FUNCTIONAL TRANSCRIPTOMICS IN Schmidtea mediterranea STEM CELLS

G. Rodríguez-Esteban, J<u>.F. Abril</u>, A. González-Sastre, J.I. Rojo-Laguna, M. Marín, E. Saló The Saló Lab & Computational Genomics Lab, Department of Genetics, UB & IBUB

1. Mapping DGE tags



2. GO and Pfam annotation





TAGS MAPPING



After discarding low-occurrence reads (left), 27,116 tags have been mapped against all publicly available transcriptomes, GeneBank ESTs and Genomic URFs of S. mediterranea (top).

Remarkably, only a 6.0% of the tags are present in all the datasets and only a 3.4% are shared by all transcriptomes, showing a divergence between them. Also, a few number of tags (1.4%) mapped exclusively over the Genomic URFs revealing potential genes not represented in the current sets of ESTs.

Number of Occurrences

6. New neoblast genes identified



α-H3P

From our differential expression analysis we have been able to identify and experimentally validate new 47 neoblastrelated genes, from which a **meis-like** (left) and three *nf-Y* (bottom) are shown here.

Kir



3. Data mining

Web accessible dynamic tables are provided for a userfriendly interaction with complex search and sorting capabilities at planarian.bio.ub.edu

		~	MSB RV				% coverage	omes rel. 98º	Transcript	
Subjec	Term		umina plus NK	GOs	Bit score	E-value	Pfam	54_90e ₁	Smed4	
			RN							
A6QR	in thiolesterase activity	ubiquiti	n454ESTABI	0004221	268.8 0004221		PF00443	1027	90e_	
3	ident protein catabolic process	Ts ^{tin-depen}	mediterranea ESTs	0006511	55.1	1e-18	PF13423	1027	90e_	
Q6P8	NA		enomic URFs	NA	93.7	7.2e-31	PF01248	10270	90e_1	
			RES from contigs		22.6	1.4e-8	PF08228	10270	90e_10270	
					14	0.000032	PF11202	10270	90e_1	
P592	ribosome		ellular_component	0008270	119.5 00082		PF01529	10271	90e_1	
NA	NA		NA	NA	NA	NA	NA	10272	90e_1	
Q637	structural constituent of ribosome		nolecular_function	0003735	21.4	1.1e-8	PF00276	10273	90e_1	
	zinc ion binding	:	nolecular_function	0005840				10273	90e_1	
	translation		iological process	0006412				0070	00- 4	
	translation		iological_process					10273	90e_1	
- 1,040 of 38	View 1,031		►> ►I 10 ▼	Page 104 of 38,	। ब २व			10273	90e_1	
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- 1,040 of 38	p-value (X2 vs Xin) 4.44e-16 0.0801	e (X1 vs Xin) 44e-16 87e-54	Iiated₂ p-value () 5.64 4.44 1.33 1.87	III Page 104 of 38, control ₂ i 214.21 570.25	Xin 51.35 24.82	X2 0.00 19.20	X1 0.00 278.21	e strand fwd fwd	90e_1 90e_100	
- 1,040 of 38	p-value (X2 vs Xin) 4.44e-16 0.0801 0.0000153	e (X1 vs Xin) 44e-16 87e-54 .00185	Image: line line line line line line line line	III Page 104 of 38, control ₂ ii 214.21 570.25 38.74	Xin 51.35 24.82 16.26	X2 0.00 19.20 0.00	X1 0.00 278.21 3.30	e strand fwd fwd fwd	90e_1 90e_100	
- 1,040 of 38	p-value (X2 vs Xin) 4.44e-16 0.0801 0.0000153 1	e (X1 vs Xin) 44e-16 87e-54 .00185 000061	Image: Additional process	III Page 104 of 38, control ₂ ii 214.21 570.25 38.74 22.26	Xin 51.35 24.82 16.26 0.00	X2 0.00 19.20 0.00 0.00	X1 0.00 278.21 3.30 14.28	e strand fwd fwd fwd fwd fwd	90e_1 90e_100 90e_1000	
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5. Expression plot

Advanced dot plot for representation of differential expression in two dimensions ease data depiction and interpretation for selection of new genes of interest.

Fold Change of X1 and X2 vs Xin



Digital Gene Expression libraries

4. Data browsing

		Position:	90e_350:27832803 (+ strand)
Planarian Smed4	54 Transcriptome Browser: 1.769 kbp from 90e 350:1.1202.889	Length:	21
	······································	Score:	2.637
Browser Select Tra	acks Community Tracks Custom Tracks Preferences	load_id:	17414.01
Search		note:	Raw Count: 1580 Adjusted Count: 433 93 Log10 Count: 2 637
Landmark or Region:			Predicted Rank: R1 Manping A times over A conting
90e 350:1.1202.889	Search Download generic Configure Go	rank	1
Examples: 90e 1, 90e 3	39190, F6AJIXP02H4KN4, F6AJIXP02FPW73, F6AJIXP02FPW*.	sequence:	
Data Source		primary id:	1090667
Planarian Smed454 Tran	scriptome Browser Scroll/Zoom: 📉 🚬 Show 1.77 kbp 🔻 🔤 Flip	gbrowse dbid	dge:database
Overview		-	°
	90e_350 <	>DGE00017414 CATGTCATAT A	.01 class=Sequence position=90e_350:27832803 (+ strand) TATTACAAT T
	0k 1k 2k	DCE00017/	114 01 Details
		DGE000174	14.01 Details
		Name:	DGE00017414.01
Region		Туре:	DGE_tag
	ok 1k 2k i i i i i i i i i i i i i i i i i i	Description:	

Abril, Cebrià, et al. (2010); Adamidi et al. (2011); Blythe et al. (2010); Boguski et al. (1993); References Labbé et al. (2012); Resch et al. (2012); Rouhana et al. (2012); Sandmann et al. (2011); genome.wustl.edu

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planarian.bio.ub.edu | compgen.bio.ub.edu | gresteban@scientist.com



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