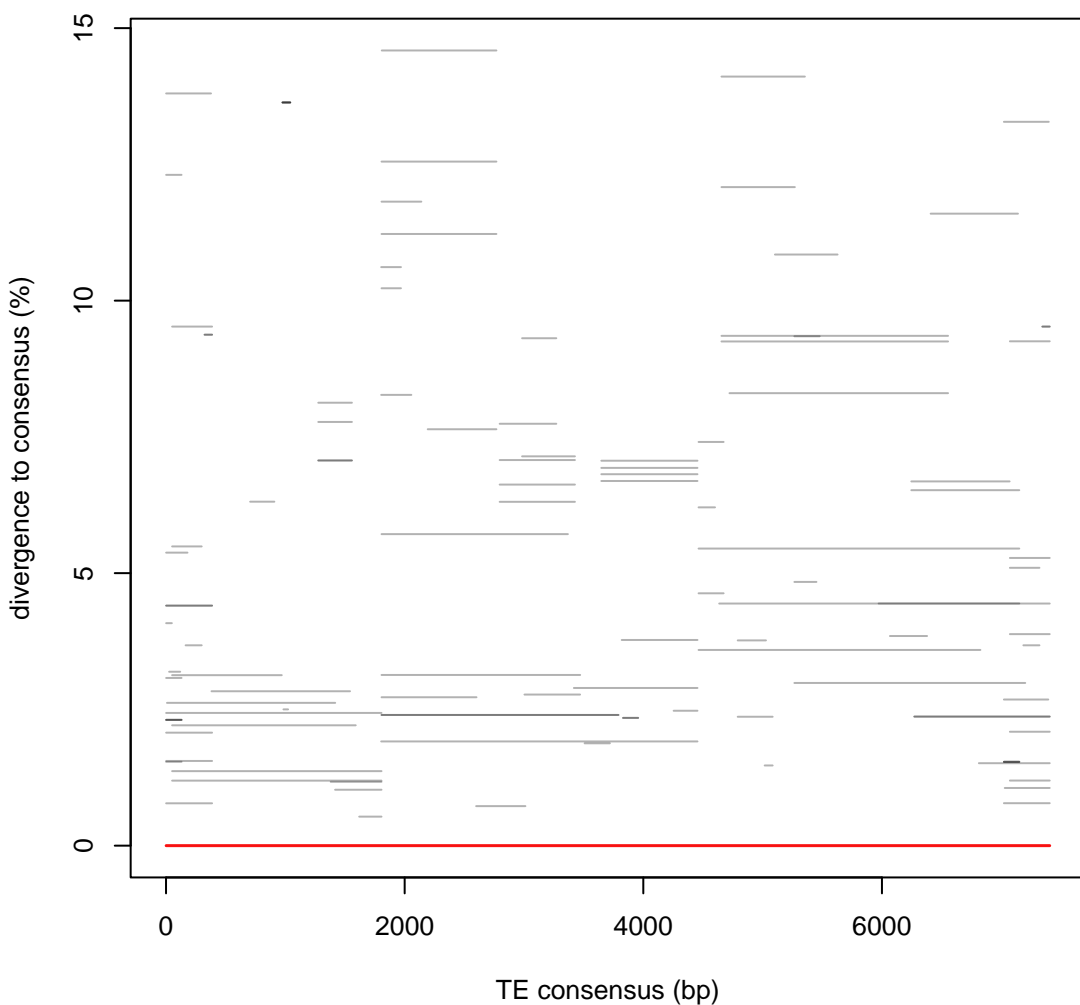
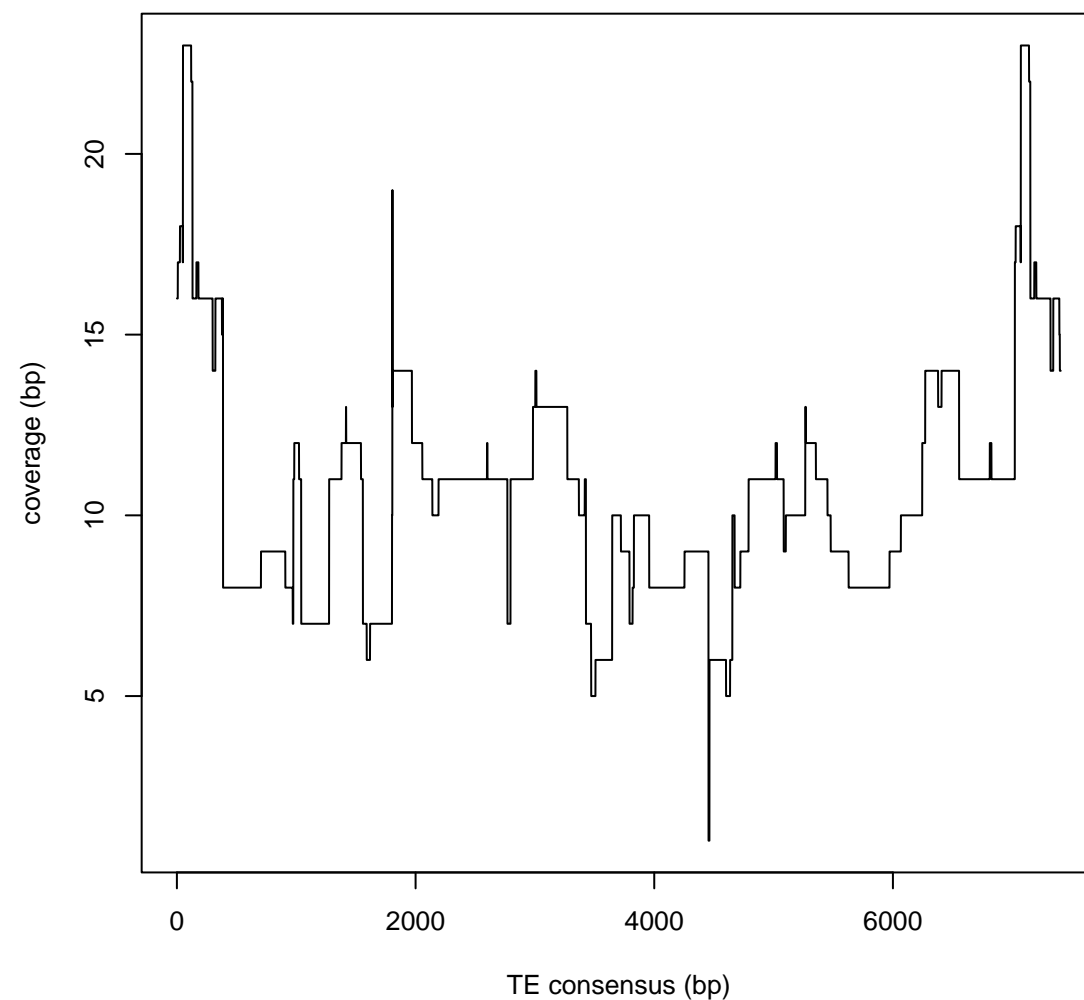


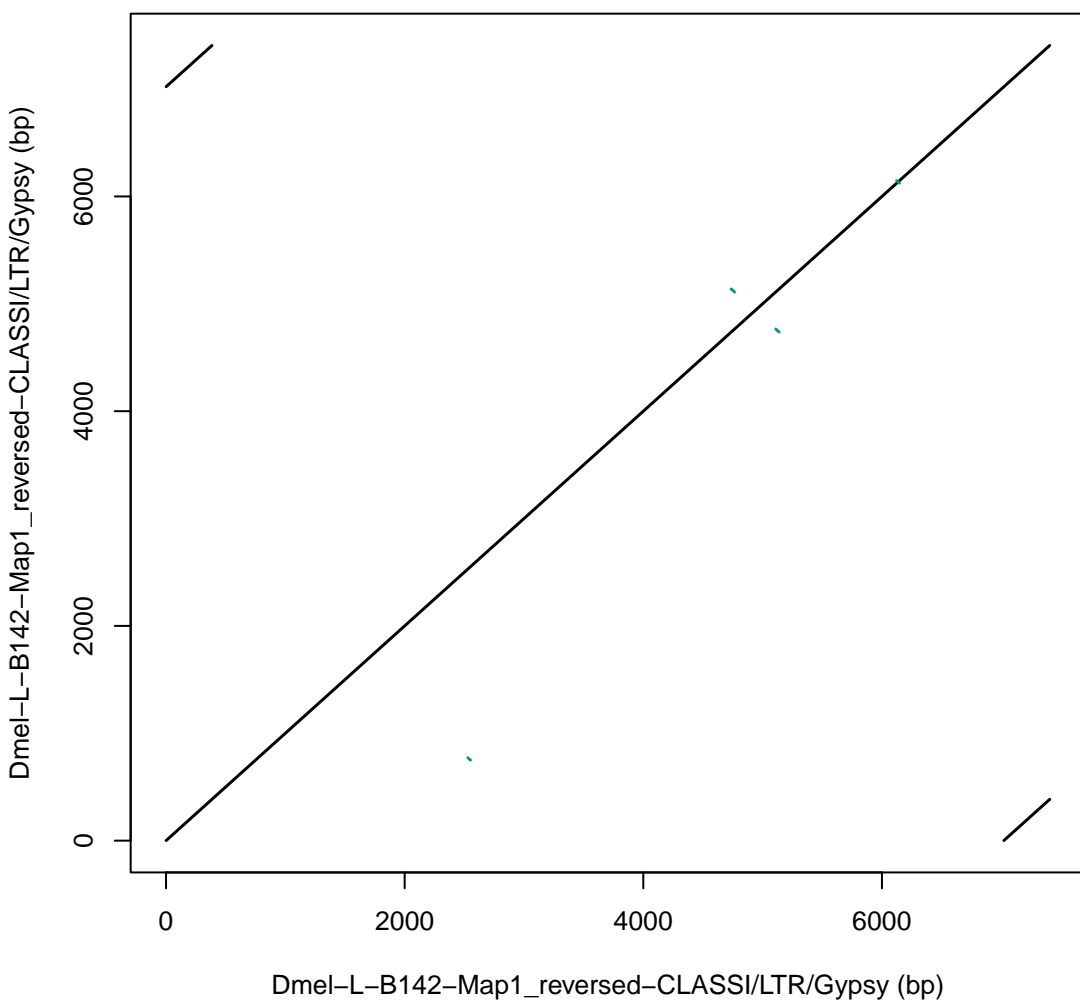
TE: Dmel-L-B142-Map1_reversed-CLASSI/LTR/Gypsy
consensus size: 7406bp; fragments: 115; full length: 1 (>=6665.4bp)



TE consensus genomic coverage



TE consensus self dotplot (blastn)



TE consensus structure and protein hits

