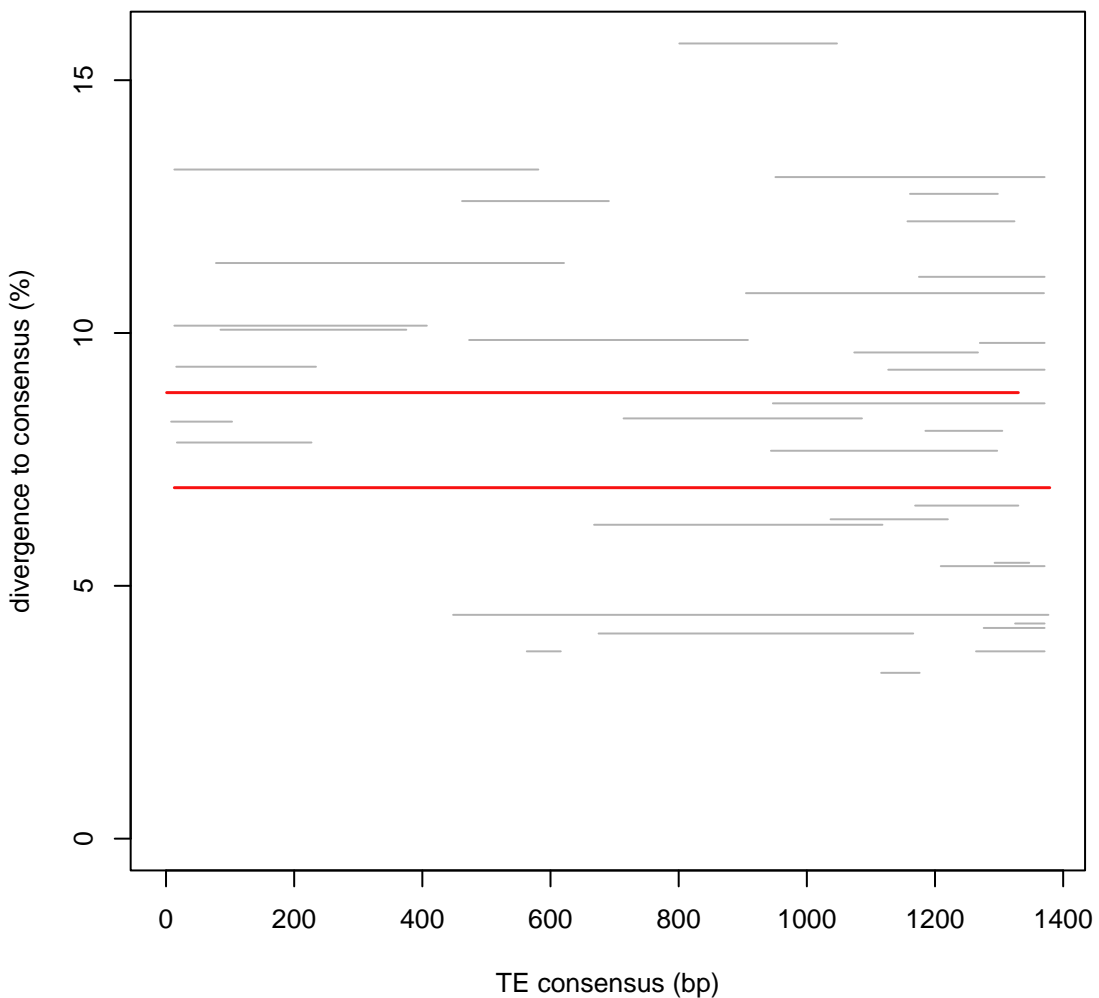
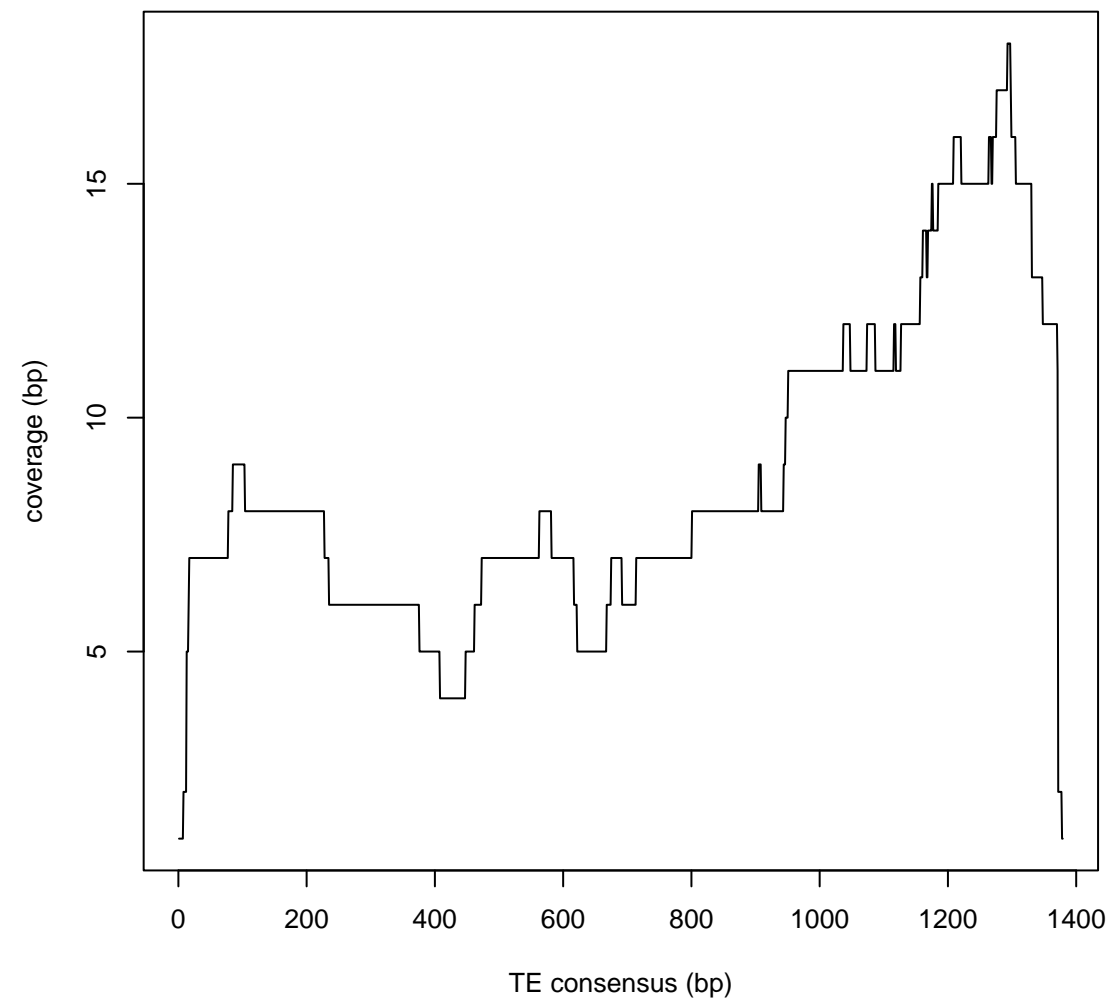


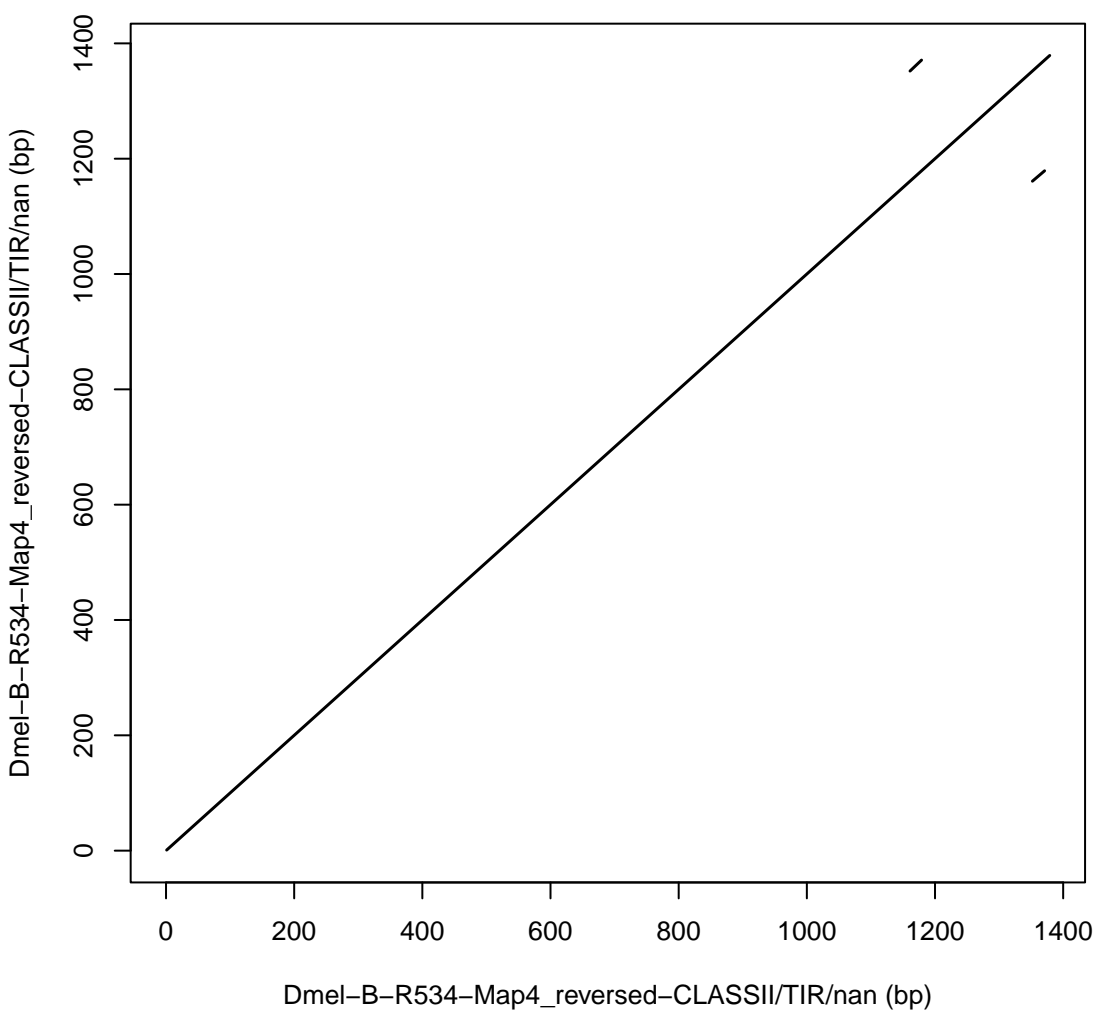
TE: Dmel-B-R534-Map4_reversed-CLASSII/TIR/nan
consensus size: 1379bp; fragments: 36; full length: 2 (≥ 1241.1 bp)



TE consensus genomic coverage



TE consensus self dotplot (blastn)



TE consensus structure and protein hits

