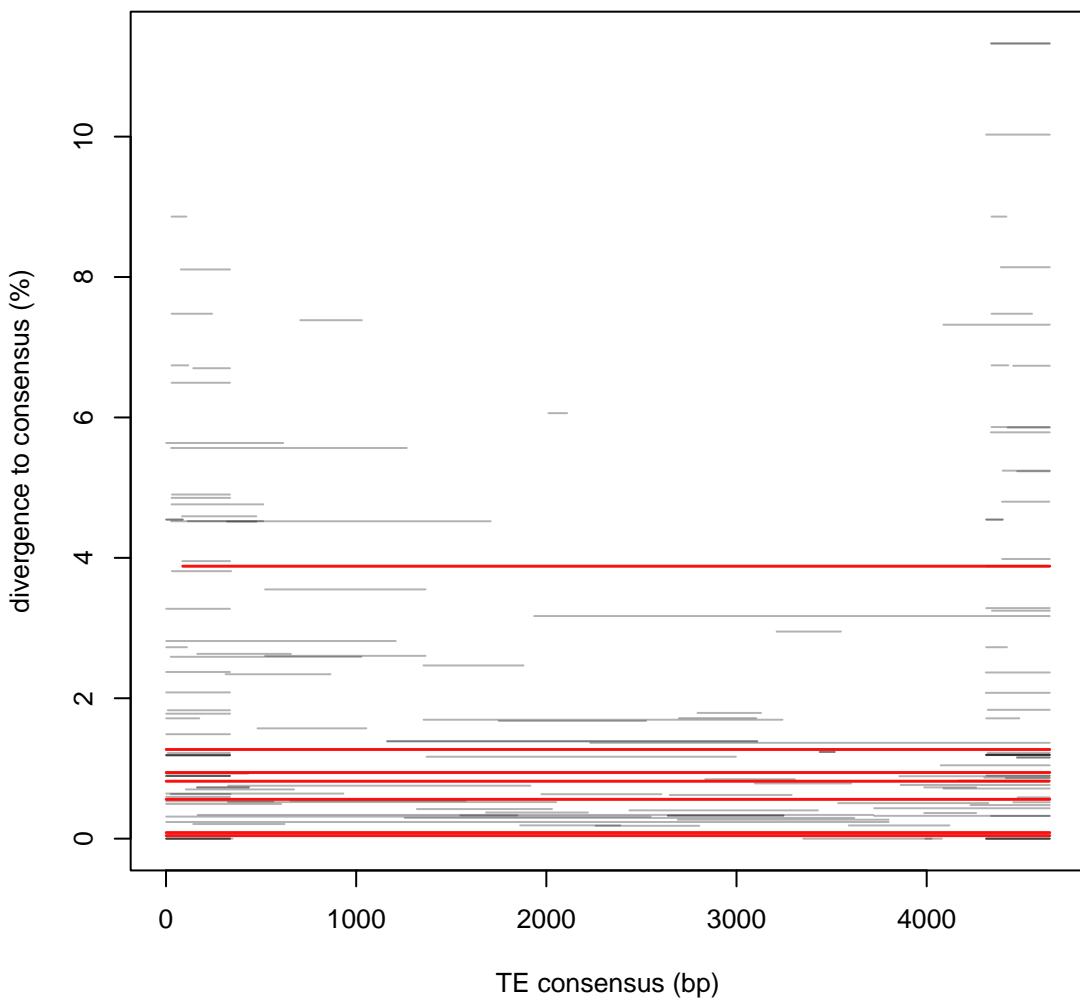
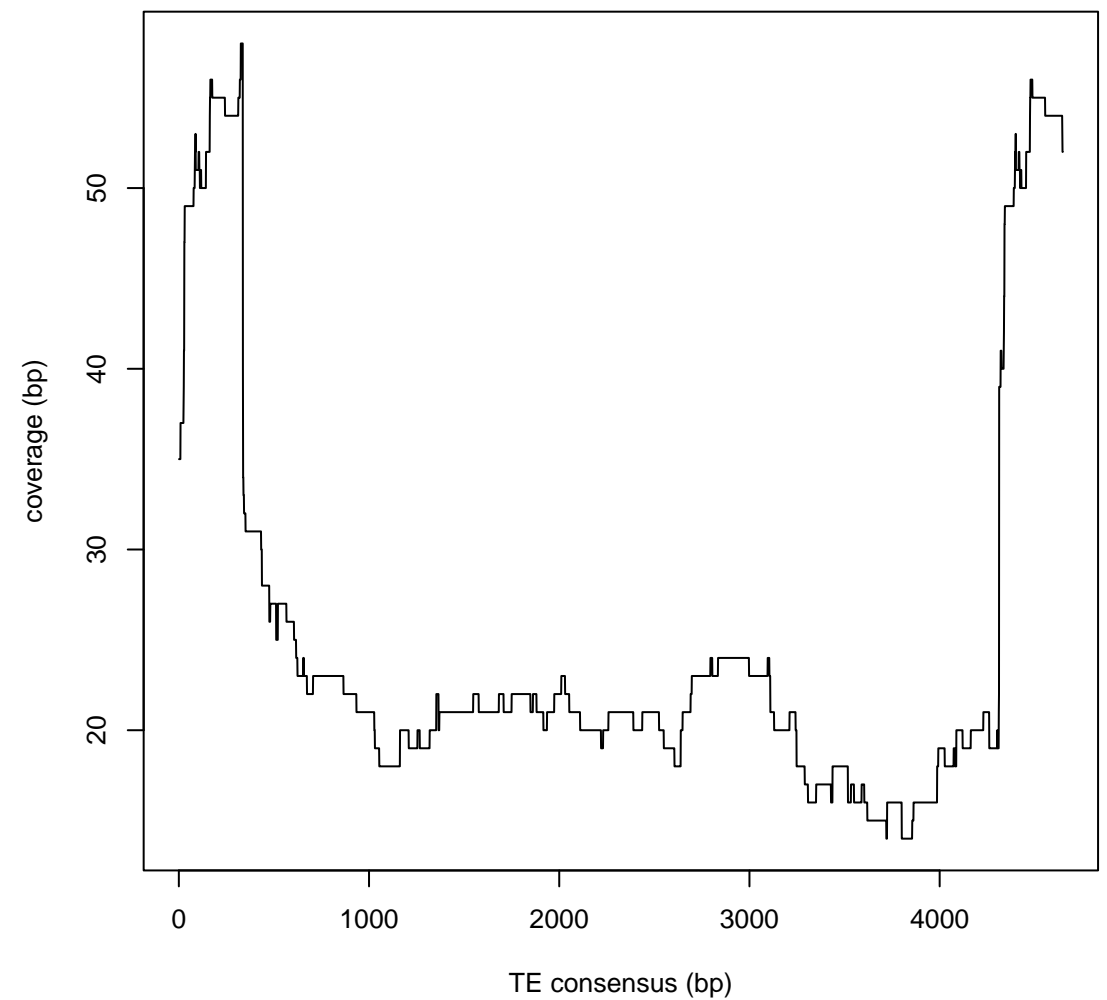


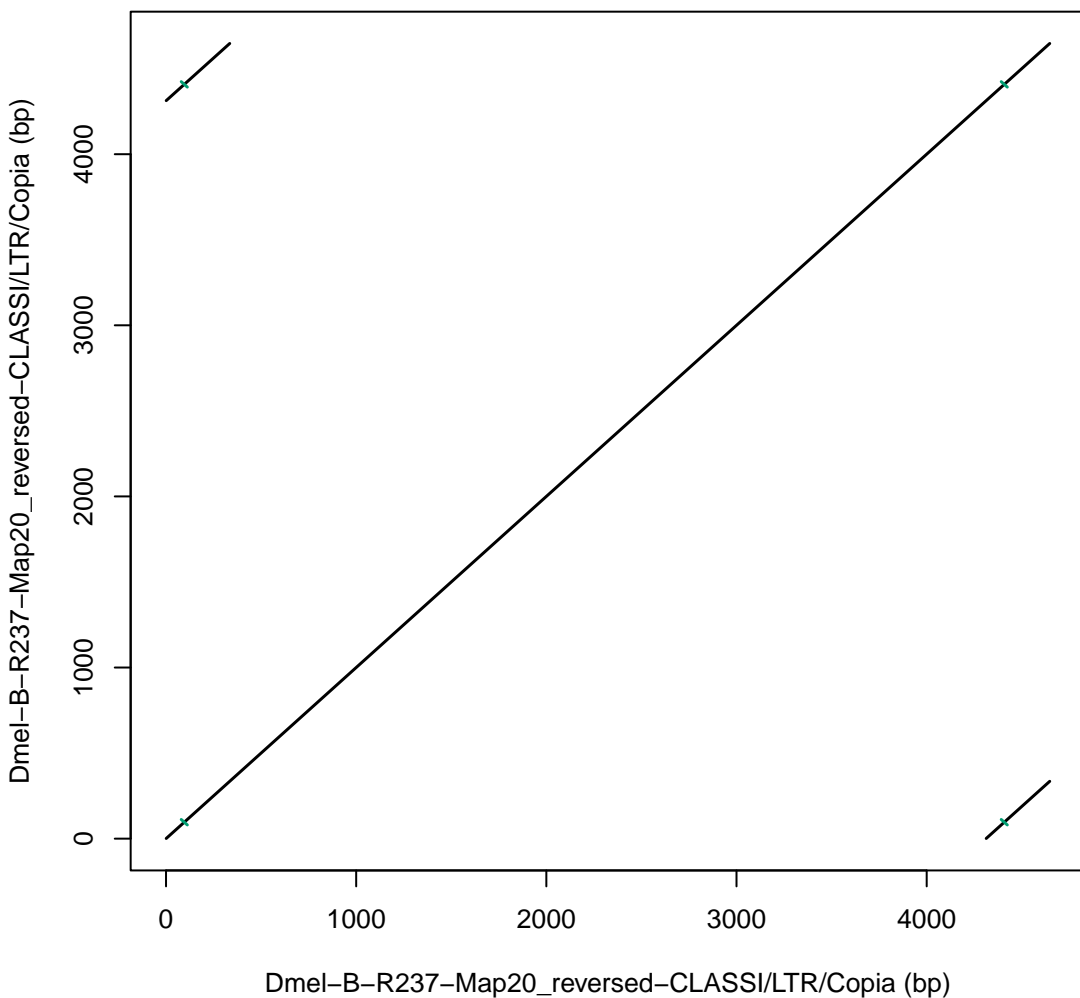
TE: Dmel-B-R237-Map20_reversed-CLASSI/LTR/Copia
consensus size: 4647bp; fragments: 157; full length: 7 (>=4182.3bp)



TE consensus genomic coverage



TE consensus self dotplot (blastn)



TE consensus structure and protein hits

