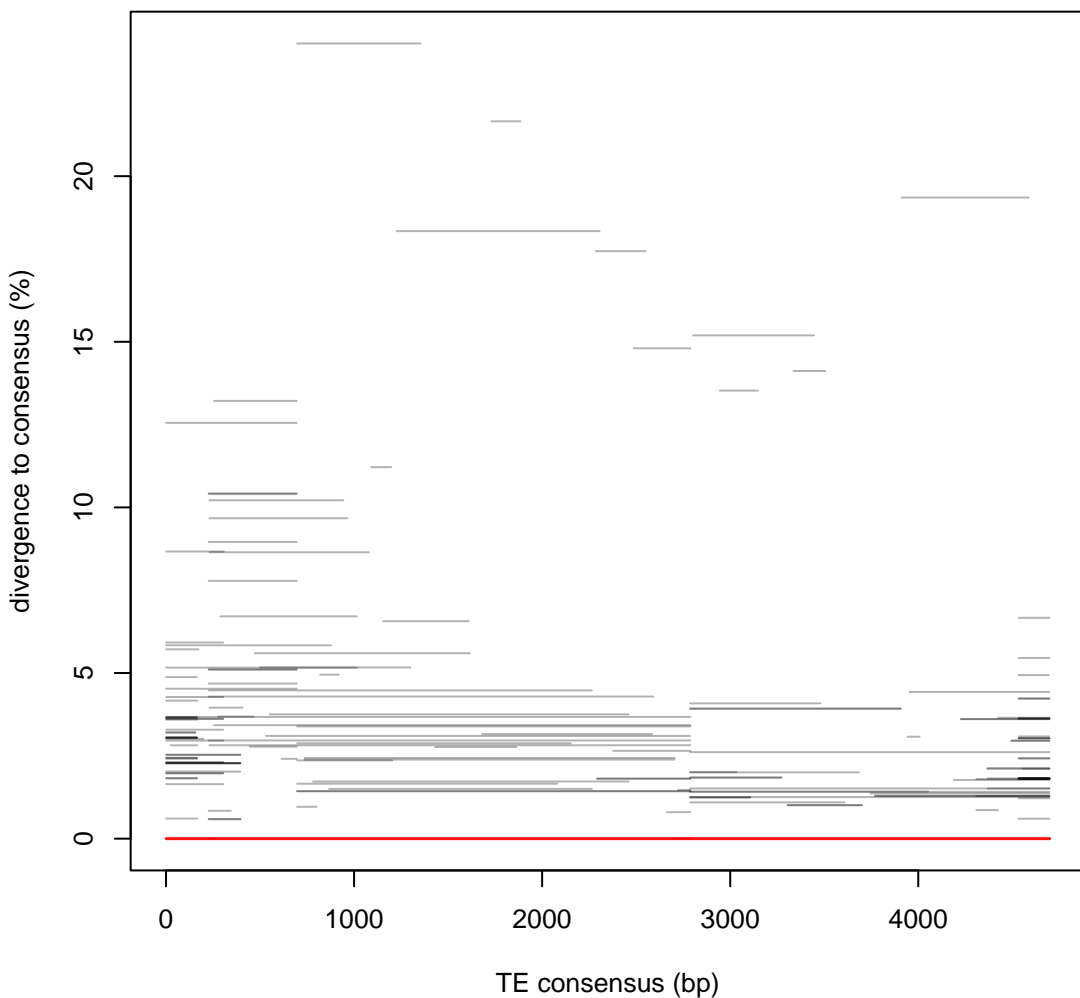
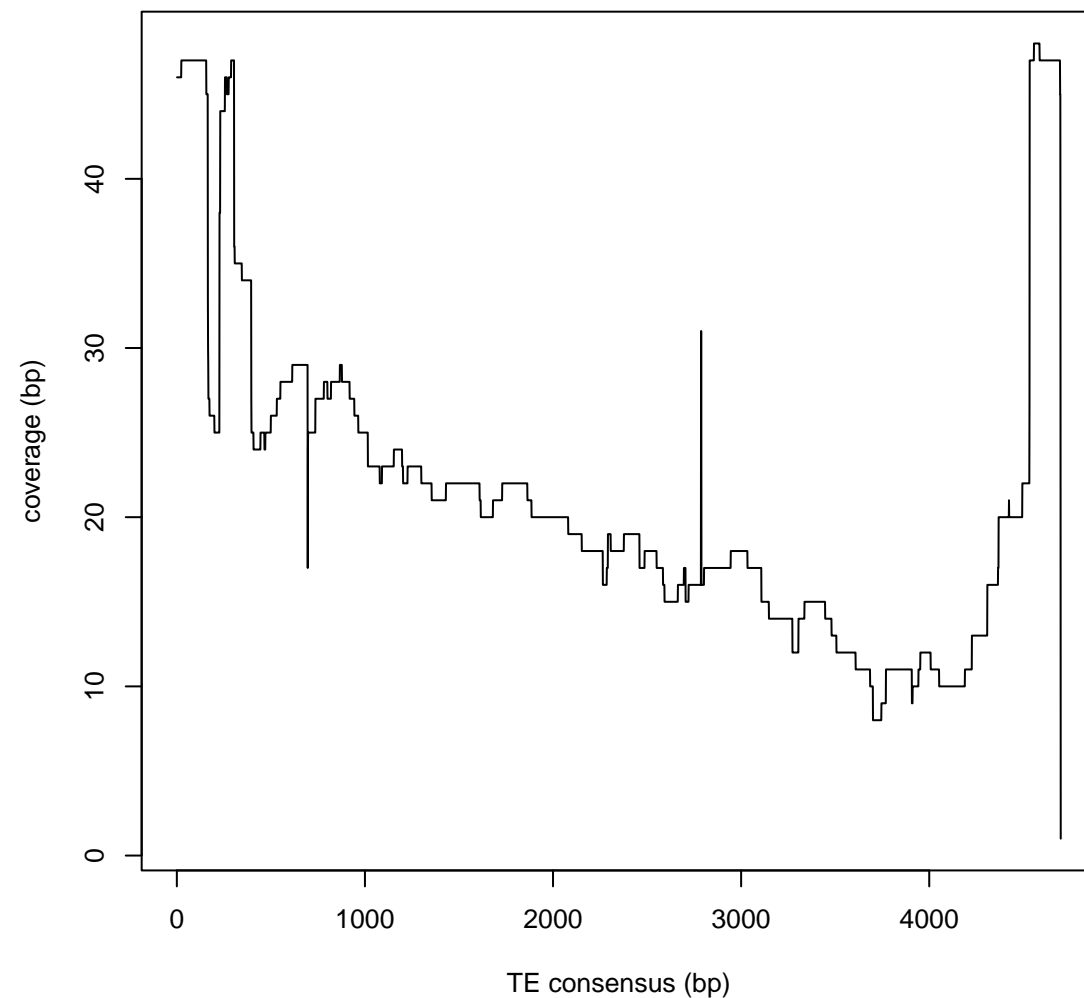


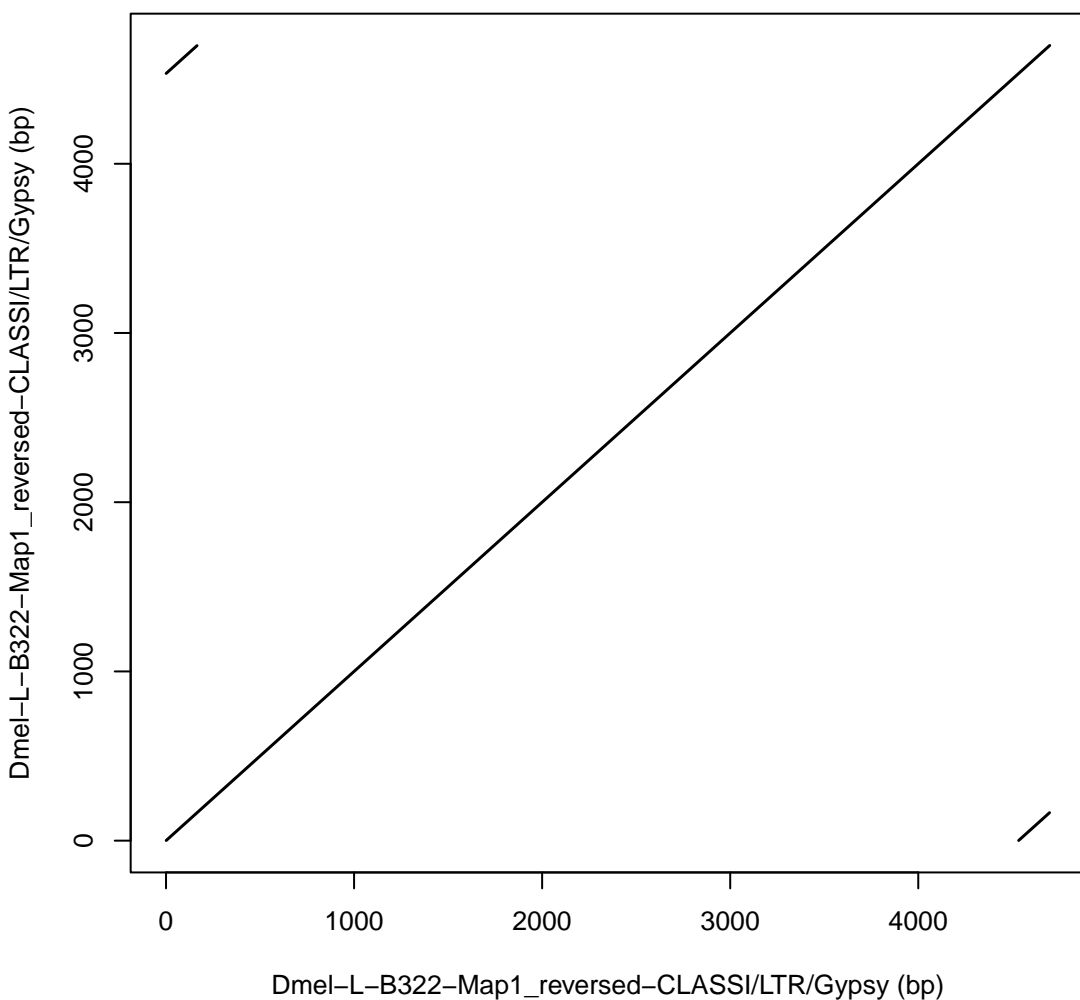
TE: Dmel-L-B322-Map1_reversed-CLASSI/LTR/Gypsy
consensus size: 4699bp; fragments: 168; full length: 1 (>=4229.1bp)



TE consensus genomic coverage



TE consensus self dotplot (blastn)



TE consensus structure and protein hits

