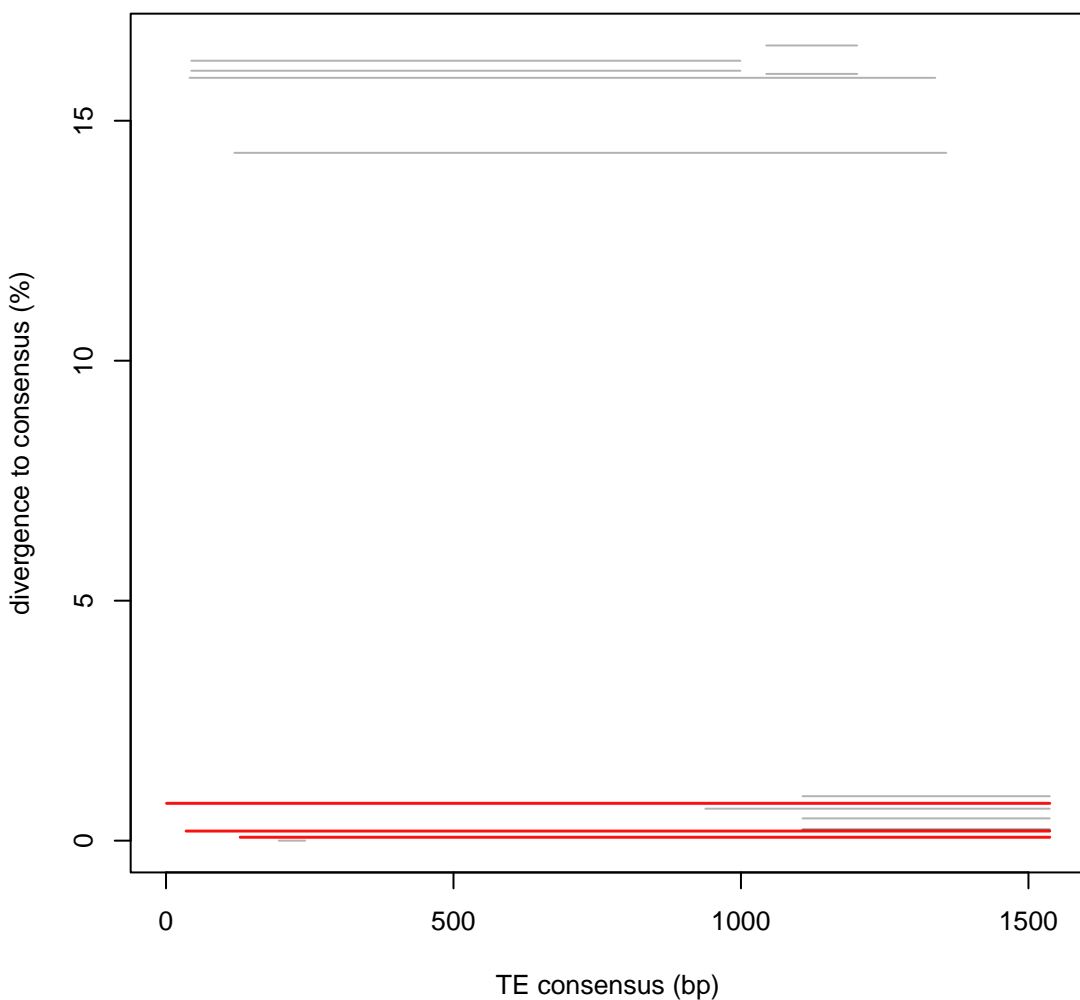
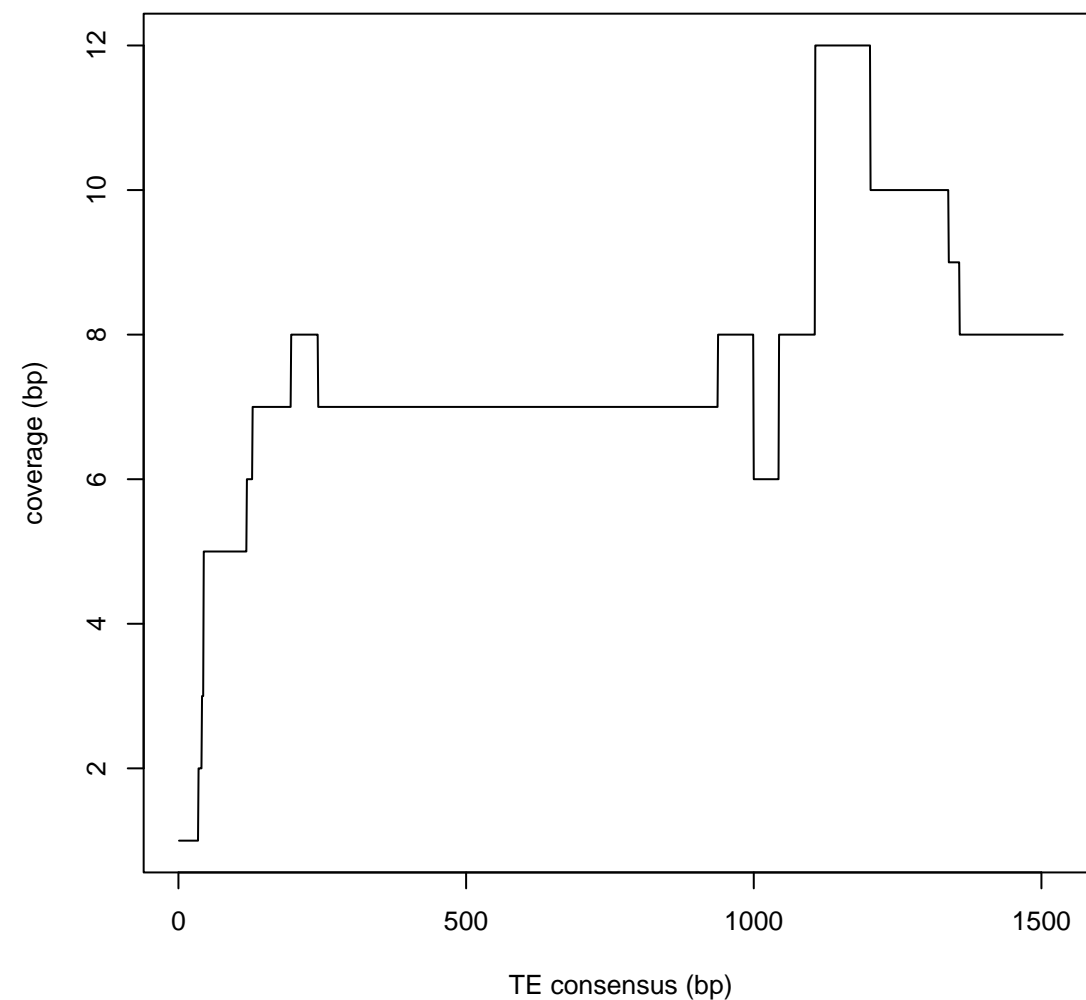


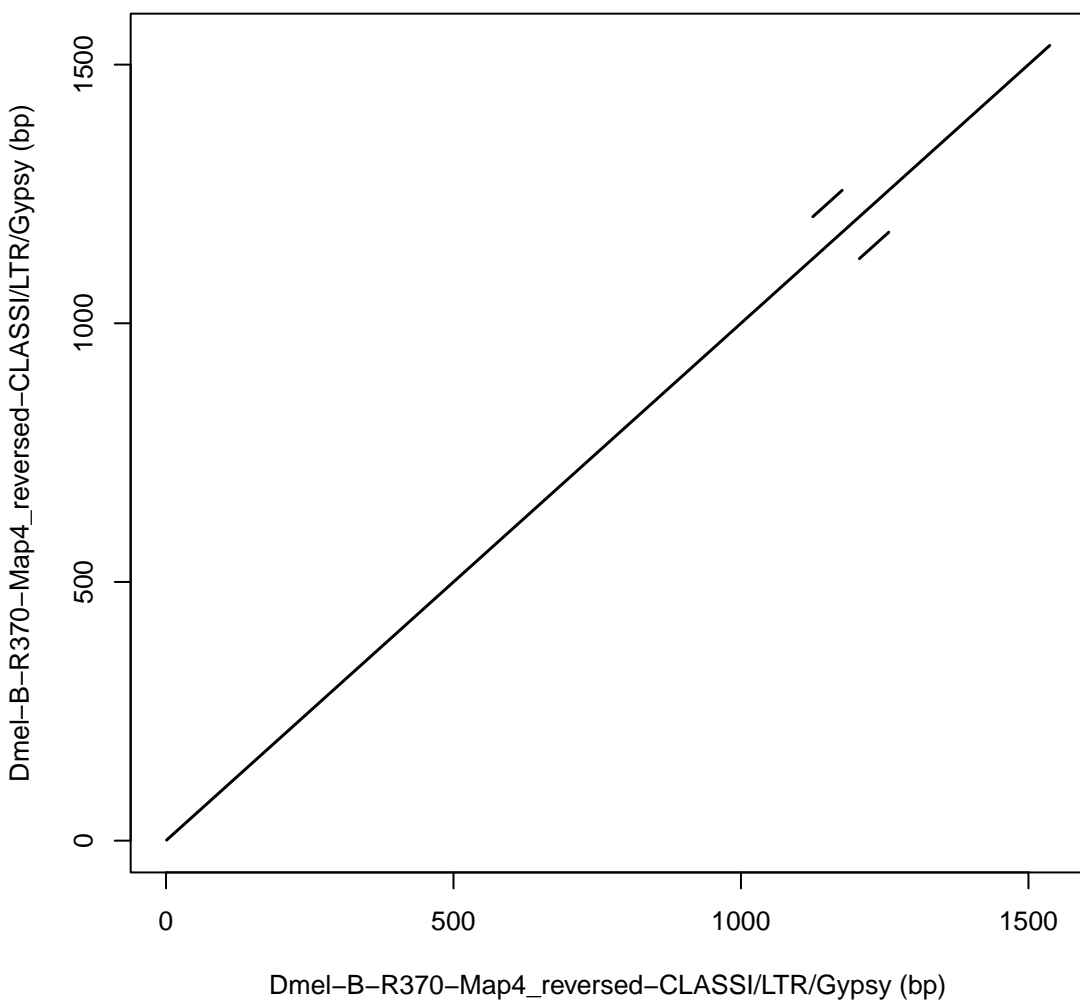
TE: Dmel-B-R370-Map4_reversed-CLASSI/LTR/Gypsy
consensus size: 1537bp; fragments: 15; full length: 3 (≥ 1383.3 bp)



TE consensus genomic coverage



TE consensus self dotplot (blastn)



TE consensus structure and protein hits

