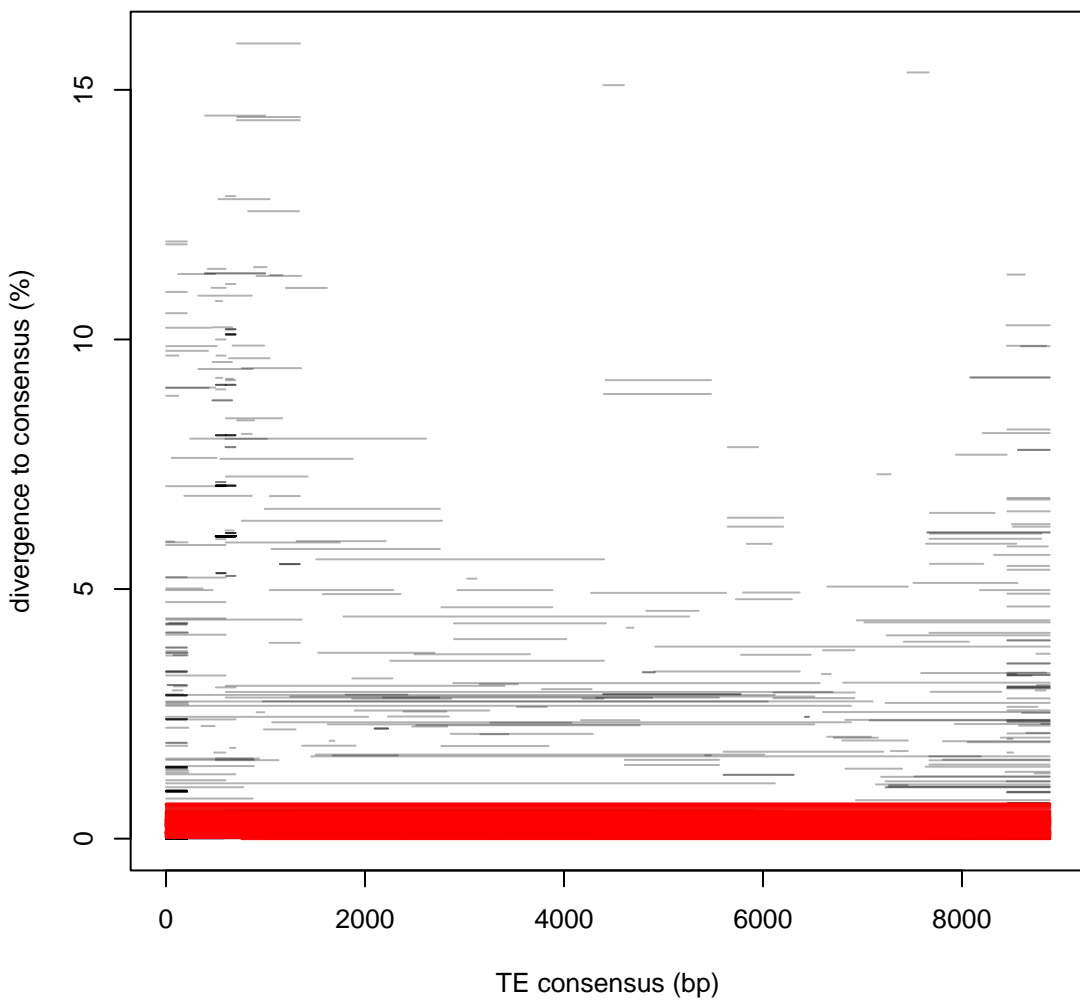
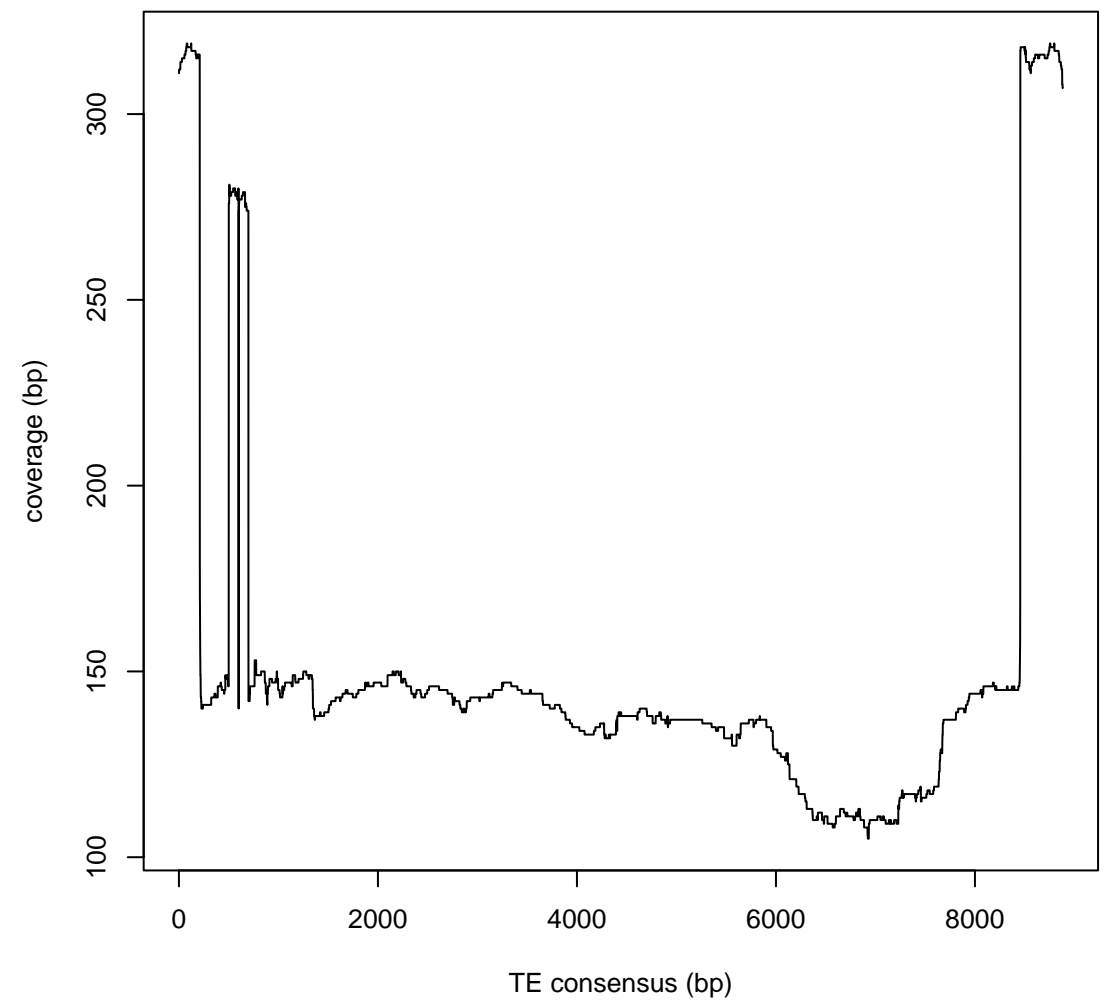


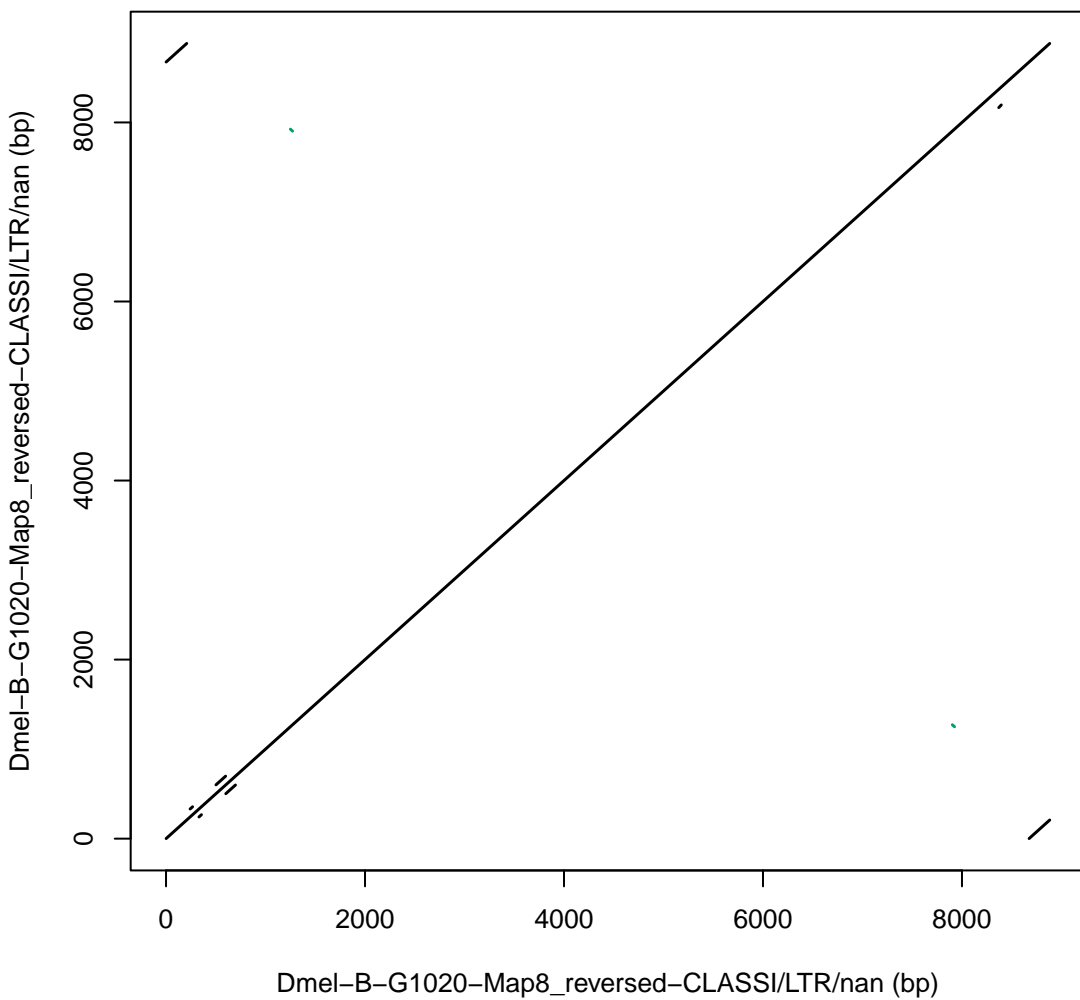
TE: Dmel-B-G1020-Map8\_reversed-CLASSI/LTR/nan  
consensus size: 8882bp; fragments: 1009; full length: 70 (>=7993.8bp)



TE consensus genomic coverage



TE consensus self dotplot (blastn)



TE consensus structure and protein hits

