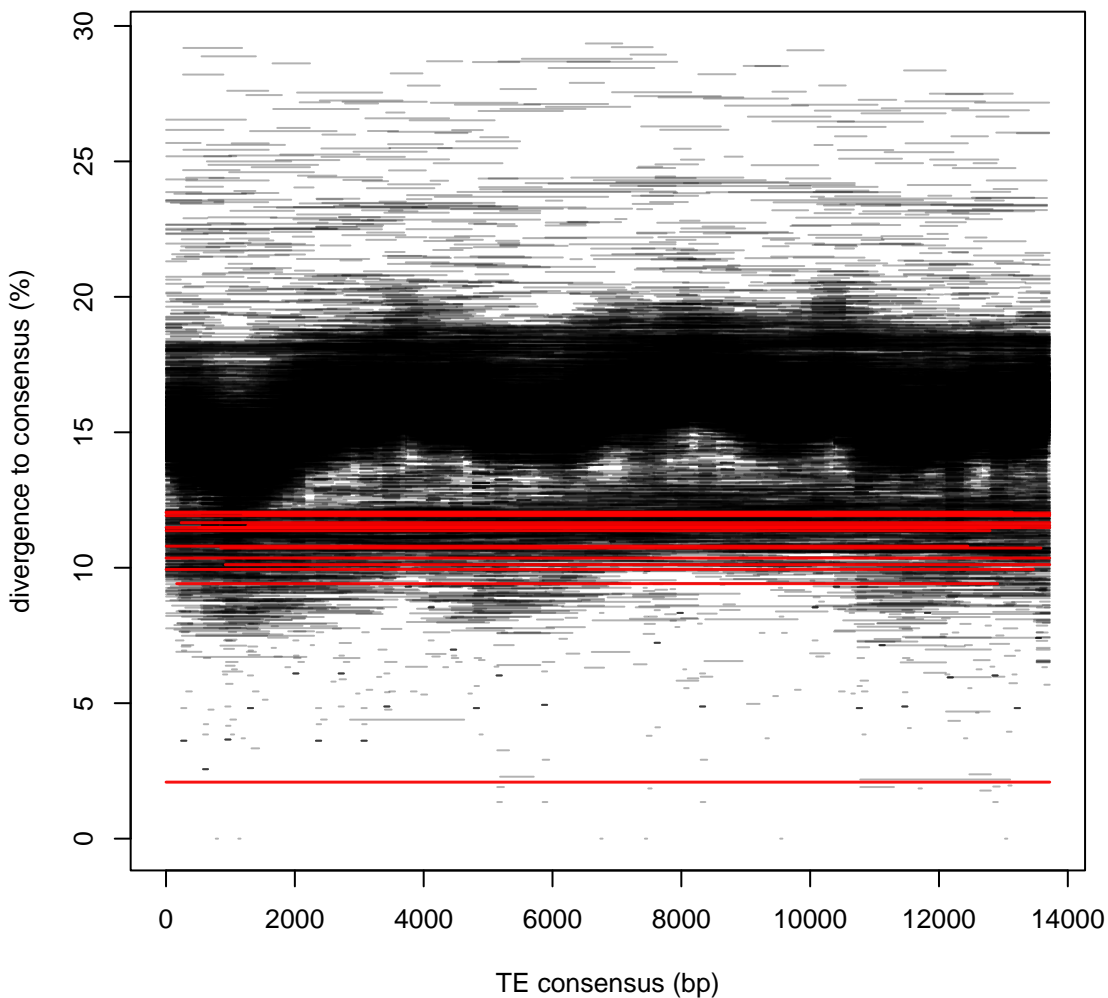
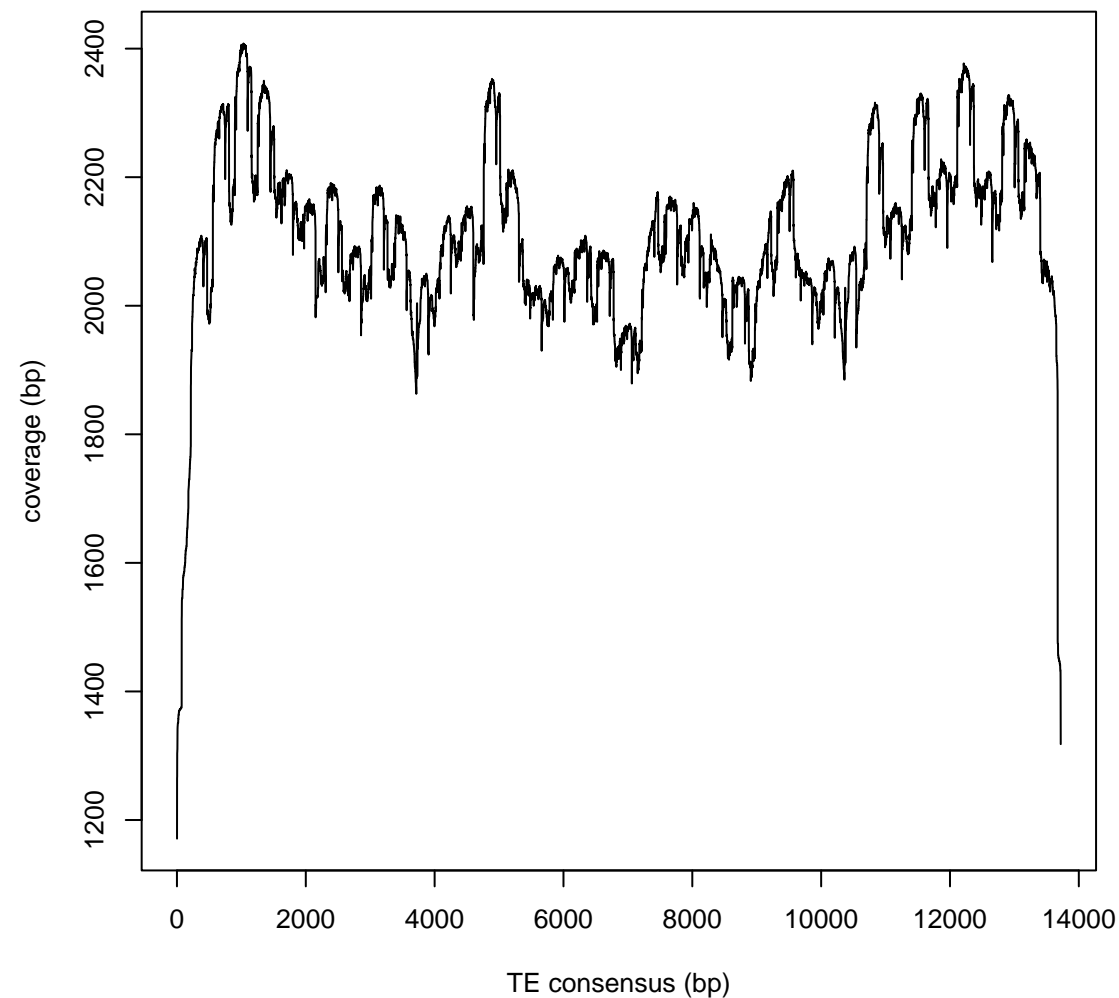


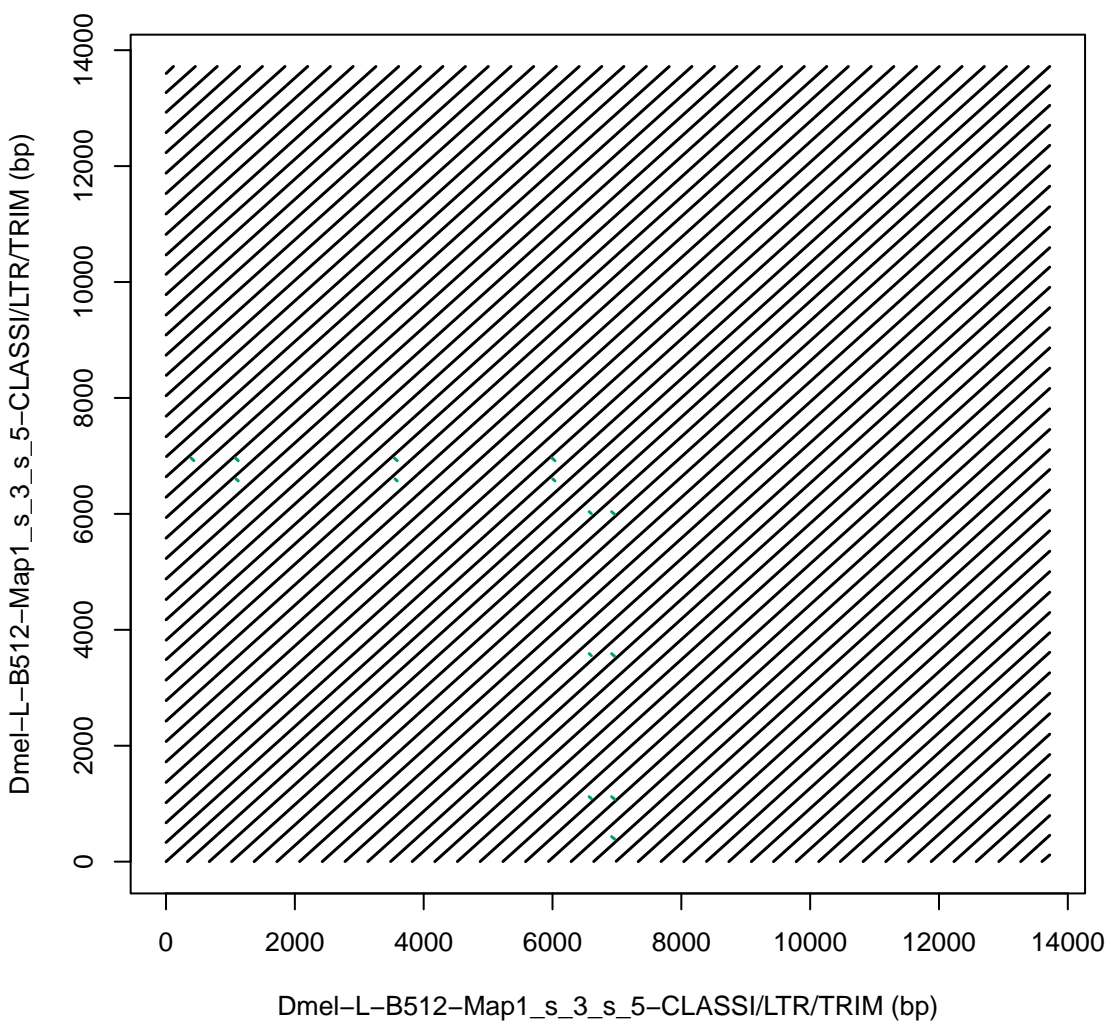
TE: Dmel-L-B512-Map1_s_3_s_5-CLASSI/LTR/TRIM
consensus size: 13719bp; fragments: 26820; full length: 17 (>=12347.1bp)



TE consensus genomic coverage



TE consensus self dotplot (blastn)



TE consensus structure and protein hits

