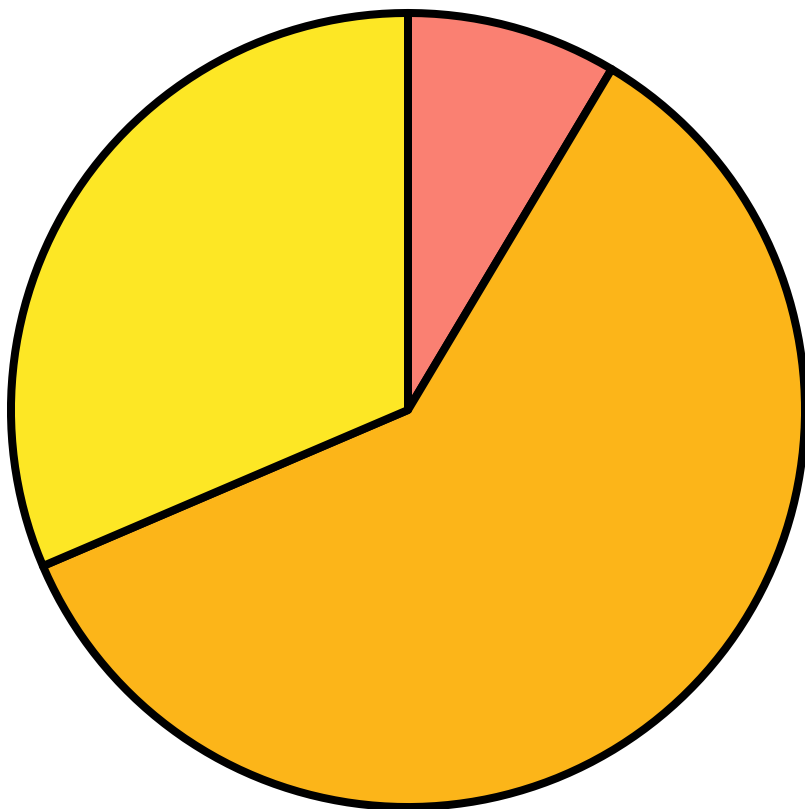





## test\_8 (35 peaks)



### REGIONS

-  PROMOTER (8.6%)
-  GENIC (60%)
-  INTERGENIC (31.4%)

**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.

PROMOTER region is the region plus/minus 500 bp upstream of the TSS and the TSS.

GENIC region is the rest of intragenic region within the transcripts not overlapping with PROMOTER.

INTERGENIC is the rest of the genome. TSS is the Transcription Start Site.

ChIPseq experiment:

*test\_8*

Number of peaks:

32

RefSeq transcripts:

6

Window factor:

10