TE: Dmel−L−B502−Map1−CLASSI/LTR/TRIM
consensus size: 4452bp; fragments: 921; full length: 1 (>=4006.8bp)

divergence to consensus (%)
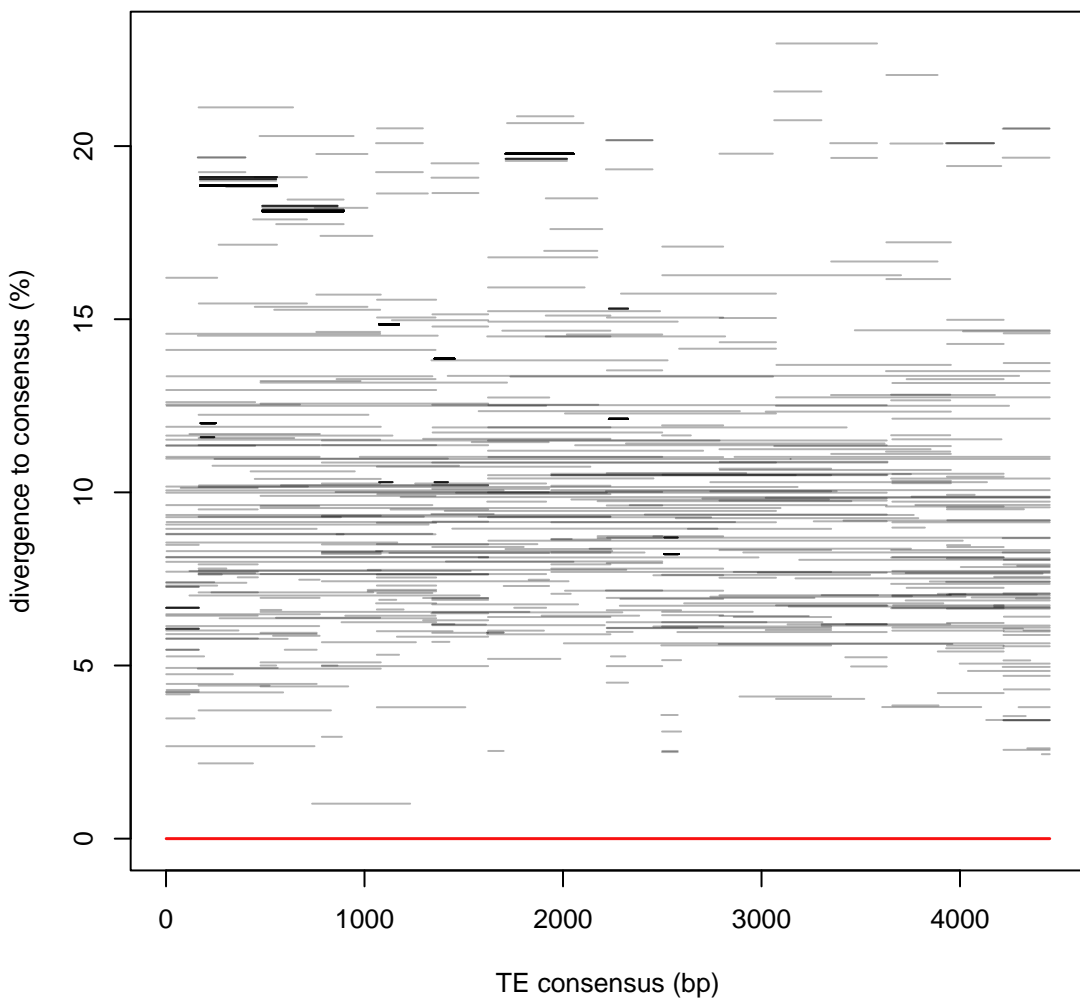
TE consensus (bp)

TE consensus genomic coverage

coverage (bp)
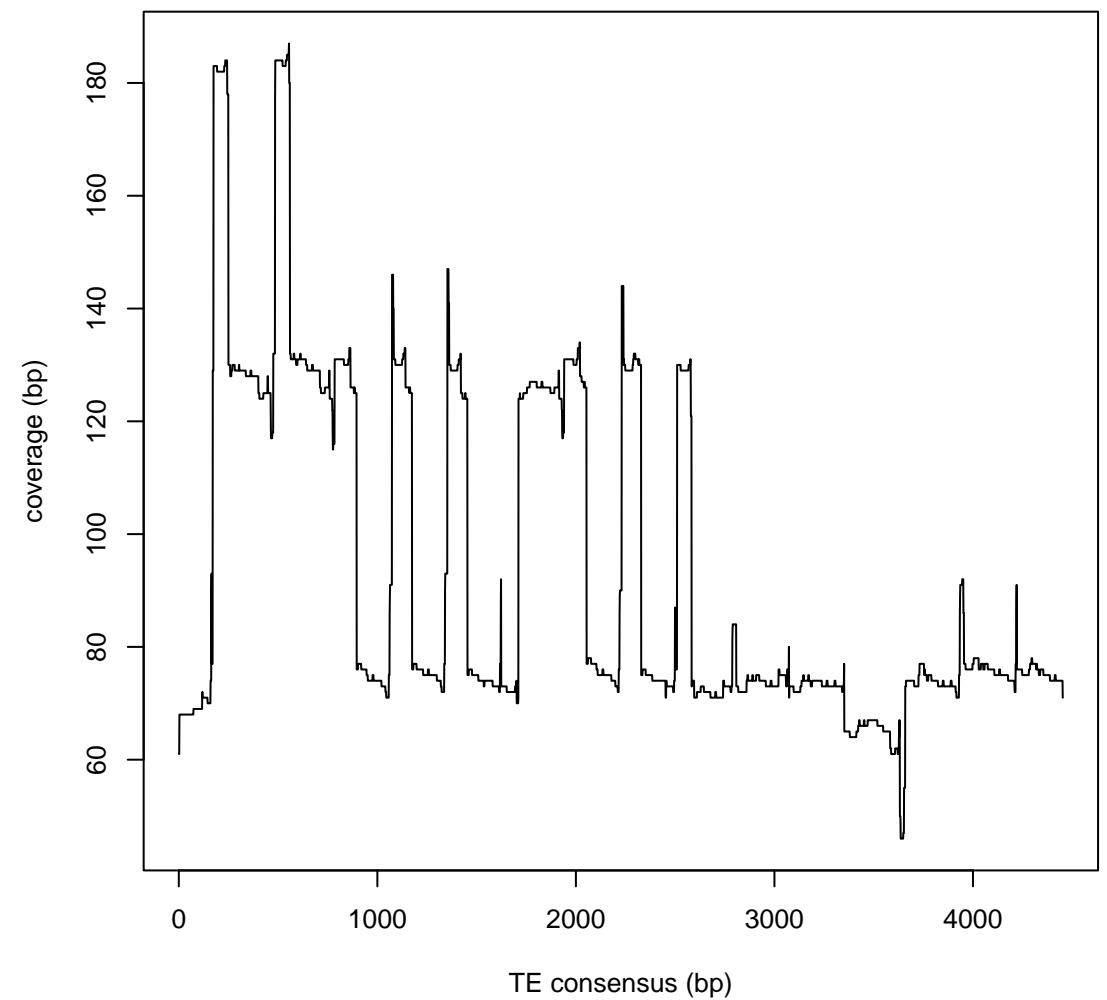
TE consensus (bp)

TE consensus self dotplot (blastn)

Dmel−L−B502−Map1−CLASSI/LTR/TRIM (bp)

Dmel−L−B502−Map1−CLASSI/LTR/TRIM (bp)
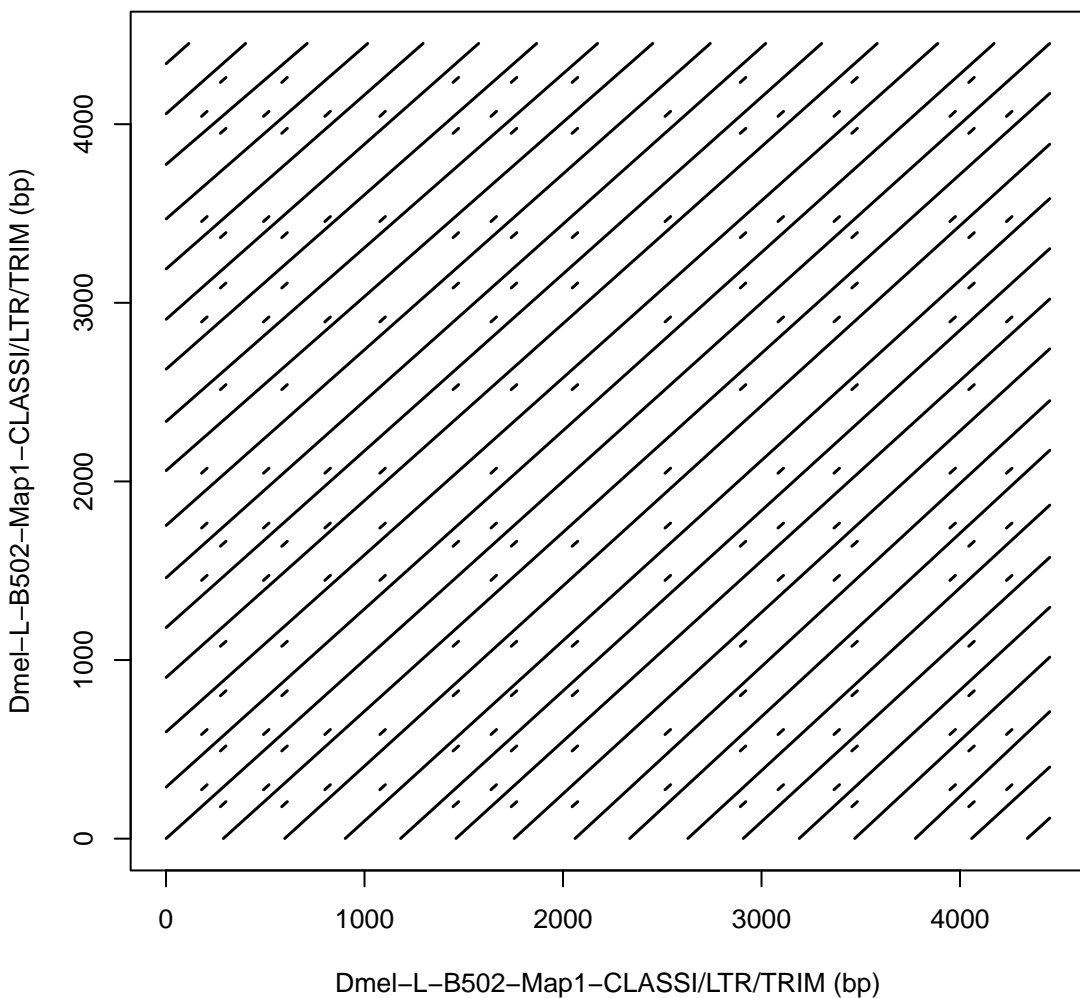
TE consensus structure and protein hits

no orf >400 bp detected

Dmel−L−B502−Map1−CLASSI/LTR/TRIM (bp)