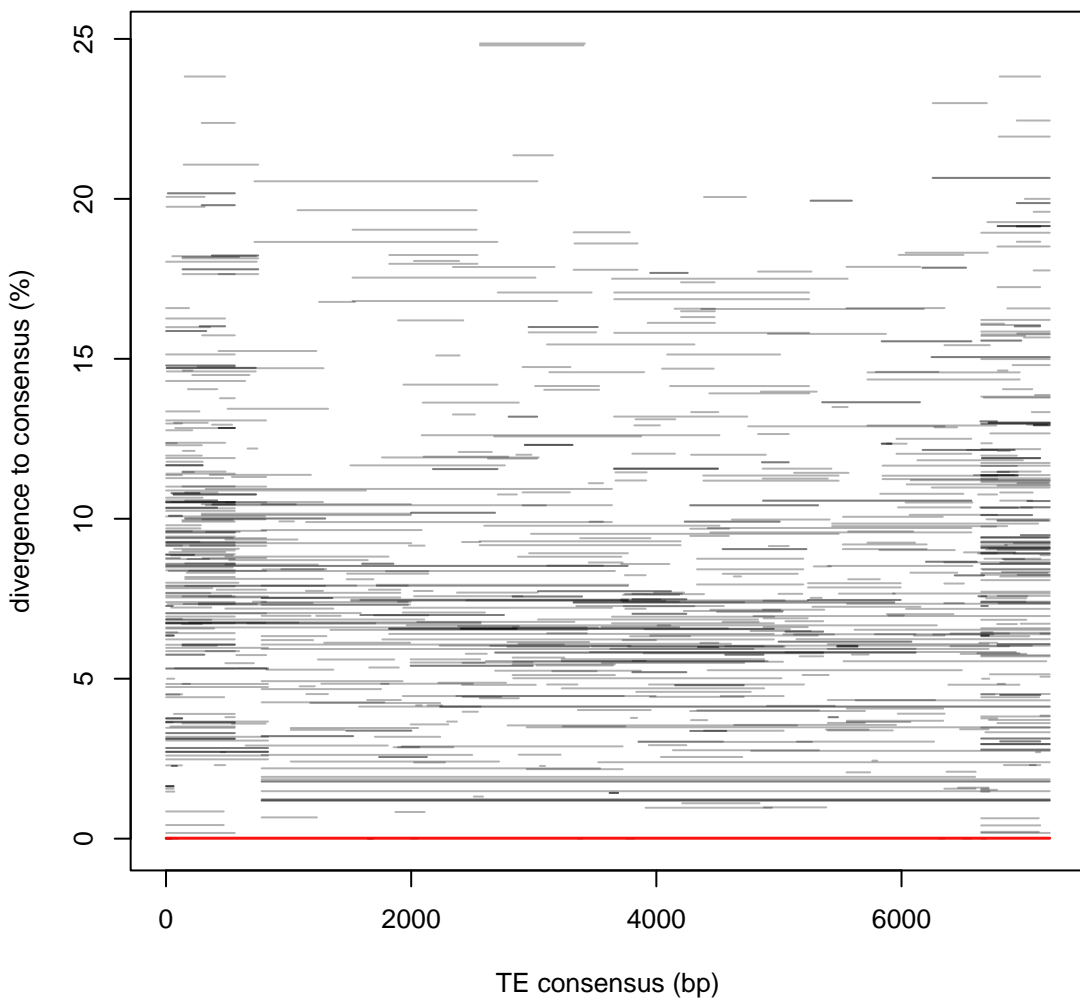
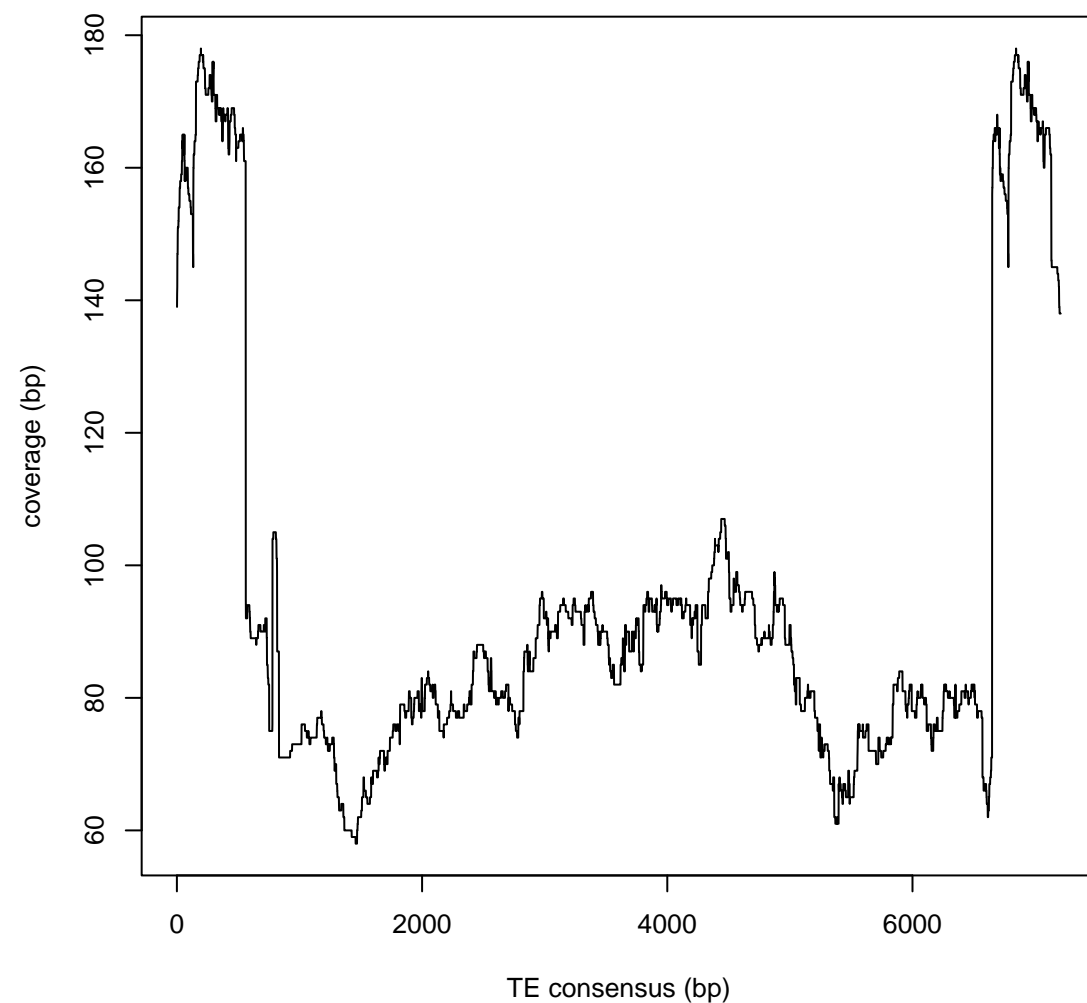


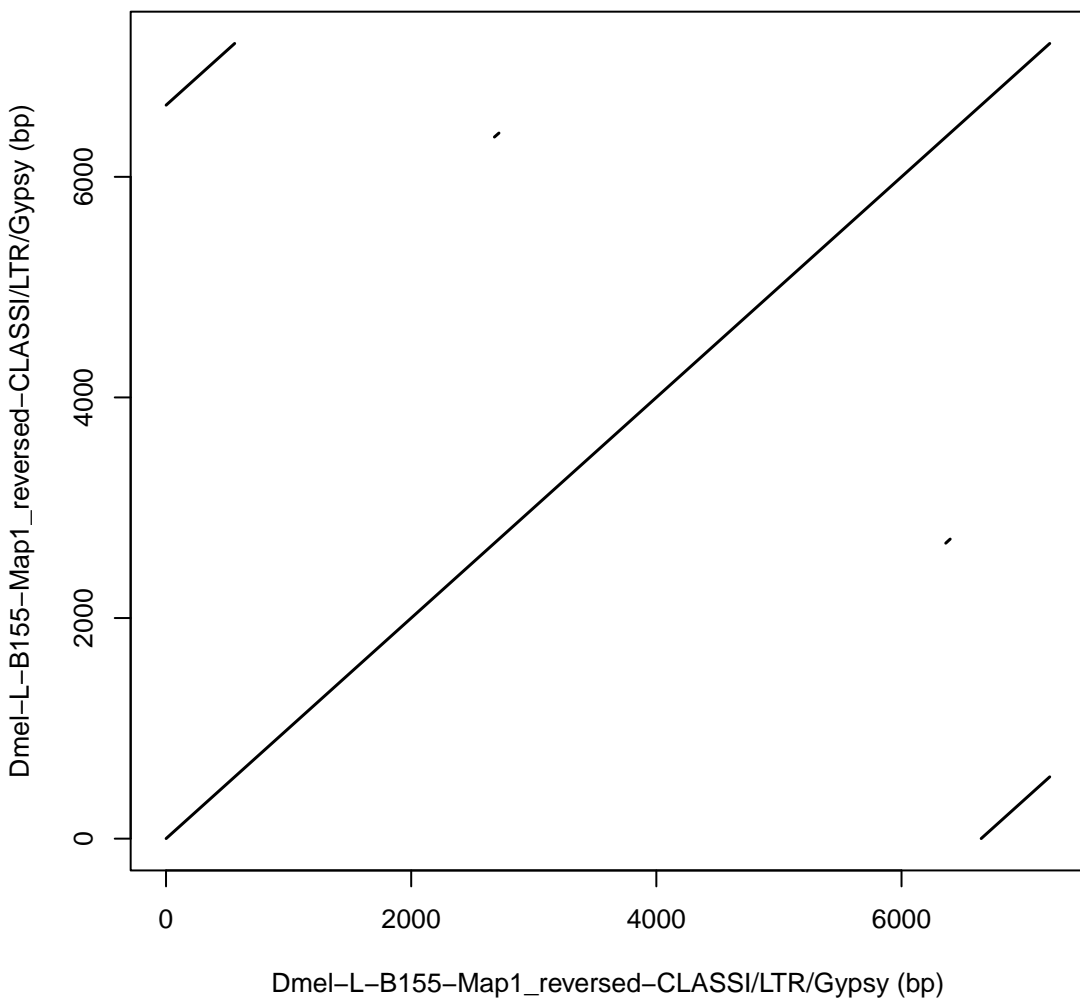
TE: Dmel-L-B155-Map1_reversed-CLASSI/LTR/Gypsy
consensus size: 7209bp; fragments: 936; full length: 1 (>=6488.1bp)



TE consensus genomic coverage



TE consensus self dotplot (blastn)



TE consensus structure and protein hits

