TE: Dmel−B−R16−Map20−CLASSI/LTR/nan
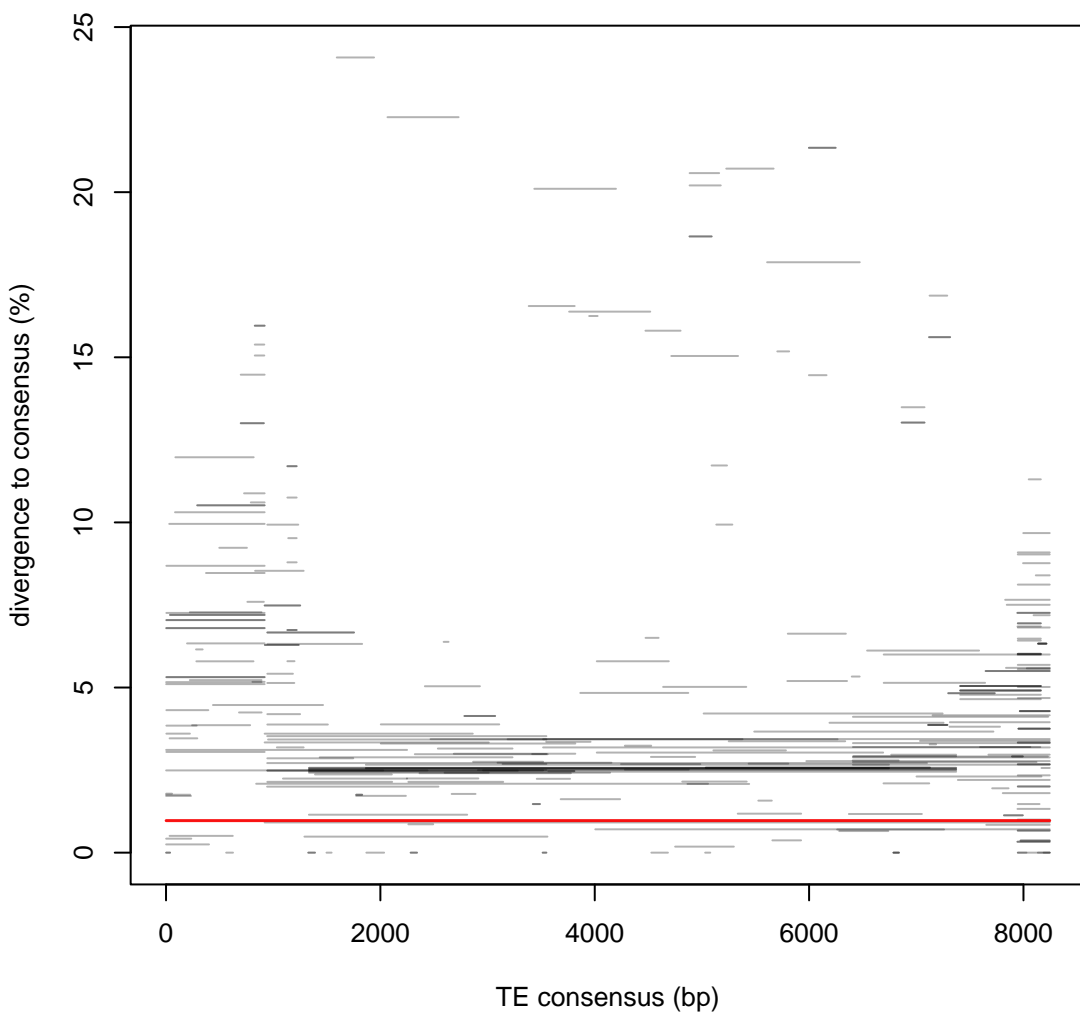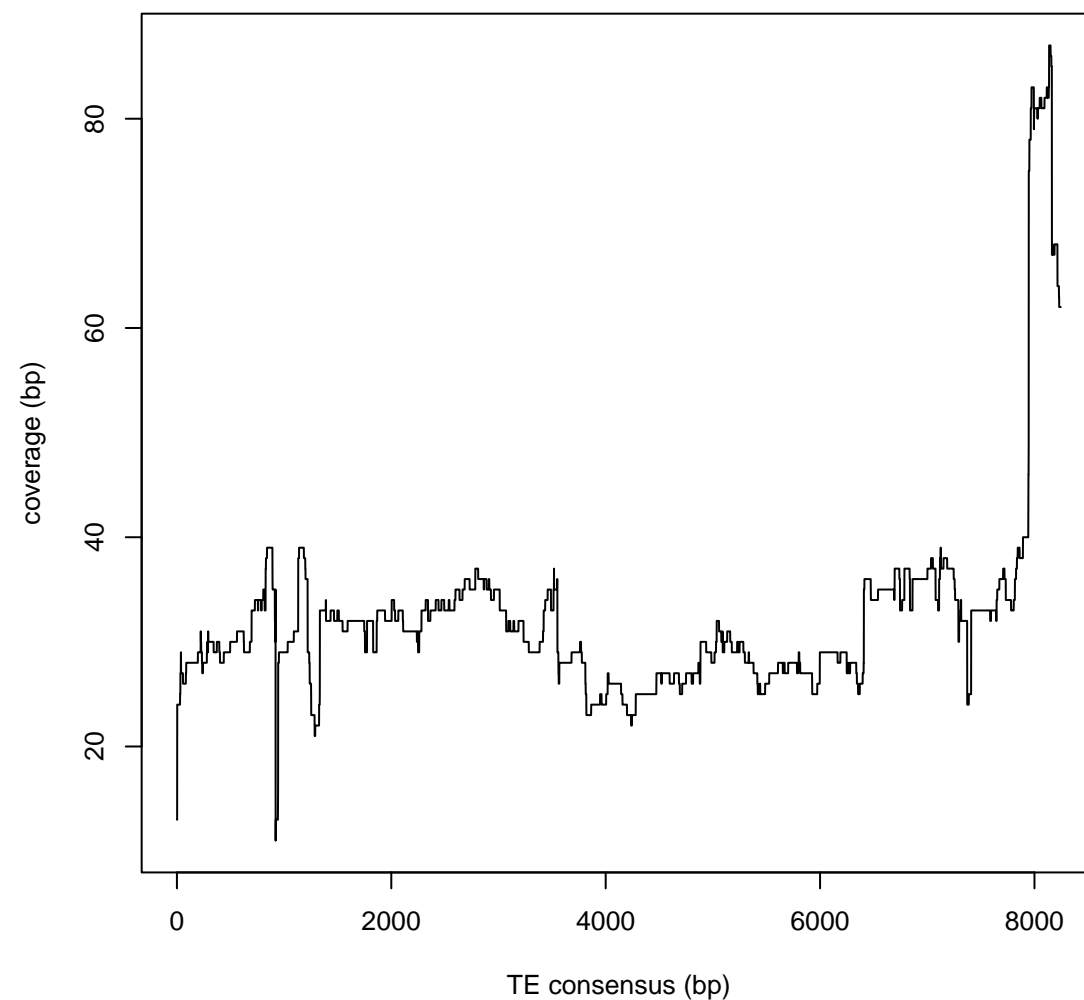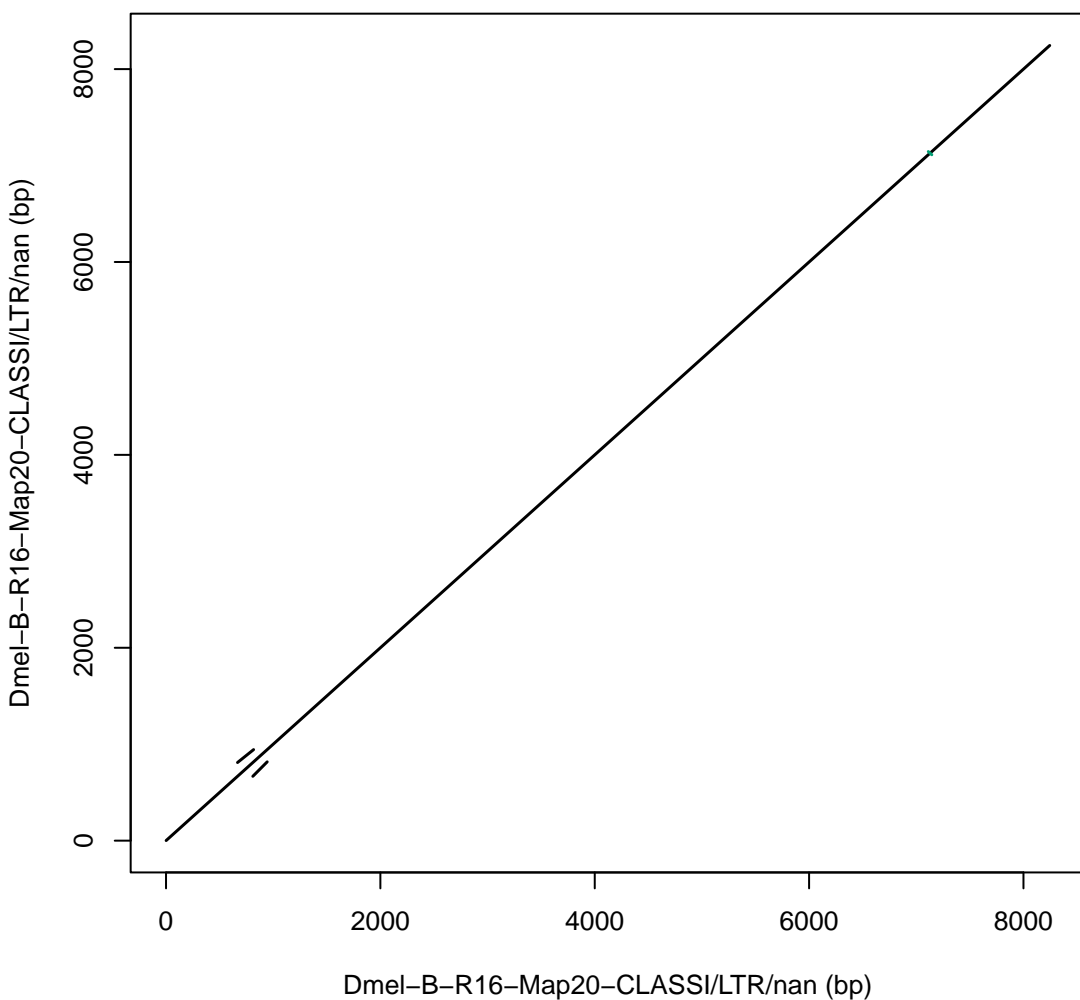consensus size: 8245bp; fragments: 314; full length: 1 (>=7420.5bp)

TE consensus genomic coverage

divergence to consensus (%)

TE consensus (bp)

coverage (bp)

TE consensus (bp)

TE consensus self dotplot (blastn)

Dmel−B−R16−Map20−CLASSI/LTR/nan (bp)

Dmel−B−R16−Map20−CLASSI/LTR/nan (bp)

TE consensus structure and protein hits

_GR_1p LTR/Gypsy

BEL−73_AA_pol LTR/Pao

BEL−224_AA_pol LTR/Pao

L1−6_Mad_pol LINE/L1

MAX_pol LTR/Pao

Copia−7_Pru LTR/Cop

Gypsy−55F_CCri_3p LTR/

BEL−10_DAn_pol LTR/P

Dmel−B−R16−Map20−CLASSI/LTR/nan (bp)