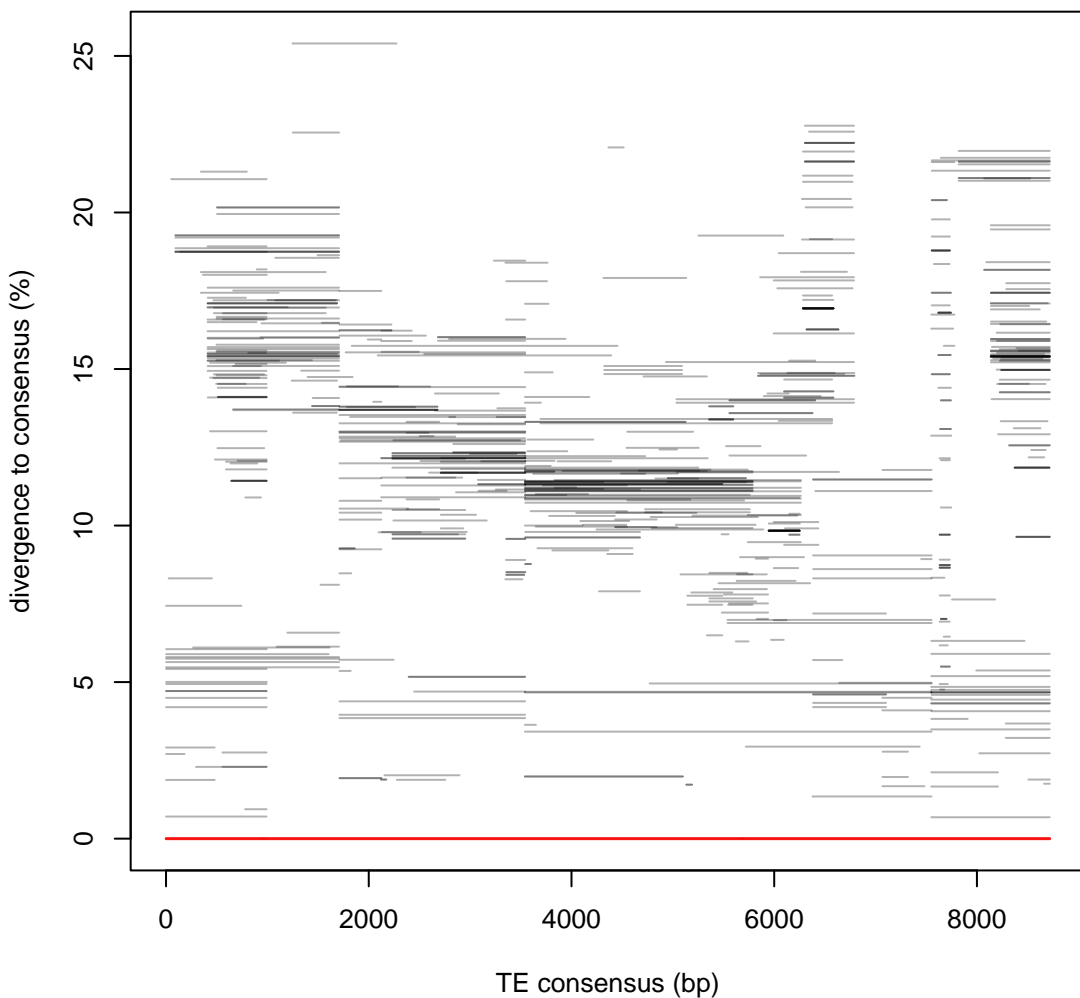
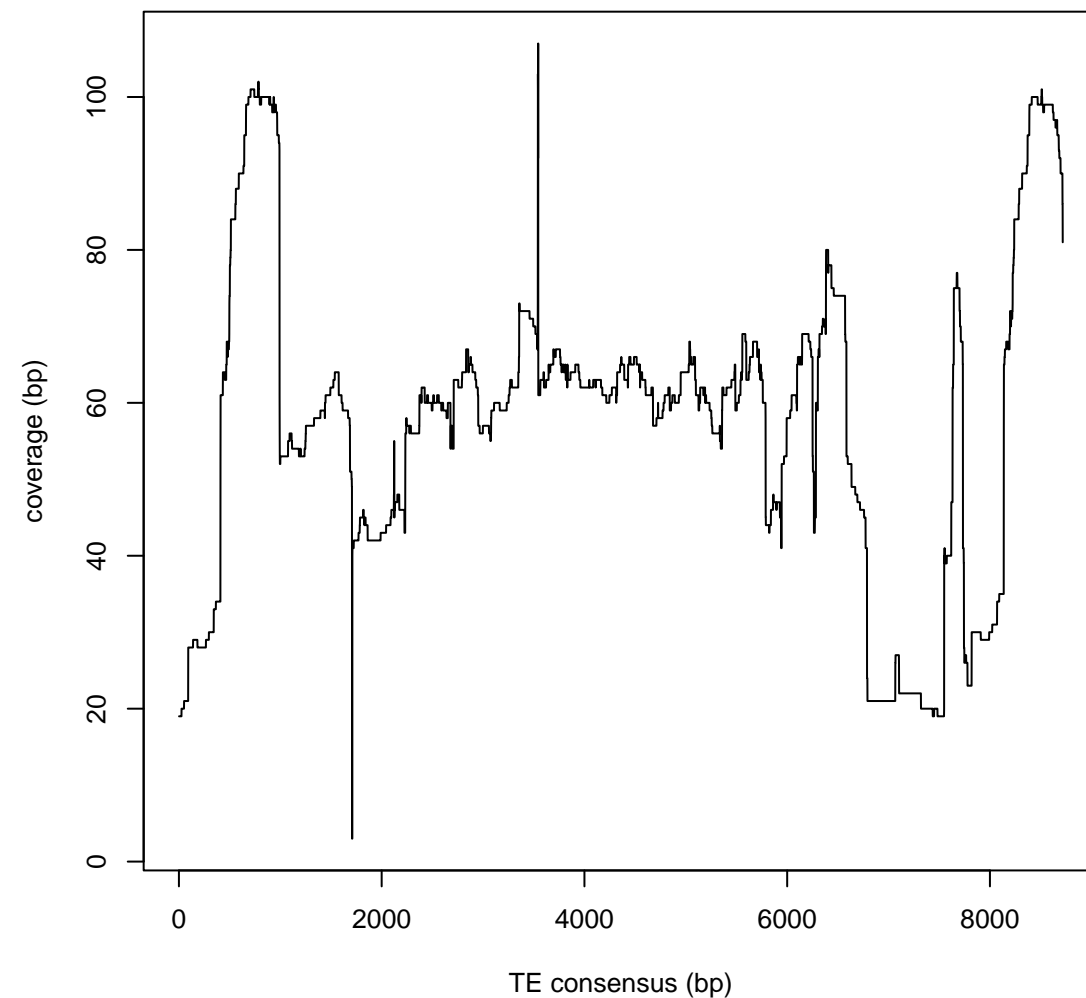


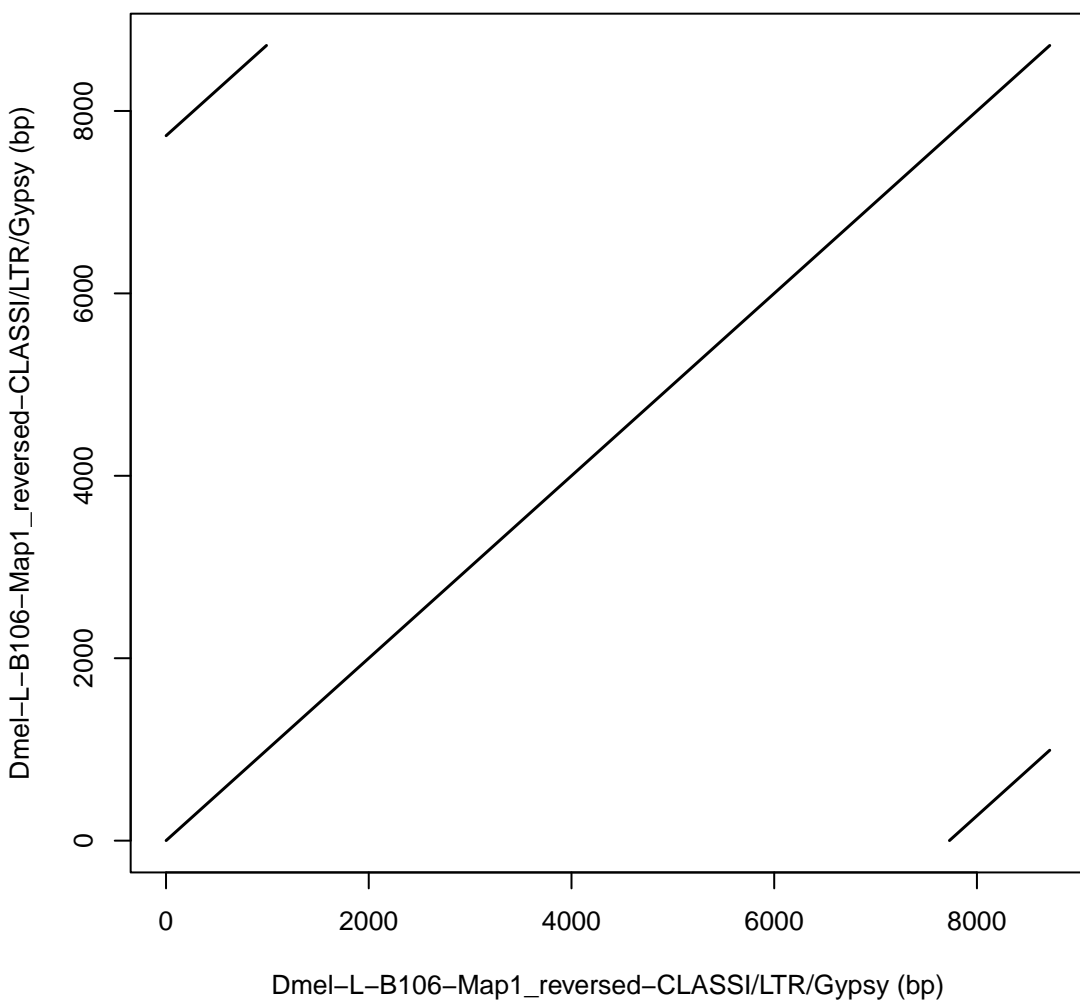
TE: Dmel-L-B106-Map1_reversed-CLASSI/LTR/Gypsy
consensus size: 8718bp; fragments: 662; full length: 1 (>=7846.2bp)



TE consensus genomic coverage



TE consensus self dotplot (blastn)



TE consensus structure and protein hits

