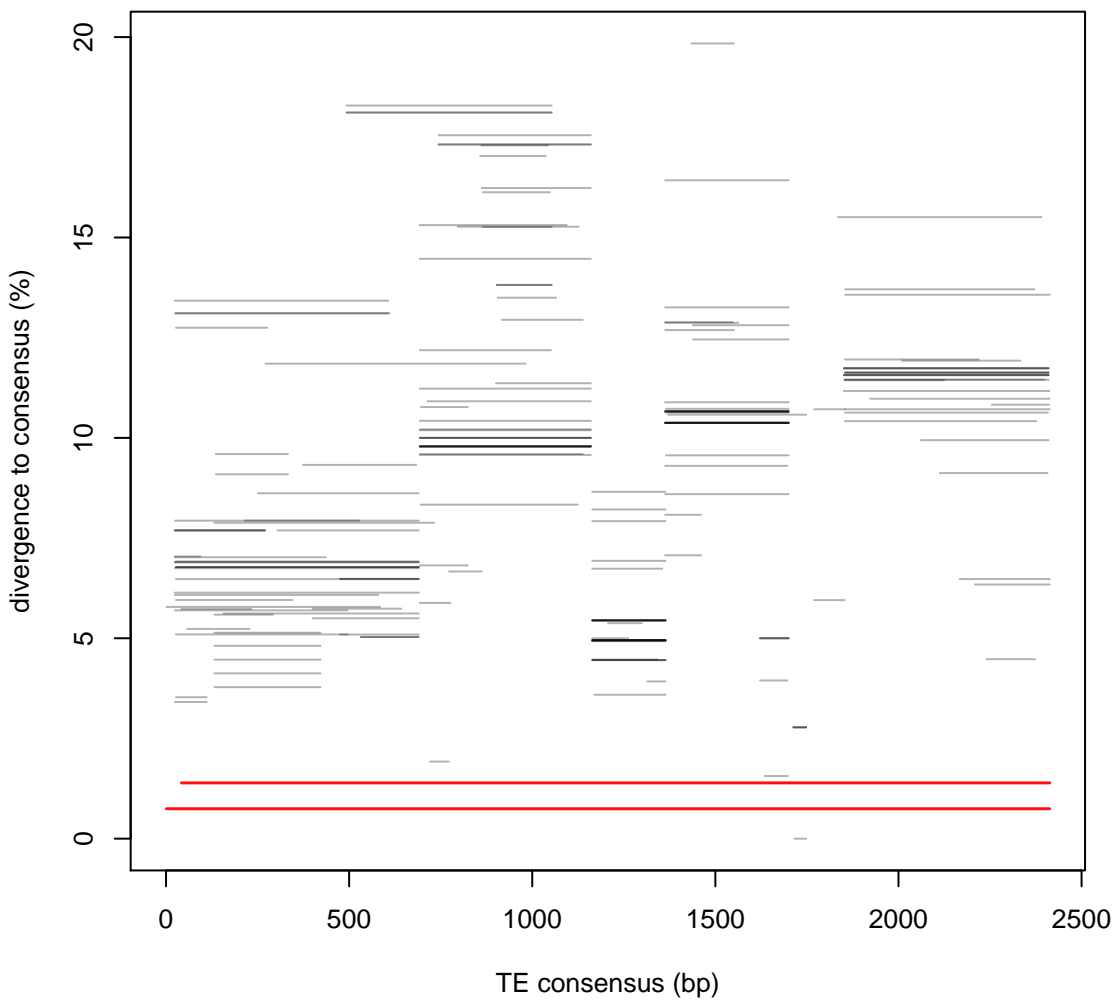
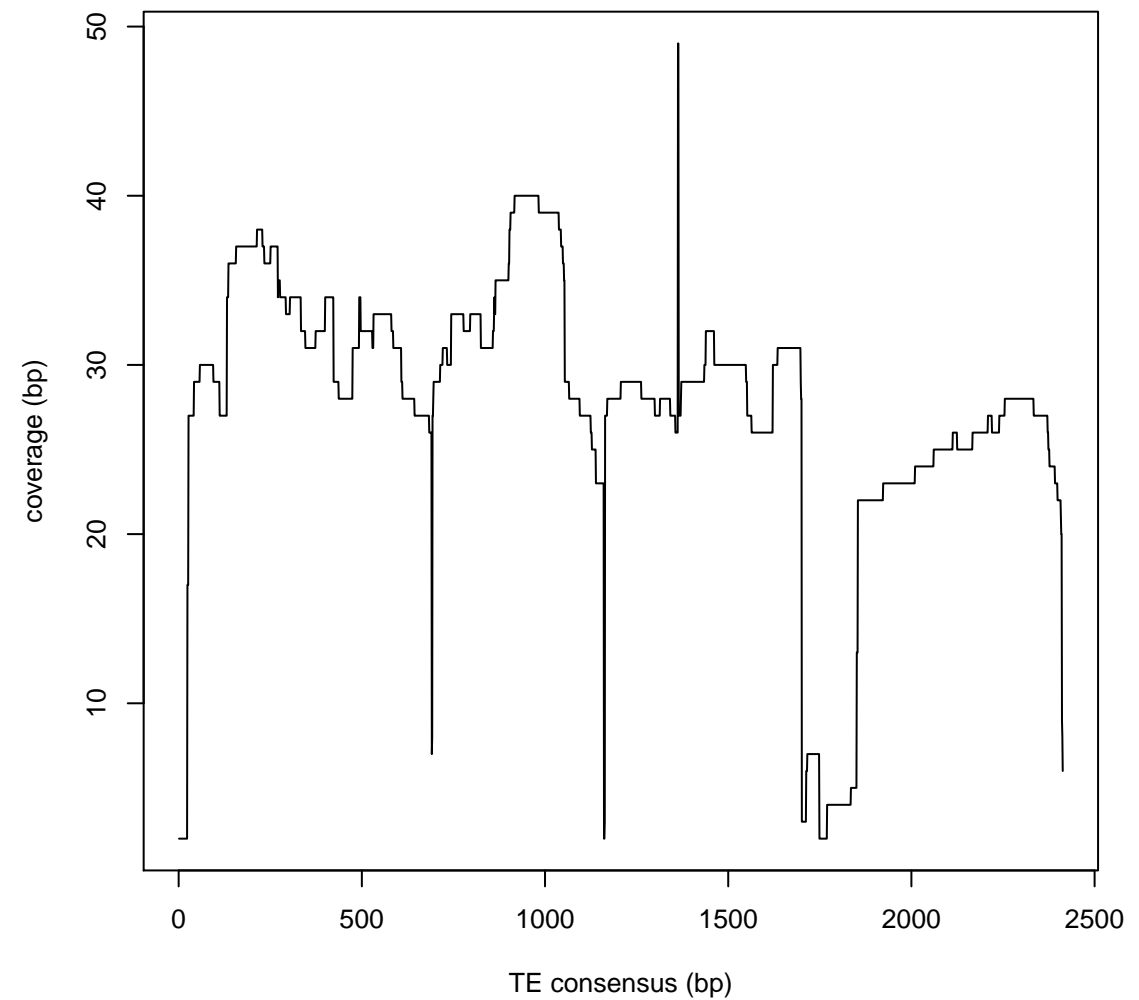


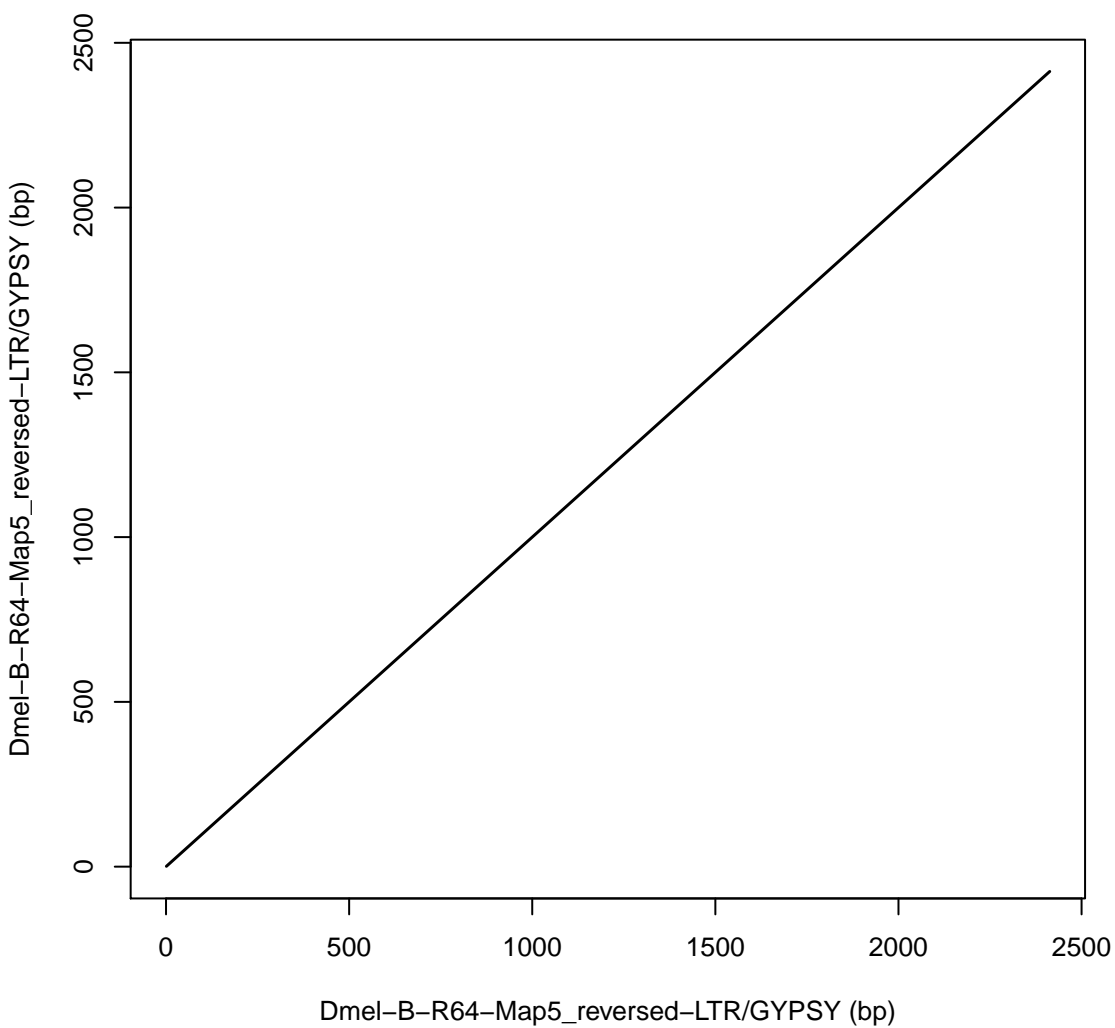
TE: Dmel-B-R64-Map5_reversed-LTR/GYPSY
consensus size: 2413bp; fragments: 191; full length: 2 (>=2171.7bp)



TE consensus genomic coverage



TE consensus self dotplot (blastn)



TE consensus structure and protein hits

