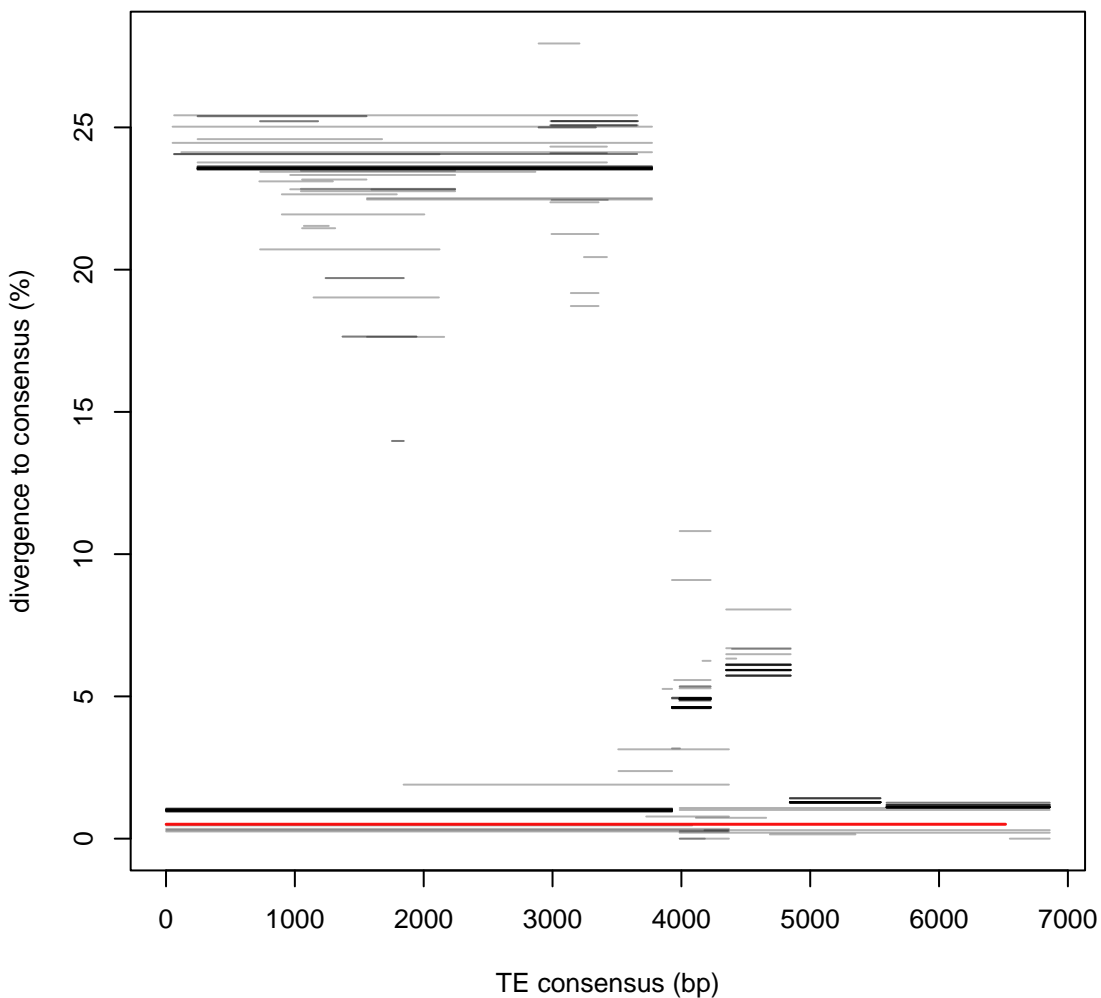
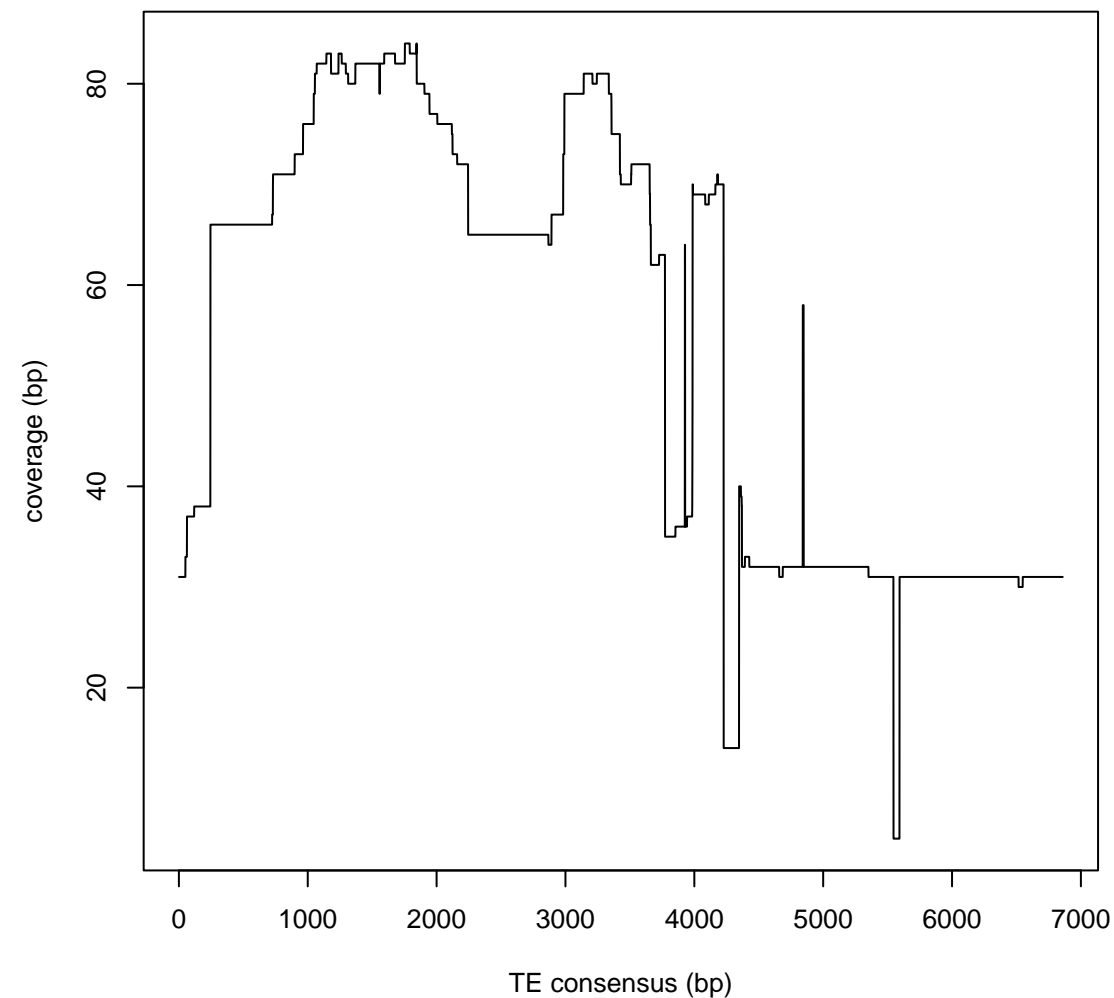


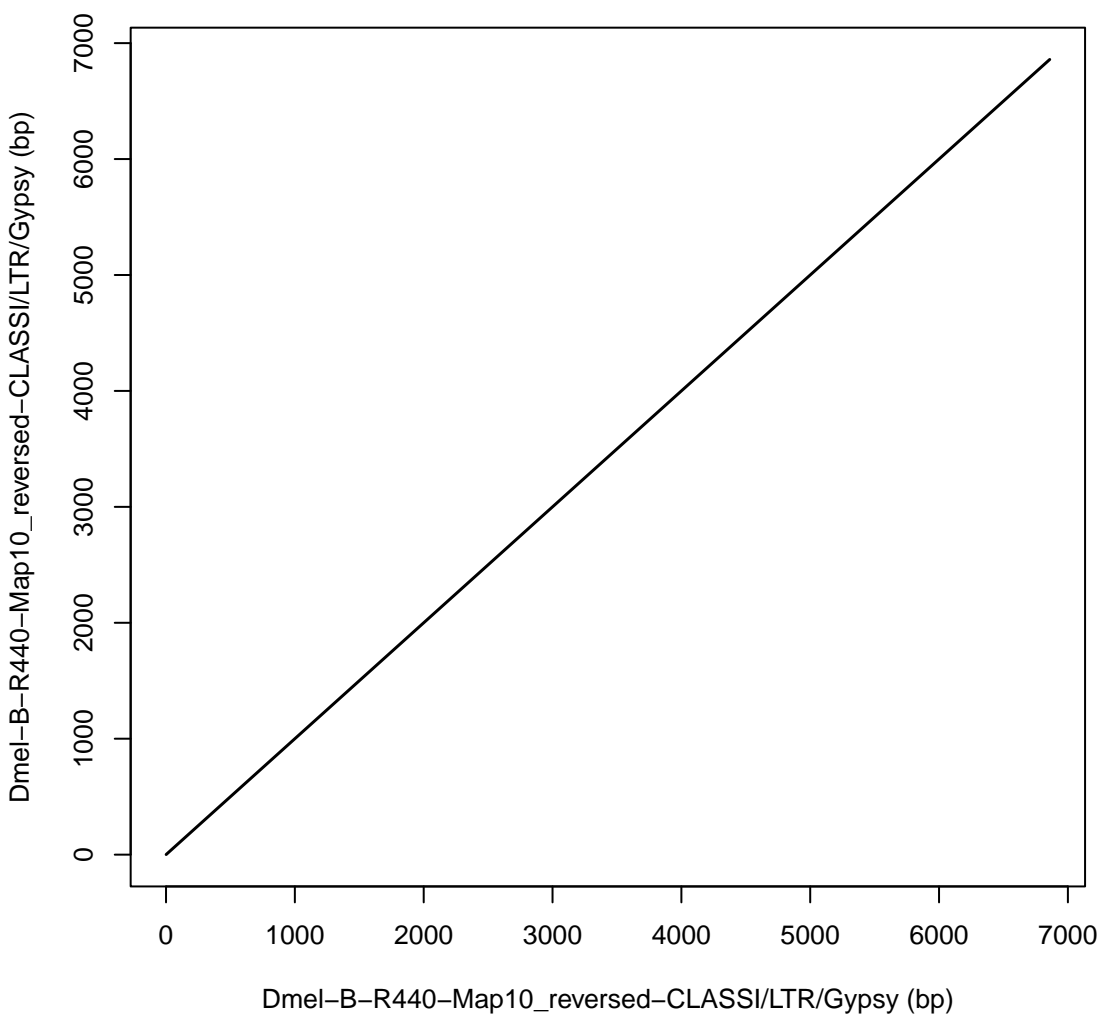
TE: Dmel-B-R440-Map10_reversed-CLASSI/LTR/Gypsy
consensus size: 6859bp; fragments: 262; full length: 1 (>=6173.1bp)



TE consensus genomic coverage



TE consensus self dotplot (blastn)



TE consensus structure and protein hits

