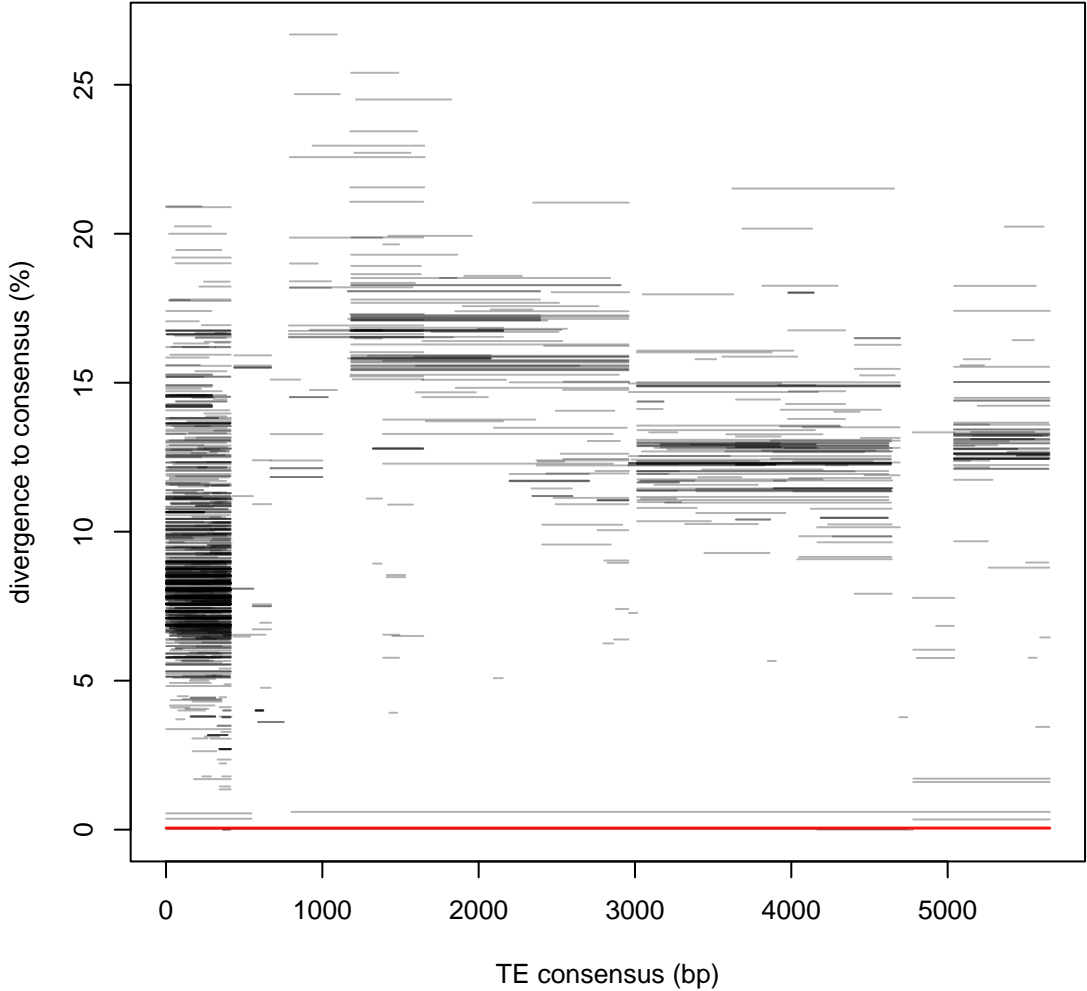
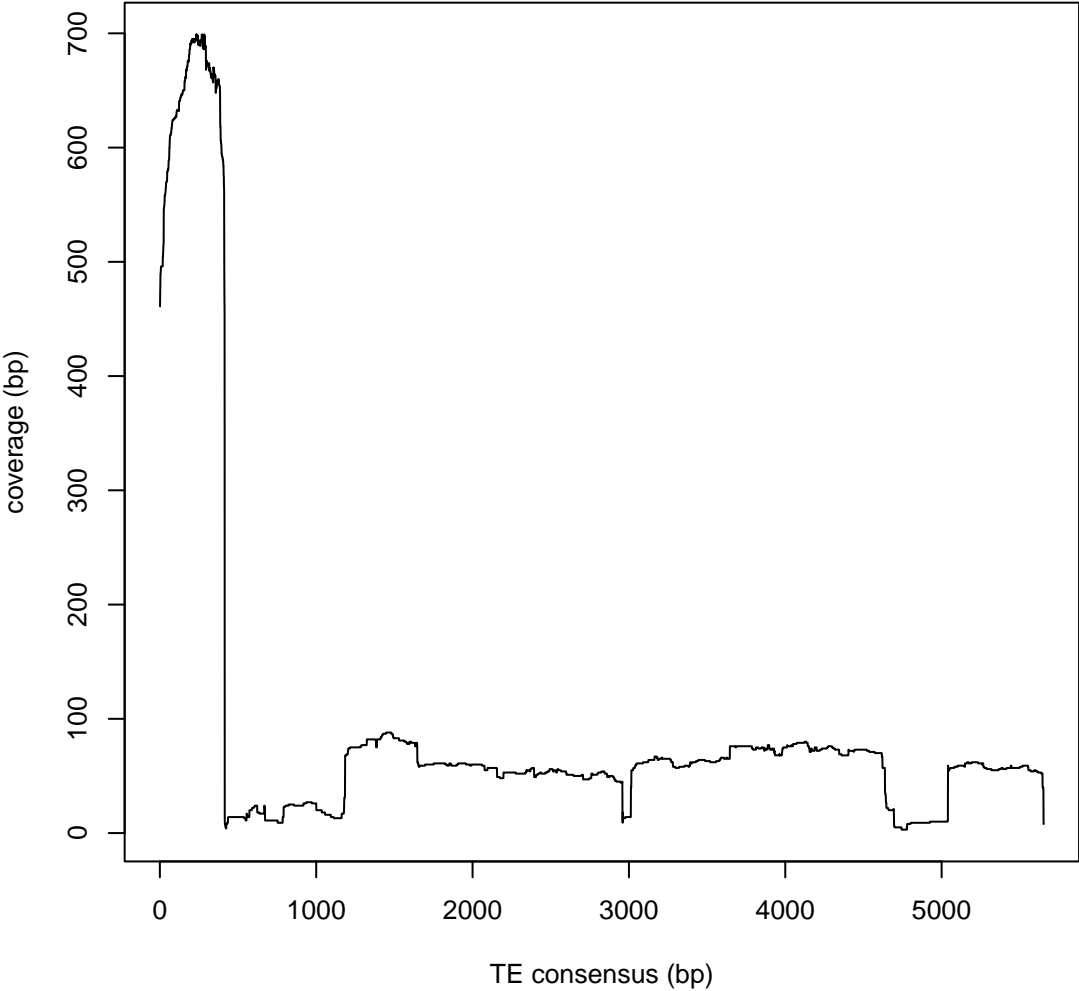


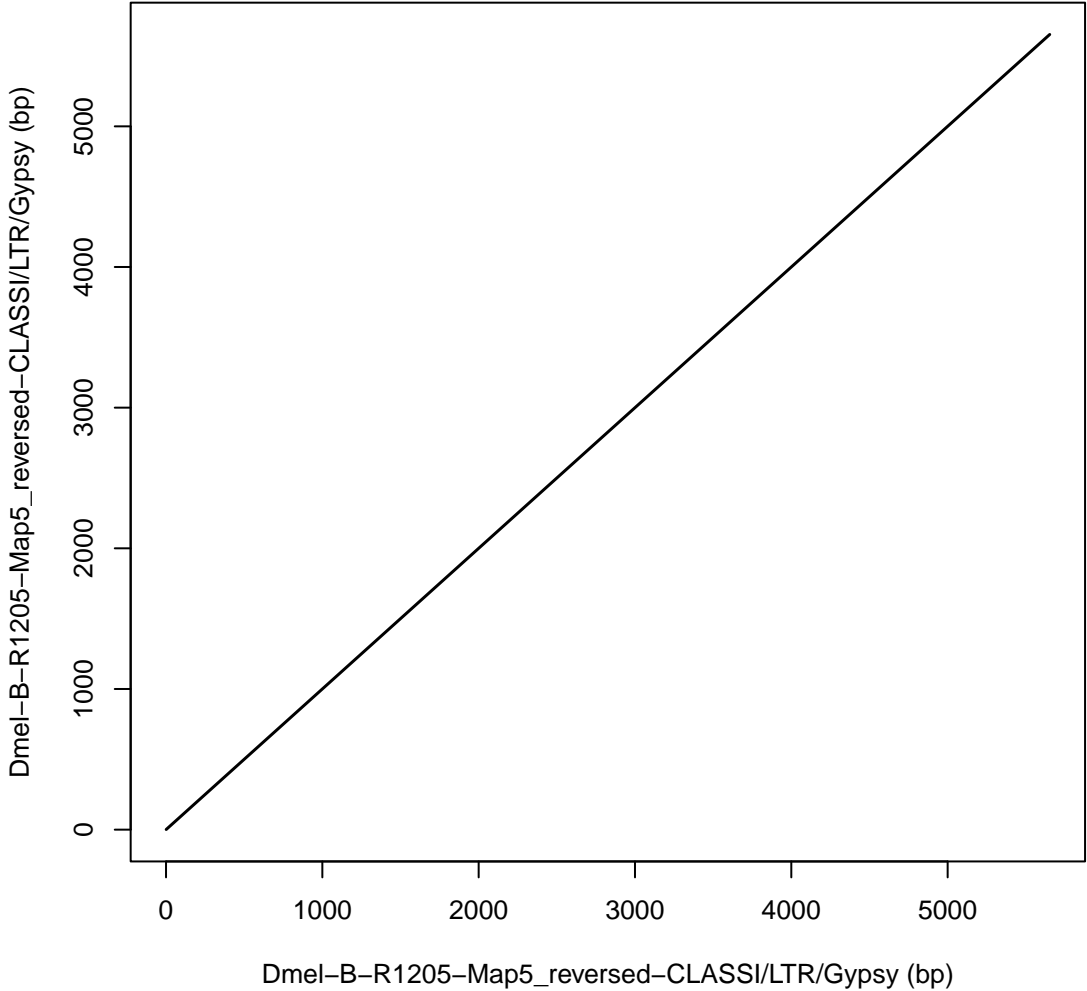
TE: Dmel-B-R1205-Map5_reversed-CLASSI/LTR/Gypsy
consensus size: 5653bp; fragments: 1234; full length: 1 (>=5087.7bp)



TE consensus genomic coverage



TE consensus self dotplot (blastn)



TE consensus structure and protein hits

