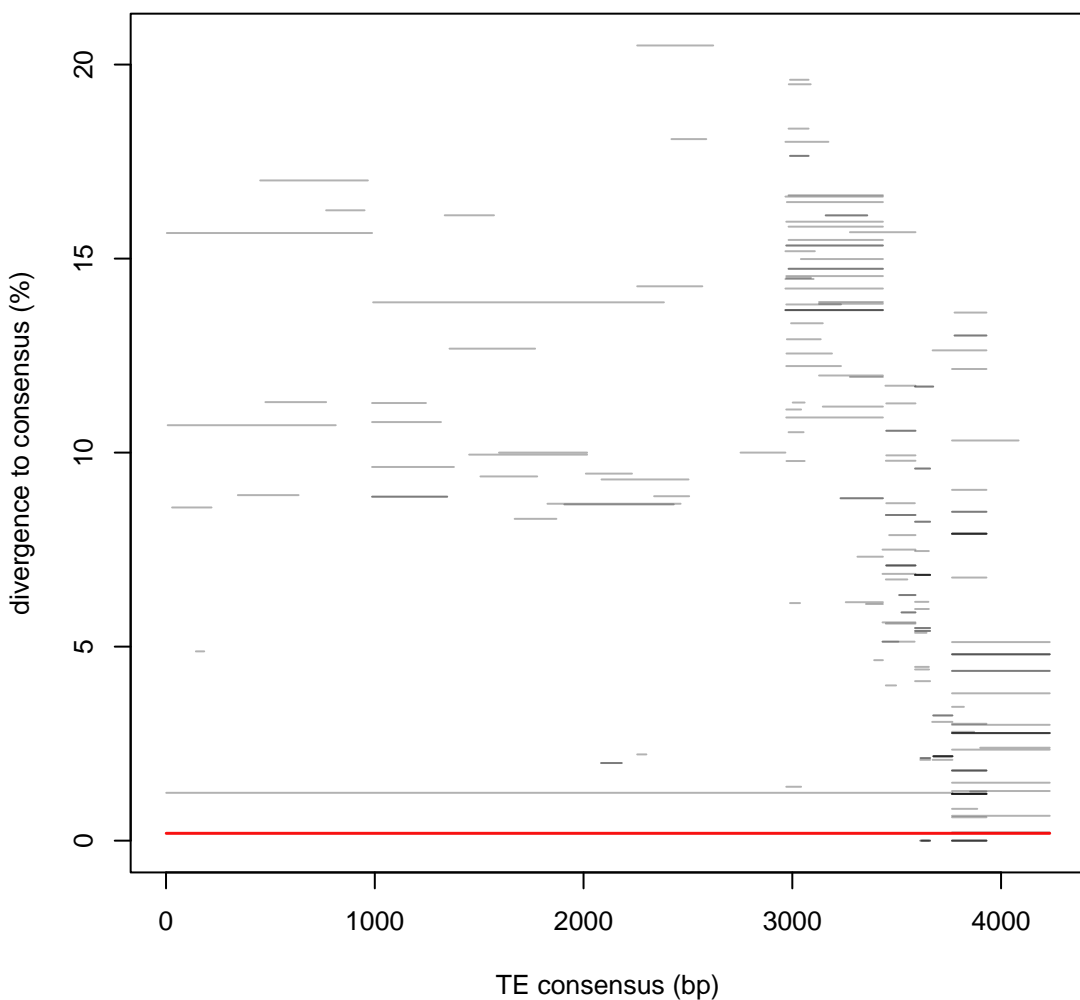
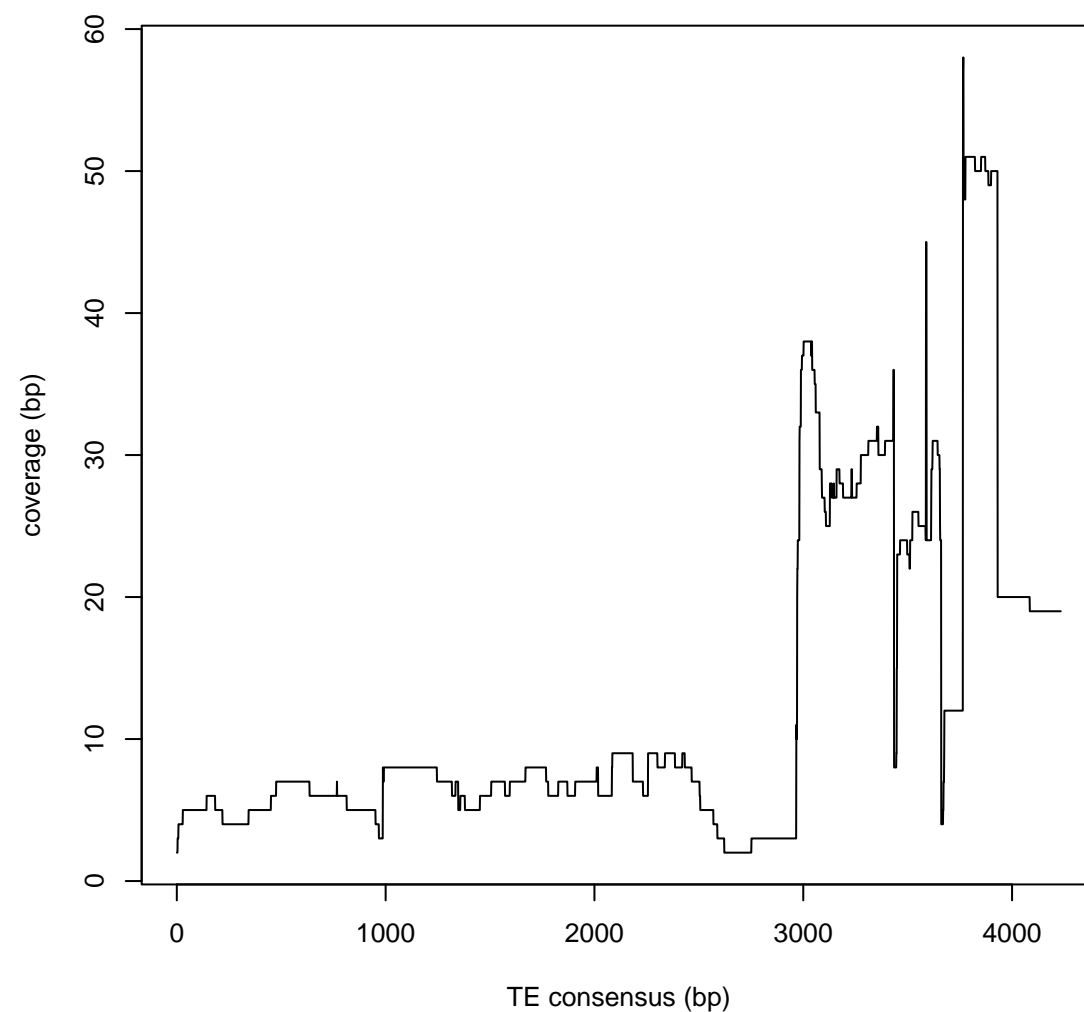


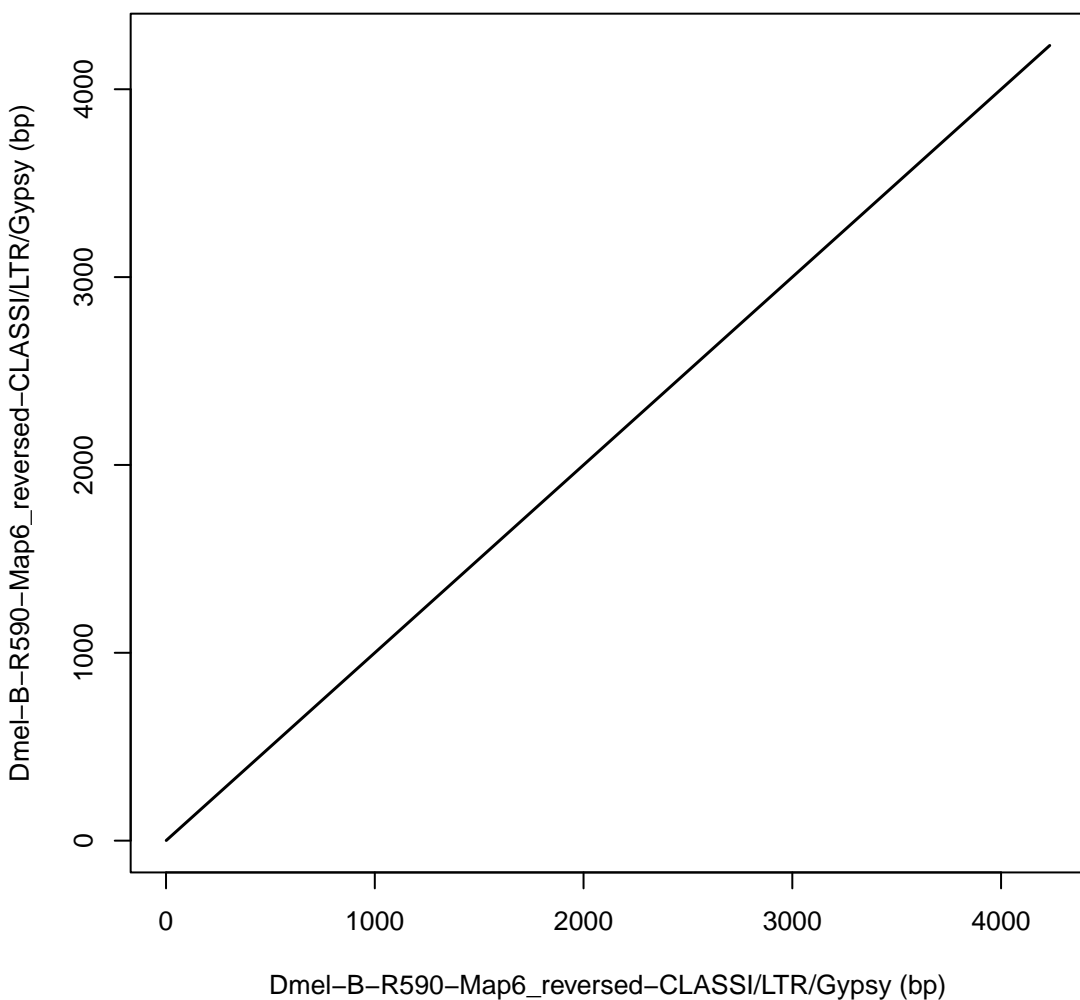
TE: Dmel-B-R590-Map6_reversed-CLASSI/LTR/Gypsy
consensus size: 4233bp; fragments: 200; full length: 1 (≥ 3809.7 bp)



TE consensus genomic coverage



TE consensus self dotplot (blastn)



TE consensus structure and protein hits

