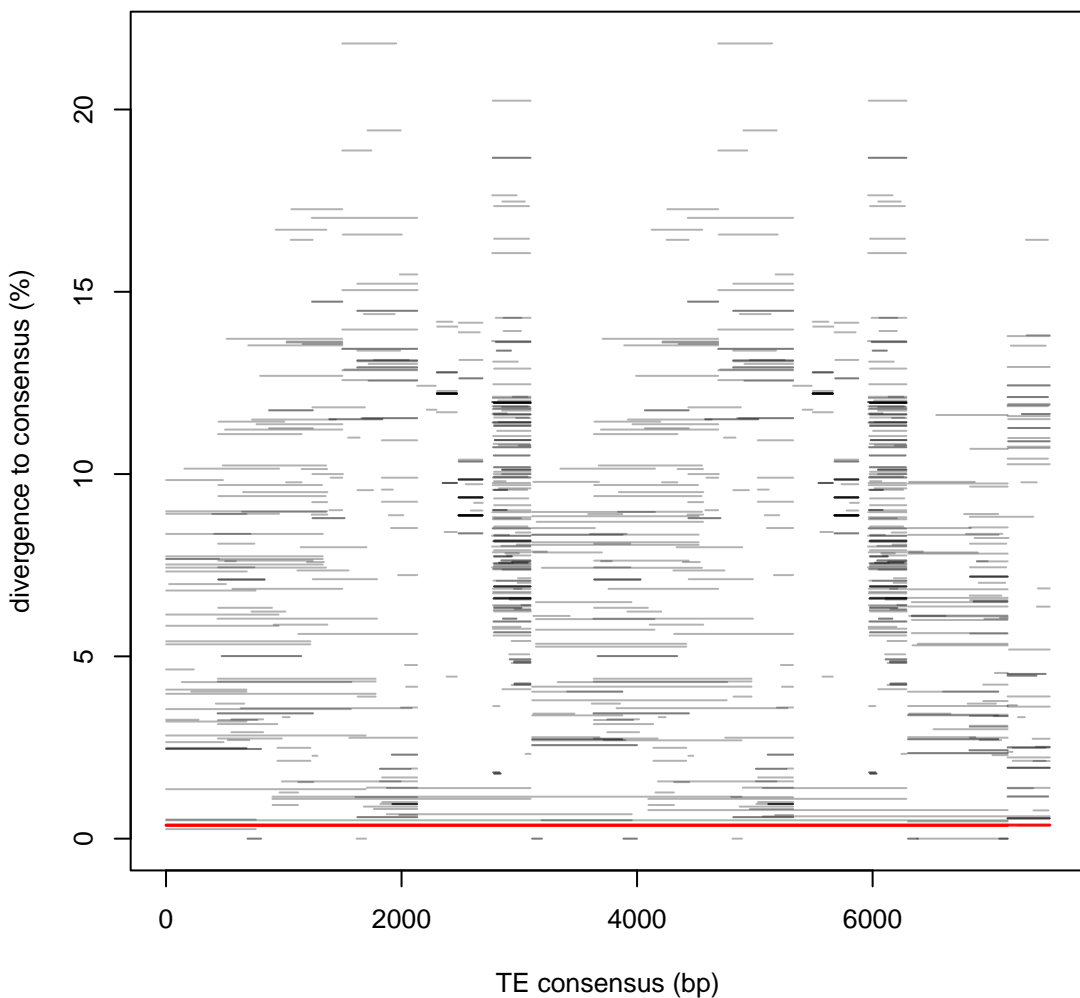
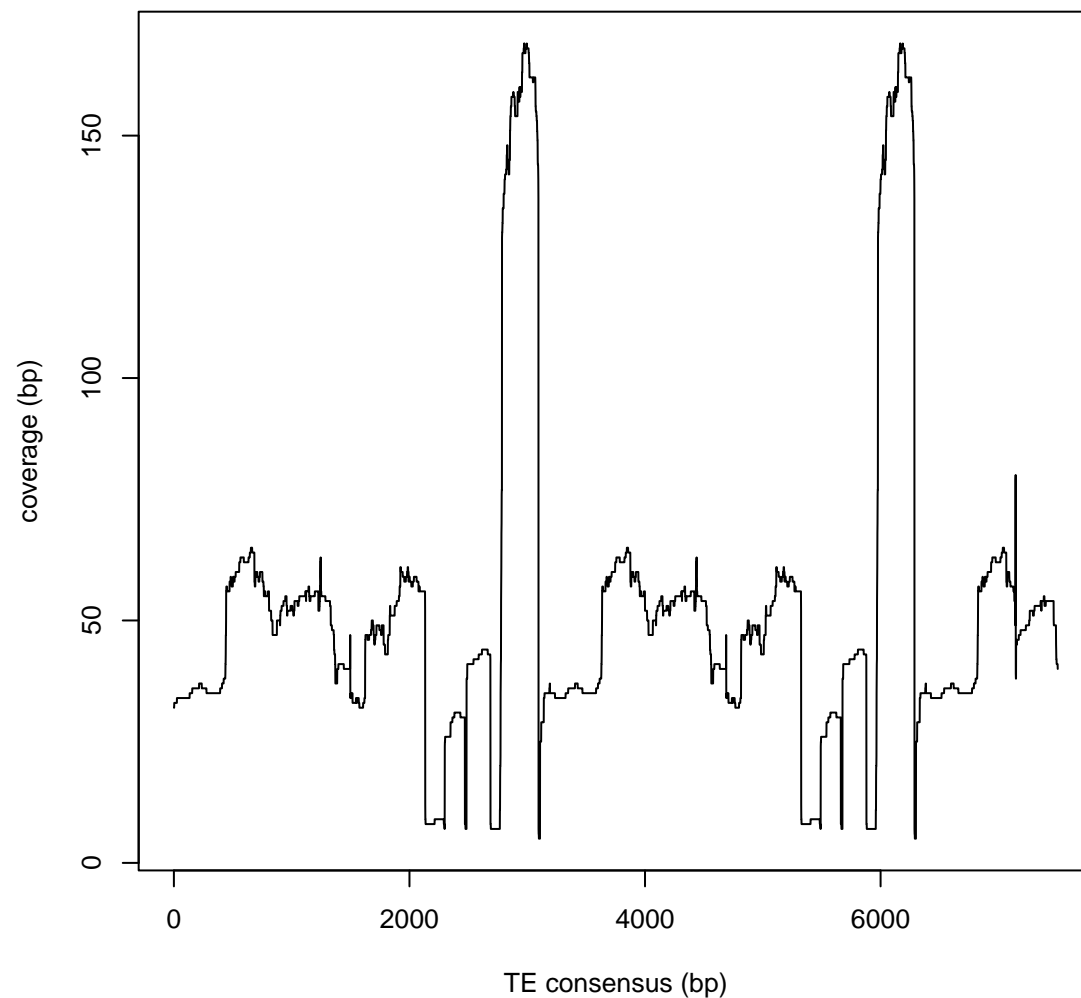


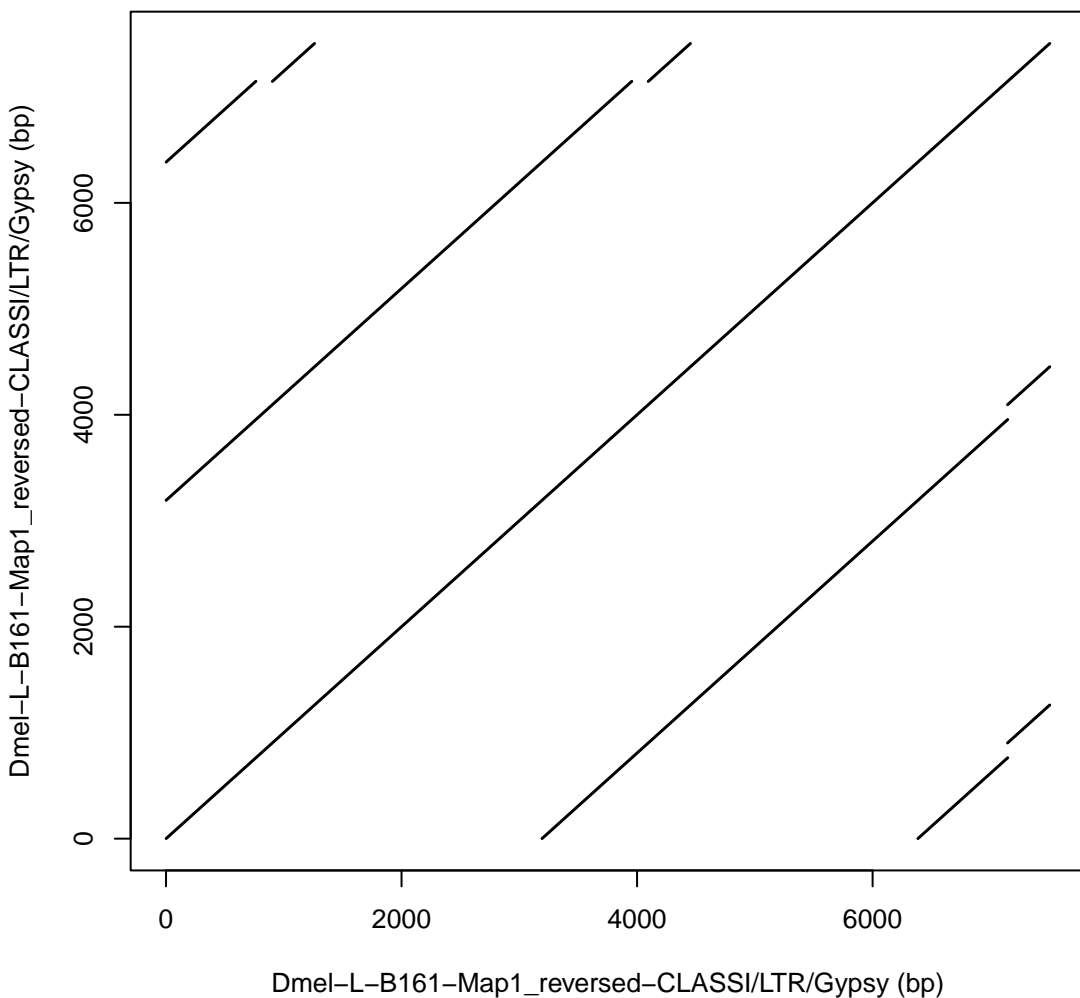
TE: Dmel-L-B161-Map1_reversed-CLASSI/LTR/Gypsy
consensus size: 7504bp; fragments: 996; full length: 2 (>=6753.6bp)



TE consensus genomic coverage



TE consensus self dotplot (blastn)



TE consensus structure and protein hits

