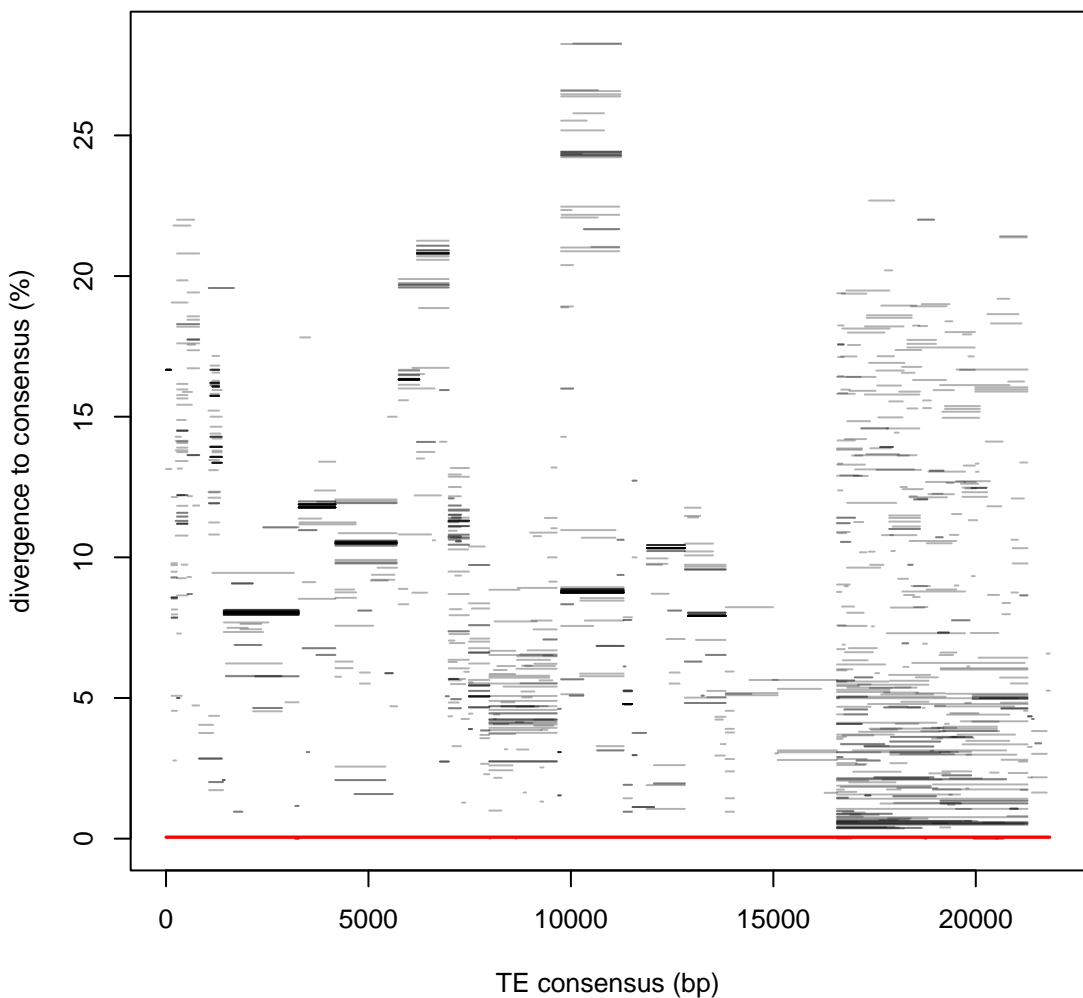
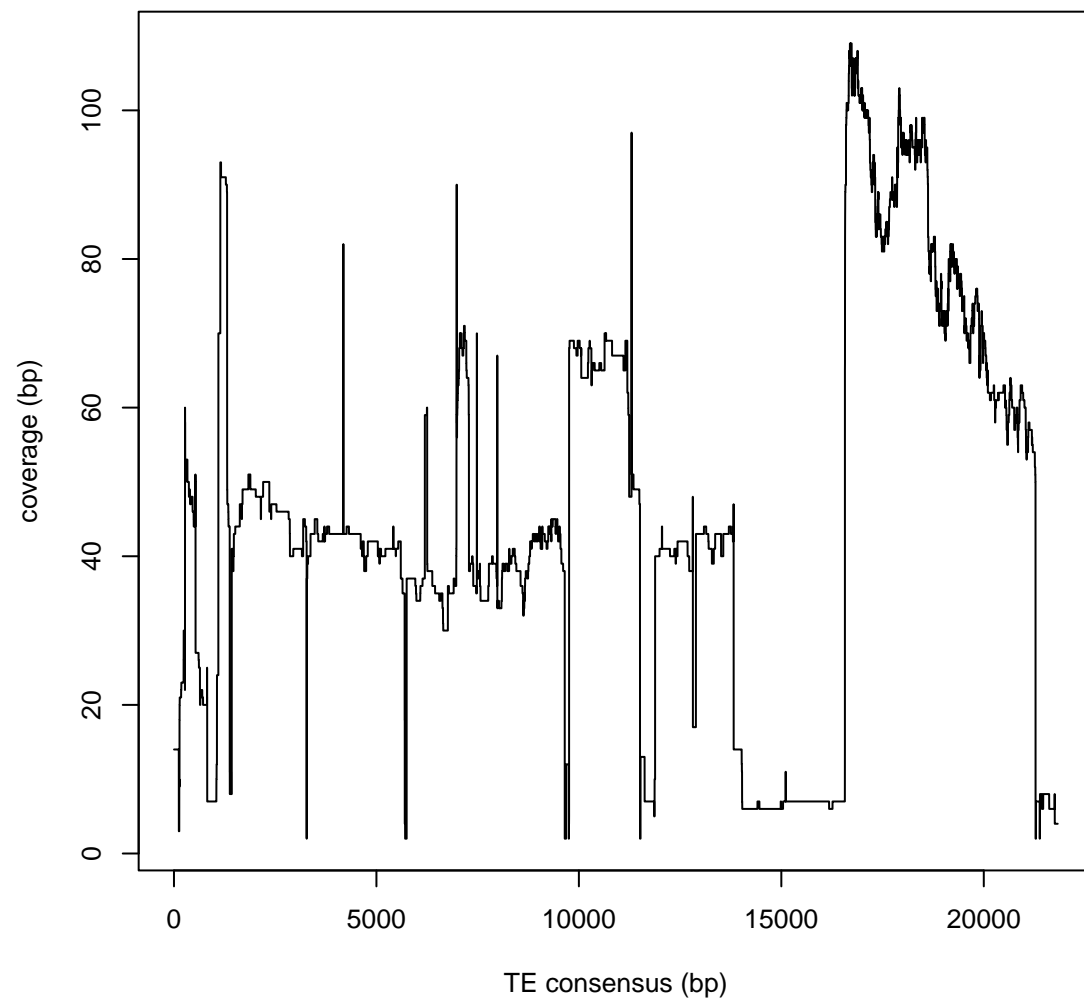


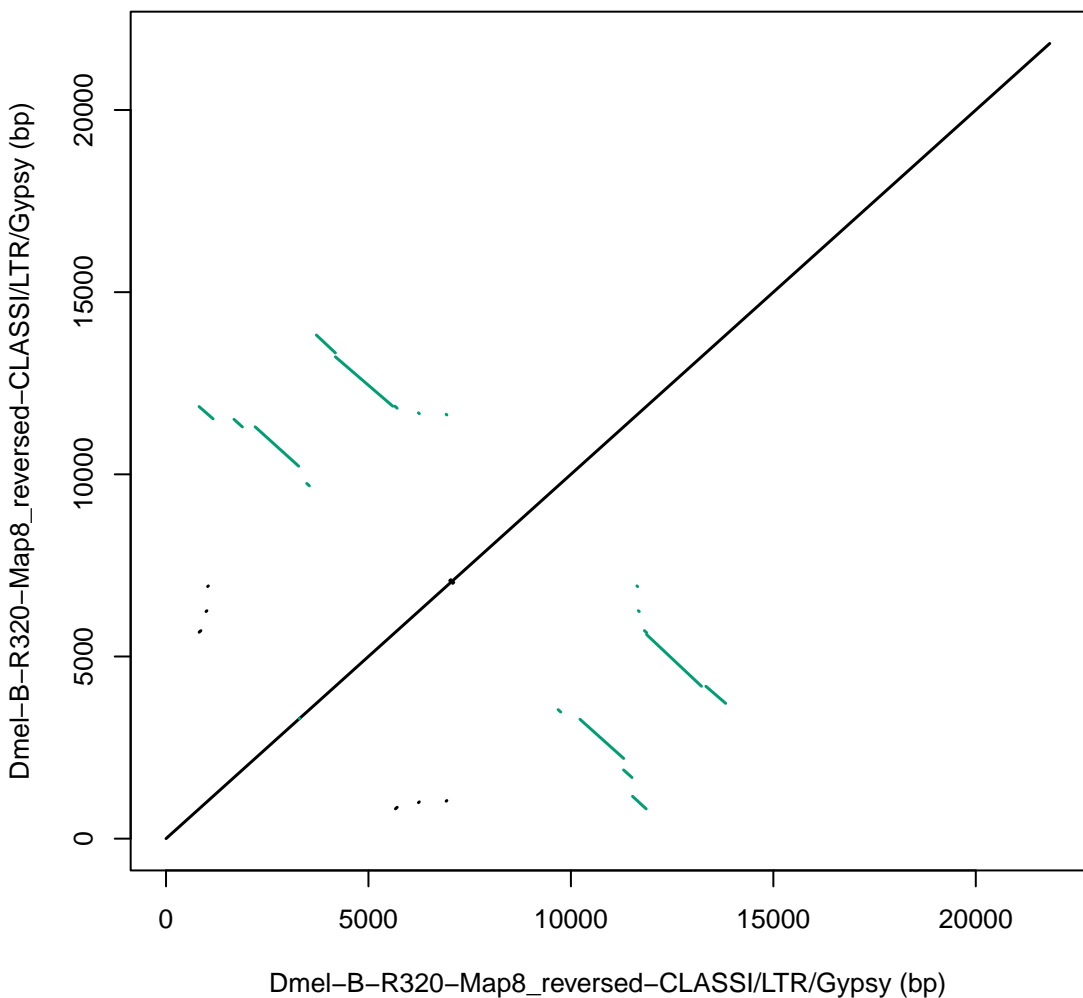
TE: Dmel-B-R320-Map8\_reversed-CLASSI/LTR/Gypsy  
consensus size: 21826bp; fragments: 1340; full length: 2 (>=19643.4bp)



TE consensus genomic coverage



TE consensus self dotplot (blastn)



TE consensus structure and protein hits

