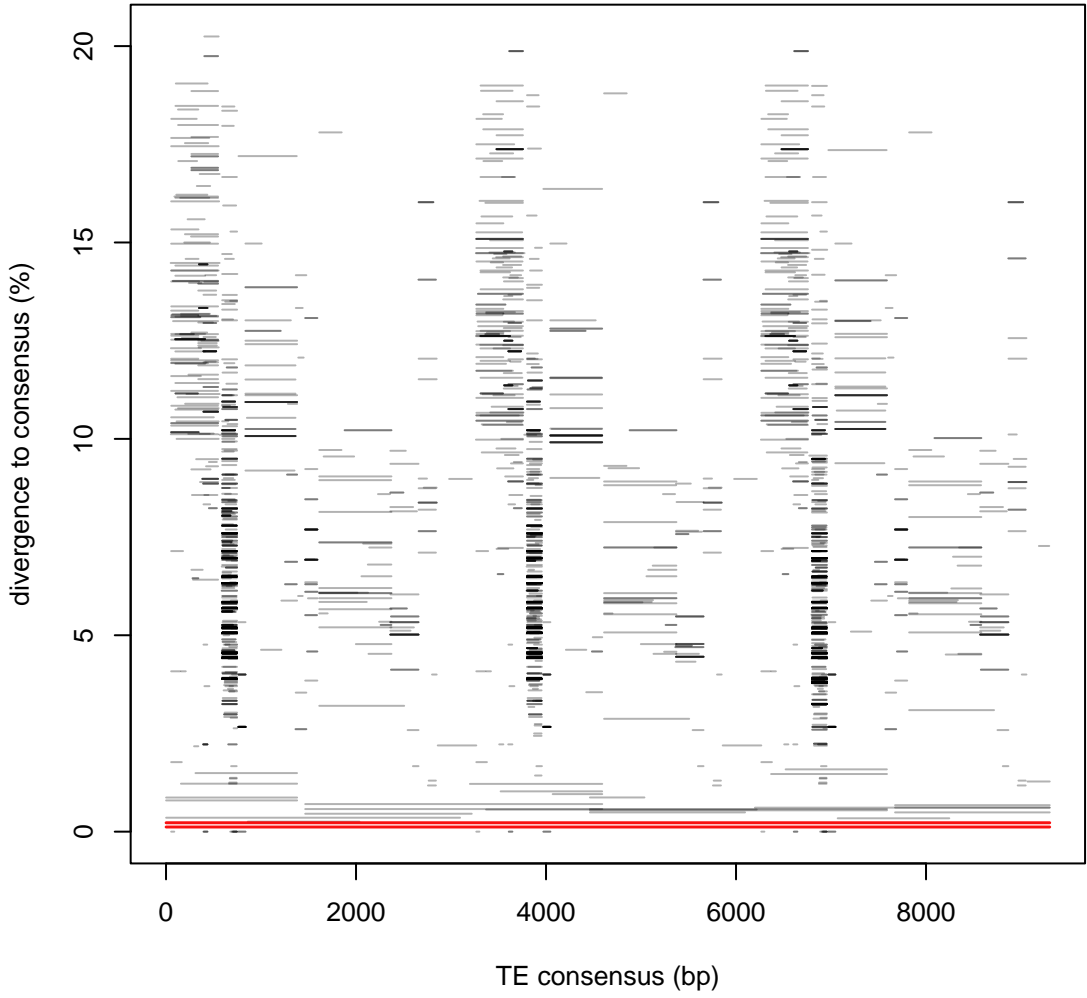
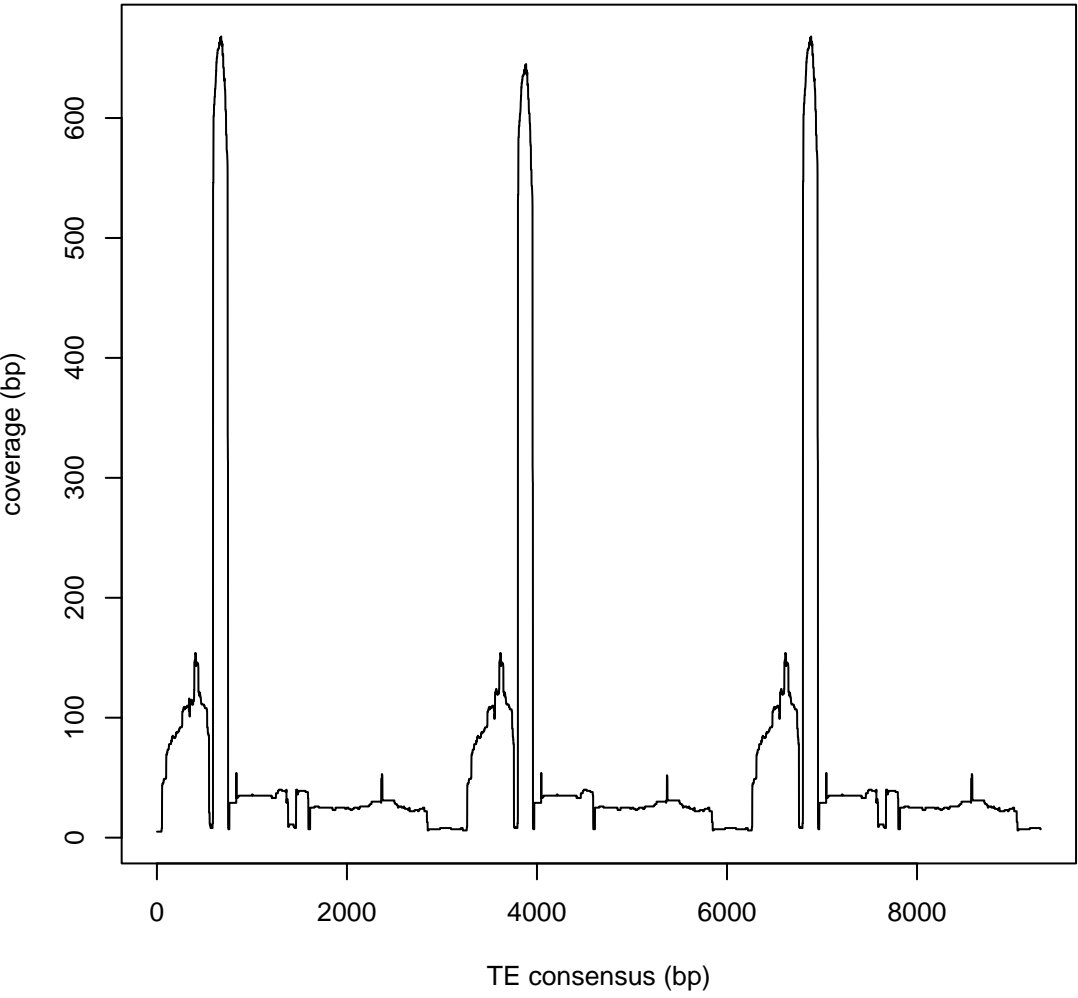


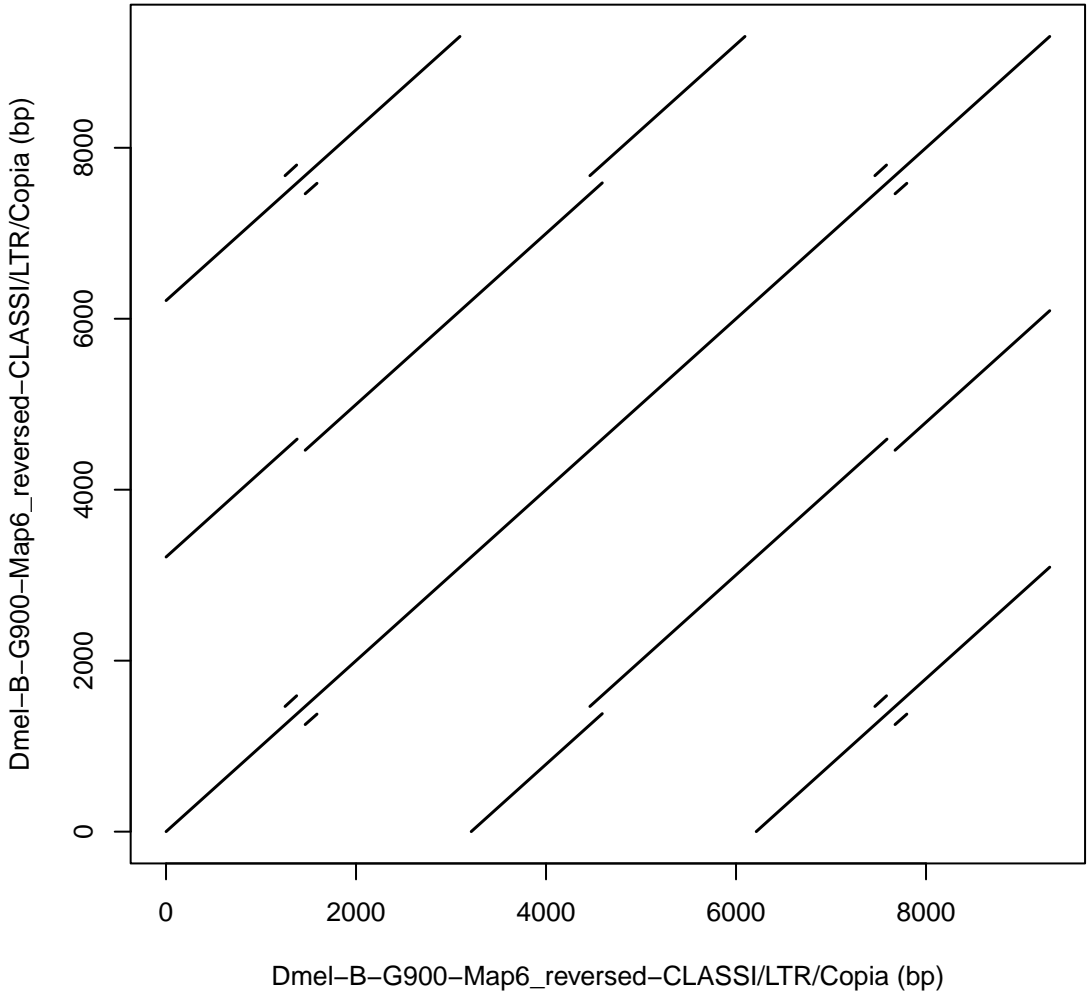
TE: Dmel-B-G900-Map6_reversed-CLASSI/LTR/Copia
consensus size: 9302bp; fragments: 3081; full length: 2 (>=8371.8bp)



TE consensus genomic coverage



TE consensus self dotplot (blastn)



TE consensus structure and protein hits

