**TE: Dmel−L−B422−Map1−LTR**
**consensus size: 3627bp; fragments: 178; full length: 7 (>=3264.3bp)**

divergence to consensus (%)
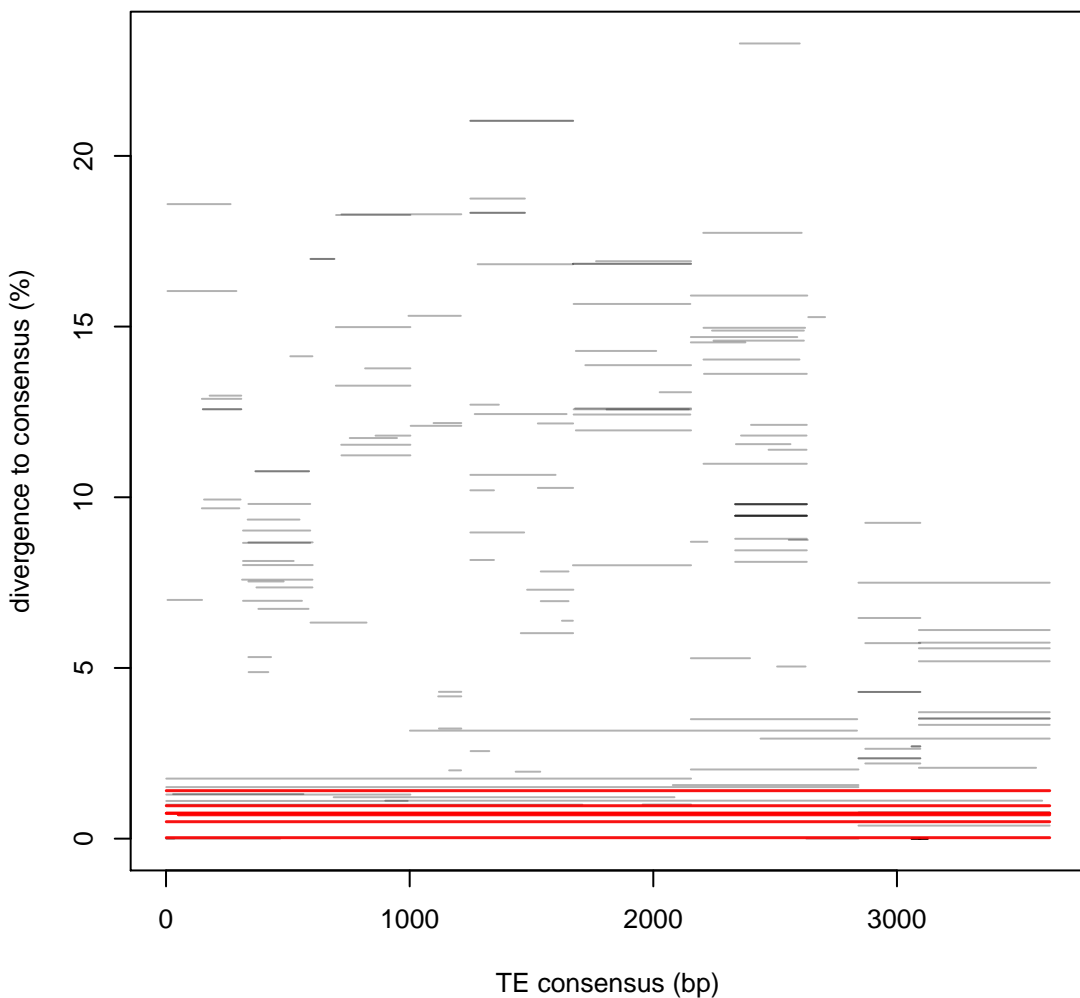
TE consensus (bp)

**TE consensus genomic coverage**

coverage (bp)
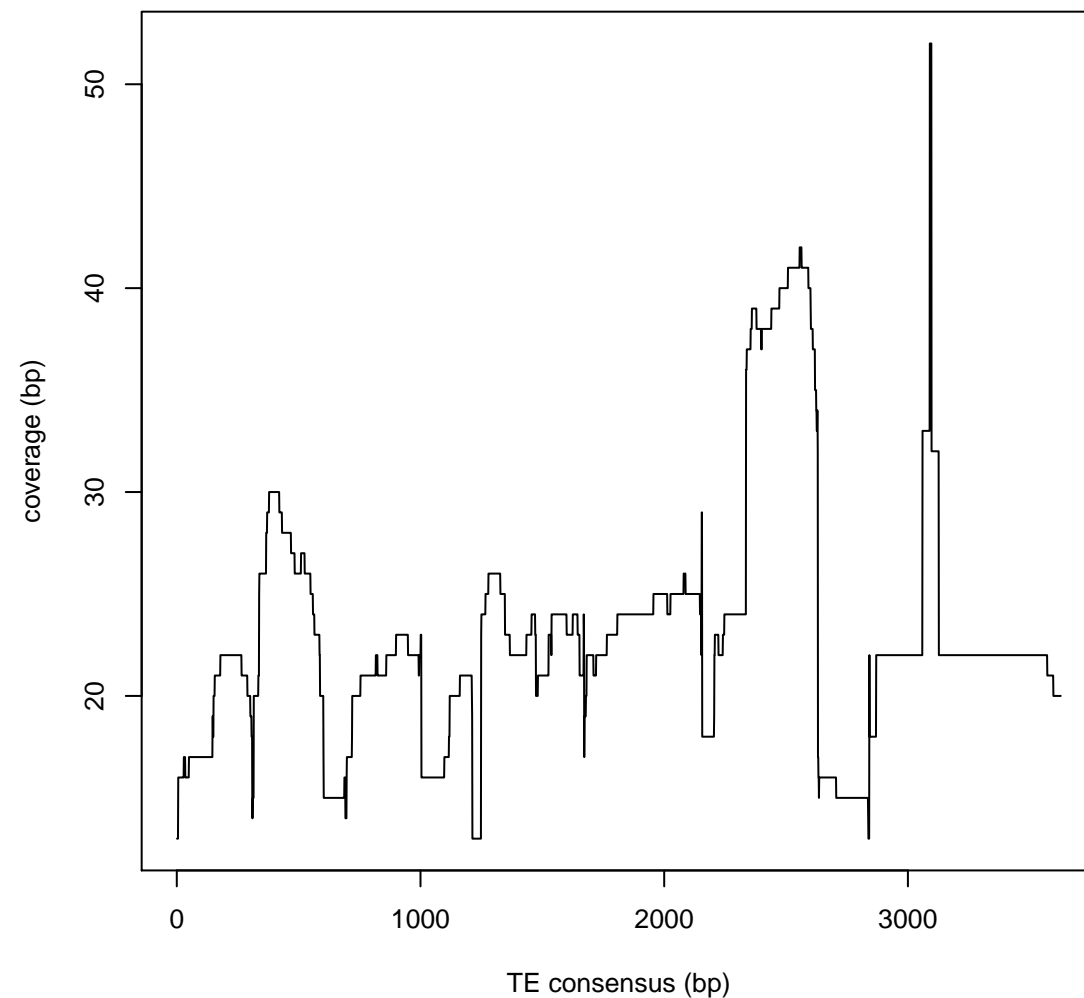
TE consensus (bp)

**TE consensus self dotplot (blastn)**

Dmel−L−B422−Map1−LTR (bp)

Dmel−L−B422−Map1−LTR (bp)
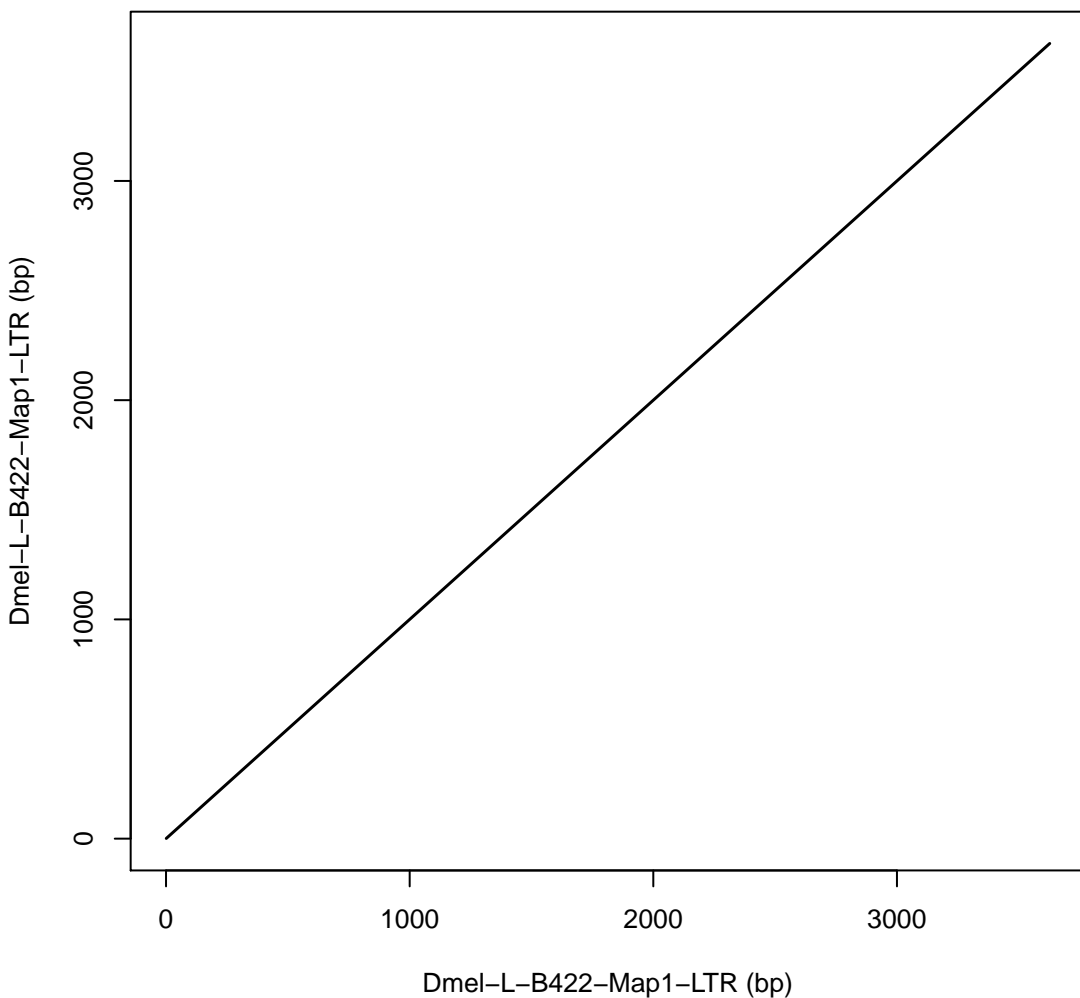
**TE consensus structure and protein hits**

BEL−75_AA_pol LTR/Pao

Copia−101_BRa LTR/Cop

Dmel−L−B422−Map1−LTR (bp)