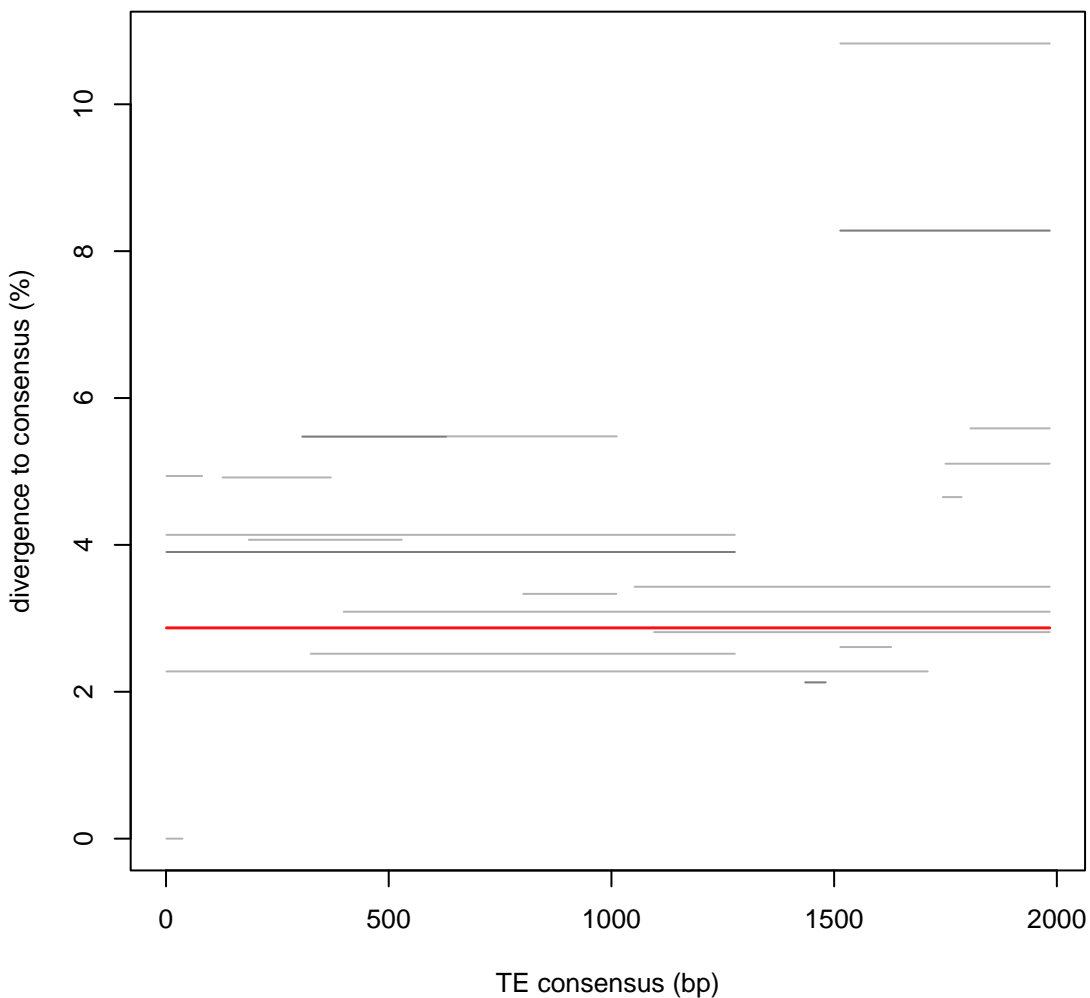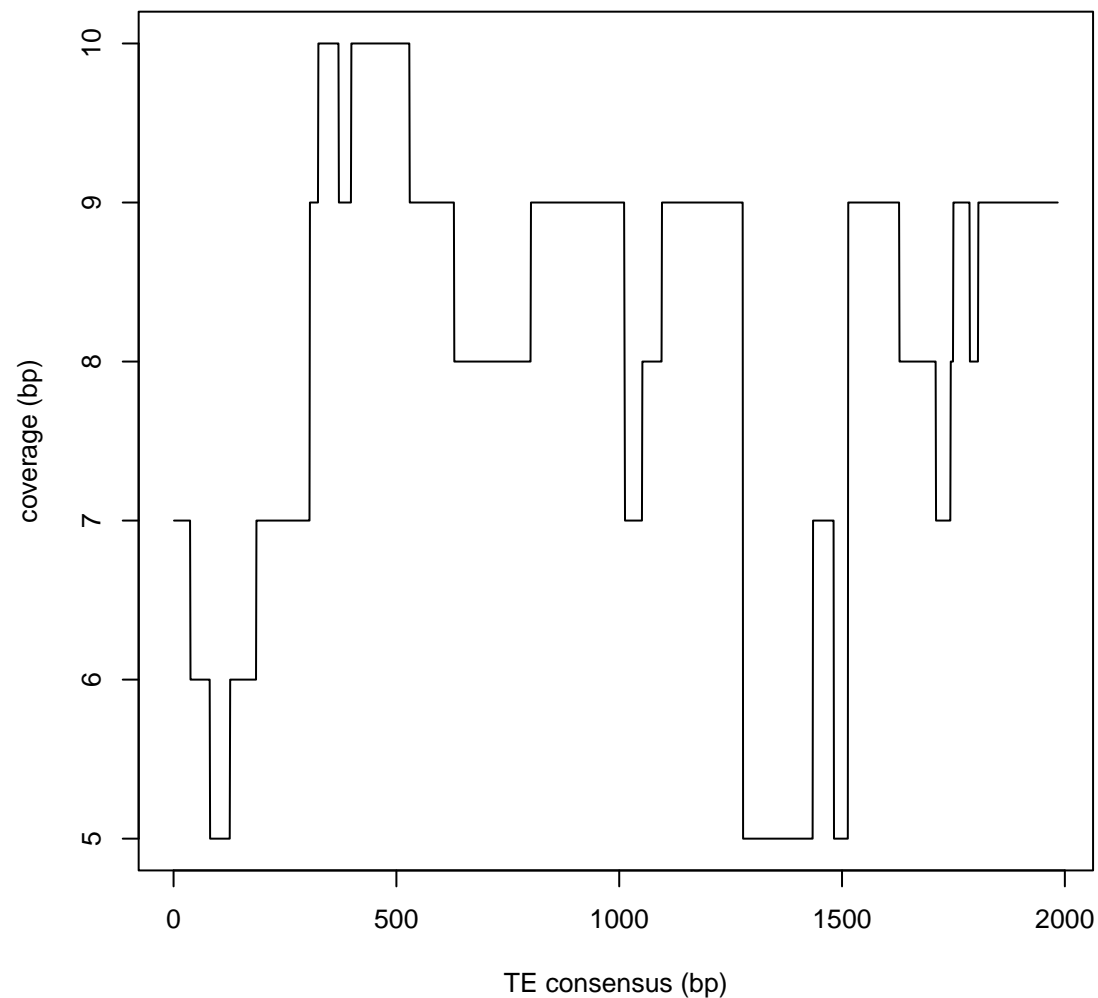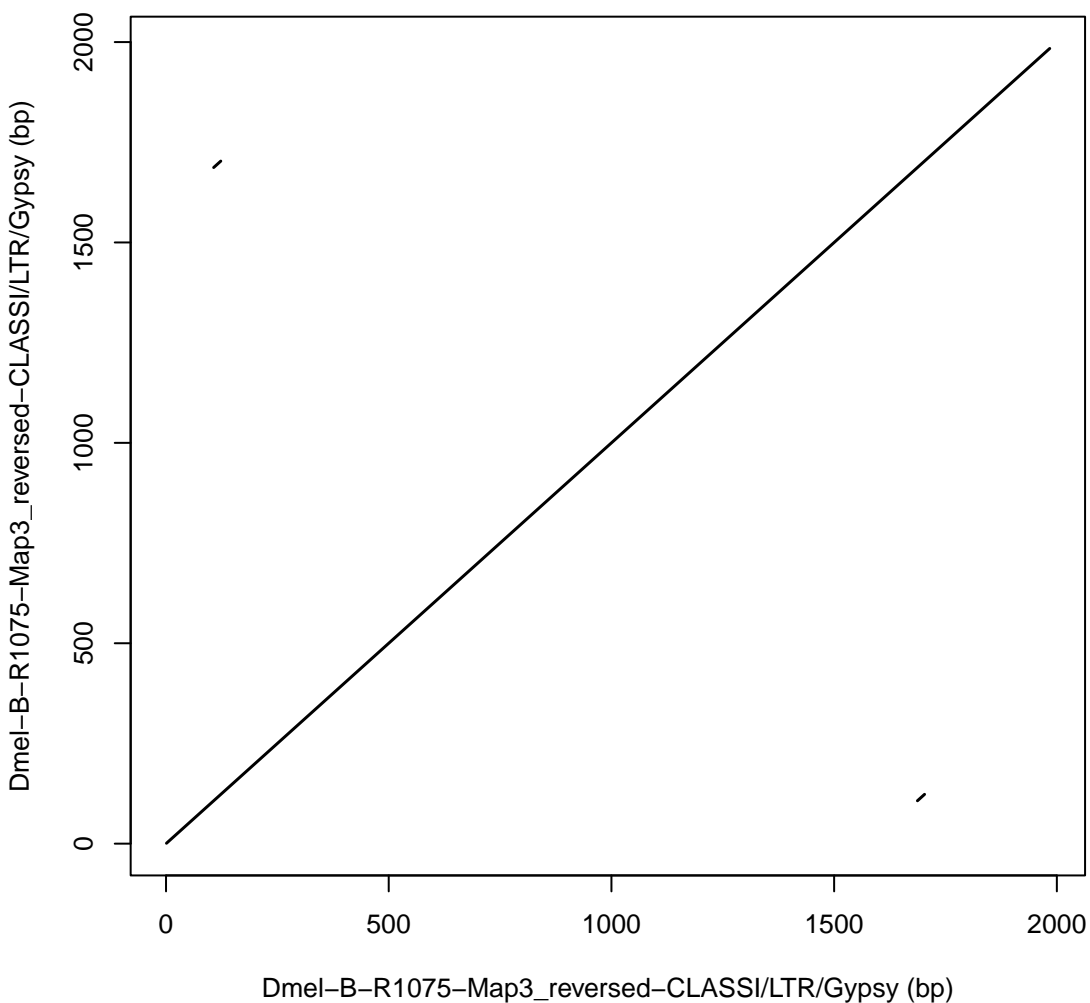**TE: Dmel−B−R1075−Map3_reversed−CLASSI/LTR/Gypsy**
consensus size: 1984bp; fragments: 25; full length: 1 (>=1785.6bp)

TE consensus genomic coverage

TE consensus self dotplot (blastn)

TE consensus structure and protein hits

Gypsy5_AG LTR/Gypsy