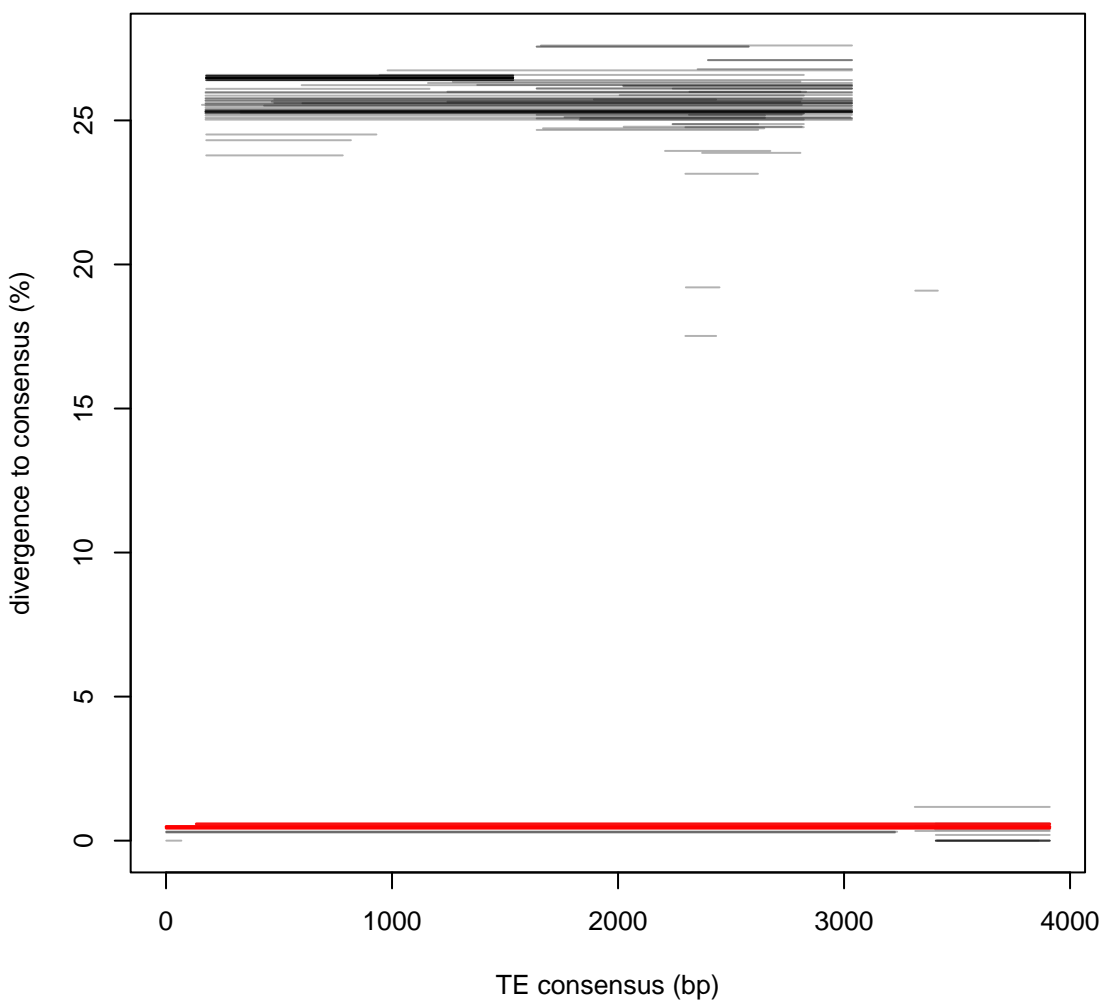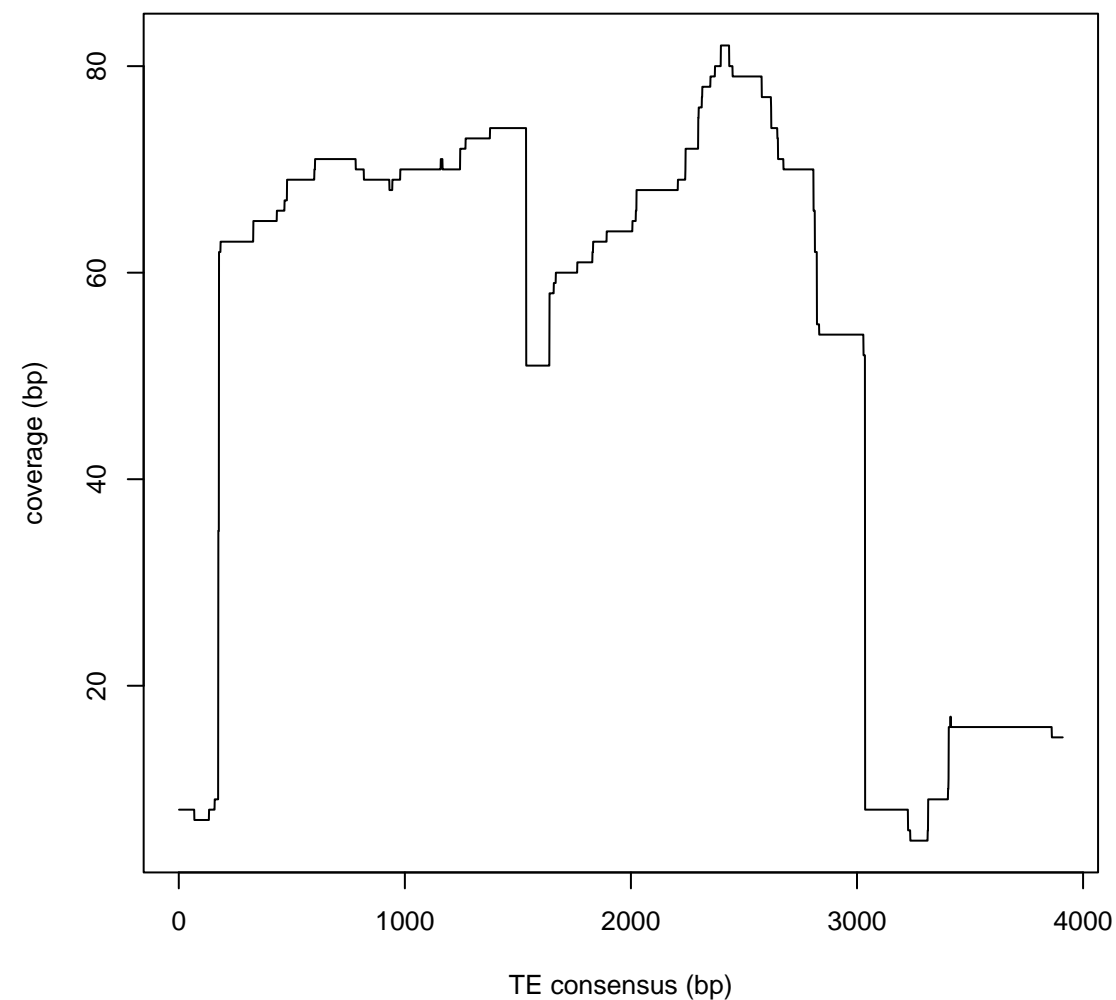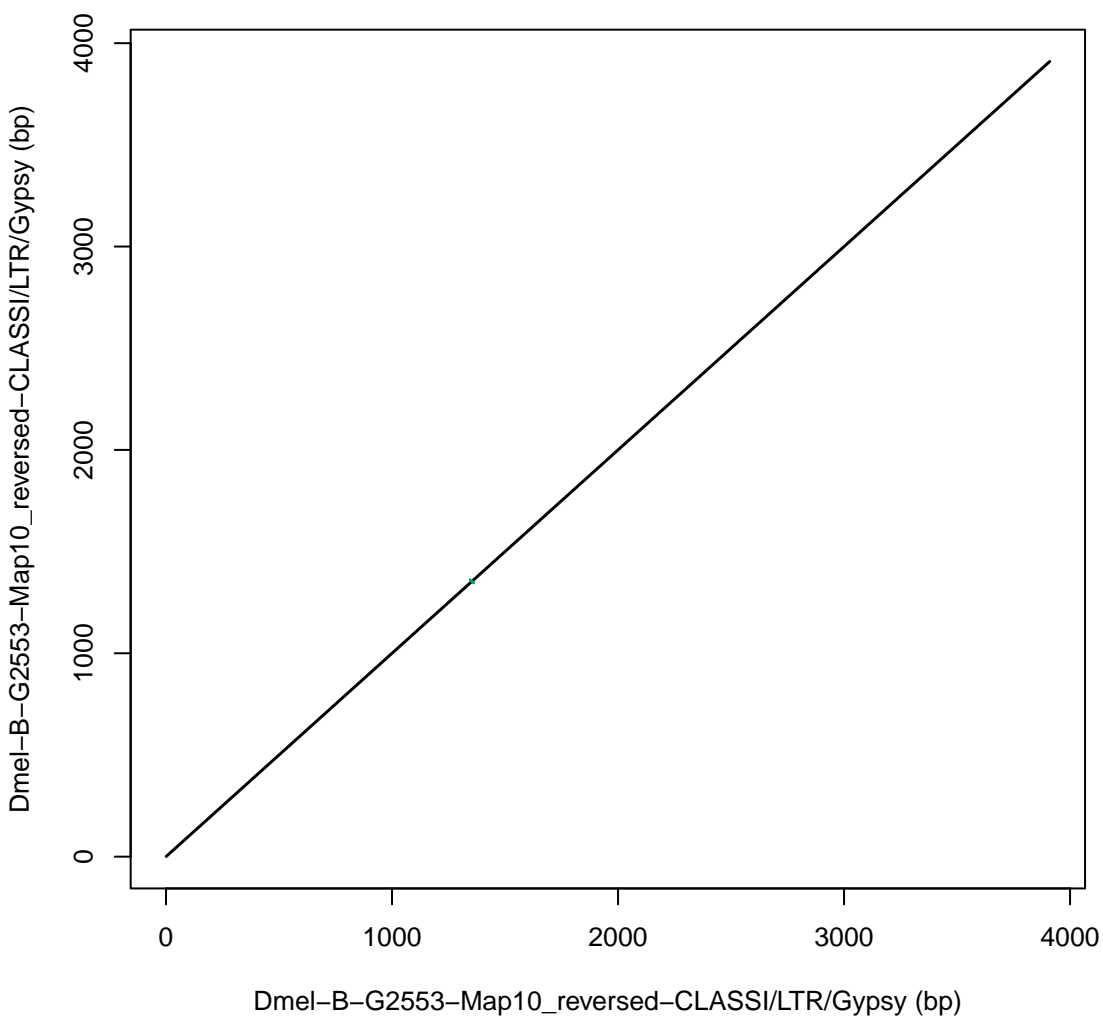**TE: Dmel−B−G2553−Map10_reversed−CLASSI/LTR/Gypsy**
consensus size: 3910bp; fragments: 122; full length: 5 (>=3519bp)

TE consensus genomic coverage

TE consensus self dotplot (blastn)

TE consensus structure and protein hits

Daphne−57_HMa_pol LINE/L2

TABOR_pol LTR/Gypsy