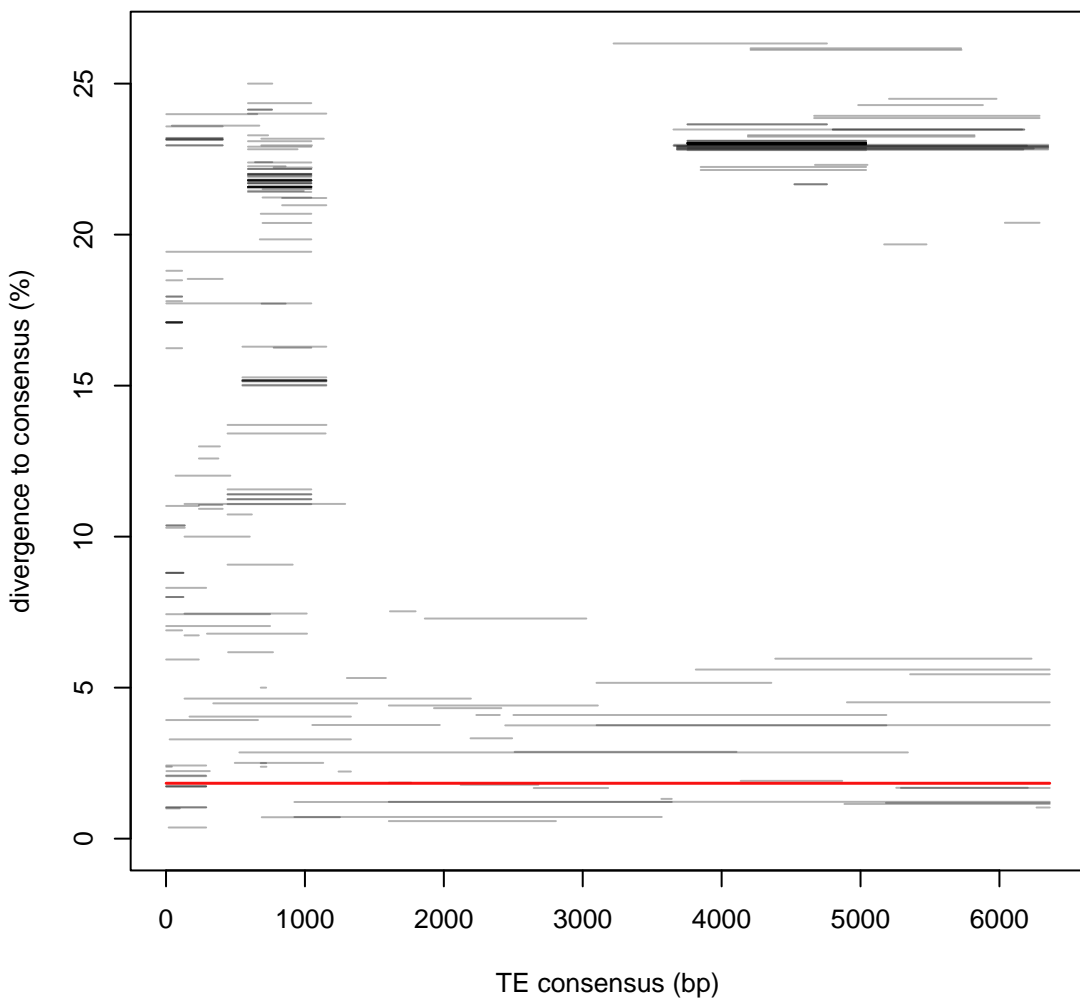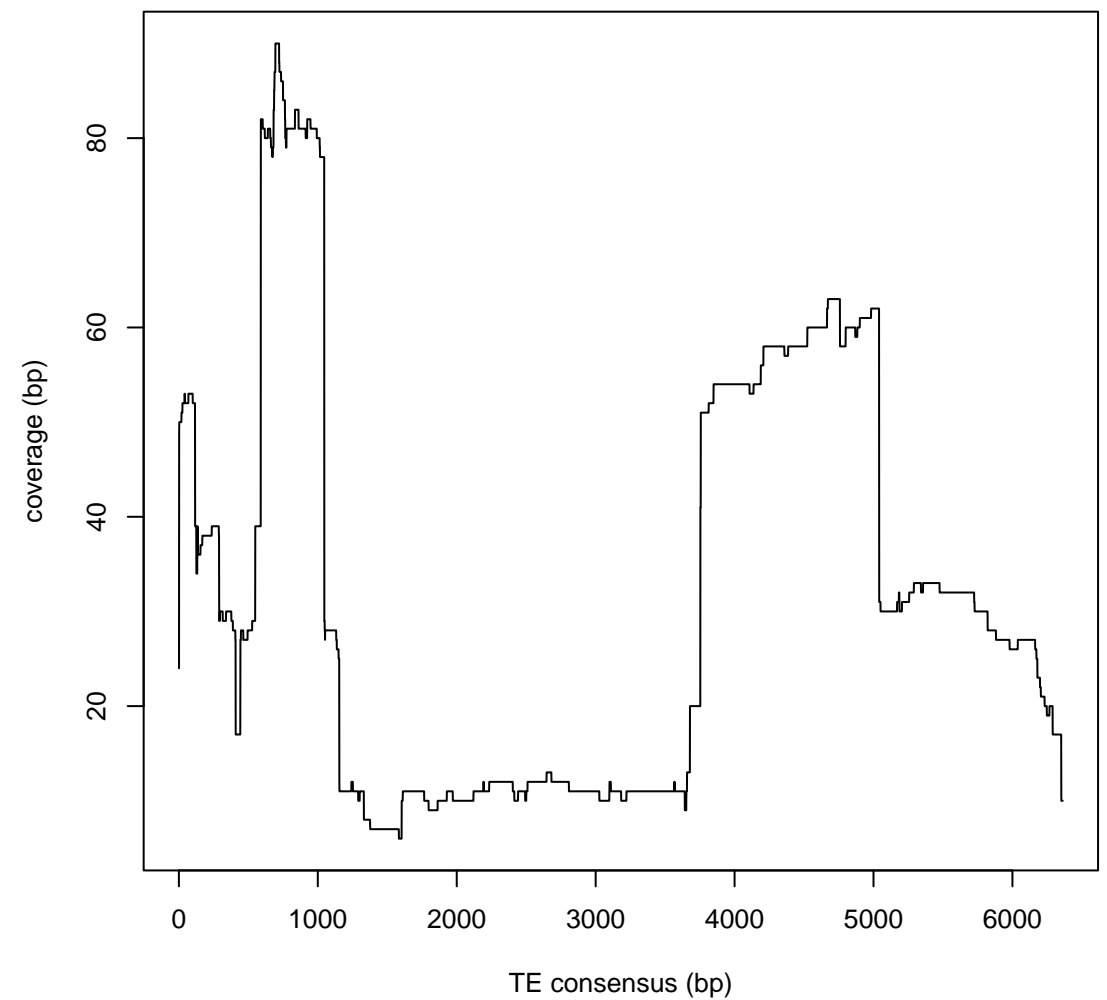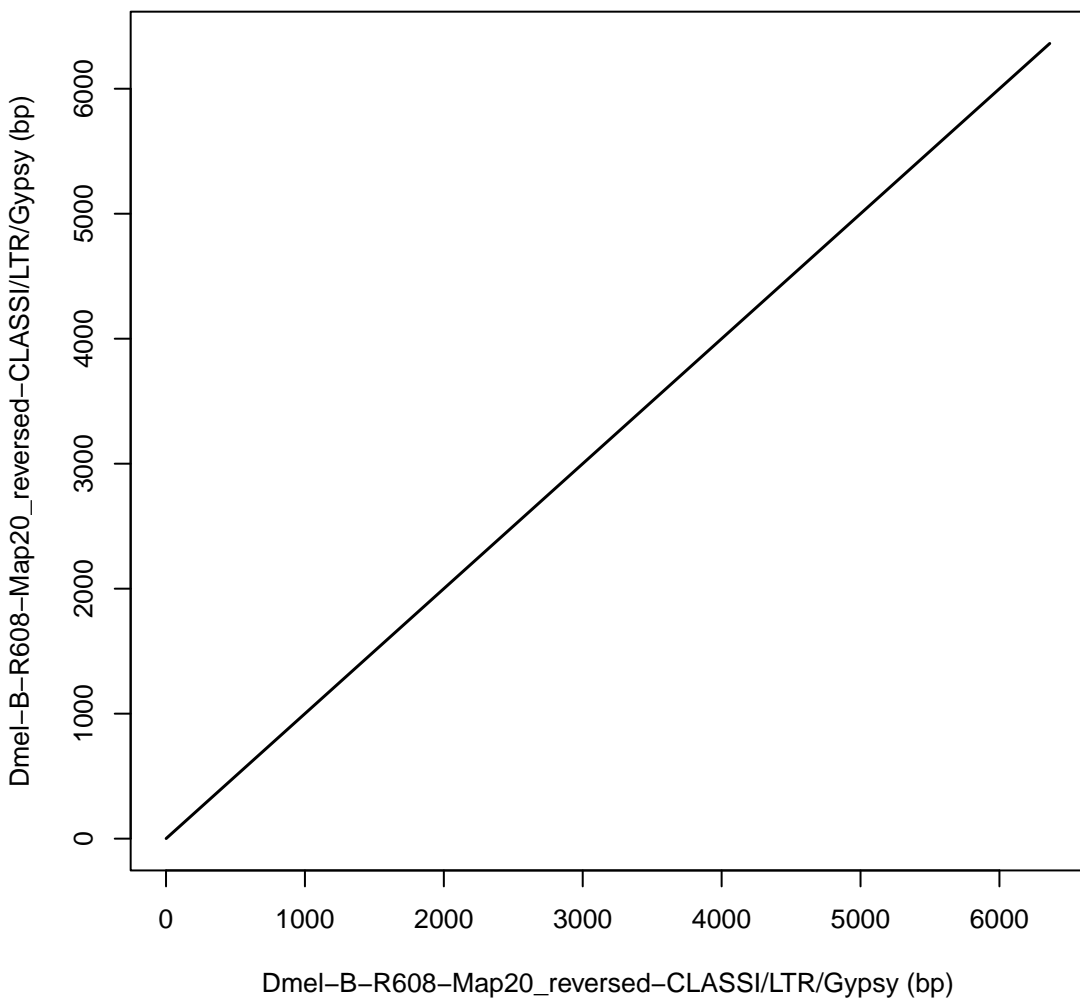**TE: Dmel−B−R608−Map20_reversed−CLASSI/LTR/Gypsy**
consensus size: 6362bp; fragments: 242; full length: 1 (>=5725.8bp)

TE consensus genomic coverage

TE consensus self dotplot (blastn)

TE consensus structure and protein hits

−9_DWil LTR/Gypsy

sy−30_SB_pol LTR/Gypsy

Gypsy−26_DPse_gag LTR/Gypsy

Gypsy−139_AA_gag LTR/Gypsy

Gypsy−588_AA_pol LTR/Gypsy

Gypsy−62_DWil_pol LTR/Gypsy

Gypsy16_AG_pol LTR/Gypsy

Gypsy−10_AMi LTR