TE: Dmel−B−R66−Map4_reversed−CLASSI/LTR/Gypsy
consensus size: 1478bp; fragments: 116; full length: 1 (>=1330.2bp)

divergence to consensus (%)
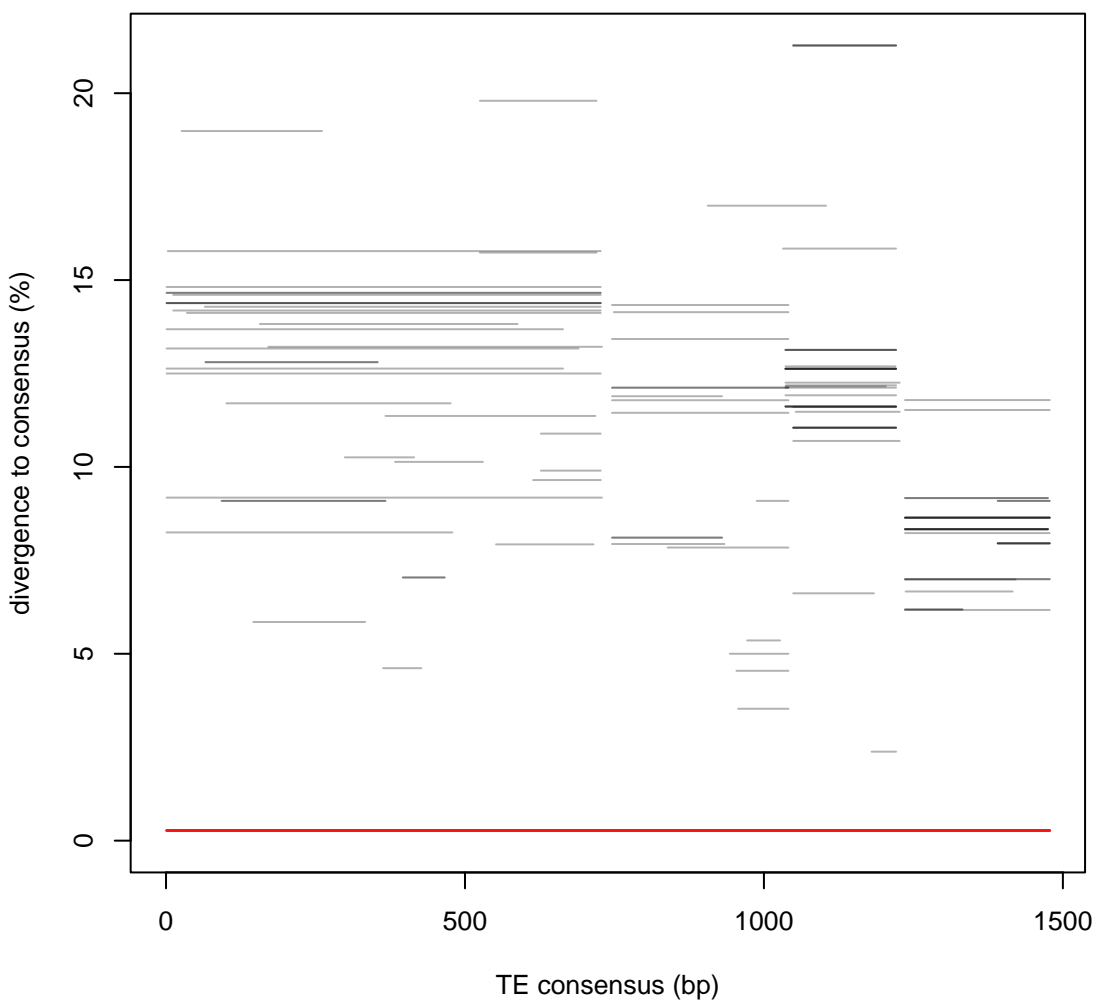
TE consensus (bp)

TE consensus genomic coverage

coverage (bp)
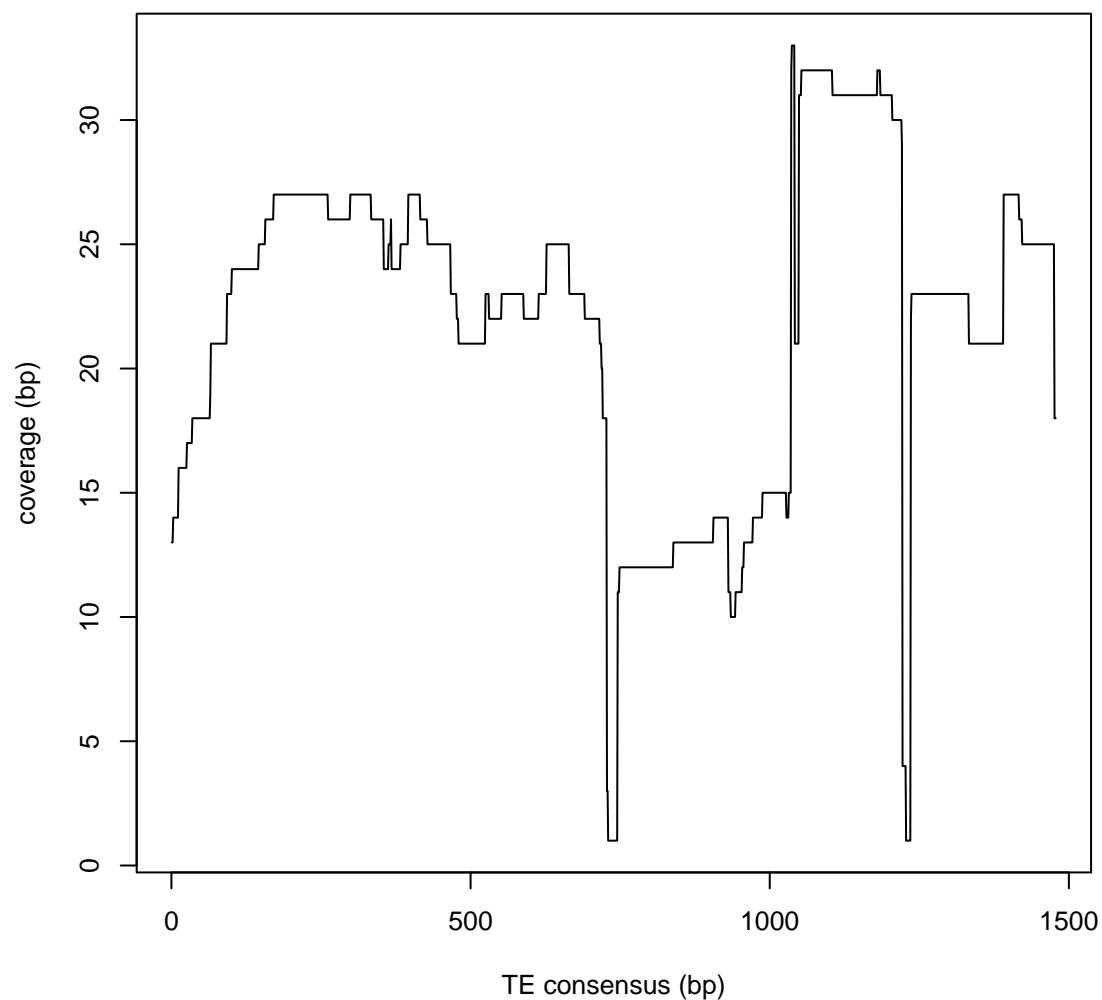
TE consensus (bp)

TE consensus self dotplot (blastn)

Dmel−B−R66−Map4_reversed−CLASSI/LTR/Gypsy (bp)

Dmel−B−R66−Map4_reversed−CLASSI/LTR/Gypsy (bp)
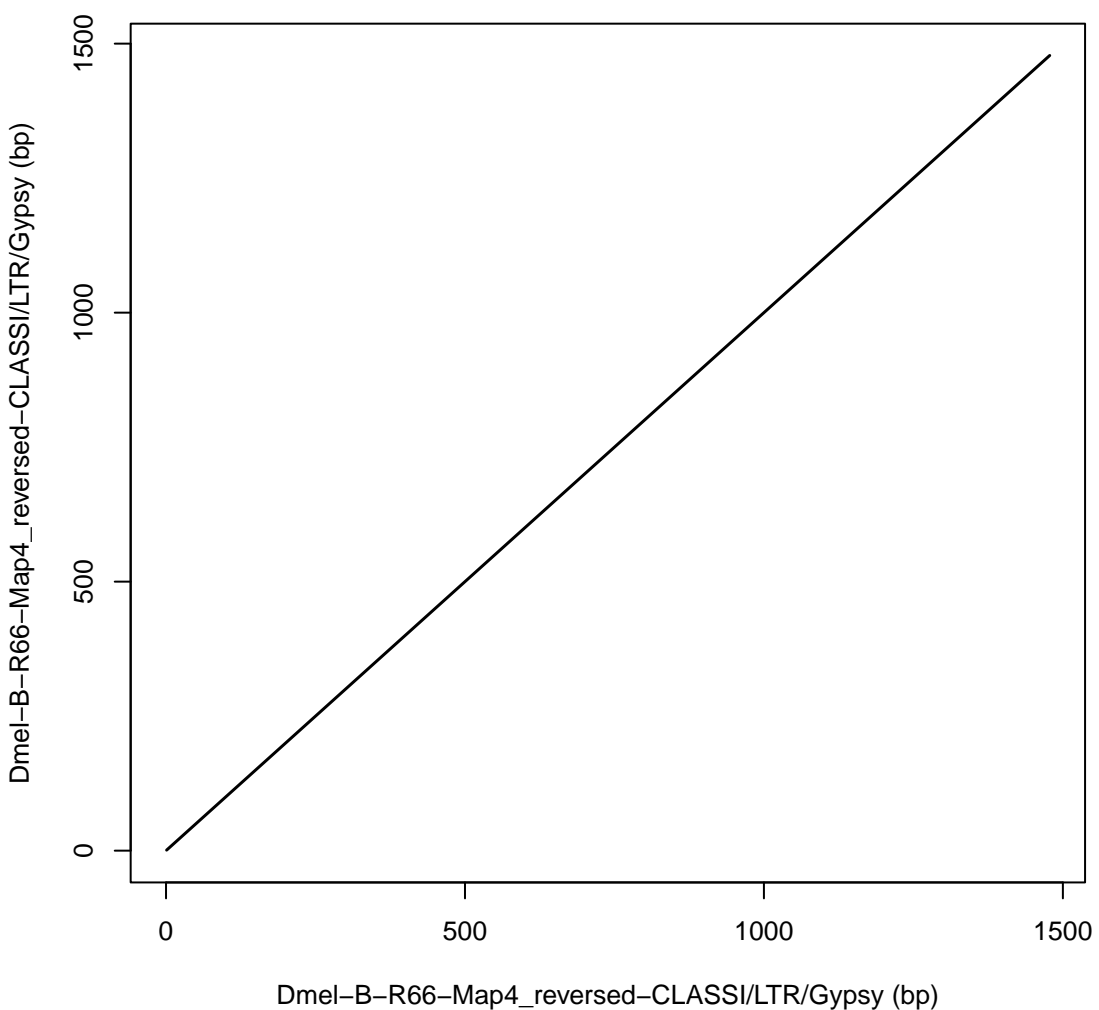
TE consensus structure and protein hits

Gypsy−29_DAn_gag LTR/Gypsy

Gypsy−14_DAn_pol LTR/Gypsy

Dmel−B−R66−Map4_reversed−CLASSI/LTR/Gypsy (bp)