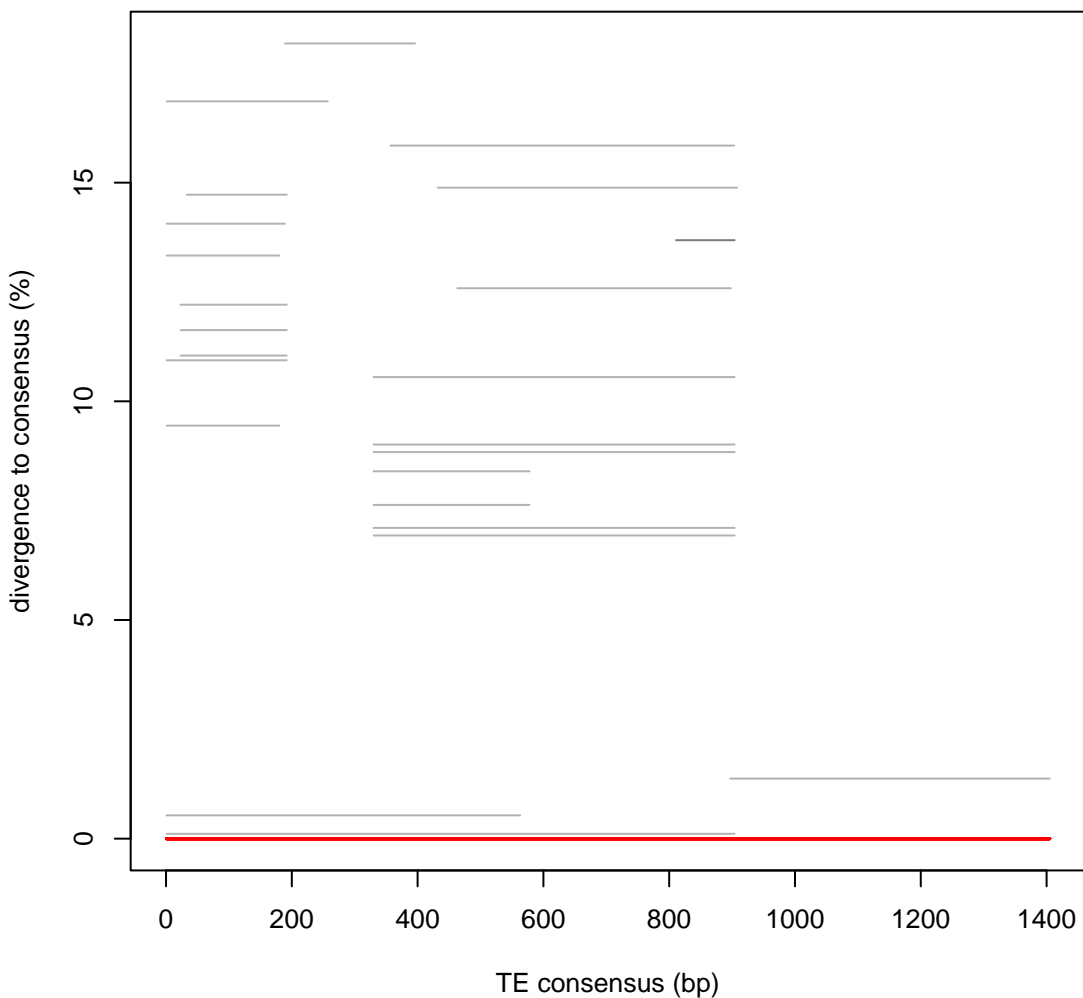
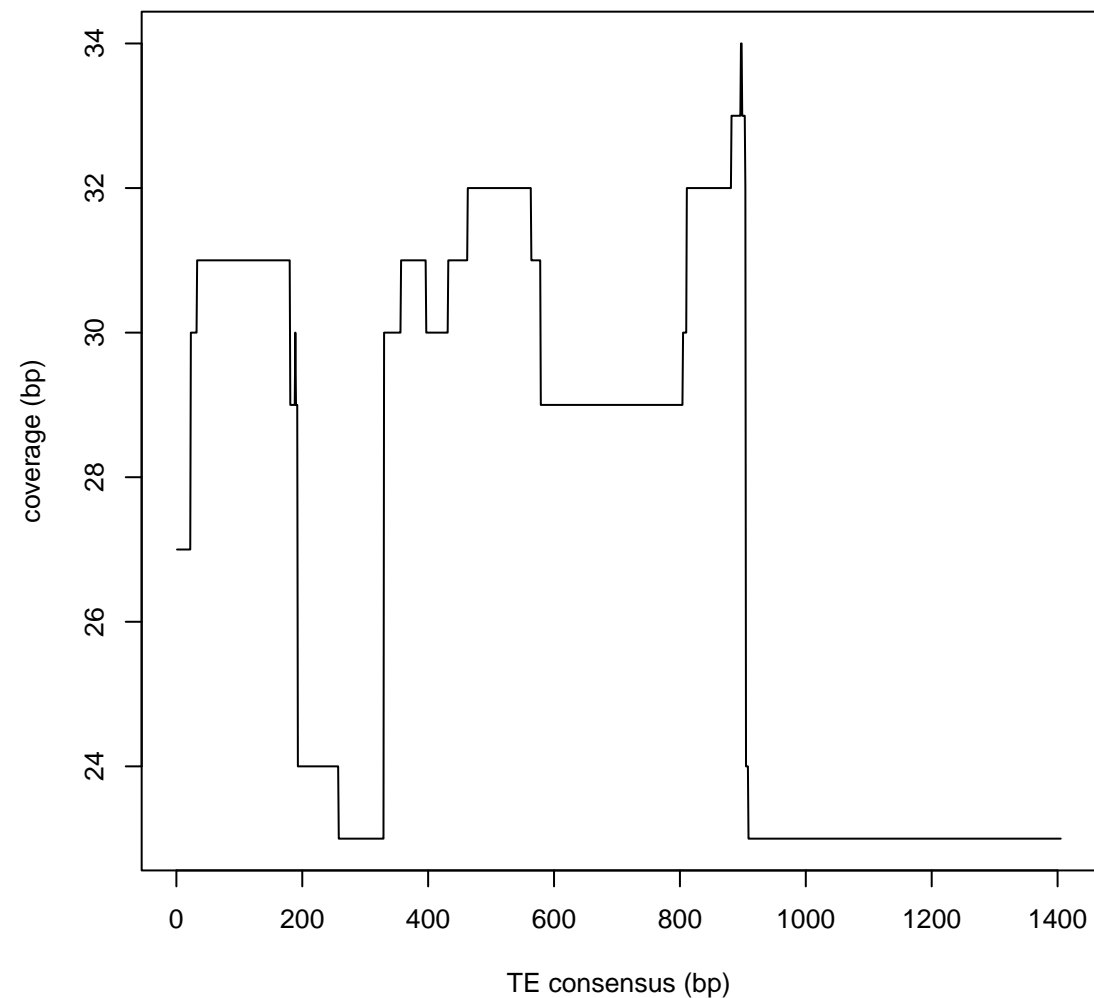


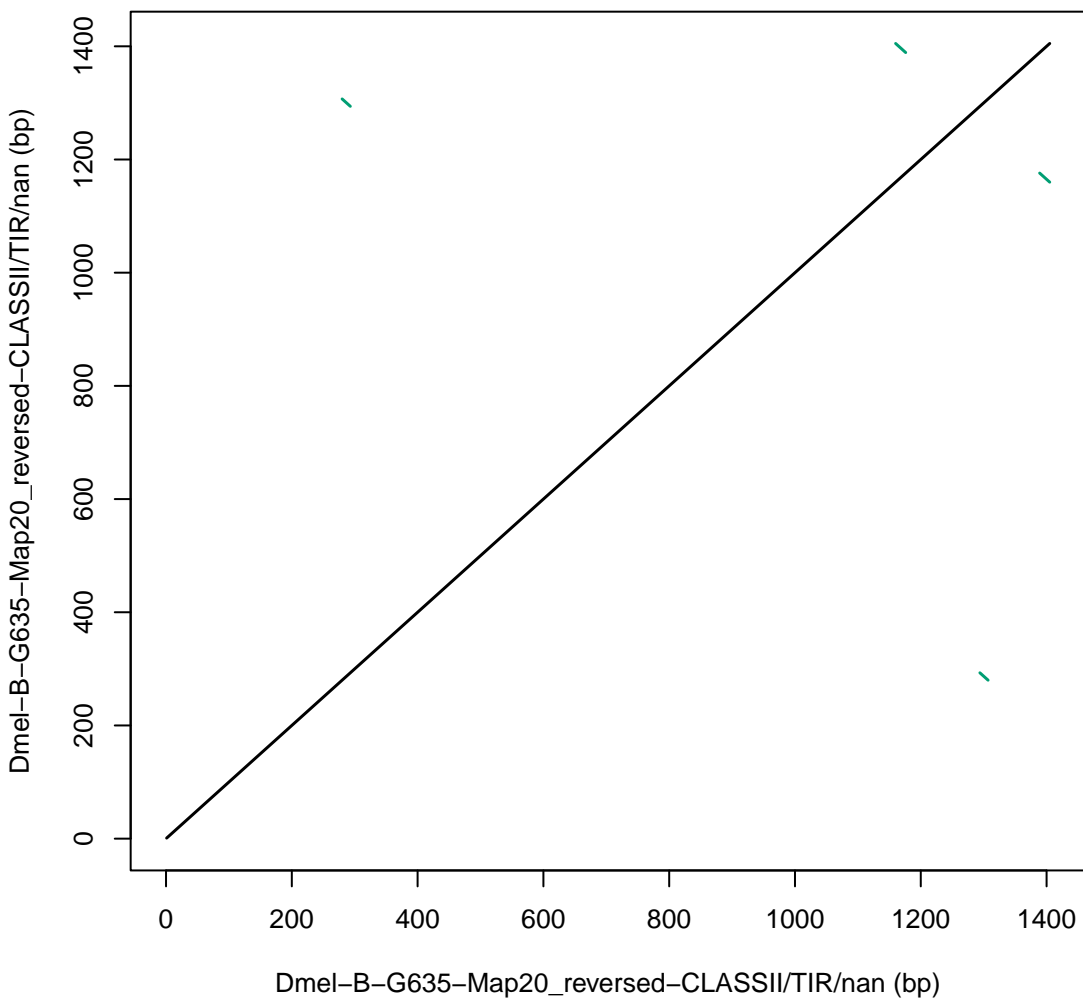
TE: Dmel-B-G635-Map20_reversed-CLASSII/TIR/nan
consensus size: 1405bp; fragments: 47; full length: 20 (>=1264.5bp)



TE consensus genomic coverage



TE consensus self dotplot (blastn)



TE consensus structure and protein hits

