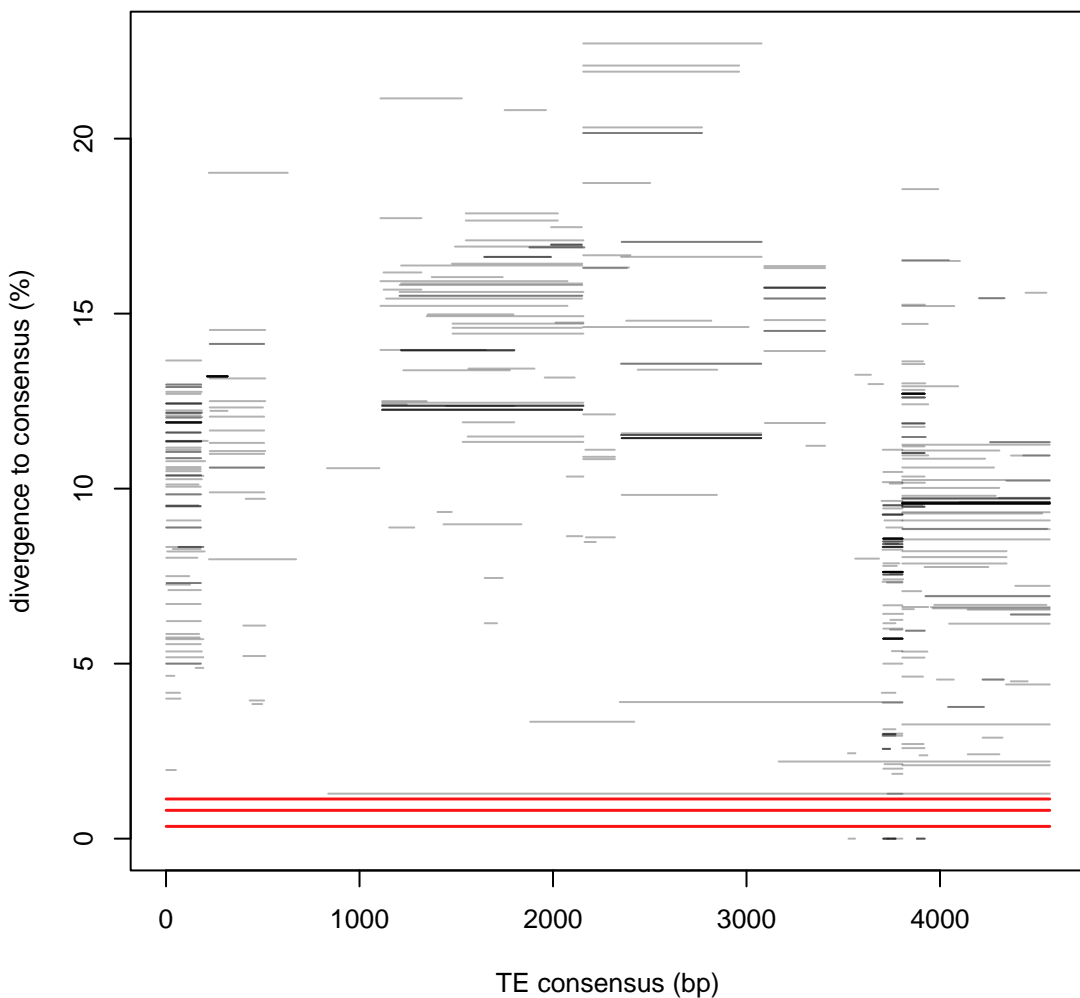
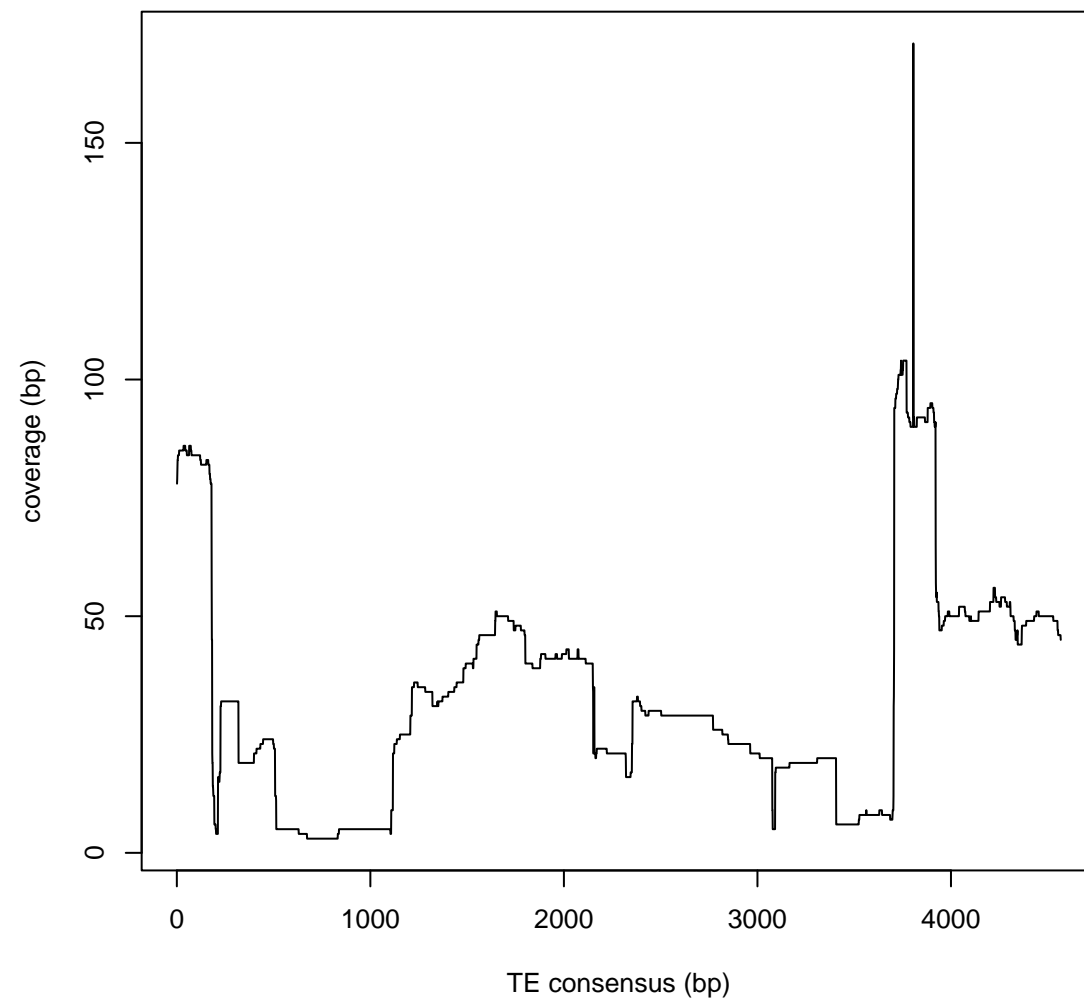


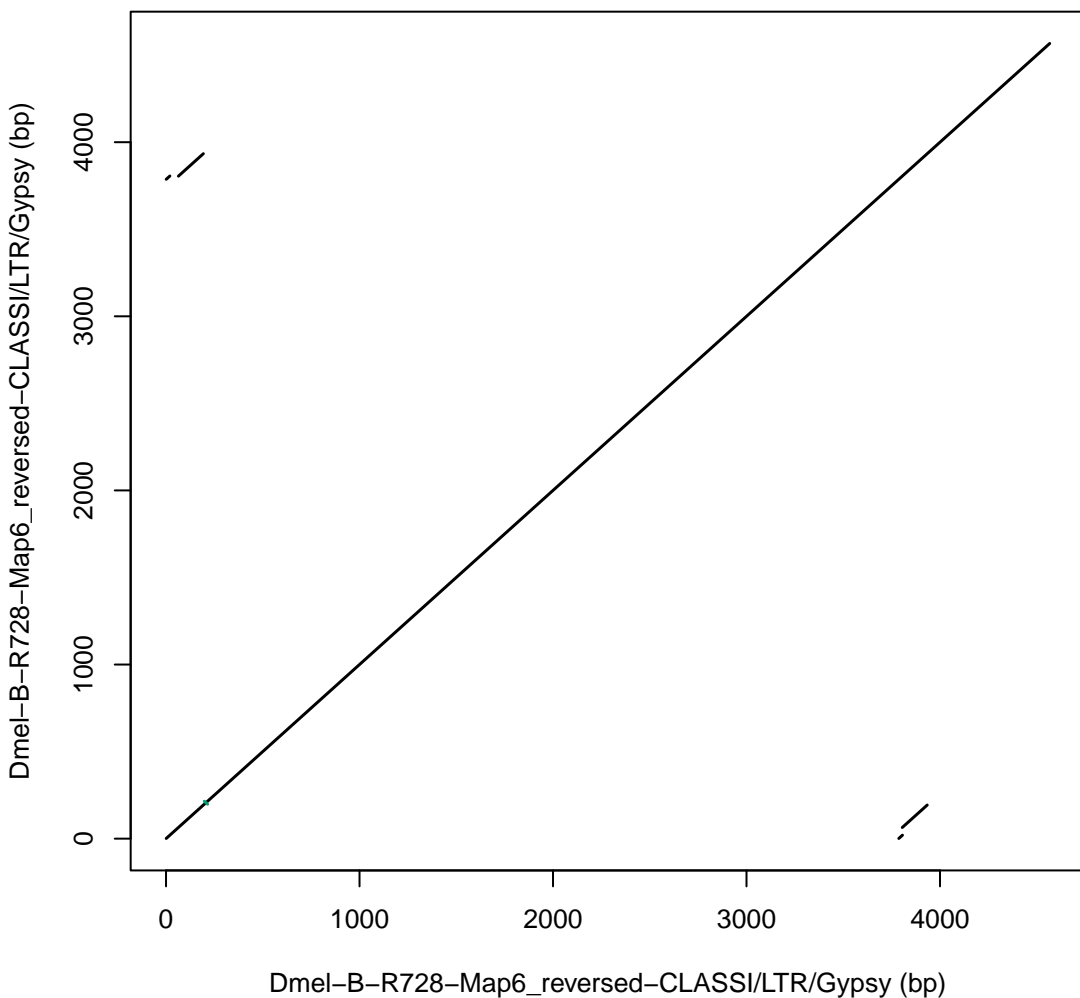
TE: Dmel-B-R728-Map6_reversed-CLASSI/LTR/Gypsy
consensus size: 4567bp; fragments: 470; full length: 3 (>=4110.3bp)



TE consensus genomic coverage



TE consensus self dotplot (blastn)



TE consensus structure and protein hits

