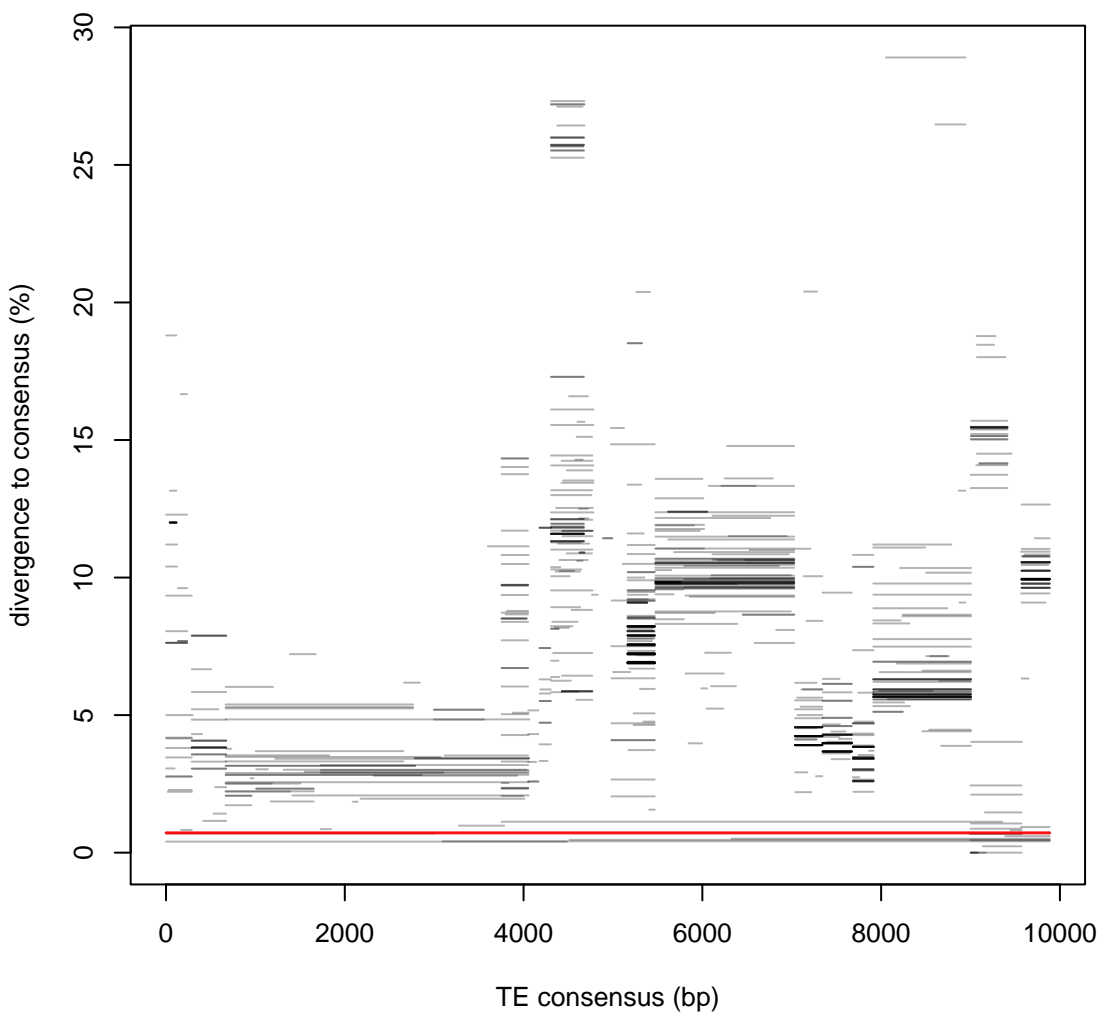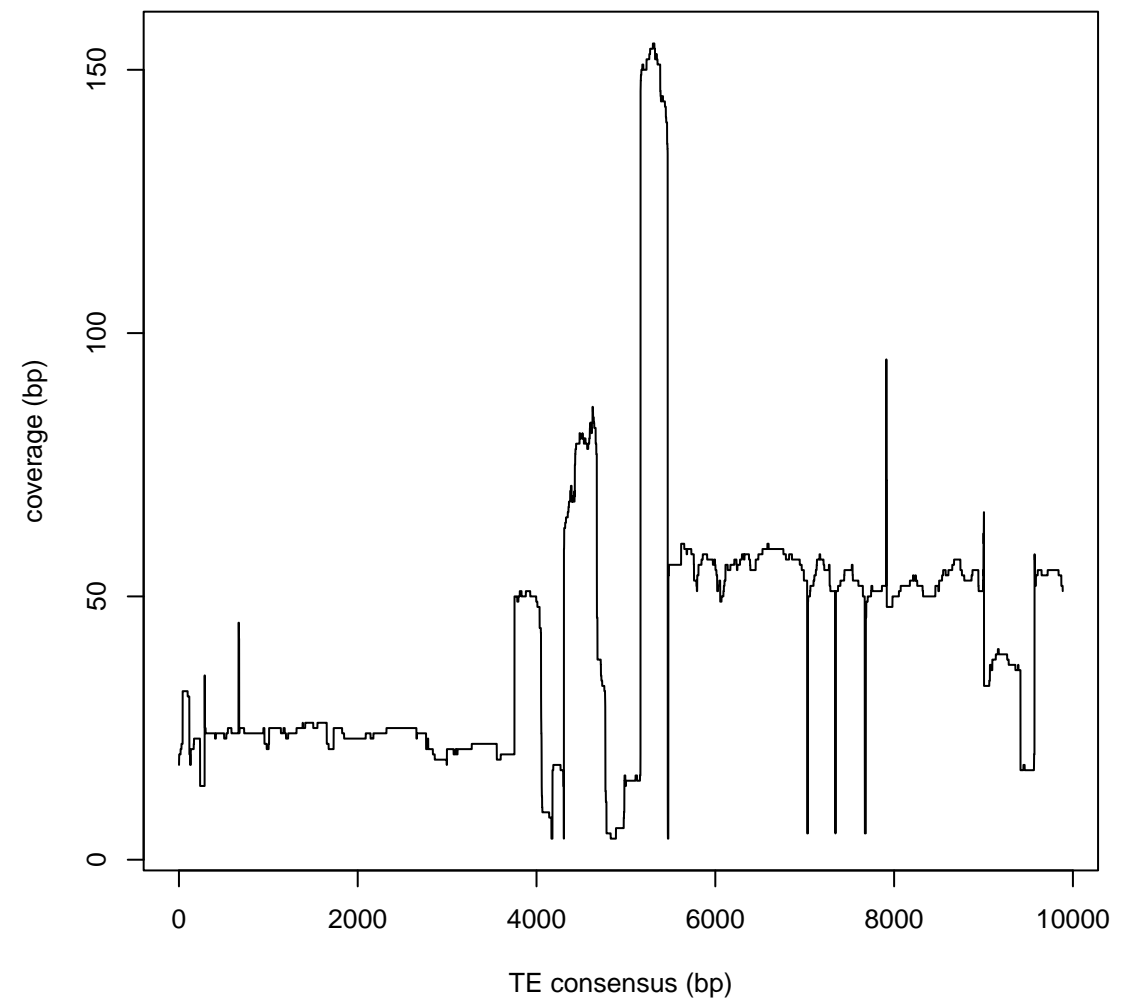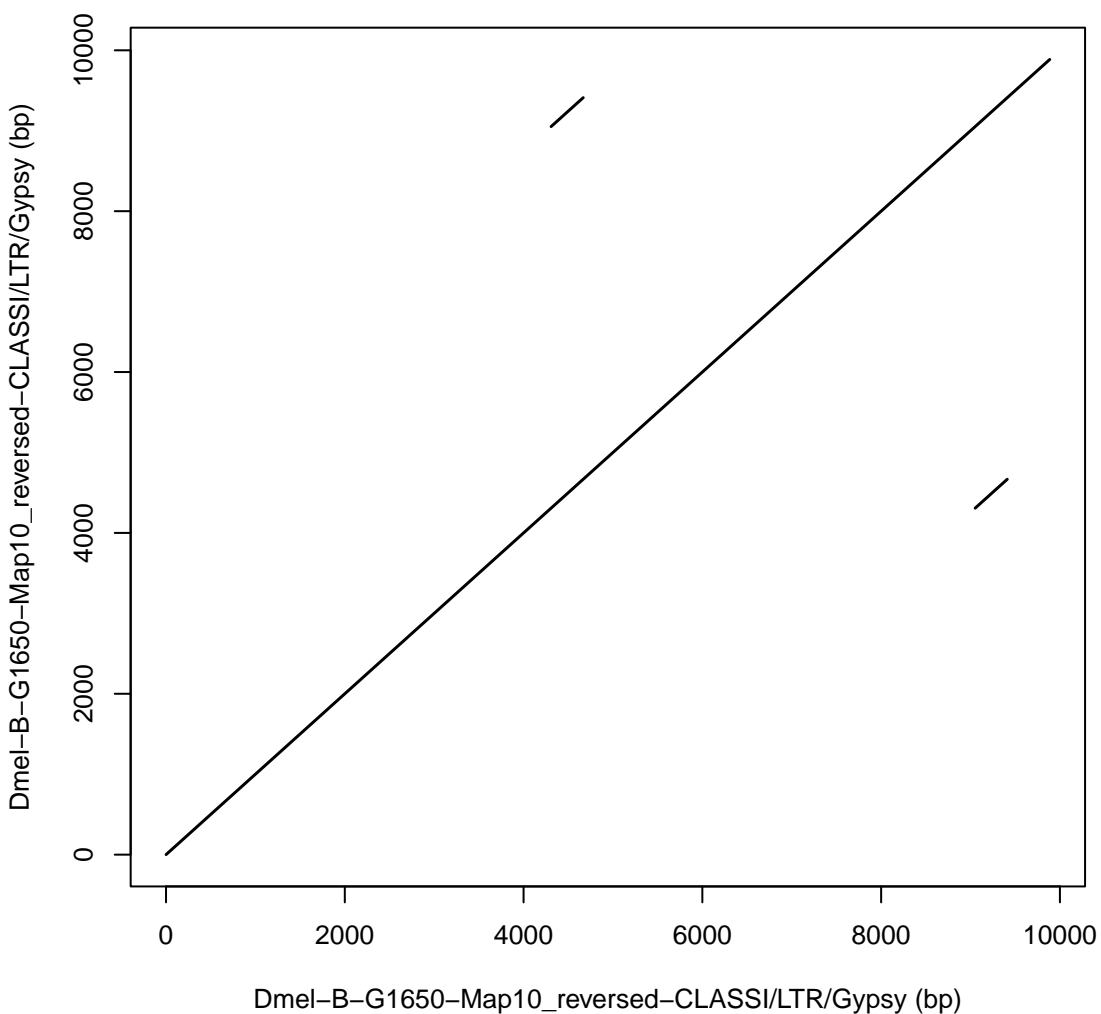**TE: Dmel–B–G1650–Map10_reversed–CLASSI/LTR/Gypsy**
consensus size: 9886bp; fragments: 807; full length: 1 (>=8897.4bp)

TE consensus genomic coverage

TE consensus self dotplot (blastn)

TE consensus structure and protein hits

Gypsy4_pol LTR/Gypsy
Gypsy–12_DVir_env LTR/Gypsy
Gypsy3_env LTR/Gypsy
ATGP5A_pol LTR/Gypsy
TRANSPAC_pol LTR/Gypsy
TRANSPAC_pol LTR/Gyp
Rover_DM_pol LT