TE: Dmel−B−G1624−Map5_reversed−CLASSI/LTR/Gypsy
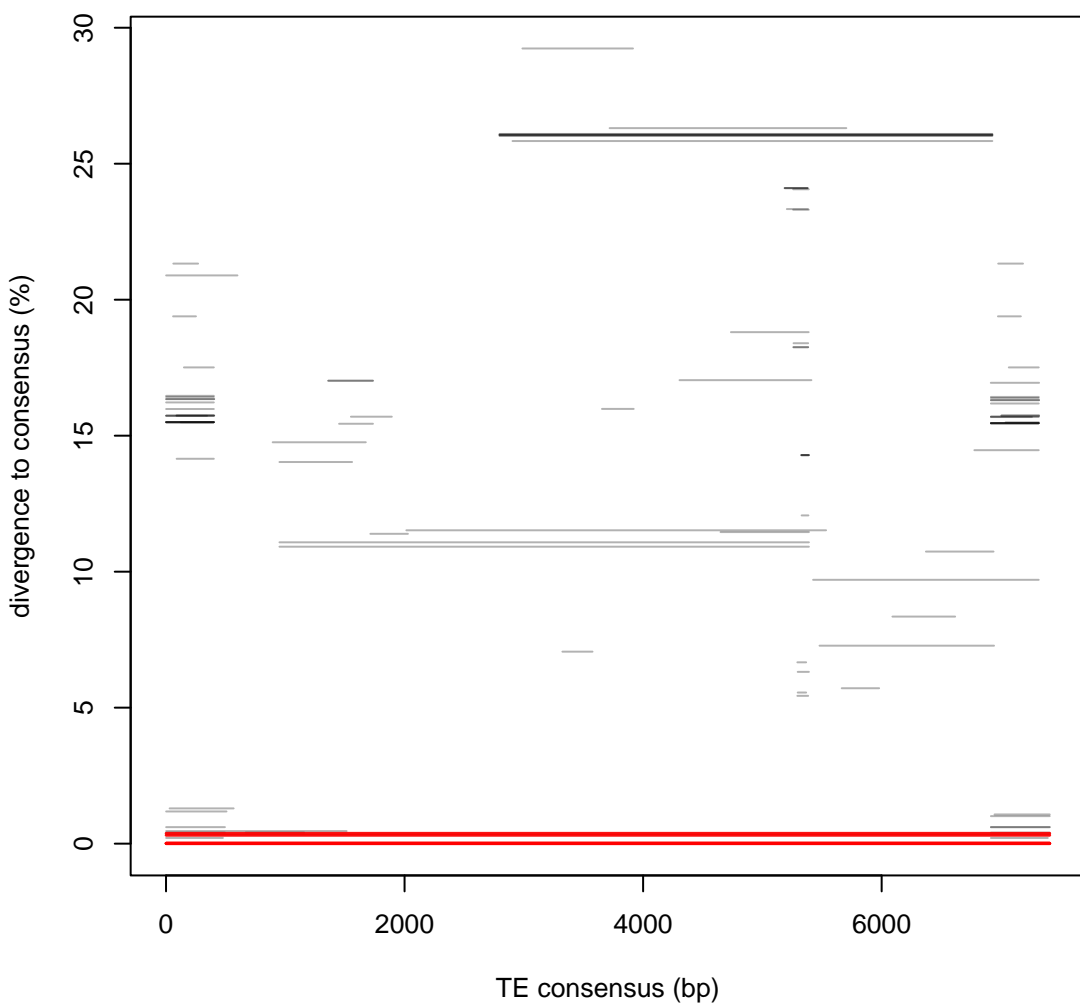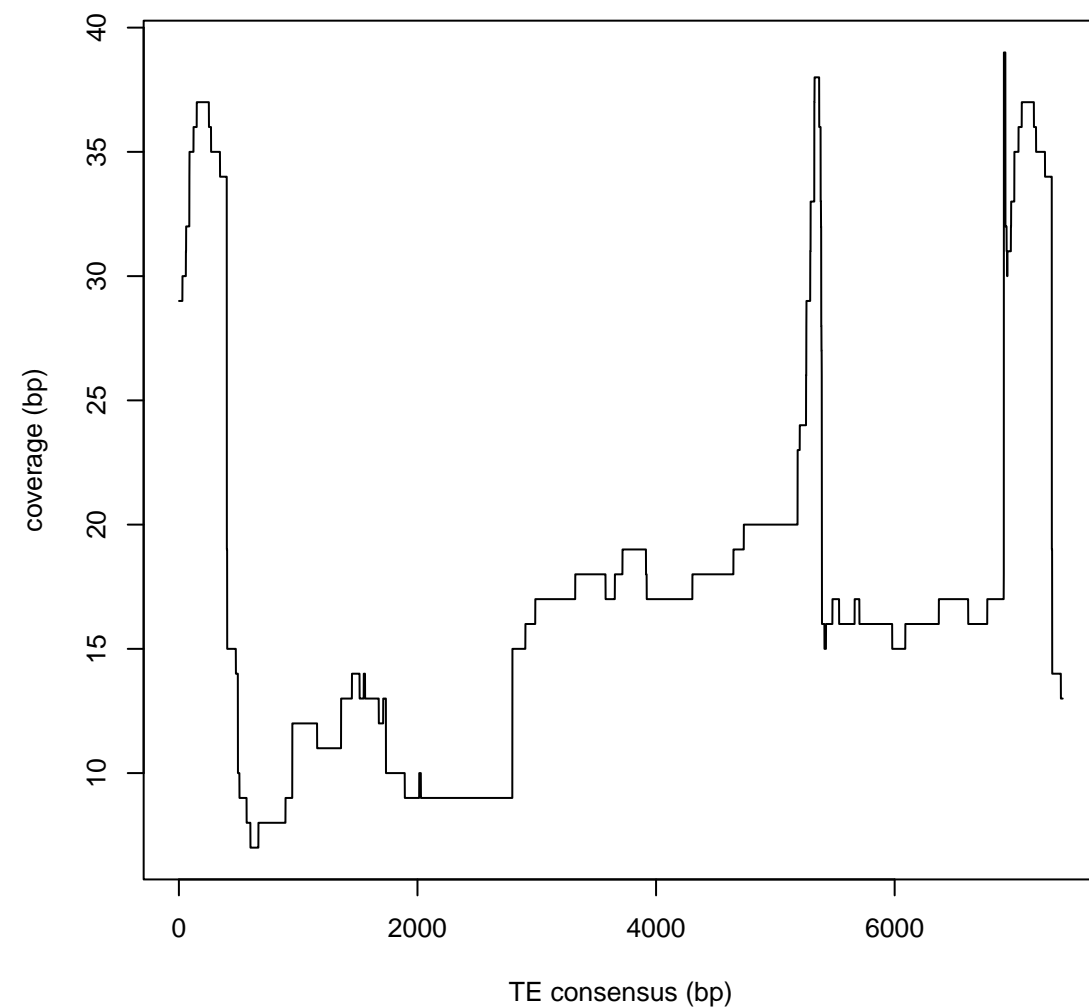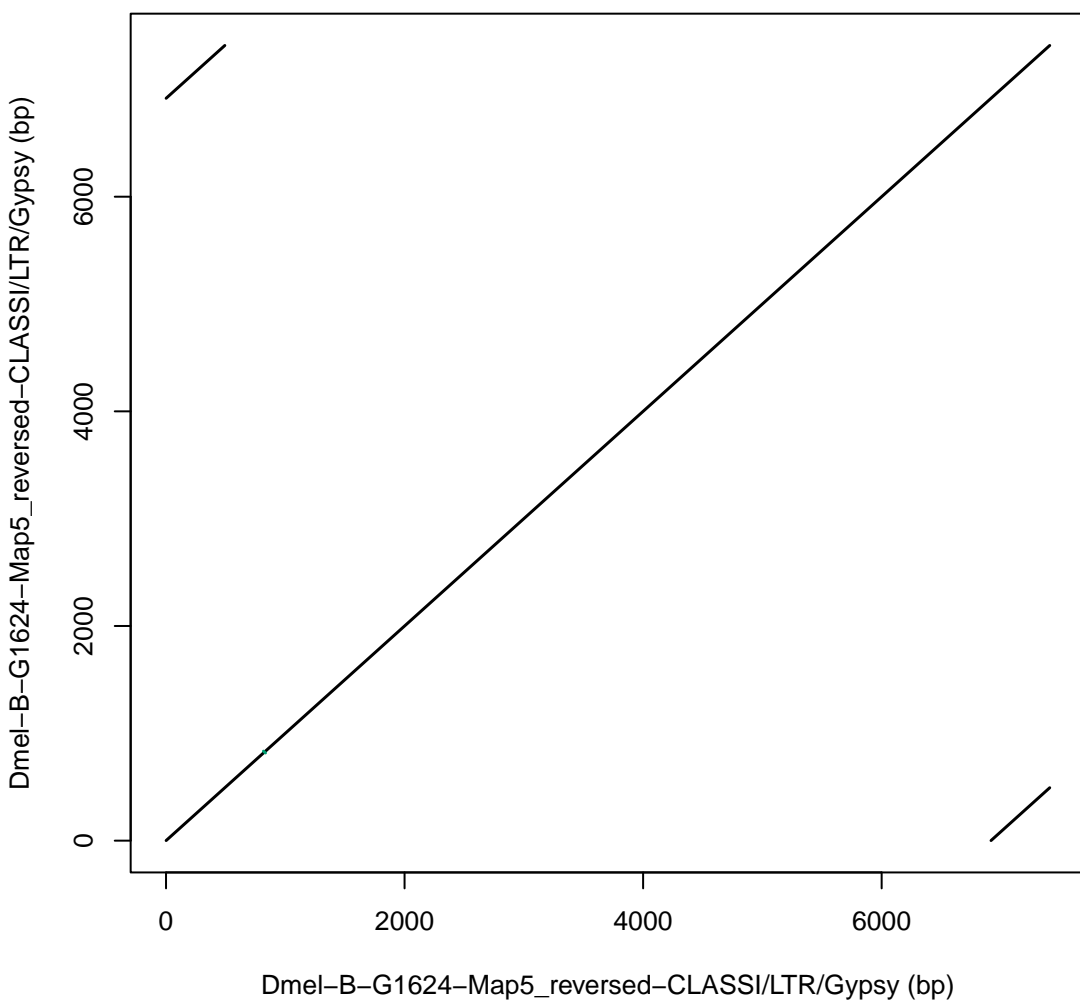## consensus size: 7409bp; fragments: 115; full length: 6 (>=6668.1bp)

TE consensus (bp)

divergence to consensus (%)

TE consensus genomic coverage

coverage (bp)

TE consensus (bp)

TE consensus self dotplot (blastn)

Dmel−B−G1624−Map5_reversed−CLASSI/LTR/Gypsy (bp)

Dmel−B−G1624−Map5_reversed−CLASSI/LTR/Gypsy (bp)

TE consensus structure and protein hits

GTWIN_gag LTR/Gypsy

Gypsy−18_BRa_1p LTR/Gypsy

GTWIN_pol LTR/Gypsy

Gypsy−1_DSim_env LTR/Gypsy

CR1−62_HM_pol LINE/CR

GTWIN_env LTR/Gypsy

Dmel−B−G1624−Map5_reversed−CLASSI/LTR/Gypsy (bp)