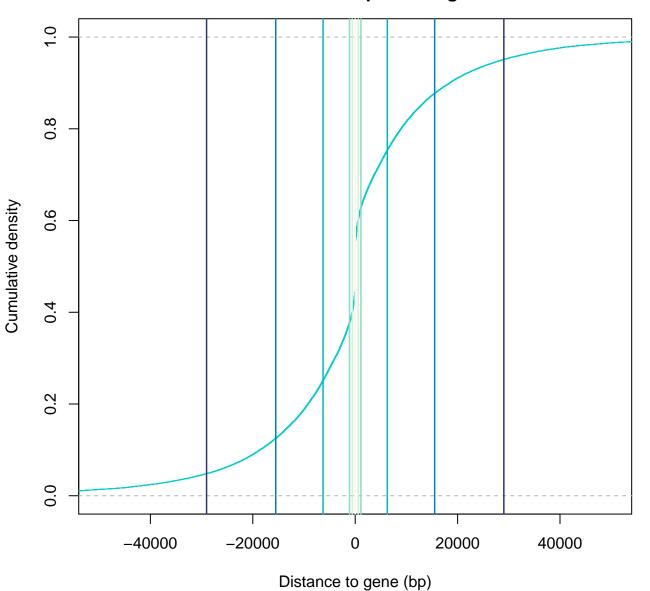
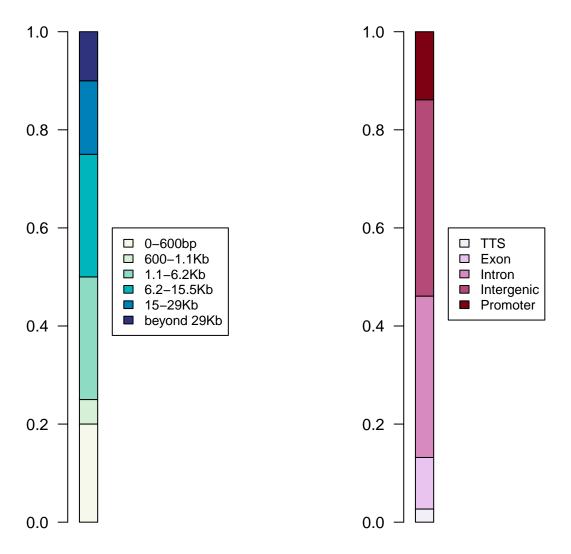
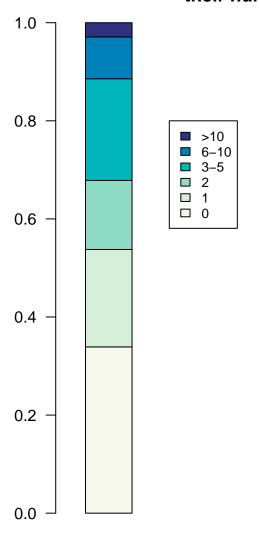
Cumulative density distribution of distance of ATAC peaks to genes

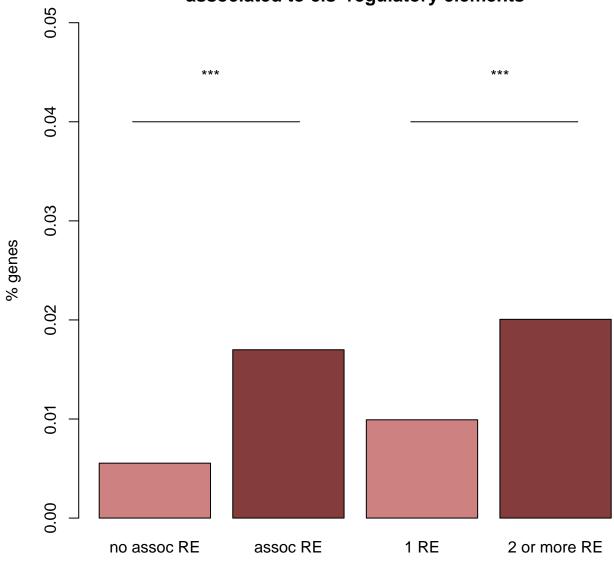




Number of genes based on their number of associated OCRs

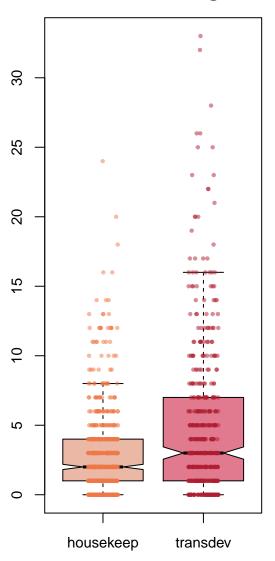


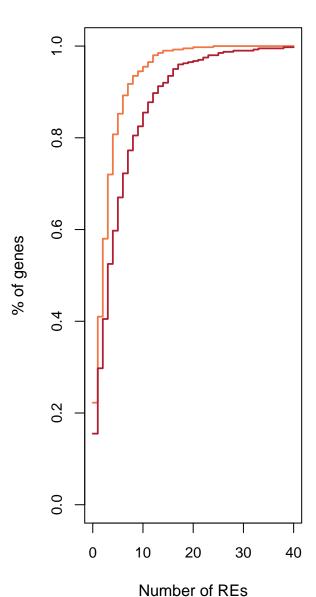
Fraction of trans-developmental genes associated to cis-regulatory elements

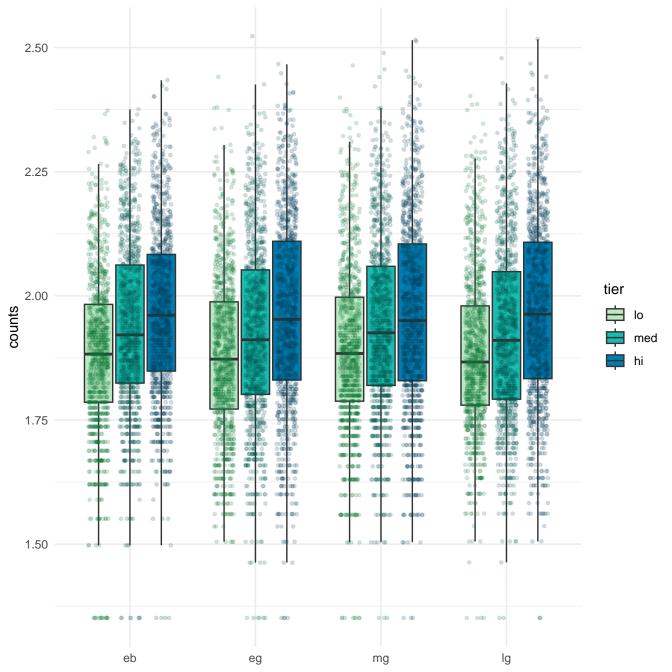


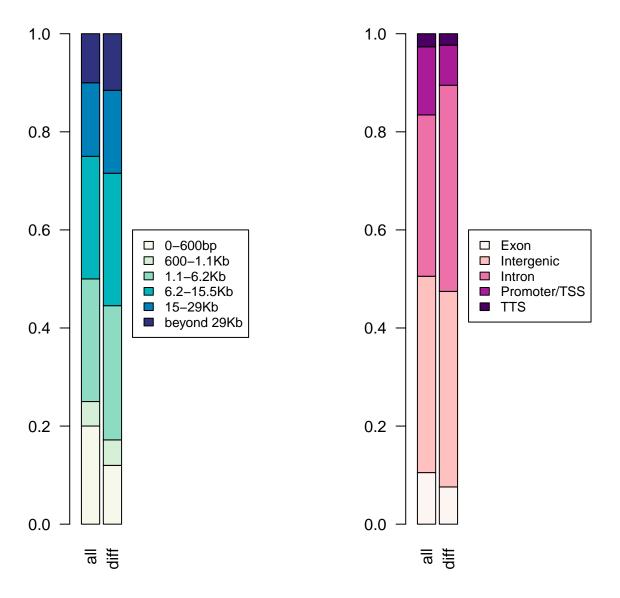
distribution of associated REs in TD and HK genes

Cumulative density









Similarity of de novo and known motifs

