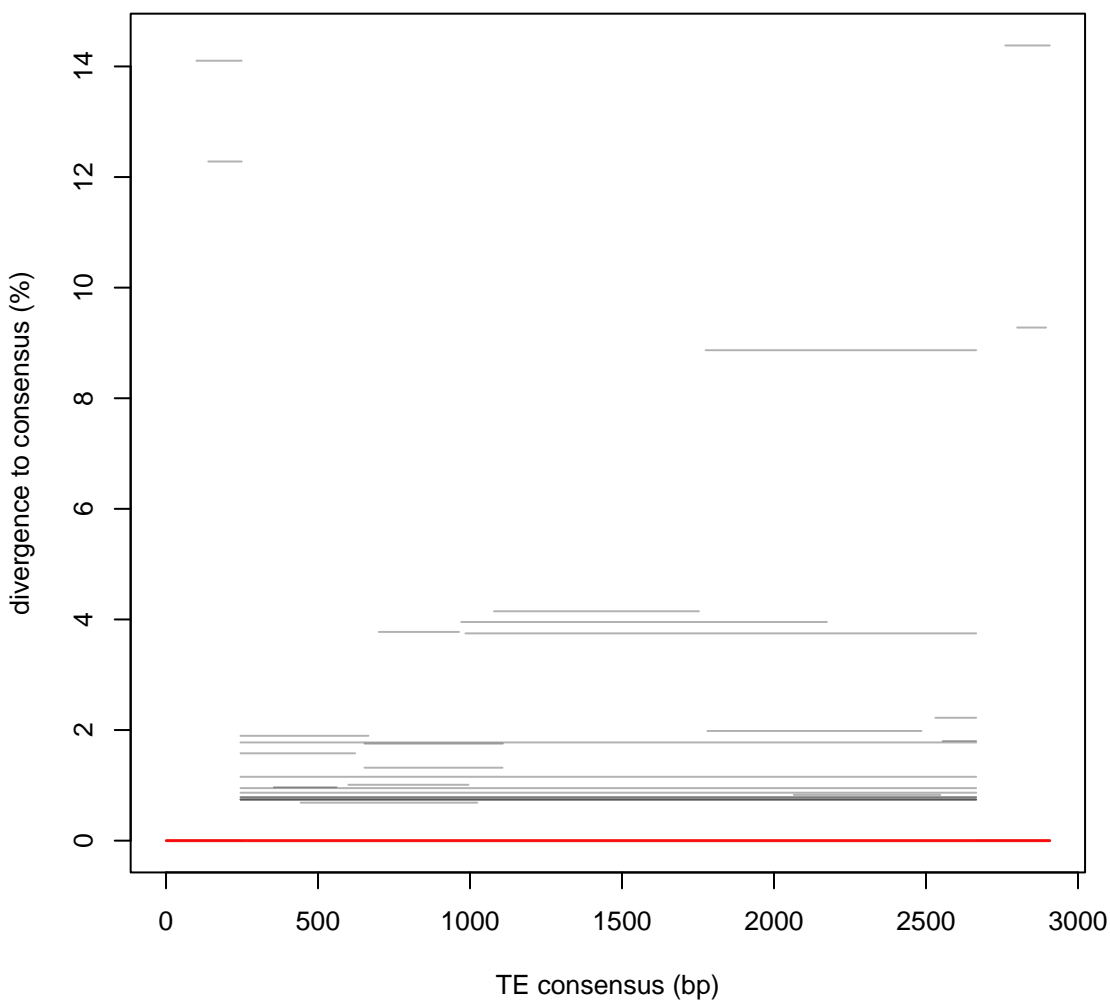
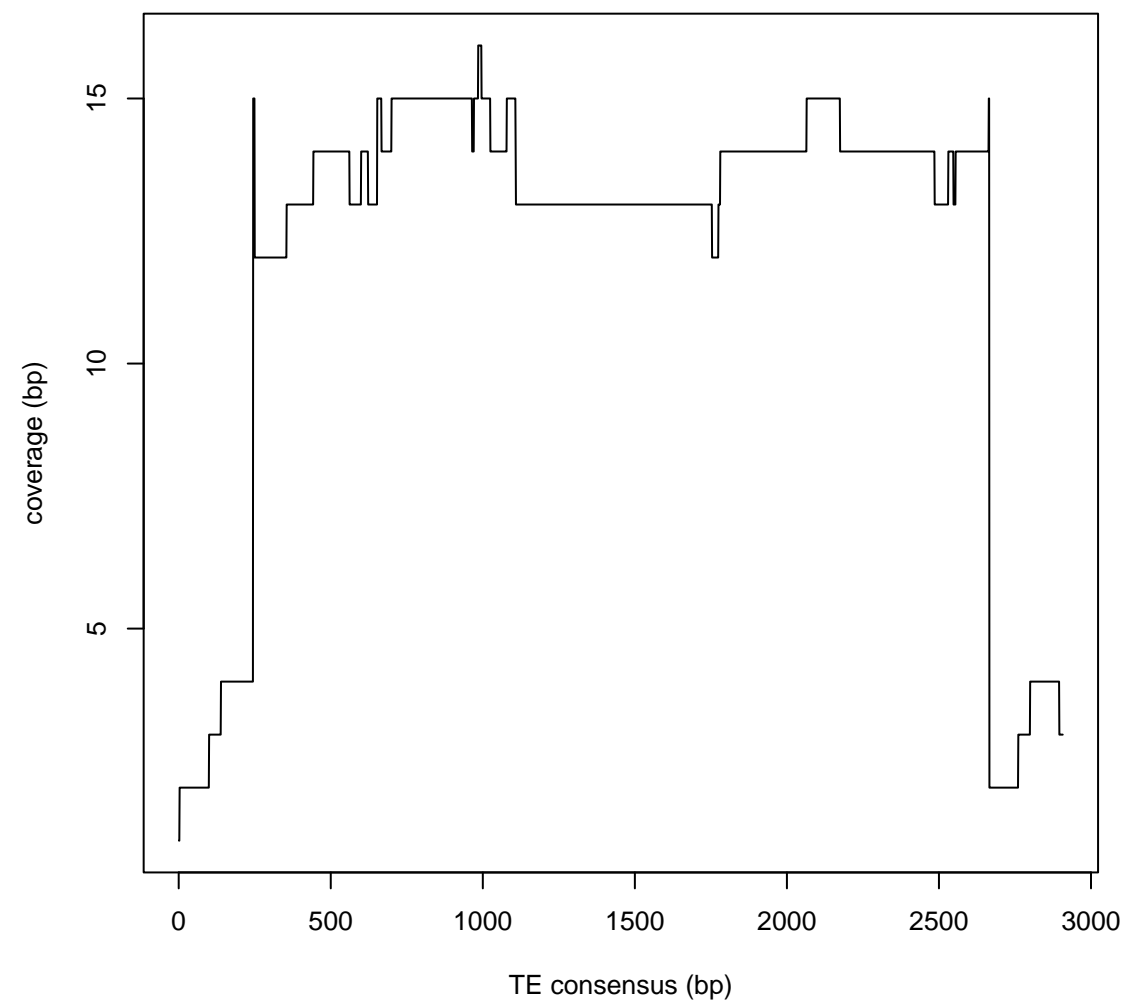


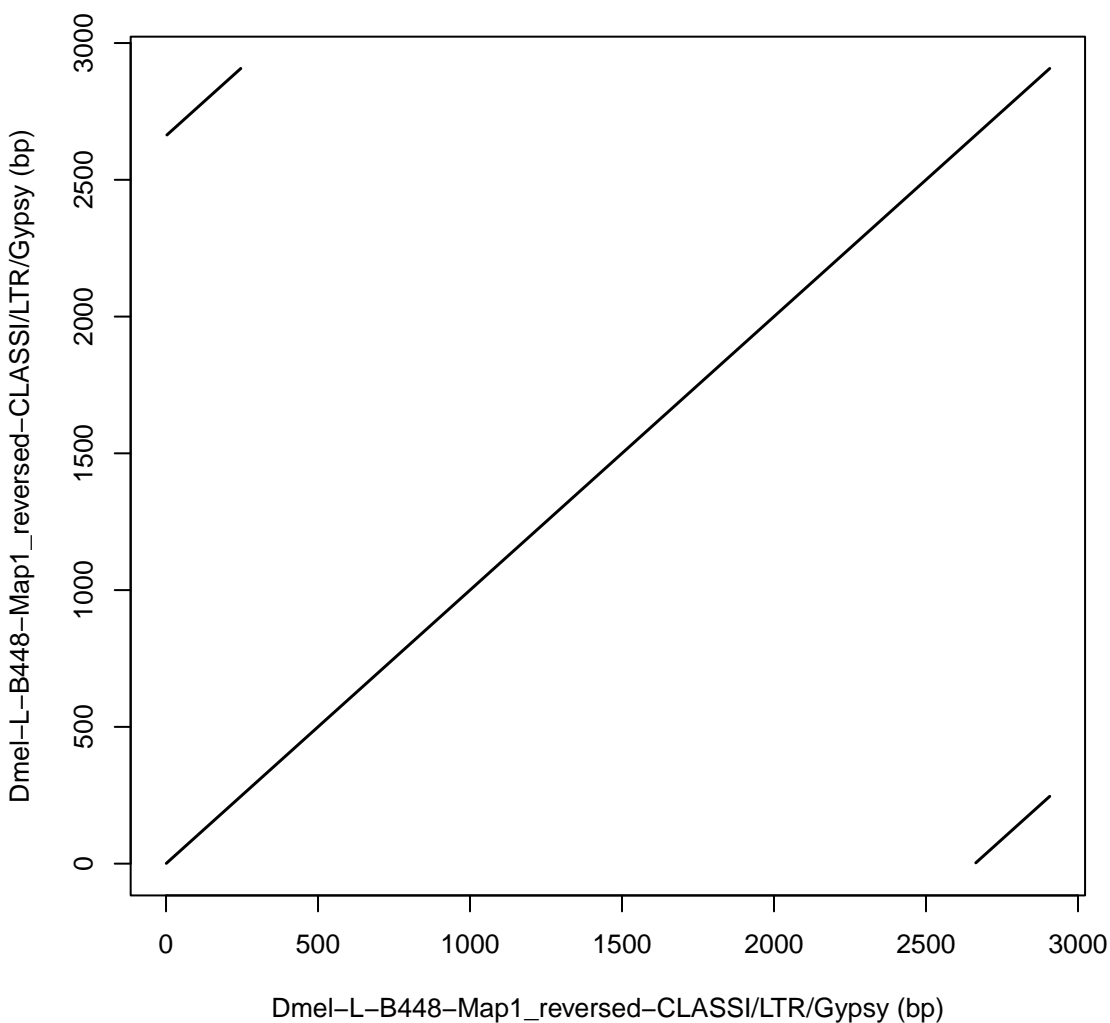
TE: Dmel-L-B448-Map1_reversed-CLASSI/LTR/Gypsy
consensus size: 2907bp; fragments: 32; full length: 1 (>=2616.3bp)



TE consensus genomic coverage



TE consensus self dotplot (blastn)



TE consensus structure and protein hits

