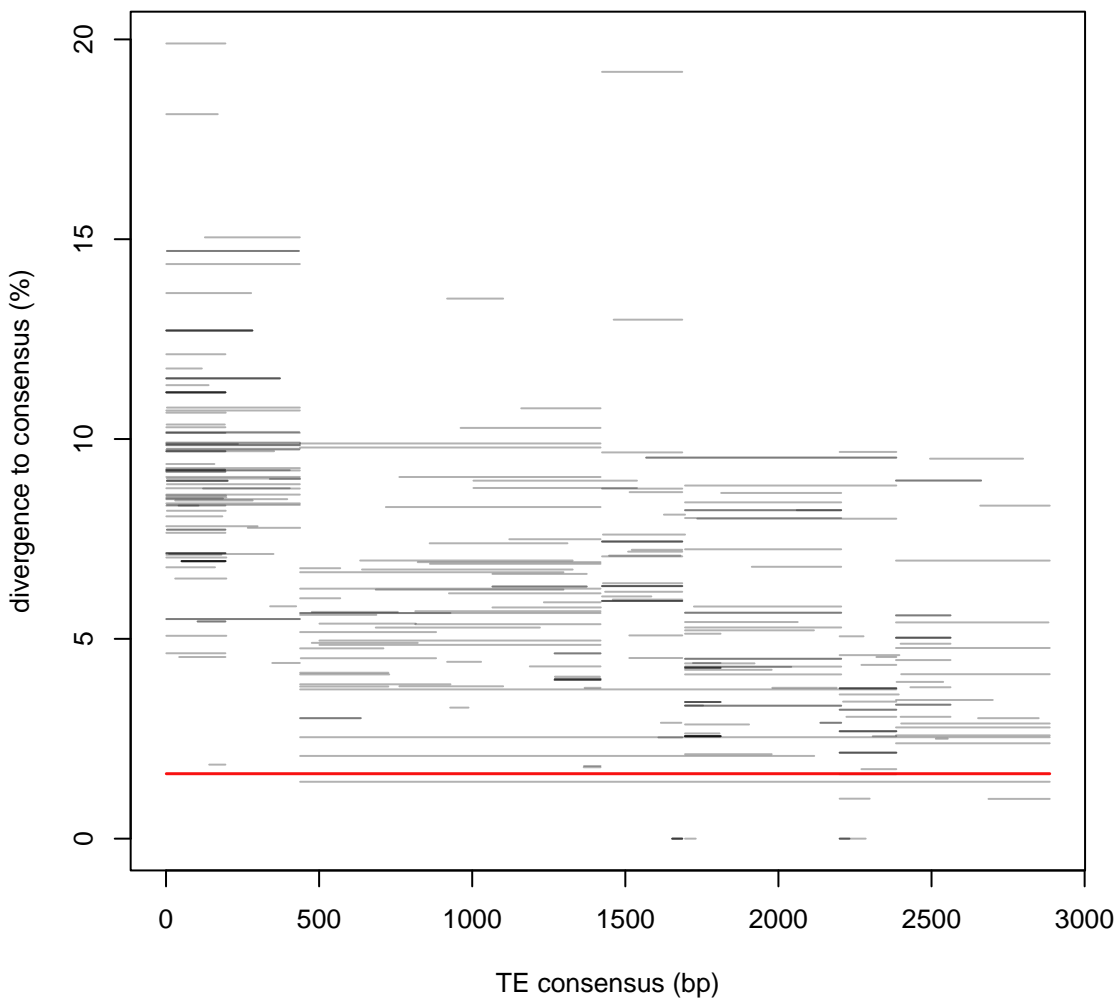
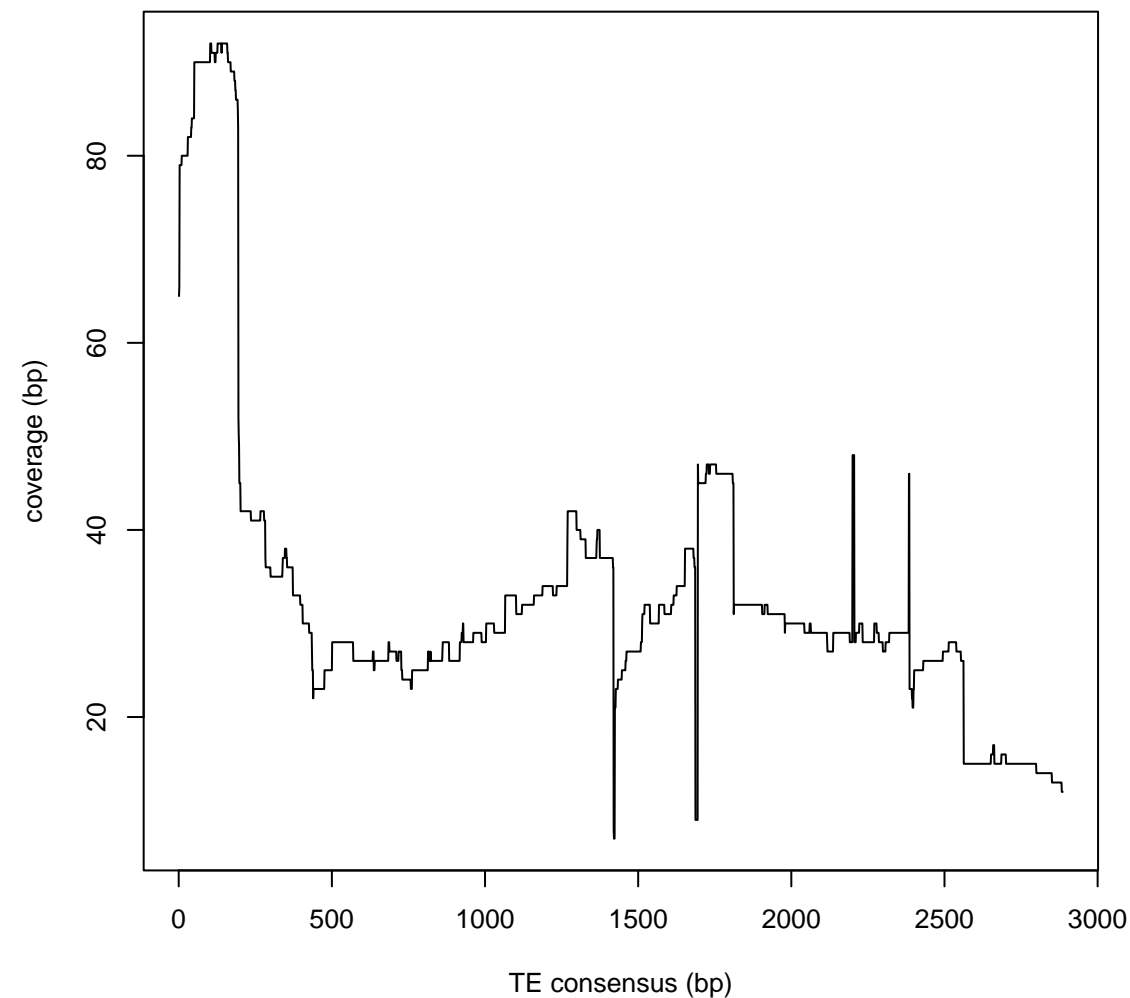


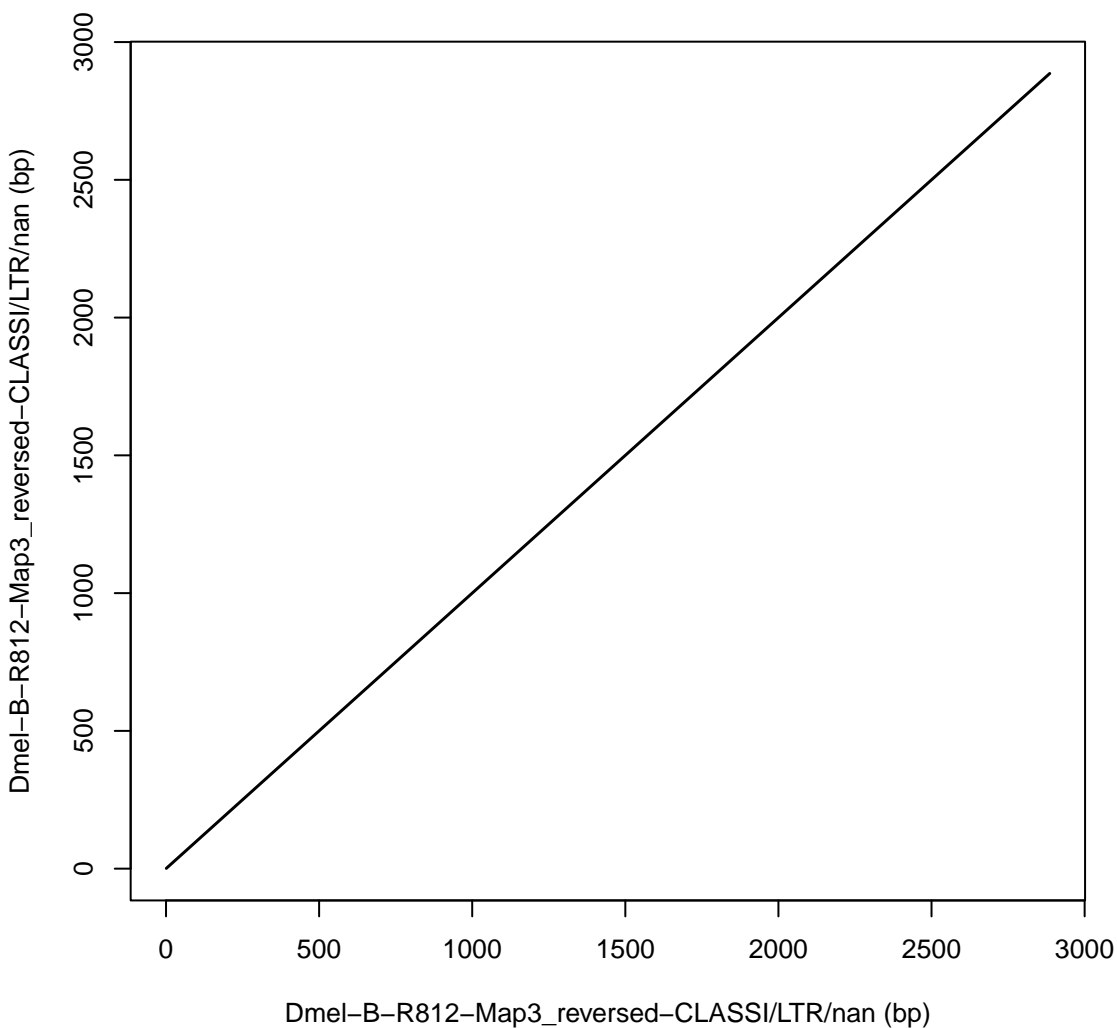
TE: Dmel-B-R812-Map3_reversed-CLASSI/LTR/nan
consensus size: 2886bp; fragments: 299; full length: 1 (>=2597.4bp)



TE consensus genomic coverage



TE consensus self dotplot (blastn)



TE consensus structure and protein hits

