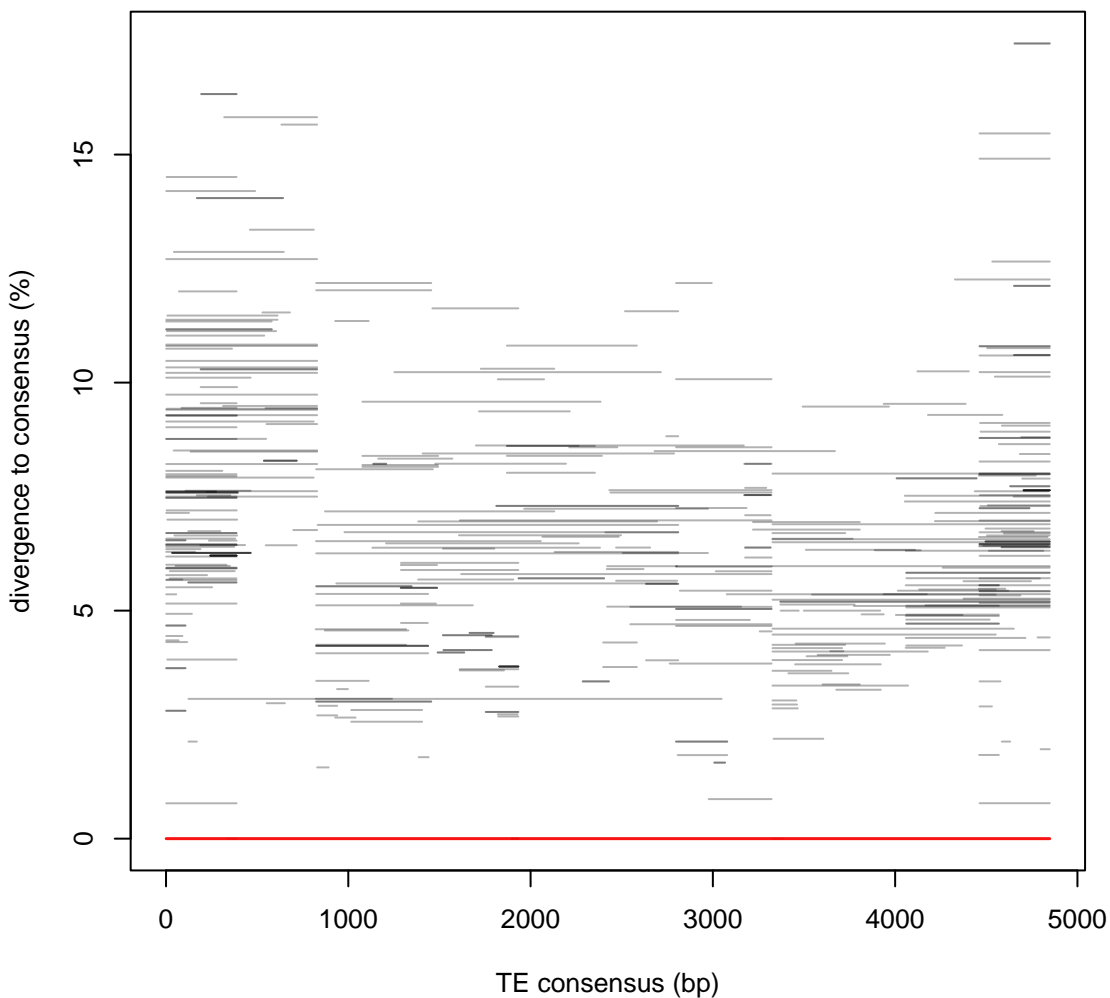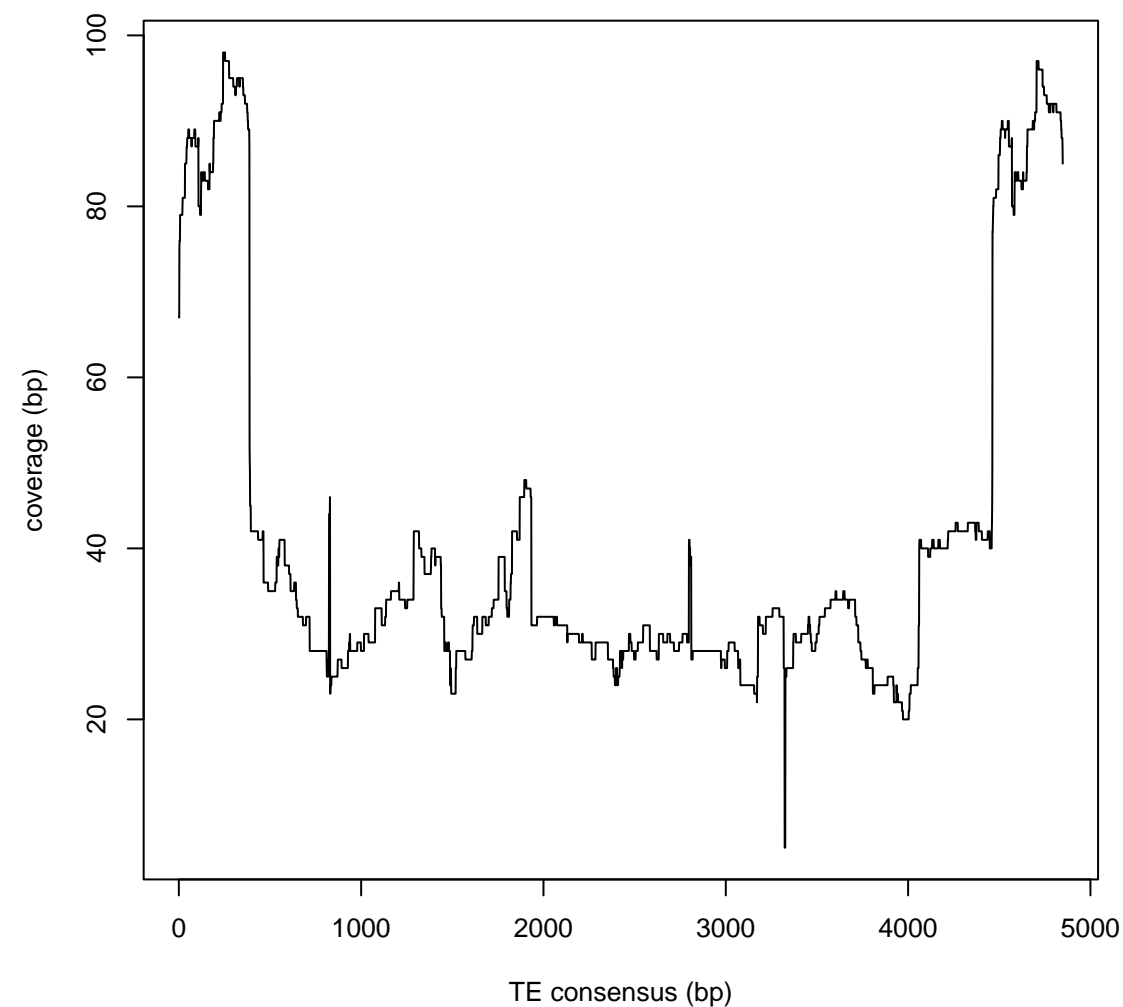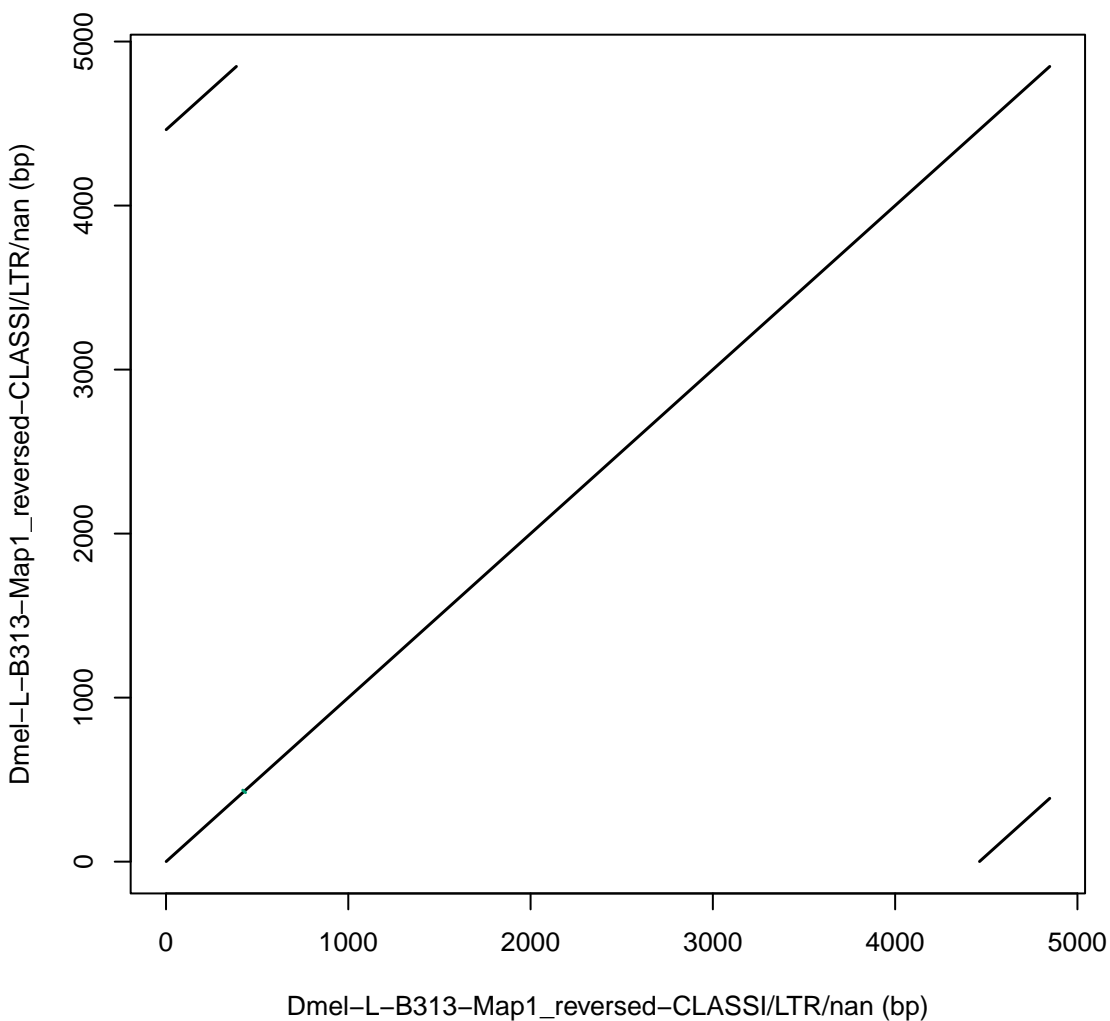**TE: Dmel−L−B313−Map1_reversed−CLASSI/LTR/nan**
consensus size: 4848bp; fragments: 439; full length: 1 (>=4363.2bp)

TE consensus genomic coverage

TE consensus self dotplot (blastn)

TE consensus structure and protein hits

ger−53_CCri_tp TIR/PIF−Harbinger
BEL−4_AA_pol LTR/Pao
BEL−2_DFi_pol LTR/Pao
BEL−616_AA_pol LTR/Pao
ATCopia6 LTR/Copia
BEL−6_DYa_pol LTR/Pao