

1 –TSV custom file available on page “Download & JBrowse”. This file is composed to 24 columns which are filled with features about ncRNAs and TEs that overlap each other.

ncRNAs features

Column 1: Region (Chr, Scaffold or Contig).
Column 2: Source of the annotation.
Column 3: Biotype of the sequence.
Column 4: Start of the sequence.
Column 5: End of the sequence.
Column 6: Length.
Column 7: Minus or Plus.
Column 8: Score.
Column 9: ID Gene.
Column 10: Name.
Column 11: Description.
Column 12: Sequence.

TEs features

Column 13: Region (Chr, Scaffold or Contig).
Column 14: Source of the annotation.
Column 15: Type of the sequence.
Column 16: Start of the sequence.
Column 17: End of the sequence.
Column 18: Length.
Column 19: Minus or Plus.
Column 20: Score.
Column 21: ID.
Column 22: Repeat name.
Column 23: Repeat type.
Column 24: Sequence.