TE: Dmel−B−G2318−Map3_reversed_s_0_s_2−CLASSI/LTR/Gypsy
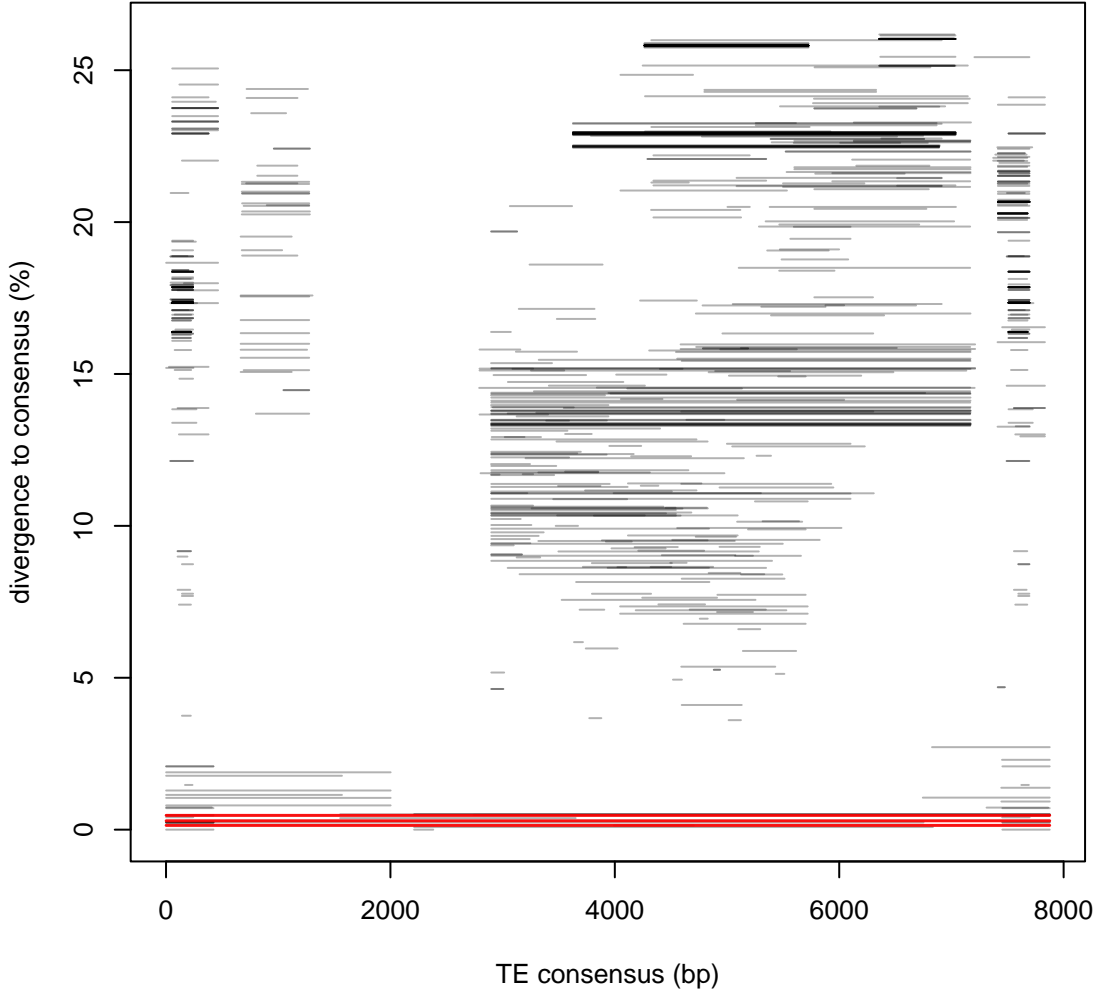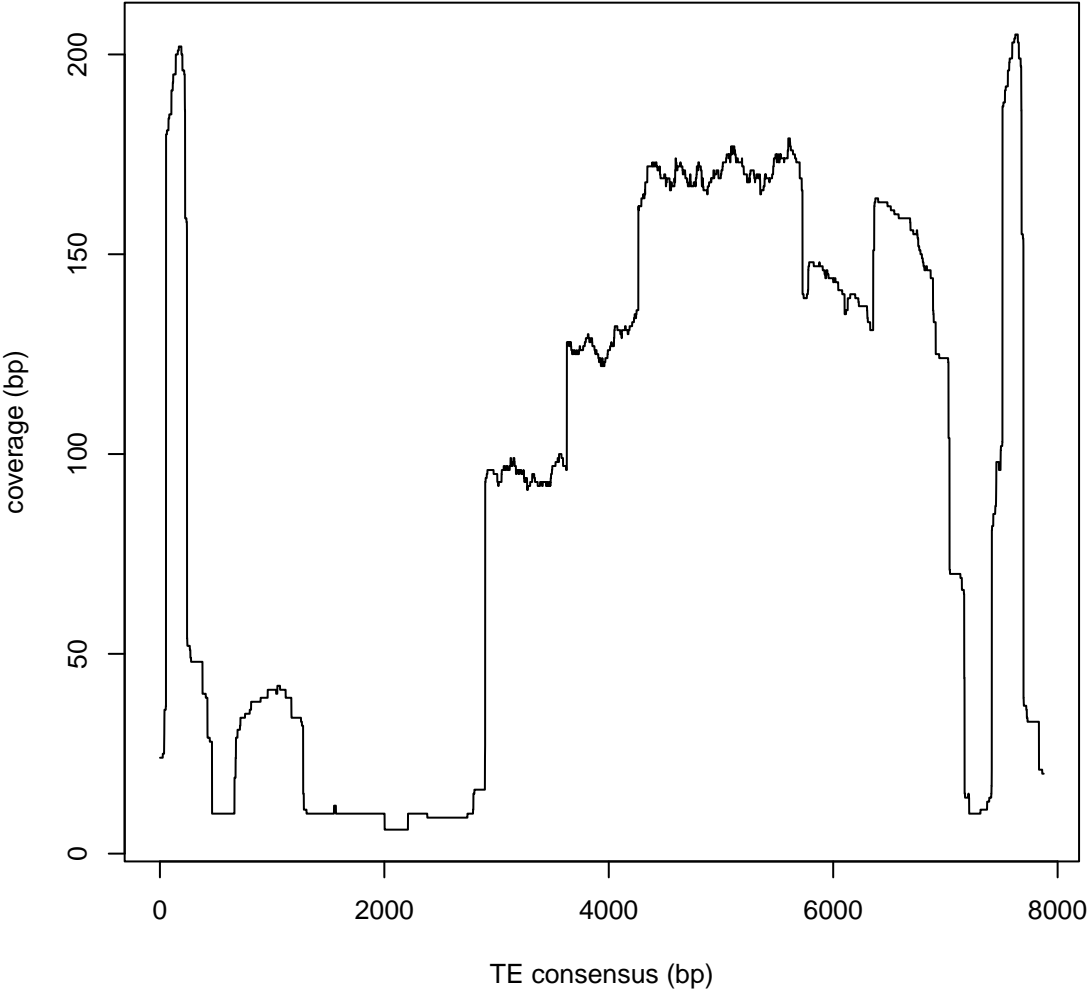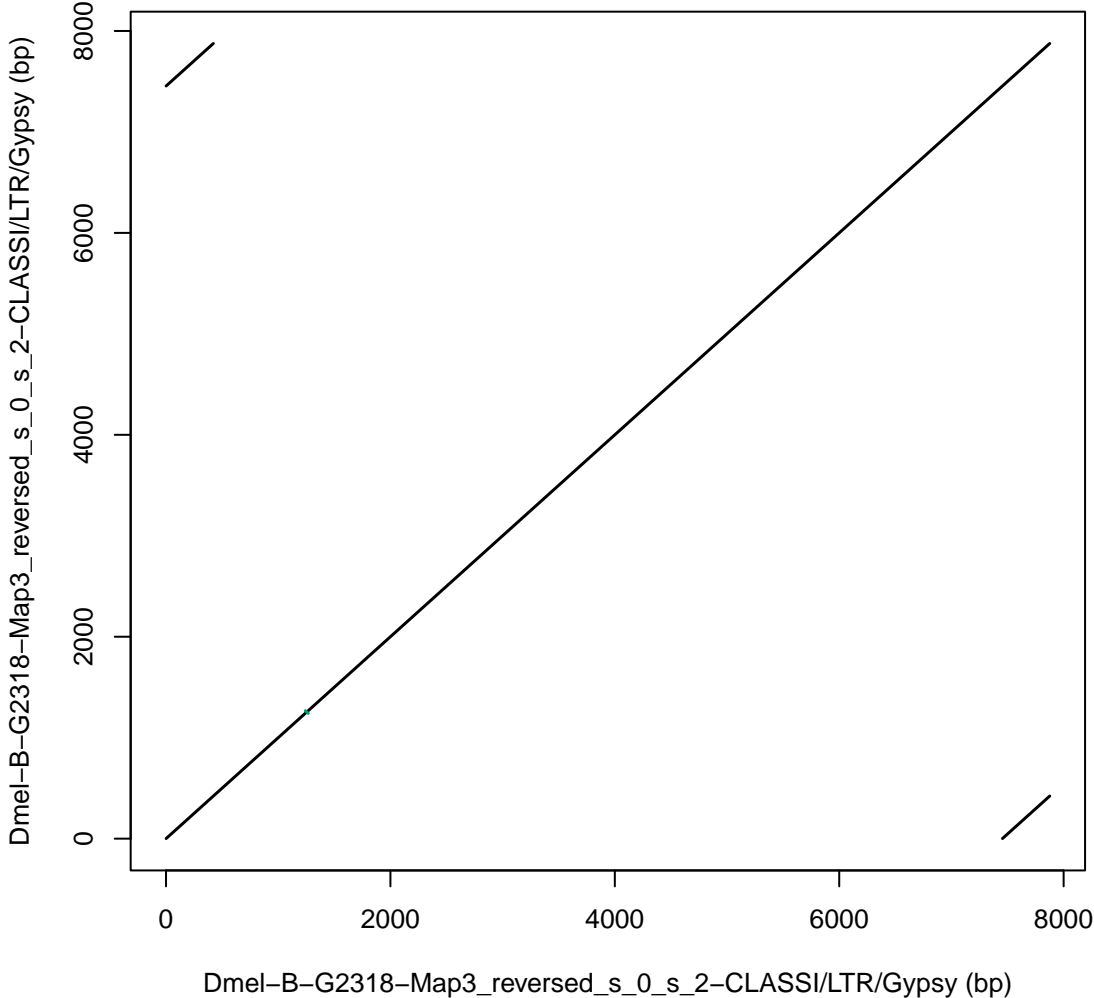**consensus size: 7876bp; fragments: 818; full length: 3 (>=7088.4bp)**

TE consensus genomic coverage

TE consensus self dotplot (blastn)

TE consensus structure and protein hits

−611_AA_pol LTR/Pao
sy−30_SB_pol LTR/Gypsy
BEL1_MH_pc1 LTR/Pao
Gypsy−276_AA_gag LTR/Gypsy
Jockey−1_DWi_pol LINE/I−Jockey
Stalker4_pol LTR/Gypsy