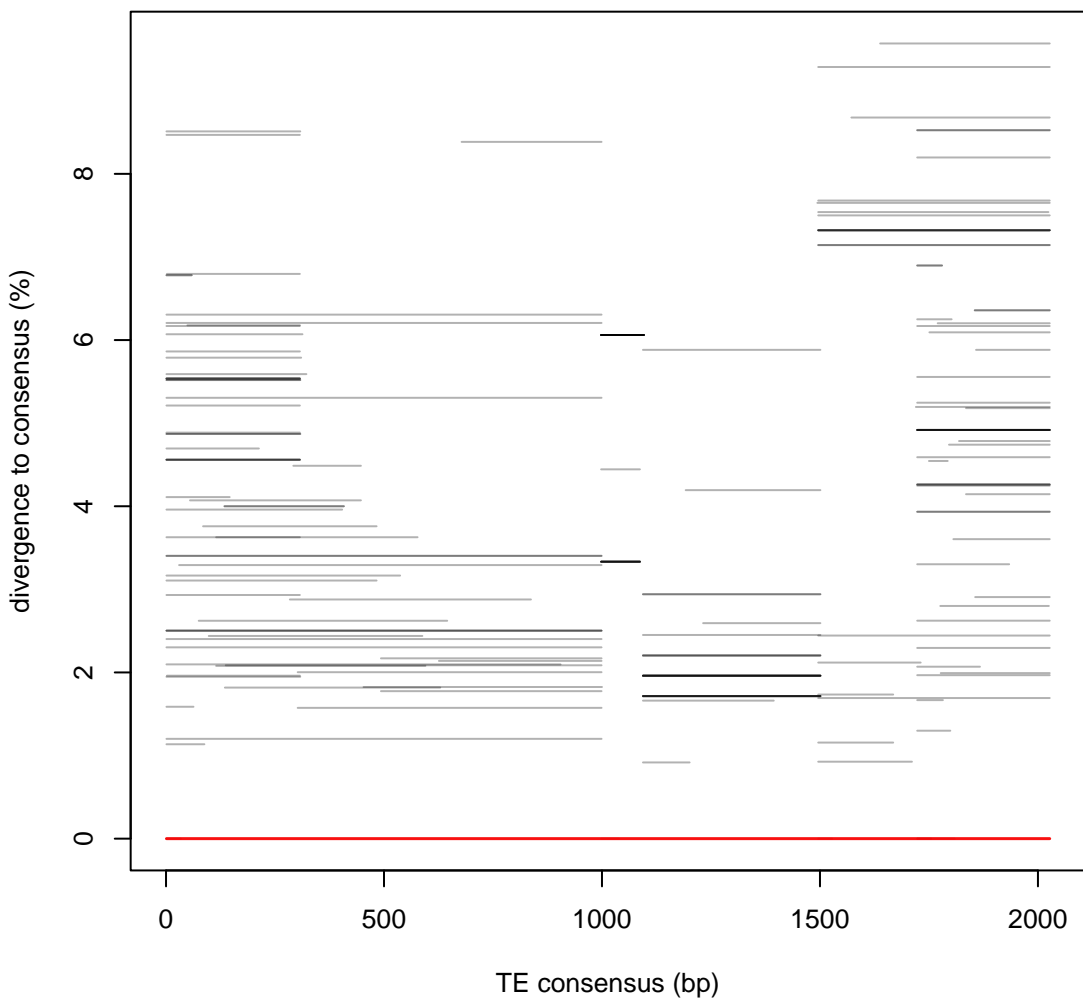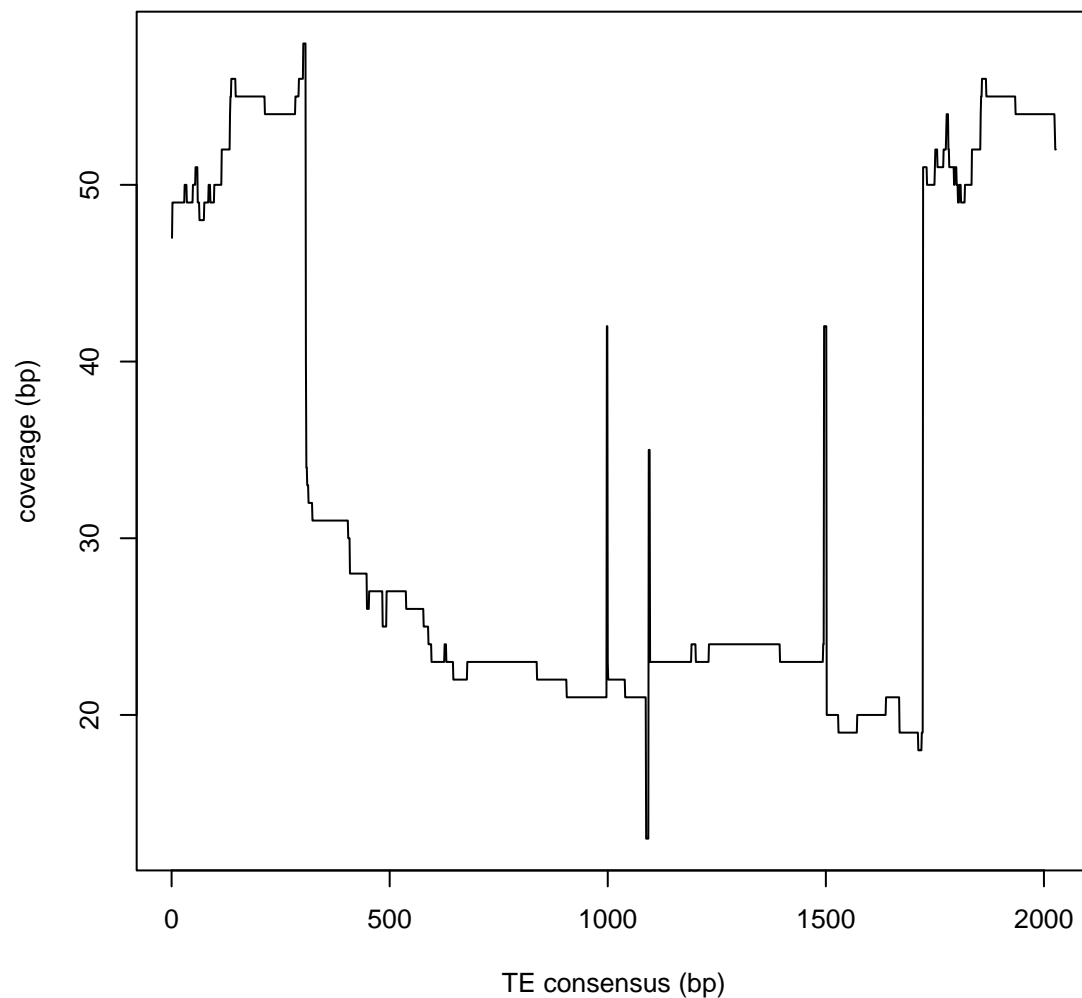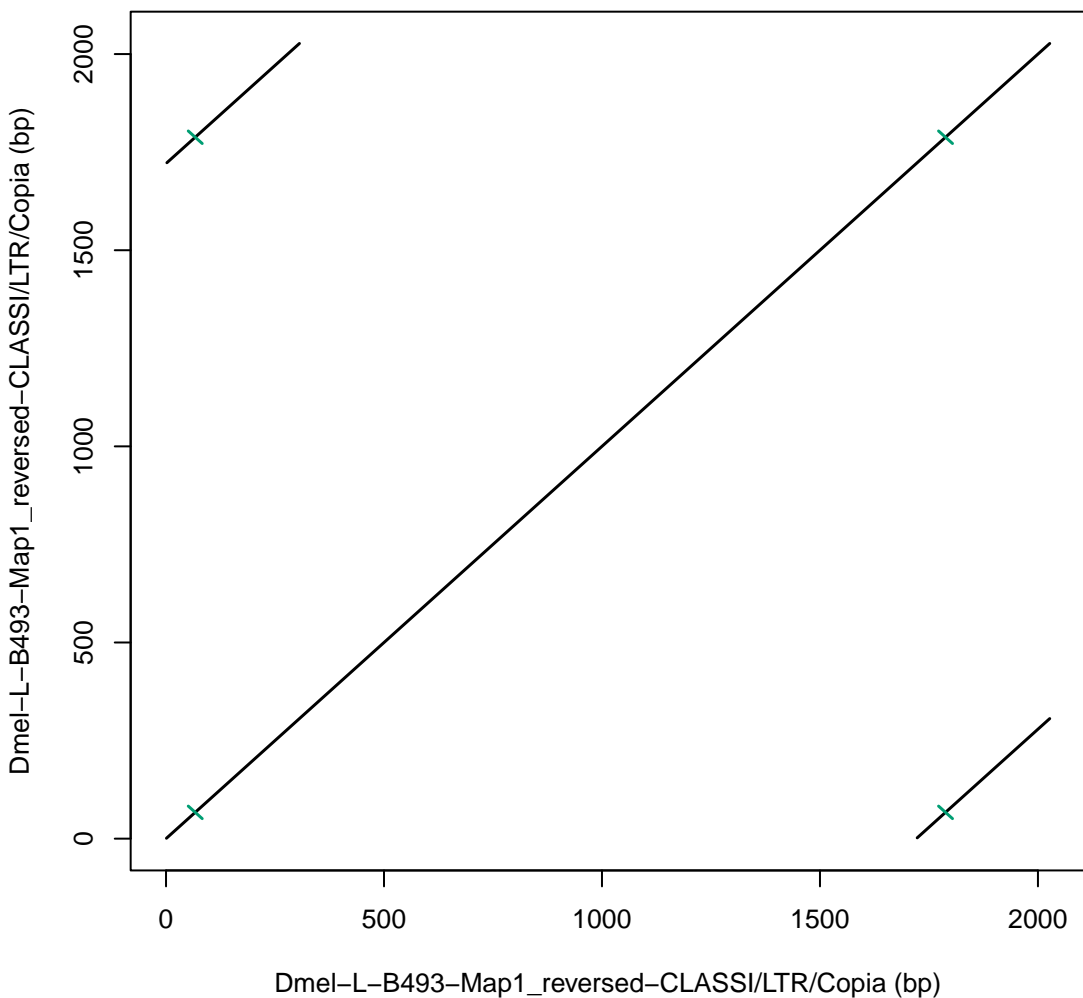**TE: Dmel−L−B493−Map1_reversed−CLASSI/LTR/Copia**
consensus size: 2027bp; fragments: 183; full length: 1 (>=1824.3bp)

TE consensus genomic coverage

TE consensus self dotplot (blastn)

TE consensus structure and protein hits

BEL24_DR_pol LTR/Pao
Copia−6_DWil LTR/Copia
DM1731 LTR/Copia