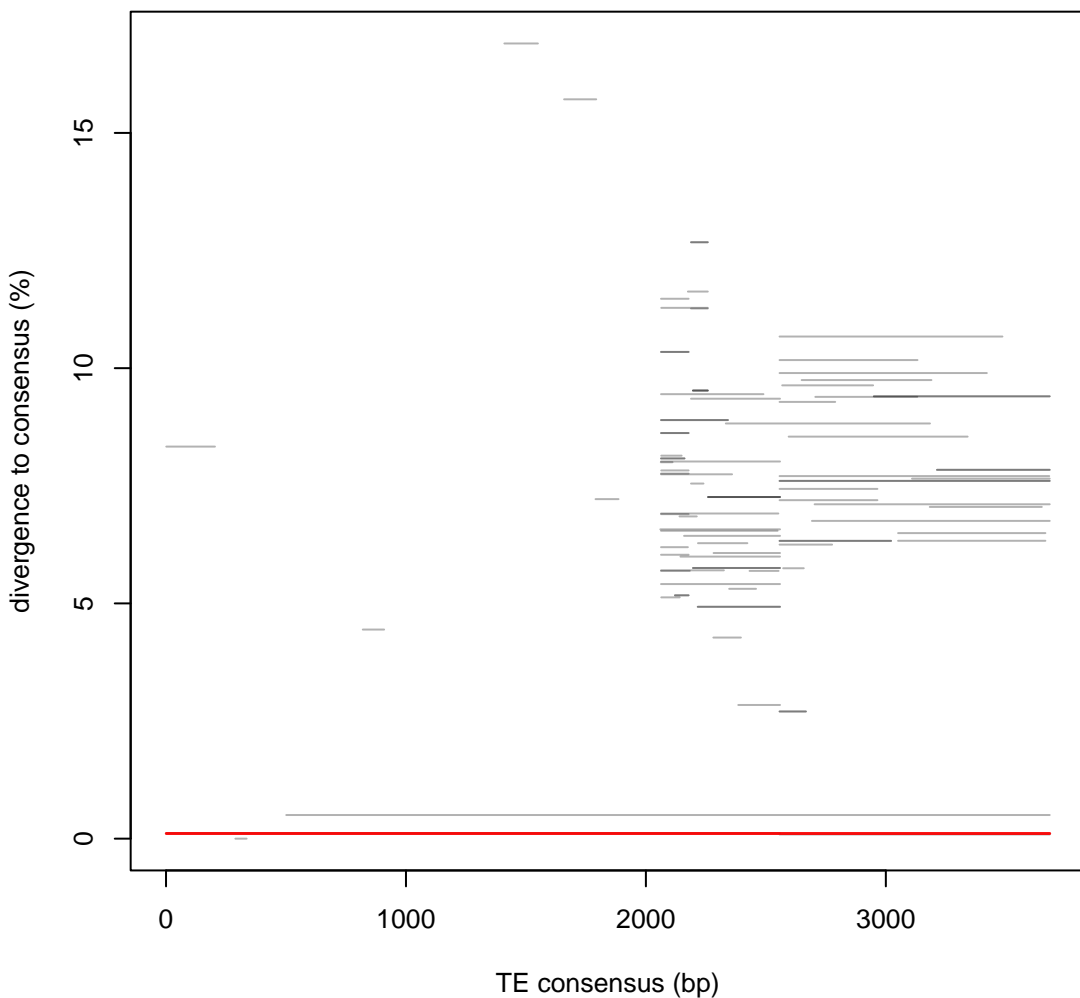
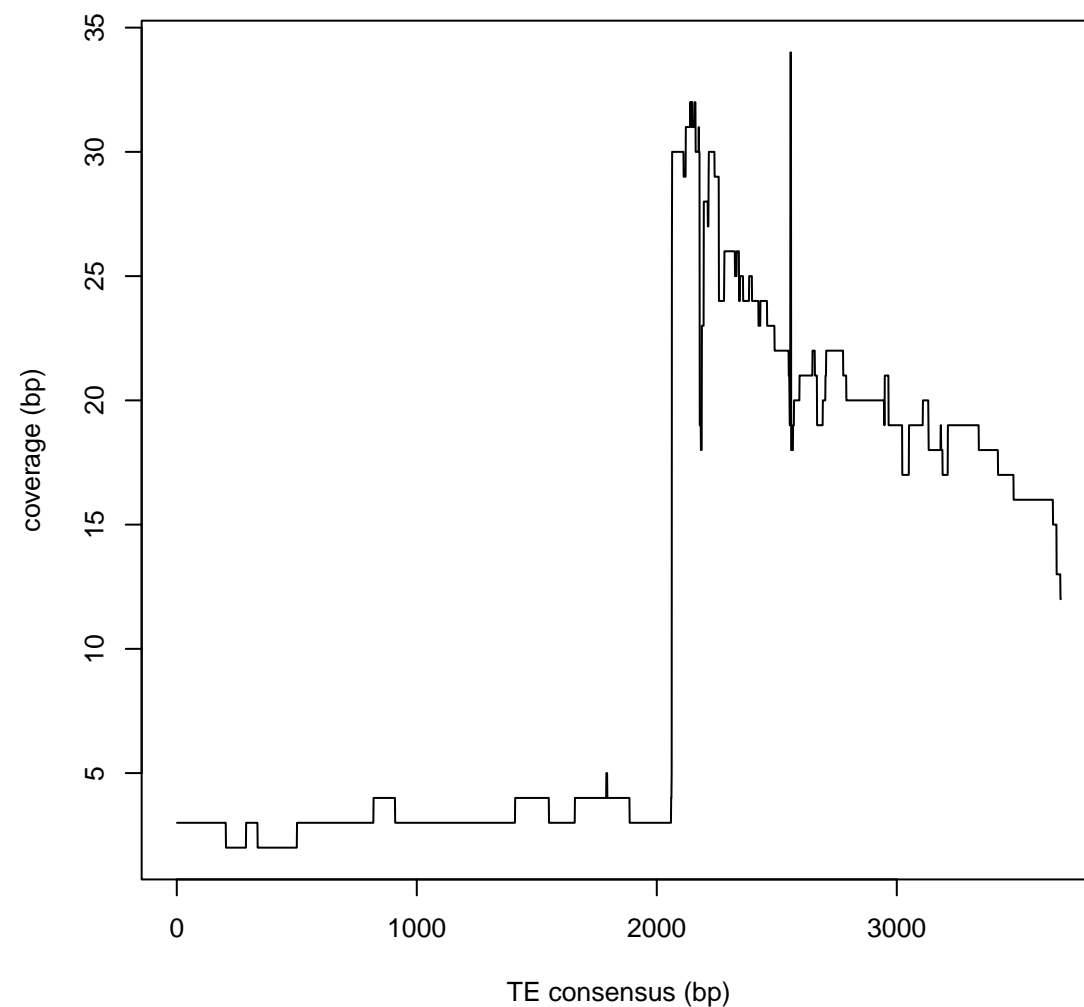


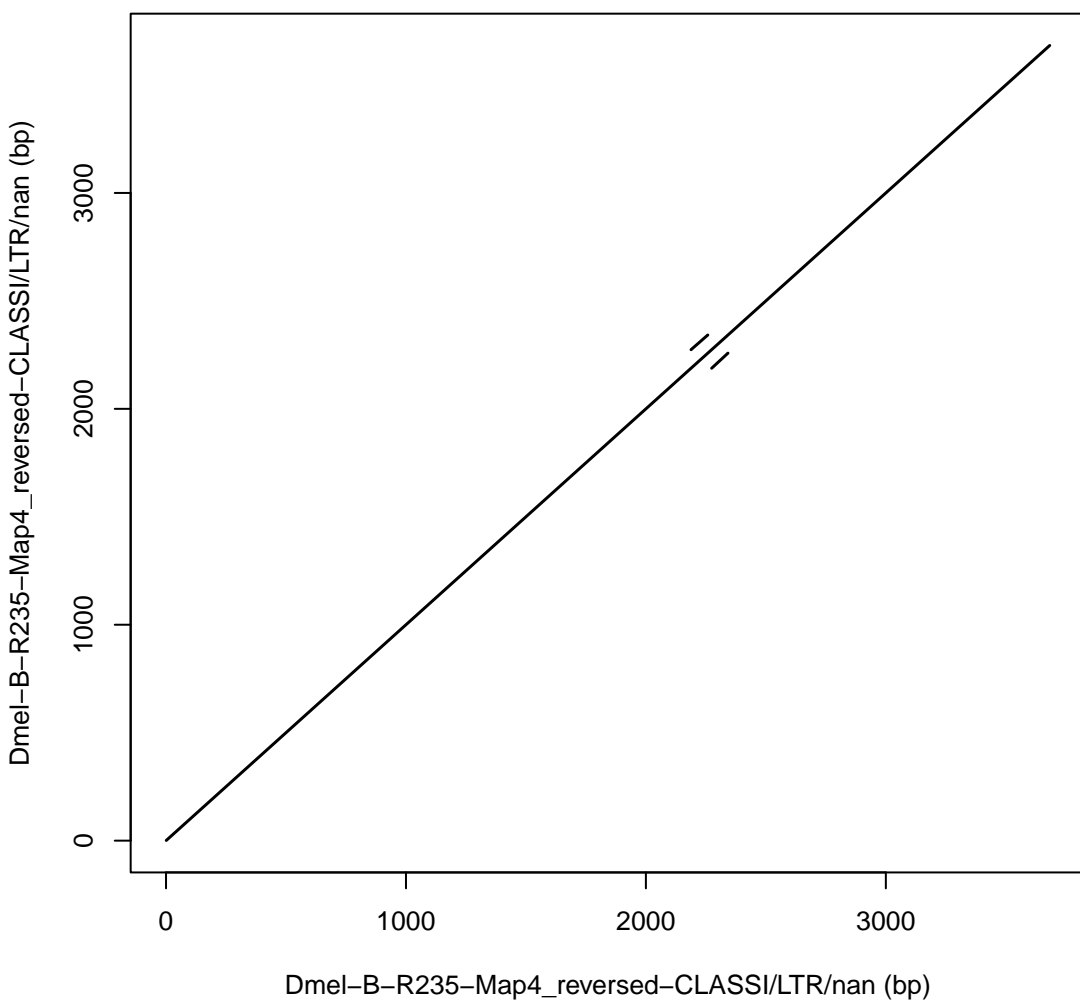
TE: Dmel-B-R235-Map4_reversed-CLASSI/LTR/nan
consensus size: 3683bp; fragments: 94; full length: 1 (>=3314.7bp)



TE consensus genomic coverage



TE consensus self dotplot (blastn)



TE consensus structure and protein hits

