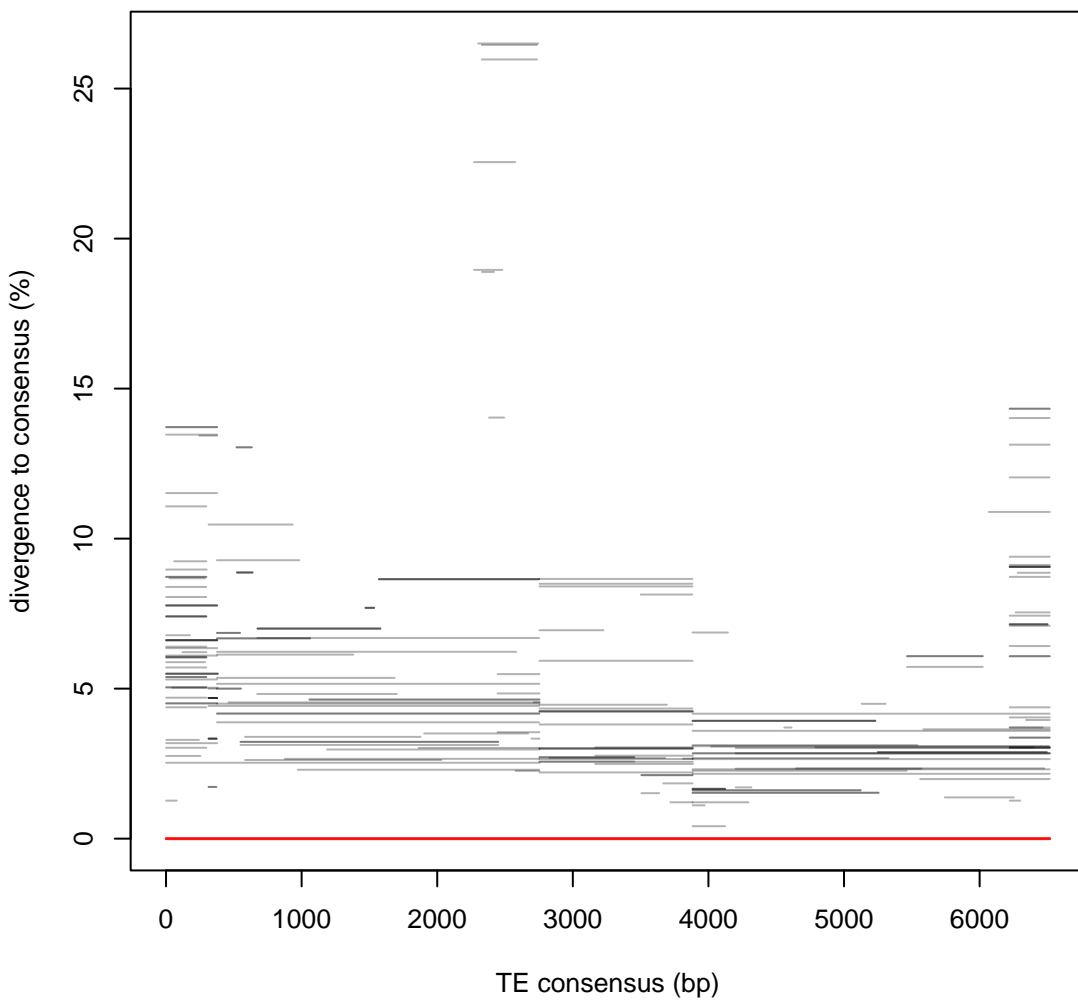
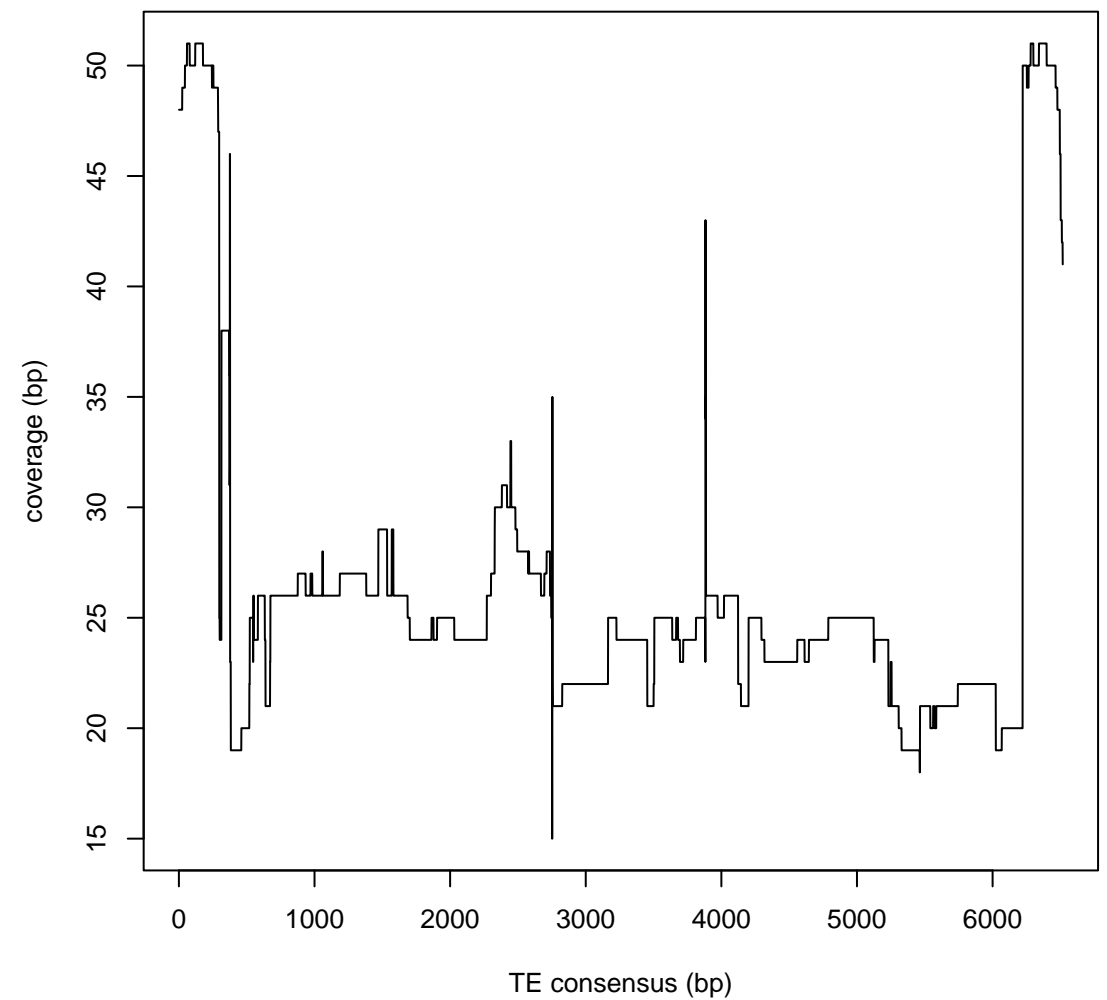


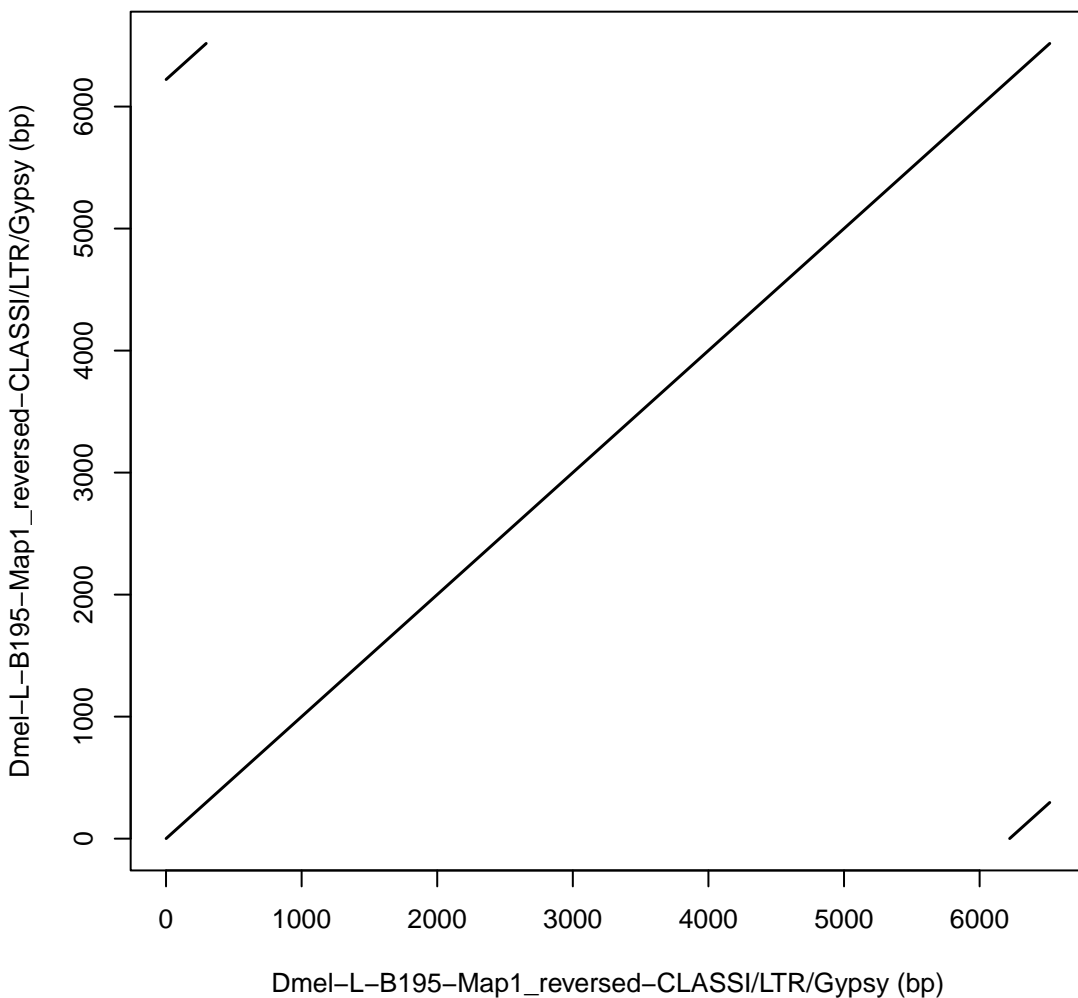
TE: Dmel-L-B195-Map1\_reversed-CLASSI/LTR/Gypsy  
consensus size: 6517bp; fragments: 231; full length: 1 (>=5865.3bp)



TE consensus genomic coverage



TE consensus self dotplot (blastn)



TE consensus structure and protein hits

