FUNCTIONAL TRANSCRIPTOMICS IN Schmidtea mediterranea STEM CELLS
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1. Mapping DGE tags

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.

6. New neoblast genes identified

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

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.

2. GO and Pfam annotation

Annotation of transcripts based on Gene Ontology (up) and domain annotation based on Pfam (right).

We have developed a computational protocol that allows to retrieve the GO IDs and their associated terms as well as the Pfam domains of a bunch of sequences in a more accurate manner and independent from Blast.

3. Data mining

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

4. Data browsing

Smed454 transcriptome browser, updated, based on Gbrowse, allows an interactive exploration of sequences and retrieving of information about expression and domains.

References
Abril, Cedre, et al. (2010); Adamidi et al. (2011); Bytte et al. (2010); Bisguier et al. (1993); Lavelle et al. (2012); Resch et al. (2012); Roush et al. (2012); Sandmann et al. (2012); genome.wustl.edu

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