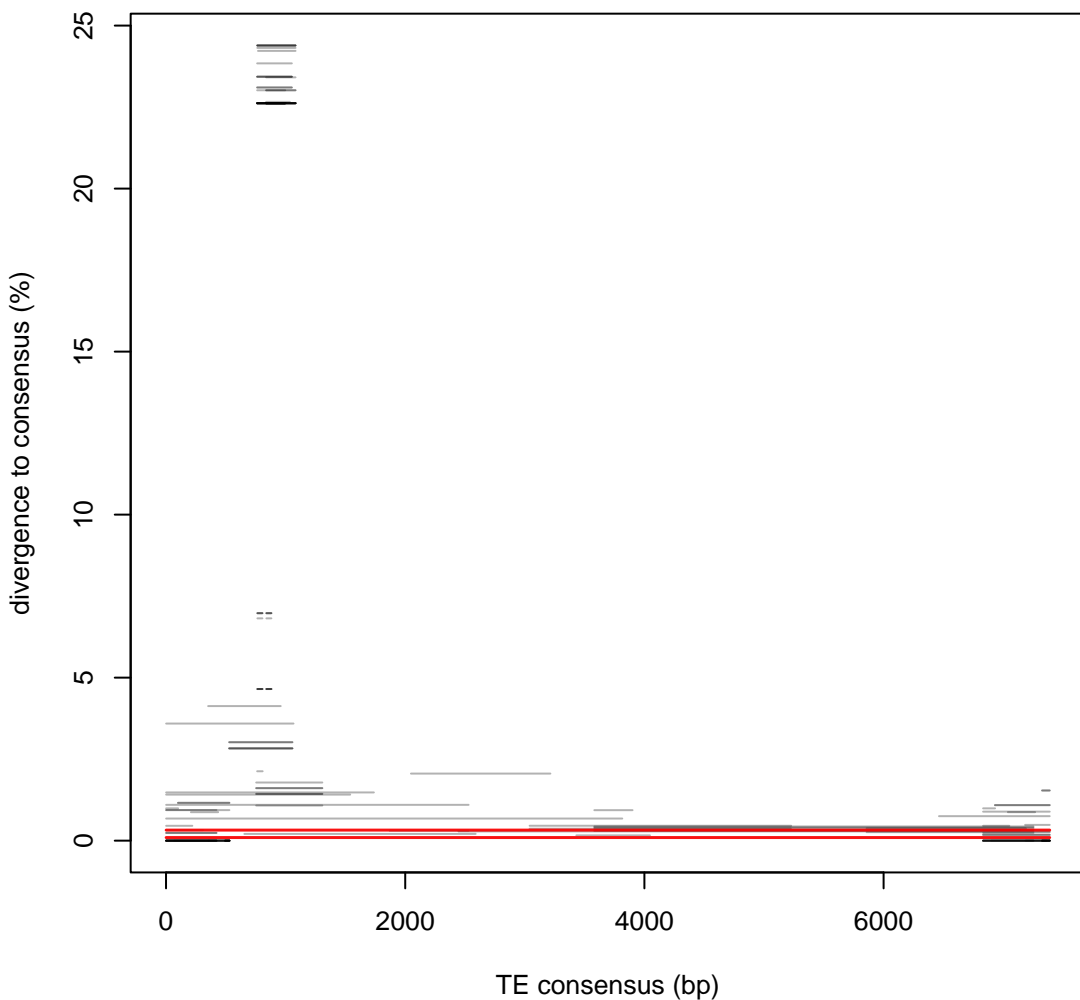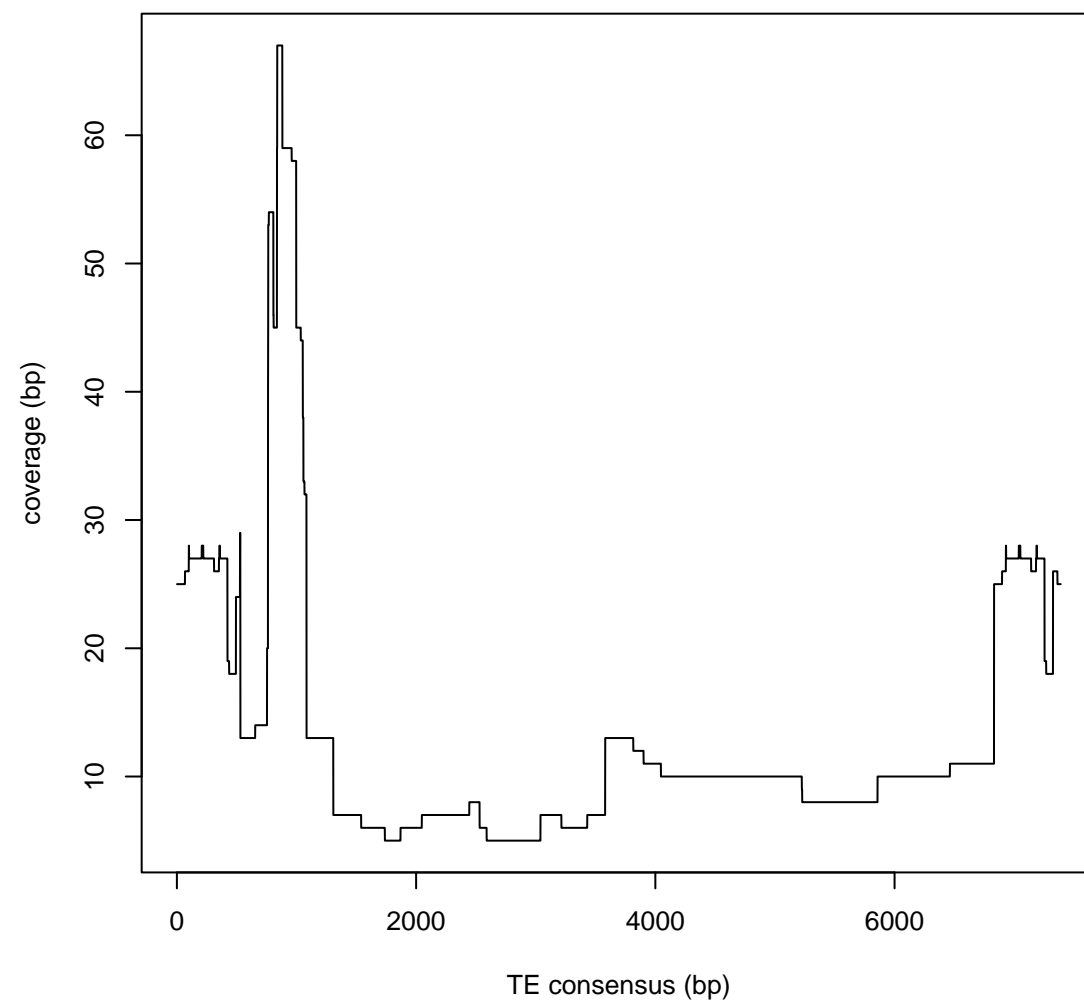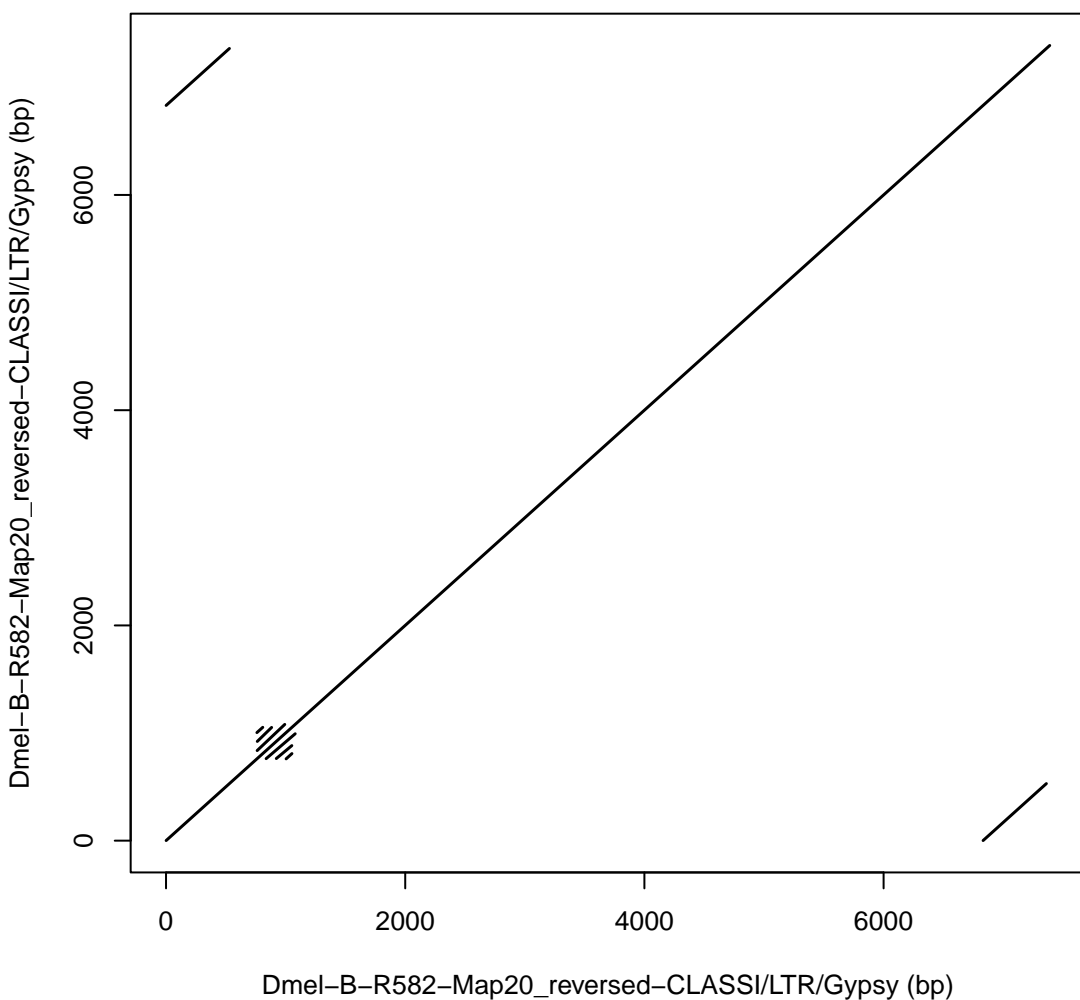**TE: Dmel−B−R582−Map20_reversed−CLASSI/LTR/Gypsy**
consensus size: 7389bp; fragments: 148; full length: 2 (>=6650.1bp)

TE consensus genomic coverage

TE consensus self dotplot (blastn)

TE consensus structure and protein hits

Gypsy−37_CQ_gag LTR/Gypsy
ACCORD_pol LTR/Gypsy
Gypsy−14_DWil LTR/Gypsy
ZAM_env LTR/Gypsy