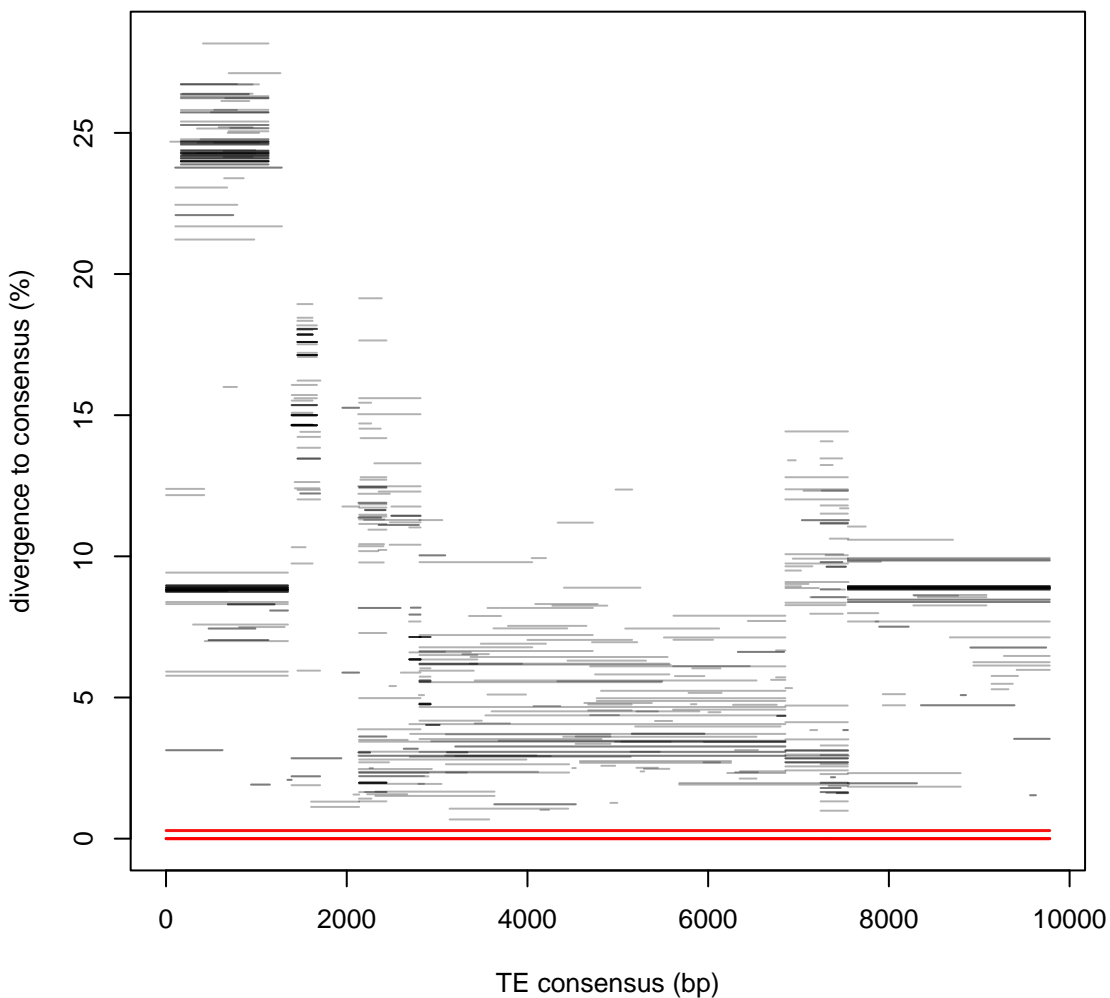
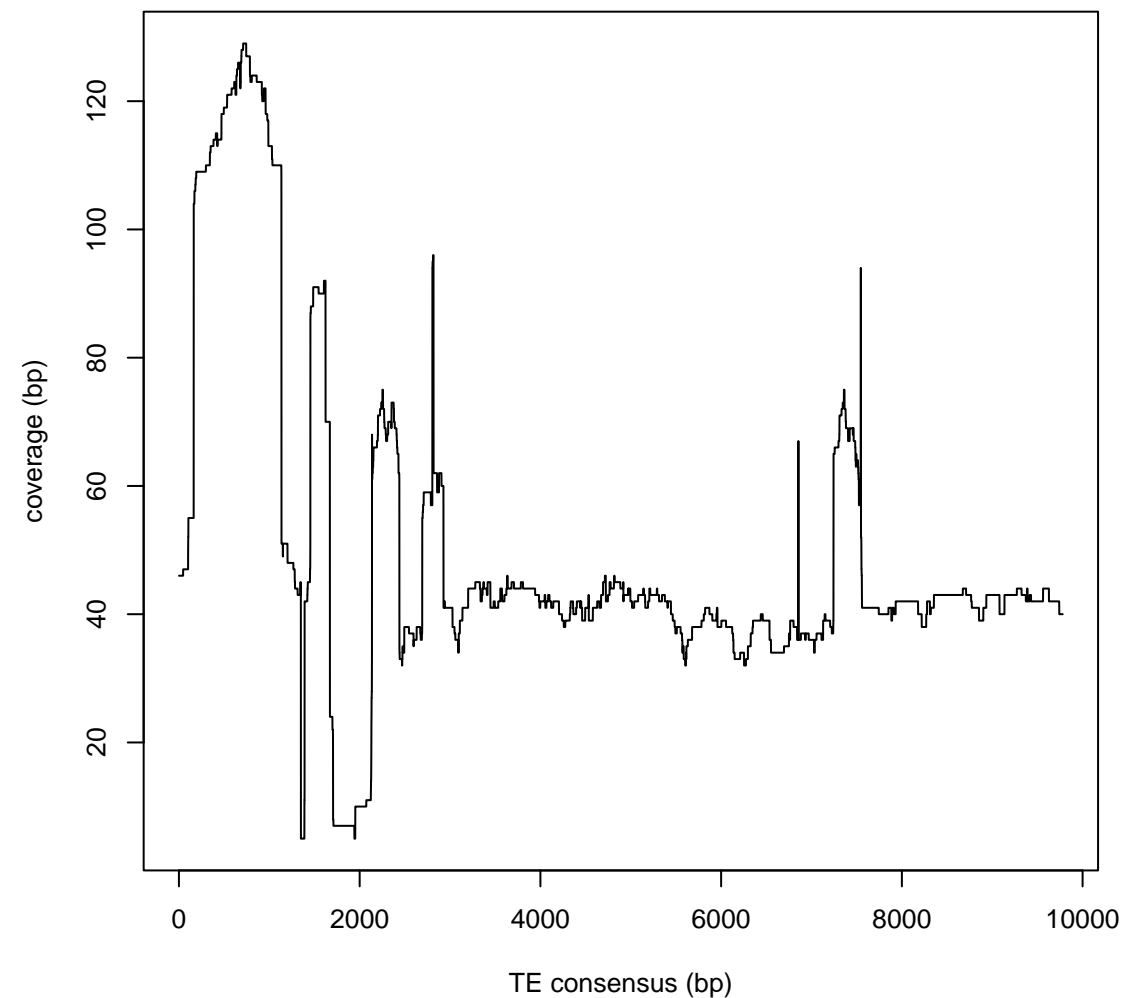


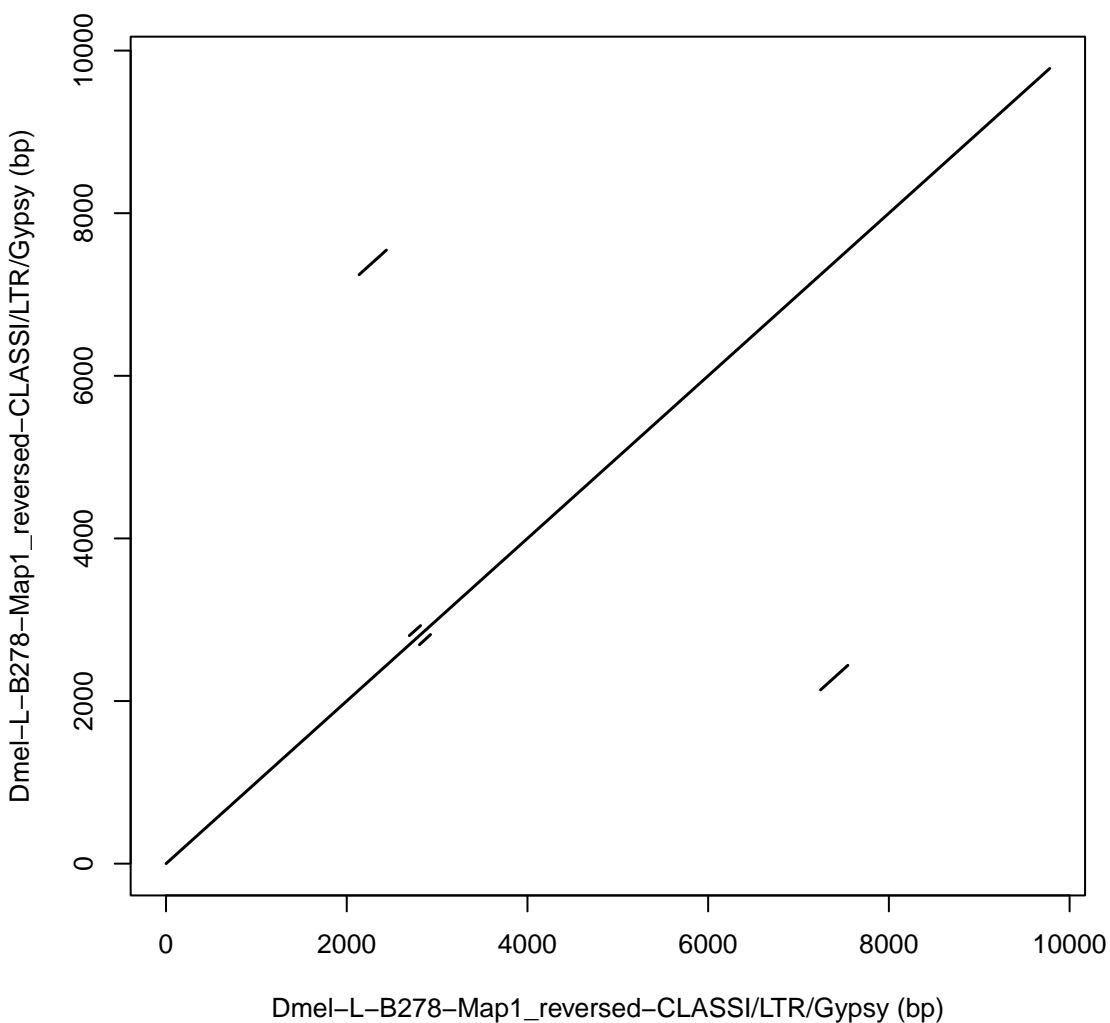
TE: Dmel-L-B278-Map1_reversed-CLASSI/LTR/Gypsy
consensus size: 9780bp; fragments: 648; full length: 3 (>=8802bp)



TE consensus genomic coverage



TE consensus self dotplot (blastn)



TE consensus structure and protein hits

