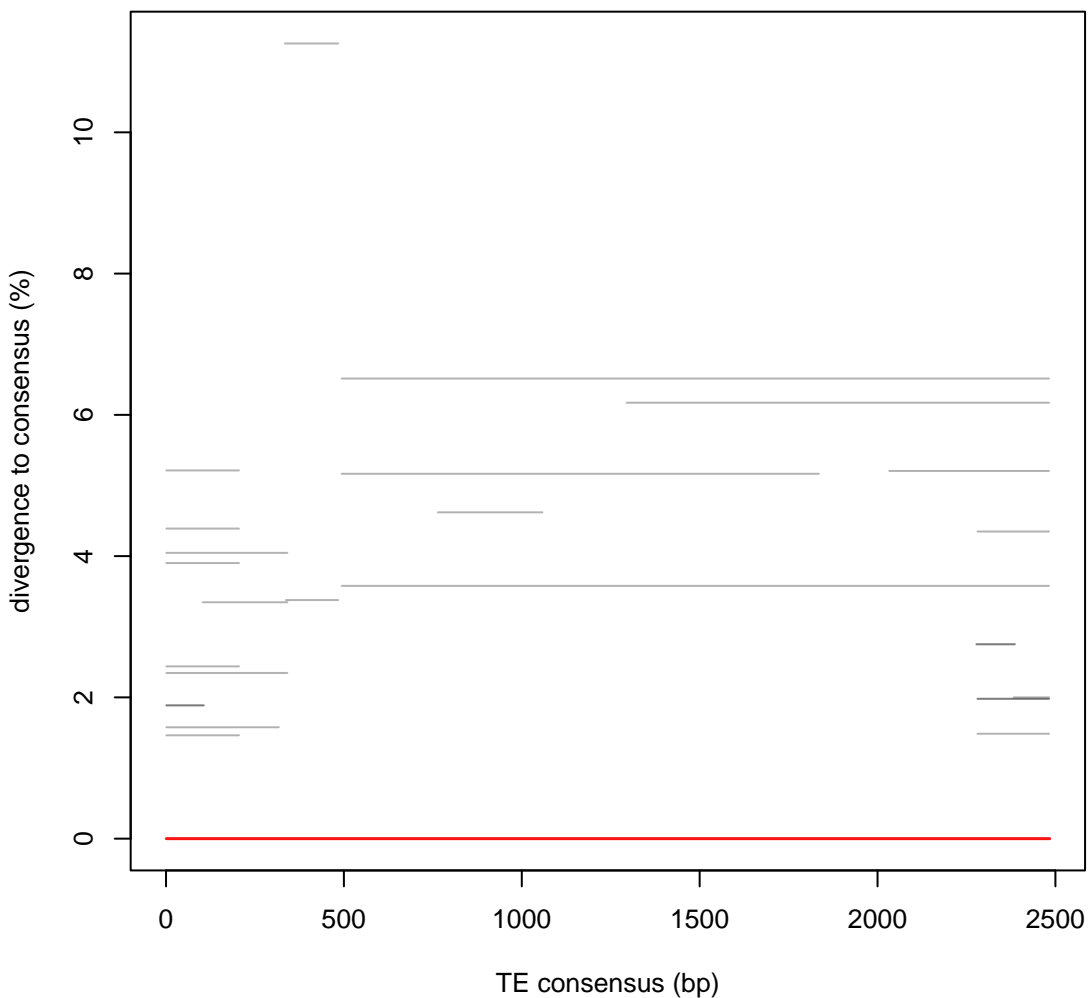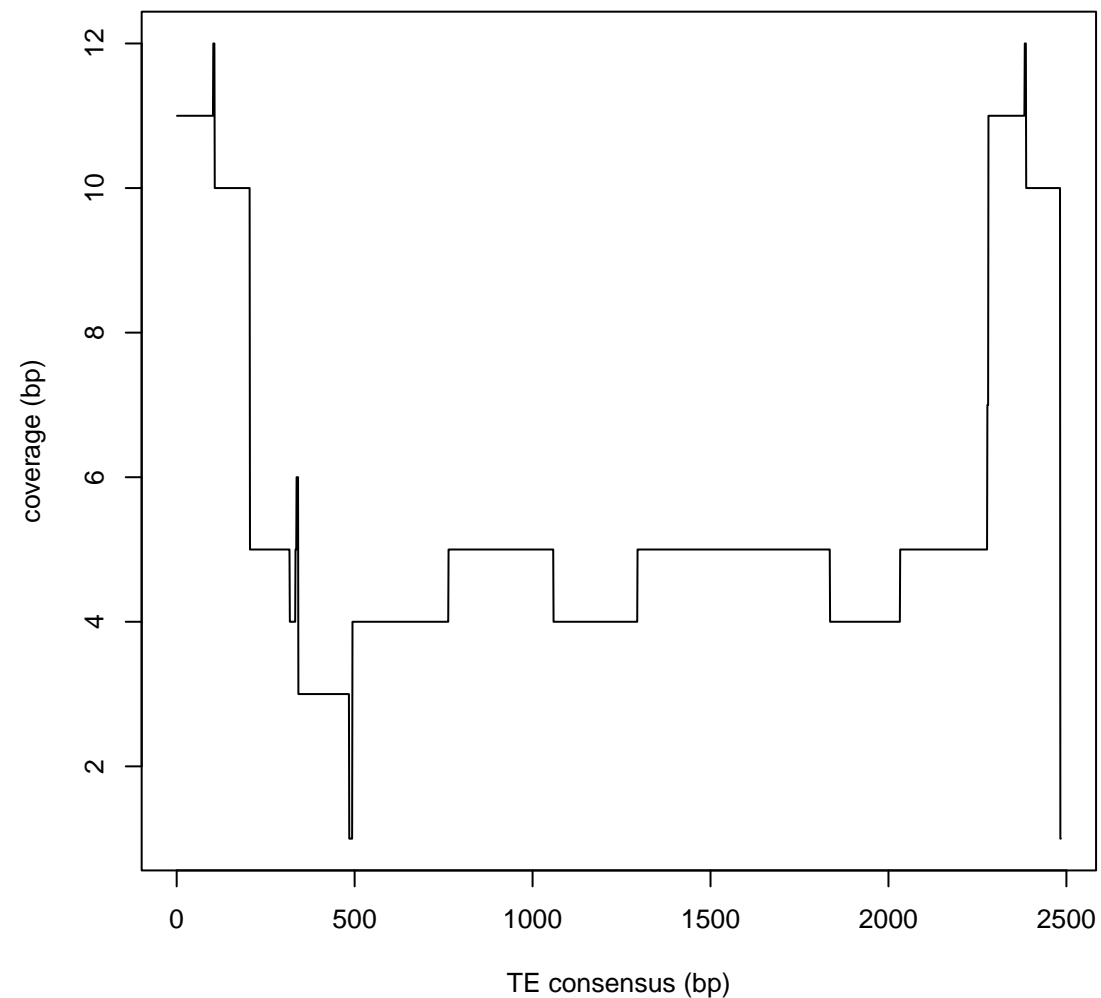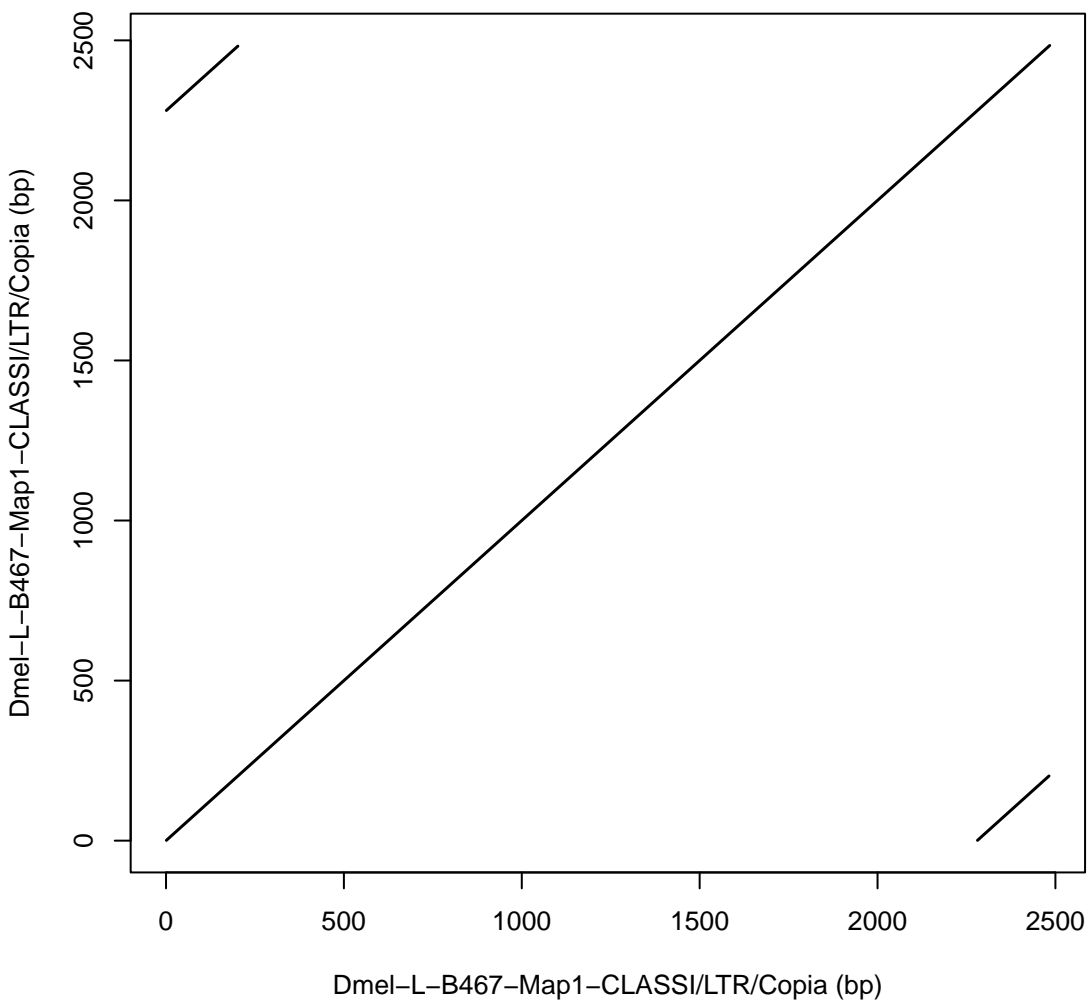# TE: Dmel−L−B467−Map1−CLASSI/LTR/Copia
consensus size: 2484bp; fragments: 27; full length: 1 (>=2235.6bp)

TE consensus (bp)

divergence to consensus (%)

TE consensus genomic coverage

coverage (bp)

TE consensus (bp)

TE consensus self dotplot (blastn)

Dmel−L−B467−Map1−CLASSI/LTR/Copia (bp)

Dmel−L−B467−Map1−CLASSI/LTR/Copia (bp)

TE consensus structure and protein hits

Copia1_DM LTR/Copia

Dmel−L−B467−Map1−CLASSI/LTR/Copia (bp)