Supplemental_Figure_S3

Self-similarity analysis of genomic regions assembled in GRCr8, but not in mRatBN7.2

Supplemental Figure_S3a: StainedGlass analysis of self-similarity in GRCr8 Chr9:22-34Mb. This analysis was performed on a block of the chromosome in which GRCr8 and mRatBN7.2 are syntenous.

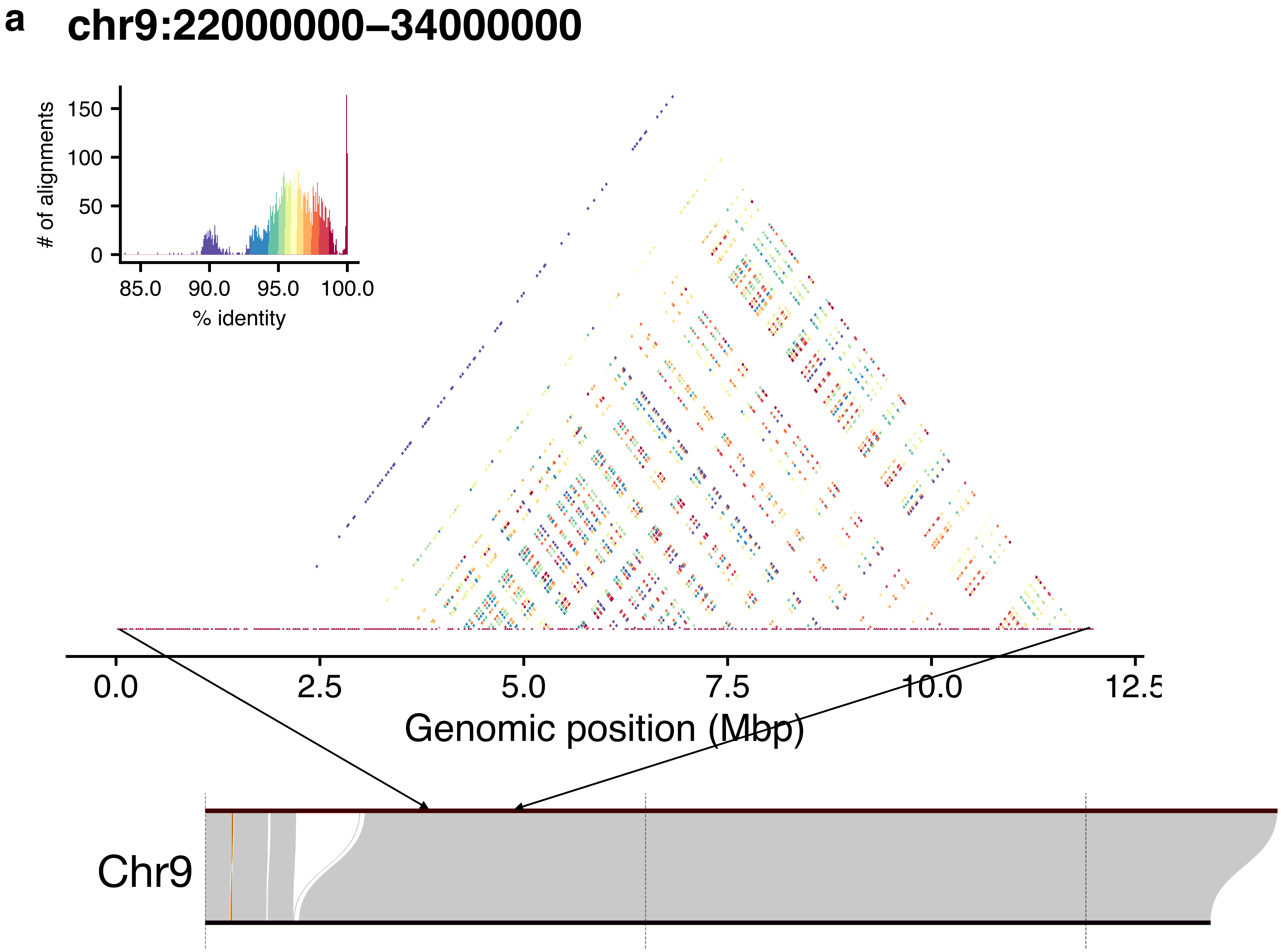
Supplemental Figure_S3b. A similar analysis as above, but spanning the region Chr9:8-20Mb of the GRCr8 assembly. This is a new element of the rat genome assembly that was largely absent from mRatBN7.2. Approximately 7Mb of this region show high self-similarity, indicating a repetitive chromosomal region.

Supplemental Figure_S3c. A similar analysis of GRCr8 Chr16 across a newly assembled block that was absent from the mRatBN7.2 assembly. Again, high self-similarity is observed in this region

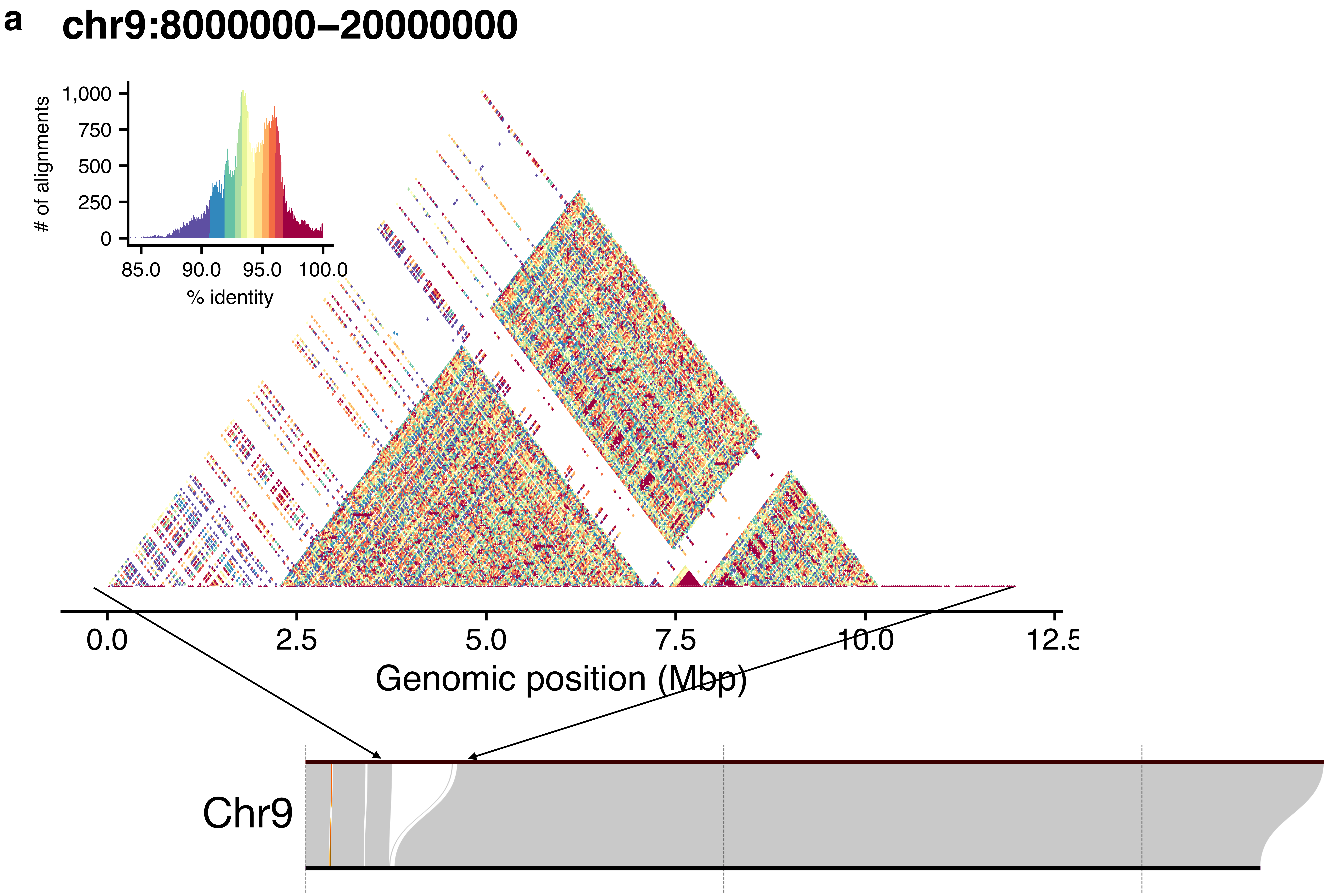
Supplemental Figure_S3d. A newly assembled region of Chr15 also shows high self-similarity

Supplemental Figure_S3e. A region of ~15MB was assembled in proximal GRCr8 Chr19 that showed high self-similarity across 15Mb. This region was not assembled in mRatBN7.2. We aligned PacBio Iso-Seq transcripts from multiple BN tissues to the GRCr8 assembly and examined alignment in this region. Aligned transcripts were observed that corresponded to annotated protein coding genes. In contrast, the lower panel shows Chr15 centromeric self-similarity that has greater self-similarity structure and lacks coding gene annotation.

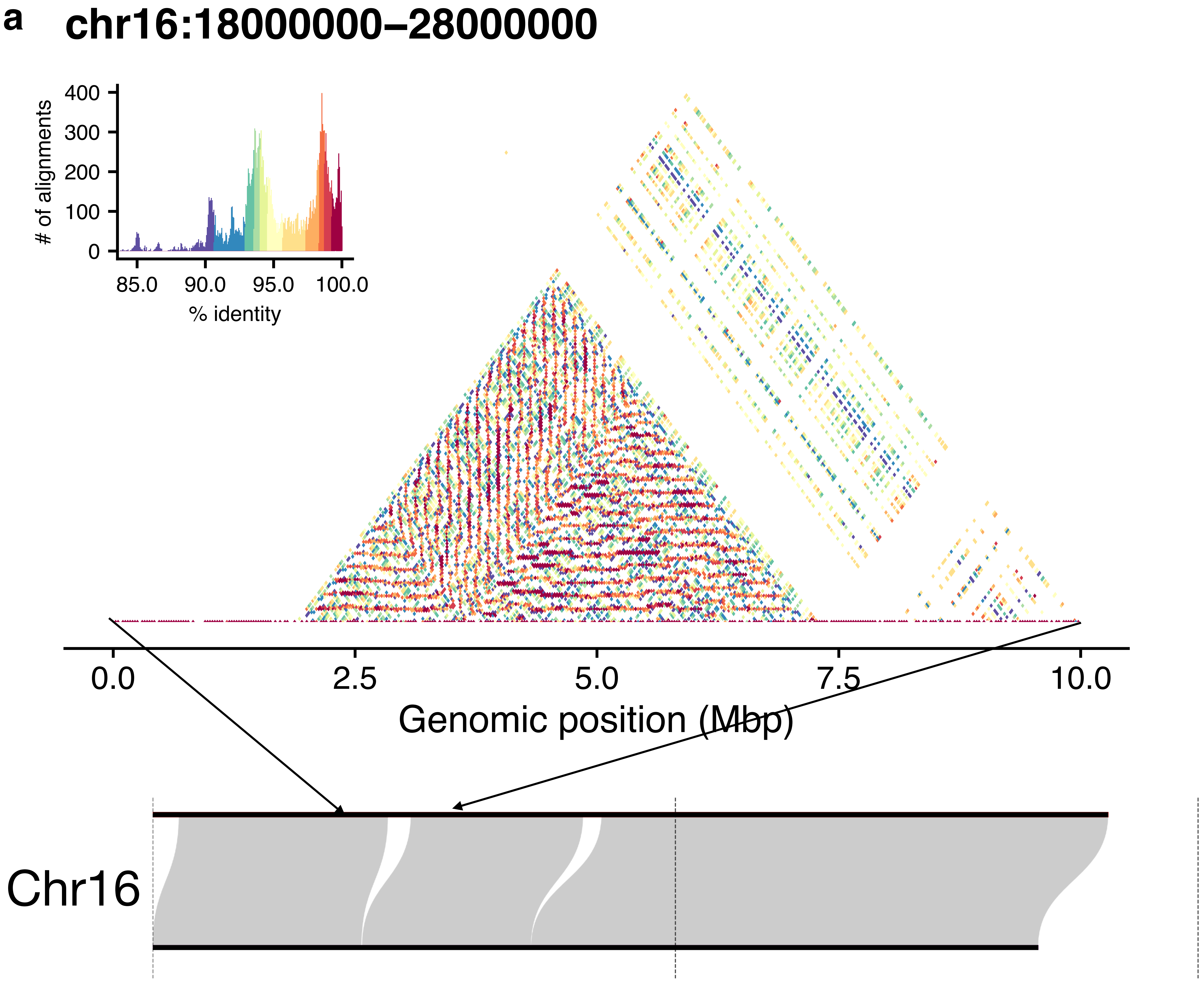
Suppl Figure 3a



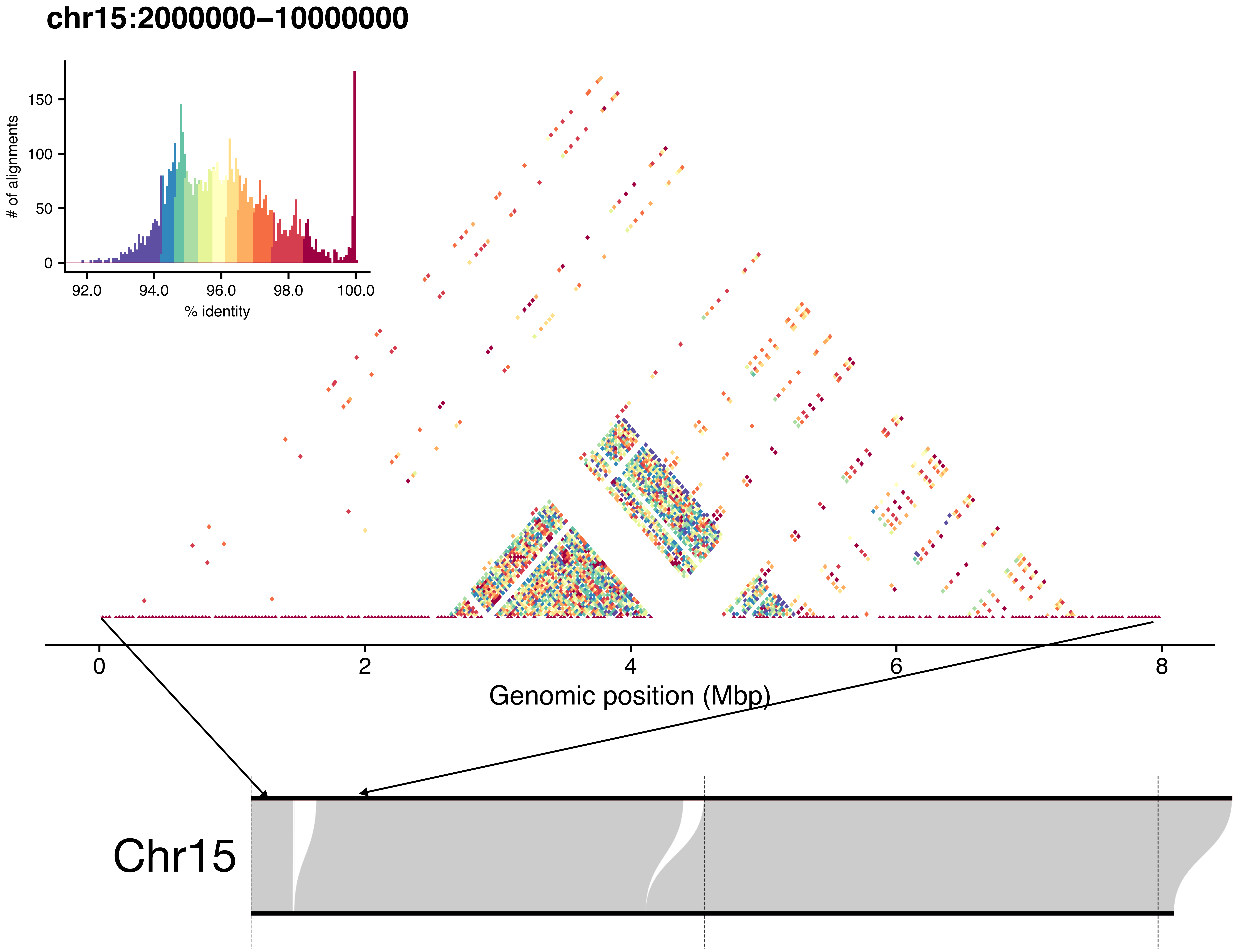
Suppl Figure 3b



Suppl Figure 3c

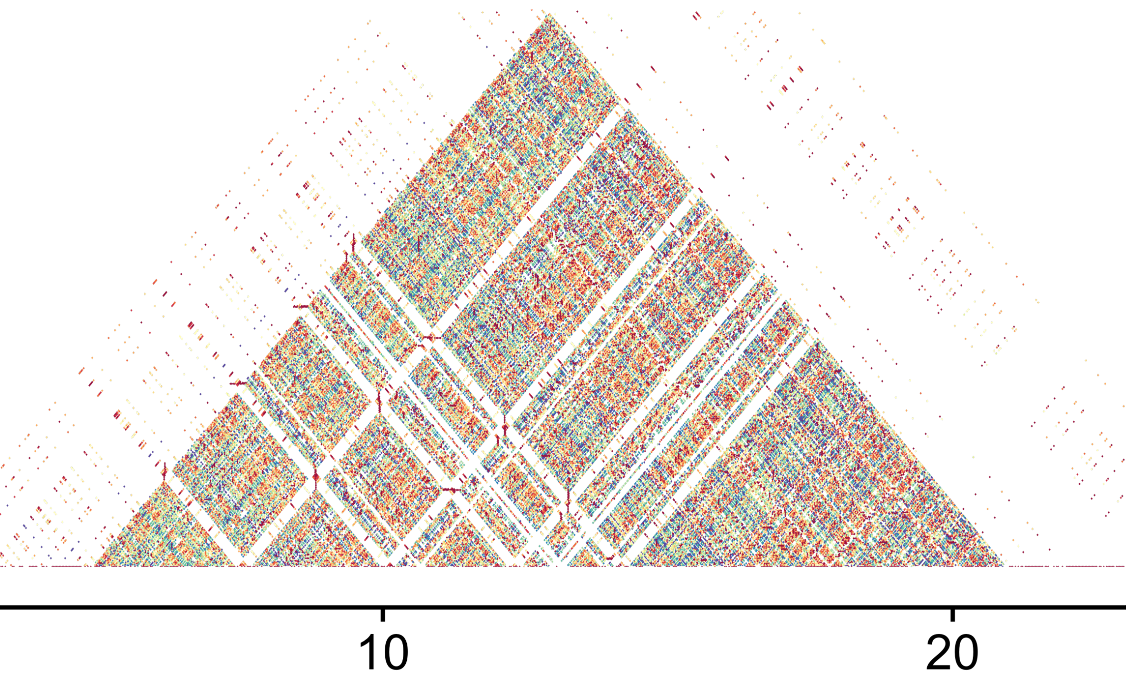


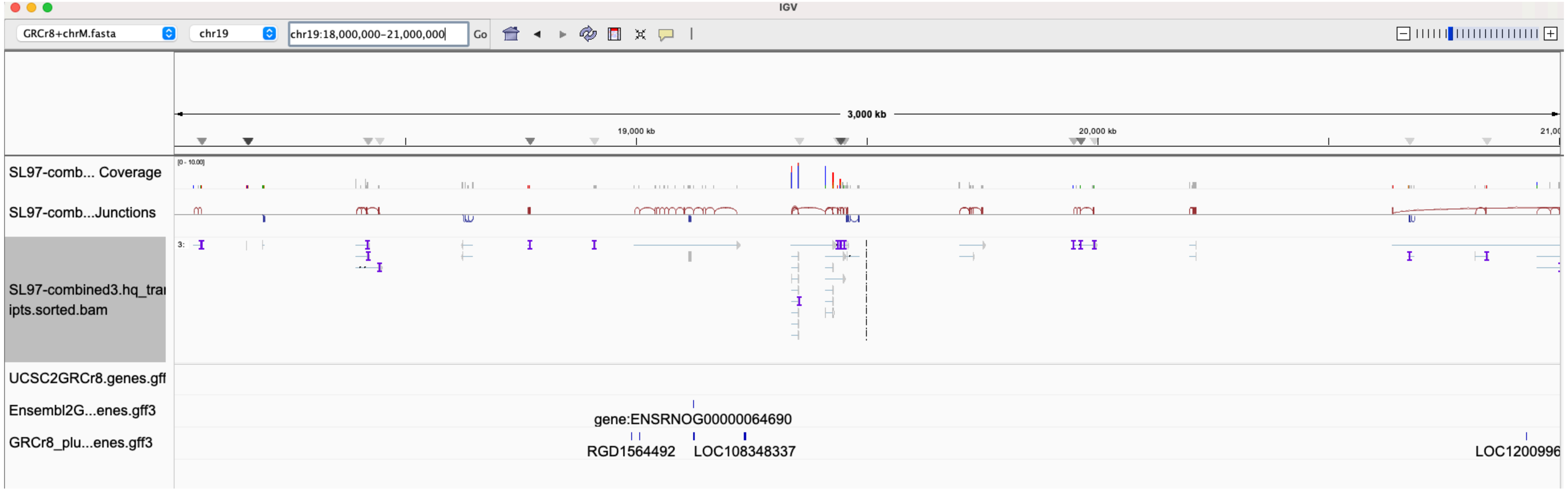
Suppl Figure 3d



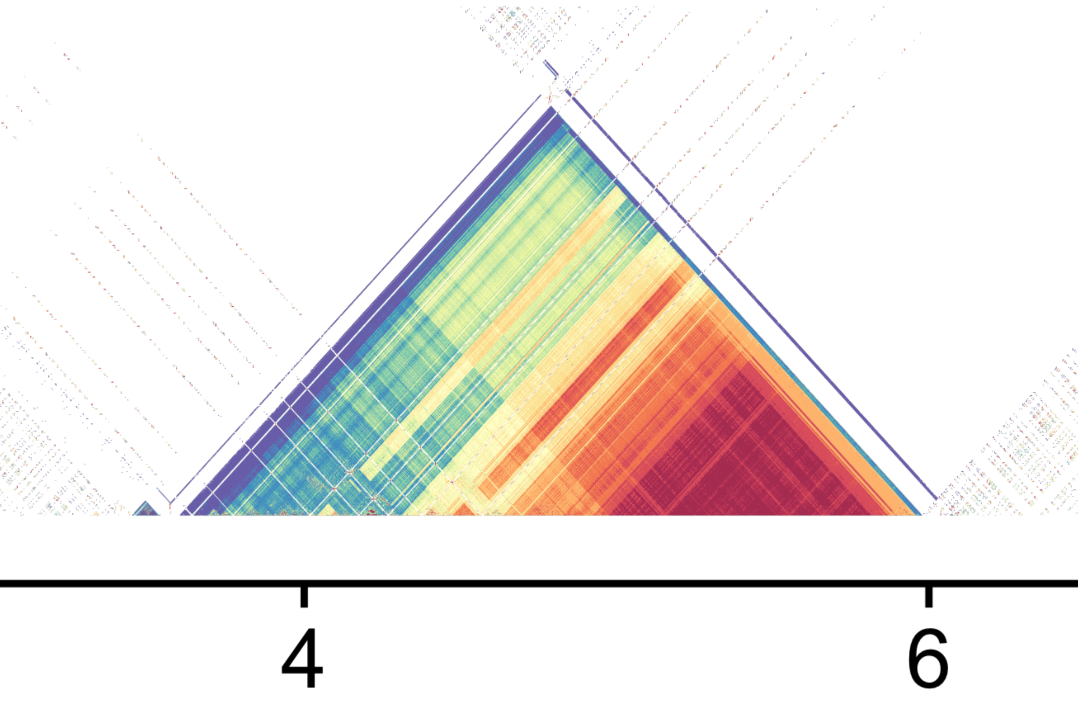
Suppl Figure 3e

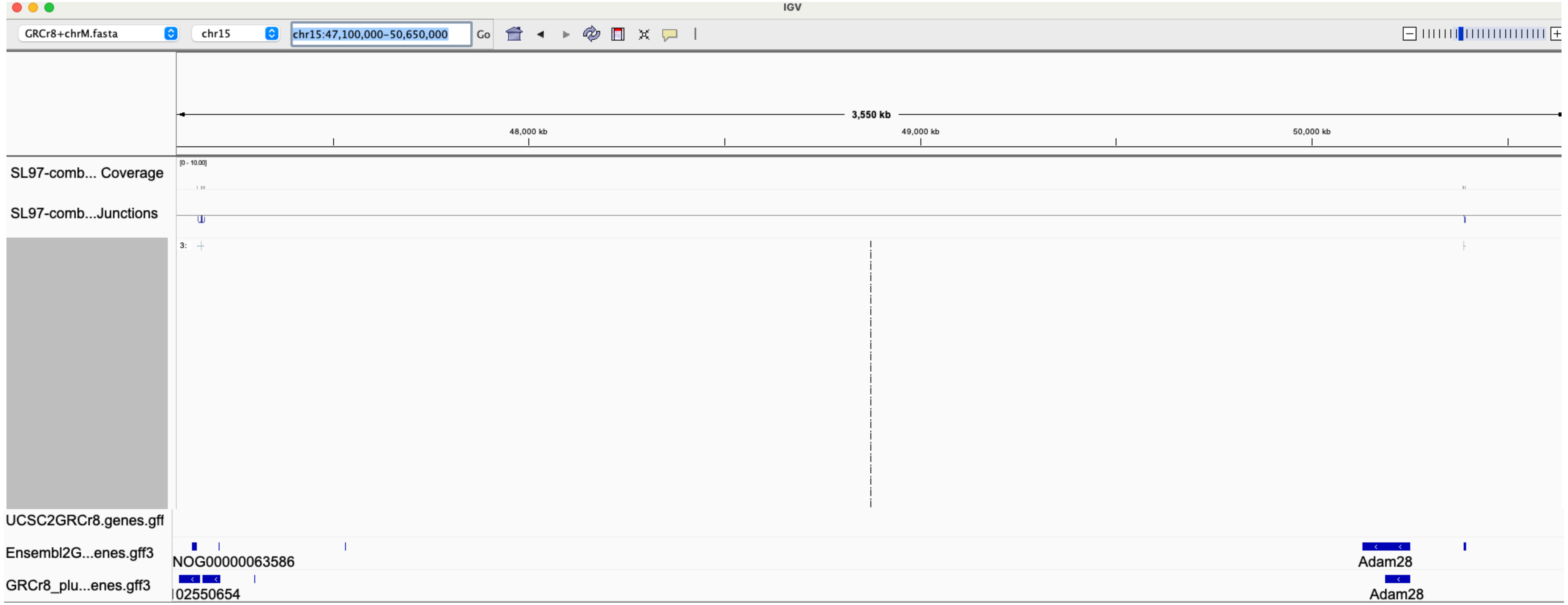
Chr19 duplicated region




GRCr8+chrM.fasta
chr19
chr19:18,000,000-21,000,000

Chr15 centromere




GRCr8+chrM.fasta
chr15
chr15:47,100,000-50,650,000