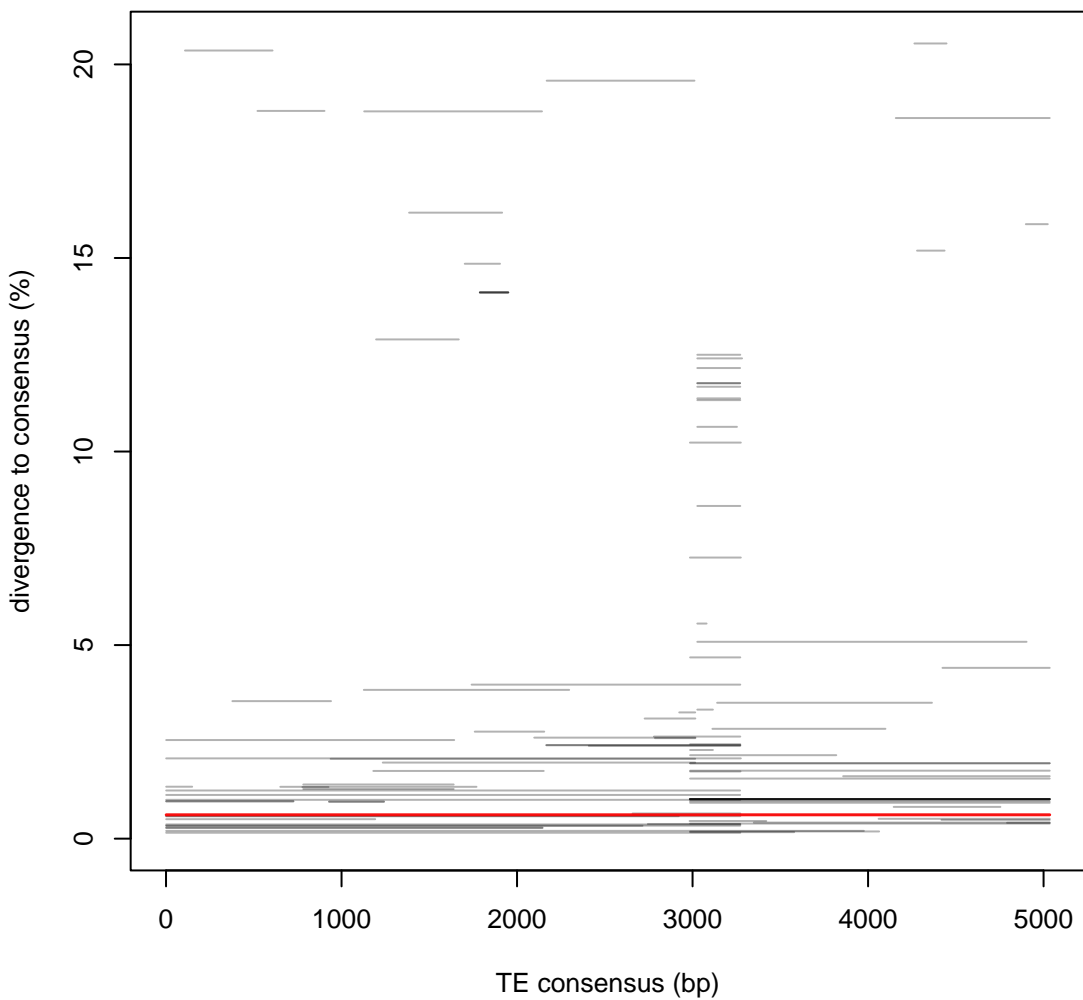
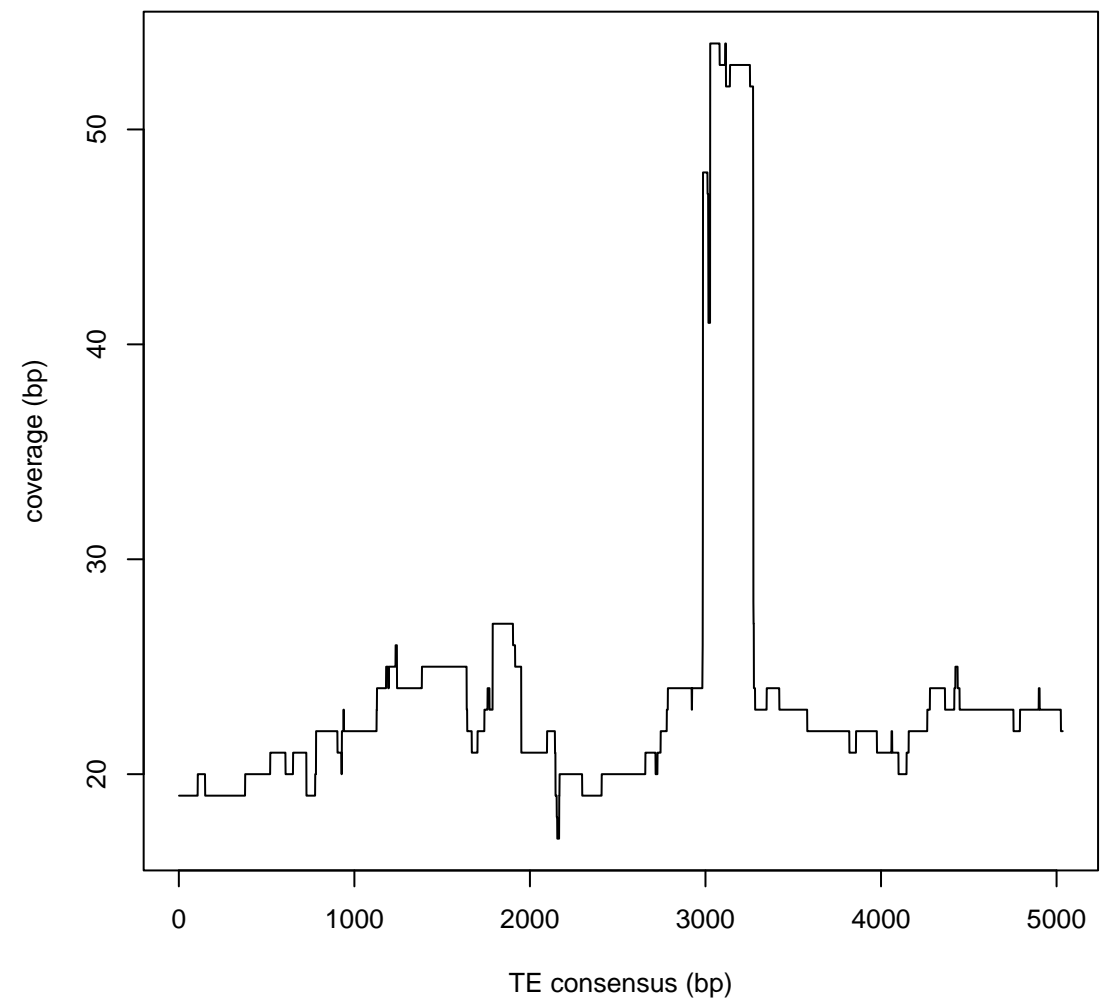


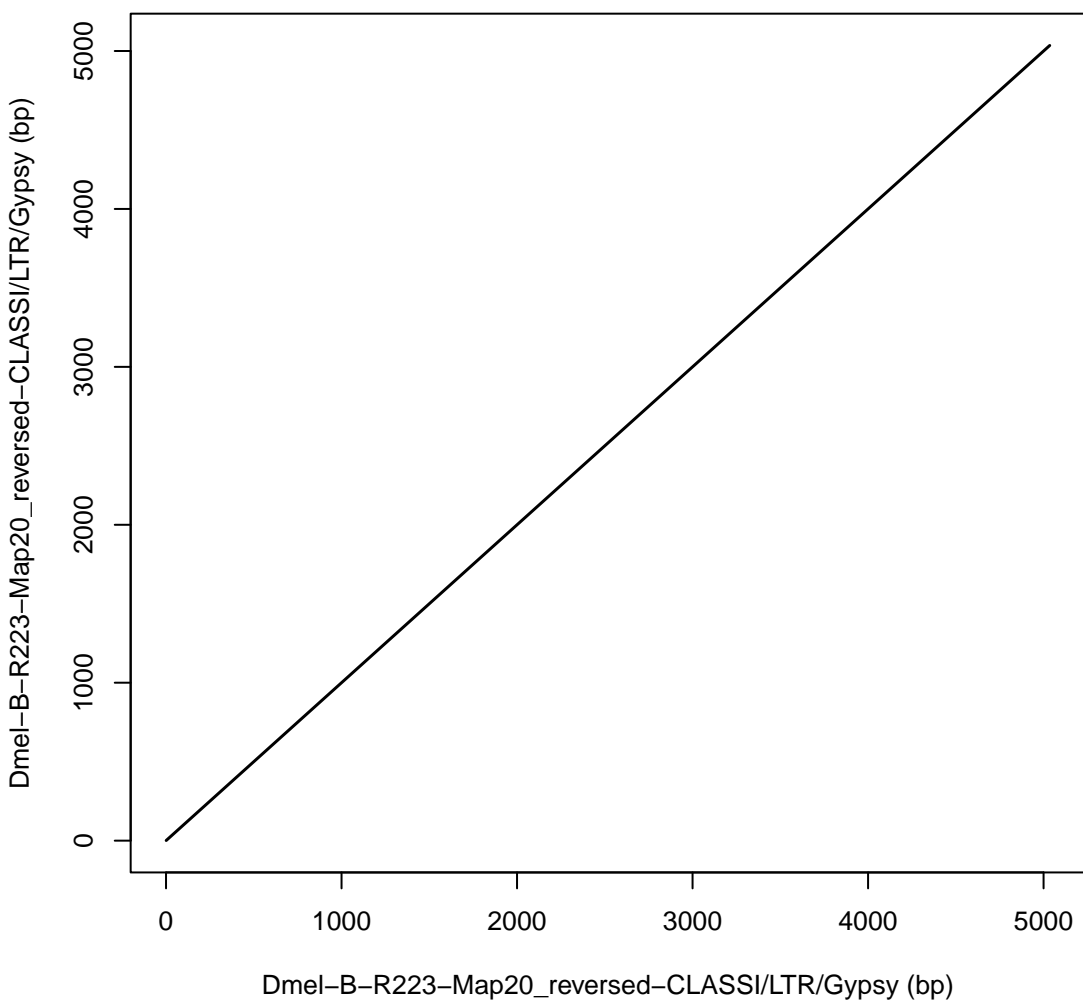
TE: Dmel-B-R223-Map20_reversed-CLASSI/LTR/Gypsy
consensus size: 5035bp; fragments: 103; full length: 1 (>=4531.5bp)



TE consensus genomic coverage



TE consensus self dotplot (blastn)



TE consensus structure and protein hits

