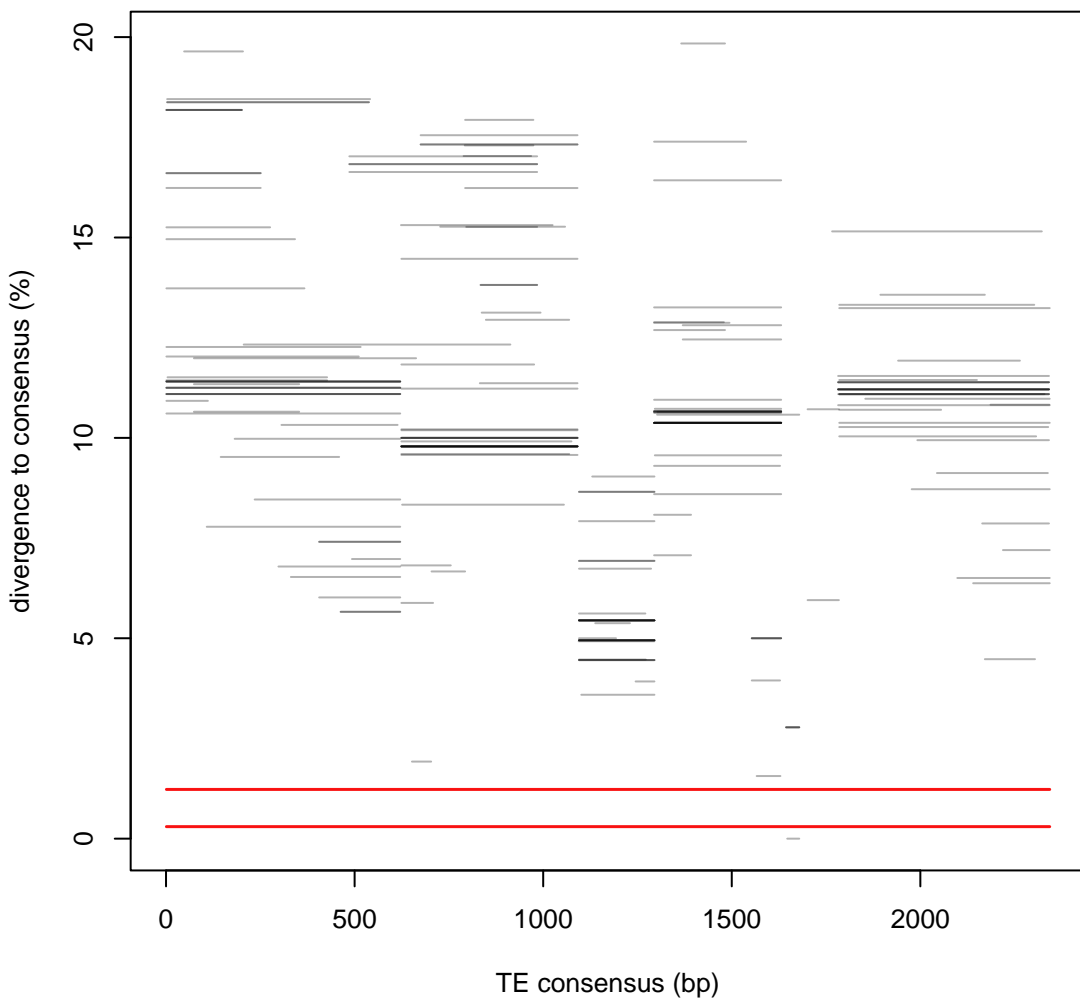
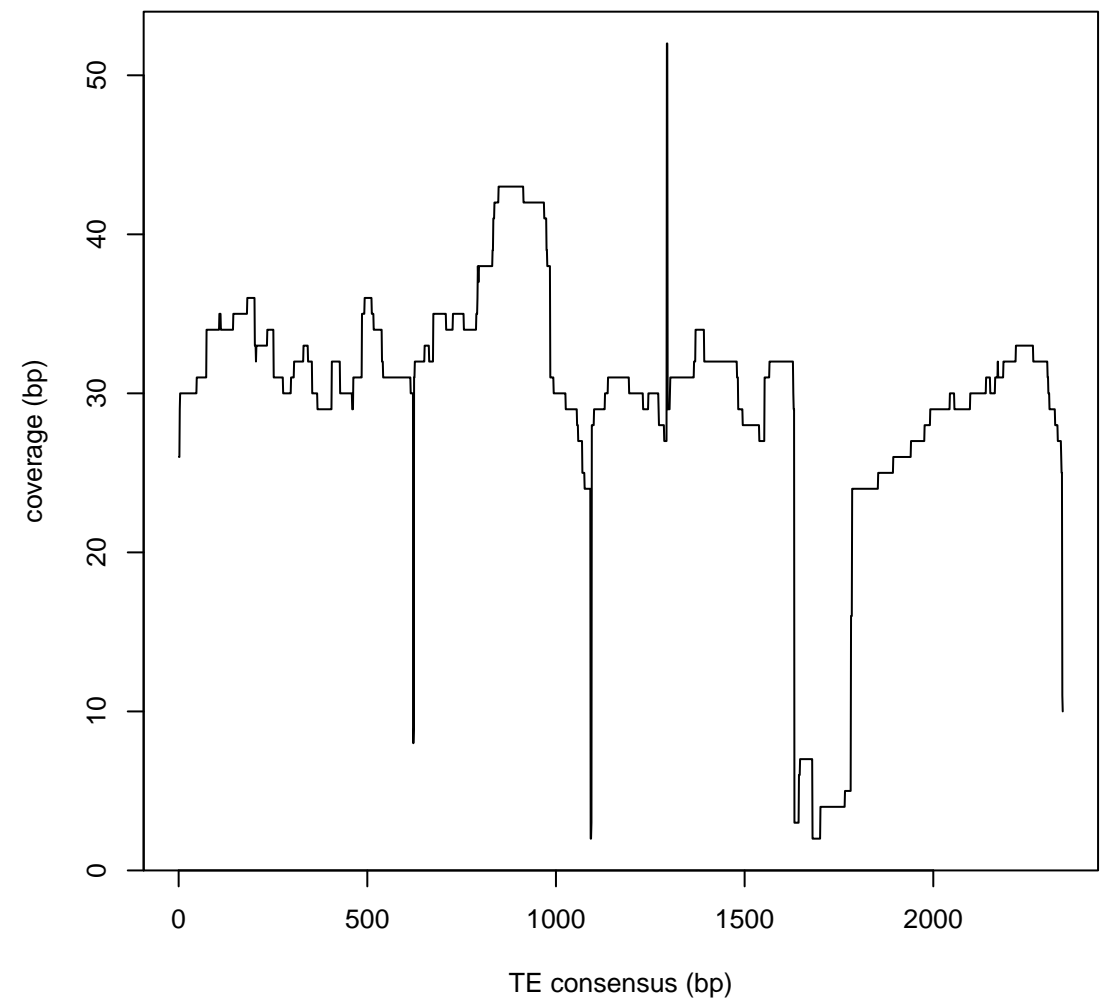


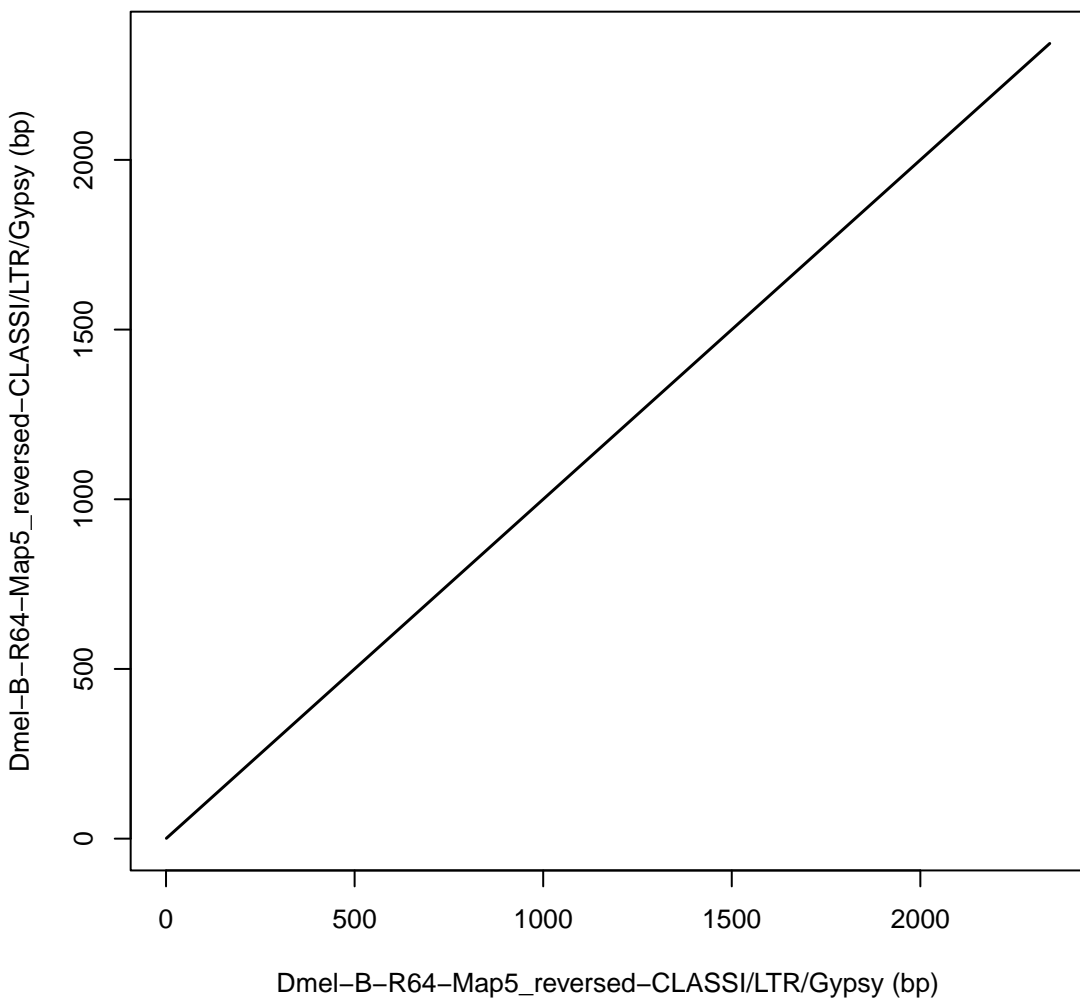
TE: Dmel-B-R64-Map5_reversed-CLASSI/LTR/Gypsy
consensus size: 2343bp; fragments: 199; full length: 2 (≥ 2108.7 bp)



TE consensus genomic coverage



TE consensus self dotplot (blastn)



TE consensus structure and protein hits

