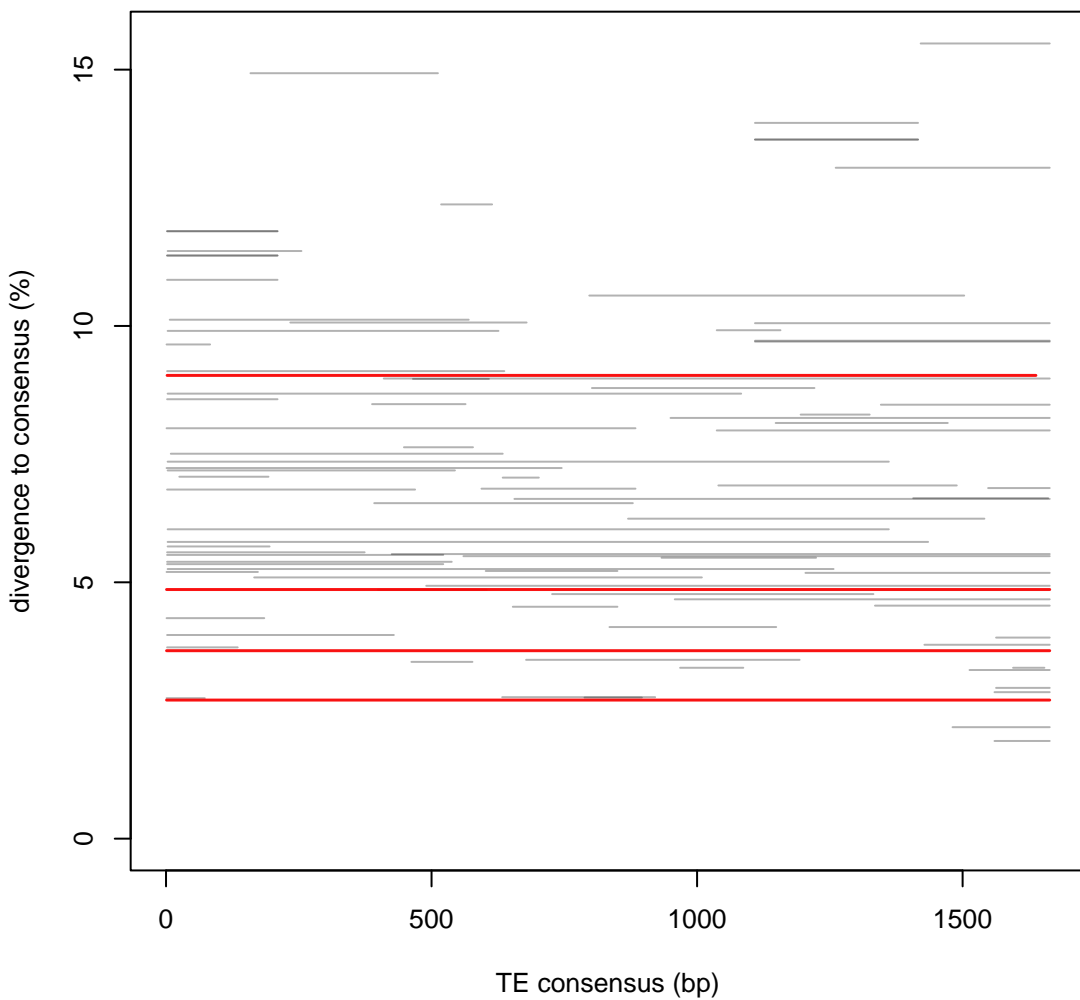
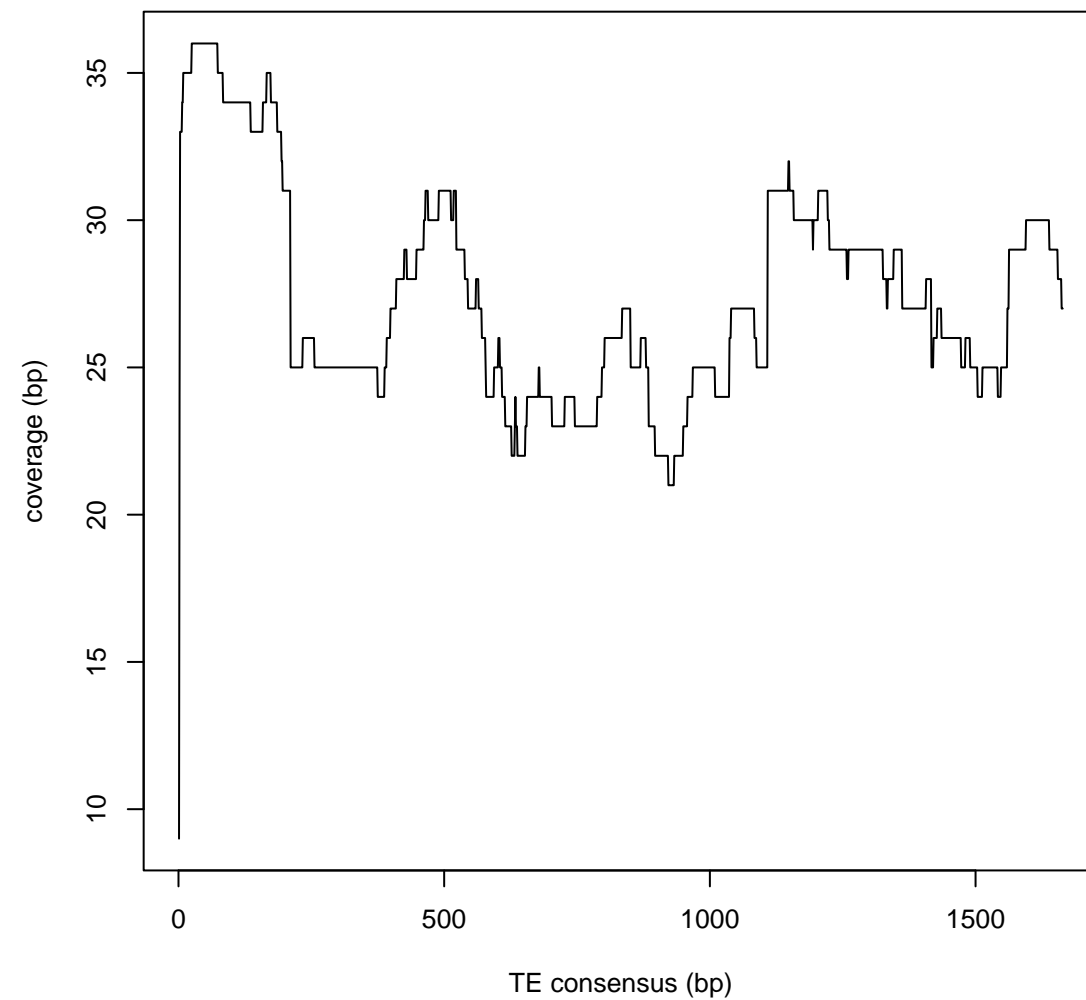


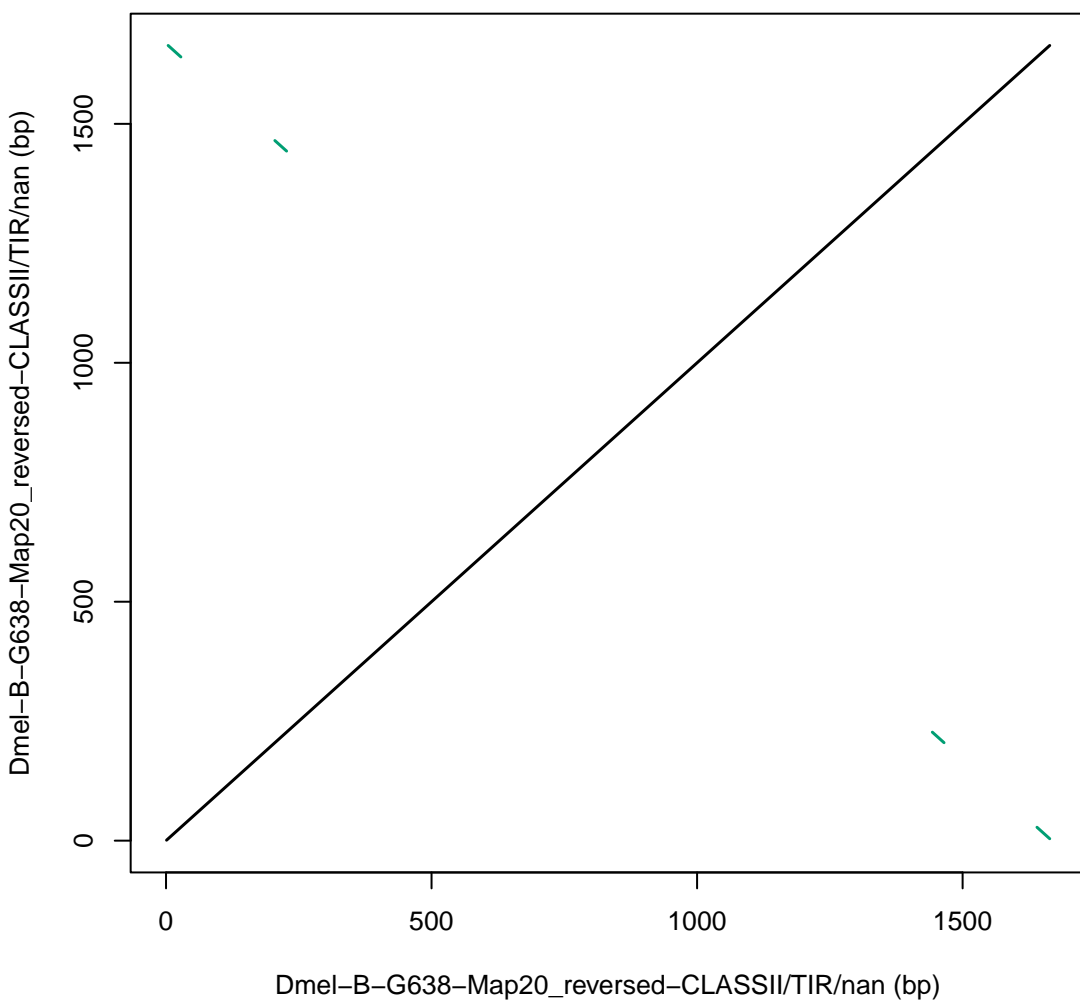
TE: Dmel-B-G638-Map20_reversed-CLASSII/TIR/nan
consensus size: 1664bp; fragments: 93; full length: 4 (≥ 1497.6 bp)



TE consensus genomic coverage



TE consensus self dotplot (blastn)



TE consensus structure and protein hits

