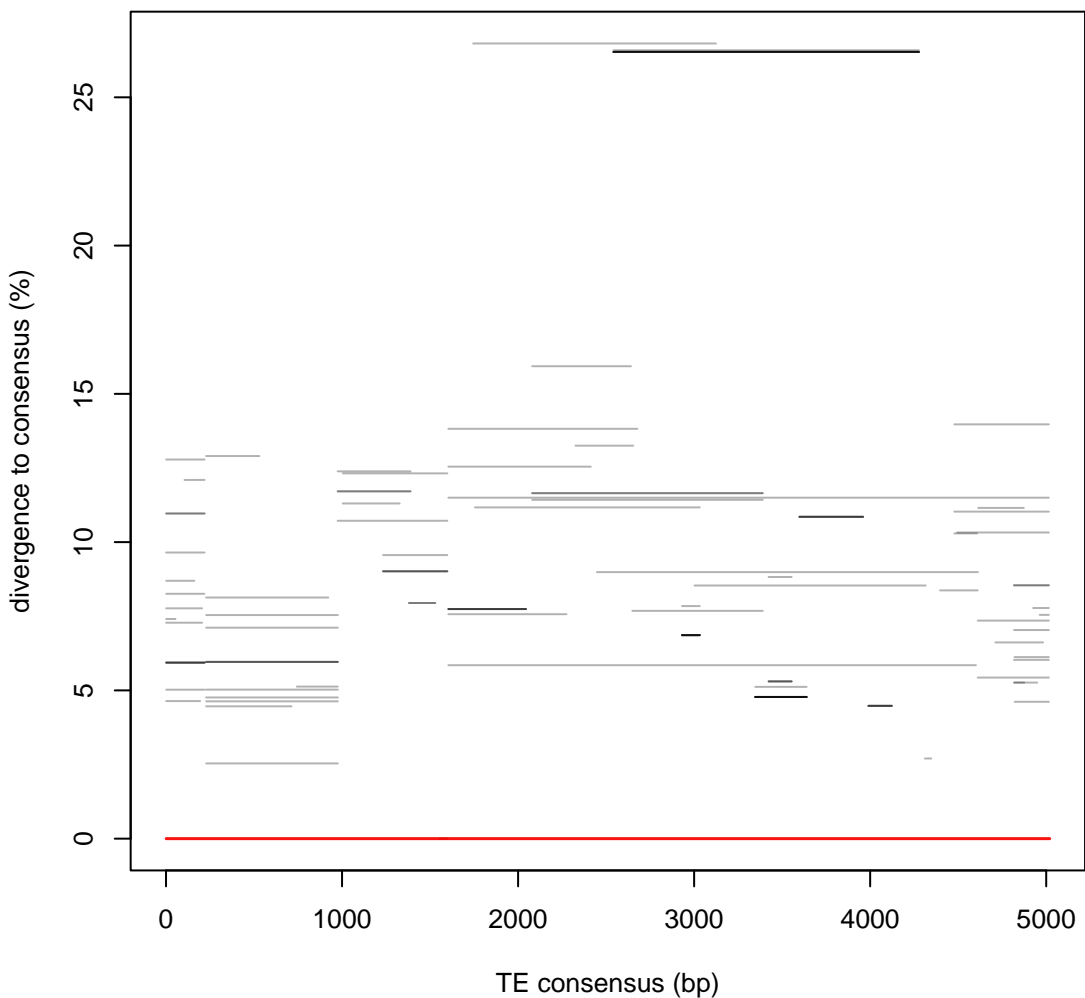
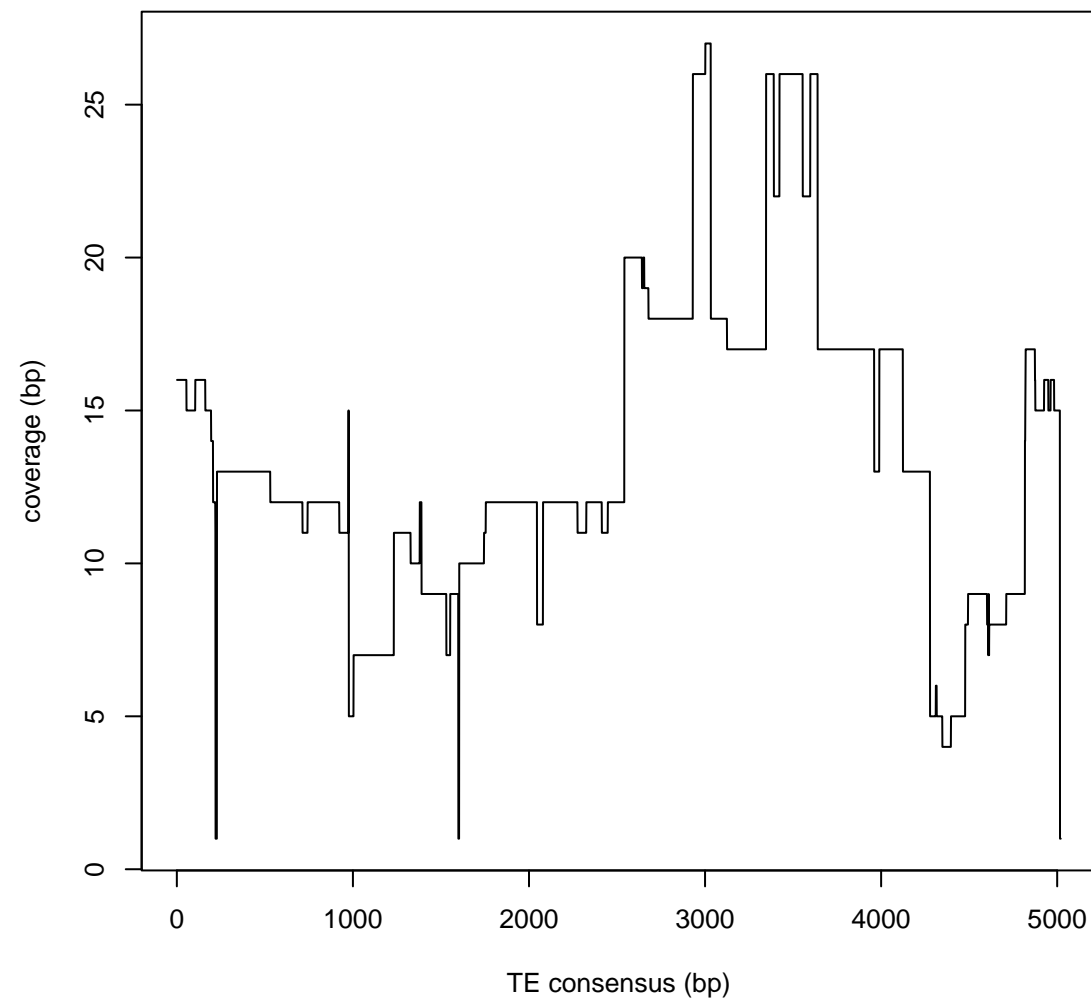


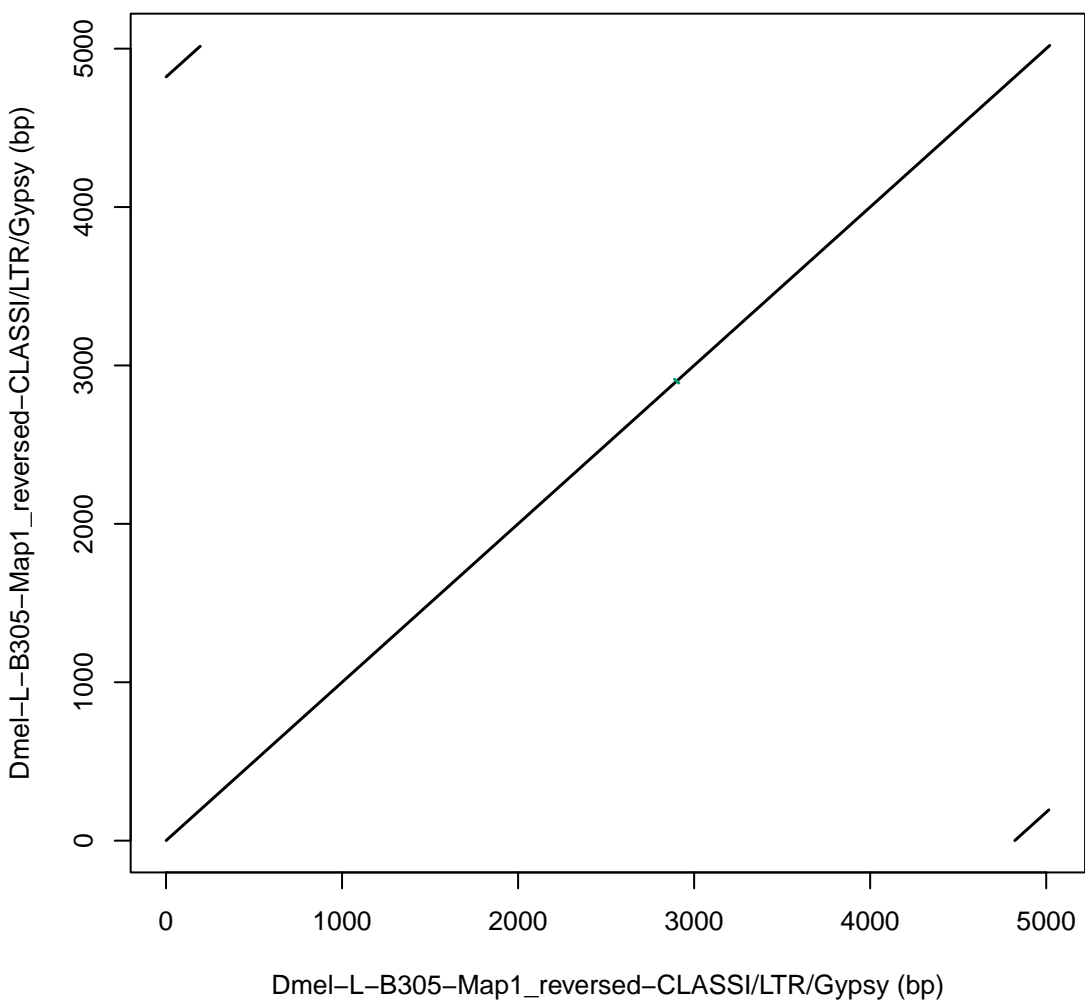
TE: Dmel-L-B305-Map1_reversed-CLASSI/LTR/Gypsy
consensus size: 5020bp; fragments: 120; full length: 1 (>=4518bp)



TE consensus genomic coverage



TE consensus self dotplot (blastn)



TE consensus structure and protein hits

