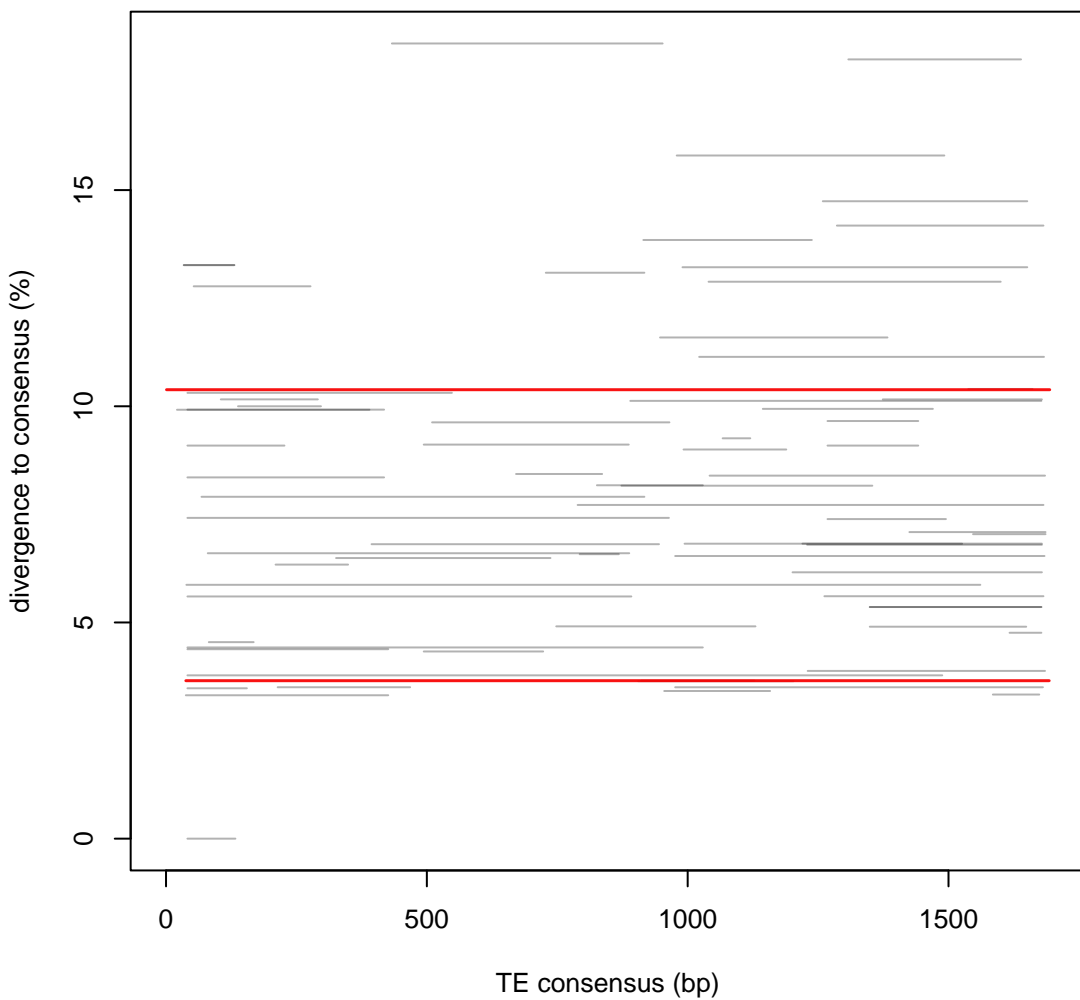
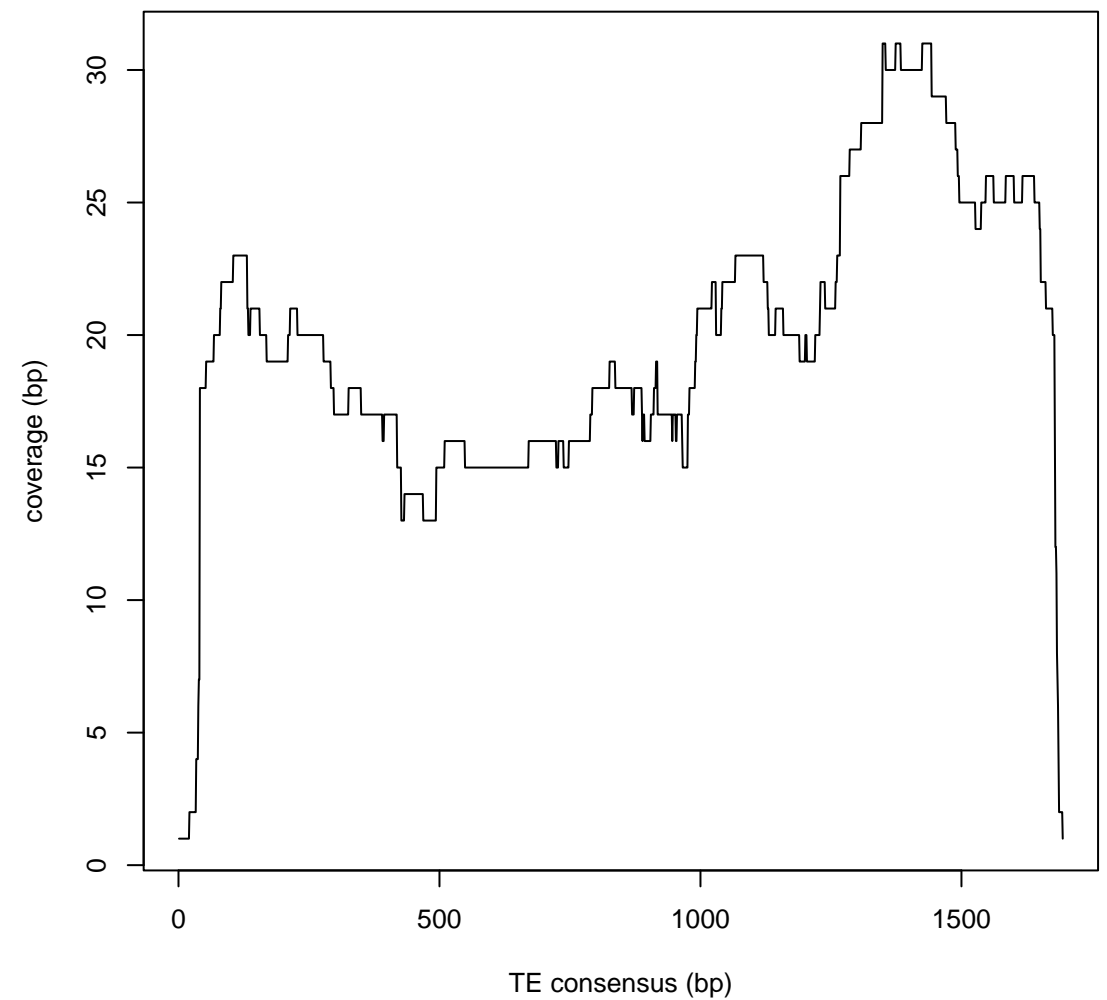


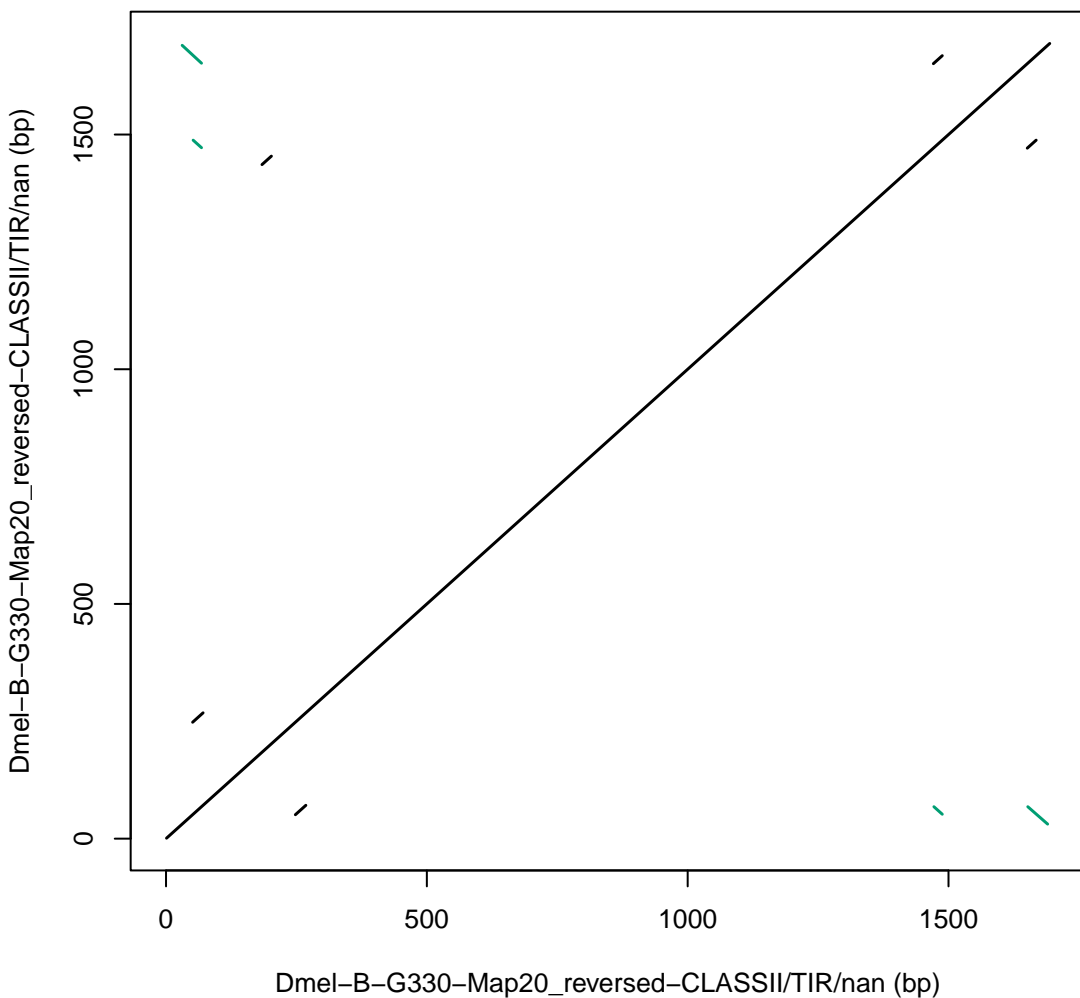
TE: Dmel-B-G330-Map20_reversed-CLASSII/TIR/nan
consensus size: 1694bp; fragments: 76; full length: 2 (≥ 1524.6 bp)



TE consensus genomic coverage



TE consensus self dotplot (blastn)



TE consensus structure and protein hits

