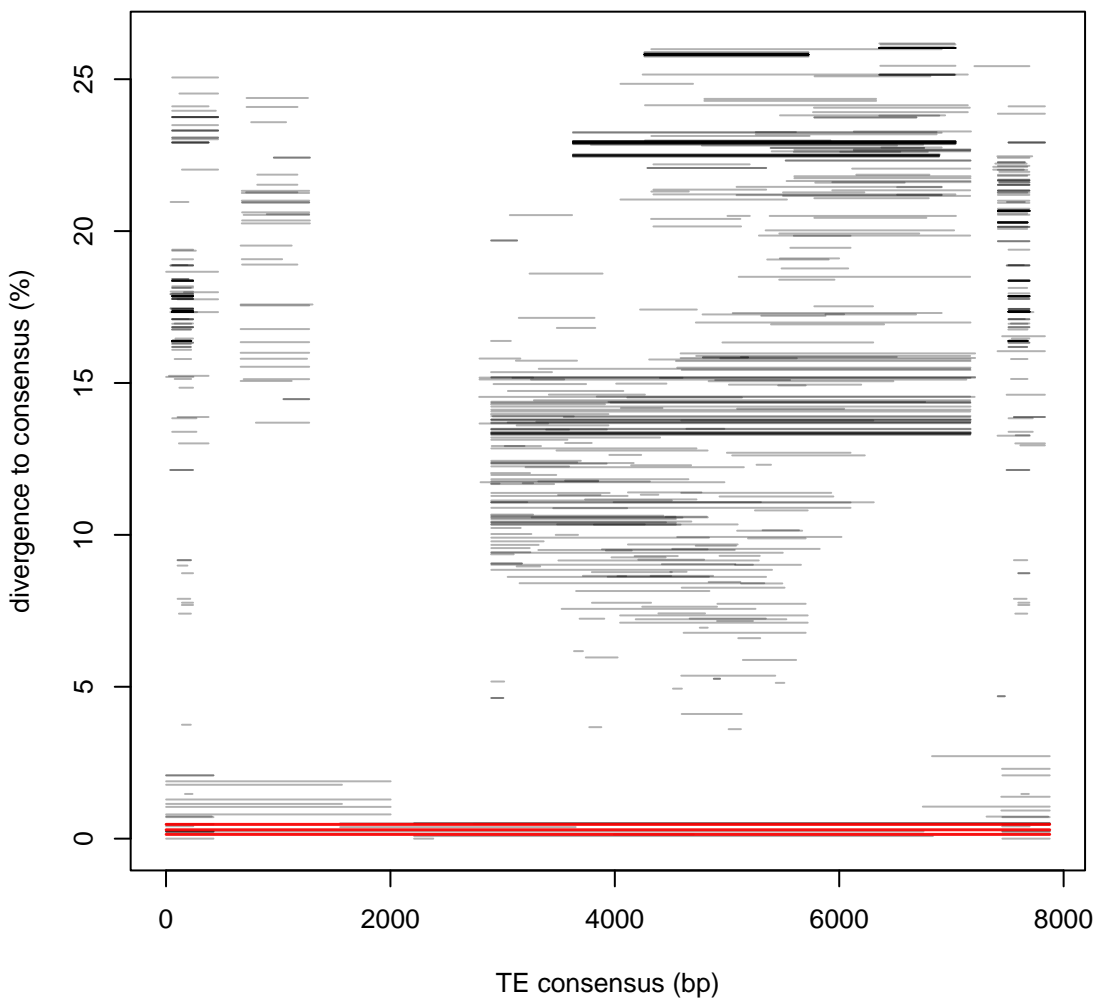
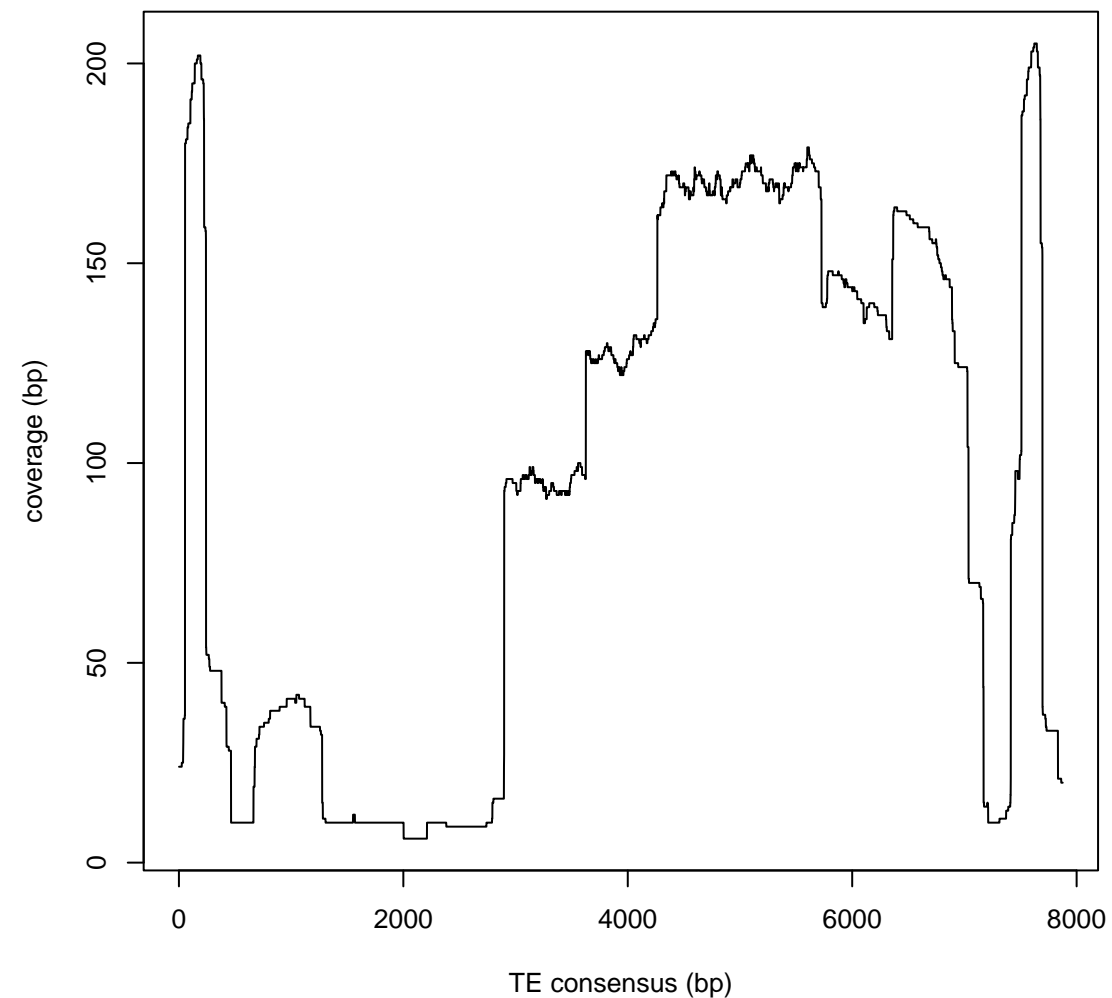


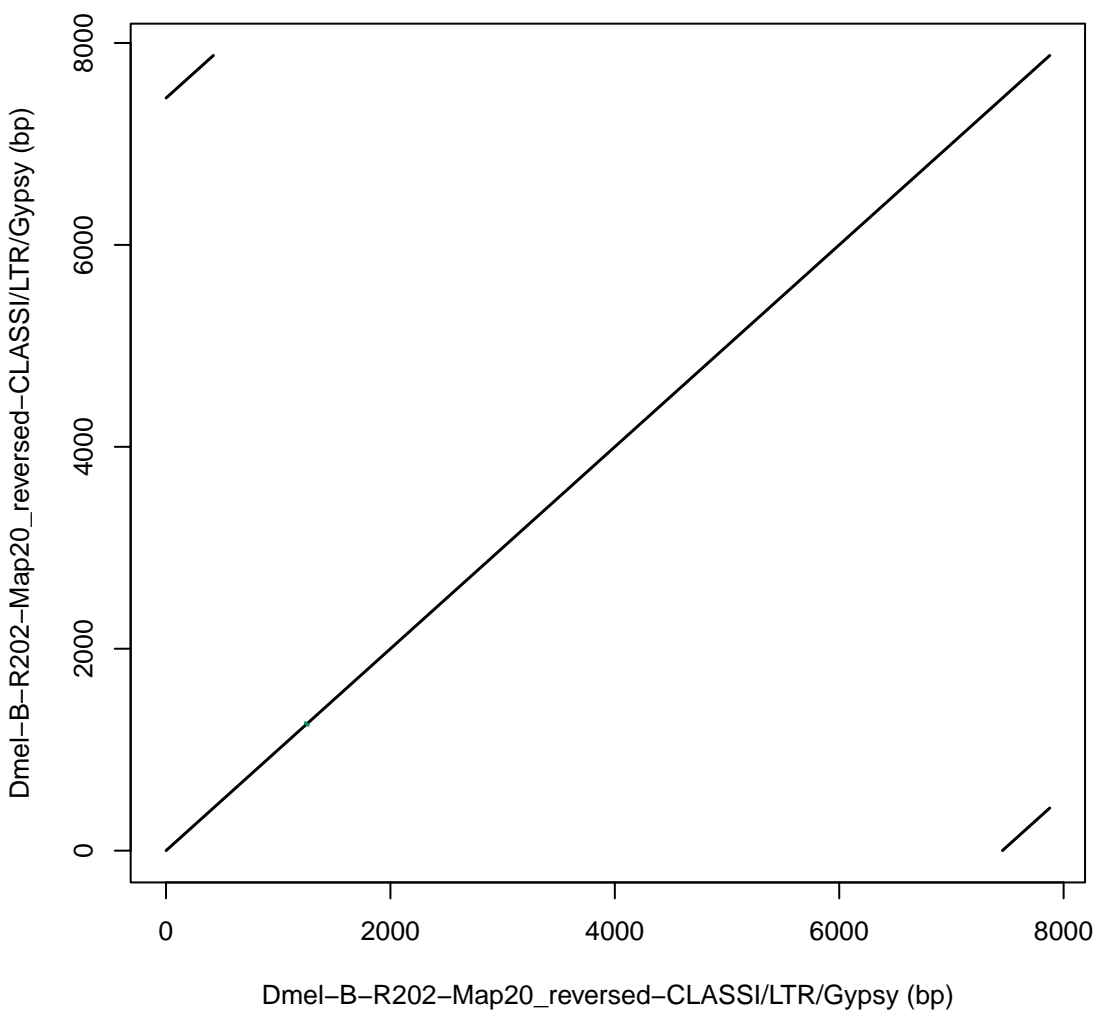
TE: Dmel-B-R202-Map20_reversed-CLASSI/LTR/Gypsy
consensus size: 7876bp; fragments: 818; full length: 3 (≥ 7088.4 bp)



TE consensus genomic coverage



TE consensus self dotplot (blastn)



TE consensus structure and protein hits

