TE: Dmel−B−G358−Map6−CLASSI/LTR/nan
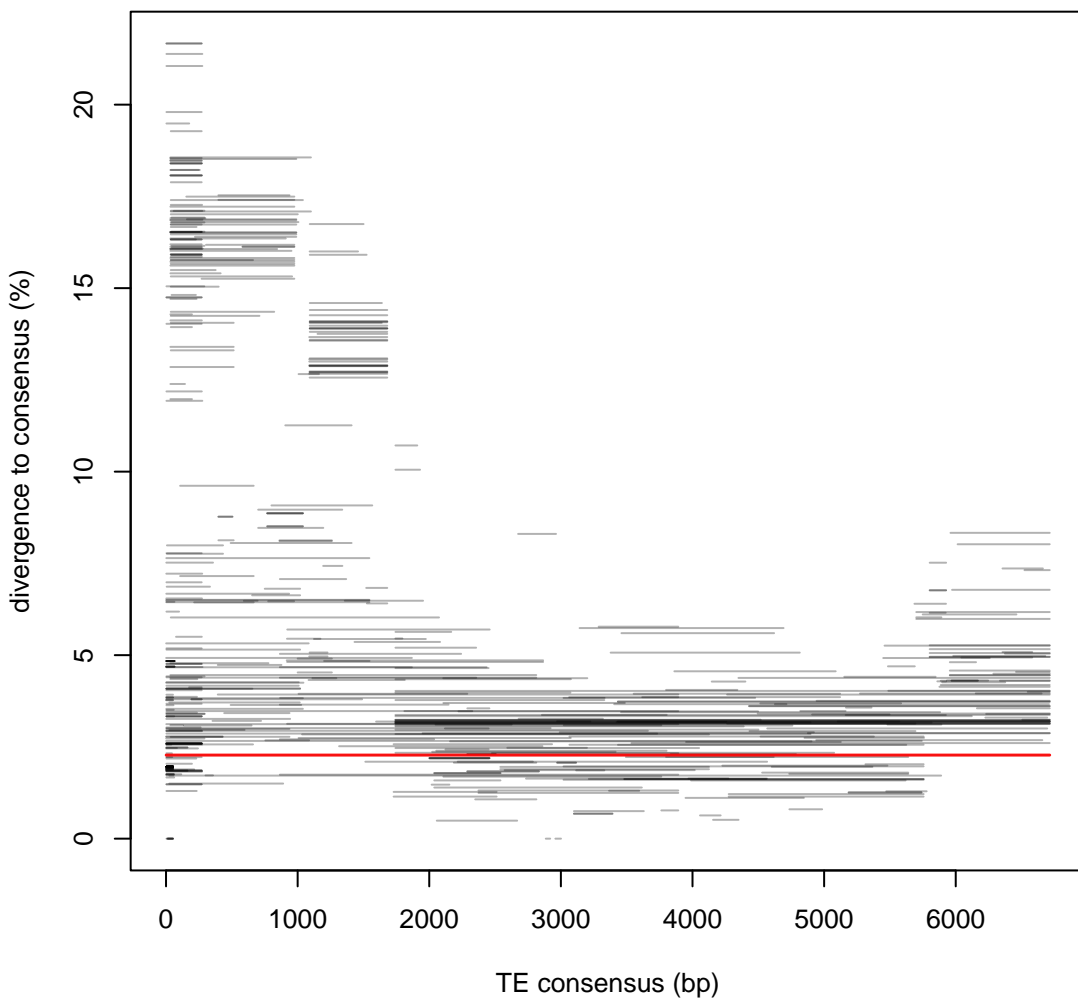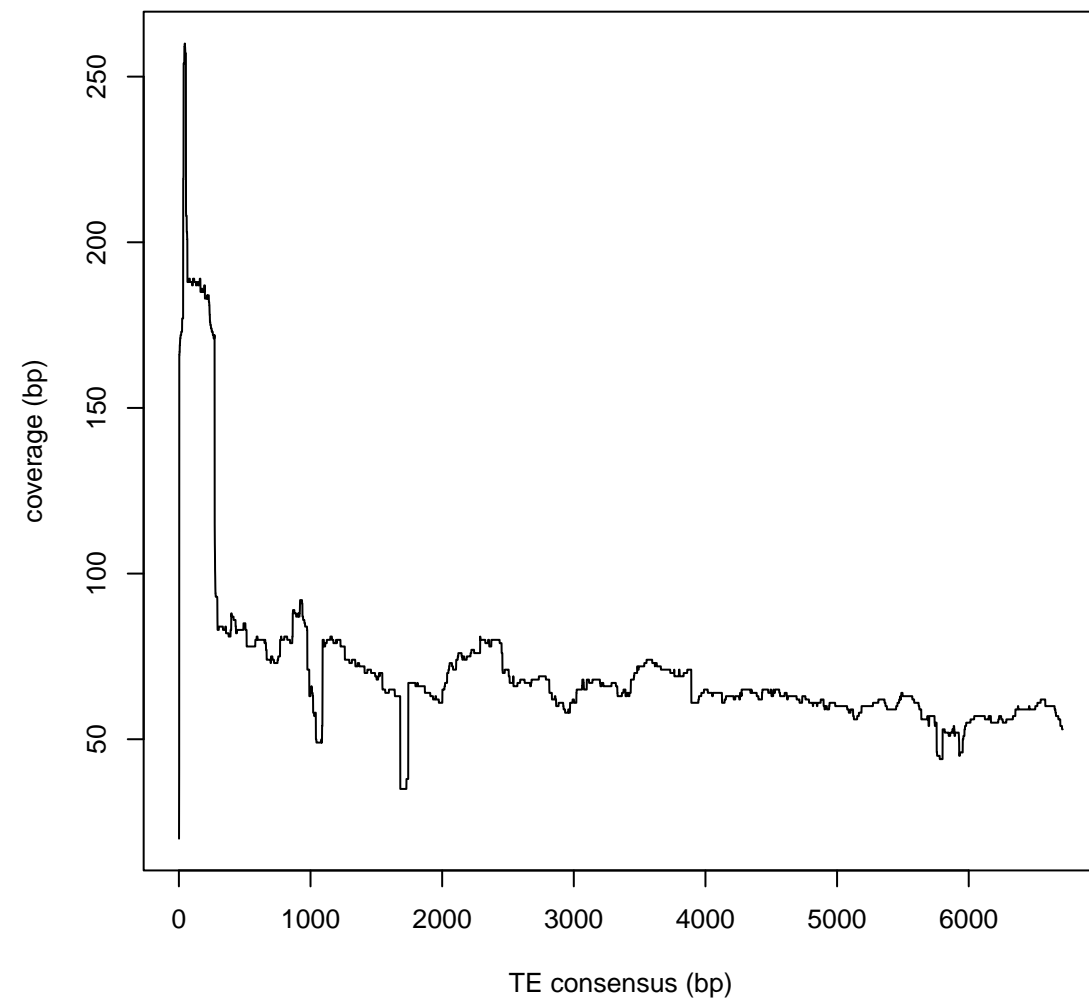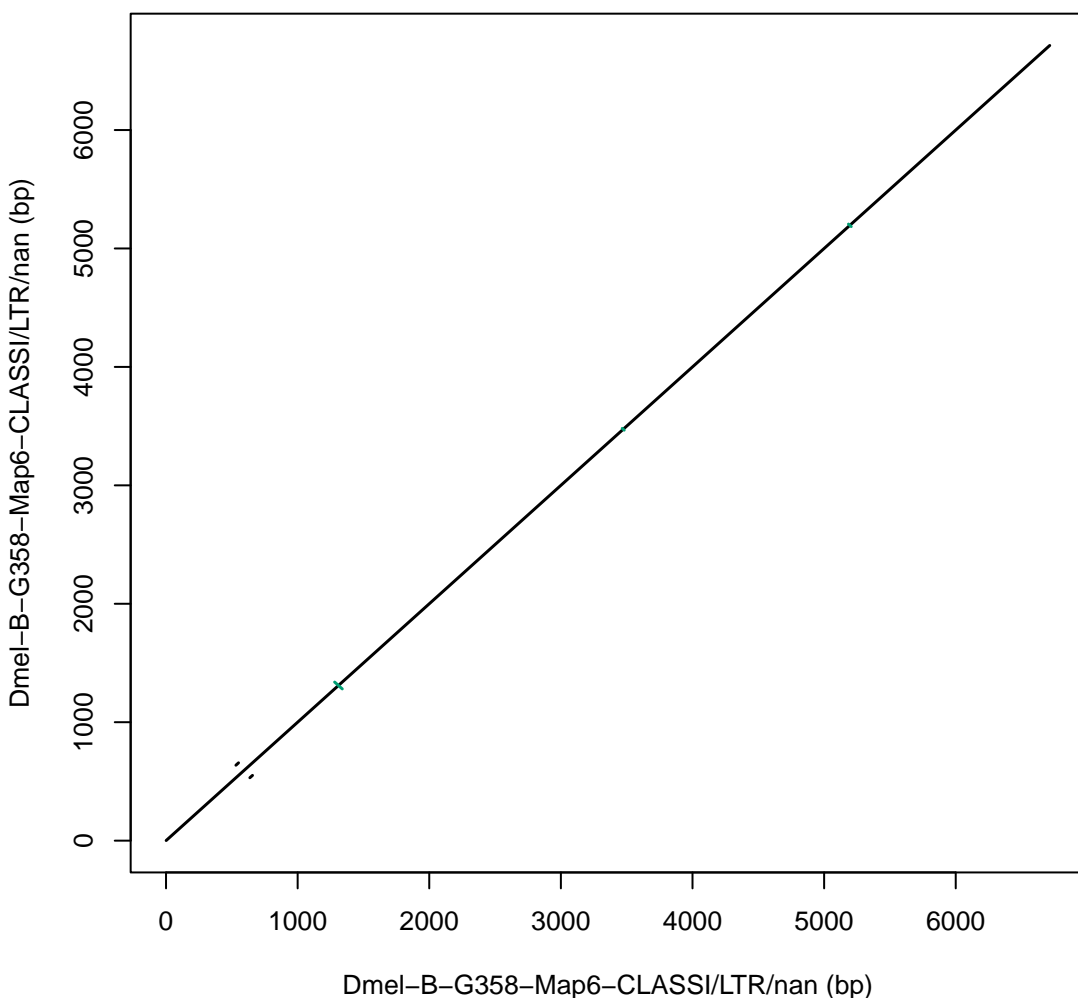consensus size: 6714bp; fragments: 572; full length: 1 (>=6042.6bp)

divergence to consensus (%)

TE consensus (bp)

TE consensus genomic coverage

coverage (bp)

TE consensus (bp)

TE consensus self dotplot (blastn)

Dmel−B−G358−Map6−CLASSI/LTR/nan (bp)

Dmel−B−G358−Map6−CLASSI/LTR/nan (bp)

TE consensus structure and protein hits

Mariner−8_HM_tp TIR/TcMar−Fot1

Copia−11_Mad LTR/Copia

BEL−10_DEl_pol LTR/Pao

BEL−15_AA_pol LTR/Pao

BEL−22_DTa_pol L

Dmel−B−G358−Map6−CLASSI/LTR/nan (bp)