Supplementary Materials

CLIPdb: a CLIP-seq database for protein-RNA interactions

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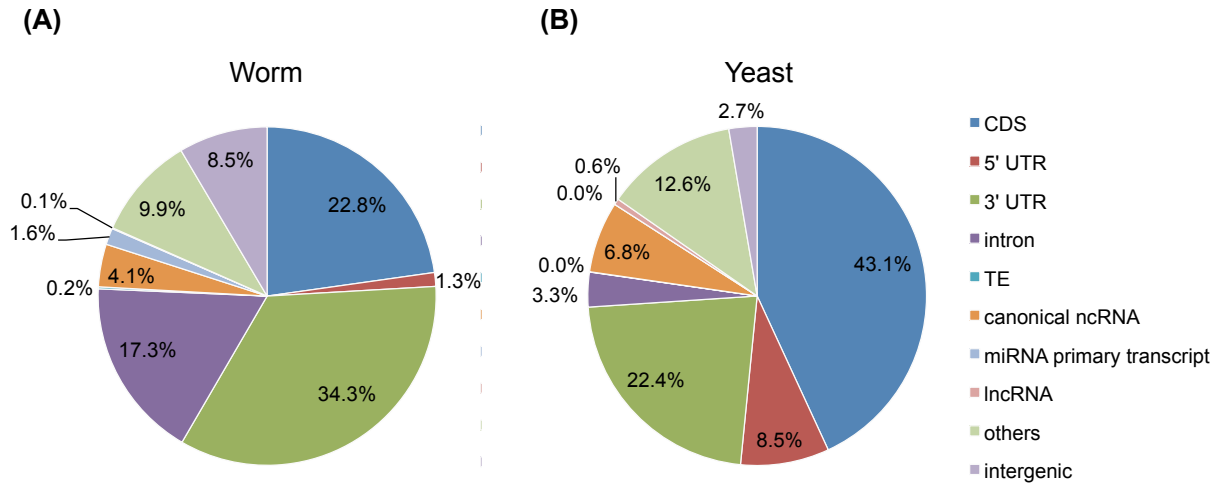
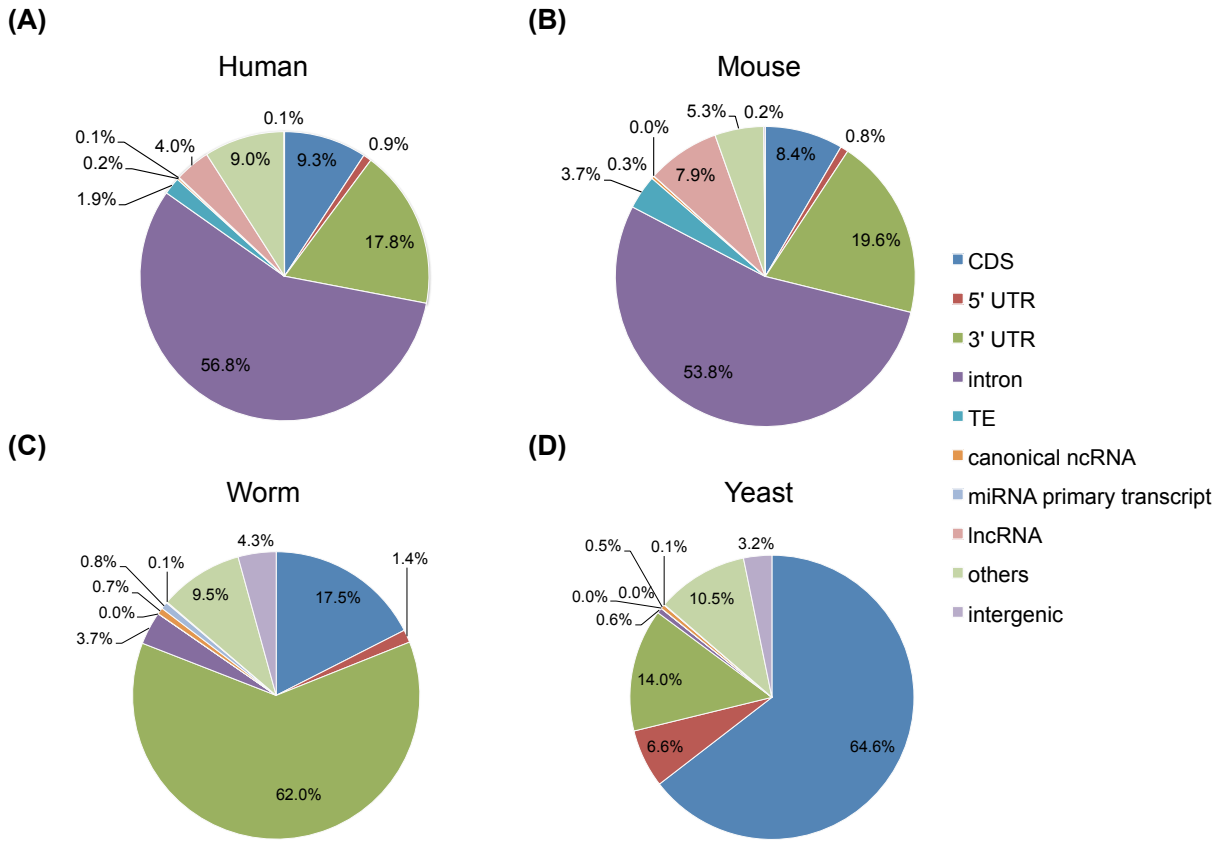
Supplementary Figure 1



Genomic distributions of RBP binding sites identified by Piranha in worm (A) and yeast (B).

Supplementary Figure 2



Genomic distributions of RBP binding sites identified by specialized tools in human (A), mouse (B), worm (C), and yeast (D). The genomic distributions of RBP binding sites generated by different methods are compared. In general, for large data sets (i.e., human and mouse), the genomic distribution of peaks called by different methods is stable. The specialized methods are more sensitive and capable of finding more peaks than the unified method (i.e., Piranha) [1].

Supplementary File 1

Summary of the CLIP-seq data sets we used and processed.

Supplementary File 2

Summary of the functional groups of RBPs in human, mouse, worm and yeast.

References

1. Wang T, Xie Y, Xiao G: **dCLIP: a computational approach for comparative CLIP-seq analyses**. *Genome biology* 2014, **15**(1):R11.