TE: Dmel−L−B232−Map1_reversed−LTR/Gypsy
consensus size: 5353bp; fragments: 209; full length: 0 (>=4817.7bp)

divergence to consensus (%)
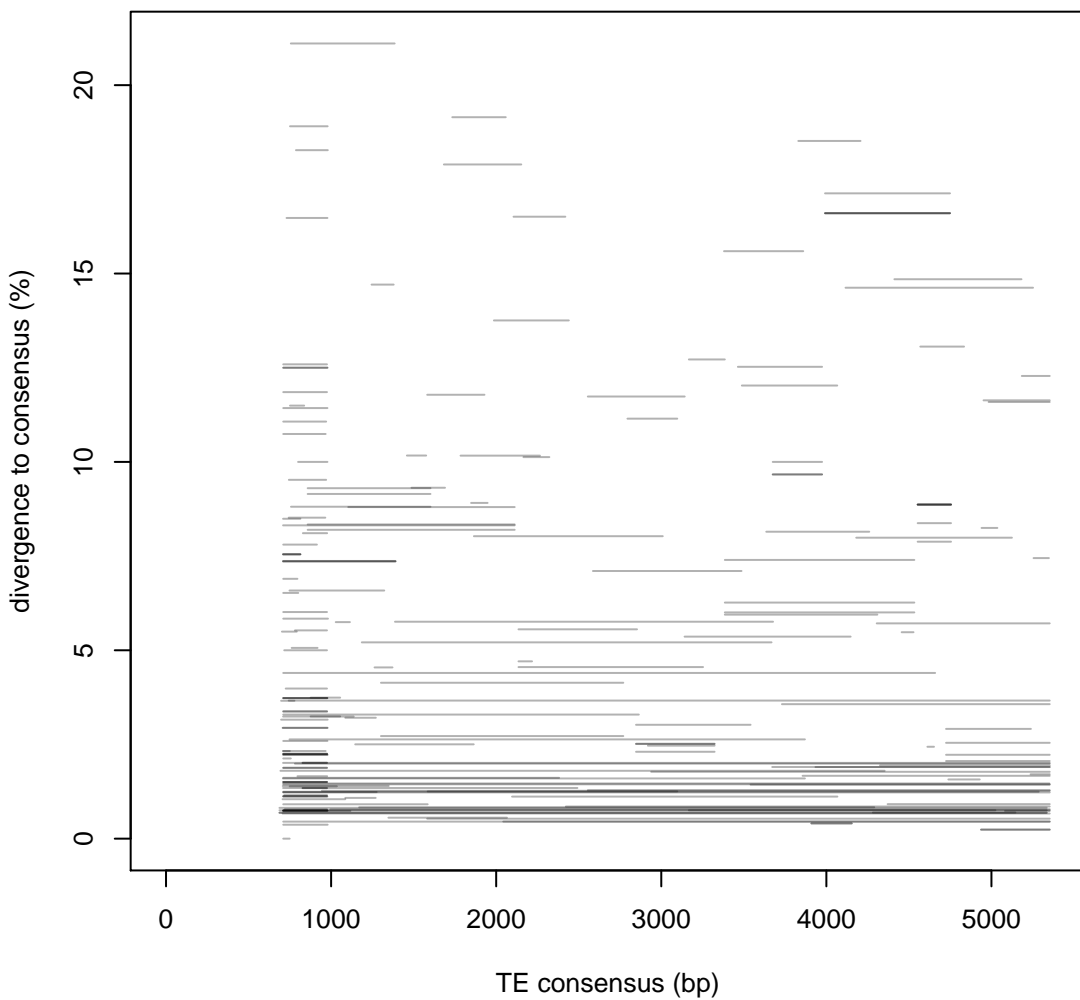
TE consensus (bp)

TE consensus genomic coverage

coverage (bp)
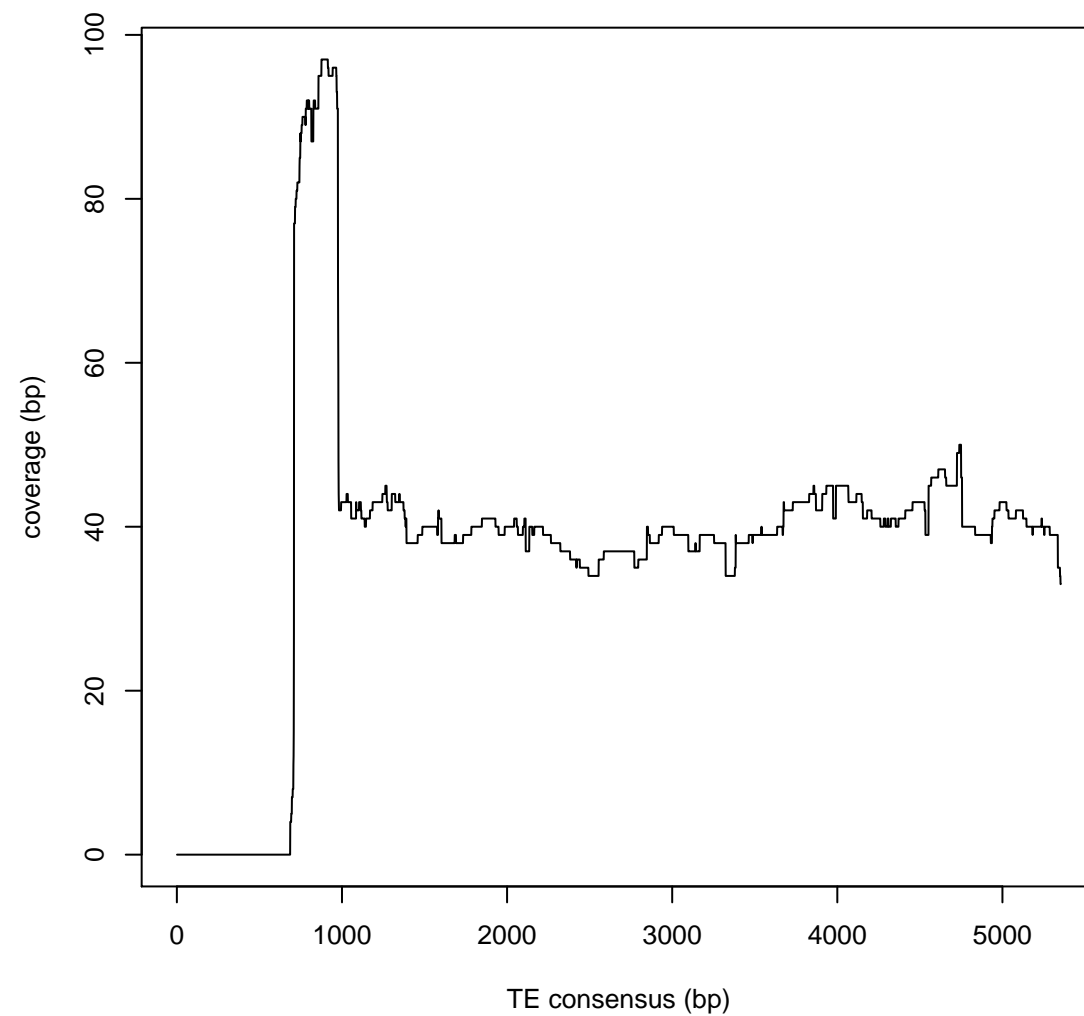
TE consensus (bp)

TE consensus self dotplot (blastn)

Dmel−L−B232−Map1_reversed−LTR/Gypsy (bp)

Dmel−L−B232−Map1_reversed−LTR/Gypsy (bp)
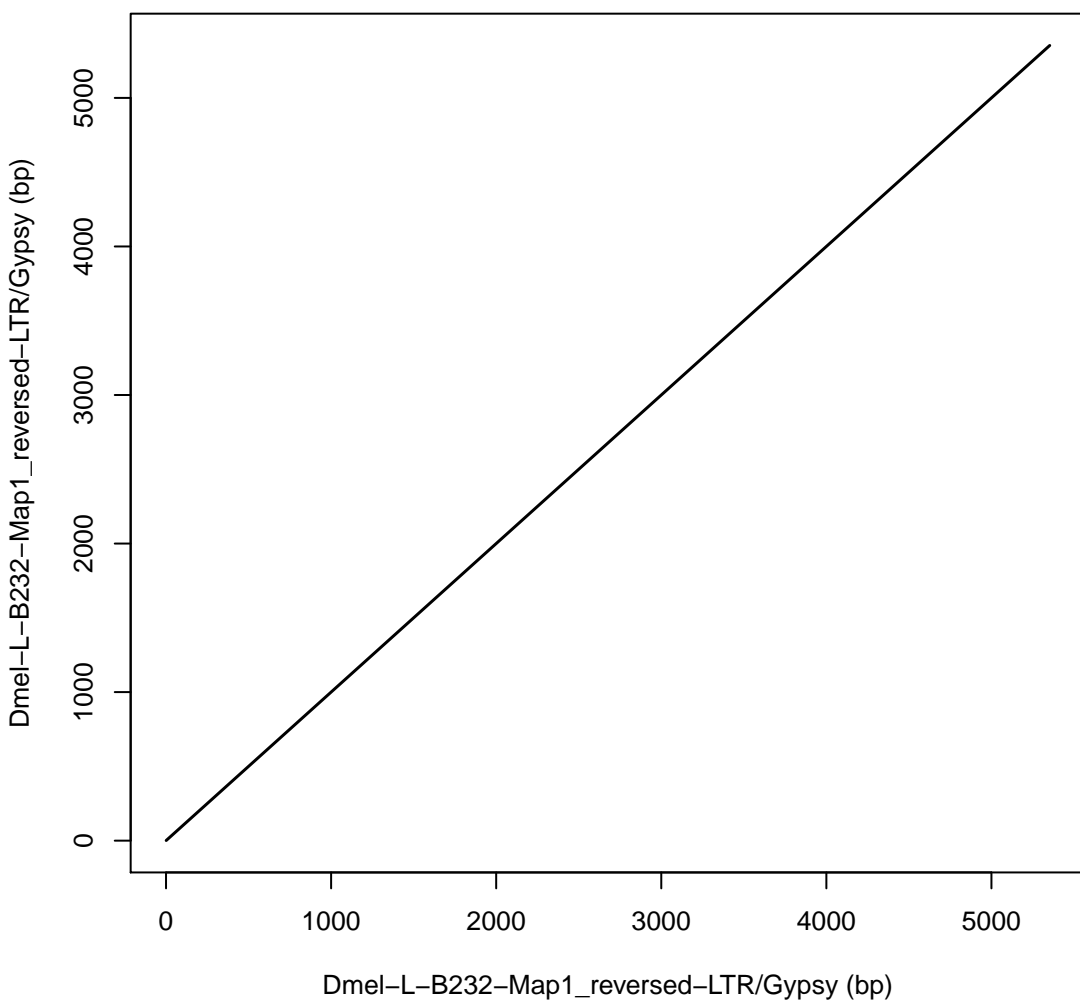
TE consensus structure and protein hits

Academ−6_CCri_tp TIR/Academ−1

Gypsy2_Dpse LTR/Gypsy

EnSpm2_PTr TIR/CMC−

Invader2 LTR/Gypsy

Dmel−L−B232−Map1_reversed−LTR/Gypsy (bp)