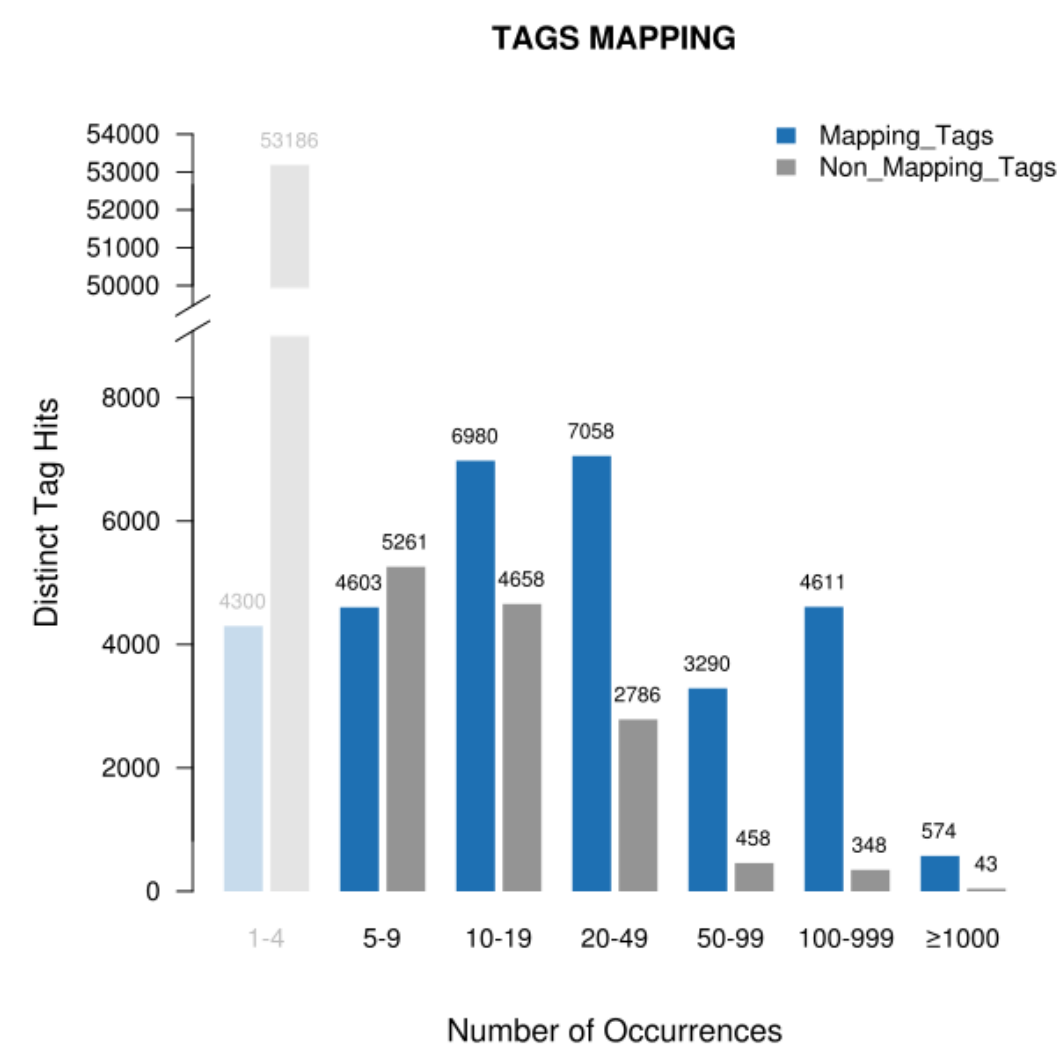
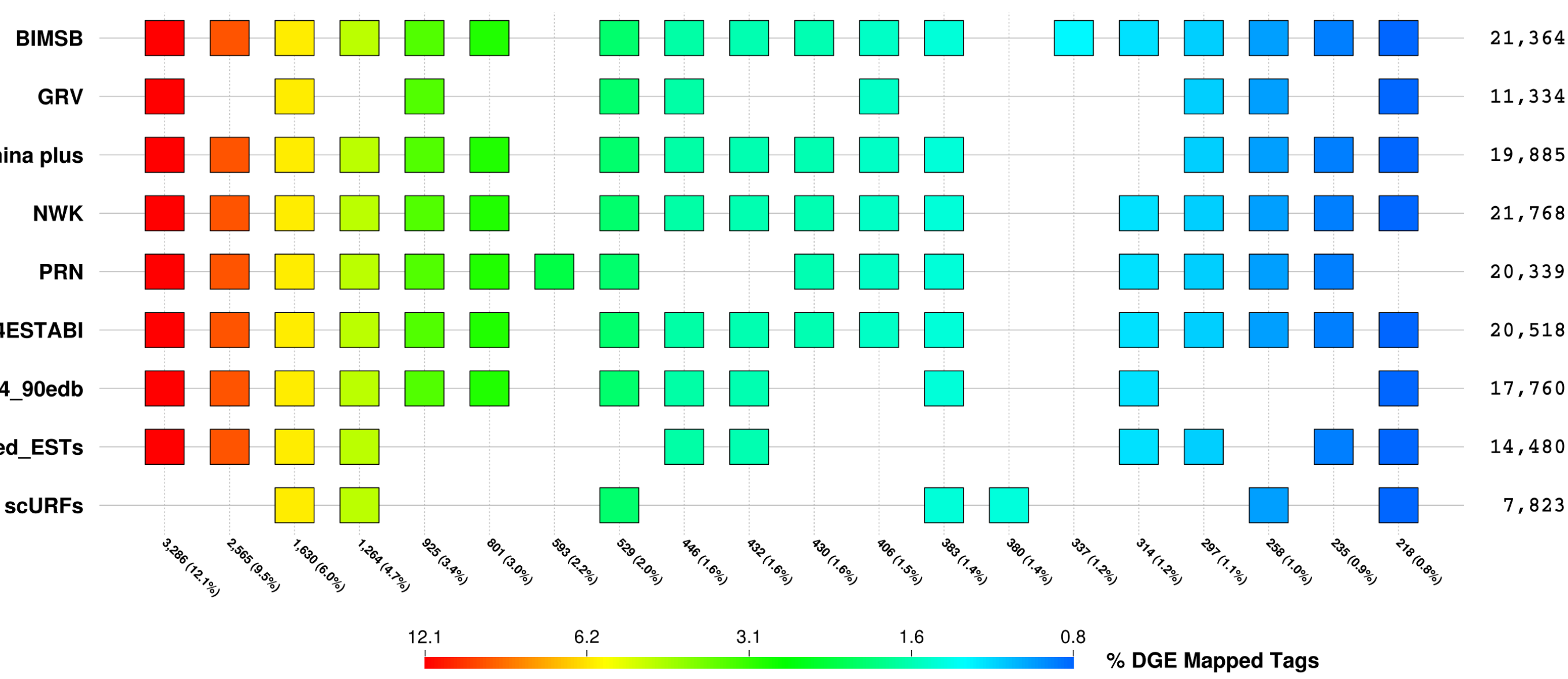


FUNCTIONAL TRANSCRIPTOMICS IN *Schmidtea mediterranea* STEM CELLS

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1. Mapping DGE tags

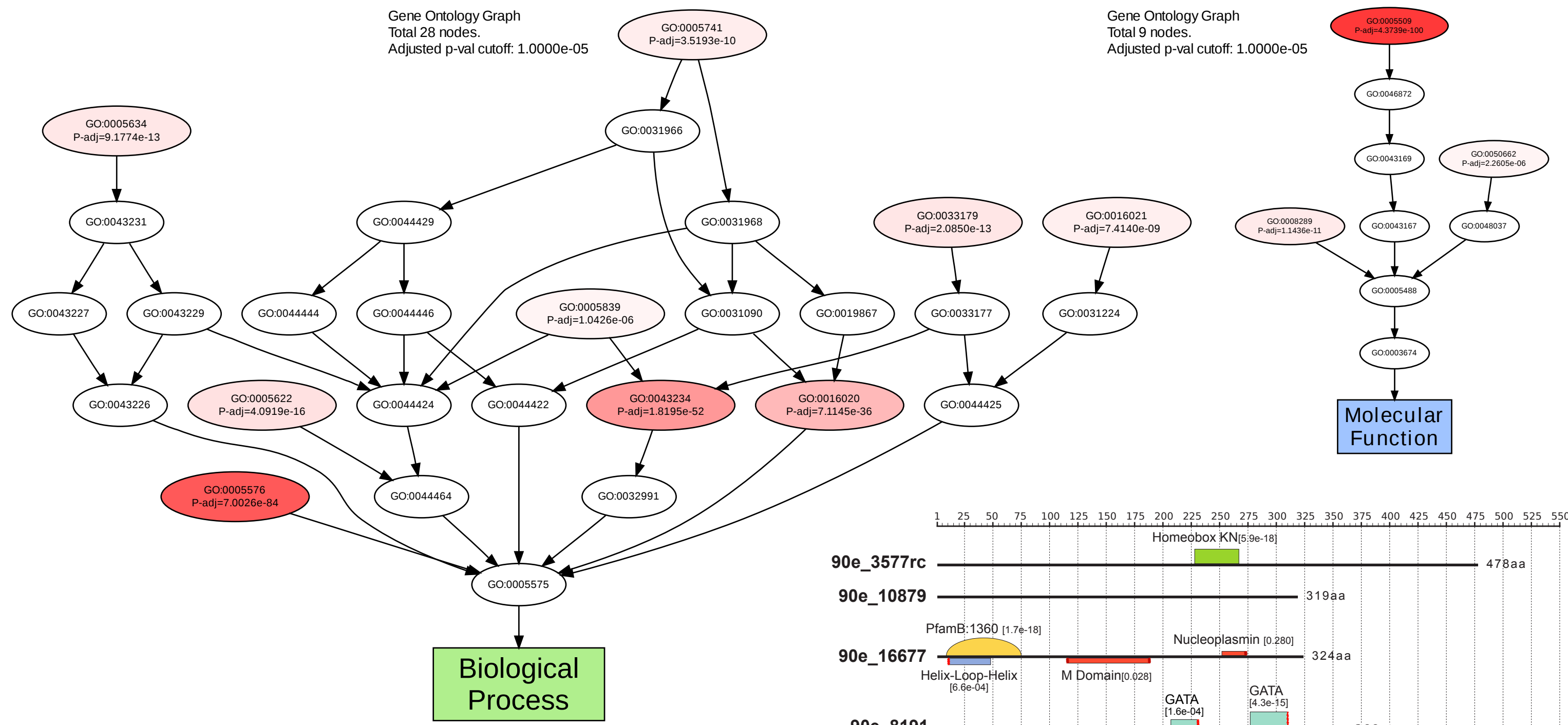
Venn Stave of DGE Mapped Tags



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.

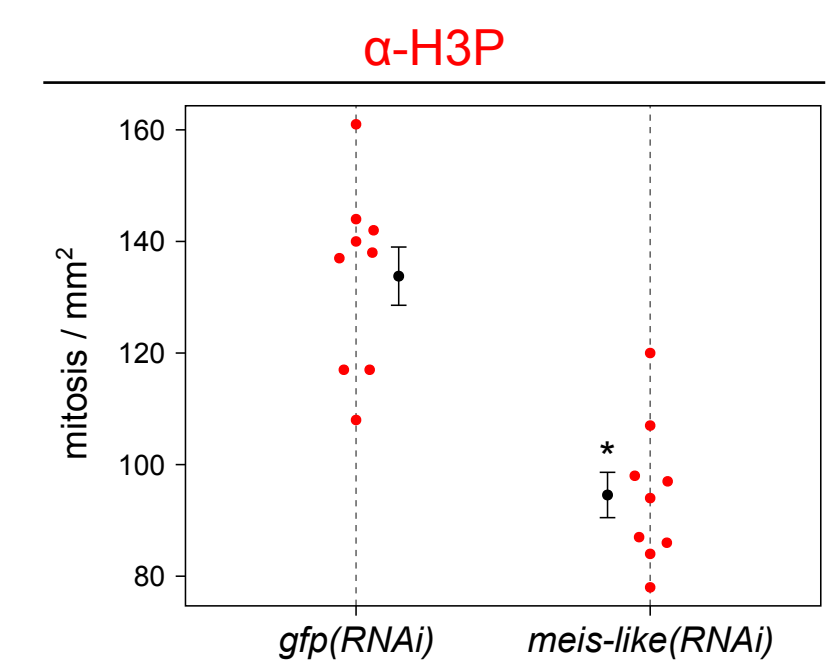
2. GO and Pfam annotation



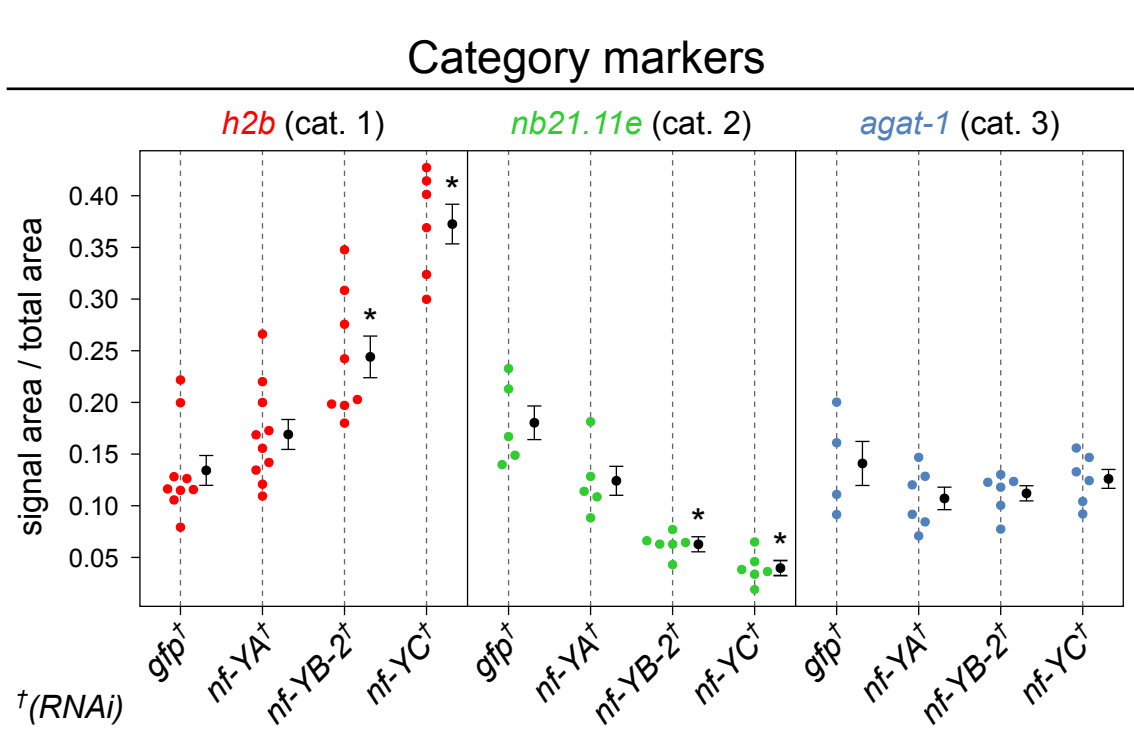
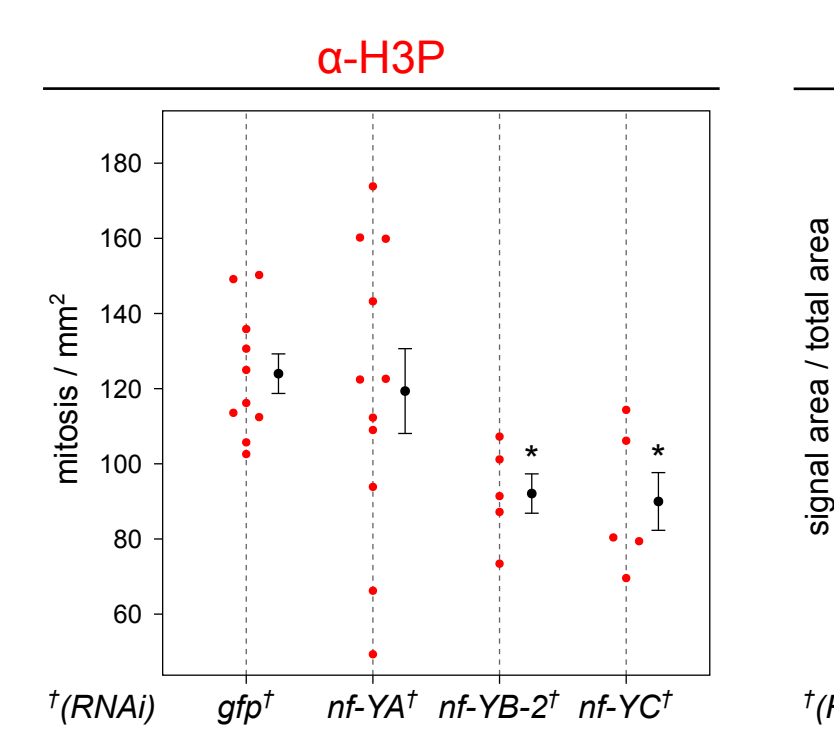
Annotation of transcripts based on Gene Ontology (up) and domain annotation based on Pfam (right).

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.

6. New neoblast genes identified



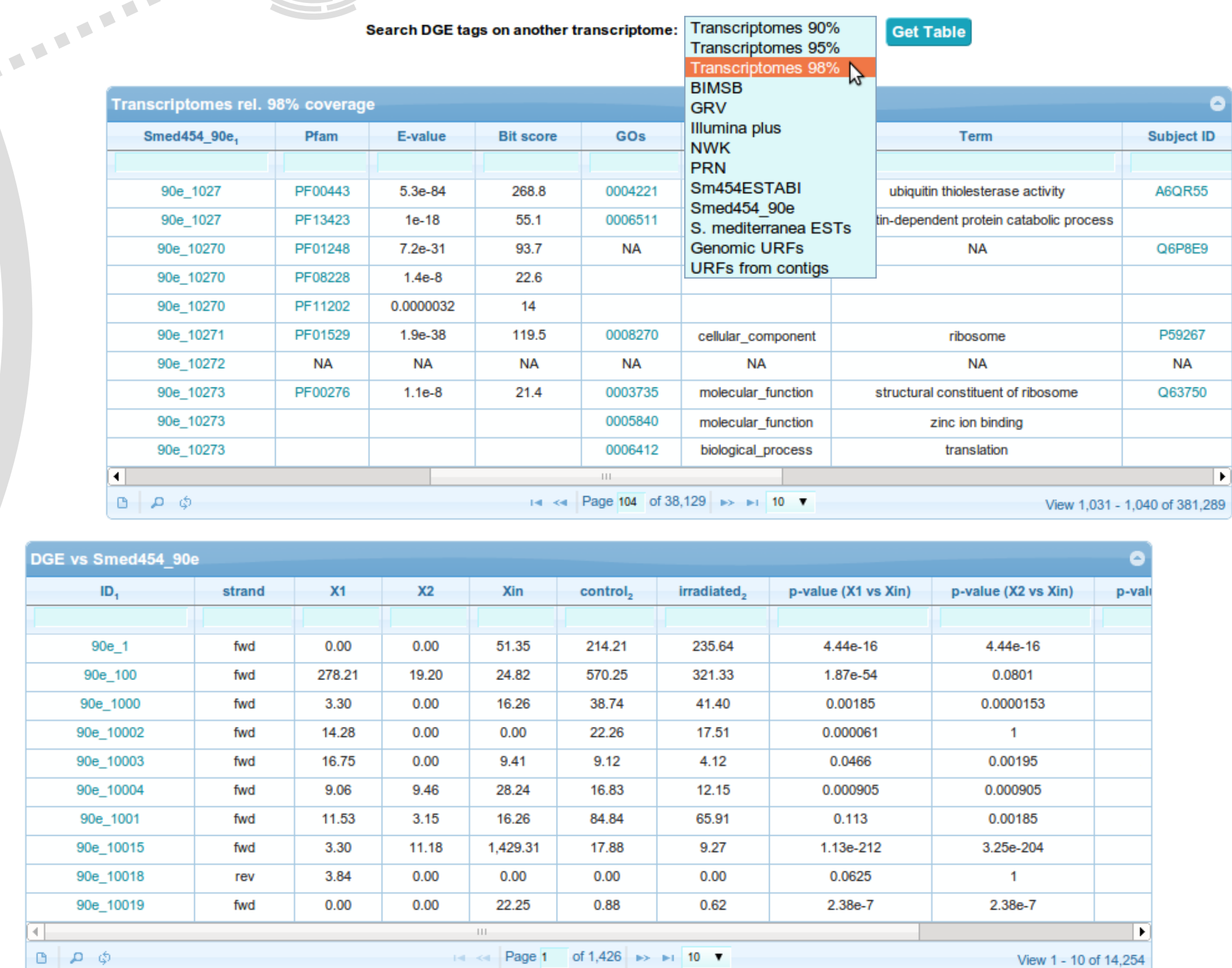
From our differential expression analysis we have been able to identify and experimentally validate new 47 neoblast-related genes, from which a *meis-like* (left) and three *nf-Y* (bottom) are shown here.



Digital Gene Expression libraries

3. Data mining

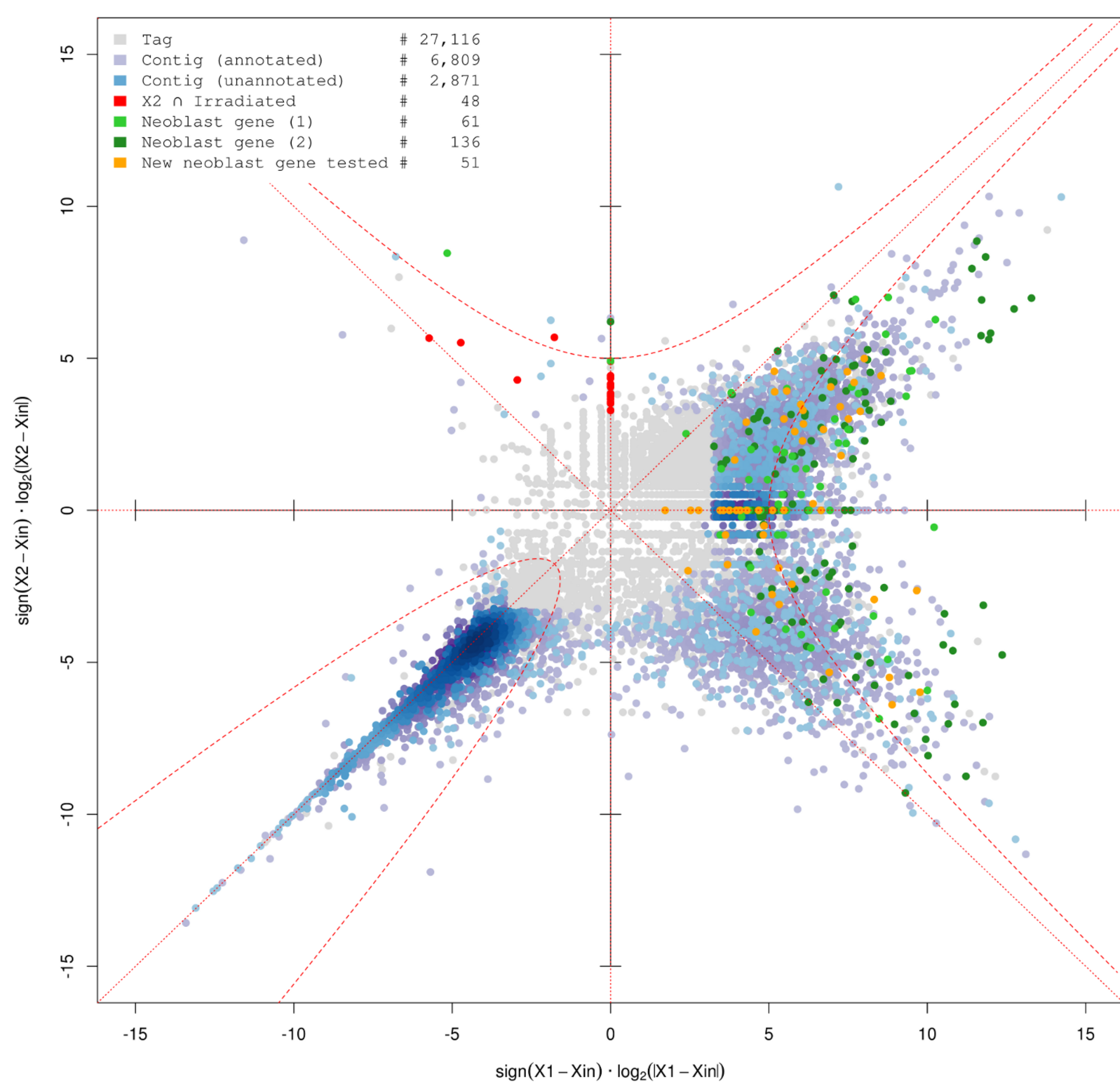
Web accessible dynamic tables are provided for a user-friendly interaction with complex search and sorting capabilities at planarian.bio.ub.edu



5. Exprn plot

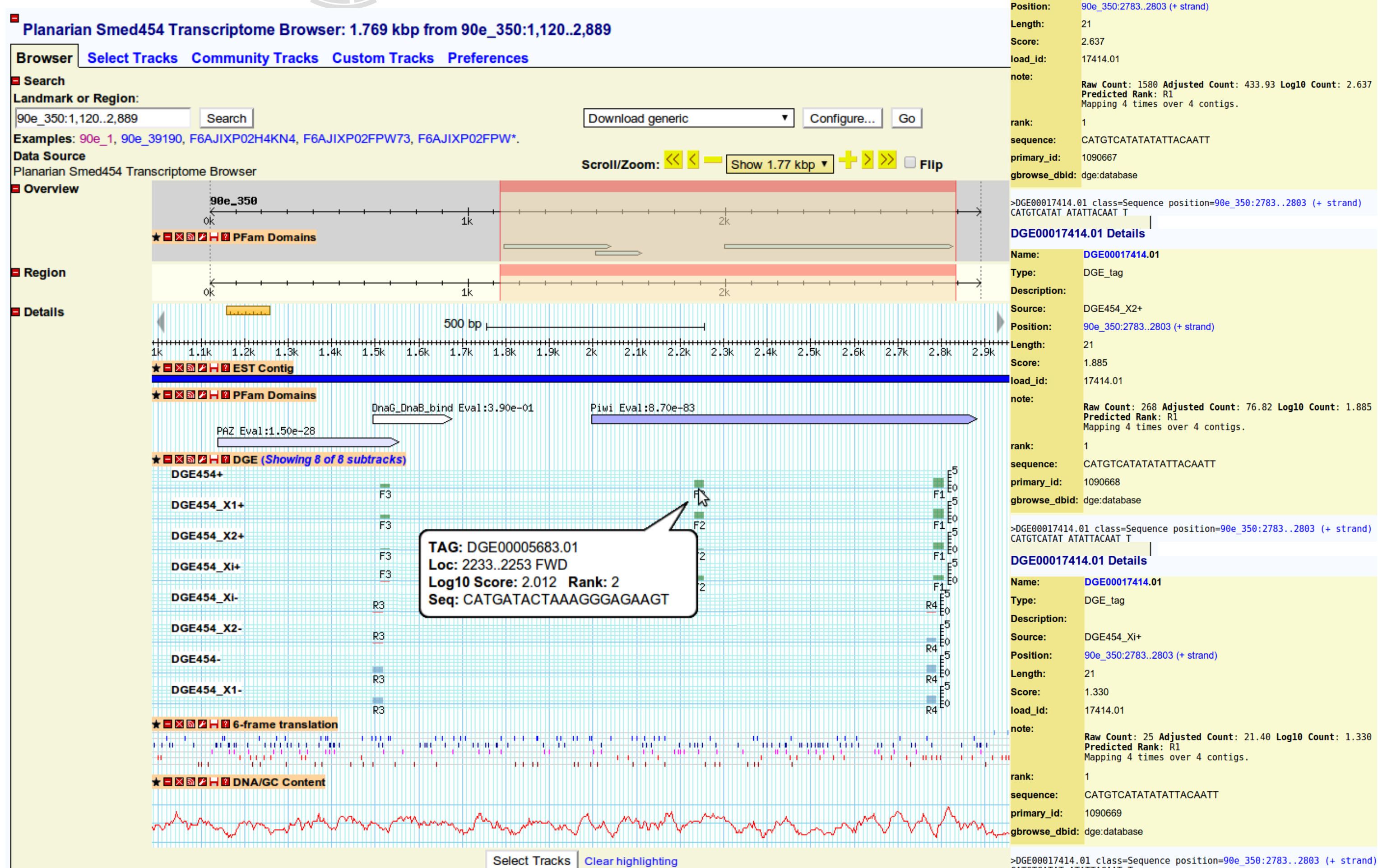
Advanced dot plot for representation of differential expression in two dimensions ease data depiction and interpretation for selection of new genes of interest.

Fold Change of X1 and X2 vs Xin



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

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