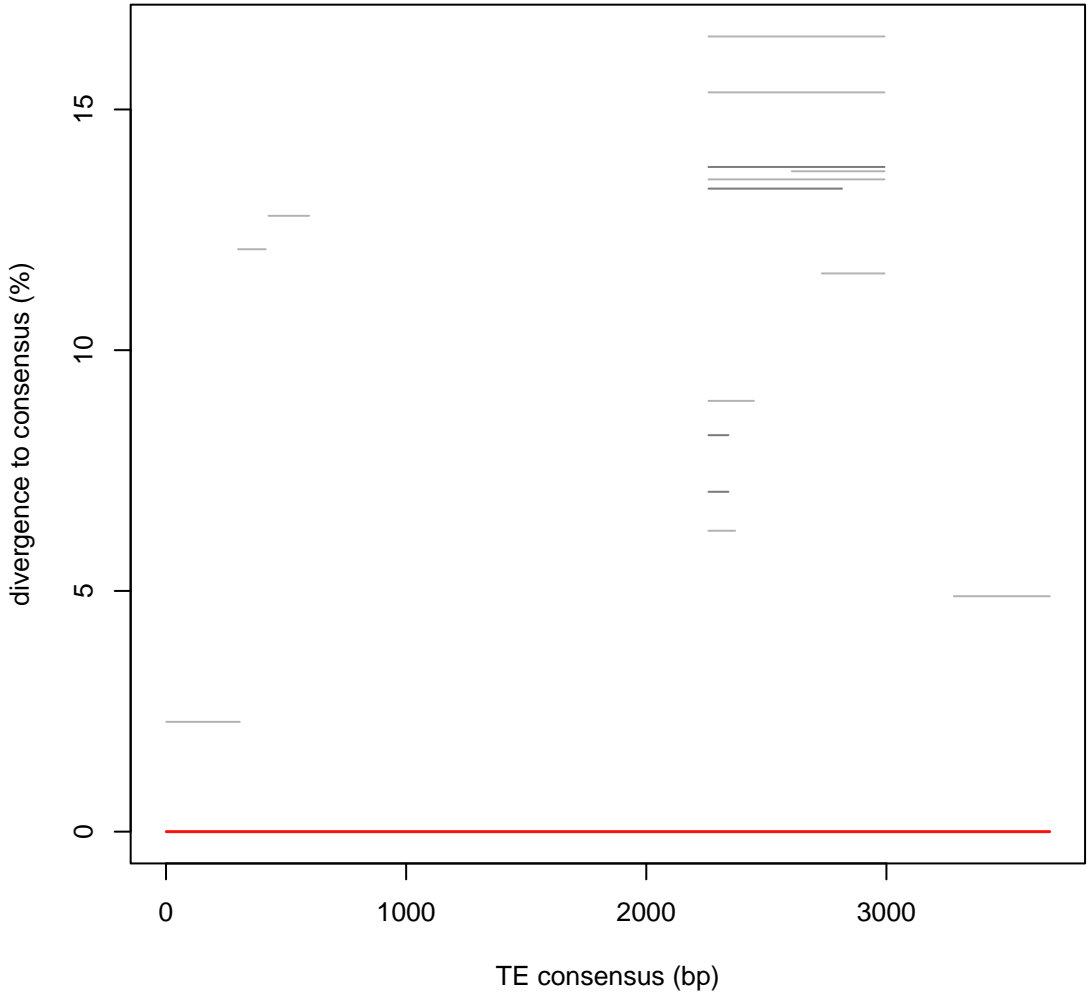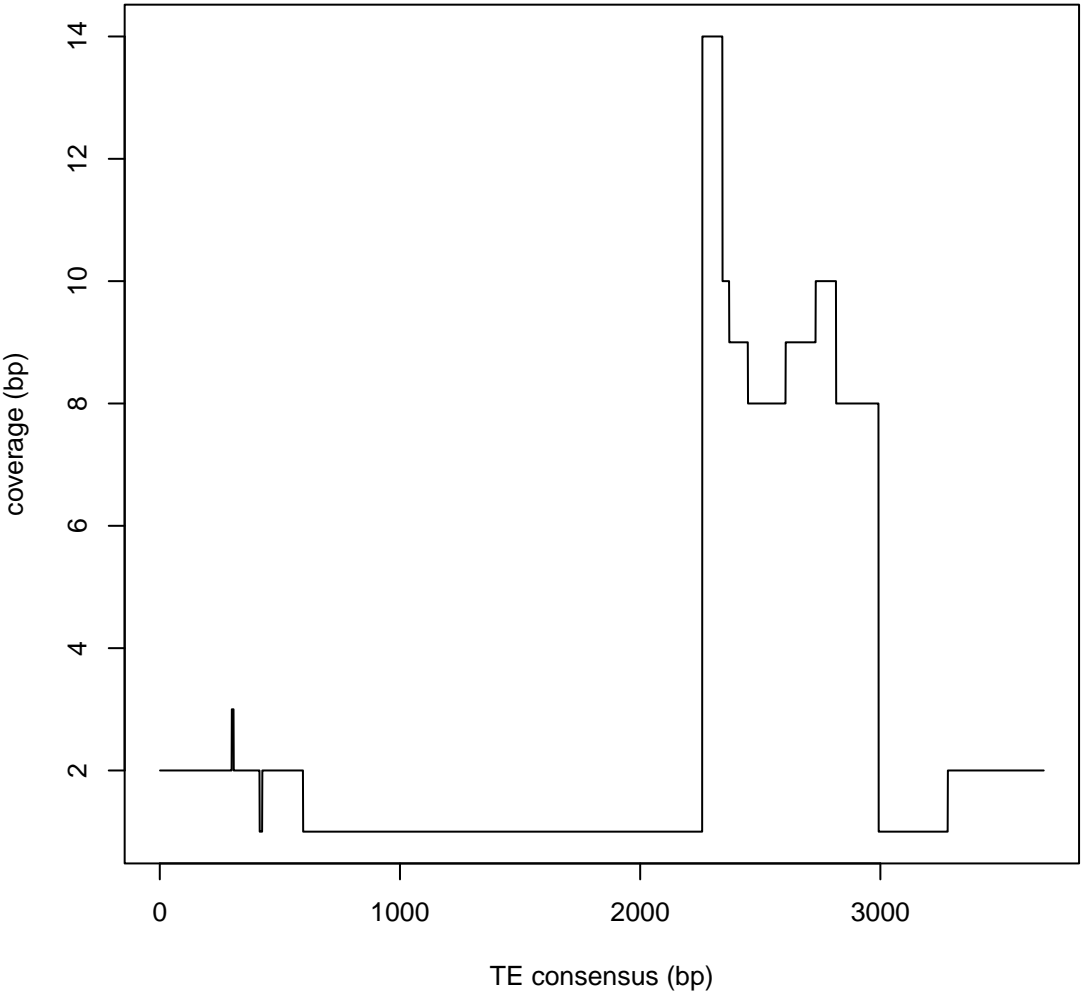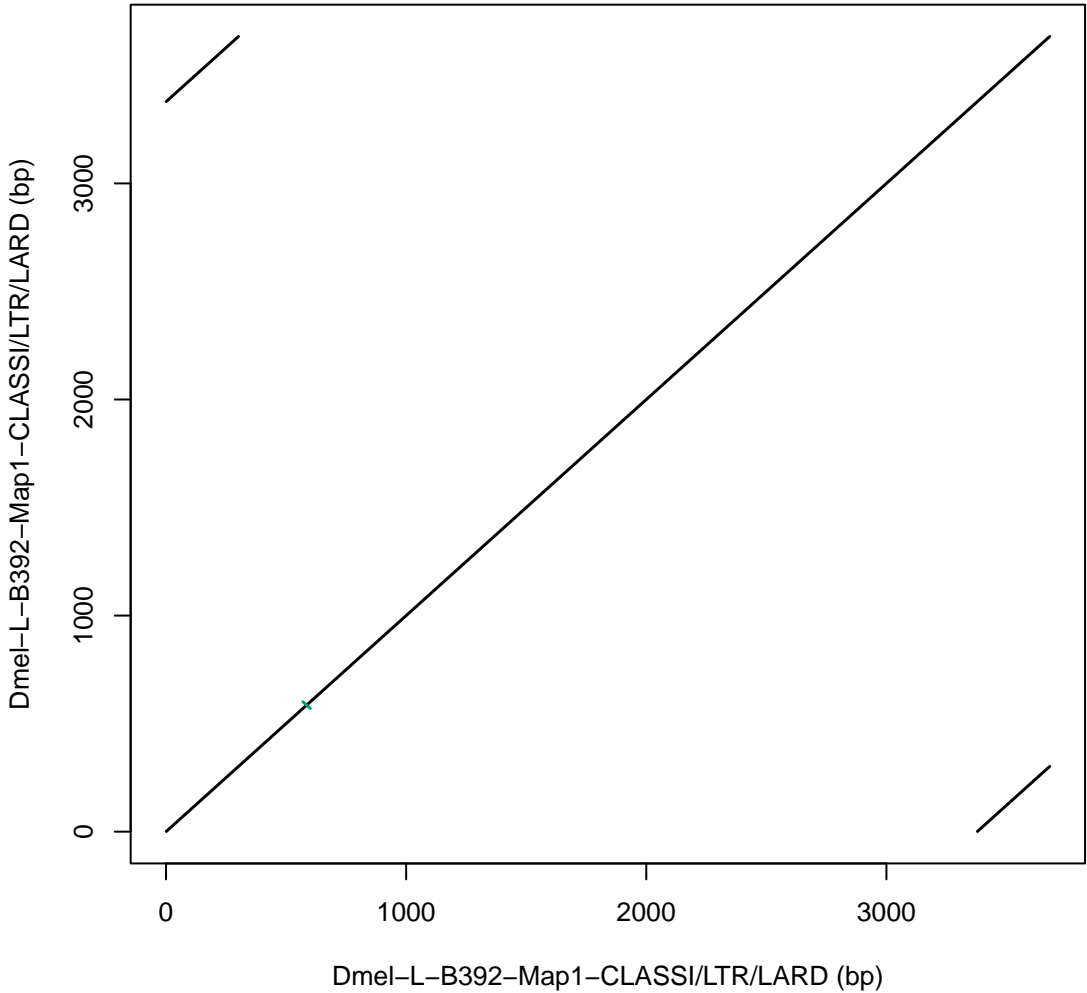# TE: Dmel−L−B392−Map1−CLASSI/LTR/LARD
consensus size: 3680bp; fragments: 20; full length: 1 (>=3312bp)

TE consensus genomic coverage

TE consensus self dotplot (blastn)

TE consensus structure and protein hits

Copia−55_VV LTR/Copia

CR1−17_AMi_pol LINE/CR1