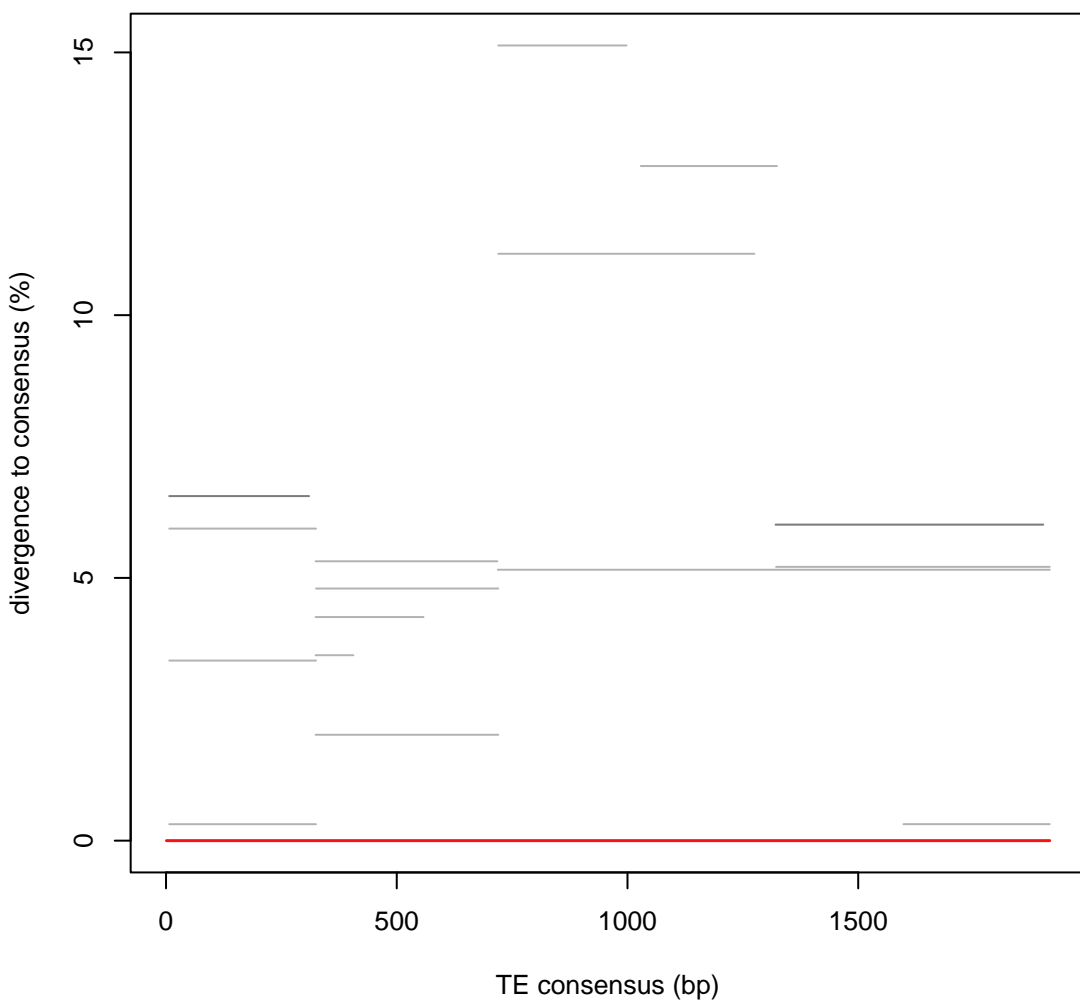
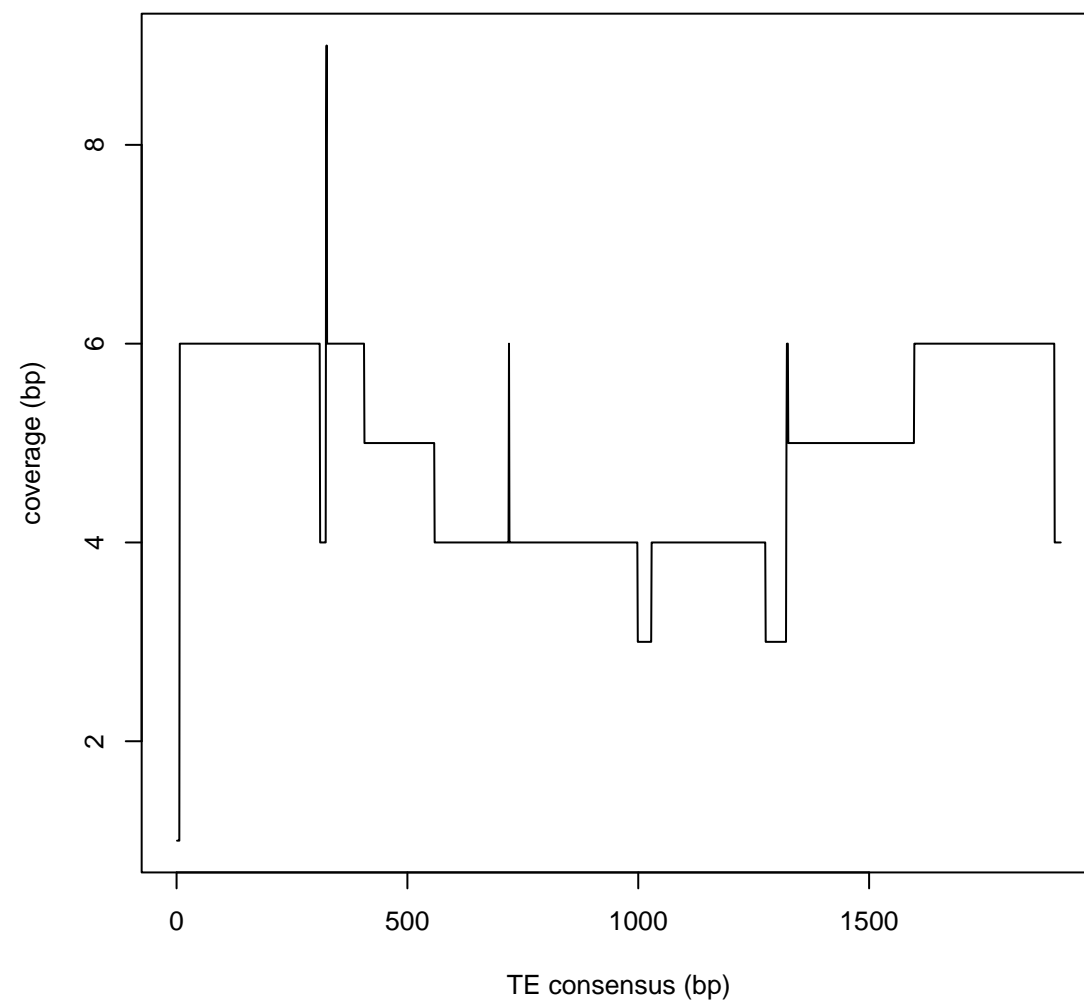


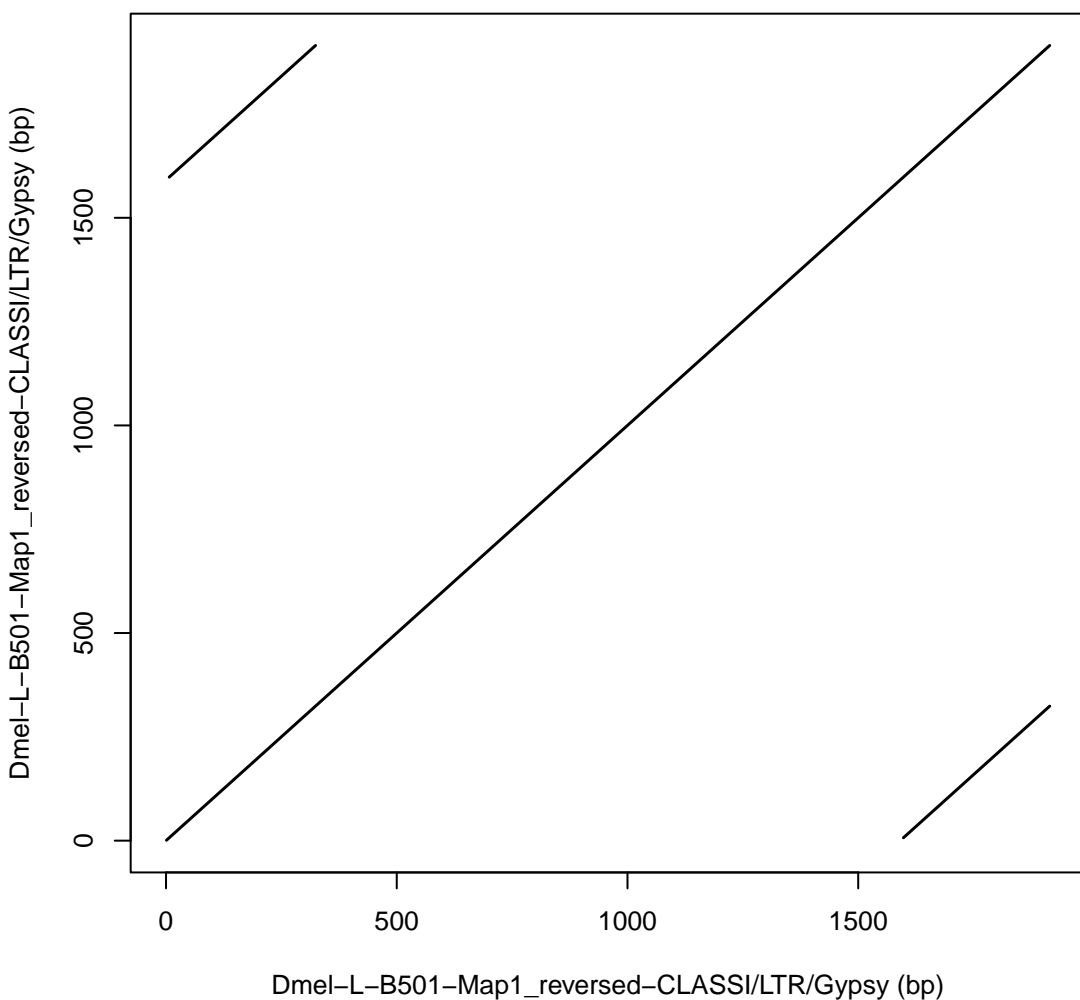
TE: Dmel-L-B501-Map1_reversed-CLASSI/LTR/Gypsy
consensus size: 1915bp; fragments: 19; full length: 1 (>=1723.5bp)



TE consensus genomic coverage



TE consensus self dotplot (blastn)



TE consensus structure and protein hits

