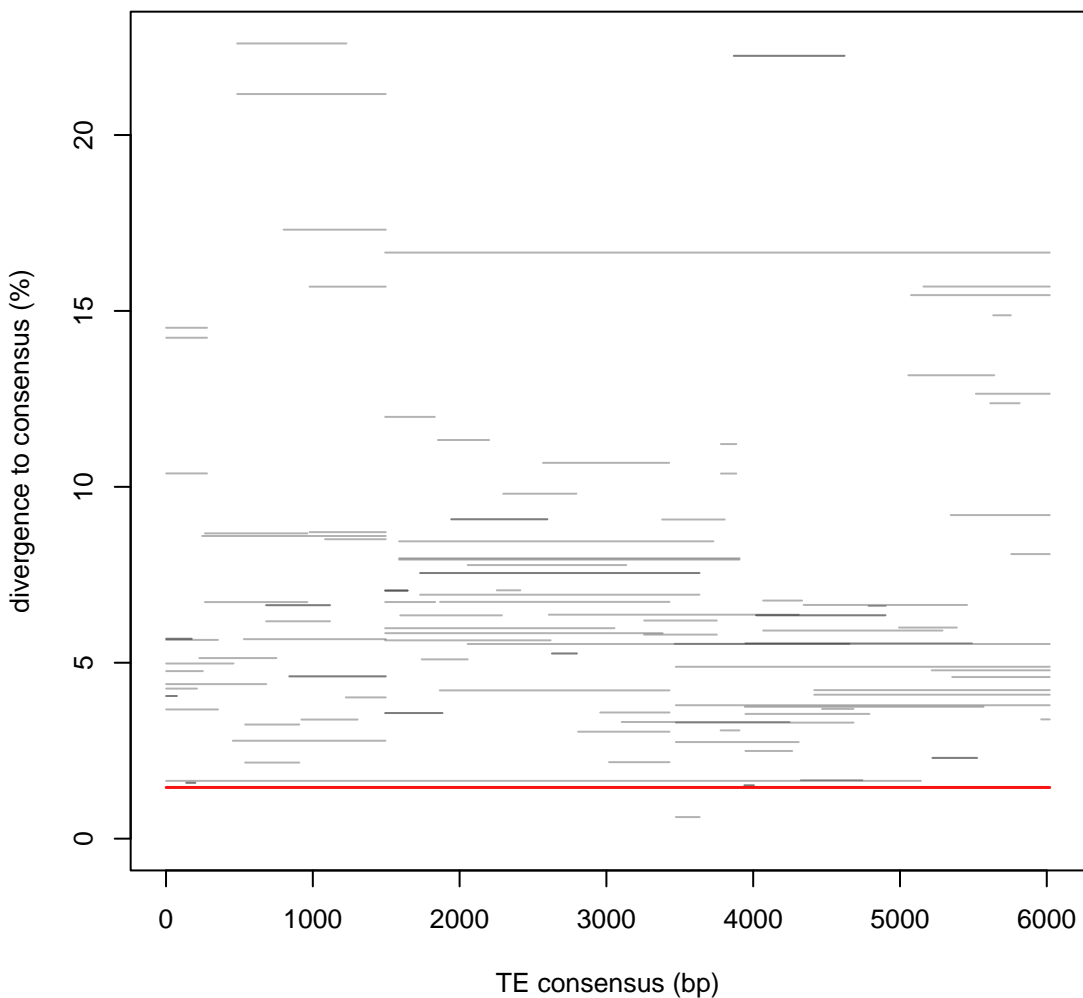
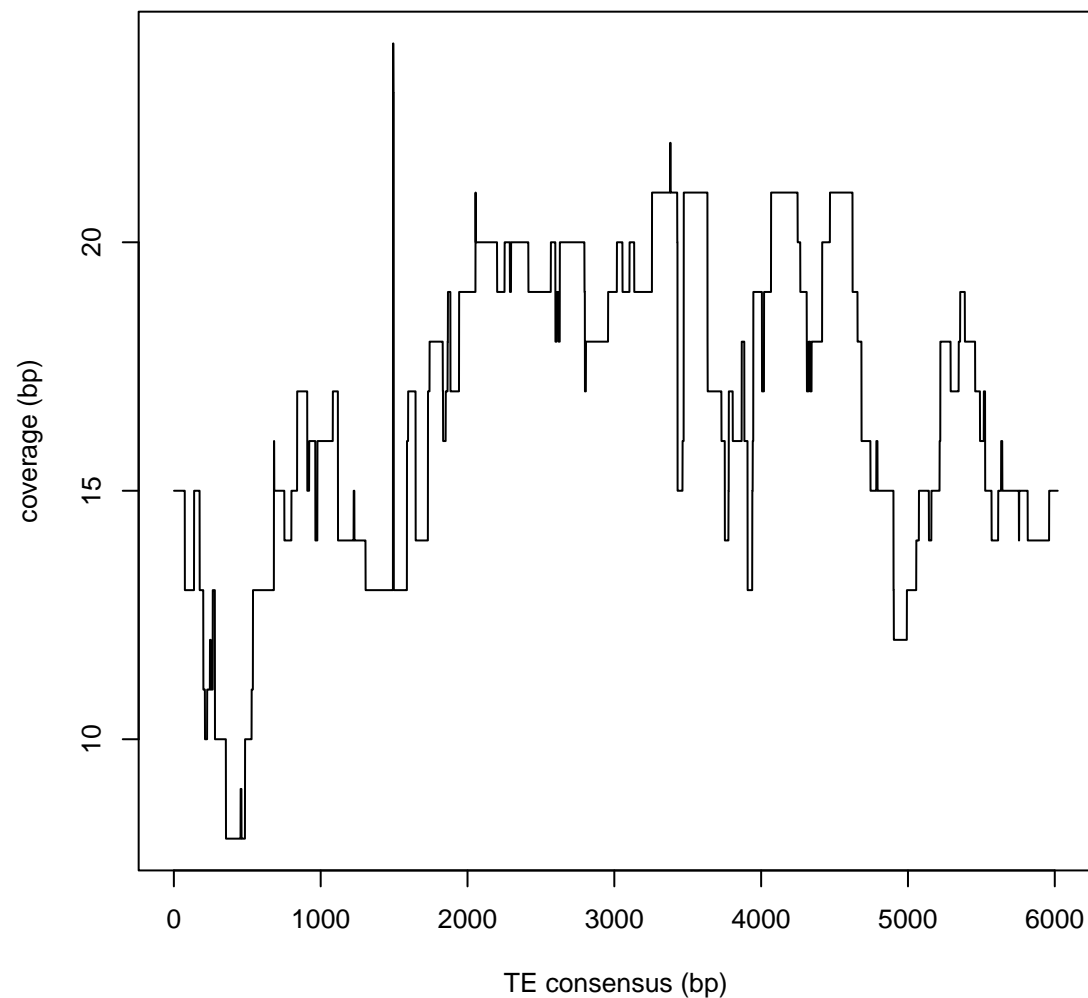


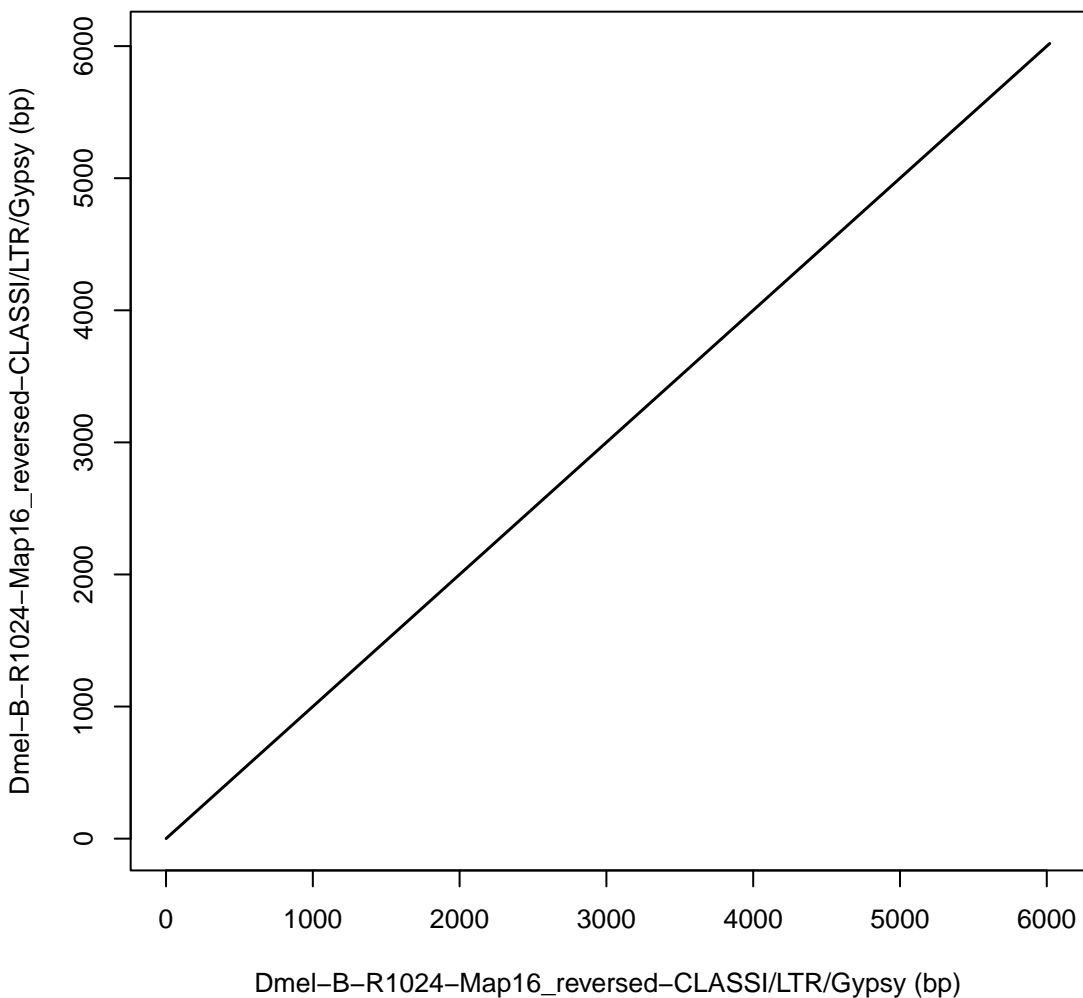
TE: Dmel-B-R1024-Map16_reversed-CLASSI/LTR/Gypsy
consensus size: 6020bp; fragments: 118; full length: 1 (>=5418bp)



TE consensus genomic coverage



TE consensus self dotplot (blastn)



TE consensus structure and protein hits

