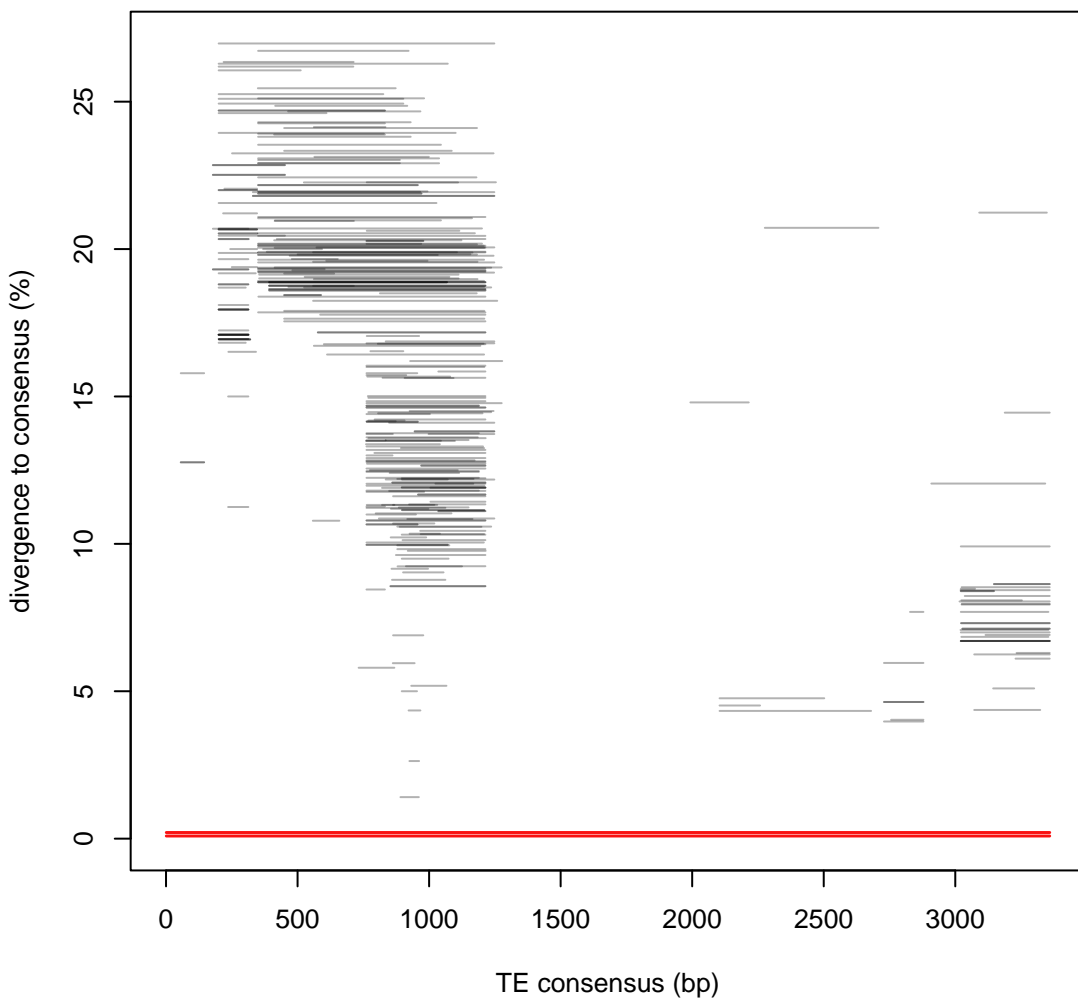
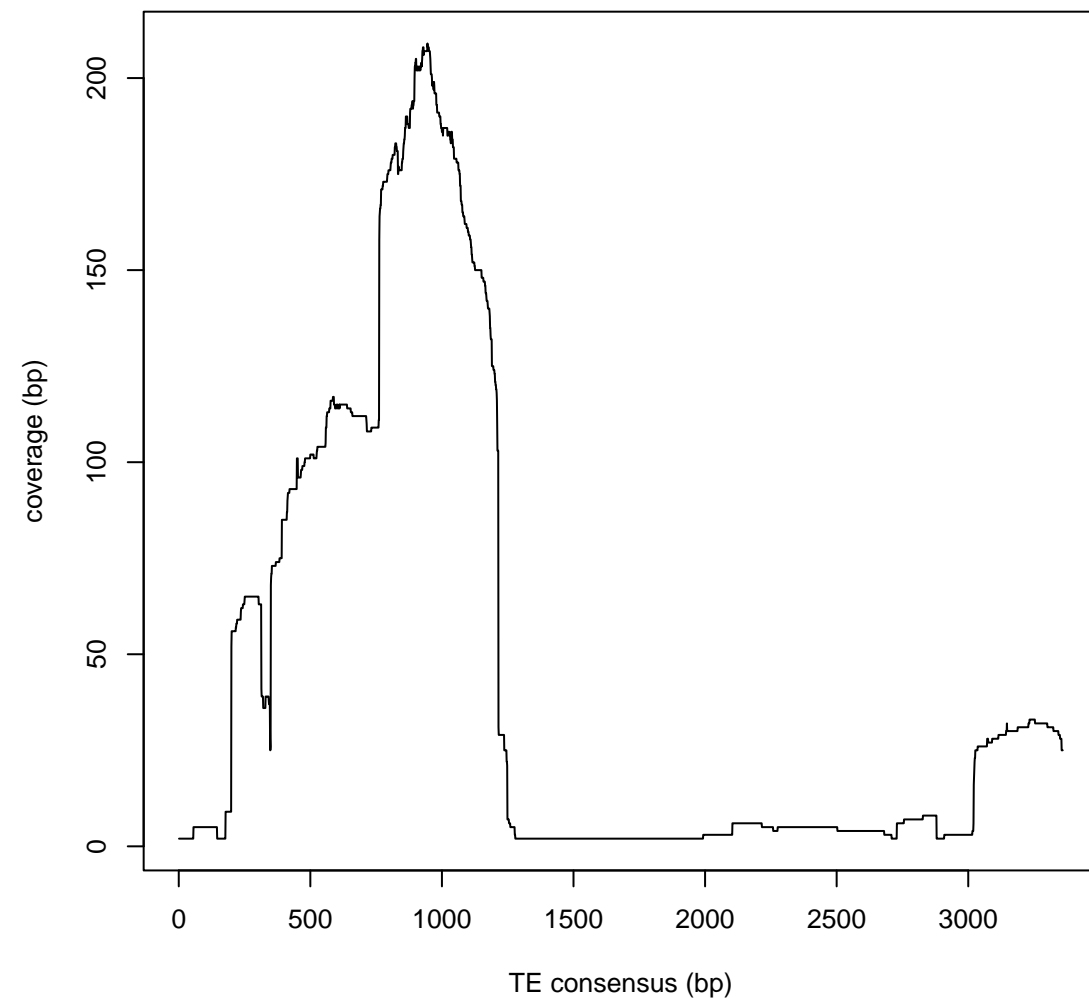


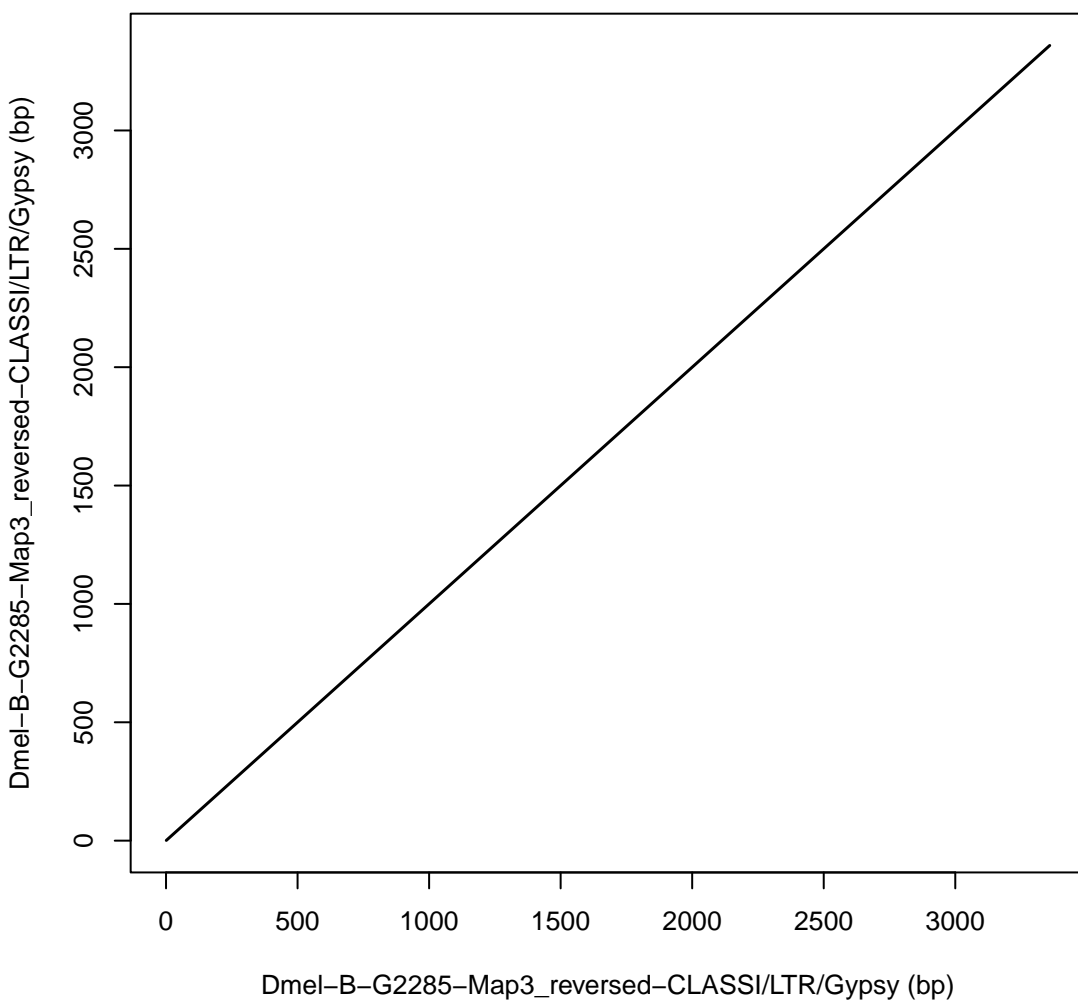
TE: Dmel-B-G2285-Map3\_reversed-CLASSI/LTR/Gypsy  
consensus size: 3359bp; fragments: 358; full length: 2 (>=3023.1bp)



TE consensus genomic coverage



TE consensus self dotplot (blastn)



TE consensus structure and protein hits

