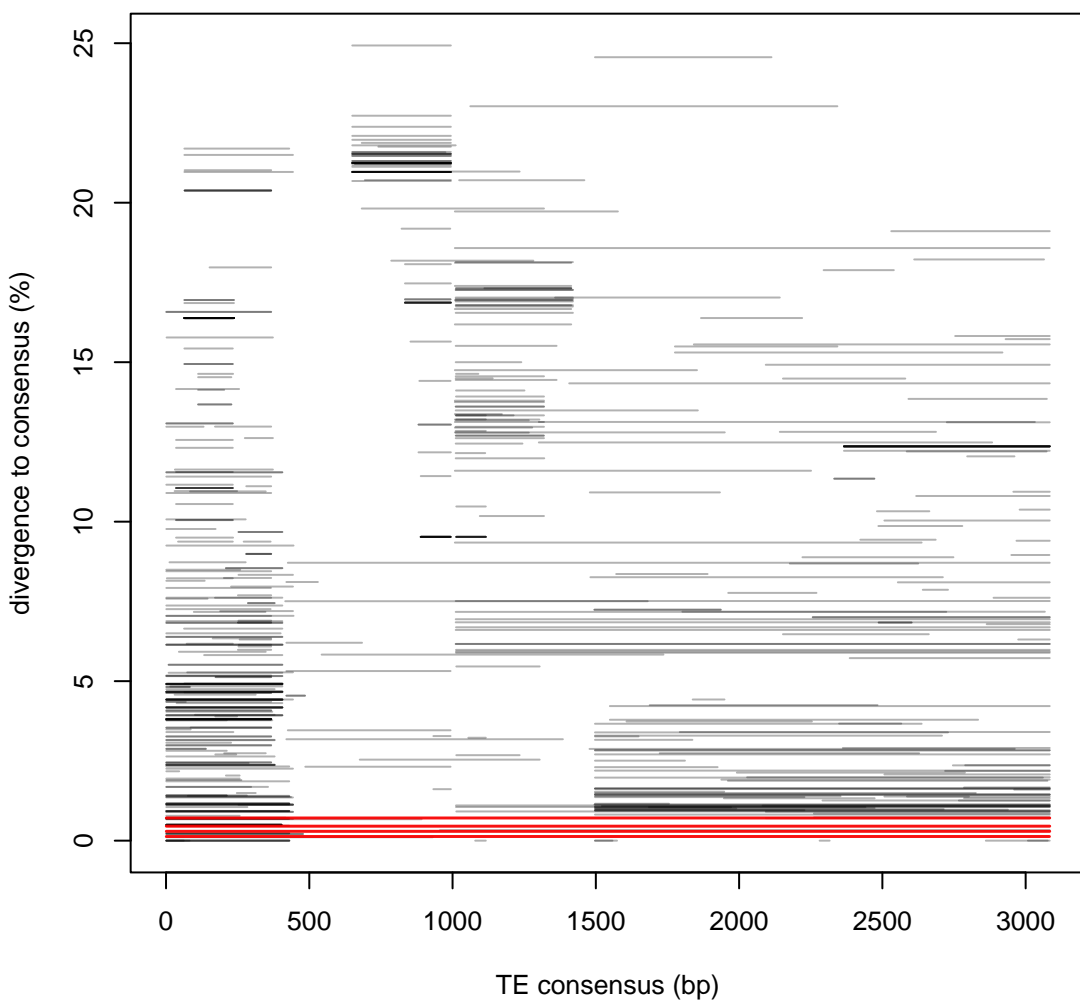
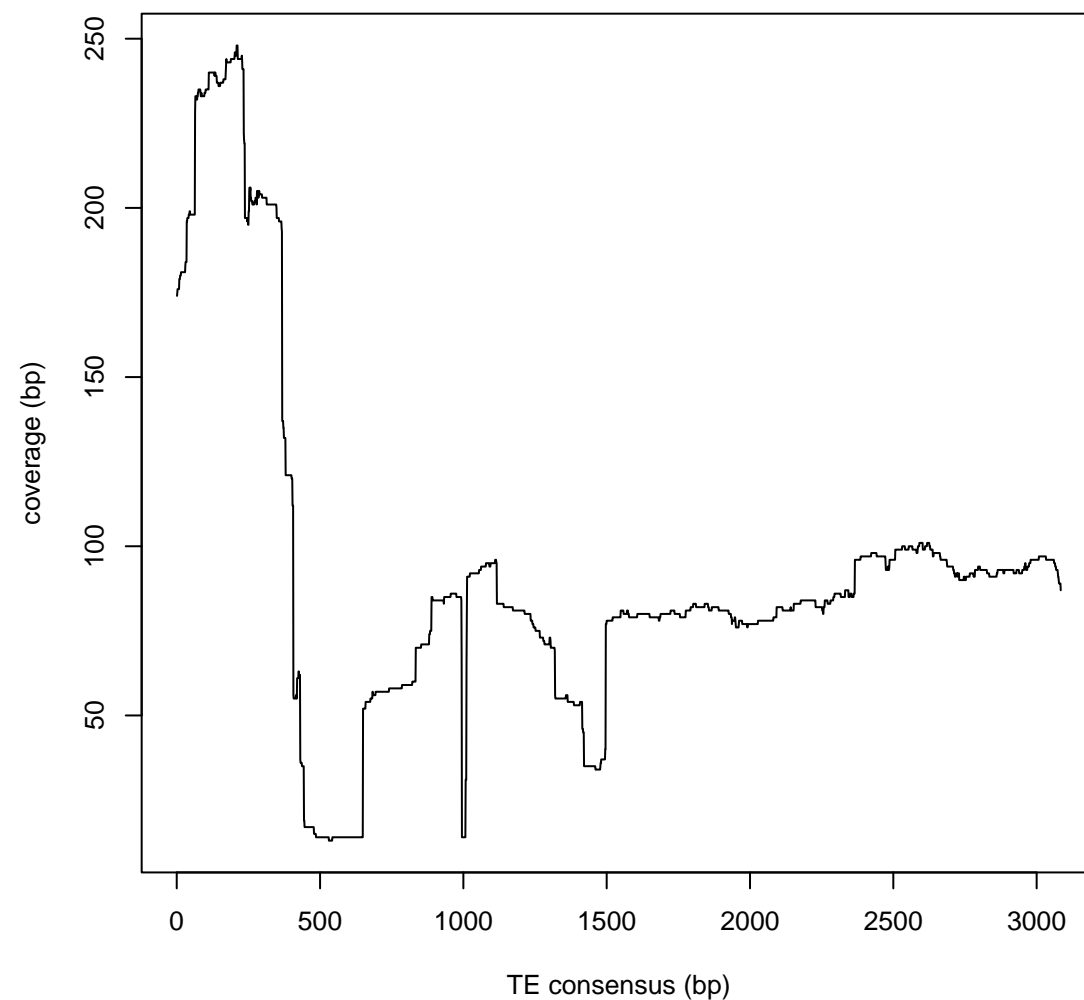


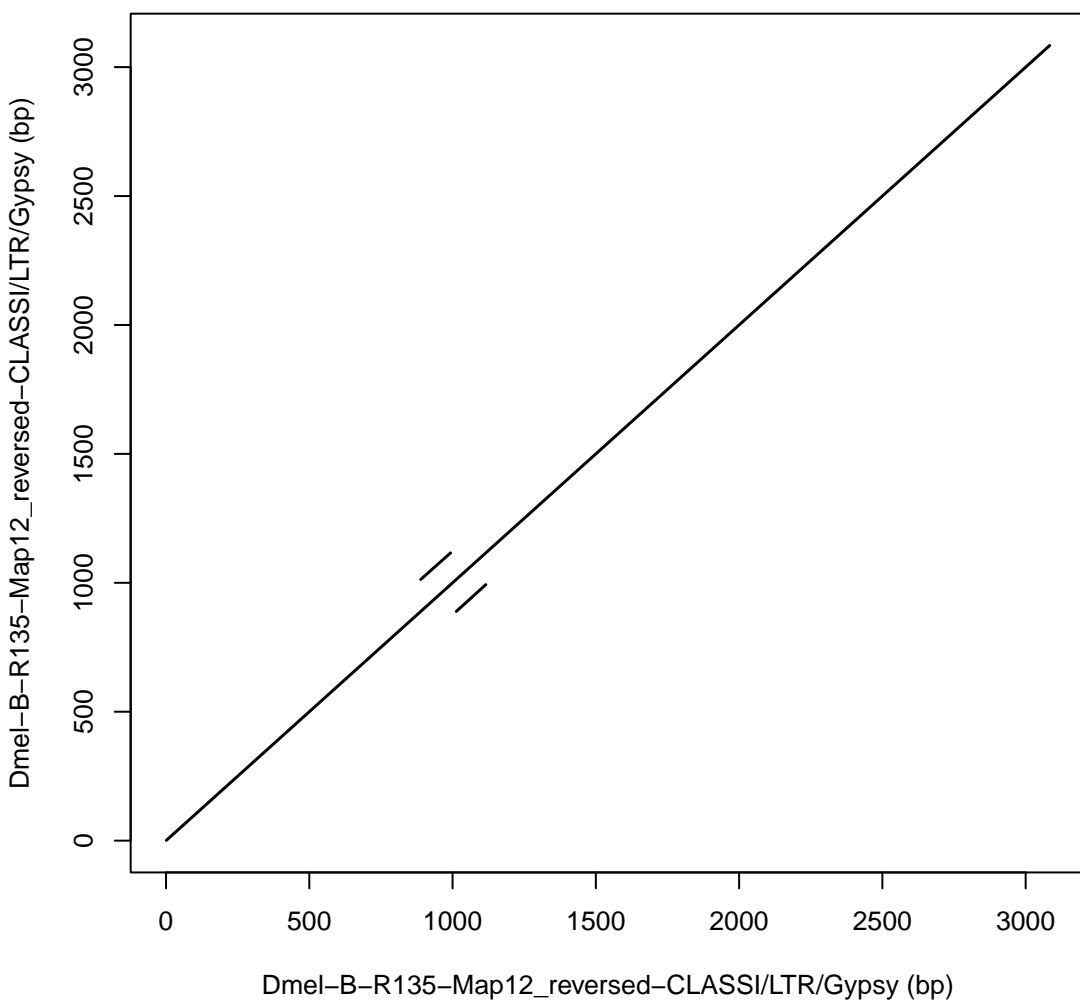
TE: Dmel-B-R135-Map12_reversed-CLASSI/LTR/Gypsy
consensus size: 3084bp; fragments: 590; full length: 4 (>=2775.6bp)



TE consensus genomic coverage



TE consensus self dotplot (blastn)



TE consensus structure and protein hits

