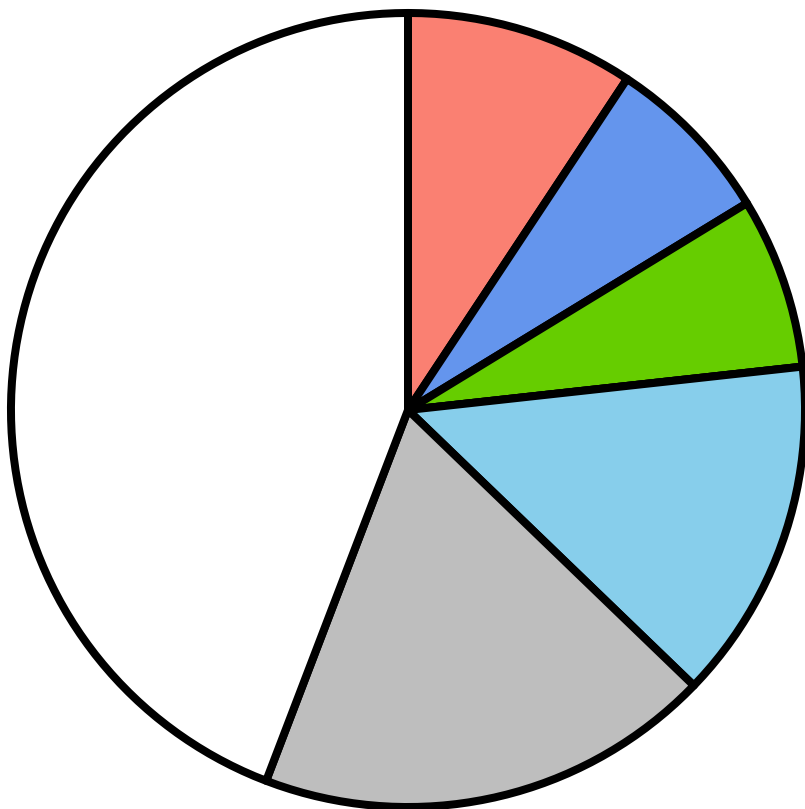


test_6 (43 peaks)



REGIONS

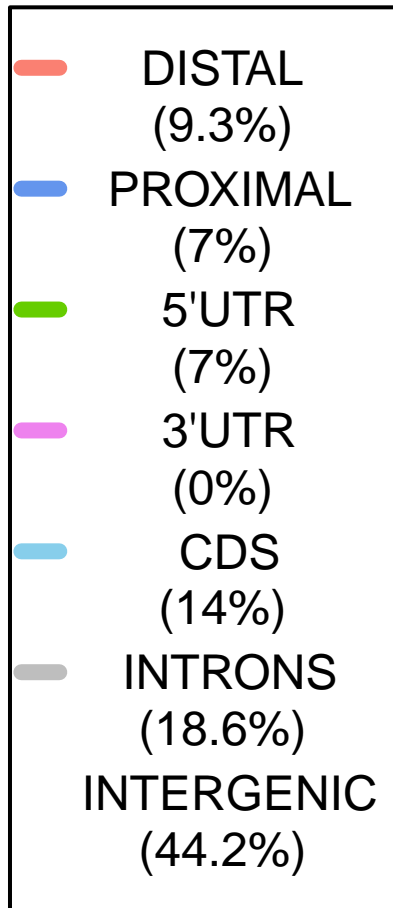


Figure legend. Distribution of ChIPseq reads across different regions of the genome.

This plot is generated by counting the number of peaks fitting on each class of region.

DISTAL region is the region within 2.5 Kbp and 0.5 Kbp upstream of the TSS. PROXIMAL region is the region within 0.5 Kbp and the TSS. UTR is UnTRanslated sequence. CDS is the protein CoDing Sequence. INTRONS are intronic regions. INTERGENIC is the rest of the genome. TSS is the Transcription Start Site.

ChIPseq experiment:

test_6

Number of peaks:

32

RefSeq transcripts:

6

Window factor:

10