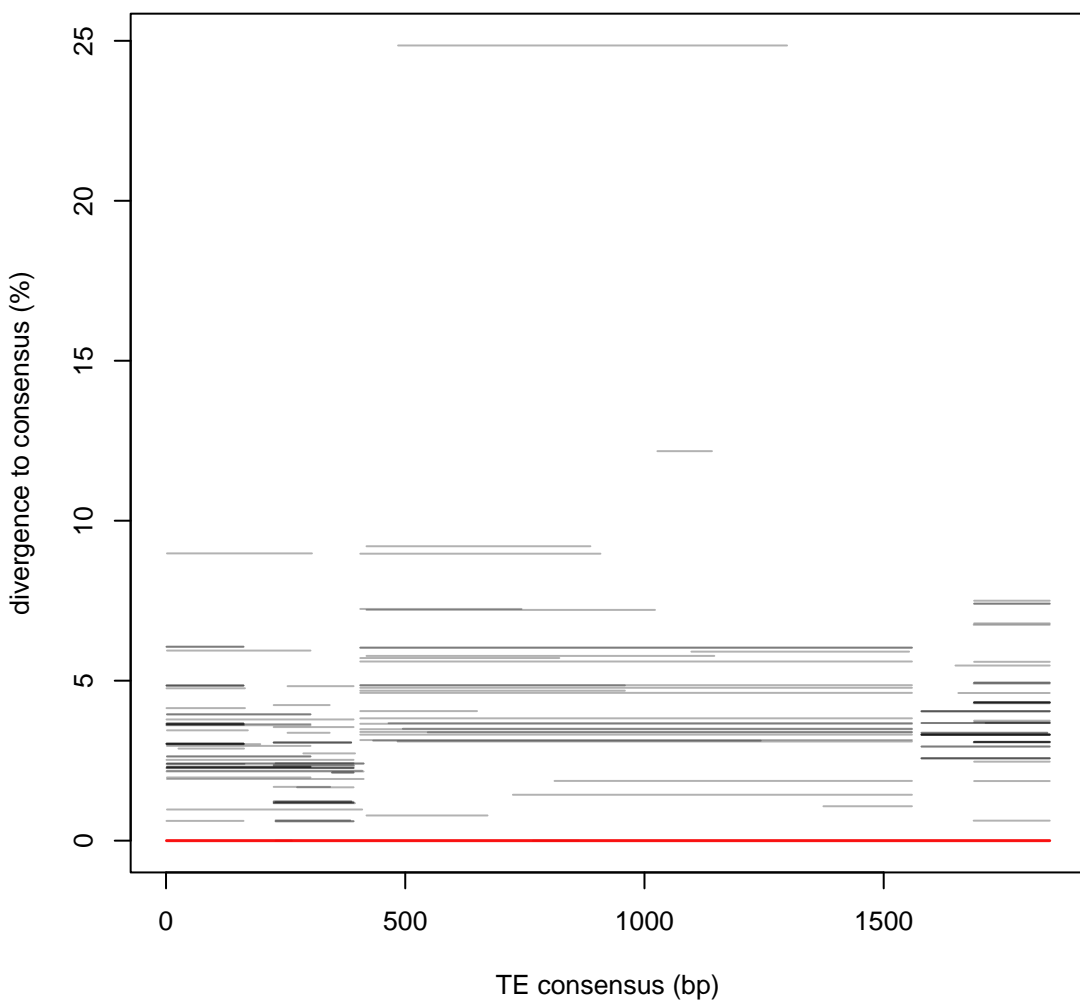
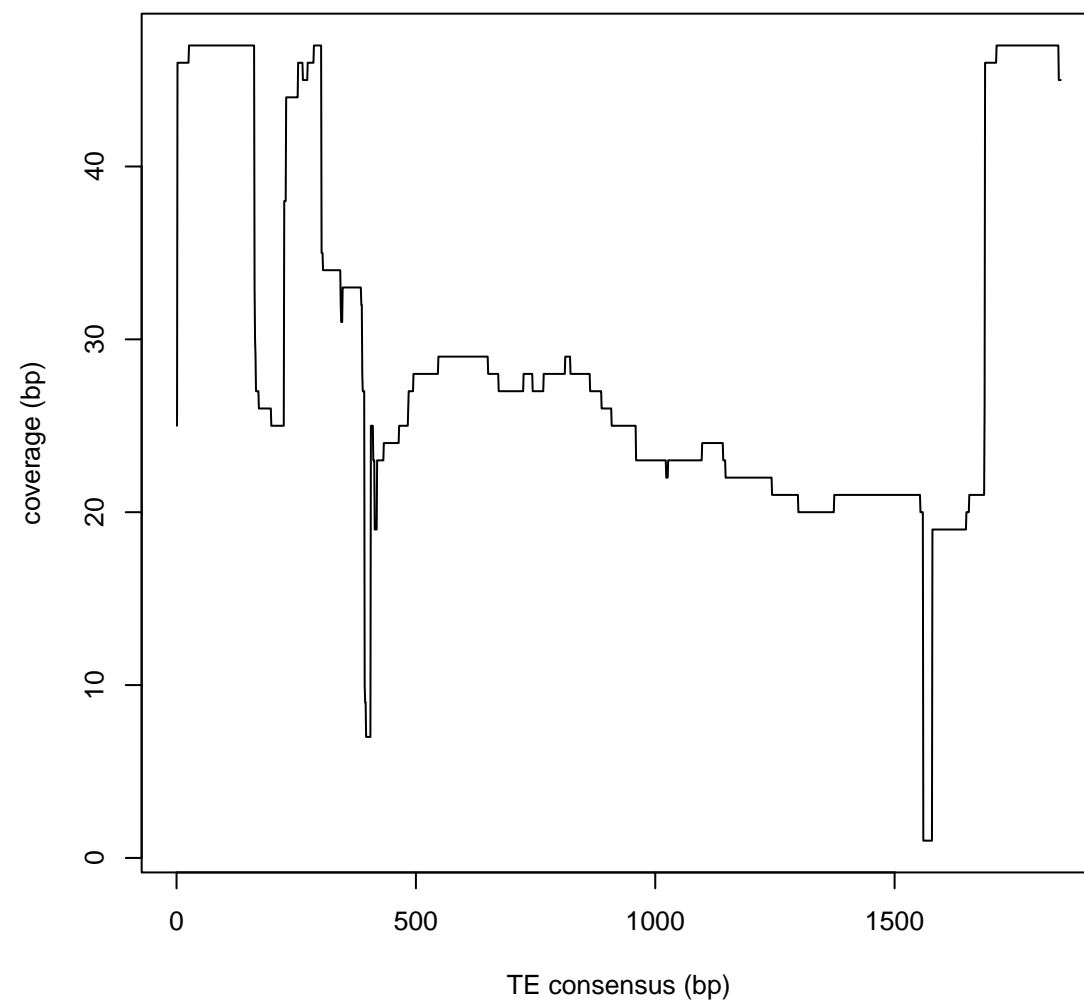


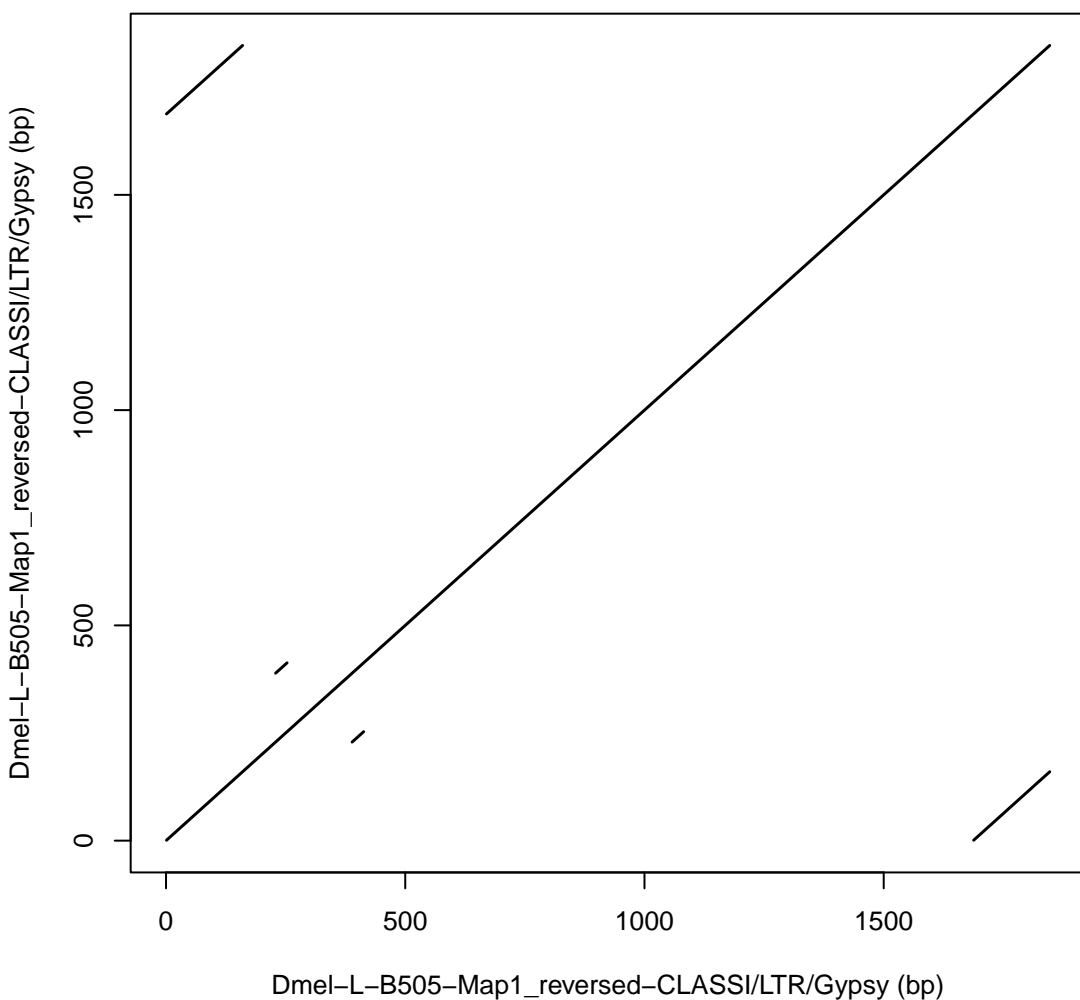
TE: Dmel-L-B505-Map1_reversed-CLASSI/LTR/Gypsy
consensus size: 1847bp; fragments: 152; full length: 1 (>=1662.3bp)



TE consensus genomic coverage



TE consensus self dotplot (blastn)



TE consensus structure and protein hits

