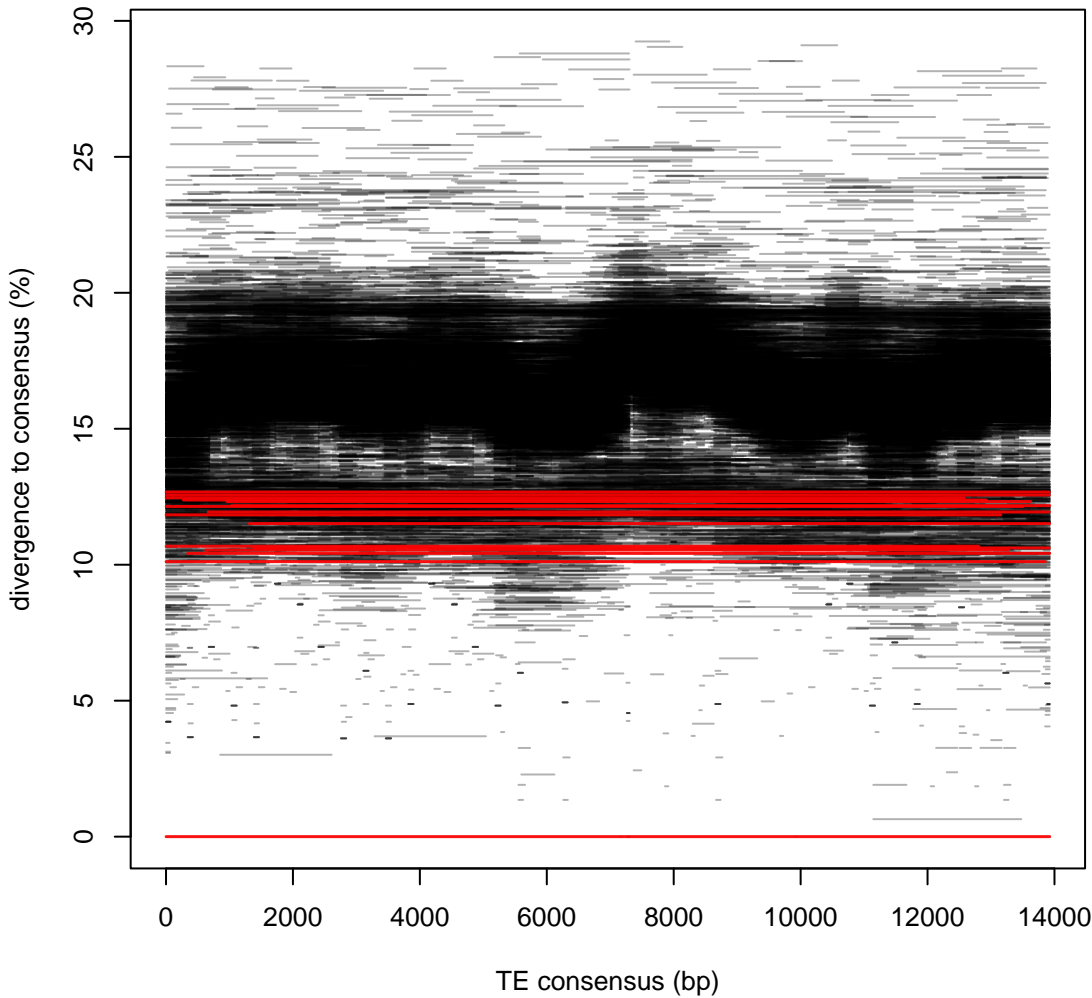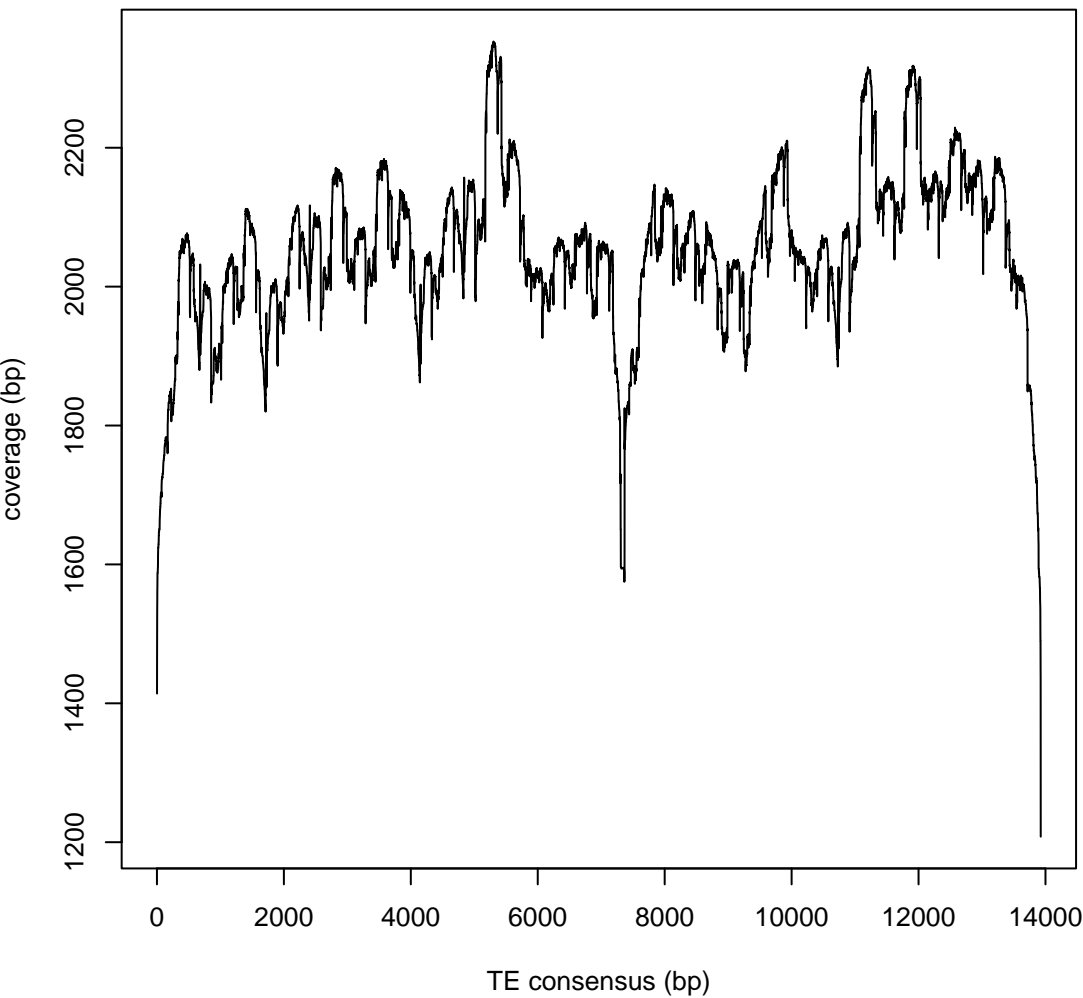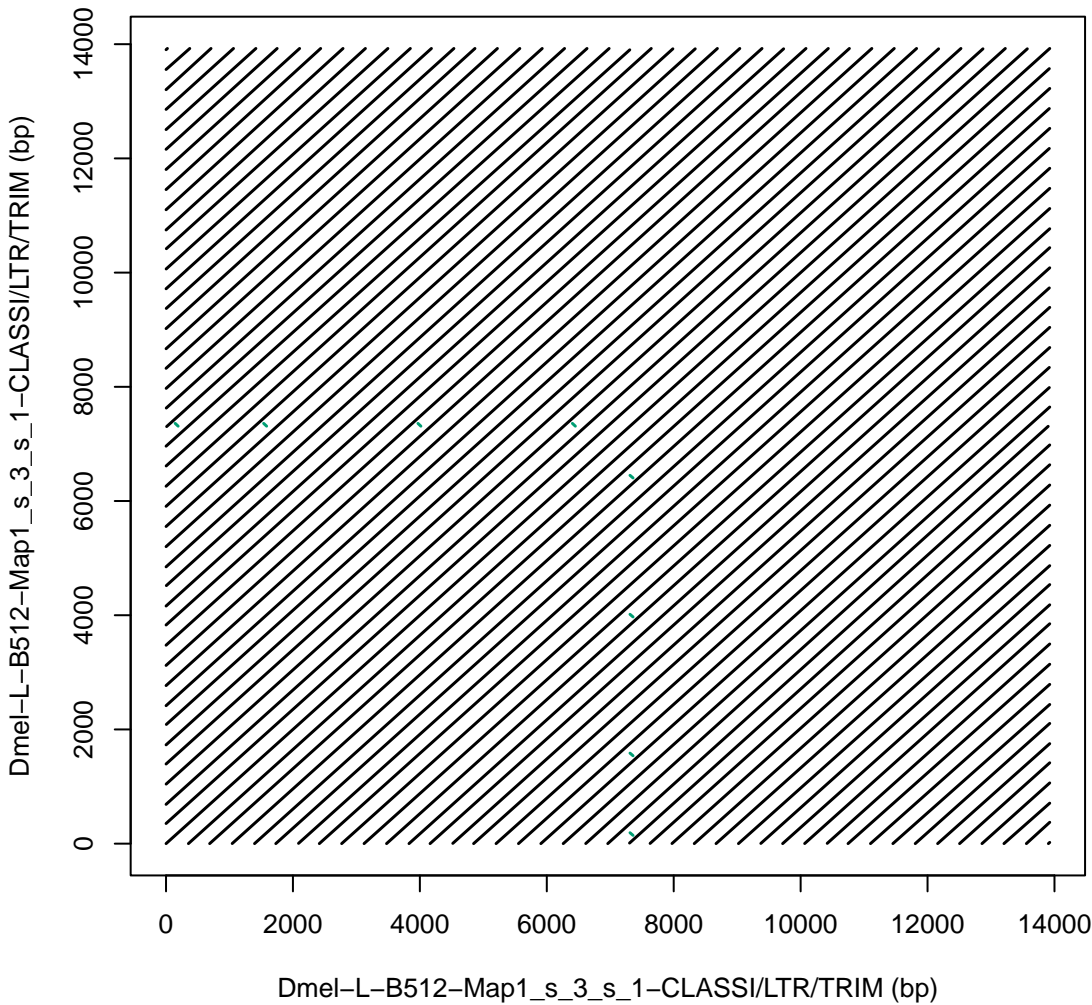**TE: Dmel−L−B512−Map1_s_3_s_1−CLASSI/LTR/TRIM**
consensus size: 13925bp; fragments: 25844; full length: 16 (>=12532.5bp)

TE consensus genomic coverage

TE consensus self dotplot (blastn)

TE consensus structure and protein hits

no orf >400 bp detected