TE: Dmel−B−G1226−Map3_reversed−LTR/GYPSY
consensus size: 5270bp; fragments: 924; full length: 2 (>=4743bp)

divergence to consensus (%)
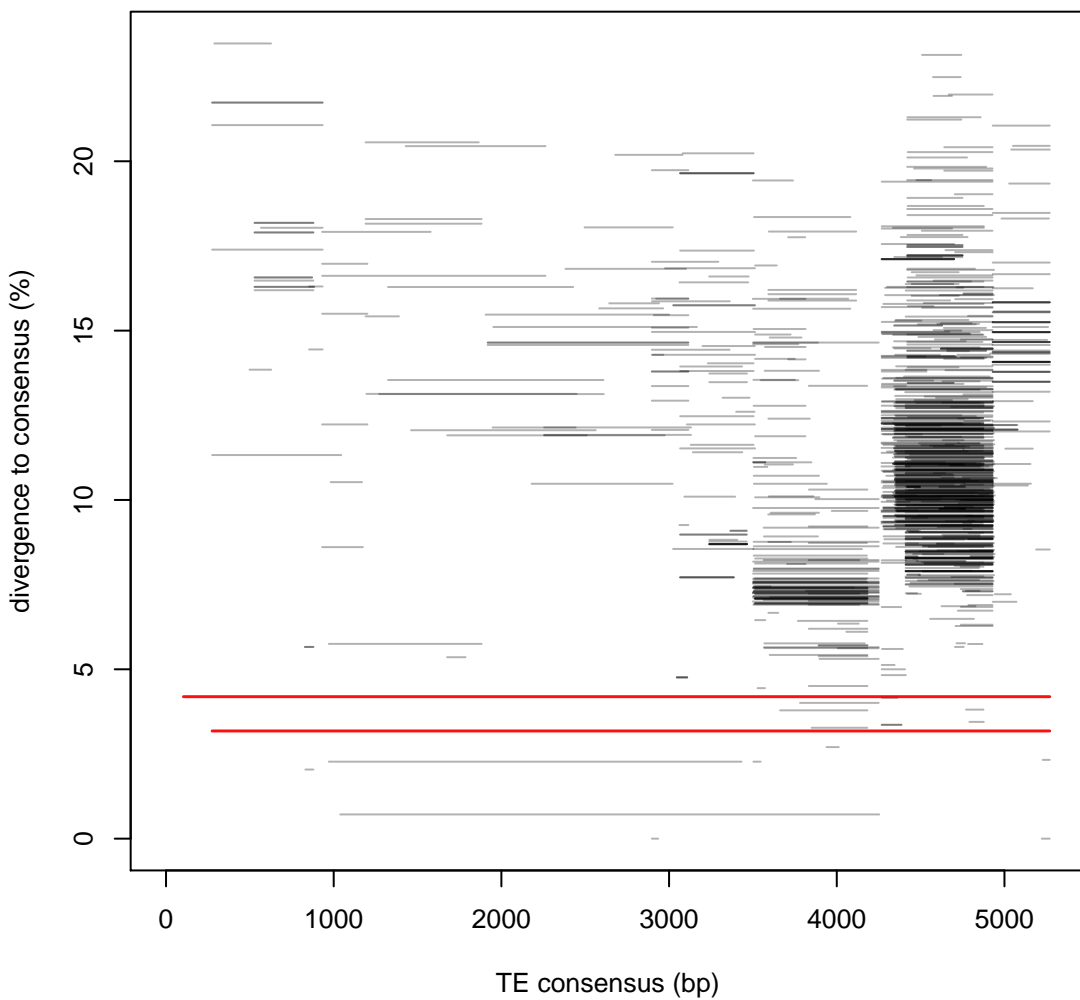
TE consensus (bp)

TE consensus genomic coverage

coverage (bp)
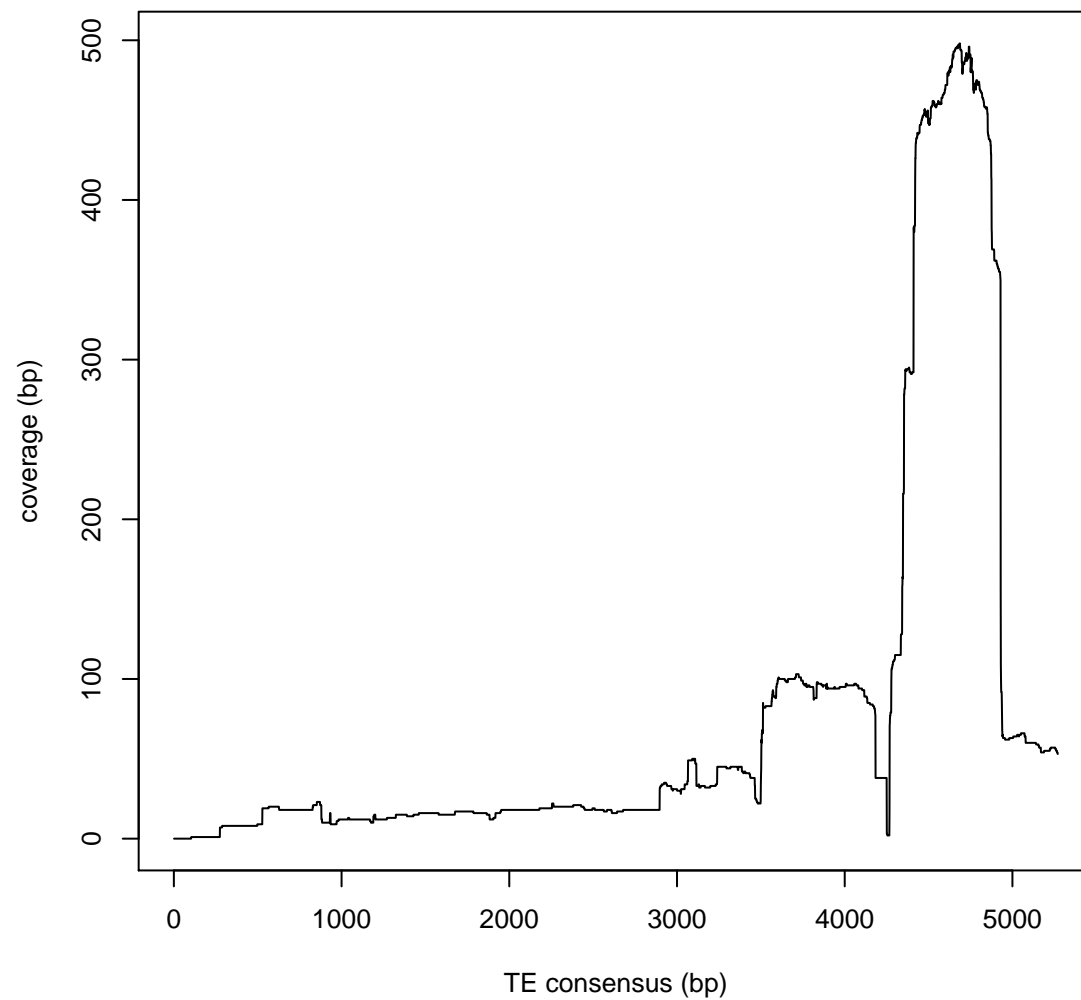
TE consensus (bp)

TE consensus self dotplot (blastn)

Dmel−B−G1226−Map3_reversed−LTR/GYPSY (bp)

Dmel−B−G1226−Map3_reversed−LTR/GYPSY (bp)
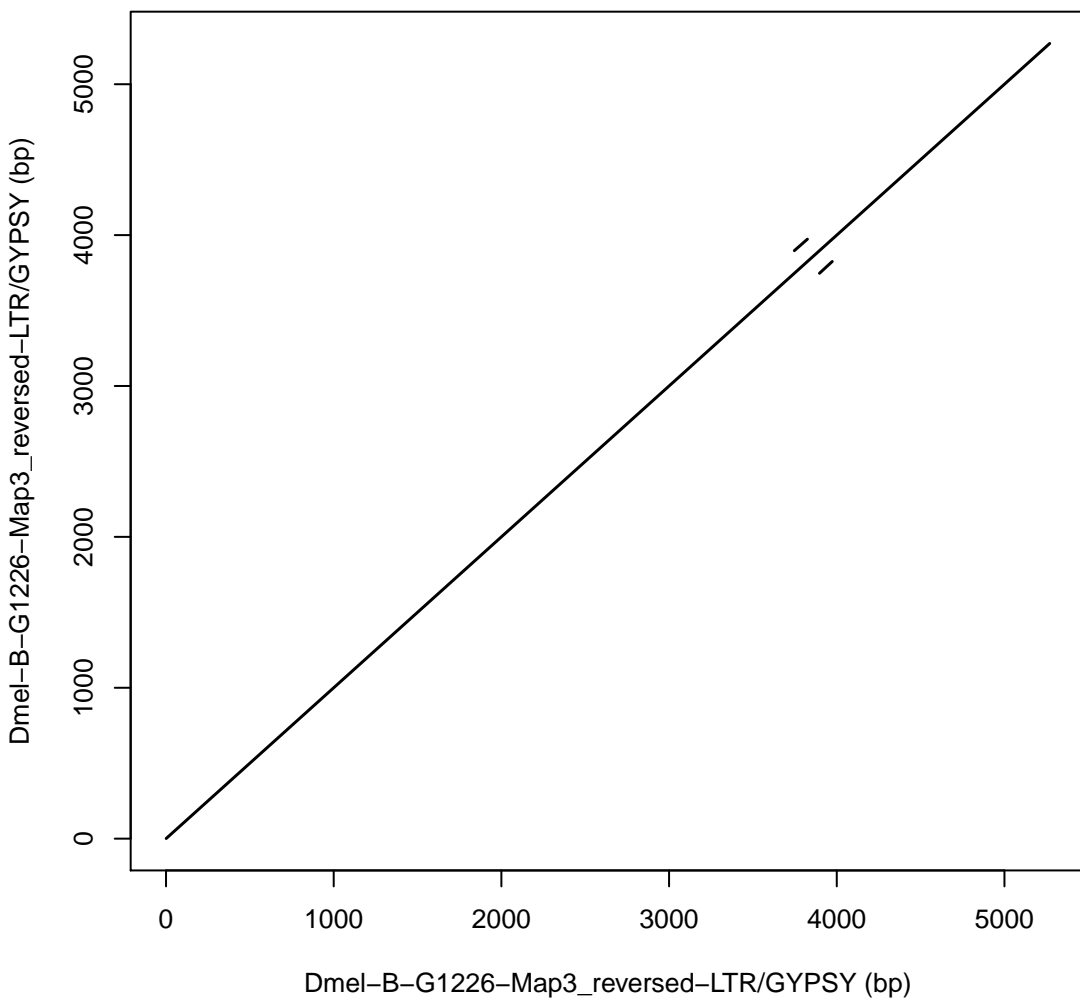
TE consensus structure and protein hits

Mariner−6_DRh_tp TIR/T

Dmel−B−G1226−Map3_reversed−LTR/GYPSY (bp)