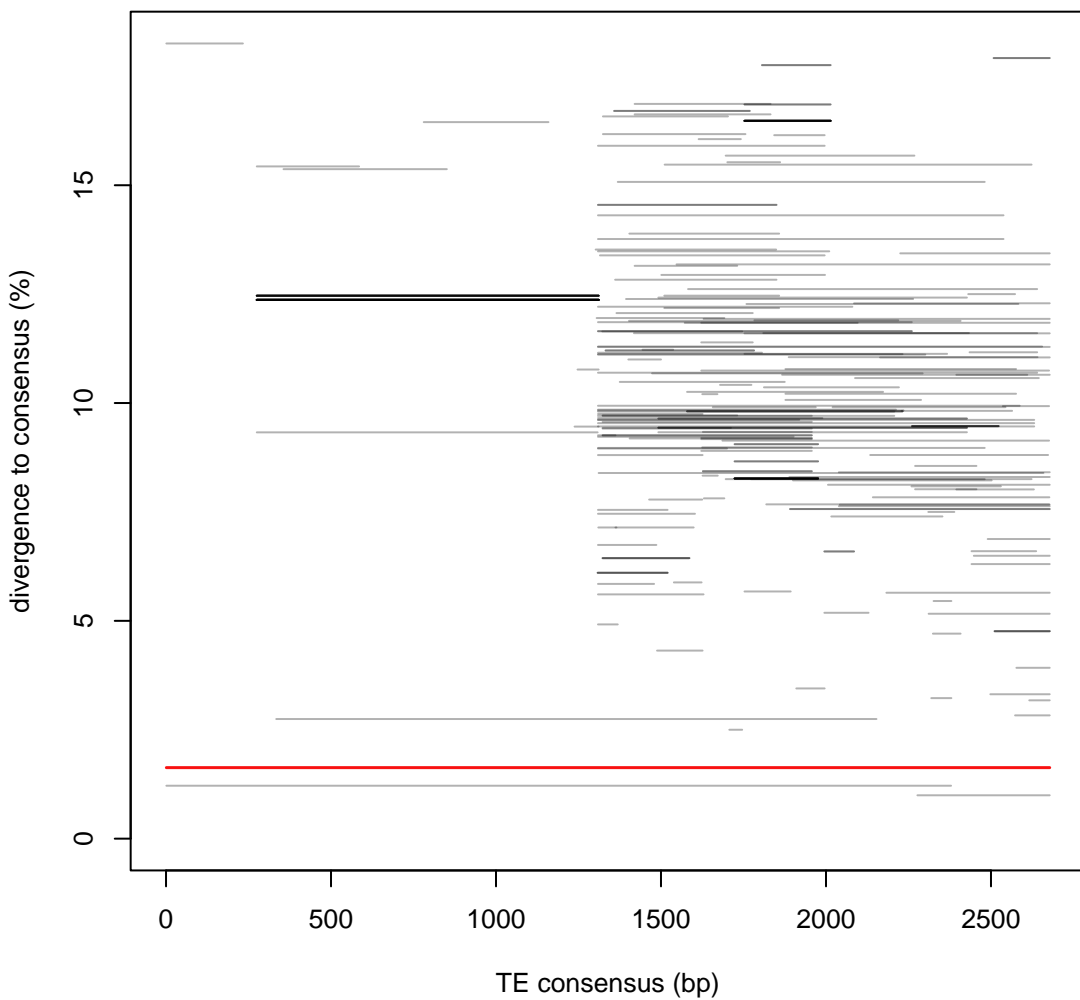
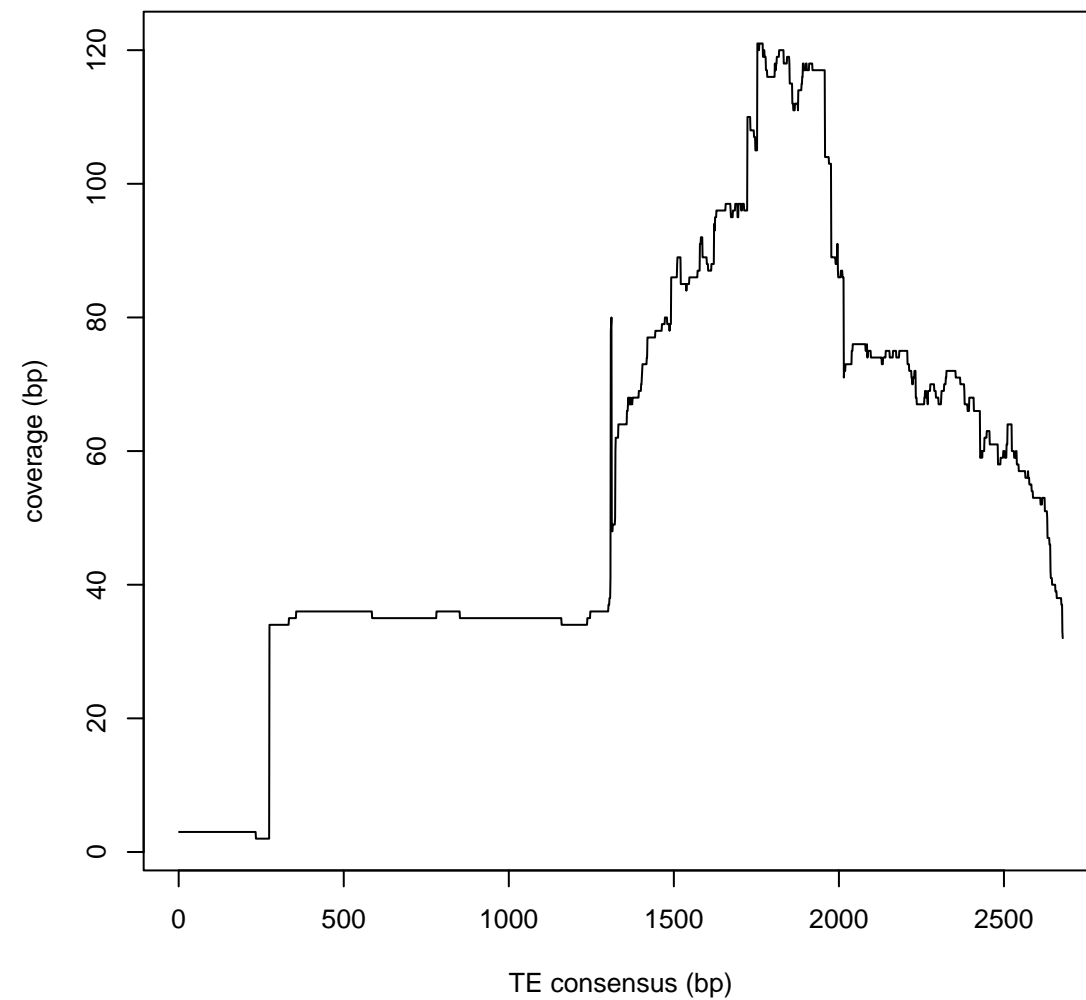


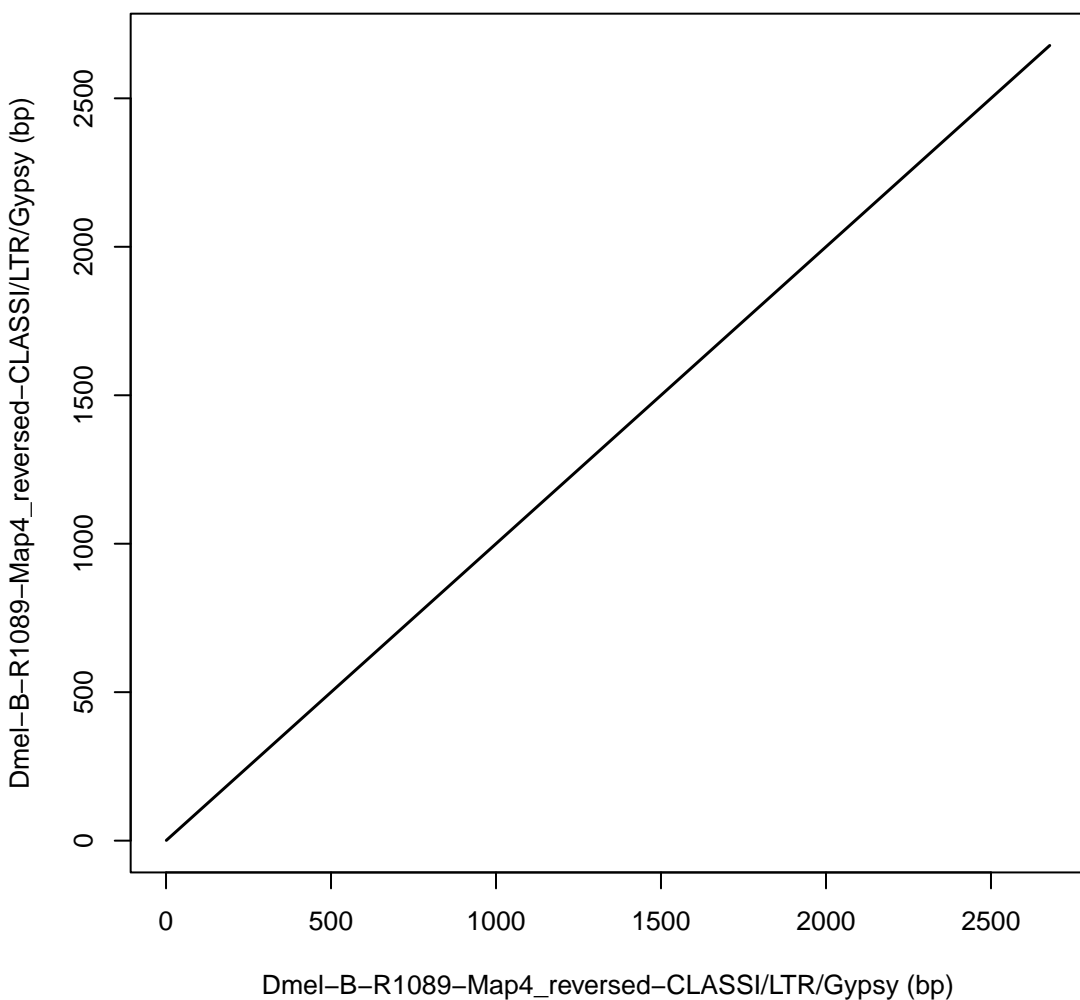
TE: Dmel-B-R1089-Map4_reversed-CLASSI/LTR/Gypsy
consensus size: 2678bp; fragments: 259; full length: 1 (>=2410.2bp)



TE consensus genomic coverage



TE consensus self dotplot (blastn)



TE consensus structure and protein hits

