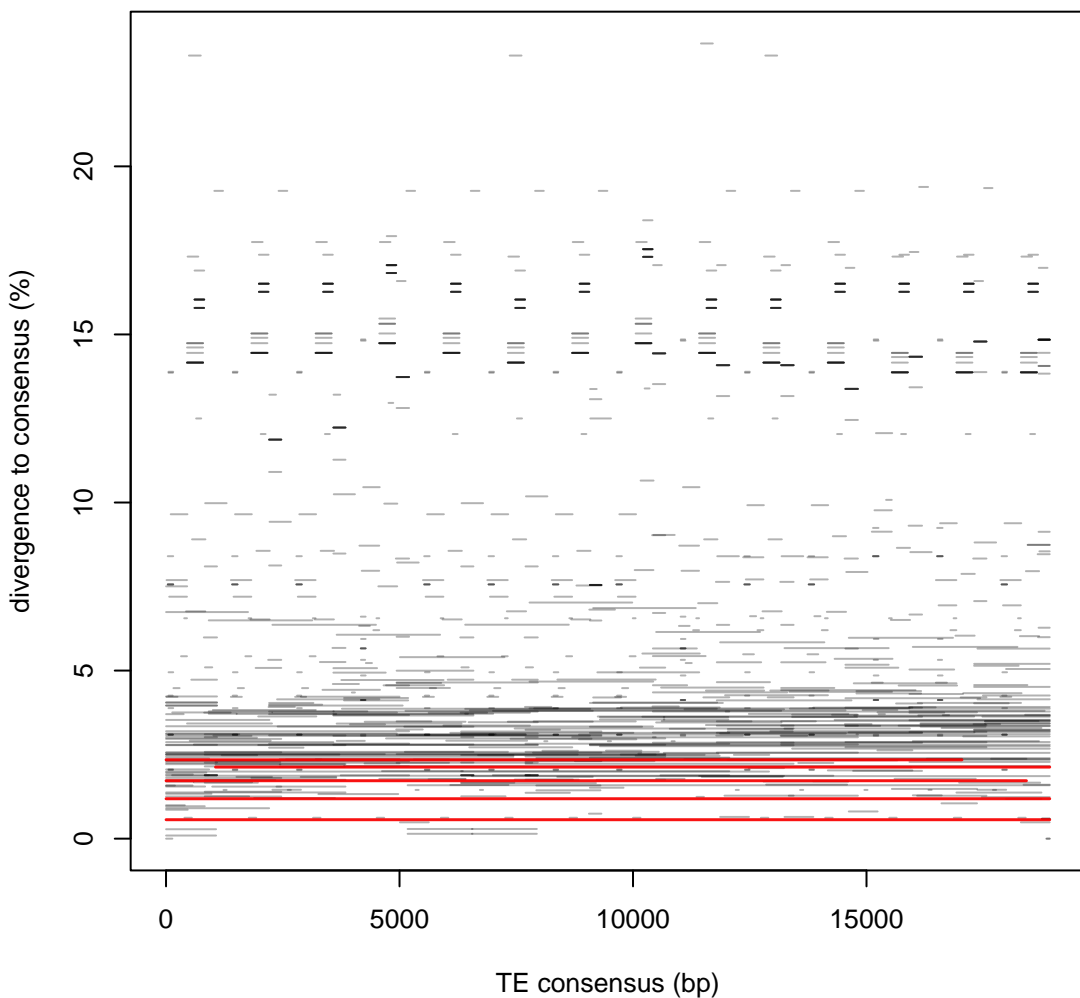
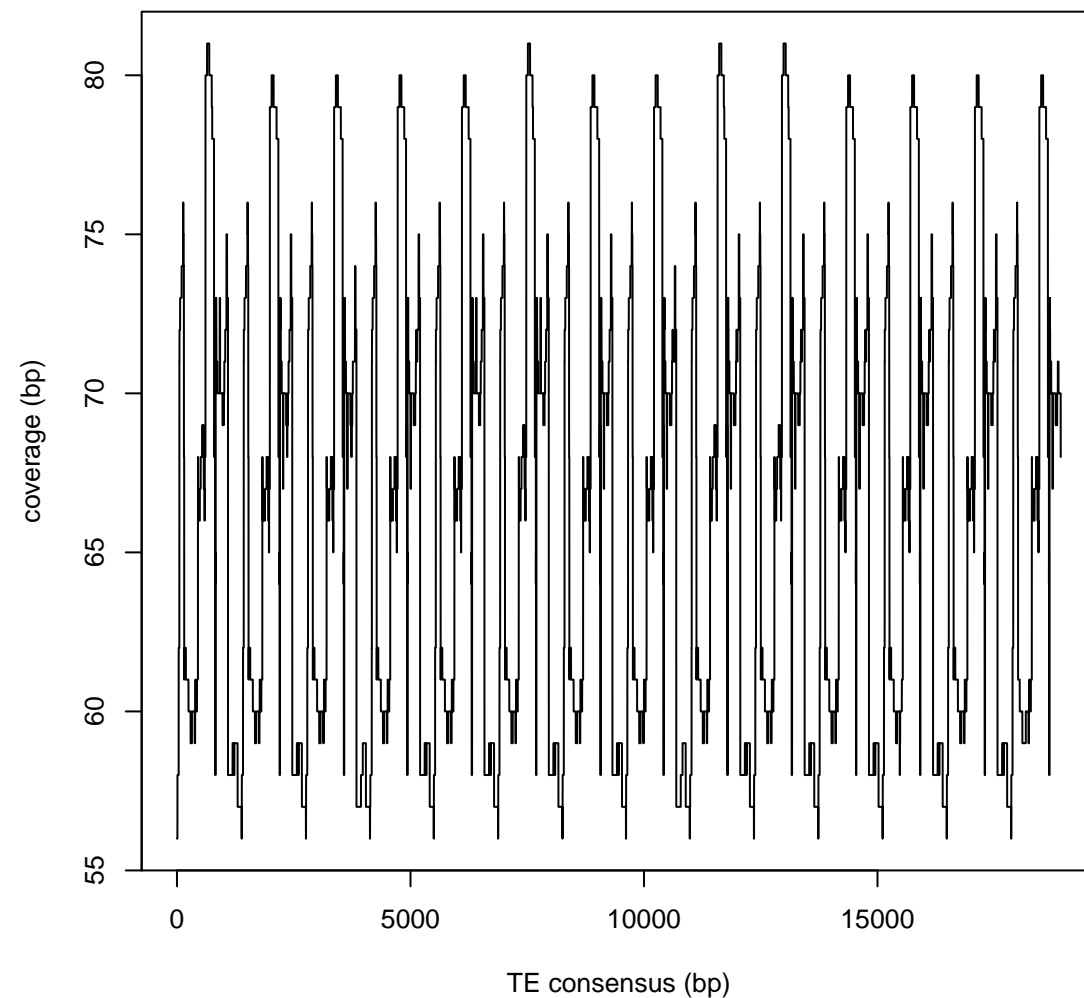


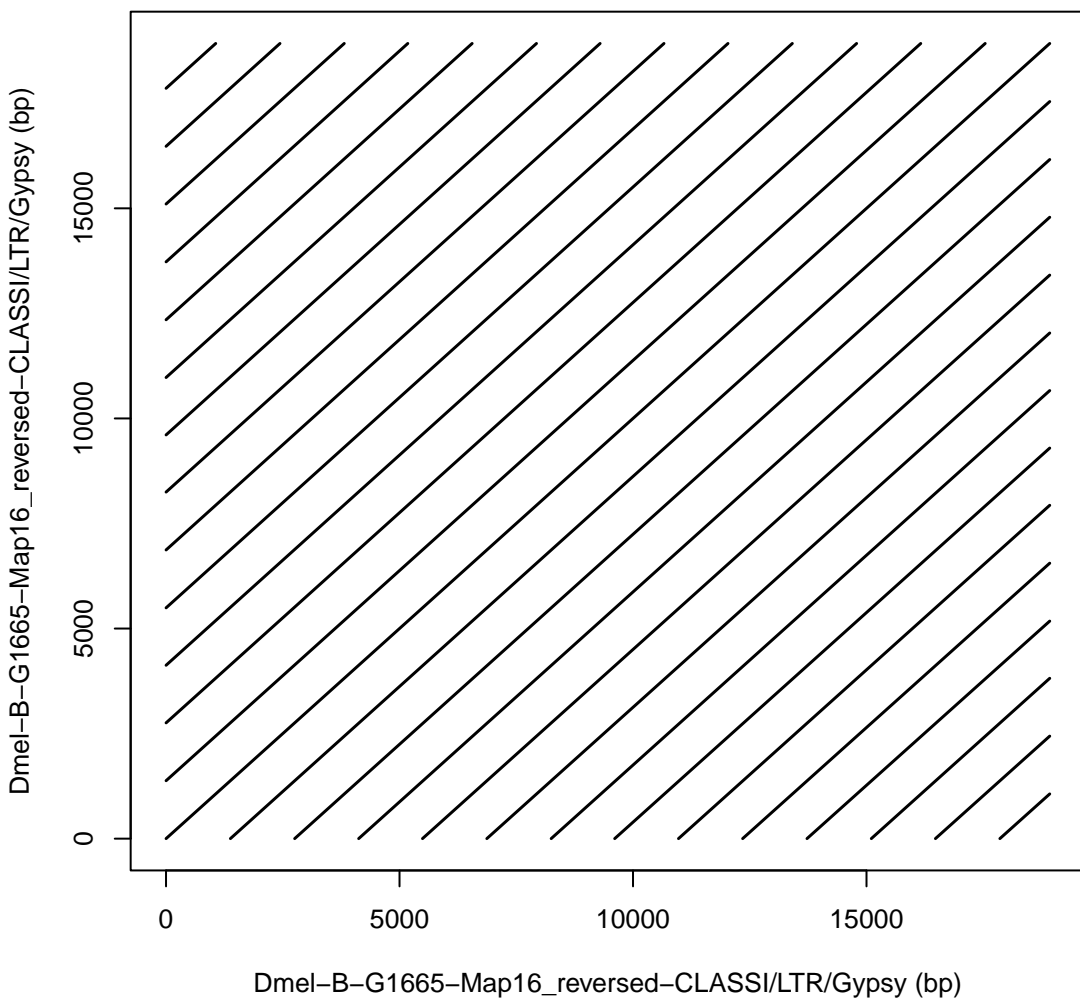
TE: Dmel-B-G1665-Map16_reversed-CLASSI/LTR/Gypsy
consensus size: 18923bp; fragments: 1254; full length: 5 (≥ 17030.7 bp)



TE consensus genomic coverage



TE consensus self dotplot (blastn)



TE consensus structure and protein hits

