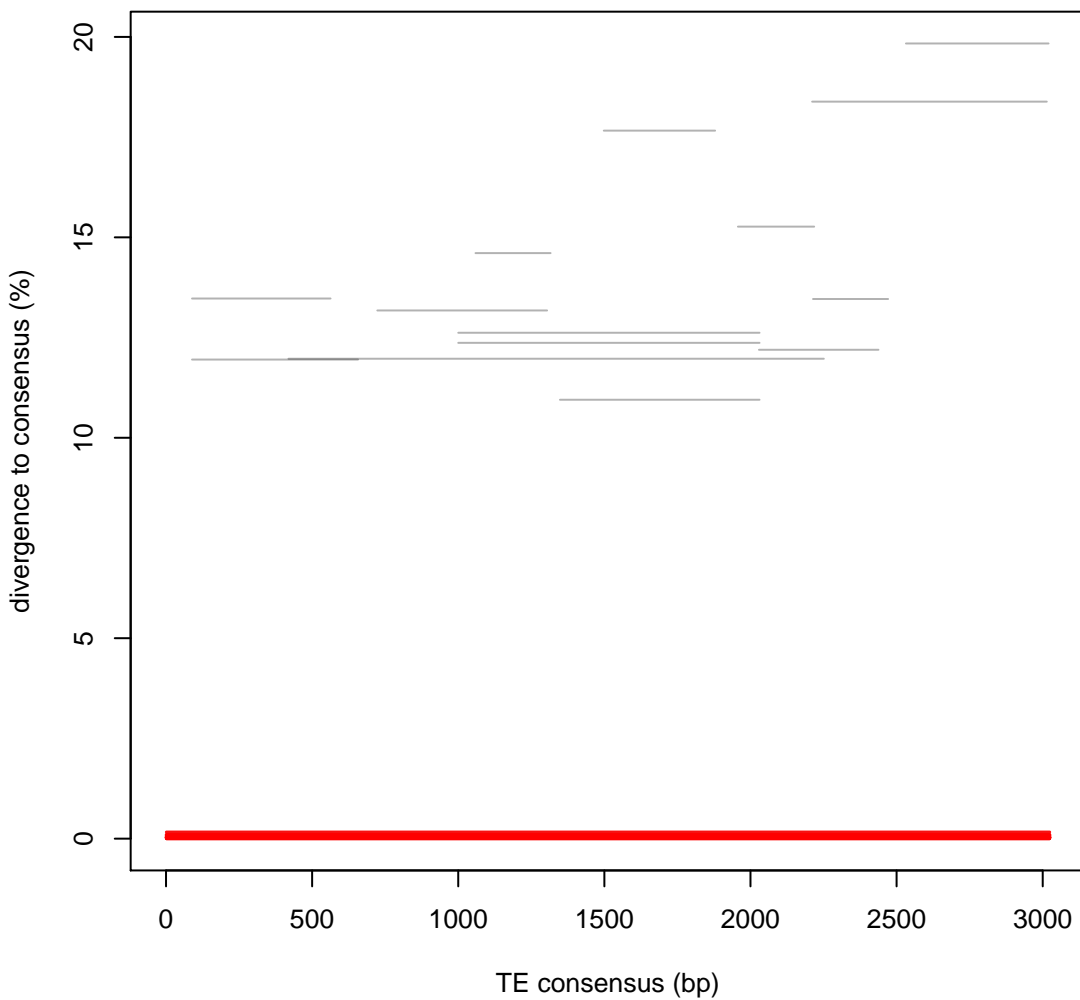
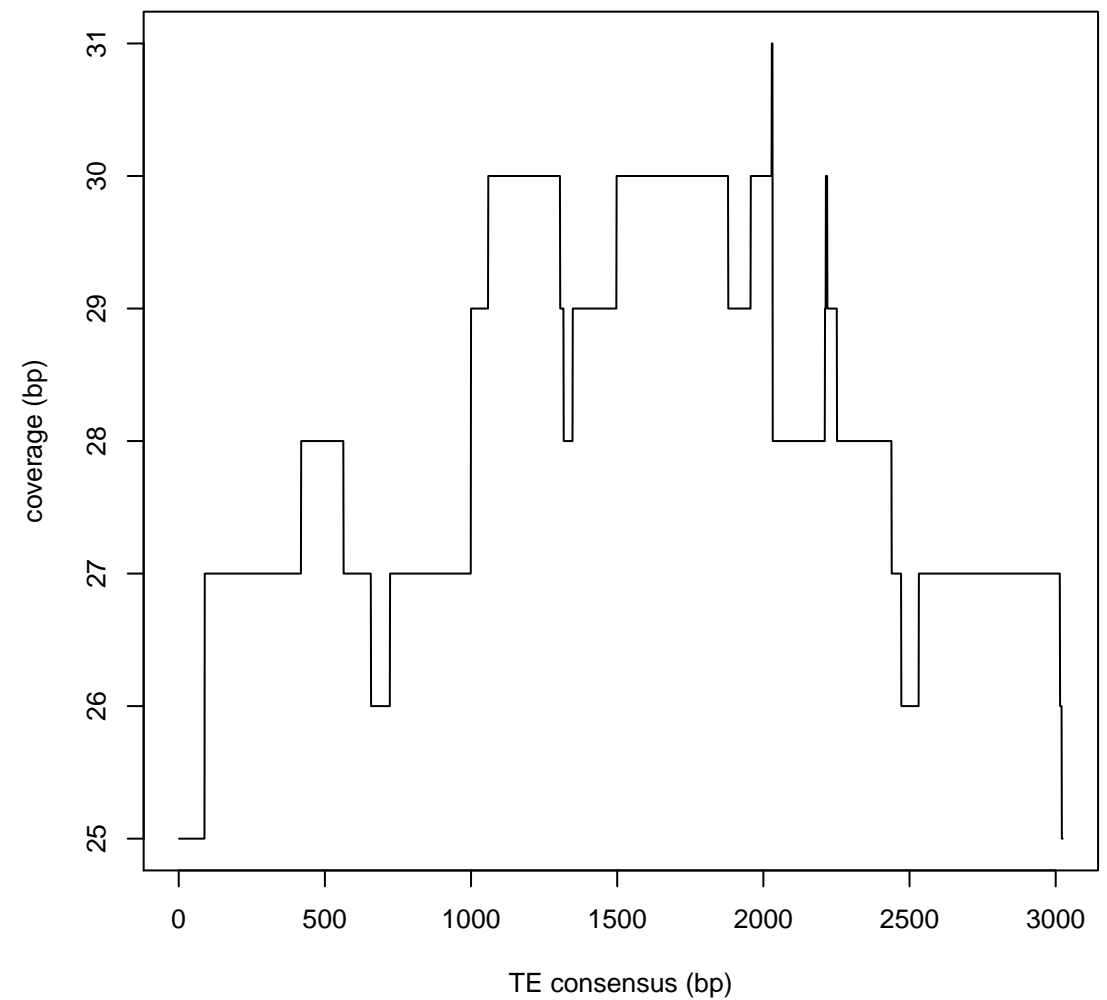


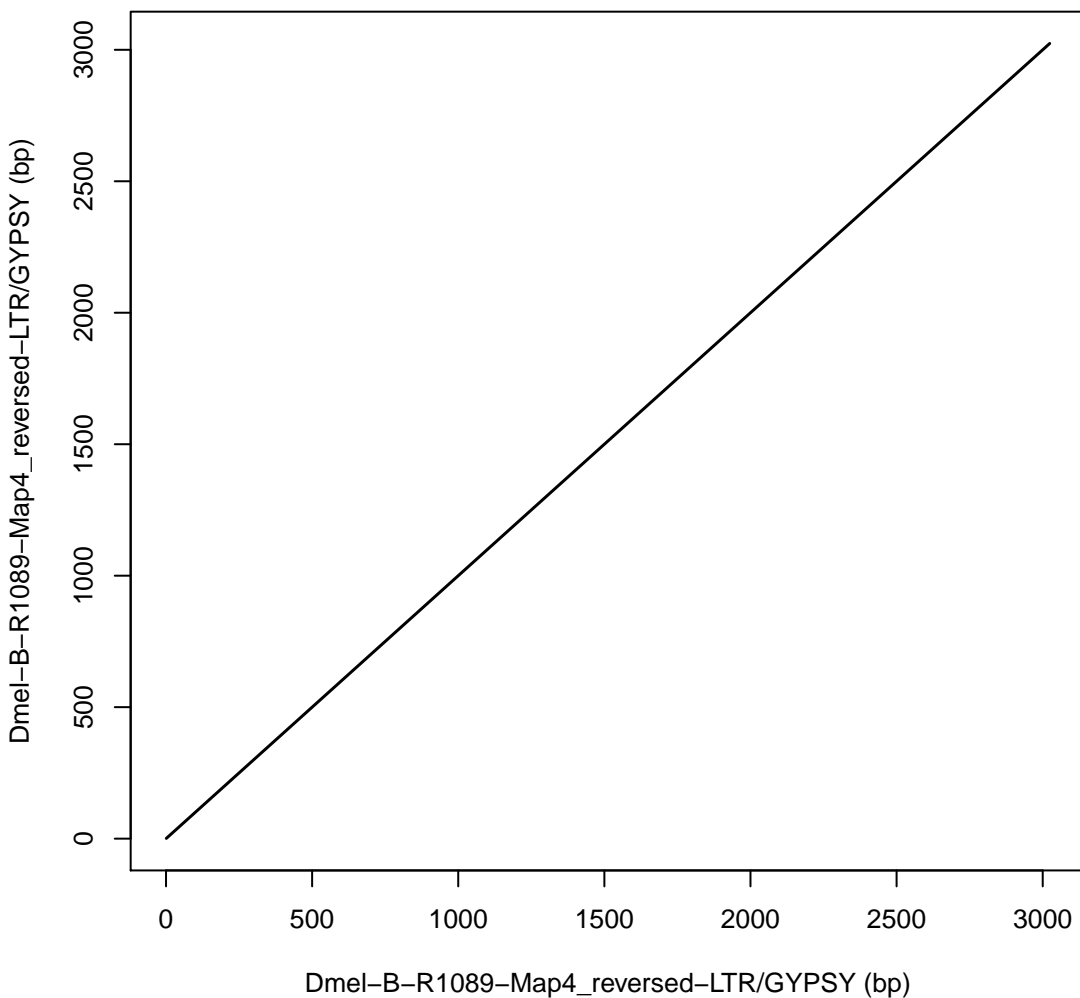
TE: Dmel-B-R1089-Map4_reversed-LTR/GYPsy
consensus size: 3024bp; fragments: 39; full length: 25 (>=2721.6bp)



TE consensus genomic coverage



TE consensus self dotplot (blastn)



TE consensus structure and protein hits

