test_3 (43 peaks)

REGIONS

- DISTAL (9.3%)
- PROXIMAL (7%)
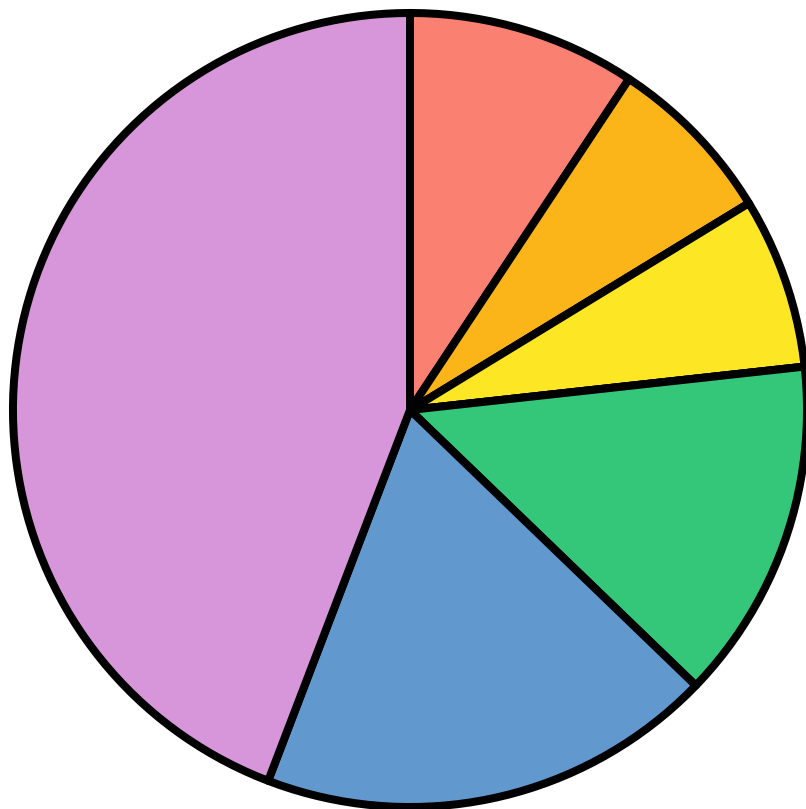- 5'UTR (7%)
- 3'UTR (0%)
- CDS (14%)
- INTRONS (18.6%)
- INTERGENIC (44.2%)

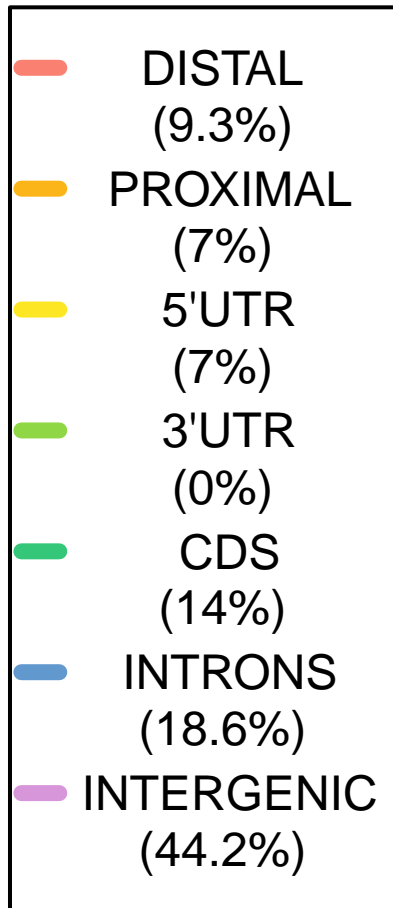SeqCode by E. Blanco [Sat Jun 5 19:52:16 2021]

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_3

Number of peaks:

32

RefSeq transcripts:

6

Window factor:

10