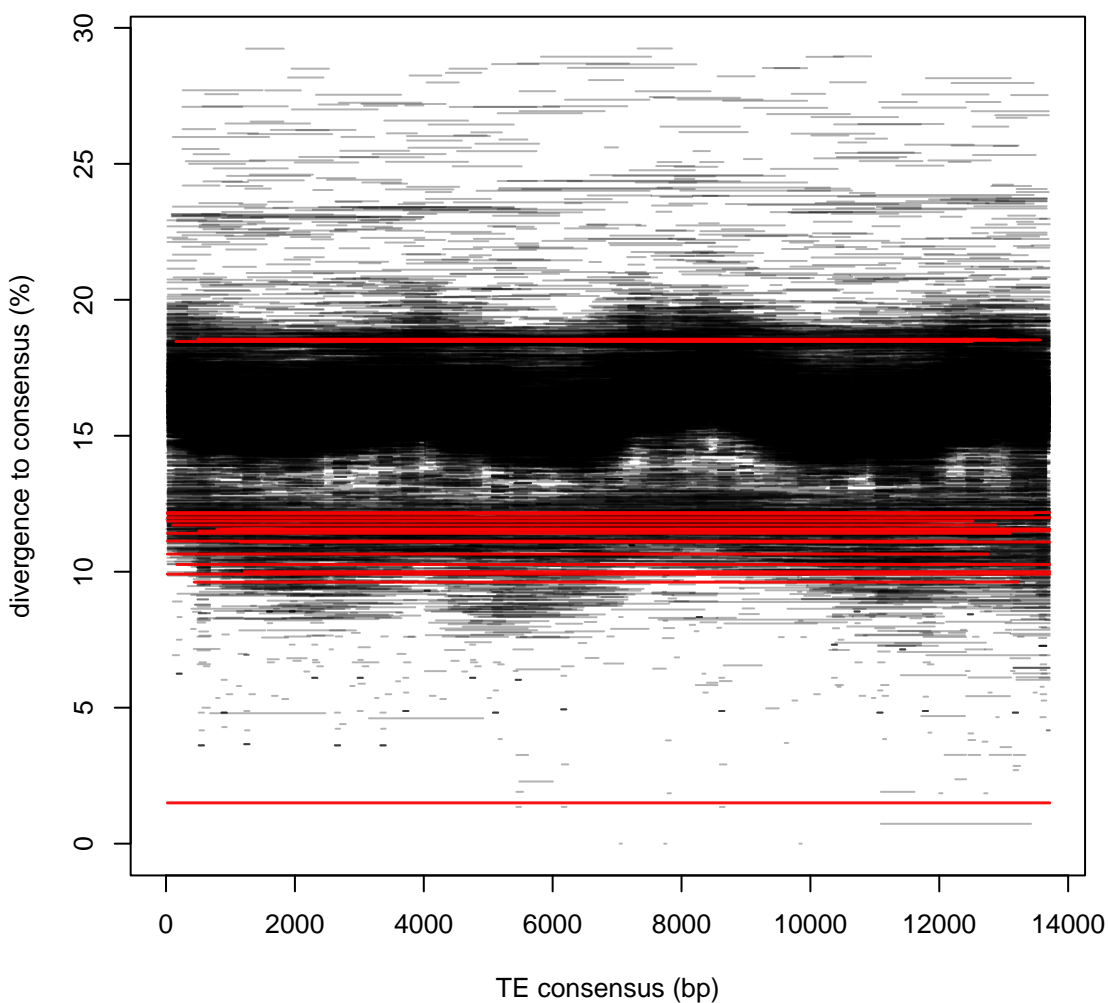
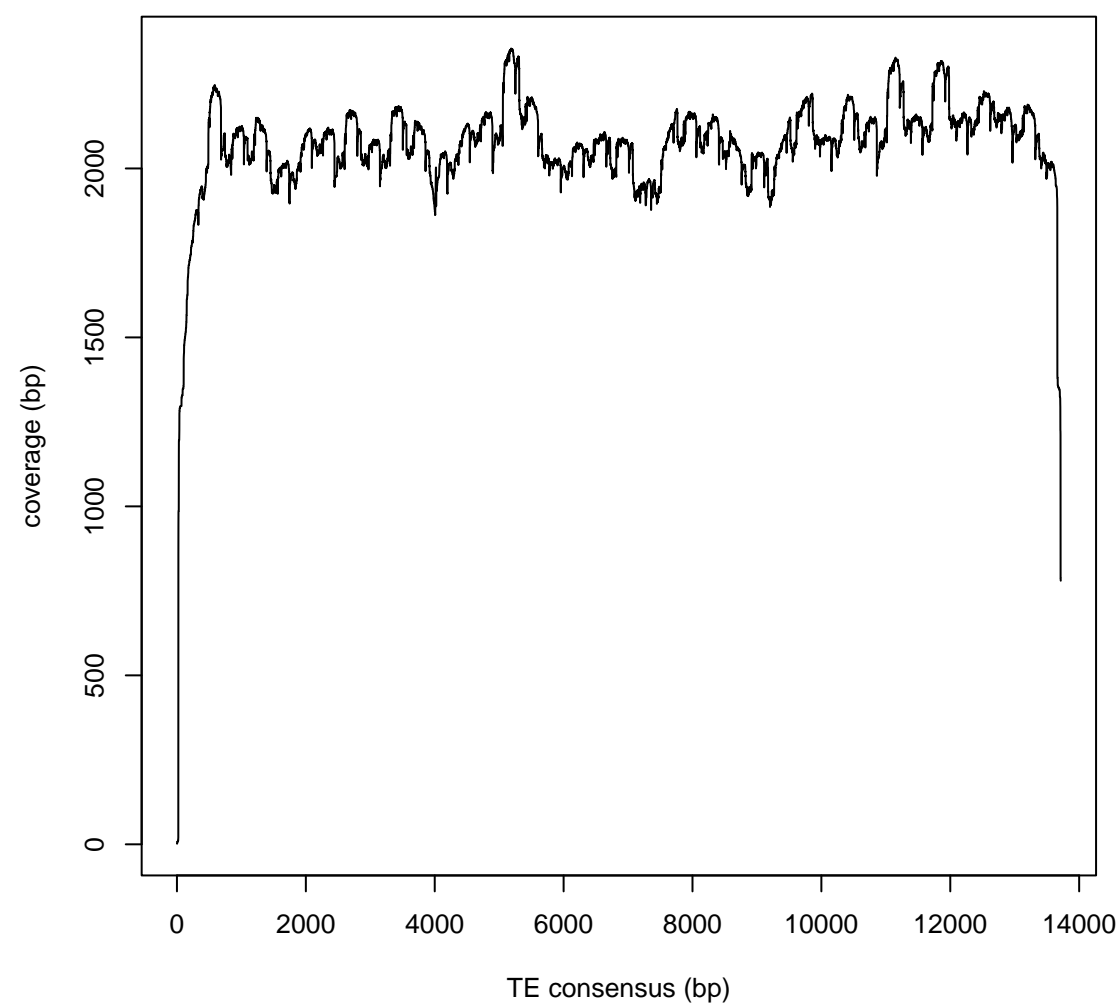


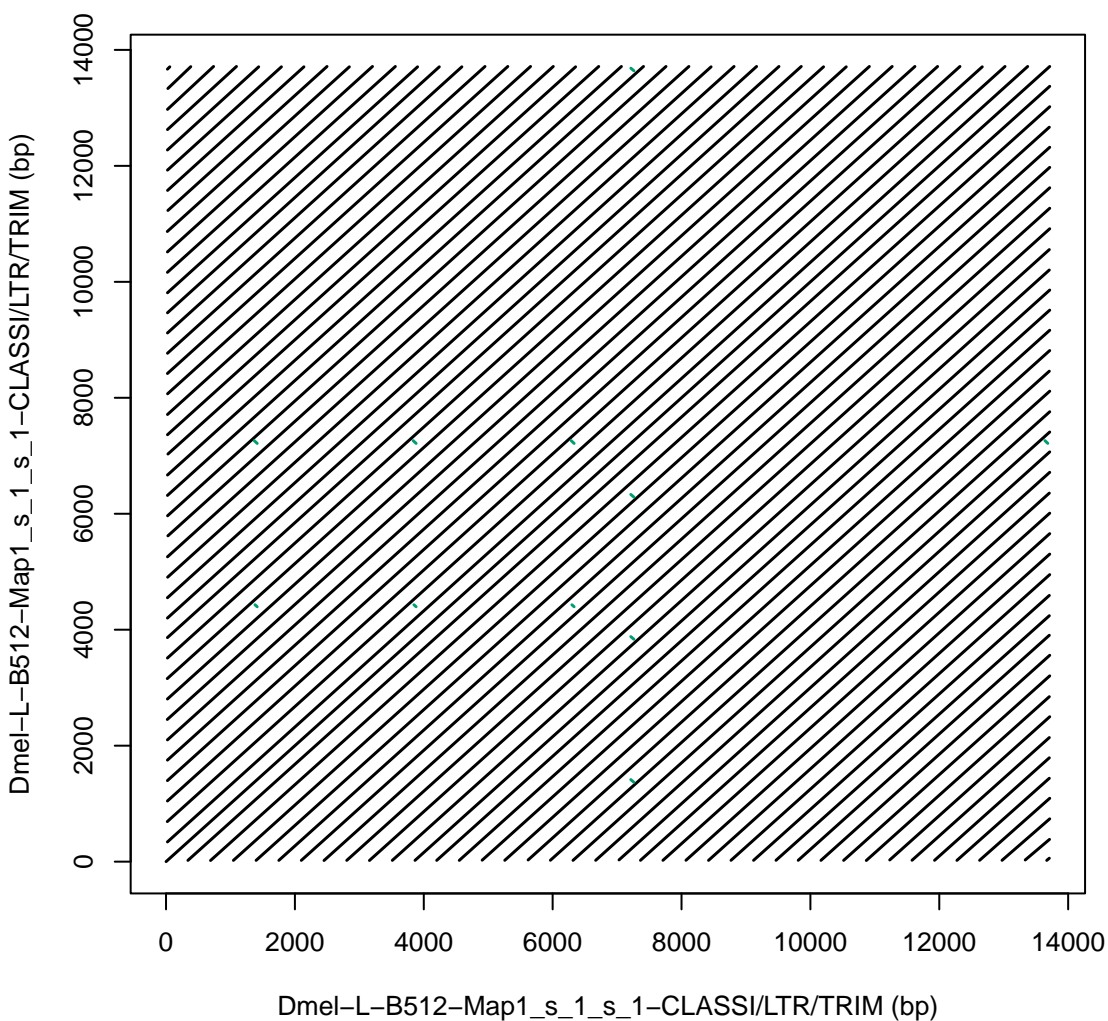
TE: Dmel-L-B512-Map1_s_1_s_1-CLASSI/LTR/TRIM
consensus size: 13714bp; fragments: 25766; full length: 21 (>=12342.6bp)



TE consensus genomic coverage



TE consensus self dotplot (blastn)



TE consensus structure and protein hits

