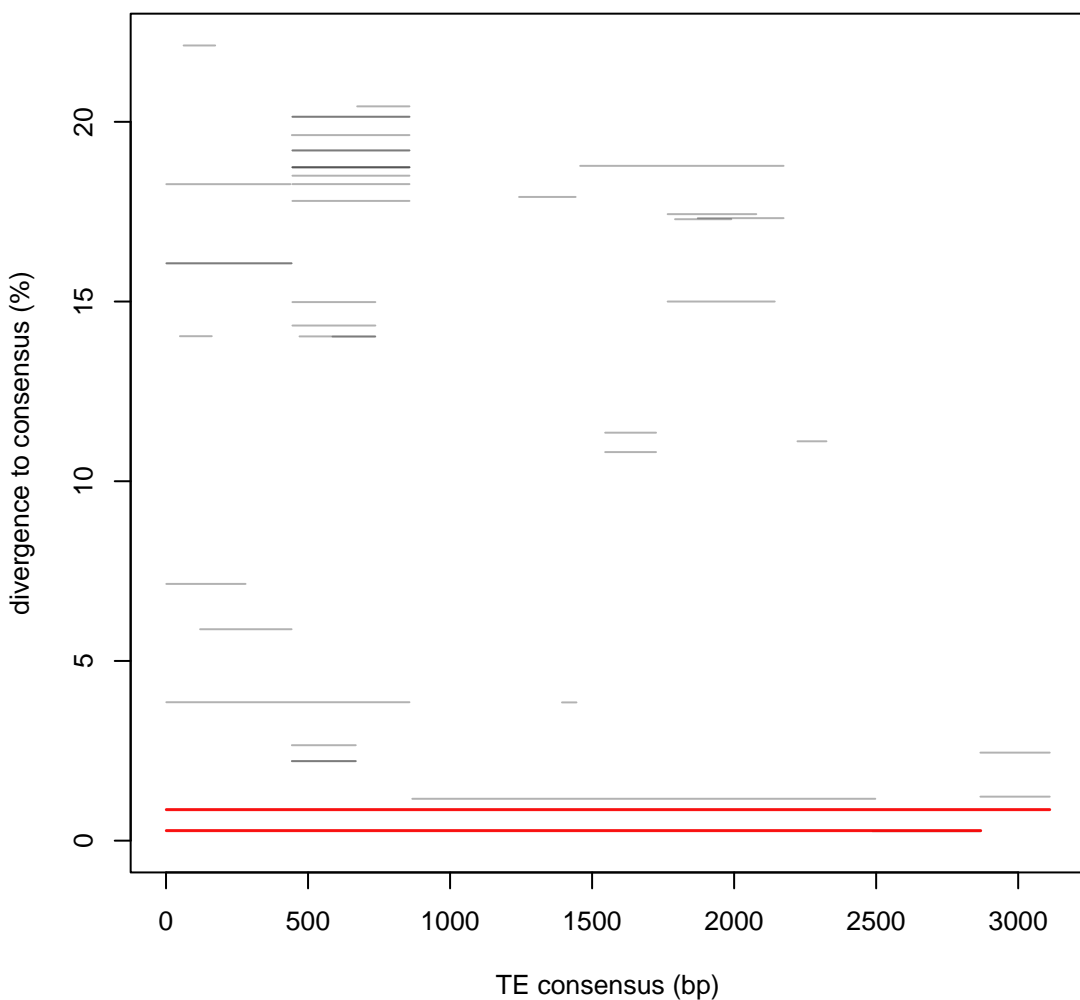
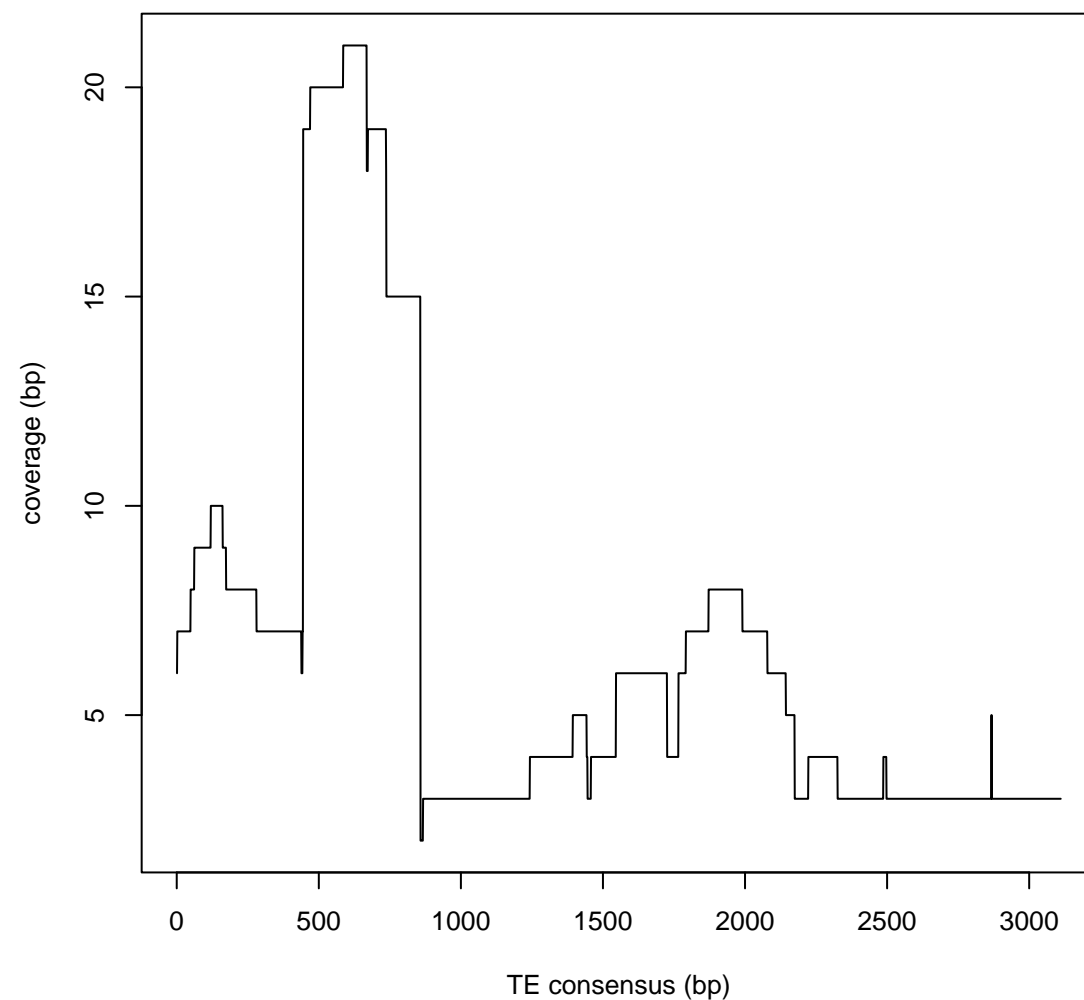


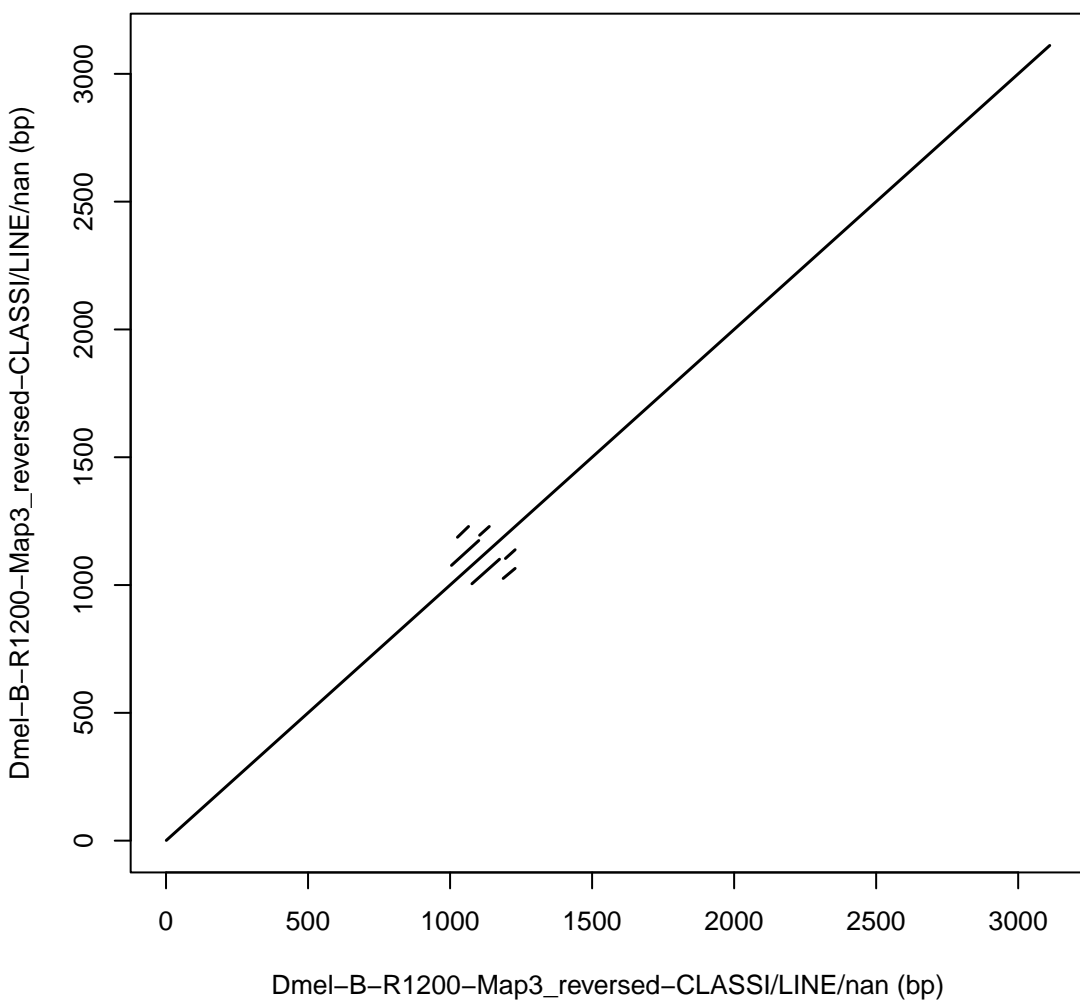
TE: Dmel-B-R1200-Map3_reversed-CLASSI/LINE/nan
consensus size: 3111bp; fragments: 43; full length: 2 (≥ 2799.9 bp)



TE consensus genomic coverage



TE consensus self dotplot (blastn)



TE consensus structure and protein hits

