**TE: Dmel−B−G1691−Map8−CLASSI/LTR/Gypsy**
**consensus size: 1379bp; fragments: 115; full length: 1 (>=1241.1bp)**

divergence to consensus (%)
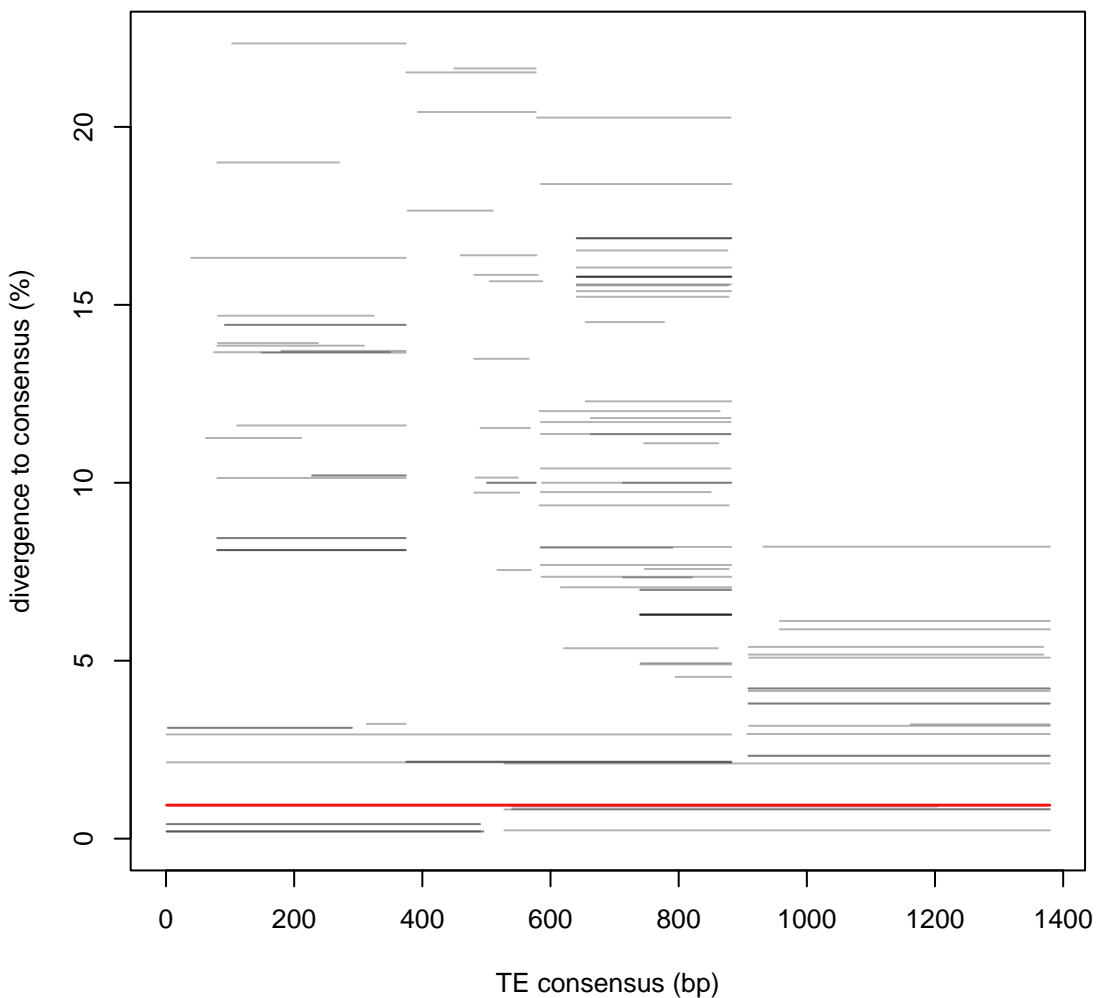
TE consensus (bp)

**TE consensus genomic coverage**

coverage (bp)
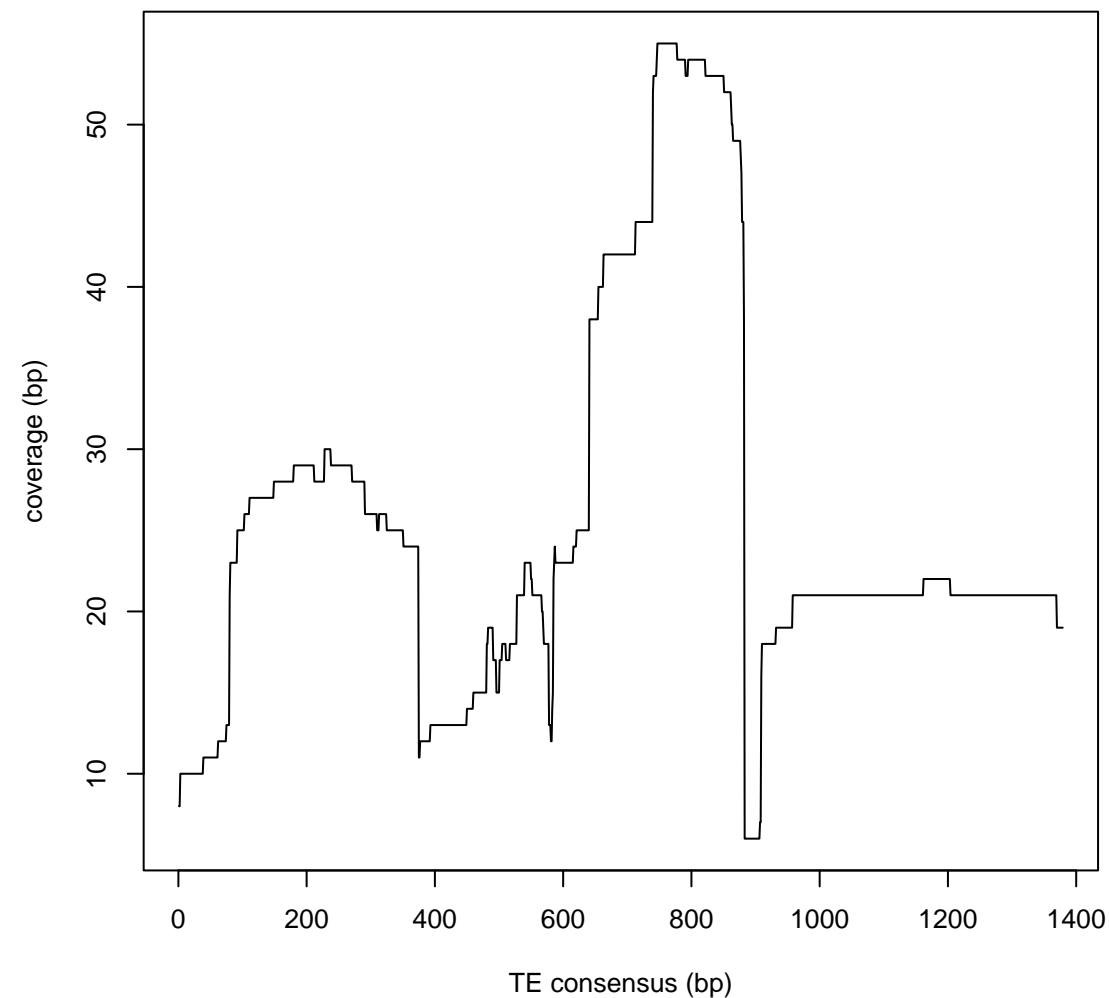
TE consensus (bp)

**TE consensus self dotplot (blastn)**

Dmel−B−G1691−Map8−CLASSI/LTR/Gypsy (bp)

Dmel−B−G1691−Map8−CLASSI/LTR/Gypsy (bp)
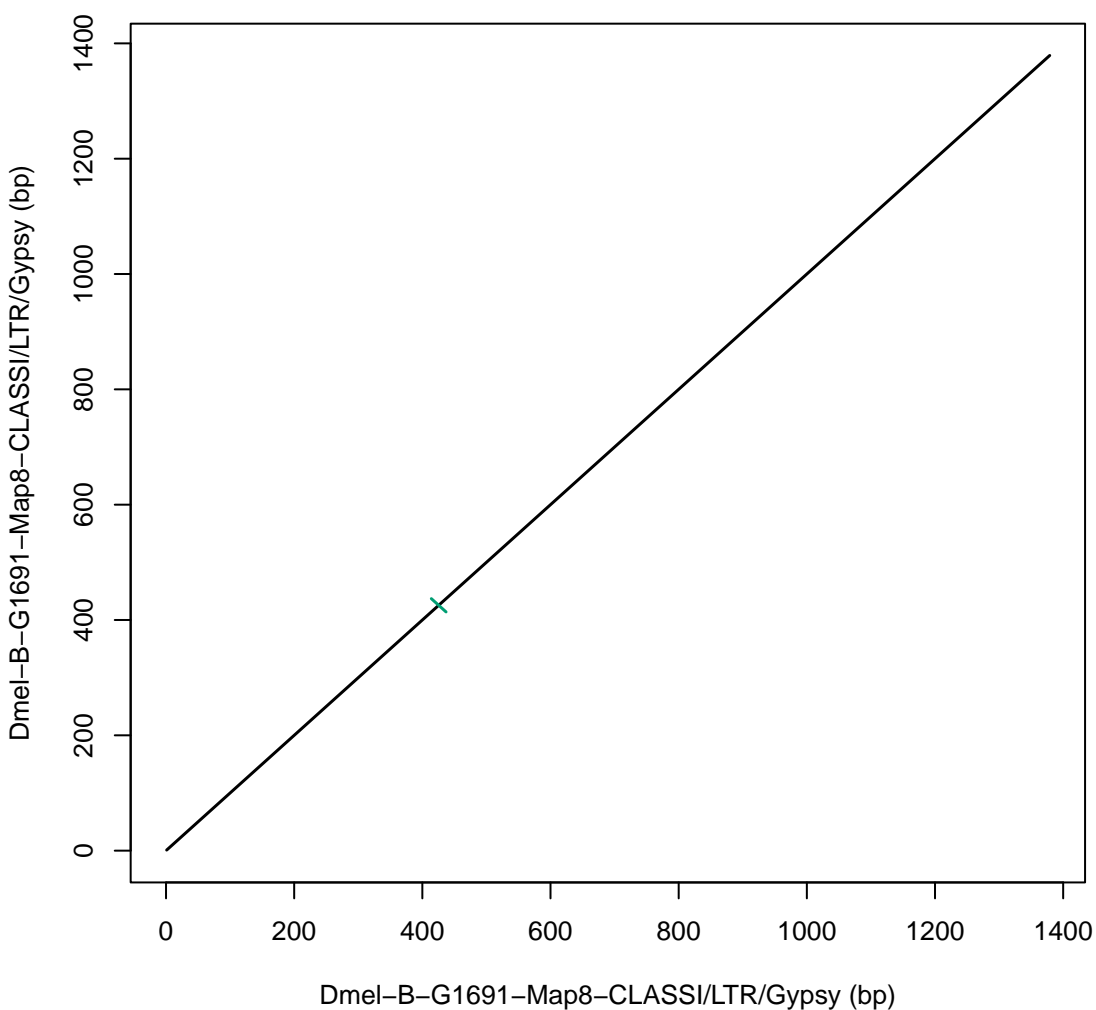
**TE consensus structure and protein hits**

no orf >400 bp detected

Dmel−B−G1691−Map8−CLASSI/LTR/Gypsy (bp)