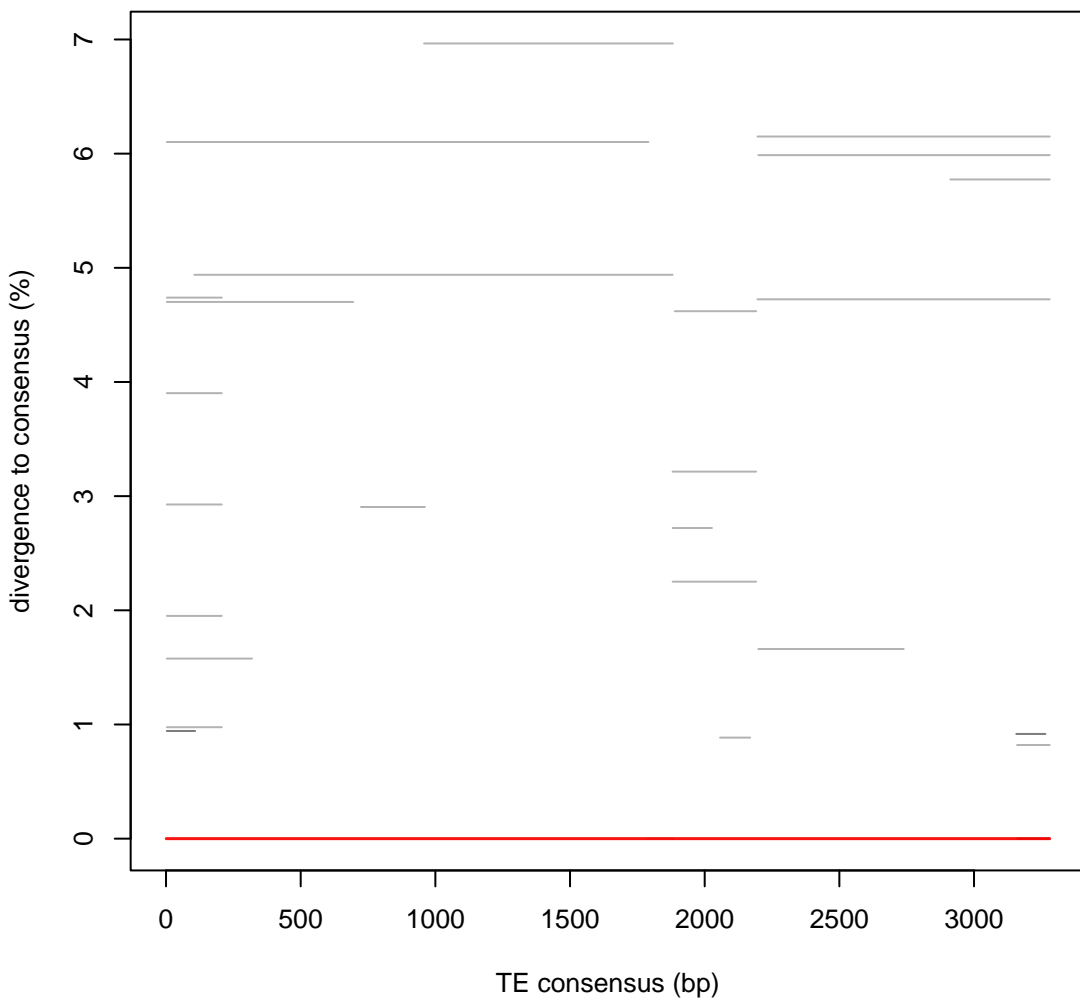
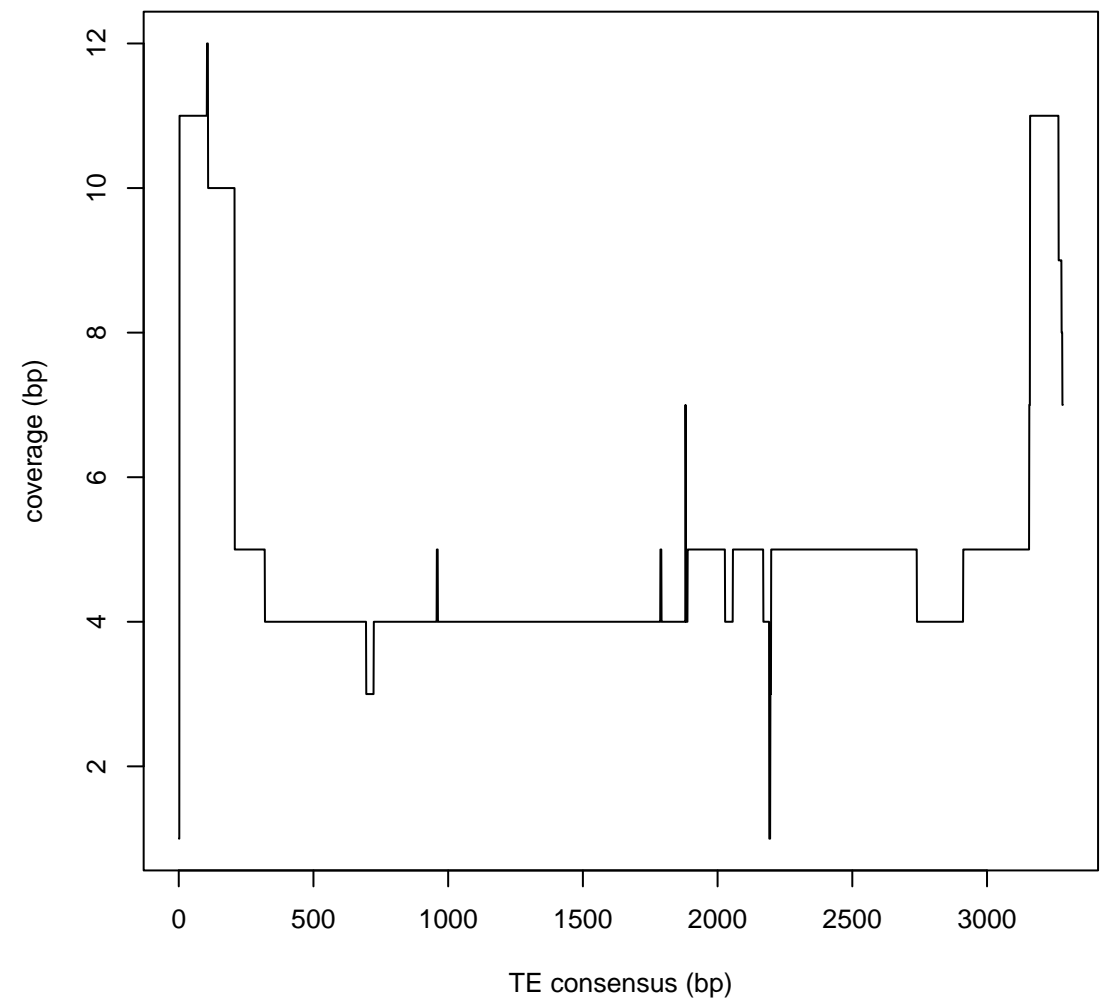


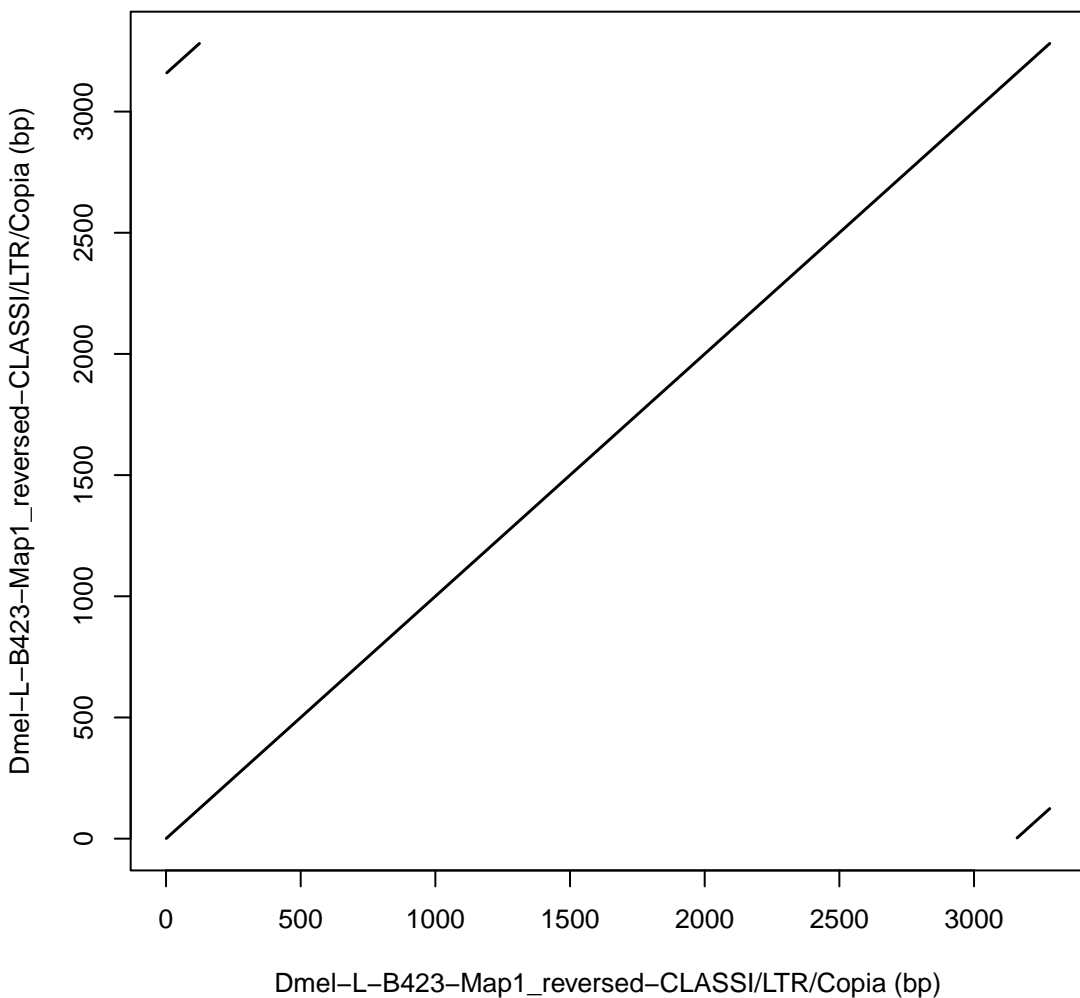
TE: Dmel-L-B423-Map1_reversed-CLASSI/LTR/Copia
consensus size: 3281bp; fragments: 31; full length: 1 (>=2952.9bp)



TE consensus genomic coverage



TE consensus self dotplot (blastn)



TE consensus structure and protein hits

