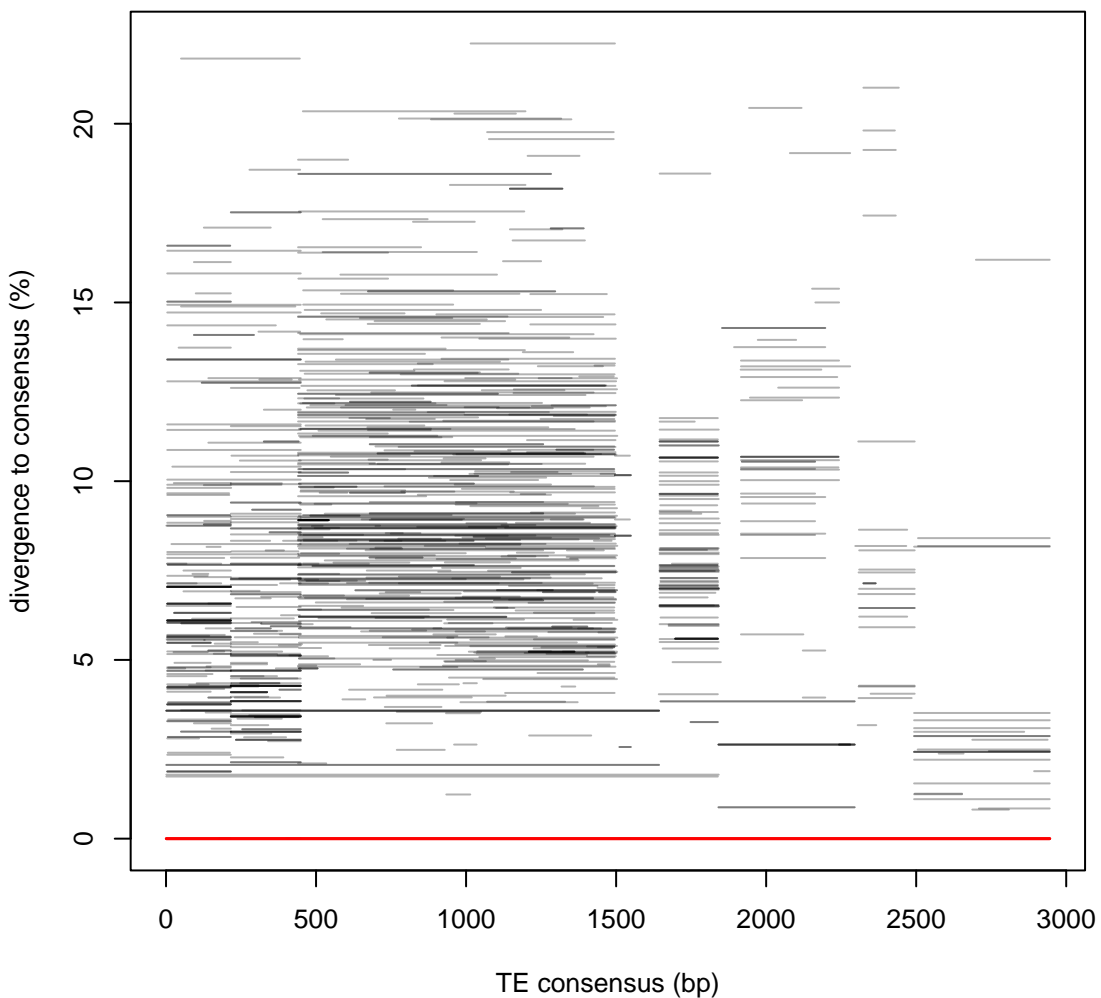
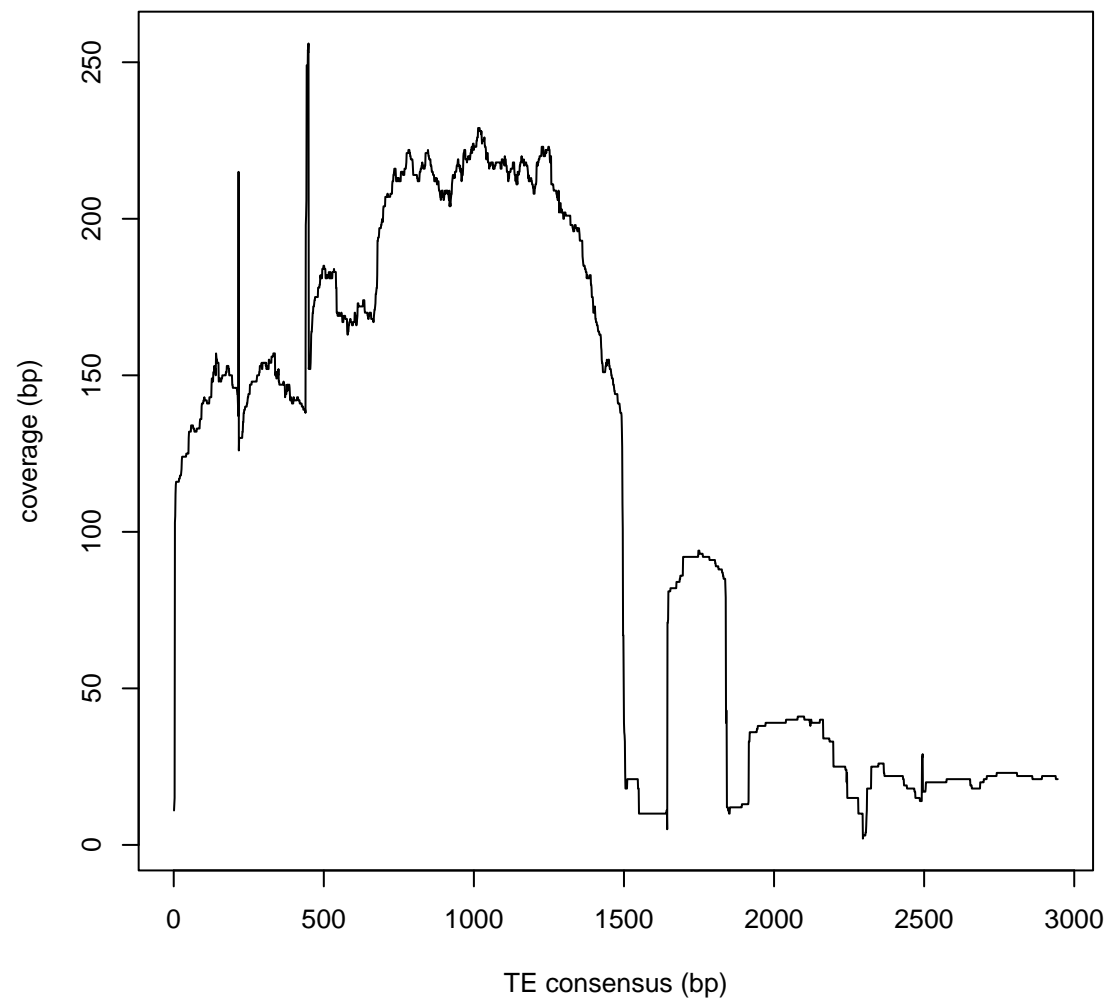


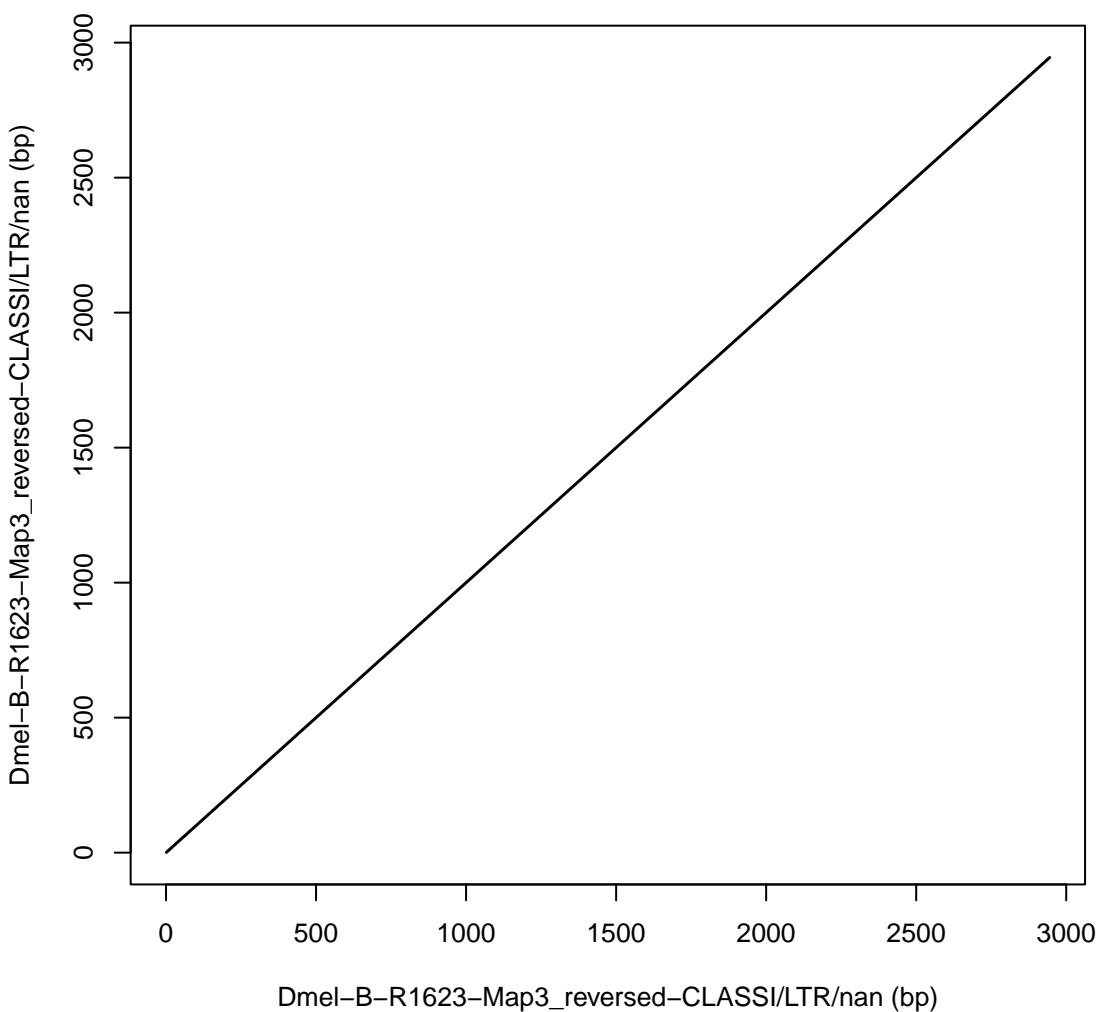
TE: Dmel-B-R1623-Map3\_reversed-CLASSI/LTR/nan  
consensus size: 2945bp; fragments: 977; full length: 2 ( $\geq 2650.5$ bp)



TE consensus genomic coverage



TE consensus self dotplot (blastn)



TE consensus structure and protein hits

