP	Notch signaling pathway
-							12	1e-06	9 / 21	BP	regulation of canonical Wnt signaling pathway
7	ENSDARG000	2.85	-1.19	0.84	zic2b	zic family member 2 (odd-paired homolog, Drosophila) b [Soi	13	2e-06	14 / 55	BP	neuron differentiation
•							14	2e-06	148 / 1761	MF	metal ion binding
8	ENSDARG000	2.75	-1.34	0.64		oligodendrocyte transcription factor 3 [Source:ZFIN;Acc:ZDB-	15	2e-06	79 / 800	MF	zinc ion binding
Ü							16	3e-06	12 / 42	BP	convergent extension
9	ENSDARG000	2.65	-1.55	0.48			17	5e-06	7 / 14	BP	regulation of Notch signaling pathway
J	2.102/110001						18	6e-06	9 / 25	MF	frizzled binding
10	ENSDARG000	2 64	-1.85	0.6	sp8b	sp8 transcription factor b [Source:ZFIN;Acc:ZDB-GENE-030	19	8e-06	65 / 643	BP	transcription, DNA-templated
10	2.102/110001	2.01	1.00	0.0			20	1e-05	8 / 21	BP	negative regulation of canonical Wnt signaling pathway
11	ENSDARG000	2.48	-1.49	0.5			21	1e-05	22 / 138	BP	cilium assembly
	LINODAIRCOOK	2.40	-1.45	0.0			22	1e-05	42 / 362	BP	regulation of transcription from RNA polymerase II promoter
12	ENSDARG000	2.47	-1.28	0.76	igsf9a	immunoglobulin superfamily, member 9a [Source:ZFIN;Acc:Zl	23	1e-05	33 / 257	BP	cell differentiation
12	ENSDARGOO	2.47	-1.20	0.76	igaiau	initialogiobalii superiariliy, member sa [oodree.21 in,700.21	24	2e-05	12 / 50	BP	pronephros development
13	ENSDARG000	2.46	-1.7	0.58		si:ch211-193l2.3 [Source:ZFIN;Acc:ZDB-GENE-141216-14	25	3e-05	9 / 30	MF	transcription cofactor activity
13	ENSDARGOO	2.40	-1.7	0.36		Si.Cit211-19312.3 [GOUICE.ZI IIN,ACC.ZDD-GEINE-141210-14	26	4e-05	26 / 190	MF	protein dimerization activity
14	ENCDAD COO	2 20	-2.26	0.4	1.0040	straign and enhancer of split-related 15, tandem duplicate 1 [S	27	4e-05	9 / 31	MF	histone–lysine N–methyltransferase activity
14	ENSDARG000	2.30	-2.20	0.4	LOCIO	150 and a string of the string	28	4e-05	6 / 13	BP	neural retina development
15	ENCDAD COO	0.00	4.00	0.0	h40	hairy-related 13 [Source:ZFIN;Acc:ZDB-GENE-050228-1]	29	4e-05	6 / 13	BP	ventral spinal cord interneuron differentiation
15	ENSDARG000	2.38	-1.82	0.6	her13	naily-related 13 [Source.ZFIN,Acc.ZDB-GENE-030226-1]	30	5e-05	8 / 25	BP	cell fate commitment
40	ENODA DOSS	0.07	4.04	0.7		paired box 3a [Source:ZFIN;Acc:ZDB-GENE-980526-52]	31	7e-05	6 / 14	BP	ATP-dependent chromatin remodeling
16	ENSDARG000	2.37	-1.24	0.7	pax3a	paired box 3a [Source:ZFIN;Acc:ZDB-GENE-980526-52]	32	1e-04	28 / 229	CC	chromosome
47	=======================================	0.00	0.00	0.55		alastic accordibations for a 22 (Course 75th) Acc 700 CENE	33	2e-04	9 / 37	MF	nucleosomal DNA binding
17	ENSDARG000	2.36	-3.36	0.55	emilin2a	a elastin microfibril interfacer 2a [Source:ZFIN;Acc:ZDB-GENE	34	2e-04	5 / 11	BP	regulation of cell morphogenesis
40							35	3e-04	14 / 83	BP	embryonic viscerocranium morphogenesis
18	ENSDARG000	2.36	-1.06	0.91	notch3	notch 3 [Source:ZFIN;Acc:ZDB-GENE-000329-5]	36	3e-04	7 / 24	BP	histone lysine methylation
							37	3e-04	12 / 66	MF	thiol-dependent ubiquitinyl hydrolase activity
19	ENSDARG000	2.3	-1.44	0.7	sox19b	SRY (sex determining region Y)-box 19b [Source:ZFIN;Acc:Z	38	4e-04	5 / 12	BP	regulation of neurogenesis
							39	4e-04	8 / 32	CC	chromatin
20	ENSDARG000	2.3	-1.78	0.62	tp63	tumor protein p63 [Source:ZFIN;Acc:ZDB-GENE-030819-1]	40	4e-04	6 / 18	BP	post–anal tail morphogenesis



ВР				СС				MF			
Rank	p-value	#in/all	Geneset	Rank	p-value	#in/all	Geneset	Rank	p-value	#in/all	Geneset
1	1e-30	179 / 1239	regulation of transcription, DNA-templated	1	5e-42	332 / 2716	nucleus	1	2e-38	266 / 2030	nucleic acid binding
2	1e-17	77 / 454	multicellular organism development	2	1e-04	28 / 229	chromosome	2	5e-32	204 / 1484	DNA binding
3	7e-14	32 / 117	Wnt signaling pathway	3	4e-04	8/32	chromatin	3	2e-18	94 / 608	RNA binding
4	9e-07	13 / 45	Notch signaling pathway	4	1e-03	6 / 22	dynein complex	4	9e-10	68 / 537	sequence-specific DNA binding
5	1e-06	9/21	regulation of canonical Wnt signaling pathway	5	2e-03	20 / 168	nucleosome	5	1e-07	23 / 115	chromatin binding
6	2e-06	14 / 55	neuron differentiation	6	2e-03	5 / 17	U2-type prespliceosome	6	6e-07	68 / 633	transcription factor activity, sequence–specific DNA binding
7	3e-06	12 / 42	convergent extension	7	6e-03	11 / 80	centrosome	7	2e-06	148 / 1761	metal ion binding
8	5e-06	7 / 14	regulation of Notch signaling pathway	8	9e-03	4 / 15	intrinsic component of the cytoplasmic side of the plasma membrane	8	2e-06	79 / 800	zinc ion binding
9	8e-06	65 / 643	transcription, DNA-templated	9	1e-02	10 / 76	cilium	9	6e-06	9 / 25	frizzled binding
10	1e-05	8 / 21	negative regulation of canonical Wnt signaling pathway	10	2e-02	16 / 153	proteinaceous extracellular matrix	10	3e-05	9/30	transcription cofactor activity
11	1e-05	22 / 138	cilium assembly	11	2e-02	9/70	cell projection	11	4e-05	26 / 190	protein dimerization activity
12	1e-05	42 / 362	regulation of transcription from RNA polymerase II promoter	12	2e-02	4 / 19	U1 snRNP	12	4e-05	9 / 31	histone-lysine N-methyltransferase activity
13	1e-05	33 / 257	cell differentiation	13	2e-02	7 / 49	nucleoplasm	13	2e-04	9 / 37	nucleosomal DNA binding
14	2e-05	12 / 50	pronephros development	14	2e-02	5 / 29	integrin complex	14	3e-04	12 / 66	thiol-dependent ubiquitinyl hydrolase activity
15	4e-05	6 / 13	neural retina development	15	3e-02	4/21	nuclear membrane	15	5e-04	9 / 42	histone binding

#### Spot Summary: B

# metagenes = 58 # genes = 1079

<r> metagenes = 0.88

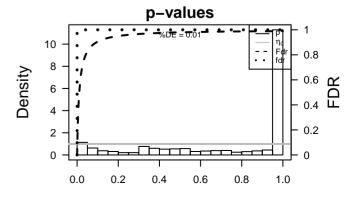
beta: r2= 3.46 / log p= -Inf

# samples with spot = 0 ( 0 %)

#### **Overview Map** Spot 30 30 20 20 10 -10 30 30 10 20 40 10 20 40 0.0 -0.5-1.0 48hpf\_pos.1 72hpf\_neg 72hpf\_pos 72hpf\_neg\_gata5 72hpf\_pos\_gata5 72hpf\_pos.1 48hpf\_pos 72hpf\_pos\_hand2 72hpf\_pos\_gata5.1

## Spot Genelist

Ra	nk	max	е	r		Description		Rank	p-value	#in/all	Gei	neset
	ID		min e	е	Syml	bol						
1	ENSDARG000	8.23	-1.2	0.5	ednrab	endothelin receptor type Ab [Source:ZFIN;Acc:ZDB-G	GENE-C	1	2e-67	254 / 2030	MF	nucleic acid binding
•								2	6e-20	39 / 168	CC	nucleosome
2	ENSDARG000	5.91	-1.27	0.58	si:dkey-	-26igtkey-26g8.5 [Source:ZFIN;Acc:ZDB-GENE-12121	14–19]	3	6e-19	44 / 229	CC	chromosome
_					-		-	4	6e-18	43 / 232	MF	protein heterodimerization activity
3	ENSDARG000	5.48	-1.21	0.55	zgc:174	115gc:174153 [Source:ZFIN;Acc:ZDB-GENE-080215-7	7]	5	1e-15	15 / 25	BP	membrane disruption in other organism
•								6	4e-14	15/30	BP	defense response to Gram-positive bacterium
4	ENSDARG000	5.31	-1.61	0.55	MGC17	r4stdkey-26g8.4 [Source:ZFIN;Acc:ZDB-GENE-12121	14-36]	7	5e-14	181 / 2716	CC	nucleus
•							•	8	4e-11	109 / 1484	MF	DNA binding
5	ENSDARG000	2.7	-1.67	0.65	ucp3	uncoupling protein 3 [Source:ZFIN;Acc:ZDB-GENE-0	040426-	9	2e-10	13 / 34	BP	chromatin silencing
•								10	4e-10	14 / 43	BP	DNA-templated transcription, initiation
6	ENSDARG000	2.65	-1.35	0.65	si:ch73-	-364th/784364h19.1 [Source:ZFIN;Acc:ZDB-GENE-031	1010-4	11	3e-09	14 / 49	CC	nuclear chromatin
·						•		12	9e-07	49 / 608	MF	RNA binding
7	ENSDARG000	2.63	-0.64	0.6	si:dkev-	-269ilk@y-239j18.2 [Source:ZFIN;Acc:ZDB-GENE-1212	214-52	13	8e-06	17 / 128	BP	innate immune response
'					,	, , . , ,		14	1e-05	10 / 49	MF	RNA-directed DNA polymerase activity
8	ENSDARG000	2.52	-1.92	0.74	zac:163	80440stone 1, H4, like [Source:ZFIN;Acc:ZDB-GENE-070	0927-1(	15	4e-05	15 / 117	BP	nucleosome assembly
O					3			16	7e-05	9 / 48	BP	RNA-dependent DNA biosynthetic process
9	ENSDARG000	2.5	-3.45	0.71		U2 spliceosomal RNA [Source:RFAM;Acc:RF00004]		17	1e-04	10 / 61	MF	ubiquitin protein ligase binding
J	2.102/000					, , , , , , , , , , , , , , , , , , , ,		18	1e-04	5 / 14	CC	U12-type spliceosomal complex
10	ENSDARG000	2 42	-4.01	0.91	ssbp3a	single stranded DNA binding protein 3a [Source:ZFIN;	:Acc:ZD	19	2e-04	12/91	BP	cellular response to DNA damage stimulus
10	2.102/000			0.01			,	20	2e-04	16 / 148	BP	DNA repair
11	ENSDARG000	24	-3.98	0.75	si:dkev-	-28iadkeg-223a13.22 [Source:ZFIN;Acc:ZDB-GENE-160	0113-78	21	2e-04	11 / 79	BP	mRNA splicing, via spliceosome
	LINODAIRCOOK	2.7	-0.50	0.70	onancy	200000121200101212100012011117,10012000 02112 100	,,,,,,,,,	22	3e-04	6 / 25	MF	histone acetyltransferase activity
12	ENSDARG000	2.34	-2.31	0.91	tonsl	tonsoku-like, DNA repair protein [Source:ZFIN;Acc:ZI	DB_GEI	23	3e-04	5 / 17	CC	U2-type prespliceosome
12	LINODAIRCOOK	2.04	-2.01	0.51	torisi	toriosita iiito, 211/110paii protoiii (200100121 iiti, 100122	JD 02.	24	5e-04	5 / 18	CC	U2 snRNP
13	ENSDARG000	23	-1.26	0.39		si:dkey-240n22.8 [Source:ZFIN;Acc:ZDB-GENE-110	0914-15	25	6e-04	5 / 19	CC	U1 snRNP
13	LINODAIRCOOK	2.0	-1.20	0.00		cliately 2 to 122.0 (course.21 my, too.255 C2.12 Tro	,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,	26	1e-03	5 / 21	CC	spindle pole
14	ENSDARG000	2 27	-3.43	0.96	stil	scl/tal1 interrupting locus [Source:ZFIN;Acc:ZDB-GEN	NF-020	27	1e-03	4 / 13	CC	U5 snRNP
14	LINSDAIRGOON	2.27	-0.40	0.50	Jui	contain morraphing local [Scarco.Li mt, too.LSS SL	020	28	1e-03	9 / 70	BP	RNA processing
15	ENSDARG000	2 26	-2.2	0.53				29	2e-03	4 / 14	BP	mitotic spindle assembly
10	LINODAIRCOOK	2.20	-2.2	0.00				30	2e-03	5/24	CC	precatalytic spliceosome
16	ENSDARG000	2.19	-0.96	0.61	tbx6	T-box 6 [Source:ZFIN;Acc:ZDB-GENE-020416-5]		31	2e-03	76 / 1427	BP	biological_process
10	LINODAIRCOOK	2.10	-0.50	0.01	lDXO	. Box 0 (Box 100.121 111, 100.125 B GETTE 620 110 0)		32	3e-03	4 / 16	BP	mitochondrial translation
17	ENSDARG000	2 13	-1.76	0.73	zac:165	55 <b>55</b> c:165555 [Source:ZFIN;Acc:ZDB-GENE-070620-1	171	33 34	3e-03	4 / 17	MF	DNA-directed DNA polymerase activity spliceosomal complex assembly
' '	LINODAIRCOOK	2.10	0	0.70	-9		,	35	3e-03 3e-03	4 / 17 9 / 80	BP CC	centrosome
18	ENSDARG000	2.1	-2.66	0.75	1.0056	277/stone 1, H4, like [Source:ZFIN;Acc:ZDB-GENE-070	0927-10	36	5e-03	5/30	MF	damaged DNA binding
10	LINODAIRCOOK	2.1	-2.00	0.70	200002	27,000.00 1,111, 1100 [000.00.21 111,100.2222 02.12 070	0027 11	37			MF	N-acetyltransferase activity
19	ENSDARG000	2.09	-0.94	0.69				38	5e-03 5e-03	5 / 30 3 / 10	CC	chromosome, telomeric region
19	LINODANGOO	2.03	-0.34	0.03				39	5e-03	3/10	CC	cullin–RING ubiquitin ligase complex
20	ENSDARG000	2.07	-2.01	0.87	cenpi	centromere protein J [Source:ZFIN;Acc:ZDB-GENE-(	030131	39 40	5e-03	3/10	CC	intraciliary transport particle B
20	LINSDARGOOI	2.01	-2.01	0.07	conpj	Controlled proton o [Courto Li III, NOC. EDD OCITE	000.01	40	00-00	3/10	CC	mademan, manoport particle D



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

#### Spot Summary: C

# metagenes = 83 # genes = 1196

<r> metagenes = 0.76

beta: r2= 1.55 / log p= -Inf

# samples with spot = 0 ( 0 %)

#### **Overview Map Spot** 40 30 30 20 20 10 -10 10 20 30 40 10 20 30 40 0.4 0.2 0.0 -0.2 -0.4 -0.648hpf\_neg 48hpf\_pos 48hpf\_pos.1 72hpf\_neg 72hpf\_pos 24hpf\_neg 72hpf\_neg\_gata5 72hpf\_pos\_gata5 72hpf\_neg\_tbx5 72hpf\_pos\_tbx5 72hpf\_pos\_hand2 72hpf\_pos.1 72hpf\_pos\_tbx5.1 72hpf\_pos\_gata5.1

#### **Spot Genelist**

ENSDARG000 1.74

ENSDARG00( 1.73

ENSDARG00( 1.72

ENSDARG000 1.7

ENSDARG00( 1.66

ENSDARG00( 1.65

20 ENSDARG001 1.65

15 ENSDARG00( 1.73

-0.36 0.71

-1.59

-0.78

-0.43

-18 054

-3.05

Rar	nk ID	max	e min e	r ;	Sym	Description bol			Rank	p-value	#in/all	Ger	neset
1	ENSDARG000	2.68	-0.85	0.63	si:dkey-	-2 <b>6g/2:117</b> 4855 [Source	e:ZFIN;Acc:ZDB-	GENE-071004-74]	1	7e-30	200 / 2030	MF	nucleic a
_									2	2e-10	62 / 608	MF	RNA bin
2	ENSDARG000	2.63	-1.19	0.39		si:ch211-39f2.3 [Sc	ource:ZFIN;Acc:Z	DB-GENE-131126-52]	3	3e-07	7 / 13	BP	RNA me
_									4	1e-06	15 / 79	BP	mRNA s
3	ENSDARG000	2.46	-1.5	0.4	kcnj1a.	6 potassium inwardly-	-rectifying chann	el, subfamily J, member '	5	1e-06	6 / 10 10 / 51	MF	RNA me
									6 7	5e-05 6e-05	17 / 135	BP MF	methyltra
4	ENSDARG000	2.35	-0.89	0.64	wu:fa26	6c@athepsin Lb [Sourc	ce:ZFIN;Acc:ZDB	-GENE-980526-285]	8	3e-04	16 / 138	CC	intracellu
_	ENODADOSS.	0.07		0.07	a:	06094-4- 0004 4 [0-		DD OENE 404044 071	9	3e-04	12 / 88	BP	mRNA p
5	ENSDARG000	2.27	-0.8	0.67	si:ukey-	-2151900 K99y - 210911.4 [50	ource:ZFIN;Acc:Z	DB-GENE-121214-37]	10	4e-04	16 / 144	BP	methylat
c	ENODADOSS.	0.40	-0.58	0.64	oiselleou	21 C 01:000 0:00	Course: ZEIN: A sec	ZDB-GENE-121214-39	11	7e-04	10 / 70	BP	RNA pro
6	ENSDARG000	2.13	-0.58	0.64	Si.ukey-	-2 <b>s</b> isyimeyo-239j16.3 [3	Source.ZFIIN,Acc	ZDB-GEINE-121214-39	12	8e-04	4/11	CC	small rib
7	ENSDARG000	2.00	-0.57	0.64	ctslb	anthonoin I b (Cours	00:7EIN: 4 00:7DB	-GENE-980526-285]	13	2e-03	7 / 42	CC	spliceos
1	ENSDARGOO	2.08	-0.57	0.64	CISID	catriepsin Lb (Sourc	Le.ZFIIN,ACC.ZDB	-GENE-900320-203]	14	2e-03	19 / 214	BP	translatio
8	ENSDARG000	2.01	-0.68	0.71	1.0010	nesietkas, 260i1 / ISa	ource:7EIN:Acc:7	DB-GENE-121214-37]	15	2e-03	4/14	BP	mitotic s
0	ENSDARGOO	2.01	-0.00	0.71	LOCIO	033040437-20311.4 [30	Juice.Zi IIV,Acc.Z	DD-GLINE-121214-5/1	16	2e-03	4 / 14	CC	U12-typ
9	ENSDARG000	1.06	-0.76	0.7	fqf8a	fibroblast growth fac	ctor 8a [Source:7	FIN;Acc:ZDB-GENE-99	17	2e-03	5 / 23	BP	cytoplas
9	ENSDARGOO	1.50	-0.70	0.7	igioa	iibiobiast growtii iac	ctor oa joodree.2	1 114,7 (00.2DB - OL14E - 55	18	3e-03	8 / 58	BP	RNA spli
10	ENSDARG000	1 03	-0.76	0.56	ece2a	endothelin convertir	na enzvme 2a IS	ource:ZFIN;Acc:ZDB-GE	19	3e-03	4 / 15	BP	mRNA p
10	LINSDARGOON	1.55	-0.70	0.50	eceza	CHGOTHCIIII CONVCIU	ing chizyinic za joi	50100.21 114,7100.2DD-GE	20	3e-03	144 / 2716	CC	nucleus
11	ENSDARG000	1.85	-0.54	0.44	sirch73.	_3xi3th78=34314.8 [Sc	ource:ZEIN:Acc:Z	DB-GENE-090313-159	21	4e-03	27 / 362	BP	regulatio
1.1	LINSDARGOON	1.00	-0.54	0.44	31.0117.3	-3434900 04014.0 [00	50100.21 11 <b>1</b> ,7100.2	DD-0ENE-030010-103	22	4e-03	42 / 643	BP	transcrip
12	ENSDARG000	1.79	-0.47	0.74					23	4e-03	5 / 26	CC	nuclear
12	LINDDANGUUI	1.13	-0.47	J.14					24	6e-03	5 / 28	MF	double-
									25	60 03	4/19	RP	enlicane

regulation of transcription from RNA polymerase II promoter transcription, DNA-templated nuclear speck double-stranded DNA binding 6e-03 4/18 spliceosomal snRNP assembly si:dkev-2993th@2-239i18.2 [Source:ZFIN:Acc:ZDB-GENE-121214-52 7e-03 3/10 BP tRNA aminoacylation 8e-03 4/19 CC U1 snRNP slc16a6a solute carrier family 16, member 6a [Source:ZFIN;Acc:ZDB-C ME rRNA binding 9e-03 4/20 regulation of pH 1e-02 3 / 11 RP CC 1e-02 13 / 147 ribosome 1e-02 3/12 CC DNA-directed RNA polymerase II, core complex si:ch211-14p21.4 [Source:ZFIN;Acc:ZDB-GENE-070912-95 1e-02 3/12 BP 1e-02 3/12 tRNA modification hsd3b7 hydroxy-delta-5-steroid dehydrogenase, 3 beta- and steroid 1e-02 4/22 transcription from RNA polymerase III promoter 1e-02 4/22 ME tRNA binding tmem44 transmembrane protein 44 [Source:ZFIN:Acc:ZDB-GENE-06 1e-02 5/34 CC catalytic step 2 spliceosome meiotic cell cycle 2e-02 4/23 RP myzap myocardial zonula adherens protein [Source:ZFIN:Acc:ZDB-38 2e-02 9/91 RP cellular response to DNA damage stimulus 39 ME cysteine-type peptidase activity 2e-02 11 / 123 hyperpolarization activated cyclic nucleotide-gated potassium 2e-02 cyclin-dependent protein kinase holoenzyme complex 3 / 13

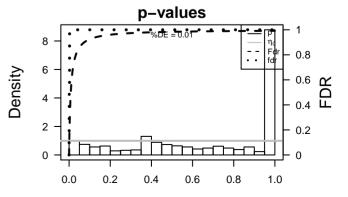
**Geneset Overrepresentation** 

nucleic acid binding RNA binding

RNA methylation mRNA splicing, via spliceosome RNA methyltransferase activity

tRNA processing methyltransferase activity intracellular ribonucleoprotein complex

mRNA processing
methylation
RNA processing
small ribosomal subunit
spliceosomal complex
translation
mitotic spindle assembly
U12-type spliceosomal complex
cytoplasmic translation
RNA splicing
mRNA polyadenylation
nucleus



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

### Spot Summary: D

# metagenes = 137 # genes = 2381

<r> metagenes = 0.63

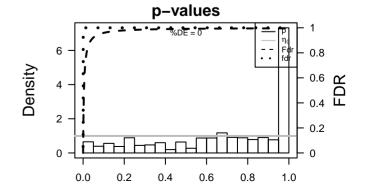
beta: r2= 1.22 / log p= -Inf

# samples with spot = 0 ( 0 %)

#### **Overview Map** Spot 30 30 20 20 10 -10 30 30 10 20 40 10 20 0.6 0.4 0.2 0.0 -0.2 -48hpf\_pos.1 72hpf\_neg 72hpf\_neg 72hpf\_pos 72hpf\_neg\_gata5 72hpf\_pos\_gata5 72hpf\_pos.1 72hpf\_neg\_tbx5 72hpf\_pos\_hand2 72hpf\_pos\_gata5.1

## **Spot Genelist**

Ra	ink ID	max	e min e	r e	Description Symbol	Rank	p-value	#in/all	Ger	neset
1	ENSDARG000	2.67	-2.18	0.35	si:ch211-213a13.2 [Source:ZFIN;Acc:ZDB-GENE-050208-{	1	1e-33	331 / 2030	MF	nucleic acid binding
						2	3e-05	13 / 43	CC	proteasome complex
2	ENSDARG000	2.63	-1.3	0.44	ampd2a adenosine monophosphate deaminase 2a [Source:ZFIN;Acc:	3	2e-04	6 / 12	BP	'de novo' protein folding
						4	3e-04	8 / 22	MF	threonine-type endopeptidase activity
3	ENSDARG000	2.63	-1.21	0.69	zgc:1584@gc:158403 [Source:ZFIN;Acc:ZDB-GENE-061215-116]	5	4e-04	6 / 13	MF	protein binding involved in protein folding
						6	4e-04	8 / 23	CC	proteasome core complex
4	ENSDARG000	2.29	-0.81	0.81		7	5e-04	11 / 42	BP	cilium movement
						8	6e-04	10 / 36	MF	endopeptidase activity
5	ENSDARG000	2.23	-0.61	0.46	pm20d1.†peptidase M20 domain containing 1, tandem duplicate 1 [Sou	9	7e-04	5 / 10	CC	chaperonin-containing T-complex
						10	7e-04	5 / 10	MF	endodeoxyribonuclease activity
6	ENSDARG000	2.22	-5.7	0.31	hand2 heart and neural crest derivatives expressed 2 [Source:ZFIN;	11	1e-03	5 / 11	BP	positive regulation of guanylate cyclase activity
						12	1e-03	6 / 16	BP	DNA integration
7	ENSDARG000	2.18	-0.75	0.77		13	3e-03	8 / 31	BP	chaperone-mediated protein folding
						14	4e-03	5 / 14	BP	transcription elongation from RNA polymerase II promoter
8	ENSDARG000	2.16	-0.86	0.65	cabp2a calcium binding protein 2a [Source:ZFIN;Acc:ZDB-GENE-05	15	5e-03	6 / 20	BP	nucleotide-excision repair
-						16	6e-03	5 / 15	BP	mRNA polyadenylation
9	ENSDARG000	2.11	-0.4	0.79		17	7e-03	14 / 80	BP	liver development
•						18	7e-03	4 / 10	MF	acetylglucosaminyltransferase activity
10	ENSDARG000	2.09	-0.6	0.69	zgc:109913[Source:ZFIN;Acc:ZDB-GENE-050522-72]	19	7e-03	4 / 10	BP	nuclear-transcribed mRNA catabolic process
10					g g ( , , , ,	20	7e-03	4 / 10	CC	proteasome core complex, alpha-subunit complex
11	ENSDARG000	2.09	-0.73	0.81	mhc1ubamajor histocompatibility complex class I UBA [Source:ZFIN;A	21	7e-03	7 / 28	MF	hydrolase activity, acting on ester bonds
	2110271110001	2.00	00	0.01	11110 1 dDd 1119 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1	22	8e-03	5 / 16	BP	response to ionizing radiation
12	ENSDARG000	2.00	-0.52	0.58	LOC571488	23	9e-03	8 / 36	CC	P-body
12	LINSDANGOO	2.03	-0.52	0.50	2003/1400	24	1e-02	4 / 11	CC	P granule
13	ENSDARG000	2.07	-0.92	0.56		25	1e-02	5 / 18	BP	spliceosomal snRNP assembly
13	ENSDARGOO	2.07	-0.92	0.36		26	2e-02	8 / 40	BP	erythrocyte differentiation
4.4	FNODADOOO	2.05	0.00	0.07	si:ch211-163c2.2 [Source:ZFIN;Acc:ZDB-GENE-160114-56	27	2e-02	8 / 40	BP	regulation of translation
14	ENSDARG000	2.05	-0.32	0.67	SI.CHZ11-103CZ.Z [Source.ZFIN,ACC.ZDB-GENE-100114-30	28	2e-02	5 / 19	BP	embryonic heart tube morphogenesis
4 5	FNODADOOO	0.04	0.75	0.05	CENE (	29	2e-02	39 / 329	BP	negative regulation of apoptotic process
15	ENSDARG000	2.04	-0.75	0.85	tmem218transmembrane protein 218 [Source:ZFIN;Acc:ZDB-GENE-(	30	2e-02	4 / 13	BP	reciprocal meiotic recombination
40						31	2e-02	8 / 42	CC	spliceosomal complex
16	ENSDARG000	2.01	-1.15	0.53	zgc:1585 <b>2</b> gc:173517 [Source:ZFIN;Acc:ZDB-GENE-071004-104]	32	2e-02	35 / 294	BP	regulation of mitotic cell cycle
						33	3e-02	5 / 21	BP	protein catabolic process
17	ENSDARG000	2	-0.43	0.76		34	3e-02	5 / 21	BP	translational elongation
4.0						35	3e-02	12 / 79	BP	cell division
18	ENSDARG000	2	-0.6	0.73	cd28 si:ch211-67e16.2 [Source:ZFIN;Acc:ZDB-GENE-070912-30	36	3e-02	4 / 15	MF	adrenergic receptor activity
						37	3e-02	4 / 15	BP	positive regulation of vasoconstriction
19	ENSDARG000	1.97	-0.54	0.73	si:ch211-si3th223;3i30m23.3 [Source:ZFIN;Acc:ZDB-GENE-060531-	38	4e-02	5 / 23	MF	fibroblast growth factor receptor binding
						39	4e-02	5 / 23	BP	gene silencing by RNA
20	ENSDARG000	1.97	-0.75	0.66	zmp:000000000000000001316 [Source:ZFIN;Acc:ZDB-GENE-140106-27	40	4e-02	4 / 16	BP	vascular endothelial growth factor receptor signaling pathway



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

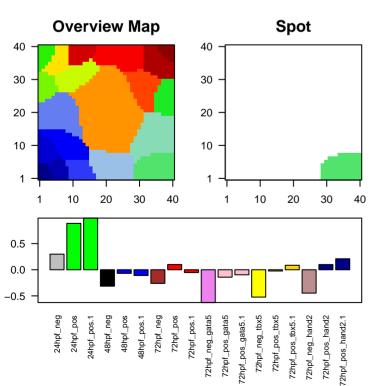
#### Spot Summary: E

# metagenes = 88 # genes = 1579

<r> metagenes = 0.83

beta: r2= 3.36 / log p= -Inf

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

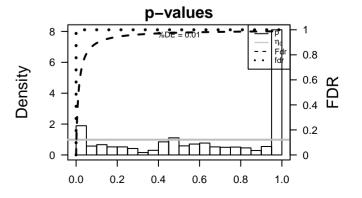


### **Spot Genelist**

Rank ID	max	e min e	r e	Symi	Description ool
1 ENSDARGO	0( 8.47	-3.84	0.32		
2 ENSDARGO	0( 8.19	-3.48	0.3		
3 ENSDARGO	0 8.13	-3.52	0.3		
4 ENSDARGO	0( 8.08	-3.28	0.26		
5 ENSDARGO	0 6.87	-3.45	0.31		
6 ENSDARGO	0 6.62	-1.54	0.13		
7 ENSDARGO	0( 5.93	-1.57	0.71	cyp7a1l	
8 ENSDARGO	0( 5.27	-3.73	0.33		
9 ENSDARGO	0( 5.15	-3.14	0.36		
10 ENSDARGO	0 5.09	-3.4	0.32		
11 ENSDARGO	0( 5.06	-3.18	0.35		
12 ENSDARGO	0( 4.97	-3.11	0.35		
13 ENSDARGO	0( 4.93	-3.21	0.36		
14 ENSDARGO	0( 4.13	-2.81	0.84	mrc1a	mannose receptor, C type 1a [Source:ZFIN;Acc:ZDB-GENE-
15 ENSDARGO	0( 4.07	-2.7	0.34		
16 ENSDARGO	0( 3.95	-1.46	0.23		zgc:158463 [Source:ZFIN;Acc:ZDB-GENE-070410-9]
17 ENSDARGO	3.89	-1.94	8.0	nkx2.7	NK2 transcription factor related 7 [Source:ZFIN;Acc:ZDB–GE
18 ENSDARGO	0( 3.75	-3.16	0.75	dnase1	4.deoxyribonuclease 1 like 4, tandem duplicate 1 [Source:ZFIN
19 ENSDARGO	0( 3.73	-2.69	0.09		
20 ENSDARGO	0( 3.53	-3.11	0.83	ikzf1	IKAROS family zinc finger 1 (Ikaros) [Source:ZFIN;Acc:ZDB-

#### Geneset Overrepresentation

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



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

#### Spot Summary: F

# metagenes = 65 # genes = 1082

<r> metagenes = 0.9

beta: r2= 6.3 / log p= -Inf

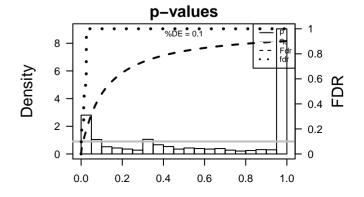
# samples with spot = 3 ( 16.7 %)

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

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

### **Spot Genelist**

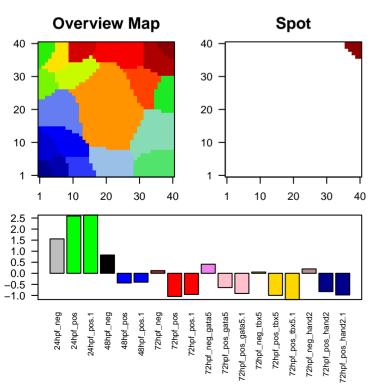
Rar	nk	max	е	r		Description	Rank	p-value	#in/all	Ge	neset
	ID		min e	•	Symb	ool .		•			
					-						
4	ENSDARG000	3.53	-2.37	0.59	aala	selectin E [Source:ZFIN;Acc:ZDB-GENE-041014-221]	1	4e-56	280 / 2716	CC	nucleus
- 1	ENSDARGOO	3.53	-2.37	0.59	sele	Selectiff E [Source:ZFIN,Acc.ZDB-GENE-041014-221]	2	4e-56 5e-38	169 / 1484	MF	DNA binding
2	ENSDARG000	3.22	-4.34	0.39		collagen, type XIV, alpha 1b [Source:ZFIN;Acc:ZDB-GENE-(	3	5e-36 5e-34	61 / 229	CC	chromosome
2	ENSDARGOO	3.22	-4.34	0.39		collagen, type XIV, alpha 15 [Source.21 IIV,Acc.2DB-GEIVE-C	4	1e-29	49 / 168	CC	nucleosome
2	ENODA DOSS	2.0	0.00	0.04			5	2e-26	33 / 78	BP	DNA replication
3	ENSDARG000	2.9	-2.63	0.61			6	5e-24	37 / 117	BP	nucleosome assembly
	=						7	8e-18	43 / 232	MF	protein heterodimerization activity
4	ENSDARG000	2.82	-0.76	0.54			8	3e-15	14 / 22	BP	DNA replication initiation
_							9	7e-15	16 / 32	BP	DNA duplex unwinding
5	ENSDARG000	2.8	-4.02	0.63	capn12	calpain 12 [Source:ZFIN;Acc:ZDB-GENE-050419-245]	10	7e-15 9e-15			DNA repair
_									31 / 148	BP BP	regulation of transcription, DNA-templated
6	ENSDARG000	2.75	-1.65	0.66	gins1	GINS complex subunit 1 (Psf1 homolog) [Source:ZFIN;Acc:ZI	11	2e-12	100 / 1239		• • • •
							12	3e-10	48 / 454	BP	multicellular organism development
7	ENSDARG000	2.69	-3.04	0.58	hbbe2	hemoglobin beta embryonic-2 [Source:ZFIN;Acc:ZDB-GENE	13	7e-10	8/11	BP	RNA export from nucleus
							14	5e-09	12 / 36	BP	protein import into nucleus
8	ENSDARG000	2.67	-2.02	0.7	f2r	coagulation factor II (thrombin) receptor [Source:ZFIN;Acc:ZE	15	7e-09	20 / 110	BP	cell cycle
							16	1e-08	16 / 72	MF	helicase activity
9	ENSDARG000	2.66	-1.9	0.66	pdia2	protein disulfide isomerase family A, member 2 [Source:ZFIN	17	1e-08	12 / 39	MF	single-stranded DNA binding
-							18	8e-08	54 / 643	BP	transcription, DNA-templated
10	ENSDARG000	2.65	-1.32	0.61	helb	helicase (DNA) B [Source:ZFIN;Acc:ZDB-GENE-030729-16	19	3e-07	16 / 91	BP	cellular response to DNA damage stimulus
.0							20	4e-07	46 / 537	MF	sequence-specific DNA binding
11	ENSDARG000	2 57	-1.21	0.59			21	4e-07	18 / 115	MF	chromatin binding
	2.102/110001	2.01		0.00			22	9e-07	9 / 29	CC	kinetochore
12	ENSDARG00	2.57	-2.05	0.49	crhbp	corticotropin releasing hormone binding protein [Source:ZFIN	23	1e-06	6 / 11	MF	DNA helicase activity
12	LINSDARGOON	2.51	-2.00	0.43	оттър	control of the contro	24	1e-06	6 / 11	MF	structural constituent of nuclear pore
10	ENCDARCOO!	0.50	0.4	0.0	fibpb	EGF containing fibulin-like extracellular matrix protein 2b [So	25	2e-06	7 / 17	MF	DNA-directed DNA polymerase activity
13	ENSDARG000	2.56	-2.1	8.0	поро	EGF containing libulin-like extracellular matrix protein 2b [50	26	3e-06	8 / 25	BP	membrane disruption in other organism
4.4	=	0.50	0.00	0.00		5040910007-40.0 [C7EIN: A7DD, CENIE 444000.1	27	1e-05	7 / 22	CC	chromosome, centromeric region
14	ENSDARG000	2.52	-2.36	0.68	si:cn211	-si2th2tt0.3227n13.3 [Source:ZFIN;Acc:ZDB-GENE-141222-:	28	1e-05	8 / 30	BP	defense response to Gram-positive bacterium
4-							29	1e-05	104 / 1787	MF	ATP binding
15	ENSDARG000	2.51	-1.21	0.83	atp2b1a	ATPase, Ca++ transporting, plasma membrane 1a [Source:Zf	30	2e-05	8 / 31	BP	lymphangiogenesis
							31	2e-05	12 / 72	BP	nucleic acid phosphodiester bond hydrolysis
16	ENSDARG000	2.48	-1.83	0.81	scube2	signal peptide, CUB domain, EGF-like 2 [Source:ZFIN;Acc:Z	32	2e-05	5 / 10	BP	adenohypophysis development
							33	2e-05	6 / 16	BP	G1/S transition of mitotic cell cycle
17	ENSDARG000	2.45	-2.43	0.7			34	2e-05	9 / 41	BP	positive regulation of cell proliferation
							35	3e-05	14 / 100	BP	peptidyl-tyrosine phosphorylation
18	ENSDARG000	2.44	-1.1	0.82	si:dkeyp-	-si2dke)/p-120h9.1 [Source:ZFIN;Acc:ZDB-GENE-070705-50	36	3e-05	9 / 43	BP	DNA-templated transcription, initiation
							37	3e-05	5 / 11	BP	mitotic spindle assembly checkpoint
19	ENSDARG000	2.41	-1.34	0.77	ell2	elongation factor, RNA polymerase II, 2 [Source:ZFIN;Acc:ZD	38	5e-05	12 / 79	BP	cell division
							39	5e-05	44 / 608	MF	RNA binding
20	ENSDARG000	2.39	-1.76	0.62	urb2	URB2 ribosome biogenesis 2 homolog (S. cerevisiae) [Sourci	40	6e-05	45 / 633	MF	transcription factor activity, sequence-specific DNA binding



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

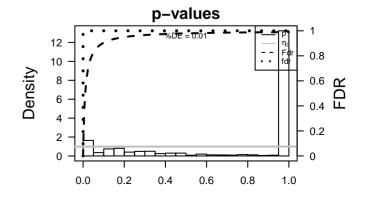
#### Spot Summary: G

# metagenes = 19 # genes = 366 <r> metagenes = 0.98 <r> genes = 0.7 beta: r2= 19.09 / log p= -Inf # samples with spot = 4 ( 22.2 %) 24hpf\_neg: 1 (100%) 24hpf\_pos : 2 ( 100 %) 48hpf\_neg: 1 (100%)



### **Spot Genelist**

Ra	nk ID	max	e min e	r e	Sym	Description bol	Rank	p-value	#in/all	Ge	neset
1	ENSDARG000	8.12	-6.4	0.86	hbbe3	hemoglobin beta embryonic-3 [Source:ZFIN;Acc:ZDB-GENE	1	4e-33	40 / 229	СС	chromosome
							2	7e-32	35 / 168	CC	nucleosome
2	ENSDARG000	7.83	-4.49	0.95	drl	draculin [Source:ZFIN;Acc:ZDB-GENE-991213-3]	3	8e-27	35 / 232	MF	protein heterodimerization activity
							4	1e-26	19 / 37	MF	nucleosomal DNA binding
3	ENSDARG000	7.74	-1.79	0.56	LOC10	0595959711-11n16.3 [Source:ZFIN;Acc:ZDB-GENE-131121-86	5	1e-24	26 / 117	BP	nucleosome assembly
							<u>6</u>	3e-19	67 / 1484	MF	DNA binding
4	ENSDARG000	7.36	-4.55	0.95	si:dkey-	-261j4.4 [Source:ZFIN;Acc:ZDB-GENE-060531-125]	7	1e-16	10 / 14	CC	hemoglobin complex
							8	1e-14	10 / 19	MF	oxygen binding
5	ENSDARG000	7.35	-4.2	0.91	blf	bloody fingers [Source:ZFIN;Acc:ZDB-GENE-050721-1]	9	1e-14	10 / 19	BP	oxygen transport
							10	1e-14	10 / 19	MF	oxygen transporter activity
6	ENSDARG000	7.06	-5.06	0.94	si:dkey-	-26/10/14/29/-261j4.3 [Source:ZFIN;Acc:ZDB-GENE-060531-124]	11	3e-13	82 / 2716	CC	nucleus
							12	1e-12	10 / 28	BP	embryonic hemopoiesis
7	ENSDARG000	6.46	-4.6	0.73		protogenin homolog b (Gallus gallus) [Source:ZFIN;Acc:ZDB-	13	6e-11	11 / 52	BP	blood vessel development
							14	7e-11	10 / 40	BP	erythrocyte differentiation
8	ENSDARG000	6.43	-3.22	0.91	stab2	stabilin 2 [Source:ZFIN;Acc:ZDB-GENE-041210-336]	15	2e-08	7 / 24	BP	myeloid cell differentiation
Ū							16	2e-08	6 / 15	BP	heme biosynthetic process
9	ENSDARG000	6.31	-1.79	0.88	ela2l	elastase 2 like [Source:ZFIN;Acc:ZDB-GENE-040511-1]	17	6e-08	13 / 145	MF	heme binding
J	2.102/1110001				O.G.Z.		18	1e-07	8 / 46	BP	mitotic cell cycle
10	ENSDARG000	6 11	-4.16	0.95	tfr1a	transferrin receptor 1a [Source:ZFIN;Acc:ZDB-GENE-04122	19	5e-07	7 / 38	BP	vasculogenesis
10	LINSDARGOON	0.11	-4.10	0.55	uiia	transienti receptor la jource. El tiv, rec. EBB-OENE-04122	20	2e-06	10 / 110	MF	protein tyrosine kinase activity
11	ENSDARG000	6	-2.33	0.91		si:ch73-299h12.2 [Source:ZFIN;Acc:ZDB-GENE-081031-7]	21	4e-06	12 / 178	MF	iron ion binding
11	ENSDARGOO	O	-2.33	0.91		SI.CH7 3-299112.2 [Source.21 IN,Acc.2DB-GENE-001031-7]	22	6e-06	4 / 10	BP	mitotic sister chromatid segregation
40	=======================================					I/C and I'V (constant)	23	7e-06	9 / 100	BP	peptidyl-tyrosine phosphorylation
12	ENSDARG000	5.97	-3.89	0.92	klf17	Kruppel-like factor 17 [Source:ZFIN;Acc:ZDB-GENE-01012!	24	9e-06	9 / 104	BP	transmembrane receptor protein tyrosine kinase signaling pathway
4.0							25	2e-05	45 / 1787	MF	ATP binding
13	ENSDARG000	5.89	-1.29	0.56	zgc:1/4	1855c:174855 [Source:ZFIN;Acc:ZDB-GENE-071004-74]	26	3e-05	9 / 121	BP	angiogenesis
							27	6e-05	7 / 75	BP	hemopoiesis
14	ENSDARG000	5.69	-3.46	0.93	gata1a	GATA binding protein 1a [Source:ZFIN;Acc:ZDB-GENE-980!	28	7e-05	5 / 34	BP	ephrin receptor signaling pathway
							29	7e-05	4 / 18	BP	cell morphogenesis
15	ENSDARG000	5.69	-3.04	0.9	gfi1b	growth factor independent 1B transcription repressor [Source	30	8e-05	7 / 79	BP	cell division
							31	9e-05	18 / 491	MF	kinase activity
16	ENSDARG000	5.53	-3.53	0.83			32	1e-04	11 / 210	MF	protein binding
							33	1e-04	4 / 21	BP	erythrocyte development
17	ENSDARG000	5.51	-4.09	0.87	znfl2a	zinc finger-like gene 2a [Source:ZFIN;Acc:ZDB-GENE-0308	34	2e-04	18 / 522	BP	phosphorylation
							35	2e-04	6 / 66	BP	sprouting angiogenesis
18	ENSDARG000	5.45	-1.91	0.8	cpox	coproporphyrinogen oxidase [Source:ZFIN;Acc:ZDB-GENE-	36	2e-04	4 / 24	BP	primitive hemopoiesis
-							37	4e-04	36 / 1506	MF	nucleotide binding
19	ENSDARG000	5.42	-2.18	0.83	hmbsb	hydroxymethylbilane synthase, b [Source:ZFIN;Acc:ZDB-GEI	38	4e-04	5 / 47	MF	nuclease activity
							39	4e-04	3 / 12	BP	hemoglobin biosynthetic process
20	ENSDARG000	5.39	-4.85	0.91	hdr	hematopoietic death receptor [Source:ZFIN;Acc:ZDB-GENE-	40	4e-04	6 / 75	MF	microtubule motor activity



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

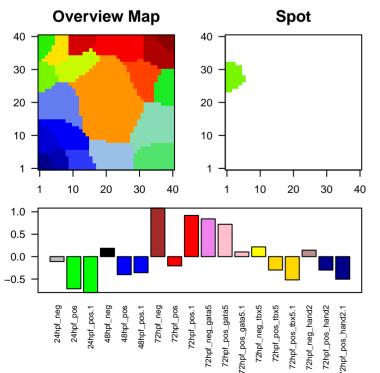
#### Spot Summary: H

# metagenes = 41

# genes = 628

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

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

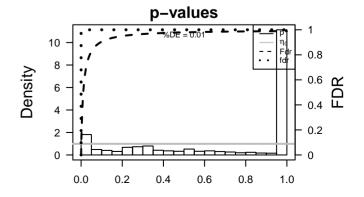


#### **Spot Genelist**

Raı	nk ID	max	e min e	r e	Description Symbol
1	ENSDARG000	11.88	-0.87	0.47	
2	ENSDARG000	7.94	-1.47	0.51	cts12 cathepsin 12 [Source:ZFIN;Acc:ZDB-GENE-050208-336]
3	ENSDARG000	5.13	-1.38	0.48	si:dkey-2si7ttifey-247k7.2 [Source:ZFIN;Acc:ZDB-GENE-031118-45]
4	ENSDARG000	4.62	-1.7	0.36	kcnj1a.4 potassium inwardly-rectifying channel, subfamily J, member
5	ENSDARG000	4.19	-2.48	0.81	and3 actinodin3 [Source:ZFIN;Acc:ZDB-GENE-040724-185]
6	ENSDARG000	4.12	-3.12	0.9	krt1-19d keratin, type 1, gene 19d [Source:ZFIN;Acc:ZDB-GENE-060
7	ENSDARG000	3.92	-3.3	0.68	cyt1 type I cytokeratin, enveloping layer [Source:ZFIN;Acc:ZDB-G
8	ENSDARG000	3.86	-2.03	0.39	kcnj1a.5 potassium inwardly-rectifying channel, subfamily J, member
9	ENSDARG000	3.84	-1.98	0.32	kcnj1a.3 potassium inwardly–rectifying channel, subfamily J, member $$
10	ENSDARG000	3.81	-3.87	0.7	zgc:1008@gc:100868 [Source:ZFIN;Acc:ZDB-GENE-040801-33]
11	ENSDARG000	3.71	-3.28	0.64	cyt1I type I cytokeratin, enveloping layer, like [Source:ZFIN;Acc:ZD
12	ENSDARG000	3.64	-2.02	0.42	prph2a peripherin 2a (retinal degeneration, slow) [Source:ZFIN;Acc:2
13	ENSDARG000	3.51	-3.12	0.69	tmem176transmembrane protein 176l.4 [Source:ZFIN;Acc:ZDB-GENE
14	ENSDARG000	3.51	-2.68	0.6	si:dkey-3%idkey-33i11.4 [Source:ZFIN;Acc:ZDB-GENE-030131-33]
15	ENSDARG000	3.45	-2.19	0.62	si:ch211-si2si2f6.4125o16.4 [Source:ZFIN;Acc:ZDB-GENE-131120-
16	ENSDARG000	3.4	-3.43	0.74	cldne claudin e [Source:ZFIN;Acc:ZDB-GENE-010328-5]
17	ENSDARG000	3.38	-4.07	0.78	krt4 keratin 4 [Source:ZFIN;Acc:ZDB-GENE-000607-83]
18	ENSDARG000	3.36	-3.38	0.65	col8a2 collagen, type VIII, alpha 2 [Source:ZFIN;Acc:ZDB-GENE-06
19	ENSDARG000	3.25	-3.18	0.46	anxa1c annexin A1c [Source:ZFIN;Acc:ZDB-GENE-030131-5274]
20	ENSDARG000	3.25	-1.91	0.4	agr1 anterior gradient 1 [Source:ZFIN;Acc:ZDB-GENE-030131-7

#### **Geneset Overrepresentation**

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



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

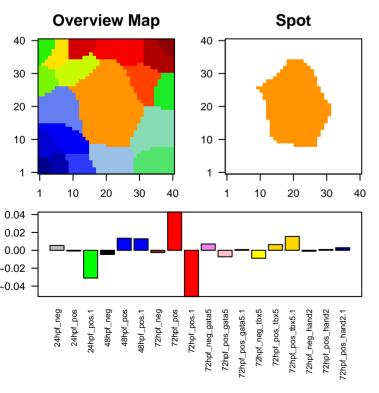
#### Spot Summary: I

# metagenes = 380 # genes = 7993

<r> metagenes = 0.02

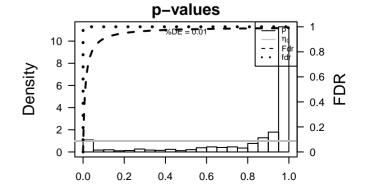
beta: r2= 0.15 / log p= -0.97

# samples with spot = 0 ( 0 %)



#### Geneset Overrepresentation

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



ВР				СС				MF			
Rank	p-value	#in/all	Geneset	Rank	p-value	#in/all	Geneset	Rank	p-value	#in/all	Geneset
1	5e-51	443 / 853	G–protein coupled receptor signaling pathway	1	8e-05	65 / 153	cell surface	1	1e-53	408 / 751	G-protein coupled receptor activity
2	1e-45	179 / 253	protein autophosphorylation	2	1e-04	220 / 634	extracellular region	2	2e-30	324 / 666	signal transducer activity
3	3e-44	213 / 329	negative regulation of apoptotic process	3	3e-02	9/17	integral component of nuclear inner membrane	3	1e-27	56 / 59	olfactory receptor activity
4	4e-40	191 / 294	regulation of mitotic cell cycle	4	1e-01	8 / 18	vacuole	4	4e-24	45 / 46	trace-amine receptor activity
5	1e-27	56 / 59	detection of chemical stimulus involved in sensory perception of smell	5	1e-01	12/31	photoreceptor outer segment	5	4e-17	109 / 192	transmembrane signaling receptor activity
6	9e-24	57 / 65	sensory perception of smell	6	1e-01	8 / 19	acetylcholine-gated channel complex	6	2e-12	264 / 652	protein serine/threonine kinase activity
7	1e-18	39 / 42	detection of chemical stimulus involved in sensory perception	7	2e-01	5/11	membrane attack complex	7	6e-09	26 / 34	G-protein coupled serotonin receptor activity
8	4e-16	68 / 102	response to stimulus	8	2e-01	22 / 65	extracellular matrix	8	4e-08	24 / 32	neurotransmitter receptor activity
9	4e-11	467 / 1298	5 signal transduction	9	2e-01	23 / 71	bicellular tight junction	9	7e-06	47 / 95	hormone activity
10	3e-10	133 / 297	immune response	10	3e-01	12/35	Golgi cisterna membrane	10	2e-05	27 / 47	chemokine activity
11	1e-09	57 / 100	neuropeptide signaling pathway	11	3e-01	4/10	integral component of peroxisomal membrane	11	2e-05	311 / 914	protein kinase activity
12	4e-08	22 / 28	G-protein coupled serotonin receptor signaling pathway	12	3e-01	233 / 809	integral component of plasma membrane	12	4e-05	79 / 191	serine-type endopeptidase activity
13	1e-04	14 / 20	response to peptide	13	3e-01	145 / 500	extracellular space	13	1e-04	10 / 12	neuropeptide receptor activity
14	2e-04	314 / 947	protein phosphorylation	14	3e-01	7 / 20	anchored component of membrane	14	1e-04	11 / 14	neuropeptide Y receptor activity
15	3e-04	24 / 45	phospholipase C-activating G-protein coupled receptor signaling pathway	15	3e-01	6/17	blood microparticle	15	7e-04	50 / 119	carbohydrate binding

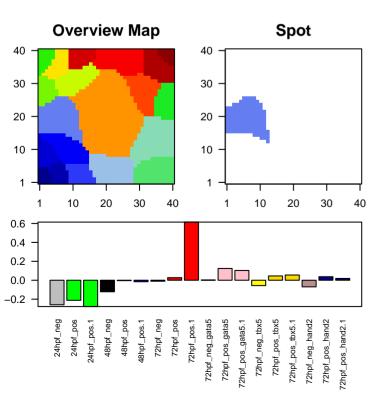
#### Spot Summary: J

# metagenes = 124 # genes = 2002

<r> metagenes = 0.5

beta: r2= 1.28 / log p= -Inf

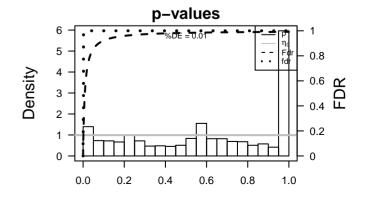
# samples with spot = 0 ( 0 %)



## **Spot Genelist**

#### Geneset Overrepresentation Description Pank n-value #in/all Consect

Rar		max	е	r		Description	Rank	p-value	#in/all	Ger	neset
	ID		min e	9	Syml	ool					
1	ENSDARG000	5.69	-0.44	0.81	slc28a1	solute carrier family 28 (concentrative nucleoside transporter)	1	5e-10	593 / 6723	СС	membrane
							2	4e-08	543 / 6248	CC	integral component of membrane
2	ENSDARG000	2.85	-1.69	0.61	si:dkeyp		3	3e-04	42 / 337	CC	endoplasmic reticulum
							4	3e-04	7 / 20	BP	retrograde vesicle-mediated transport, Golgi to ER
3	ENSDARG000	2.61	-2.6	0.52	plekhf1	pleckstrin homology domain containing, family F (with FYVE o	5	4e-04	28 / 198	CC	Golgi membrane
							6	4e-04	29 / 209	CC	endoplasmic reticulum membrane
4	ENSDARG000	2.61	-1.29	0.23	tg	thyroglobulin [Source:ZFIN;Acc:ZDB-GENE-030519-1]	7	4e-04	8 / 27	CC	recycling endosome
							8	4e-04	8 / 27	BP	ubiquitin-dependent ERAD pathway
5	ENSDARG000	2.57	-1.31	0.66			9	6e-04	27 / 194	BP	lipid metabolic process
-							10	7e-04	74 / 712	BP	oxidation-reduction process
6	ENSDARG000	2.41	-1.24	-0.09	si:dkey-	38j;t8k@y-30j16.3 [Source:ZFIN;Acc:ZDB-GENE-141212-294]	11	1e-03	7 / 25	BP	steroid biosynthetic process
-							12	2e-03	6 / 19	BP	very long-chain fatty acid biosynthetic process
7	ENSDARG000	2.33	-0.59	0.16	drd3	dopamine receptor D3 [Source:ZFIN;Acc:ZDB-GENE-02111	13	2e-03	103 / 1084	BP	transport
•							14	2e-03	157 / 1761	MF	metal ion binding
8	ENSDARG000	2.3	-1.15	0.63	LOC100	0000832	15	2e-03	18 / 119	MF	monooxygenase activity
•							16	2e-03	37 / 317	CC	Golgi apparatus
9	ENSDARG000	2.22	-1.2	0.36	si:ch211	I-si52h2314-157c3.4 [Source:ZFIN;Acc:ZDB-GENE-030131-84	17	2e-03	5 / 14	CC	autophagosome
·						,	18	2e-03	61 / 591	BP	transmembrane transport
10	ENSDARG000	2.21	-0.29	0.68		si:ch211-167j6.4 [Source:ZFIN;Acc:ZDB-GENE-070912-14	19	2e-03	55 / 522	MF	oxidoreductase activity
10						, , , , , , , , , , , , , , , , , , , ,	20	3e-03	45 / 410	CC	mitochondrion
11	ENSDARG000	2 18	-0.77	0.56	si:dkev-	-29988224239b22.2 [Source:ZFIN;Acc:ZDB-GENE-131120-8]	21	3e-03	189 / 2189	CC	cytoplasm
	2110271110001	20	0	0.00	,		22	3e-03	10 / 51	BP	ER to Golgi vesicle-mediated transport
12	ENSDARG000	2 13	-2.02	0.51	mylkb	myosin light chain kinase b [Source:ZFIN;Acc:ZDB-GENE-0	23	3e-03	7 / 28	MF	protein domain specific binding
12	LIVODAIROOOI	2.10	-2.02	0.01	,	,g	24	4e-03	14 / 88	MF	guanyl-nucleotide exchange factor activity
13	ENSDARG000	2.05	-1.18	0.46	aqp9b	aquaporin 9b [Source:ZFIN;Acc:ZDB-GENE-070911-1]	25	4e-03	4 / 10	BP	receptor clustering
13	LIVODAIROOOI	2.00	-1.10	0.40	adpob	aquaponir ob [course.2: int, too.255 C212 C70077 1]	26	4e-03	140 / 1580	CC	cellular_component
14	ENSDARG000	2.02	-1.85	0.12	c6	complement component 6 [Source:ZFIN;Acc:ZDB-GENE-04	27	4e-03	41 / 375	BP	positive regulation of GTPase activity
14	LINSDARGOON	2.02	-1.00	0.12	co	complement of pource. Entry tooled Bridge	28	5e-03	8 / 38	CC	trans-Golgi network
15	ENSDARG000	2	-1.03	0.34	kcne4	potassium voltage-gated channel, Isk-related family, membe	29	5e-03	7 / 31	BP	one-carbon metabolic process
13	LINSDARGOON	2	-1.03	0.54	KUIICH	potassium voitage gated charmer, isk-related family, membe	30	5e-03	8/39	CC	connexin complex
16	ENSDARG000	2	-1.67	0.36	700:103	5@5c:193505 [Source:ZFIN;Acc:ZDB-GENE-030131-7103]	31	5e-03	8 / 39	MF	G-protein coupled receptor binding
10	LINSDARGOON	2	-1.07	0.50	2g0.100	02g0.100000 [000100.21 114,700.2255-02142-000101-7100]	32	6e-03	9 / 48	CC	heterotrimeric G-protein complex
17	ENSDARG000	2	-0.98	0.51	ch25hl1	.1cholesterol 25-hydroxylase like 1, tandem duplicate 1 [Source	33	7e-03	27 / 229	MF	transporter activity
17	ENSDARGOO	2	-0.30	0.51	CHZJIII	, photosicrof 25-riyaroxylase like 1, tandern dupileate 1 [oodid	34	7e-03	13 / 85	MF	isomerase activity
18	ENSDARG000	1.00	-2.26	0.13		U2 spliceosomal RNA [Source:RFAM;Acc:RF00004]	35	7e-03	6 / 25	CC	mitochondrial large ribosomal subunit
10	LINODARGUUI	1.88	-2.20	-0.13		02 spirocosomai (NYA (Source.N. AWI,Acc.N. 00004)	36	7e-03	6 / 25	BP	tricarboxylic acid cycle
19	ENCOADCOO	1.00	-2.85	0.25	cyp51	cytochrome P450, family 51 [Source:ZFIN;Acc:ZDB-GENE-(	37	7e-03	5 / 18	BP	phospholipase C-activating dopamine receptor signaling pathway
19	ENSDARG000	1.99	-2.83	0.25	сурот	cytochrome r 450, lamily 51 [Source.ZFIN,Acc.ZDB-GENE-C	38	8e-03	7/33	MF	NAD binding
20	ENODADO:	4.00	2.20	0.04		LI4 online commol BNA (Source: BEAM: Acc: BE000001	39	8e-03	4/12	CC	endoplasmic reticulum lumen
20	ENSDARG000	1.99	-3.36	-0.01		U1 spliceosomal RNA [Source:RFAM;Acc:RF00003]	40	8e-03	126 / 1437	MF	molecular_function



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

#### Spot Summary: K

# metagenes = 102 # genes = 1561

<r> metagenes = 0.74

beta: r2= 2.13 / log p= -Inf

# samples with spot = 0 ( 0 %)

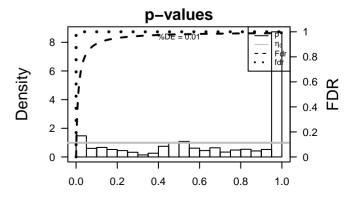
#### **Overview Map** Spot 30 30 20 20 10 -10 30 30 10 20 40 10 20 0.2 0.0 -0.2 -0.4 48hpf\_neg 48hpf\_pos 48hpf\_pos.1 72hpf\_neg 72hpf\_nes 72hpf\_neg\_gata5 72hpf\_pos\_gata5 72hpf\_pos.1 72hpf\_neg\_tbx5 72hpf\_pos\_hand2 72hpf\_pos\_gata5.1

### **Spot Genelist**

Raı	nk ID	max	e min e	r e	Syml	Description ool
1	ENSDARG000	2.94	-4.03	0.59		Metazoan signal recognition particle RNA [Source:RFAM;Acc
2	ENSDARG000	2.85	-5.47	0.46	cbx7a	chromobox homolog 7a [Source:ZFIN;Acc:ZDB-GENE-0504
3	ENSDARG000	2.83	-1.77	0.4		si:dkeyp-86h10.3 [Source:ZFIN;Acc:ZDB-GENE-100922-65
4	ENSDARG000	2.63	-3.12	0.55		Metazoan signal recognition particle RNA [Source:RFAM;Acc
5	ENSDARG000	2.62	-1.45	0.29	si:dkey-	-18/5ill/@y8-125i10.3 [Source:ZFIN;Acc:ZDB-GENE-060526-19
6	ENSDARG000	2.59	-1.38	0.68		death associated protein 1b [Source:ZFIN;Acc:ZDB-GENE-(
7	ENSDARG000	2.46	-5.71	0.68		Metazoan signal recognition particle RNA [Source:RFAM;Acc
8	ENSDARG000	2.24	-1.13	0.44	si:dkey-	-16/2#169/3102g19.3 [Source:ZFIN;Acc:ZDB-GENE-091204-2;
9	ENSDARG000	2.23	-3.57	0.65		Metazoan signal recognition particle RNA [Source:RFAM;Acc
10	ENSDARG000	2.22	-4.69	0.93	zgc:165	5 <b>2g</b> c:165573 [Source:ZFIN;Acc:ZDB-GENE-070615-27]
11	ENSDARG000	2.12	-3.78	0.71		Metazoan signal recognition particle RNA [Source:RFAM;Acc
12	ENSDARG000	2.09	-1.65	0.74	si:dkey-	-18iottk@y-10o6.2 [Source:ZFIN;Acc:ZDB-GENE-070705-284]
13	ENSDARG000	2.06	-0.5	0.51		si:ch211-165f21.7 [Source:ZFIN;Acc:ZDB-GENE-070912-1
14	ENSDARG000	2.05	-0.89	0.29		zinc finger protein 70 [Source:HGNC Symbol;Acc:HGNC:131-
15	ENSDARG000	2.02	-1.21	0.6		si:ch1073–190k2.1 [Source:ZFIN;Acc:ZDB-GENE-131127-4
16	ENSDARG000	2	-1.71	0.5		Metazoan signal recognition particle RNA [Source:RFAM;Acc
17	ENSDARG000	1.98	-3.06	0.52		Small Cajal body specific RNA 6 [Source:RFAM;Acc:RF0047
18	ENSDARG000	1.97	-1.97	0.72		Metazoan signal recognition particle RNA [Source:RFAM;Acc
19	ENSDARG000	1.95	-1.69	0.62	si:dkey-	-28/4il/4e)2-234i14.2 [Source:ZFIN;Acc:ZDB-GENE-131127-59
20	ENSDARG000	1.93	-0.98	0.47		si:ch211-194m7.4 [Source:ZFIN;Acc:ZDB-GENE-131125-8

#### Geneset Overrepresentation

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

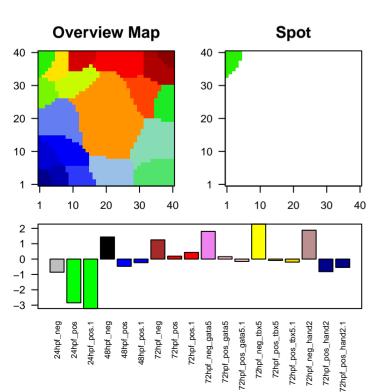


ВР				СС				MF			
Rank	p-value	#in/all	Geneset	Rank	p-value	#in/all	Geneset	Rank	p-value	#in/all	Geneset
1	5e-45	80 / 214	translation	1	1e-50	72 / 147	ribosome	1	2e-51	72 / 144	structural constituent of ribosome
2	4e-14	15 / 23	cytoplasmic translation	2	2e-29	32 / 47	cytosolic large ribosomal subunit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

#### Spot Summary: L

# metagenes = 29 # genes = 578 <r> metagenes = 0.96 <r> genes = 0.72 beta: r2= 31.47 / log p= -Inf # samples with spot = 5 ( 27.8 %) 48hpf\_neg: 1 (100%) 72hpf\_neg: 1 (100%) 72hpf\_neg\_gata5 : 1 ( 100 %)

72hpf\_neg\_hand2:1(100%)

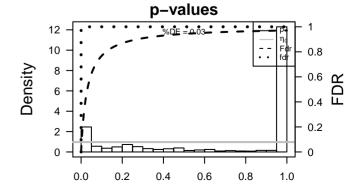


#### **Spot Genelist**

Rai	nk ID	max	e min e	r e	Symb	Description pol
1	ENSDARG000	5.44	-2.17	0.6	opn1sw	2 opsin 1 (cone pigments), short–wave–sensitive 2 [Source:ZFI
2	ENSDARG000	5.4	-5.6	0.82	muc5.1	mucin 5.1, oligomeric mucus/gel-forming [Source:ZFIN;Acc:Z
3	ENSDARG000	5.34	-6.98	0.81	matn1	matrilin 1 [Source:ZFIN;Acc:ZDB-GENE-050307-3]
4	ENSDARG000	5.22	-3.71	0.6	opn1mw	Plopsin 1 (cone pigments), medium-wave-sensitive, 1 [Source:
5	ENSDARG000	5.19	-6.04	0.55	atp1a1a	.2ATPase, Na+/K+ transporting, alpha 1a polypeptide, tandem (
6	ENSDARG000	5.16	-4.48	0.55	opn1sw	1 opsin 1 (cone pigments), short-wave-sensitive 1 [Source:ZFI
7	ENSDARG000	5.14	-4.55	0.79	rho	rhodopsin [Source:ZFIN;Acc:ZDB-GENE-990415-271]
8	ENSDARG000	5.09	-5.91	0.78	and2	actinodin2 [Source:ZFIN;Acc:ZDB-GENE-041105-2]
9	ENSDARG000	5.01	-4.88	0.79	opn1lw2	e opsin 1 (cone pigments), long-wave-sensitive, 2 [Source:ZFI
10	ENSDARG000	4.9	-3.66	0.8	and1	actinodin1 [Source:ZFIN;Acc:ZDB-GENE-030131-9105]
11	ENSDARG000	4.85	-4.47	0.79	npas4a	neuronal PAS domain protein 4a [Source:ZFIN;Acc:ZDB-GEI
12	ENSDARG000	4.83	-5.45	0.81	arr3a	arrestin 3a, retinal (X-arrestin) [Source:ZFIN;Acc:ZDB-GENE
13	ENSDARG000	4.82	-3.89	0.68	gnb3b	guanine nucleotide binding protein (G protein), beta polypepti
14	ENSDARG000	4.76	-5.55	0.83	col10a1	acollagen, type X, alpha 1a [Source:ZFIN;Acc:ZDB-GENE-03
15	ENSDARG000	4.72	-8.26	0.94	col11a2	collagen, type XI, alpha 2 [Source:ZFIN;Acc:ZDB-GENE-000
16	ENSDARG000	4.71	-3.52	0.74	rcvrn3	recoverin 3 [Source:ZFIN;Acc:ZDB-GENE-040426-1661]
17	ENSDARG000	4.57	-3.71	0.69	pde6c	phosphodiesterase 6C, cGMP-specific, cone, alpha prime [Si
18	ENSDARG000	4.55	-3.73	0.79		
19	ENSDARG000	4.55	-4.06	0.71	gnat2	guanine nucleotide binding protein (G protein), alpha transdu
20	ENSDARG000	4.49	-6.7	0.86		si:dkey-65b12.6 [Source:ZFIN;Acc:ZDB-GENE-060526-32\$

#### **Geneset Overrepresentation**

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



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

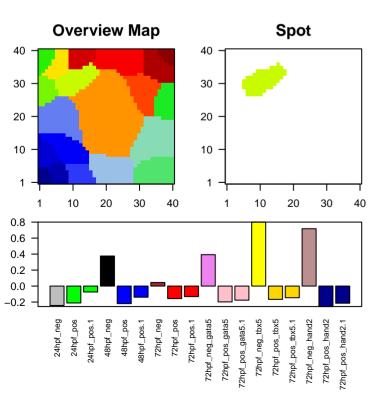
#### Spot Summary: M

# metagenes = 76 # genes = 1213

<r> metagenes = 0.8

beta: r2= 2.25 / log p= -Inf

# samples with spot = 0 ( 0 %)



#### **Spot Genelist**

20 ENSDARG001 1.94

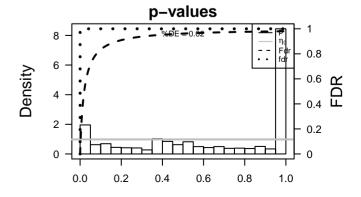
-2.11 0.26

Raı	nk ID	max	e min e	r e	Symi	Description bol	Rank	p-value	#in/all	Gei	neset
1	ENSDARG000	2.78	-2.13	0.6	mmp9	matrix metallopeptidase 9 [Source:ZFIN;Acc:ZDB-GENE-04	1	3e-21	75 / 499	ВР	ion trans
2	ENSDARG000	2.71	-1.53	0.58	zgc:110	1425c:110425 [Source:ZFIN;Acc:ZDB-GENE-050522-103]	2 3 4	1e-17 3e-14 8e-14	49 / 270 31 / 138 401 / 6723	MF BP CC	ion chan potassiu membra
3	ENSDARG000	2.4	-1.48	0.67	zgc:658	85 <b>2</b> gc:65851 [Source:ZFIN;Acc:ZDB-GENE-030131-9669]	5 6	1e-13 3e-13	107 / 1162 375 / 6248	СС	plasma i
4	ENSDARG000	2.28	-1.17	0.28		si:ch211-166i24.1 [Source:ZFIN;Acc:ZDB-GENE-091204-3	7 8	9e-13 1e-12	30 / 147 23 / 86	BP MF	potassiu voltage-
5	ENSDARG000	2.17	-1.56	0.7	ano3	anoctamin 3 [Source:ZFIN;Acc:ZDB-GENE-111031-3]	9 10	1e-12 1e-12	28 / 130 28 / 130	BP MF	regulatio
6	ENSDARG000	2.13	-2.08	0.73	rnf34b	ring finger protein 34b [Source:ZFIN;Acc:ZDB-GENE-07100	11 12	2e-11 8e-11	22 / 90 19 / 70	MF BP	potassiu protein h
7	ENSDARG000	2.09	-1.28	0.66	panx2	pannexin 2 [Source:ZFIN;Acc:ZDB-GENE-050419-55]	13 14	6e-10 2e-09	18 / 70 28 / 176	BP BP	sodium i
8	ENSDARG000	2.08	-1.44	0.78	znf804a	a zinc finger protein 804A [Source:ZFIN;Acc:ZDB-GENE-0709	15 16	1e-08 5e-08	20 / 103 24 / 155	BP CC	cell-cell synapse
9	ENSDARG000	2.07	-1.79	0.71	Irfn5a	leucine rich repeat and fibronectin type III domain containing	17 18	6e-08 7e-08	8 / 15 14 / 56	MF CC	sodium o
10	ENSDARG000	2.06	-1.04	0.29	pcolce2	ta procollagen C-endopeptidase enhancer 2a [Source:ZFIN;Acc	19 20	8e-08 2e-07	85 / 1084 15 / 69	BP MF	transpor extracell
11	ENSDARG000	2.01	-1.71	0.83		neuronal pentraxin receptor a [Source:ZFIN;Acc:ZDB-GENE-	21 22	5e-07 6e-07	9 / 25 66 / 809	MF CC	GABA-A
12	ENSDARG000	2.01	-1.43	0.79	nrxn1b	neurexin 1b [Source:ZFIN;Acc:ZDB-GENE-070206-3]	23 24	2e-06 2e-06	92 / 1295 51 / 591	BP BP	signal tra transme
13	ENSDARG000	2	-1.12	0.88	si:ch21	1-sigsti2ft5l,8195b15.8 [Source:ZFIN;Acc:ZDB-GENE-131127-(	25 26	9e-06 2e-05	13 / 71 7 / 21	MF CC	calmodu GABA-A
14	ENSDARG000	1.98	-0.96	0.27			27 28	2e-05 2e-05	21 / 175 17 / 124	BP MF	nervous receptor
15	ENSDARG000	1.97	-1.67	0.19	crybb1l	1 crystallin, beta B1, like 1 [Source:ZFIN;Acc:ZDB-GENE-100	29 30	3e-05 4e-05	55 / 717 13 / 80	MF CC	postsyna
16	ENSDARG000	1.96	-1.18	0.67	kcna1a	potassium voltage-gated channel, shaker-related subfamily,	31 32	4e-05 5e-05	11 / 59 15 / 106	MF BP	syntaxin
17	ENSDARG000	1.96	-1.64	0.73	prickle2	ta prickle homolog 2a [Source:ZFIN;Acc:ZDB-GENE-061110-1	33 34	5e-05 8e-05	5/11 23/219	BP CC	signaling cell junc
18	ENSDARG000	1.96	-1.92	0.73	grm4	glutamate receptor, metabotropic 4 [Source:ZFIN;Acc:ZDB-C	35 36	1e-04 1e-04	11 / 65 35 / 413	BP BP	sodium i

si:dkev-38icdl@9-33c12.3 [Source:ZFIN:Acc:ZDB-GENE-030131-732

Small nucleolar RNA SNORA73 family [Source:RFAM;Acc:RF

rtariit	۳		//III/all	00.	10001
1	3e-	-21	75 / 499	BP	ion transport
	1e-	-17	49 / 270	MF	ion channel activity
3	3e-	-14	31 / 138	BP	potassium ion transport
4	8e-	-14	401 / 6723	CC	membrane
2 3 4 5 6 7	1e-	-13	107 / 1162	CC	plasma membrane
6	3e-	-13	375 / 6248	CC	integral component of membrane
7	9e-	-13	30 / 147	BP	potassium ion transmembrane transport
8	1e-	-12	23 / 86	MF	voltage-gated potassium channel activity
9	1e-	-12	28 / 130	BP	regulation of ion transmembrane transport
10	1e-	-12	28 / 130	MF	voltage-gated ion channel activity
11	2e-	-11	22 / 90	MF	potassium channel activity
12	8e-	-11	19/70	BP	protein homooligomerization
13	6e-	-10	18 / 70	BP	sodium ion transmembrane transport
14	2e-	-09	28 / 176	BP	ion transmembrane transport
15	1e-	-08	20 / 103	BP	cell-cell signaling
16	5e-	-08	24 / 155	CC	synapse
17	6e-	-08	8 / 15	MF	sodium channel activity
18	7e-	-08	14 / 56	CC	voltage-gated potassium channel complex
19	8e-	-08	85 / 1084	BP	transport
20	2e-	-07	15 / 69	MF	extracellular ligand-gated ion channel activity
21	5e-	-07	9 / 25	MF	GABA-A receptor activity
22	6e-	-07	66 / 809	CC	integral component of plasma membrane
23	2e-	-06	92 / 1295	BP	signal transduction
24	2e-	-06	51 / 591	BP	transmembrane transport
25	9e-	-06	13 / 71	MF	calmodulin binding
26	2e-	-05	7 / 21	CC	GABA-A receptor complex
27	2e-	-05	21 / 175	BP	nervous system development
28	2e-	-05	17 / 124	MF	receptor activity
29	3e-	-05	55 / 717	MF	calcium ion binding
30	4e-	-05	13 / 80	CC	postsynaptic membrane
31	4e-	-05	11 / 59	MF	syntaxin binding
32	5e-	-05	15 / 106	BP	calcium ion transmembrane transport
33	5e-	-05	5 / 11	BP	signaling
34	8e-	-05	23 / 219	CC	cell junction
35	1e-	-04	11 / 65	BP	sodium ion transport
36	1e-	-04	35 / 413	BP	intracellular signal transduction
37	1e-	-04	12/79	MF	calcium channel activity
38	1e-	-04	12 / 79	BP	excitatory postsynaptic potential
39	2e-	-04	19 / 172	BP	homophilic cell adhesion via plasma membrane adhesion molecu
40	2e-	-04	32 / 375	BP	positive regulation of GTPase activity



BP				CC				MF			
Rank p-	-value	#in/all	Geneset	Rank	p-value	#in/all	Geneset	Rank	p-value	#in/all	Geneset
1 Зе	e–21	75 / 499	ion transport	1	8e-14	401 / 6723	membrane	1	1e-17	49 / 270	ion channel activity
2 3e	e-14	31 / 138	potassium ion transport	2	1e-13	107 / 1162	plasma membrane	2	1e-12	23 / 86	voltage-gated potassium channel activity
3 9e	e-13	30 / 147	potassium ion transmembrane transport	3	3e-13	375 / 6248	integral component of membrane	3	1e-12	28 / 130	voltage-gated ion channel activity
4 1e	e-12	28 / 130	regulation of ion transmembrane transport	4	5e-08	24 / 155	synapse	4	2e-11	22 / 90	potassium channel activity
5 8e	e-11	19 / 70	protein homooligomerization	5	7e-08	14 / 56	voltage-gated potassium channel complex	5	6e-08	8 / 15	sodium channel activity
6 6e	e-10	18 / 70	sodium ion transmembrane transport	6	6e-07	66 / 809	integral component of plasma membrane	6	2e-07	15 / 69	extracellular ligand–gated ion channel activity
7 26	e-09	28 / 176	ion transmembrane transport	7	2e-05	7 / 21	GABA-A receptor complex	7	5e-07	9 / 25	GABA-A receptor activity
8 1e	e-08	20 / 103	cell-cell signaling	8	4e-05	13 / 80	postsynaptic membrane	8	9e-06	13 / 71	calmodulin binding
9 86	e-08	85 / 1084	transport	9	8e-05	23 / 219	cell junction	9	2e-05	17 / 124	receptor activity
10 2e	e-06	92 / 1295	signal transduction	10	3e-04	9/51	presynapse	10	3e-05	55 / 717	calcium ion binding
11 2e	e-06	51 / 591	transmembrane transport	11	2e-03	4 / 13	presynaptic membrane	11	4e-05	11 / 59	syntaxin binding
12 26	e-05	21 / 175	nervous system development	12	3e-03	4 / 15	cytoplasmic dynein complex	12	1e-04	12 / 79	calcium channel activity
13 5e	e-05	15 / 106	calcium ion transmembrane transport	13	3e-03	4 / 15	histone acetyltransferase complex	13	4e-04	8 / 42	voltage-gated calcium channel activity
14 5e	e-05	5/11	signaling	14	6e-03	4 / 18	motile cilium	14	9e-04	6 / 27	calmodulin-dependent protein kinase activity
15 1e	e-04	11 / 65	sodium ion transport	15	8e-03	4 / 19	axon	15	1e-03	6 / 28	protein domain specific binding

#### Spot Summary: N

# metagenes = 45

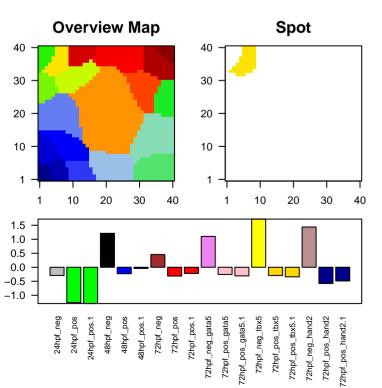
# genes = 810

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

# samples with spot = 4 ( 22.2 %)

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

72hpf\_neg\_tbx5 : 1 ( 100 %) 72hpf\_neg\_hand2 : 1 ( 100 %)

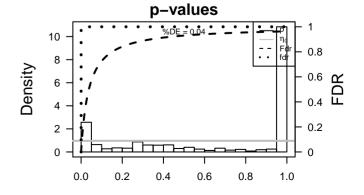


#### **Spot Genelist**

Rar	nk ID	max	e min e	r	Symb	Description ool
1	ENSDARG000	3.87	-1.49	0.84	slc6a17	solute carrier family 6 (neutral amino acid transporter), memb
2	ENSDARG000	3.35	-1.77	0.92	atp1a3a	ATPase, Na+/K+ transporting, alpha 3a polypeptide [Source:2
3	ENSDARG000	3.22	-1.74	0.88	elavl3	ELAV like neuron-specific RNA binding protein 3 [Source:ZFI
4	ENSDARG000	3.21	-2.79	0.57	LOC100	535713
5	ENSDARG000	3.18	-2.43	0.67	egr4	early growth response 4 [Source:ZFIN;Acc:ZDB-GENE-0802
6	ENSDARG000	3.14	-1.84	0.86	slitrk1	SLIT and NTRK-like family, member 1 [Source:ZFIN;Acc:ZDE
7	ENSDARG000	3.13	-1.56	0.93	csmd2	CUB and Sushi multiple domains 2 [Source:ZFIN;Acc:ZDB-G
8	ENSDARG000	3.1	-3.27	0.91	cacna1a	acalcium channel, voltage-dependent, P/Q type, alpha 1A sub
9	ENSDARG000	3.08	-2.8	0.75	syngap1	æynaptic Ras GTPase activating protein 1a [Source:ZFIN;Acc
10	ENSDARG000	3.08	-2.11	0.83	syn2b	synapsin IIb [Source:ZFIN;Acc:ZDB-GENE-051127-49]
11	ENSDARG000	3.02	-2.23	0.74	evx2	even-skipped homeobox 2 [Source:ZFIN;Acc:ZDB-GENE-9i
12	ENSDARG000	2.99	-1.76	0.73	dlx4a	distal-less homeobox 4a [Source:ZFIN;Acc:ZDB-GENE-980
13	ENSDARG000	2.98	-2.28	0.73	pcsk1	proprotein convertase subtilisin/kexin type 1 [Source:ZFIN;Ac
14	ENSDARG000	2.97	-3.26	0.59	st8sia2	ST8 alpha-N-acetyl-neuraminide alpha-2,8-sialyltransferas
15	ENSDARG000	2.96	-1.66	0.85	sez6a	seizure related 6 homolog a [Source:ZFIN;Acc:ZDB-GENE-(
16	ENSDARG000	2.94	-2.03	0.56	admb	adrenomedullin b [Source:ZFIN;Acc:ZDB-GENE-120221-6]
17	ENSDARG000	2.9	-2.16	0.62	fat2	FAT atypical cadherin 2 [Source:ZFIN;Acc:ZDB-GENE-1110
18	ENSDARG000	2.88	-1.98	0.83		si:dkeyp-27e10.3 [Source:ZFIN;Acc:ZDB-GENE-041210-9€
19	ENSDARG000	2.86	-1.72	0.8	syngap1	bsynaptic Ras GTPase activating protein 1b [Source:ZFIN;Acc
20	ENSDARG000	2.84	-2.02	0.85	si:dkey-	1इத்தும் ஓ_175g6.2 [Source:ZFIN;Acc:ZDB_GENE_030131_80€

#### **Geneset Overrepresentation**

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



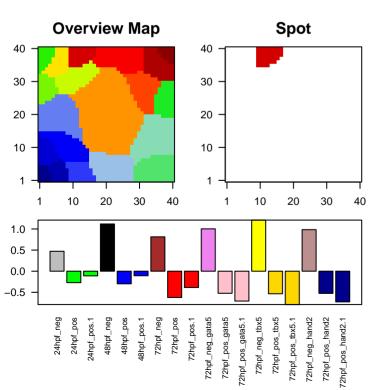
ВР				СС				MF			
Rank	p-value	#in/all	Geneset	Rank	p-value	#in/all	Geneset	Rank	p-value	#in/all	Geneset
1	6e-25	40 / 172	homophilic cell adhesion via plasma membrane adhesion molecules	1	5e-21	312 / 6723	membrane	1	3e-17	67 / 717	calcium ion binding
2	9e-22	50 / 333	cell adhesion	2	4e-20	95 / 1162	plasma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

#### Spot Summary: O

# metagenes = 41
# genes = 757

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

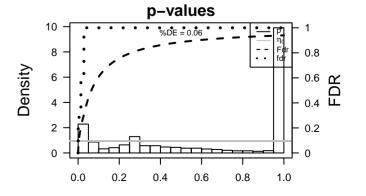
# samples with spot = 5 ( 27.8 %)
 48hpf\_neg : 1 ( 100 %)
 72hpf\_neg : 1 ( 100 %)
 72hpf\_neg\_gata5 : 1 ( 100 %)
 72hpf\_neg\_hand2 : 1 ( 100 %)



#### **Spot Genelist**

Raı	nk ID	max	e min e	r e	Symb	Description ool	Rank	p-value	#in/all	Gei	neset
1	ENSDARG000	3.14	-2.31	0.84	frem2a	Fras1 related extracellular matrix protein 2a [Source:ZFIN;Acı	1	2e-27	108 / 1239	BP	regulatio
2	ENSDARG000	3.08	-2.37	0.64		tubby like protein 4b [Source:ZFIN;Acc:ZDB-GENE-130530-	2	3e-24 1e-20	65 / 537 107 / 1484	MF MF	DNA bin
3	ENSDARG000	2.97	-2.6	0.69		zmp:0000001081 [Source:ZFIN;Acc:ZDB-GENE-140106-41	4 5	2e-16 7e-14	146 / 2716 38 / 333	CC BP MF	cell adhe
4	ENSDARG000	2.87	-3.42	0.75	si:dkeyp-	-র্রাঝেker/p-77h1.4 [Source:ZFIN;Acc:ZDB-GENE-050208-18]	6 7 8	1e-13 5e-11 2e-10	54 / 633 24 / 172 16 / 78	BP BP	transcrip homophi axon gui
5	ENSDARG000	2.85	-1.86	0.77	vcanb	versican b [Source:ZFIN;Acc:ZDB-GENE-030131-2185]	9 10	3e-09 7e-09	37 / 454 10 / 32	BP BP	multicelli retinal ga
6	ENSDARG000	2.81	-1.92	0.83	Irrn1	leucine rich repeat neuronal 1 [Source:ZFIN;Acc:ZDB-GENE	11 12	9e-09 2e-08	48 / 717 44 / 643	MF BP	calcium i
7	ENSDARG000	2.79	-1.66	0.73	col4a6	collagen, type IV, alpha 6 [Source:ZFIN;Acc:ZDB-GENE-101	13 14	9e-08 5e-06	18 / 147 9 / 48	BP BP	brain de
8	ENSDARG000	2.78	-1.46	0.53	abi3bpb	ABI family, member 3 (NESH) binding protein b [Source:ZFIN	15 16	7e-06 2e-05	7 / 28 12 / 100	BP BP	retina me
9	ENSDARG000	2.72	-4	0.72	mxra5b	matrix-remodelling associated 5b [Source:ZFIN;Acc:ZDB-GE	17 18	2e-05 2e-05	56 / 1162 16 / 175	CC BP	plasma r nervous
10	ENSDARG000	2.69	-2.29	0.72	Irfn5b	leucine rich repeat and fibronectin type III domain containing	19 20	4e-05 6e-05	12 / 110 26 / 413	MF BP	protein ty intracellu
11	ENSDARG000	2.67	-1.51	0.76		ryanodine receptor 2 [Source:HGNC Symbol;Acc:HGNC:1048	21 22	8e-05 8e-05	226 / 6723 6 / 28	CC BP	membrai skeletal
12	ENSDARG000	2.66	-1.67	0.76	col4a5	collagen, type IV, alpha 5 (Alport syndrome) [Source:ZFIN;Ac	23 24	1e-04 1e-04	7 / 41 211 / 6248	MF CC	RNA pol
13	ENSDARG000	2.65	-2.02	0.59	aspn	asporin (LRR class 1) [Source:ZFIN;Acc:ZDB-GENE-04110!	25 26	2e-04 2e-04	7 / 44 28 / 491	BP MF	neuron o kinase a
14	ENSDARG000	2.65	-2.8	0.87	thsd7aa	thrombospondin, type I, domain containing 7Aa [Source:ZFIN	27 28	2e-04 2e-04	7 / 45 9 / 76	BP BP	actin cyt
15	ENSDARG000	2.63	-1.69	0.97	nova2	neuro-oncological ventral antigen 2 [Source:ZFIN;Acc:ZDB-(	29 30	2e-04 3e-04	13 / 149 7 / 49	BP MF	cell surfa
16	ENSDARG000	2.62	-2.43	0.6	zgc:1018	8 <b>29</b> c:101810 [Source:ZFIN;Acc:ZDB-GENE-041121-7]	31 32	5e-04 5e-04	7 / 52 5 / 25	MF BP	negative
17	ENSDARG000	2.54	-3.15	0.8			33 34 35	5e-04 6e-04 6e-04	28 / 522 7 / 54 22 / 375	BP BP BP	phospho fin regen positive
18	ENSDARG000	2.53	-1.54	0.81	stmn2a	stathmin 2a [Source:ZFIN;Acc:ZDB-GENE-041010-85]	36 37	6e-04 7e-04	15 / 210 4 / 16	MF BP	protein b
19	ENSDARG000	2.52	-1.6	0.71	entpd5a	ectonucleoside triphosphate diphosphohydrolase 5a [Source:	38 39	9e-04 1e-03	12 / 153 10 / 115	CC MF	proteina
20	ENSDARG000	2.52	-1.65	0.93	dclk1b	doublecortin-like kinase 1b [Source:ZFIN;Acc:ZDB-GENE-0	40	2e-03	10 / 113	MF	protein t

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



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

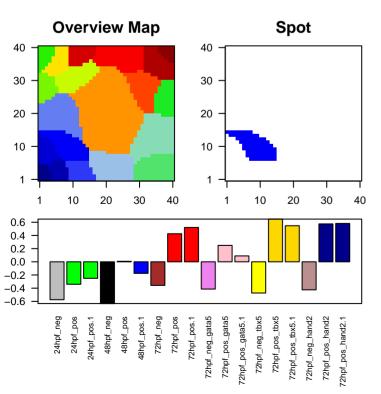
### Spot Summary: P

# metagenes = 80 # genes = 1254

<r> metagenes = 0.82

beta: r2= 4.04 / log p= -Inf

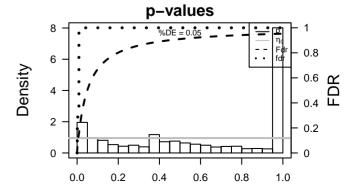
# samples with spot = 0 ( 0 %)



### **Spot Genelist**

Rar	nk ID	max	e min e	r ∋	Symb	Description ool	Rank	p-value	#in/all	Ger	neset
1	ENSDARG000	6.21	-1.42	0.4	scpp5	secretory calcium-binding phosphoprotein 5 [Source:ZFIN;Ac	1	3e-21	94 / 712	ВР	oxidation
							2	8e-20	76 / 522	MF	oxidored
2	ENSDARG000	3.42	-1.9	0.41	pcyt1bb	phosphate cytidylyltransferase 1, choline, beta b [Source:ZFII	3	2e-10	50 / 414	BP	metaboli
							4	2e-09	389 / 6723	CC	membra
3	ENSDARG000	3.22	-3.48	0.69	cfh	complement factor H [Source:ZFIN;Acc:ZDB-GENE-050208	5	1e-08	46 / 410	CC	mitochor
							6	1e-08	51 / 480	MF	catalytic
4	ENSDARG000	3.14	-2.4	0.49	cyp1b1	cytochrome P450, family 1, subfamily B, polypeptide 1 [Sourc	7	2e-08	361 / 6248	CC	integral of
							8	2e-08	8 / 13	BP	response
5	ENSDARG000	2.92	-1.62	0.78	sepp1b	selenoprotein P, plasma, 1b [Source:ZFIN;Acc:ZDB-GENE-C	9	3e-08	24 / 145	MF	heme bii
							10	3e-08	10 / 24	CC	respirato
6	ENSDARG000	2.92	-2.18	0.9	tagapa	T-cell activation RhoGTPase activating protein a [Source:ZFI	11	6e-08	21 / 119	MF	monooxy
							12	8e-08	20 / 110	MF	oxidored
7	ENSDARG000	2.91	-3.06	0.83	agt	angiotensinogen [Source:ZFIN;Acc:ZDB-GENE-030131-120	13	1e-07	26 / 178	MF	iron ion l
-							14	1e-07	9 / 21	MF	NADH d
8	ENSDARG000	2.88	-1.91	0.81	dpydb	dihydropyrimidine dehydrogenase b [Source:ZFIN;Acc:ZDB-(	15	2e-06	9 / 27	MF	oxidored
•					.,		16	4e-06	27 / 229	MF	transpor
9	ENSDARG00	2.86	-1.8	0.83	abcb11b	ATP-binding cassette, sub-family B (MDR/TAP), member 111	17	6e-06	51 / 591	BP	transme
•							18	1e-05	9 / 33	MF	oxidored
10	ENSDARG00	2.85	-2.98	0.57	hsp70l	heat shock cognate 70-kd protein, like [Source:ZFIN;Acc:ZDI	19	4e-05	6 / 16	MF	acyl-Co
10	2.102/11000	2.00	2.00	0.01		(	20	4e-05	7 / 23	CC	mitochor
11	ENSDARG000	2.84	-3.3	0.67	cvn24a1	cytochrome P450, family 24, subfamily A, polypeptide 1 [Sour	21	6e-05	5/11	MF	oxidored
	LINODAINOOO	2.04	-0.0	0.07	oype iai	oyloomonio i 100, taniny 21, oabianiny 71, polypopilao i (coa	22	8e-05	7 / 25	BP	ATP syn
12	ENSDARG000	2 02	-2.28	0.69	oirob211	-\$6\$\$2 -264f5.2 [Source:ZFIN;Acc:ZDB-GENE-080303-2]	23	1e-04	5 / 12	MF	FMN bin
12	ENSDARGOO	2.02	-2.20	0.09	SI.CHZ I I	-20412.21 -20413.2 [300106.21 114,A00.2DB-3E14E-000303-2]	24	1e-04	5 / 12	CC	mitochor
10	ENCDA DOOG	0.70	-1.4	0.87	ch25h	cholesterol 25-hydroxylase [Source:ZFIN;Acc:ZDB-GENE-0	25	2e-04	68 / 969	MF	hydrolas
13	ENSDARG00	2.78	-1.4	0.87	CHZ5H	Cholesterol 25-hydroxylase [Source.2Filit,ACC.2DB-GENE-0	26	2e-04	10 / 57	MF	flavin ad
4.4	=	0.70	4.00	0.04		CECAA III.a II.aid biadiaa 7 (Causaa 751N) Aaa 700 CENE 44	27	2e-04	8 / 38	CC	apical pl
14	ENSDARG000	2.78	-1.92	0.81		SEC14-like lipid binding 7 [Source:ZFIN;Acc:ZDB-GENE-14	28	3e-04	18 / 161	CC	mitochor
4-					1 70 4		29	4e-04	14 / 109	BP	apoptoti
15	ENSDARG000	2.76	-2.97	0.51	nsp/0.1	heat shock cognate 70-kd protein, tandem duplicate 2 [Sourc	30	4e-04	7 / 31	MF	hydroge
							31	4e-04	15 / 122	BP	inflamma
16	ENSDARG000	2.75	-3.08	0.49	si:ch211	-នុវិត្សាជា 1:8-256m1.8 [Source:ZFIN;Acc:ZDB-GENE-131127-4	32	5e-04	108 / 1761	MF	metal ior
							33	7e-04	6 / 25	MF	tumor ne
17	ENSDARG000	2.73	-1.98	0.85	serpinc1	serpin peptidase inhibitor, clade C (antithrombin), member 1 [	34	7e-04	4 / 10	BP	response
							35	7e-04	5 / 17	MF	hydrolas
18	ENSDARG000	2.71	-1.4	0.19	tbx18	T-box 18 [Source:ZFIN;Acc:ZDB-GENE-020529-2]	36	7e-04	5 / 17	BP	regulation
							37	8e-04	7 / 35	CC	peroxiso
19	ENSDARG000	2.69	-4.1	0.81		RAB44, member RAS oncogene family [Source:ZFIN;Acc:ZD	38	8e-04	70 / 1066	CC	intracellu
							39	1e-03	4 / 11	BP	mitochor
20	ENSDARG000	2.67	-2.47	0.72	cyp1a	cytochrome P450, family 1, subfamily A [Source:ZFIN;Acc:ZE	40	1e-03	4/11	BP	nitrogen

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



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

#### Spot Summary: Q

```
# metagenes = 18

# genes = 335

<r> metagenes = 0.98

<r> genes = 0.8

beta: r2= 59.39 / log p= -Inf

# samples with spot = 10 (55.6 %)

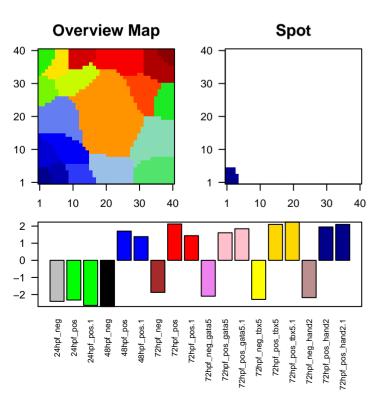
48hpf_pos : 2 (100 %)

72hpf_pos = 2 (100 %)

72hpf_pos_gata5 : 2 (100 %)

72hpf_pos_tbx5 : 2 (100 %)

72hpf_pos_hand2 : 2 (100 %)
```



#### **Spot Genelist**

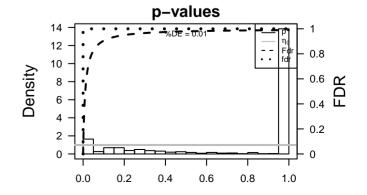
20 ENSDARG001 4.4

-6.51 0.98

Raı	nk ID	max	e min e	r ∋	Syml	Description ool	Rank	p-value	#in/all	Ge	neset
1	ENSDARG000	5.16	-6.13	0.97	oacyl	O-acyltransferase like [Source:ZFIN;Acc:ZDB-GENE-09071	1	2e-18	43 / 712	ВР	oxidation
2	ENSDARG000	4.98	-7.11	0.96	wu:fc46	htva::fc46h12 [Source:ZFIN;Acc:ZDB-GENE-030131-3611]	2	3e-17 5e-14	36 / 522 10 / 23	MF BP	lipoprote
3	ENSDARG000	4.9	-4.2	0.7	zgc:112	28gc:112265 [Source:ZFIN;Acc:ZDB-GENE-050626-133]	4 5	4e-12 2e-11	7/10	CC BP	chylomic
4	ENSDARG000	4.88	-6.93	0.96	si:dkey-	25/18/18/2-251110.2 [Source:ZFIN;Acc:ZDB-GENE-050506-10.	6 7 8	5e-11 6e-10 6e-10	9 / 30 6 / 10 6 / 10	BP CC BP	pigmenta high-der triglyceri
5	ENSDARG000	4.84	-5.75	0.78	serpina	Ilserine (or cysteine) proteinase inhibitor, clade A (alpha-1 anti	9 10	6e-10 1e-09	7/17 6/11	CC BP	blood mi choleste
6	ENSDARG000	4.78	-3.37	0.81	c3a.3	complement component c3a, duplicate 3 [Source:ZFIN;Acc:Z	11 12	2e-09 3e-09	6 / 12 28 / 634	BP CC	choleste
7	ENSDARG000	4.72	-6.07	0.65	vmhcl	ventricular myosin heavy chain-like [Source:ZFIN;Acc:ZDB-(	13 14	4e-09 3e-08	6 / 13 6 / 17	BP MF	choleste
8	ENSDARG000	4.71	-7.81	0.93	gch2	GTP cyclohydrolase 2 [Source:ZFIN;Acc:ZDB-GENE-00120	15 16	3e-08 8e-08	6 / 17 11 / 109	MF BP	choleste negative
9	ENSDARG000	4.69	-4.69	0.66	agxtb	alanine-glyoxylate aminotransferase b [Source:ZFIN;Acc:ZDI	17 18	1e-07 7e-07	7 / 33 19 / 414	MF BP	endopep metaboli
10	ENSDARG000	4.67	-4.1	0.77	plg	plasminogen [Source:ZFIN;Acc:ZDB-GENE-030131-1411]	19 20	4e-06 6e-06	4 / 10 4 / 11	CC BP	melanos purine n
11	ENSDARG000	4.58	-3.93	0.68	fga	fibrinogen alpha chain [Source:ZFIN;Acc:ZDB-GENE-03101	21 22	8e-06 1e-05	5 / 24 5 / 25	BP BP	nucleosi cellular r
12	ENSDARG000	4.57	-5.01	0.81	serpina	1 serpin peptidase inhibitor, clade A (alpha-1 antiproteinase, ar	23 24	1e-05 2e-05	5 / 26 5 / 29	BP BP	melanoc cellular r
13	ENSDARG000	4.53	-5.75	0.99		si:dkey-73n8.3 [Source:ZFIN;Acc:ZDB-GENE-141219-27]	25 26	4e-05 4e-05	5 / 32 8 / 105	MF MF	oxidored lipid bind
14	ENSDARG000	4.53	-4.41	0.81	fgb	fibrinogen beta chain [Source:ZFIN;Acc:ZDB-GENE-030131	27 28	4e-05 7e-05	5 / 33 17 / 480	MF MF	NAD bin catalytic
15	ENSDARG000	4.51	-4.97	0.96	zgc:113	14gc:113142 [Source:ZFIN;Acc:ZDB-GENE-050220-2]	29 30	1e-04 1e-04	17 / 500 13 / 321	MF	GTPase
16	ENSDARG000	4.47	-7.23	0.97	xdh	xanthine dehydrogenase [Source:ZFIN;Acc:ZDB-GENE-070	31 32	2e-04 3e-04	3/10	MF BP	protein b melanos
17	ENSDARG000	4.45	-2.24	0.72	plxdc1	plexin domain containing 1 [Source:ZFIN;Acc:ZDB-GENE-08	33 34 35	3e-04 3e-04	4 / 27 4 / 27 5 / 50	BP BP BP	developr response lipid cata
18	ENSDARG000	4.44	-6.92	0.97	zgc:162	159c:162150 [Source:ZFIN;Acc:ZDB-GENE-070410-23]	36 37	3e-04 3e-04 3e-04	3/12	BP BP	aromatic negative
19	ENSDARG000	4.42	-4.7	0.64	tnnc1a	troponin C type 1a (slow) [Source:ZFIN;Acc:ZDB-GENE-030	38	3e-04 3e-04	3/12	BP	platelet a

bscl2| Bernardinelli-Seip congenital lipodystrophy 2, like [Source:ZF

1	2e-18	43 / 712	BP	oxidation-reduction process
	3e-17	36 / 522	MF	oxidoreductase activity
ร์	5e-14	10 / 23	BP	lipoprotein metabolic process
4	4e-12	7/10	CC	chylomicron
5	2e-11	12 / 67	BP	lipid transport
6	5e-11	9/30	BP.	pigmentation
7	6e-10	6/10	CC	high-density lipoprotein particle
2 3 4 5 6 7 8	6e-10	6/10	BP	triglyceride catabolic process
9	6e-10	7 / 17	CC	blood microparticle
10	1e-09	6/11	BP	cholesterol homeostasis
11	2e-09	6 / 12	BP	cholesterol biosynthetic process
12	3e-09	28 / 634	CC	extracellular region
13	4e-09	6 / 13	BP	cholesterol efflux
14	3e-08	6 / 17	MF	cholesterol binding
15	3e-08	6 / 17	MF	cholesterol transporter activity
16	8e-08	11 / 109	BP	negative regulation of endopeptidase activity
17	1e-07	7 / 33	MF	endopeptidase inhibitor activity
18	7e-07	19 / 414	BP	metabolic process
19	4e-06	4 / 10	CC	melanosome
20	6e-06	4 / 11	BP	purine nucleotide biosynthetic process
21	8e-06	5 / 24	BP	nucleoside metabolic process
22	1e-05	5 / 25	BP	cellular response to estrogen stimulus
23	1e-05	5 / 26	BP	melanocyte differentiation
24	2e-05	5 / 29	BP	cellular response to xenobiotic stimulus
25	4e-05	5 / 32	MF	oxidoreductase activity, acting on the CH-OH group of donors, NAD or NAI
26	4e-05	8 / 105	MF	lipid binding
27	4e-05	5/33	MF	NAD binding
28	7e-05	17 / 480	MF	catalytic activity
29	1e-04	17 / 500	CC	extracellular space
30	1e-04	13 / 321	MF	GTPase activity
31	2e-04	3 / 10	MF	protein binding, bridging
32	3e-04	3/11	BP	melanosome organization
33	3e-04	4 / 27	BP	developmental pigmentation
34	3e-04	4 / 27	BP	response to bacterium
35	3e-04	5 / 50	BP	lipid catabolic process
36	3e-04	3 / 12	BP	aromatic amino acid family metabolic process
37	3e-04	3 / 12	BP	negative regulation of insulin receptor signaling pathway
38	3e-04	3 / 12	BP	platelet activation
39	4e-04	3 / 13	BP	response to toxic substance
40	5e-04	17 / 561	MF	GTP binding



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

#### Spot Summary: R

# metagenes = 40 # genes = 621

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

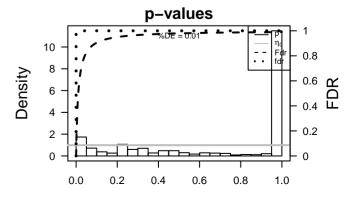
# samples with spot = 3 ( 16.7 %)

72hpf\_pos\_tbx5 : 2 ( 100 %)

#### **Overview Map** Spot 30 30 20 20 10 -10 30 30 10 20 40 10 20 0.5 0.0 -0.5 -1.0 -1.5 -2.0 48hpf\_pos.1 72hpf\_neg 72hpf\_pos 72hpf\_neg\_gata5 72hpf\_pos\_gata5 48hpf\_pos 72hpf\_pos.1 72hpf\_neg\_tbx5 72hpf\_pos\_hand2 72hpf\_pos\_gata5.1

### **Spot Genelist**

Rai	nk	max	е	r		Description	Rank	p-value	#in/all	Ge	neset
	ID		min e	Э	Symb	ool					
1	ENSDARG000	5.99	-1.86	0.39		si:ch211-220f21.2 [Source:ZFIN;Acc:ZDB-GENE-160113-1	1	7e-10	9 / 23	СС	troponin complex
•							ż	2e-09	23 / 231	MF	actin binding
2	ENSDARG00	4.89	-6.08	0.63		si:dkey-9l20.3 [Source:ZFIN;Acc:ZDB-GENE-090313-369]	3	8e-09	35 / 522	MF	oxidoreductase activity
_							4	3e-08	41 / 712	BP	oxidation-reduction process
3	ENSDARG00	4.72	-2.88	0.52	si:ch211	-sixh220-5i17m20.5 [Source:ZFIN;Acc:ZDB-GENE-030131-	5	1e-07	40 / 717	MF	calcium ion binding
·							6	2e-07	6 / 13	BP	regulation of muscle contraction
4	ENSDARG00	4.58	-2.18	0.63	zgc:1119	923c:111983 [Source:ZFIN;Acc:ZDB-GENE-050417-335]	7	4e-07	11 / 70	CC	myosin complex
•					-		8	9e-07	13 / 109	BP	negative regulation of endopeptidase activity
5	ENSDARG00	4.25	-3.15	0.44	si:ch211	-sistlesy-239b22.1 [Source:ZFIN;Acc:ZDB-GENE-131119-12	9	1e-06	7 / 26	BP	mitophagy
Ü						•	10	2e-06	5/11	BP	cellular response to nitrogen starvation
6	ENSDARG00	4.19	-1.87	0.68	hal	histidine ammonia-lyase [Source:ZFIN;Acc:ZDB-GENE-070	11	2e-06	5/11	MF	ferric iron binding
Ü							12	2e-06	6 / 19	BP	gluconeogenesis
7	ENSDARG00	4.15	-2.21	0.64	oxct1b	3-oxoacid CoA transferase 1b [Source:ZFIN;Acc:ZDB-GENE	13	6e-06	5 / 13	BP	iron ion transport
•						•	14	7e-06	25 / 414	BP	metabolic process
8	ENSDARG00	4.09	-6.65	0.6	krt17	keratin 17 [Source:ZFIN;Acc:ZDB-GENE-060503-86]	15	1e-05	67 / 1761	MF	metal ion binding
O						, ,	16	1e-05	27 / 480	MF	catalytic activity
9	ENSDARG00	3.79	-2.85	0.68	si:ch211	-si9392111.3195b11.3 [Source:ZFIN;Acc:ZDB-GENE-141222-(	17	1e-05	6 / 24	BP	cellular iron ion homeostasis
Ü						, , , , , , , , , , , , , , , , , , , ,	18	1e-05	5 / 15	BP	response to mechanical stimulus
10	ENSDARG00	3.79	-2.06	0.52	icn2	ictacalcin 2 [Source:ZFIN;Acc:ZDB-GENE-070822-9]	19	1e-05	6 / 25	MF	glutathione transferase activity
10						, , , , , , , , , , , , , , , , , , , ,	20	1e-05	12 / 120	MF	motor activity
11	ENSDARG00	3.78	-3.48	0.7	mtp	microsomal triglyceride transfer protein [Source:ZFIN;Acc:ZD	21	5e-05	6 / 31	BP	autophagosome assembly
				***		, , , , , , , , , , , , , , , , , , , ,	22	6e-05	9 / 79	MF	steroid hormone receptor activity
12	ENSDARG00	3 73	-2.36	0.7		phosphorylase, glycogen, liver [Source:ZFIN;Acc:ZDB-GENE	23	8e-05	9 / 81	BP	steroid hormone mediated signaling pathway
12	2.102/110001	0.10	2.00	0		1 ,	24	8e-05	6/33	MF	endopeptidase inhibitor activity
13	ENSDARG00	3.72	-2.88	0.62	fabp10a	fatty acid binding protein 10a, liver basic [Source:ZFIN;Acc:ZI	25	9e-05	6/34	BP	glycolytic process
10						,	26	1e-04	4 / 12	BP	response to activity
14	ENSDARG000	3.72	-3.24	0.59		si:ch211-217k17.9 [Source:ZFIN;Acc:ZDB-GENE-061207-2	27	2e-04	7 / 53	BP	autophagy
1-7	2.102/110001					, , , , , , , , , , , , , , , , , , , ,	28	2e-04	13 / 178	MF	iron ion binding intracellular receptor signaling pathway
15	ENSDARG00	3.63	-2.04	0.68	zgc:1720	05thc:172051 [Source:ZFIN;Acc:ZDB-GENE-080219-23]	29 30	2e-04	6 / 40 4 / 15	BP BP	, , ,
					•	g ( , ,,	30 31	3e-04 3e-04	4 / 15	MF	cardiac muscle contraction
16	ENSDARG00	3.62	-2.04	0.66	gc	group-specific component (vitamin D binding protein) [Source	32	3e-04 3e-04	4 / 15	BP	nucleoside diphosphate kinase activity nucleoside diphosphate phosphorylation
10					•	3 - 1 - 1 - 1 - 1 - 1 - 1 - 1 - 1 - 1 -	32 33	3e-04 3e-04	4 / 15	BP	skeletal muscle contraction
17	ENSDARG000	3.61	-2.02	0.74	LOC108	1sigch211-212c13.8 [Source:ZFIN;Acc:ZDB-GENE-131118-2	33 34	6e-04	55 / 1580	CC	cellular_component
.,	2.102/110001				200.00	, , , , , , , , , , , , , , , , , , , ,	35	7e-04	6 / 49	BP	cell-matrix adhesion
18	ENSDARG00	3.56	-1.31	0.54		jacalin 10 [Source:ZFIN;Acc:ZDB-GENE-071004-126]	36	1e-03	5 / 35	BP	sarcomere organization
						,	37	1e-03	3/10	BP	glycogen biosynthetic process
19	ENSDARG00	3.53	-3.48	0.64	g6pca.2	glucose-6-phosphatase a, catalytic subunit, tandem duplicat	38	1e-03	9/119	BP	regulation of cell proliferation
					3-1		39	2e-03	3/113	BP	photoperiodism
20	ENSDARG000	3.52	-2.88	0.85	uroc1	urocanate hydratase 1 [Source:ZFIN;Acc:ZDB-GENE-08102	40	2e-03	4 / 25	BP	tricarboxylic acid cycle
20	2.400/110000	3.02	2.00	3.00	31001	,	70	_3 00	. , 20	Di	,



### Spot Summary: S

```
# metagenes = 31

# genes = 520

<r> metagenes = 0.97

<r> genes = 0.75

beta: r2= 20.77 / log p= -Inf

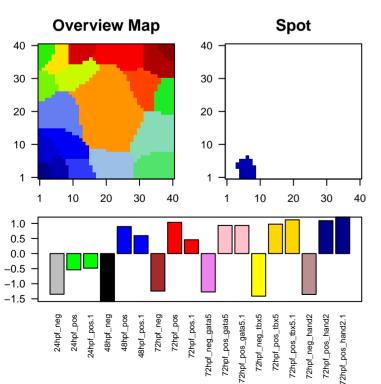
# samples with spot = 8 ( 44.4 %)

48hpf_pos : 1 ( 50 %)

72hpf_pos : 1 ( 50 %)

72hpf_pos_gata5 : 2 ( 100 %)

72hpf_pos_hand2 : 2 ( 100 %)
```



#### **Spot Genelist**

max e

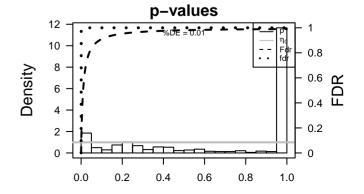
Rank

itai	ÏD		min e		Symb	ool
1	ENSDARG000	4.01	-2.52	0.6		
2	ENSDARG000	3.99	-4.09	0.77	myl7	myosin, light chain 7, regulatory [Source:ZFIN;Acc:ZDB-GEN
3	ENSDARG000	3.62	-3.18	0.71	plaua	plasminogen activator, urokinase a [Source:ZFIN;Acc:ZDB-G
4	ENSDARG000	3.51	-4.07	0.77	hspb7	heat shock protein family, member 7 (cardiovascular) [Source
5	ENSDARG000	3.42	-2.94	0.67	Irrc10	leucine rich repeat containing 10 [Source:ZFIN;Acc:ZDB-GEI
6	ENSDARG000	3.41	-3.37	0.76	mybpc3	myosin binding protein C, cardiac [Source:ZFIN;Acc:ZDB-GE
7	ENSDARG000	3.33	-5.73	0.71	slc8a1a	solute carrier family 8 (sodium/calcium exchanger), member 1
8	ENSDARG000	3.24	-3.98	0.76		ryanodine receptor 2b (cardiac) [Source:ZFIN;Acc:ZDB-GEN
9	ENSDARG000	3.24	-2.94	0.8		
10	ENSDARG000	3.15	-3.12	0.64	lmod2b	leiomodin 2 (cardiac) b [Source:ZFIN;Acc:ZDB-GENE-0412'
11	ENSDARG000	3.14	-3.74	0.69	qdpra	quinoid dihydropteridine reductase a [Source:ZFIN;Acc:ZDB-
12	ENSDARG000	3.1	-3	0.6	LOC100	150660 polymerization promoting protein [Source:ZFIN;Acc:ZI
13	ENSDARG000	2.98	-3.59	0.88	mrc1b	mannose receptor, C type 1b [Source:ZFIN;Acc:ZDB-GENE-
14	ENSDARG000	2.97	-3	0.88		si:ch211-194m7.3 [Source:ZFIN;Acc:ZDB-GENE-131121-1
15	ENSDARG000	2.81	-2.52	0.86	si:ch211	-30912316-209f23.6 [Source:ZFIN;Acc:ZDB-GENE-141211-7
16	ENSDARG000	2.78	-4.04	0.9	ctss2.1	cathepsin S, ortholog2, tandem duplicate 1 [Source:ZFIN;Acc
17	ENSDARG000	2.77	-2.86	0.73	myh7bb	myosin, heavy chain 7B, cardiac muscle, beta b [Source:ZFIN
18	ENSDARG000	2.75	-2.5	0.94	hmox1a	heme oxygenase 1a [Source:ZFIN;Acc:ZDB-GENE-030131-
19	ENSDARG000	2.73	-2.21	0.75		adhesion G protein-coupled receptor G3 [Source:ZFIN;Acc:Z
20	ENSDARG000	2.72	-3.38	0.9	il10ra	interleukin 10 receptor, alpha [Source:ZFIN;Acc:ZDB-GENE-

Description

#### **Geneset Overrepresentation**

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



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

### Spot Summary: T

# metagenes = 44
# genes = 722

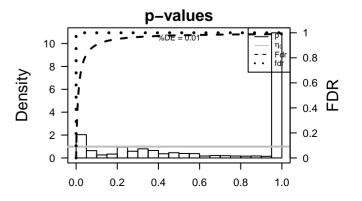
<r> metagenes = 0.94 <r> genes = 0.6 beta: r2= 7.01 / log p= -Inf

# samples with spot = 0 ( 0 %)

#### **Overview Map** Spot 30 30 20 20 10 -10 20 30 20 30 10 40 10 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**

Ra	Rank max e r			Description	Rank	p-value	#in/all	neset			
	ID		min e	Э	Syml	ool					
					-						
4	ENSDARG000	2 50	-3.41	0.69	vmhc	ventricular myosin heavy chain [Source:ZFIN;Acc:ZDB-GENI	1	9e-11	40 / 480	MF	catalytic activity
ı	ENSDARGOO	3.39	-3.41	0.09	VIIIIC	ventricular myosiir neavy chain joodioc.21 m,766.200-0211	2	1e-08	33 / 414	BP	metabolic process
2	ENCDA DC00	2.24	-3.58	0.62	-140-	C-type lectin domain containing 19A [Source:ZFIN;Acc:ZDB-	3	6e-08	9/31	MF	hydrogen ion transmembrane transporter activity
2	ENSDARG000	3.21	-3.58	0.62	ciec i 9a	C-type lectiff domain containing 19A [Source.ZFIN,Acc.ZDB-	4	3e-07	14 / 101	CC	endosome
2	FNODADOOS	0.00	0.00	0.50	-IO F	NK2 homeobox 5 [Source:ZFIN;Acc:ZDB-GENE-980526-32	5	9e-07	8/31	BP	ATP hydrolysis coupled proton transport
3	ENSDARG000	2.88	-2.32	0.56	nkx2.5	INC HOMEODOX 5 [Source.ZFIN,ACC.ZDB-GENE-980520-52	6	1e-06	17 / 164	BP	carbohydrate metabolic process
	FNODADOOS	0.00	4.0	0.75	overno 21	D	7	1e-06	16 / 147	BP	vesicle-mediated transport
4	ENSDARG00	2.82	-1.8	0.75	synpozi	b synaptopodin 2-like b [Source:ZFIN;Acc:ZDB-GENE-09082	8	2e-06	7 / 25	MF	proton–transporting ATPase activity, rotational mechanism
_	=					750	9	2e-06	19 / 210	BP	intracellular protein transport
5	ENSDARG000	2.81	-2.63	0.65		myosin, heavy chain 7B, cardiac muscle, beta a [Source:ZFIN	10	7e-06	9/53	MF	pyridoxal phosphate binding
_							11	1e-05	5 / 13	CC	proton-transporting V-type ATPase, V0 domain
6	ENSDARG00	2.73	-1.88	0.66	hebp2	heme binding protein 2 [Source:ZFIN;Acc:ZDB-GENE-04042	12	2e-05	6/23	BP	retrograde transport, endosome to Golgi
_							13	2e-05 2e-05	8 / 47	BP	proton transport
7	ENSDARG00	2.7	-3.16	0.66	mylk2	myosin light chain kinase 2 [Source:ZFIN;Acc:ZDB-GENE-0]	14	3e-05	22 / 321	MF	GTPase activity
_							15	4e-05	50 / 1066	CC	intracellular
8	ENSDARG000	2.64	-2.08	0.78	mibp	muscle-specific beta 1 integrin binding protein [Source:ZFIN;	16	4e-05	9 / 64	MF	hydrolase activity, acting on glycosyl bonds
_							17	5e-05	14 / 156	BP	small GTPase mediated signal transduction
9	ENSDARG000	2.64	-3.7	0.53	LOC565	15/15/h211-233h19.2 [Source:ZFIN;Acc:ZDB-GENE-061009-	18	6e-05	31 / 561	MF	GTP binding
							19	7e-05	5 / 18	CC	endosome membrane
10	ENSDARG000	2.51	-1.81	0.67	csrp3	cysteine and glycine-rich protein 3 (cardiac LIM protein) [Sou	20	8e-05	9/71	CC	endomembrane system
							21	1e-04	17 / 231	MF	actin binding
11	ENSDARG000	2.46	-1.35	0.65	nppb	natriuretic peptide B [Source:ZFIN;Acc:ZDB-GENE-130530-	22	1e-04	8 / 59	BP	actin filament organization
							23	2e-04	5 / 21	BP	muscle contraction
12	ENSDARG000	2.44	-2.75	0.7	mylk3	myosin light chain kinase 3 [Source:ZFIN;Acc:ZDB-GENE-0:	24	2e-04	48 / 1084	BP	transport
							25	2e-04	83 / 2189	CC	cytoplasm
13	ENSDARG000	2.43	-3.39	0.76	gata4	GATA binding protein 4 [Source:ZFIN;Acc:ZDB-GENE-98052	26	3e-04	4 / 13	BP	cellular response to oxidative stress
							27	3e-04	4 / 13	BP	vesicle organization
14	ENSDARG000	2.4	-3.18	0.56	si:ch73-	-2xi8xt2735248e21.5 [Source:ZFIN;Acc:ZDB-GENE-120215-2!	28	3e-04	7 / 51	CC	lysosomal membrane
							29	3e-04	5 / 24	BP	metal ion transport
15	ENSDARG000	2.39	-2.43	0.74	popdc2	popeye domain containing 2 [Source:ZFIN;Acc:ZDB-GENE-I	30	3e-04	6 / 37	BP	myofibril assembly
							31	4e-04	5 / 25	BP	phosphatidylinositol dephosphorylation
16	ENSDARG000	2.37	-1.55	0.74			32	4e-04	212 / 6723	CC	membrane
							33	4e-04	43 / 969	MF	hydrolase activity
17	ENSDARG000	2.36	-4.29	0.52	obsl1a	obscurin-like 1a [Source:ZFIN;Acc:ZDB-GENE-060503-64§	34	4e-04	6/39	CC	Z disc
							35	6e-04	4 / 16	MF	FAD binding
18	ENSDARG000	2.33	-2.97	0.77	gata5	GATA binding protein 5 [Source:ZFIN;Acc:ZDB-GENE-98052	36	7e-04	6 / 42	MF	SNAP receptor activity
							37	8e-04	4 / 17	CC	Arp2/3 protein complex
19	ENSDARG000	2.32	-2.15	0.64	alpk3a	alpha-kinase 3a [Source:ZFIN;Acc:ZDB-GENE-050419-48]	38	1e-03	8 / 79	MF	phosphatidylinositol binding
							39	1e-03	20 / 355	CC	cytosol
20	ENSDARG000	2.32	-2.72	0.5	crestin	crestin [Source:ZFIN;Acc:ZDB-GENE-000208-13]	40	1e-03	12 / 161	CC	mitochondrial inner membrane



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