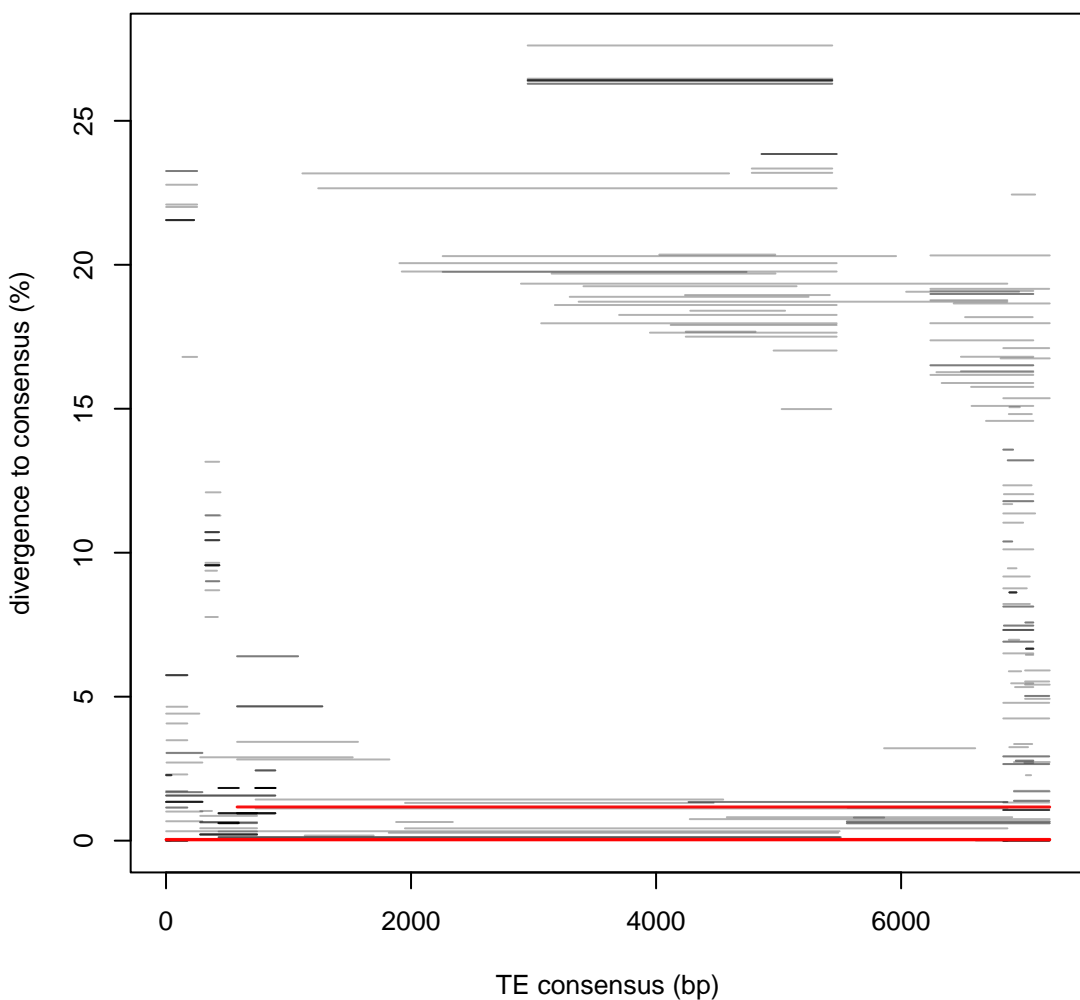
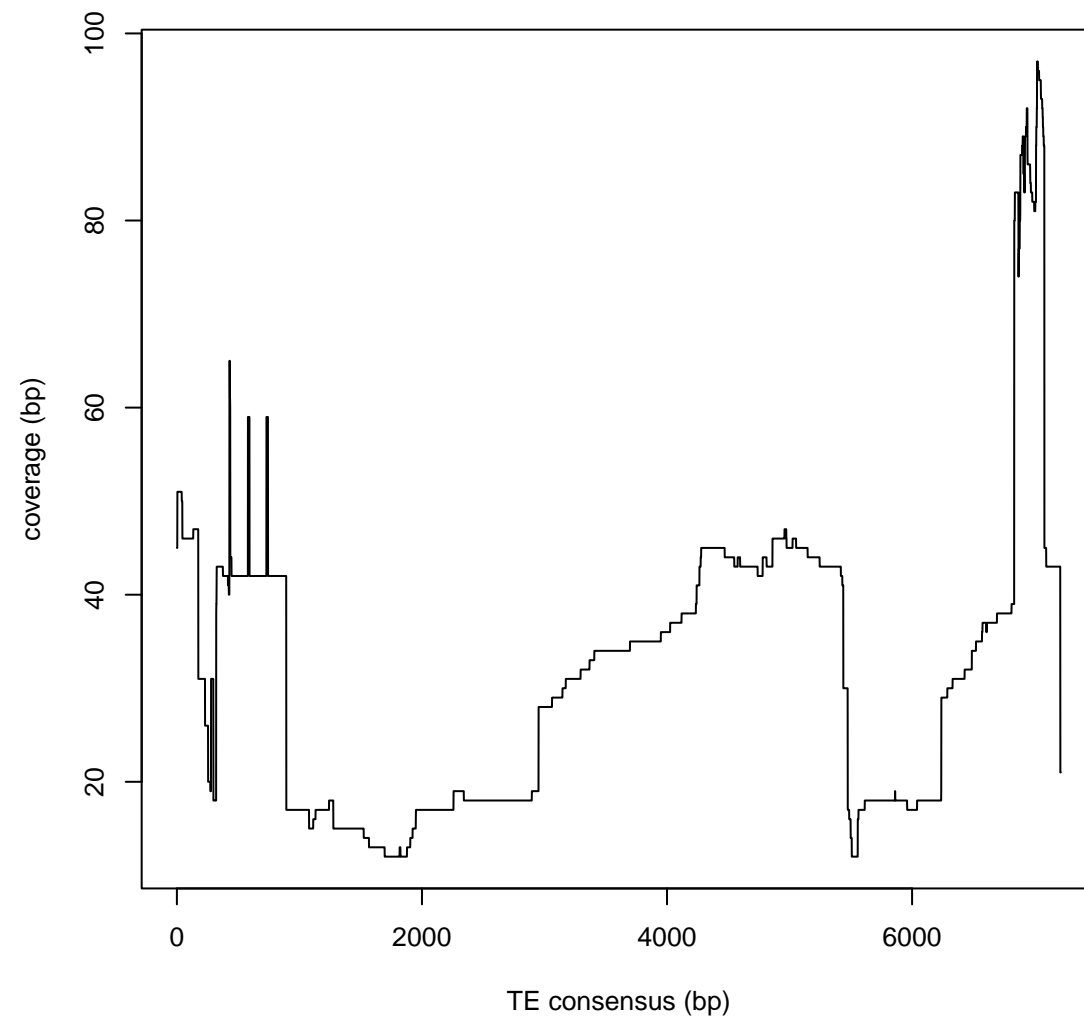


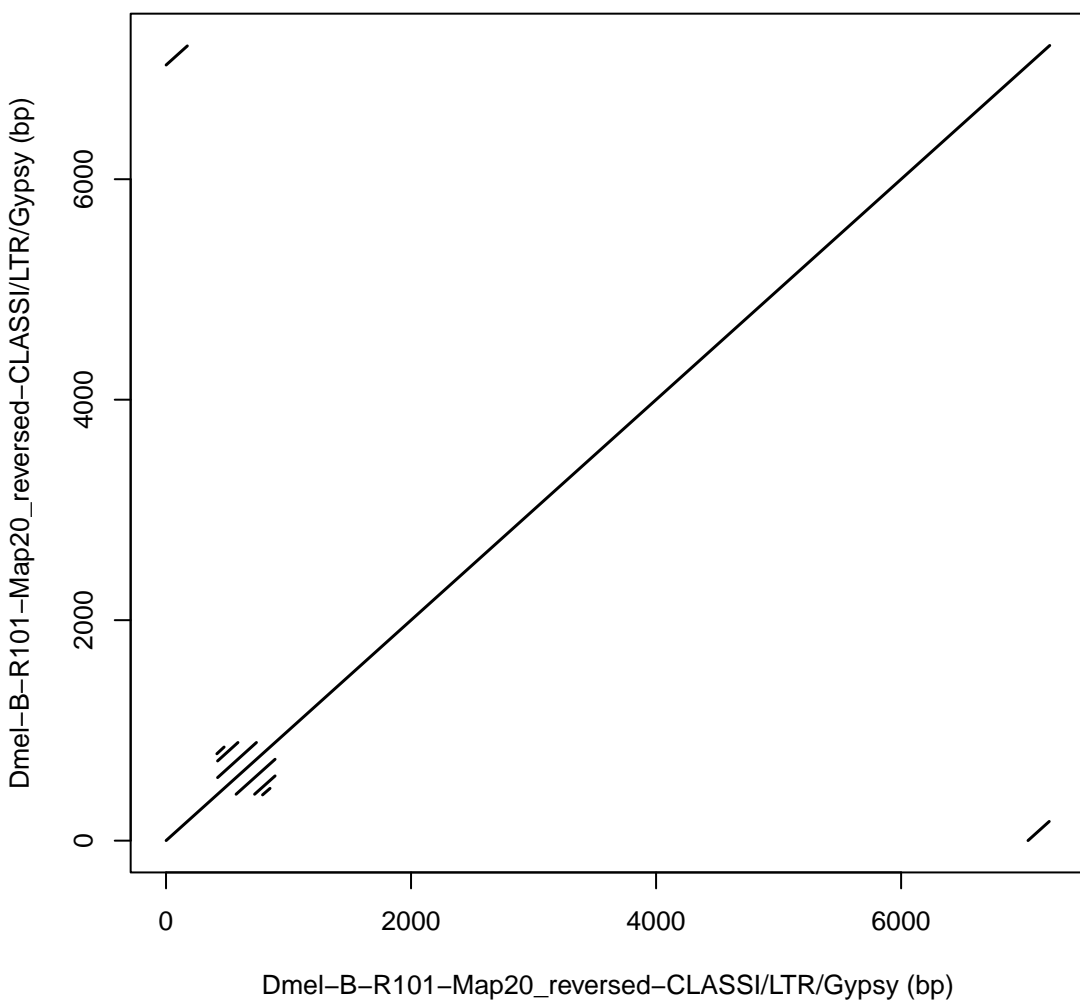
TE: Dmel-B-R101-Map20_reversed-CLASSI/LTR/Gypsy
consensus size: 7213bp; fragments: 308; full length: 3 (>=6491.7bp)



TE consensus genomic coverage



TE consensus self dotplot (blastn)



TE consensus structure and protein hits

