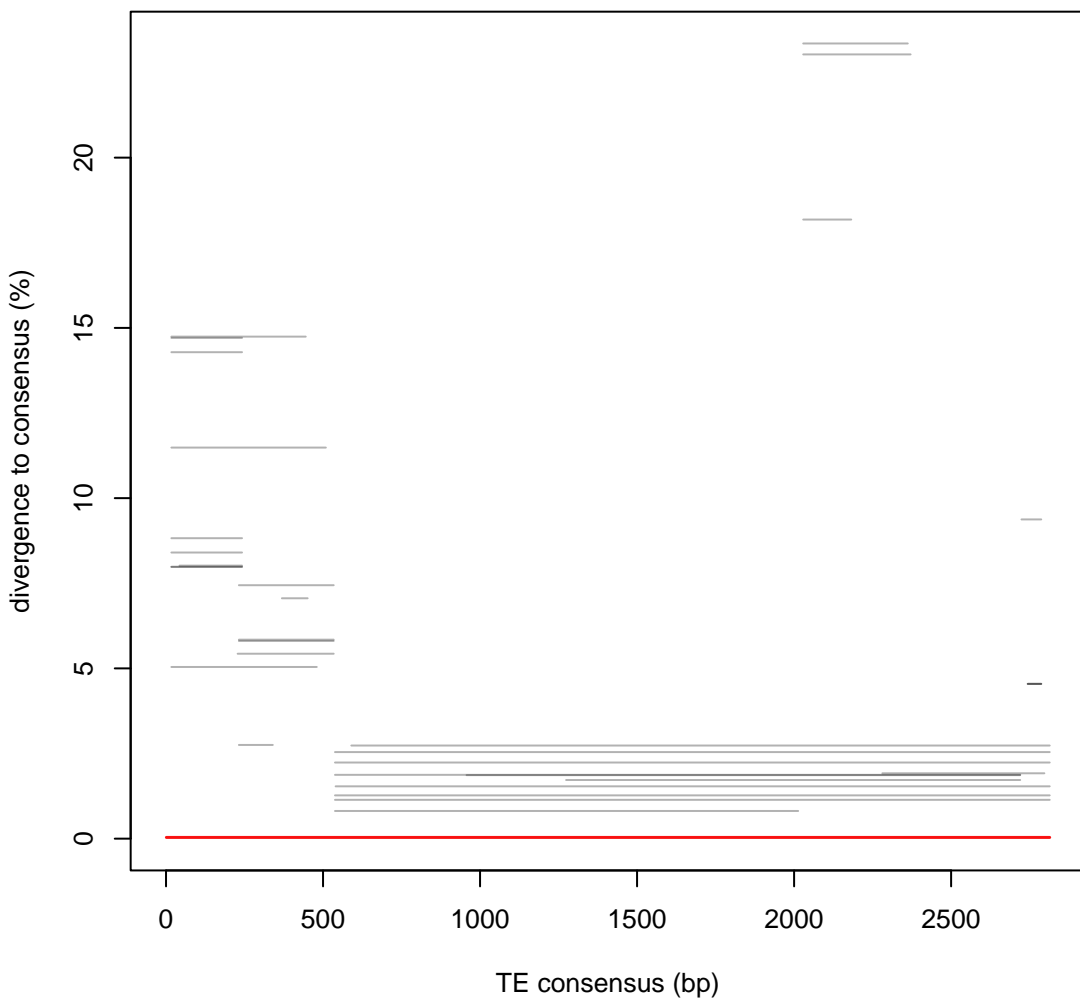
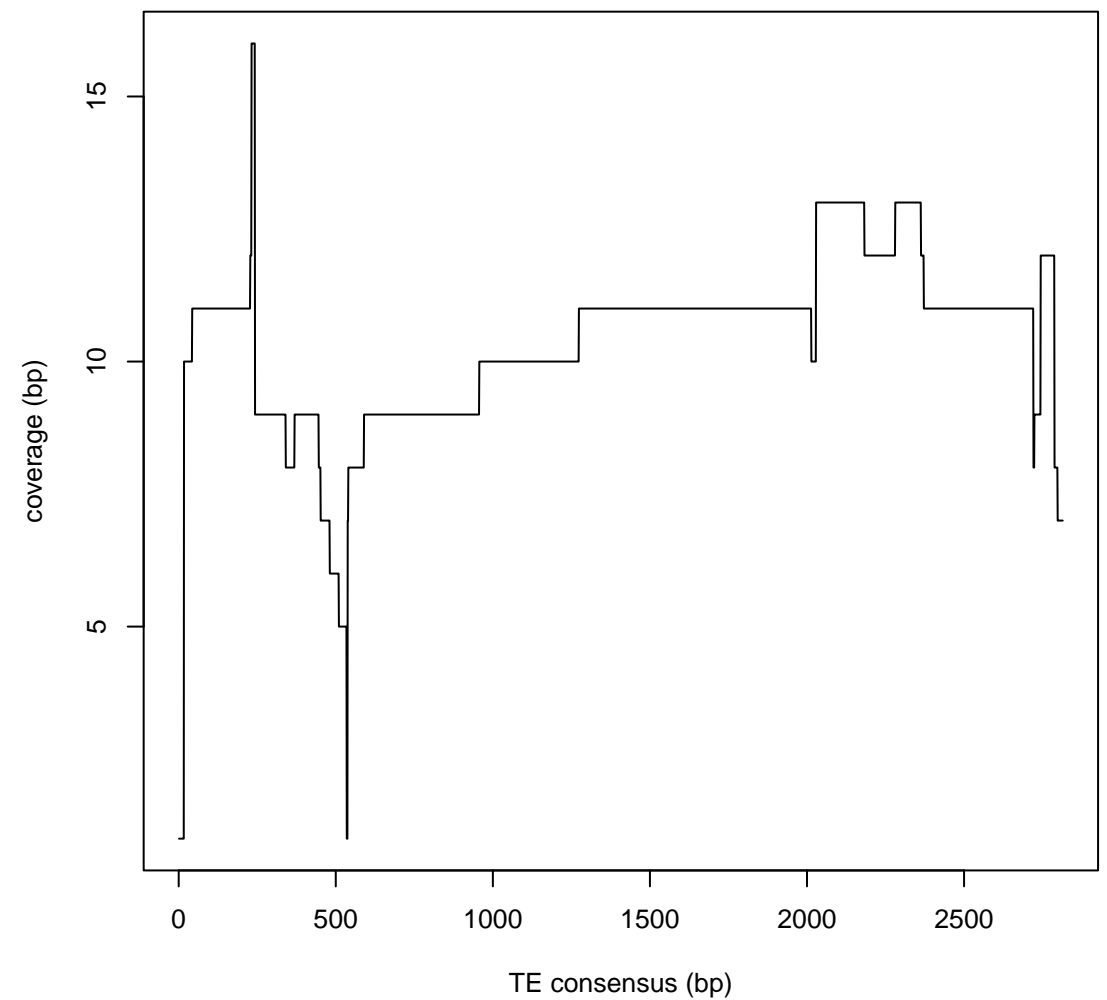


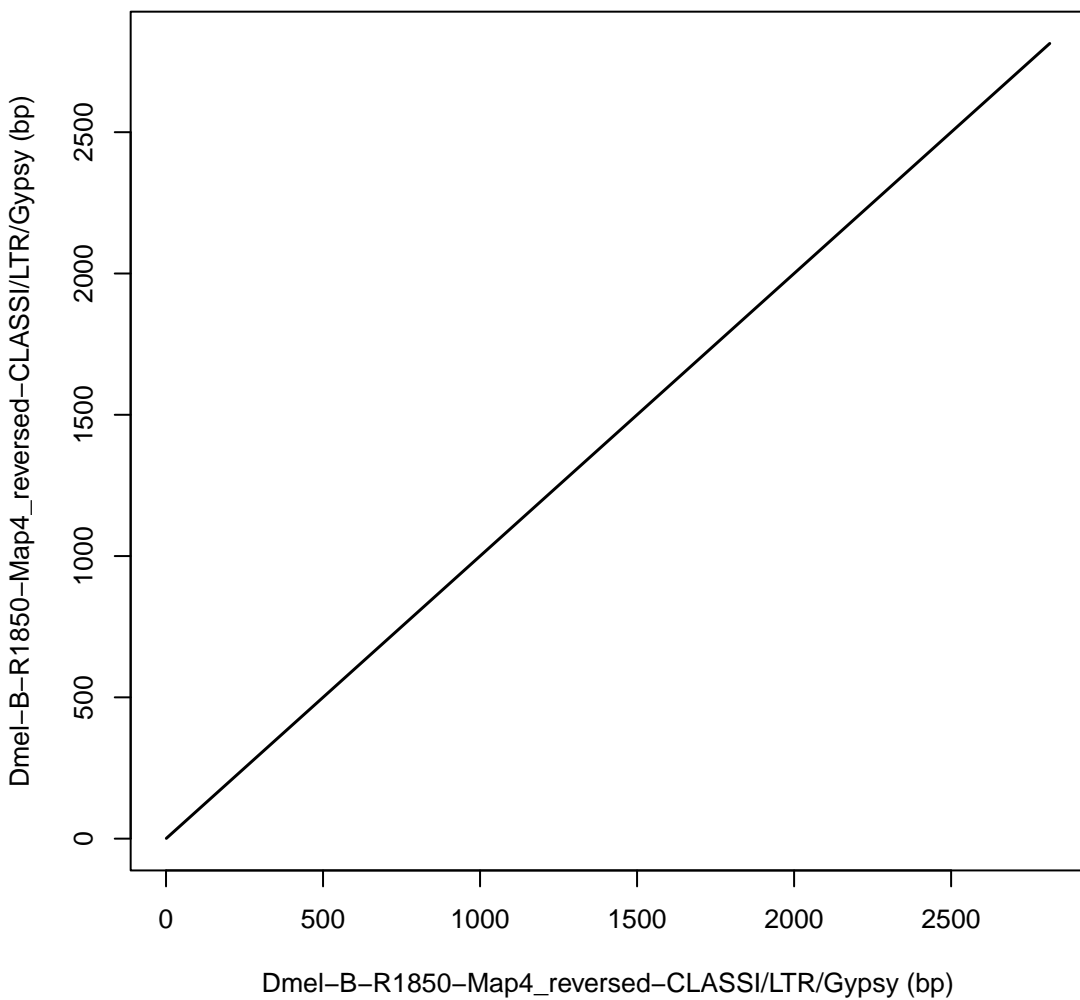
TE: Dmel-B-R1850-Map4\_reversed-CLASSI/LTR/Gypsy  
consensus size: 2814bp; fragments: 35; full length: 1 (>=2532.6bp)



TE consensus genomic coverage



TE consensus self dotplot (blastn)



TE consensus structure and protein hits

