TE: Dmel−L−B313−Map1_reversed−LTR/nan
consensus size: 4849bp; fragments: 283; full length: 1 (>=4364.1bp)

divergence to consensus (%)
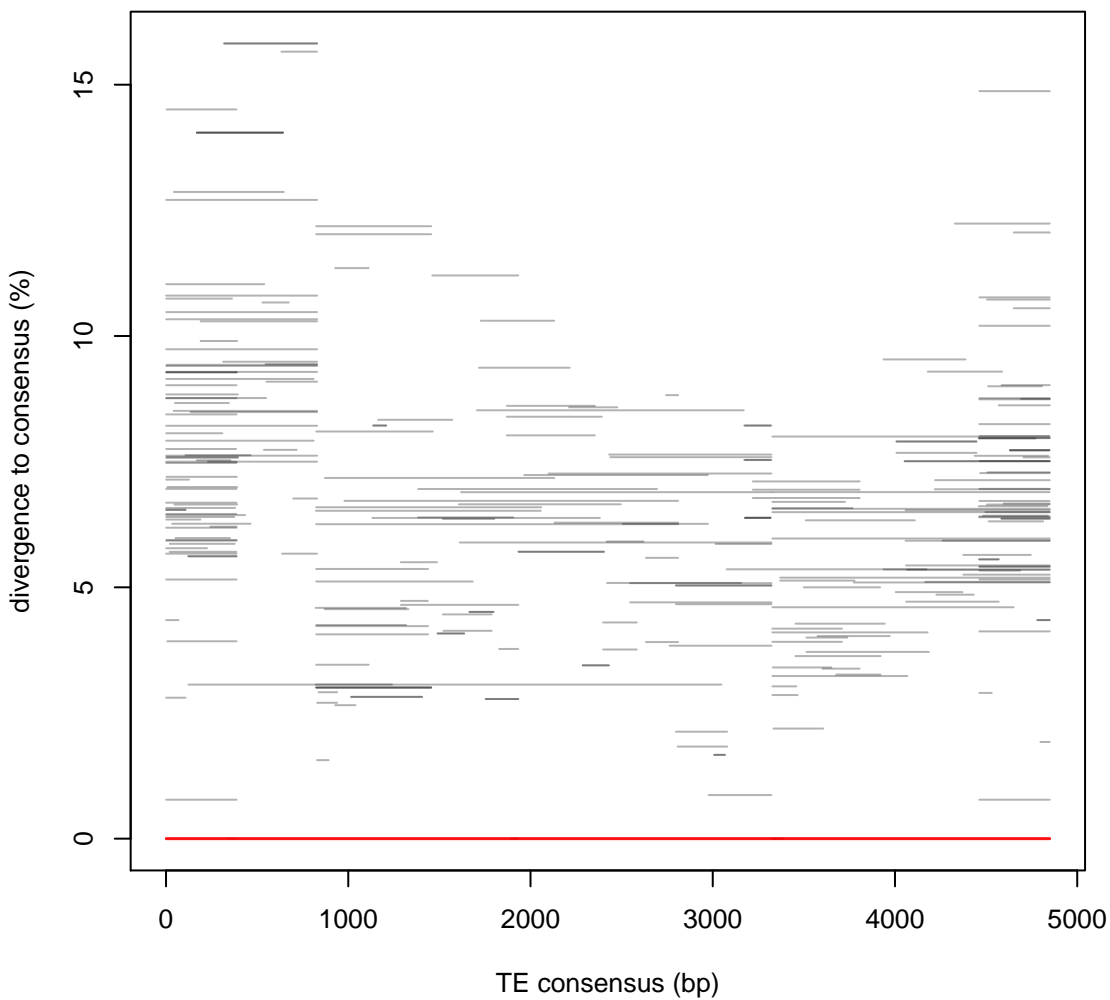
TE consensus (bp)

TE consensus genomic coverage

coverage (bp)
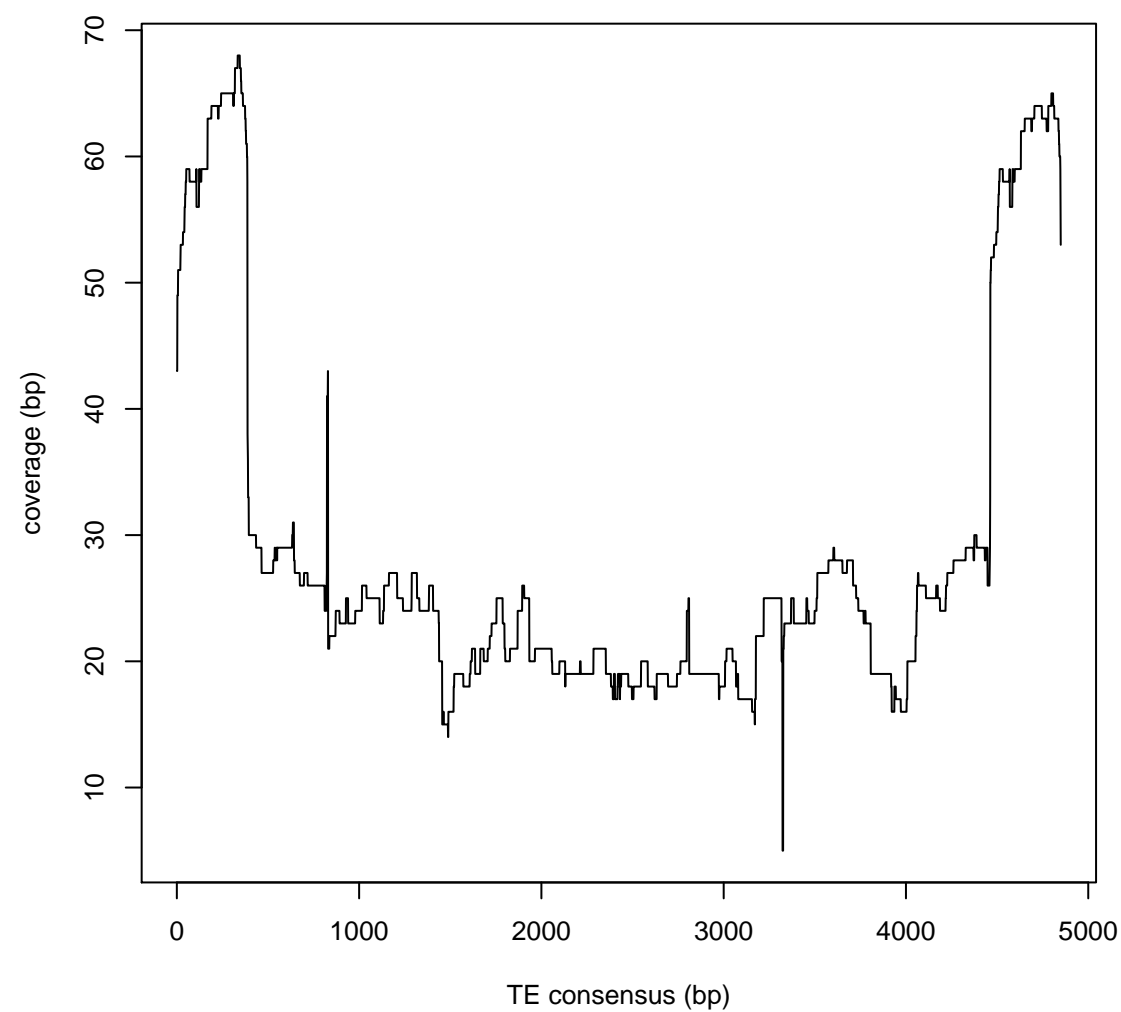
TE consensus (bp)

TE consensus self dotplot (blastn)

Dmel−L−B313−Map1_reversed−LTR/nan (bp)

Dmel−L−B313−Map1_reversed−LTR/nan (bp)
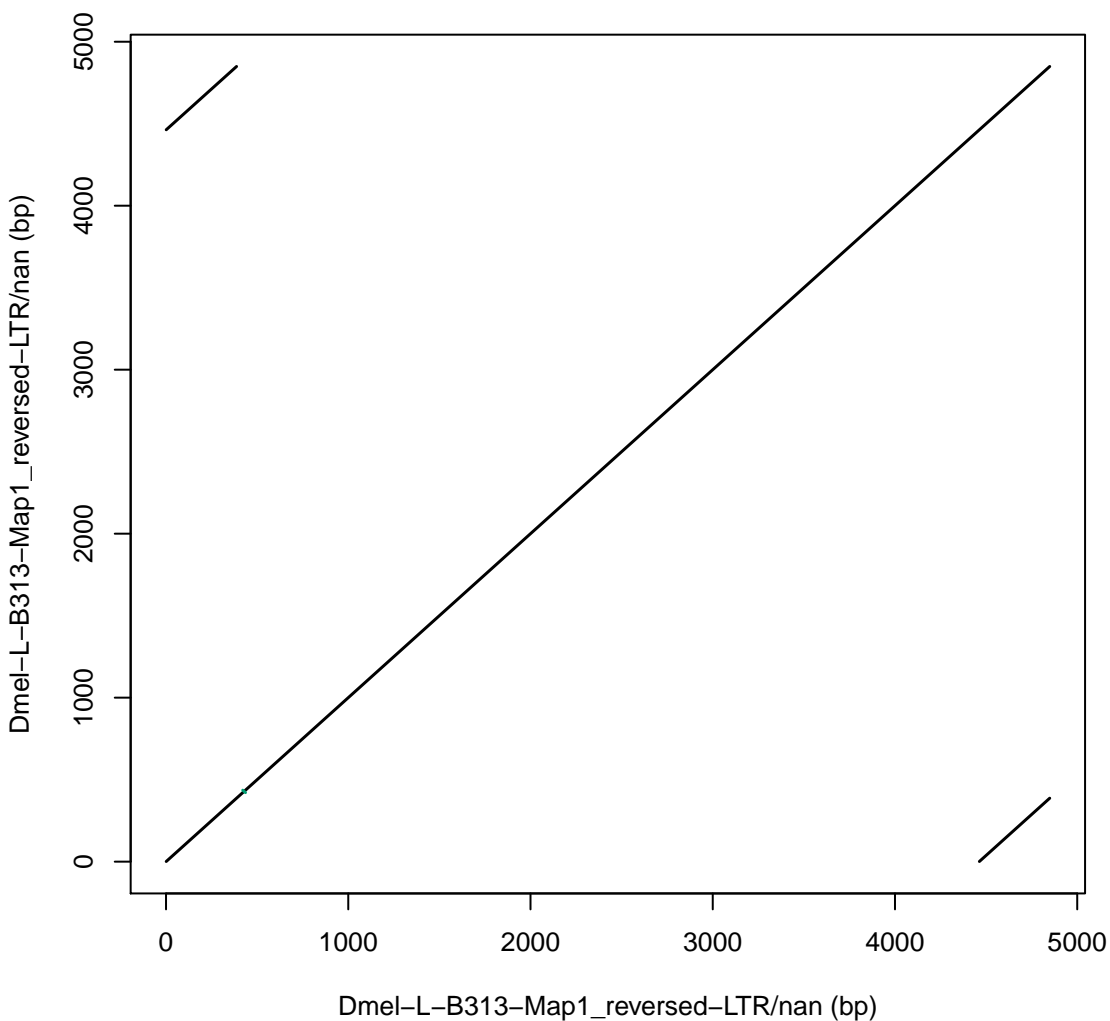
TE consensus structure and protein hits

Dmel−L−B313−Map1_reversed−LTR/nan (bp)

Dmel−L−B313−Map1_reversed−LTR/nan (bp)