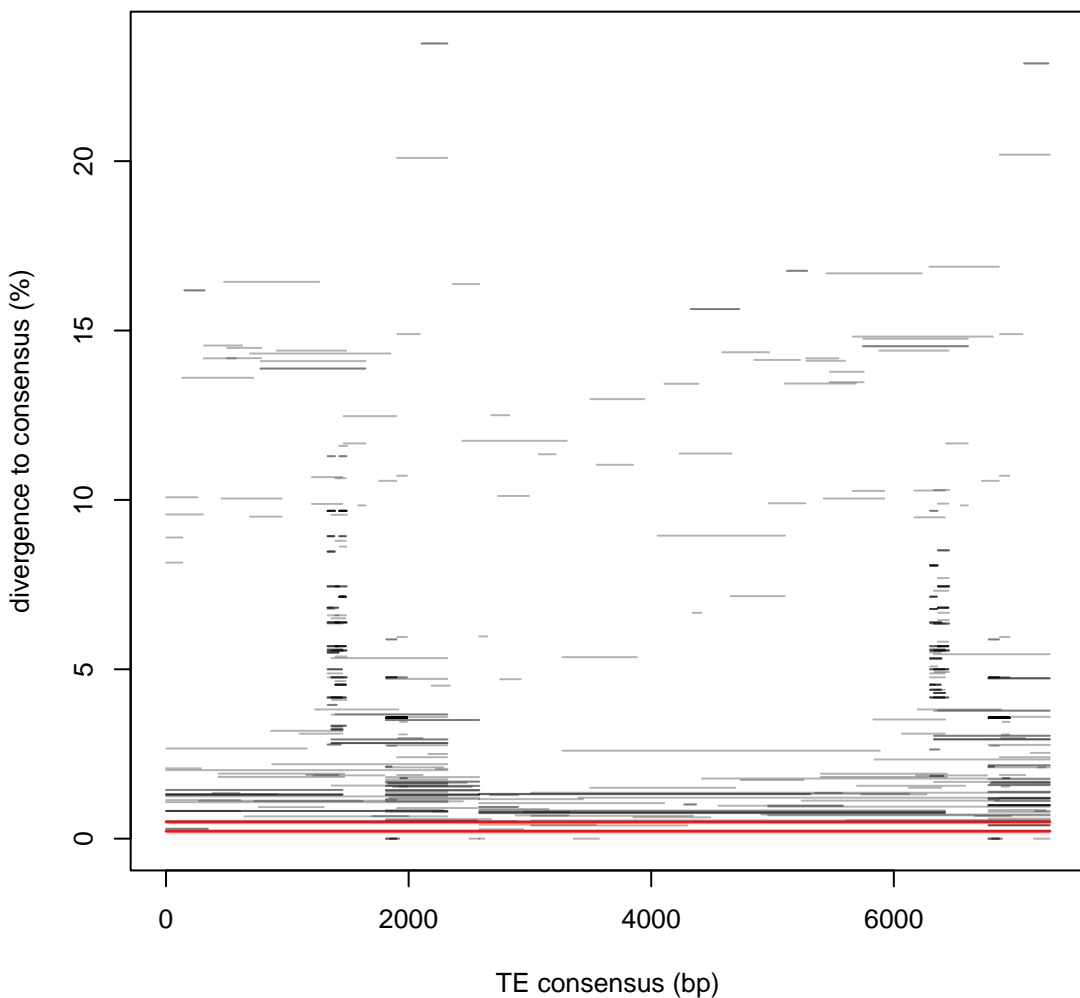
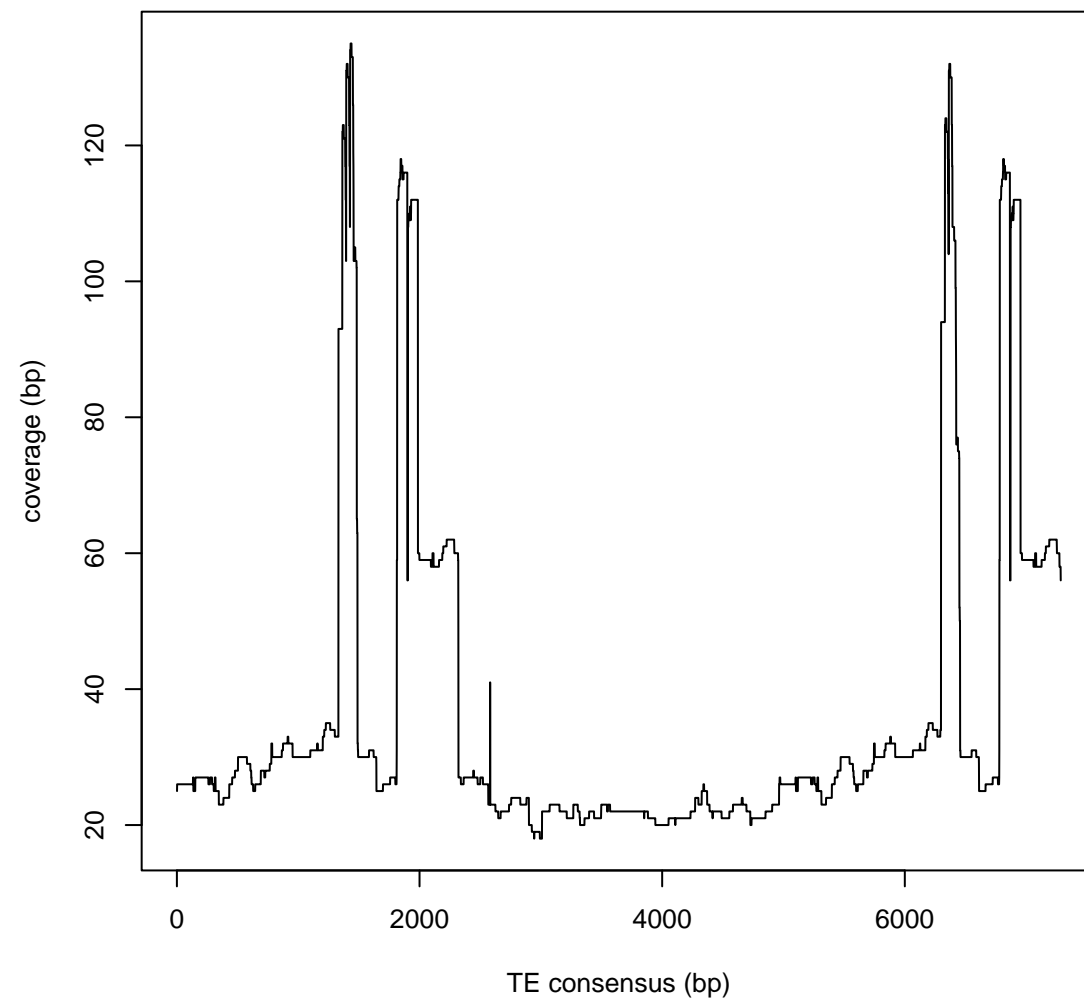


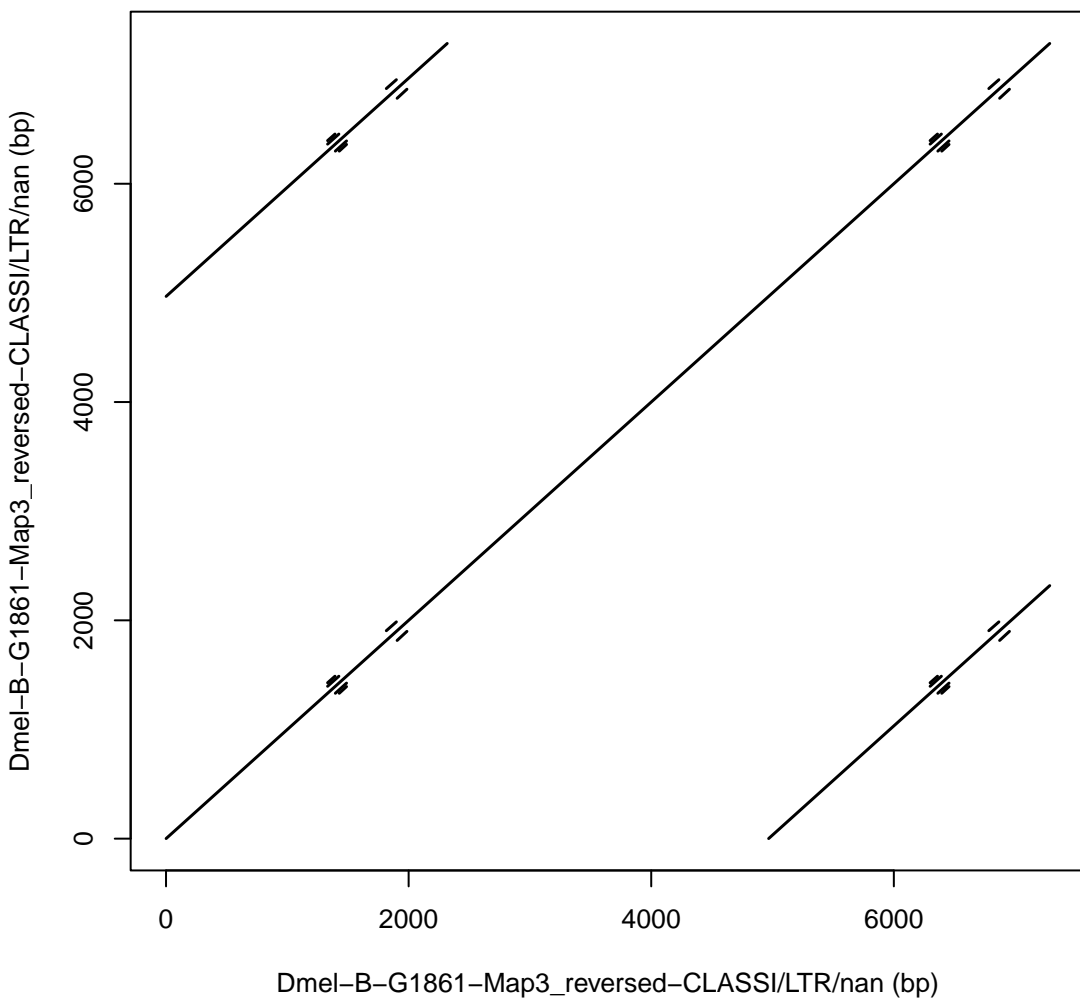
TE: Dmel-B-G1861-Map3_reversed-CLASSI/LTR/nan
consensus size: 7285bp; fragments: 735; full length: 2 (>=6556.5bp)



TE consensus genomic coverage



TE consensus self dotplot (blastn)



TE consensus structure and protein hits

