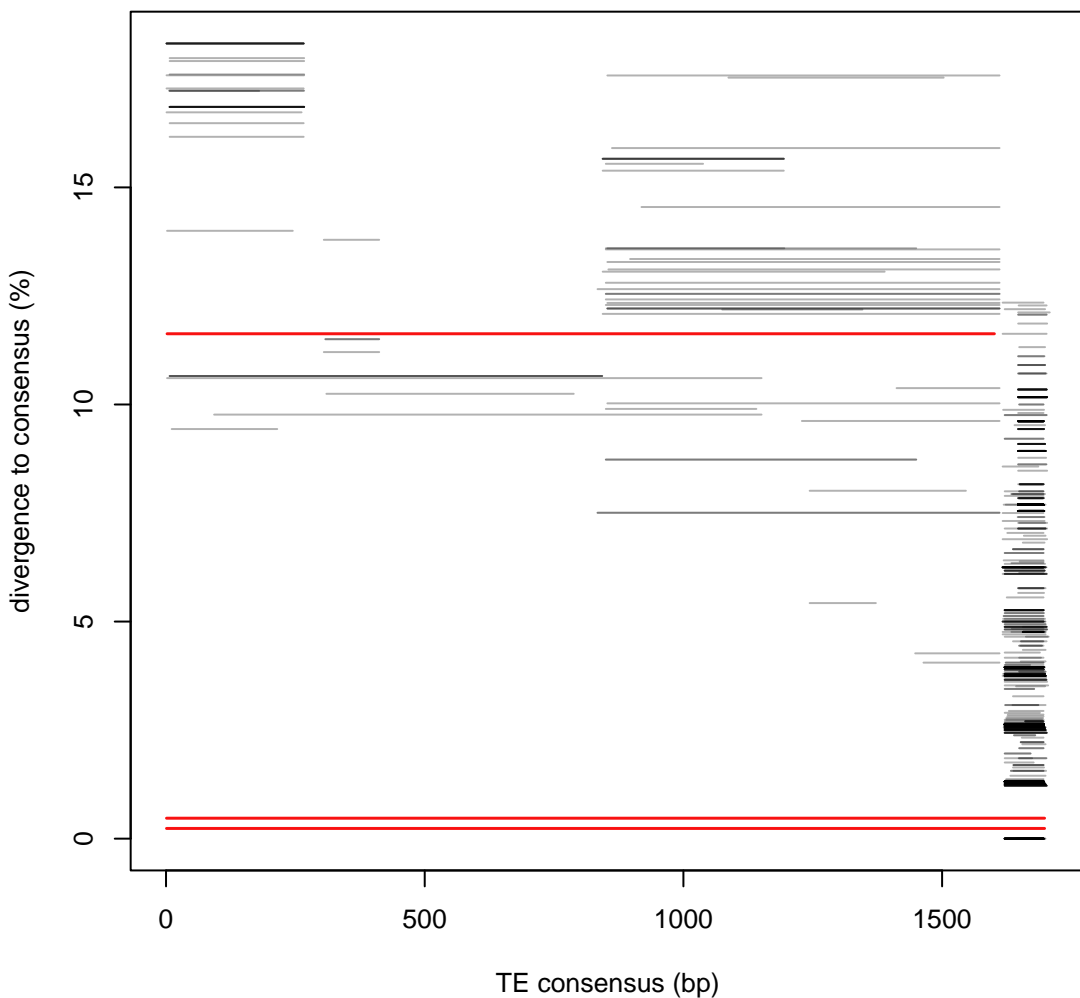
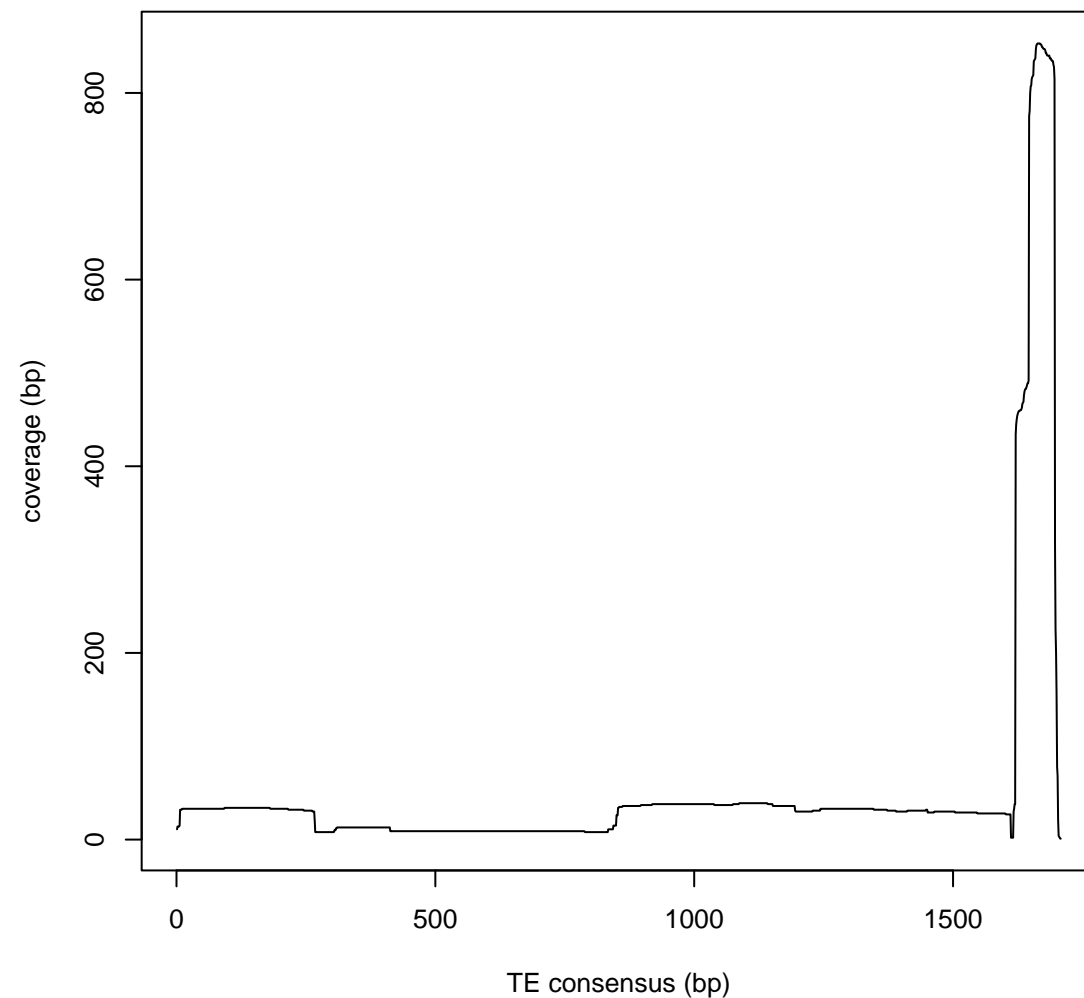


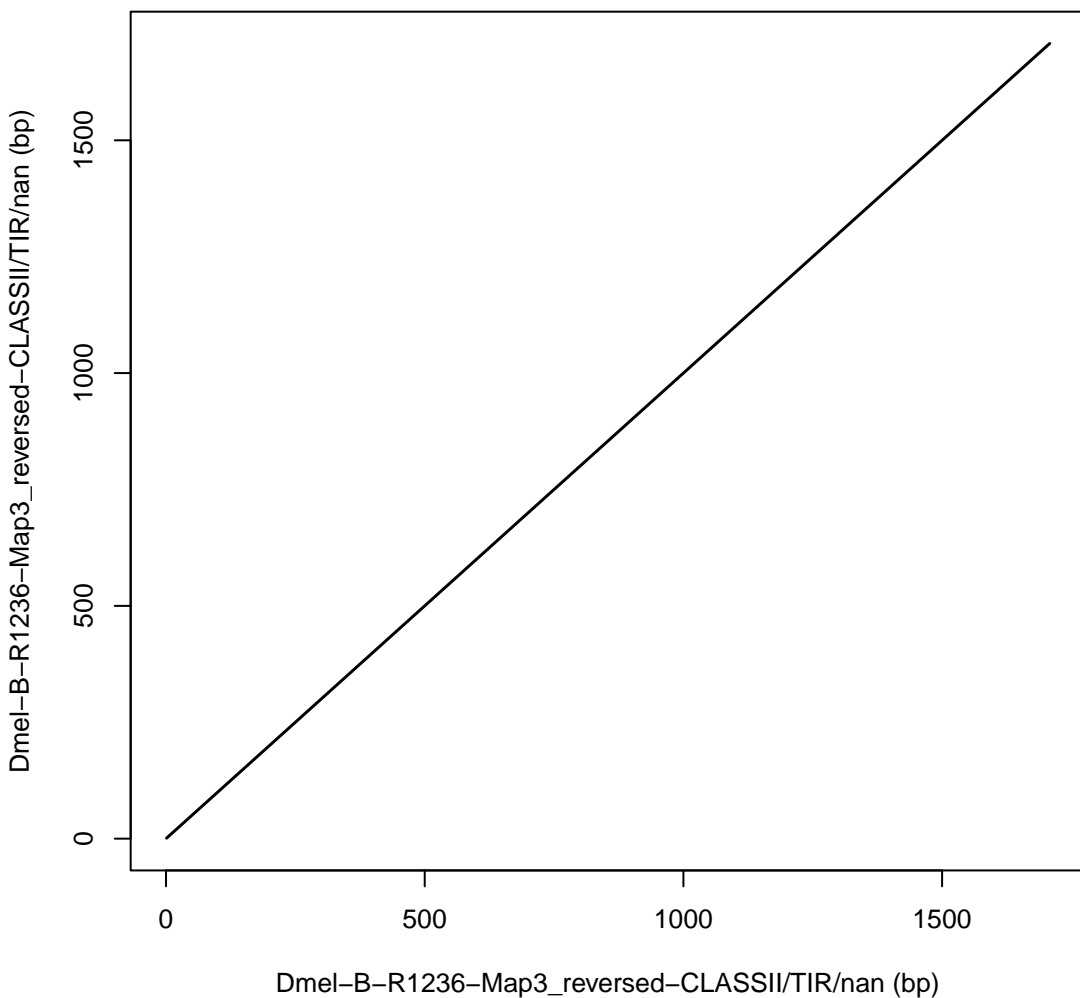
TE: Dmel-B-R1236-Map3\_reversed-CLASSII/TIR/nan  
consensus size: 1708bp; fragments: 931; full length: 3 ( $\geq 1537.2$ bp)



TE consensus genomic coverage



TE consensus self dotplot (blastn)



TE consensus structure and protein hits

