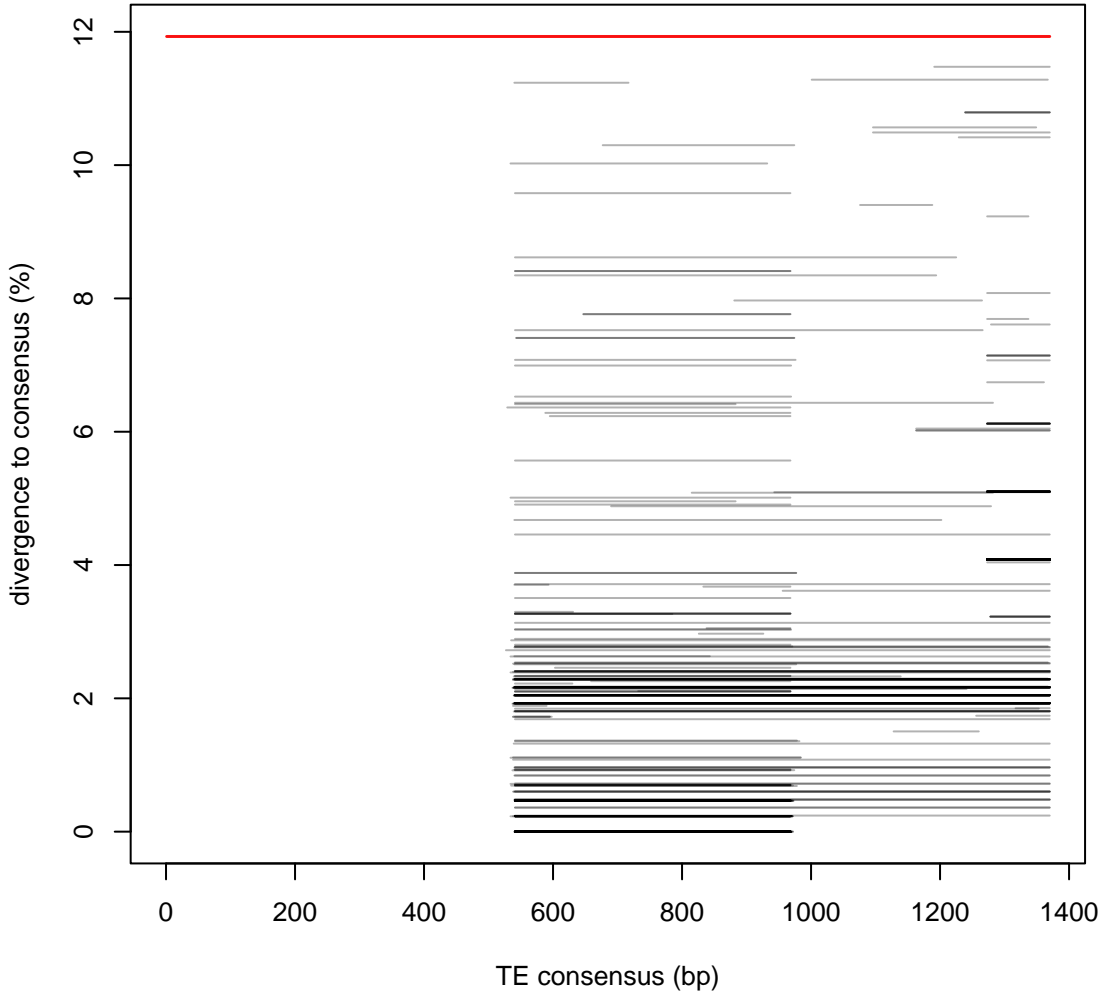
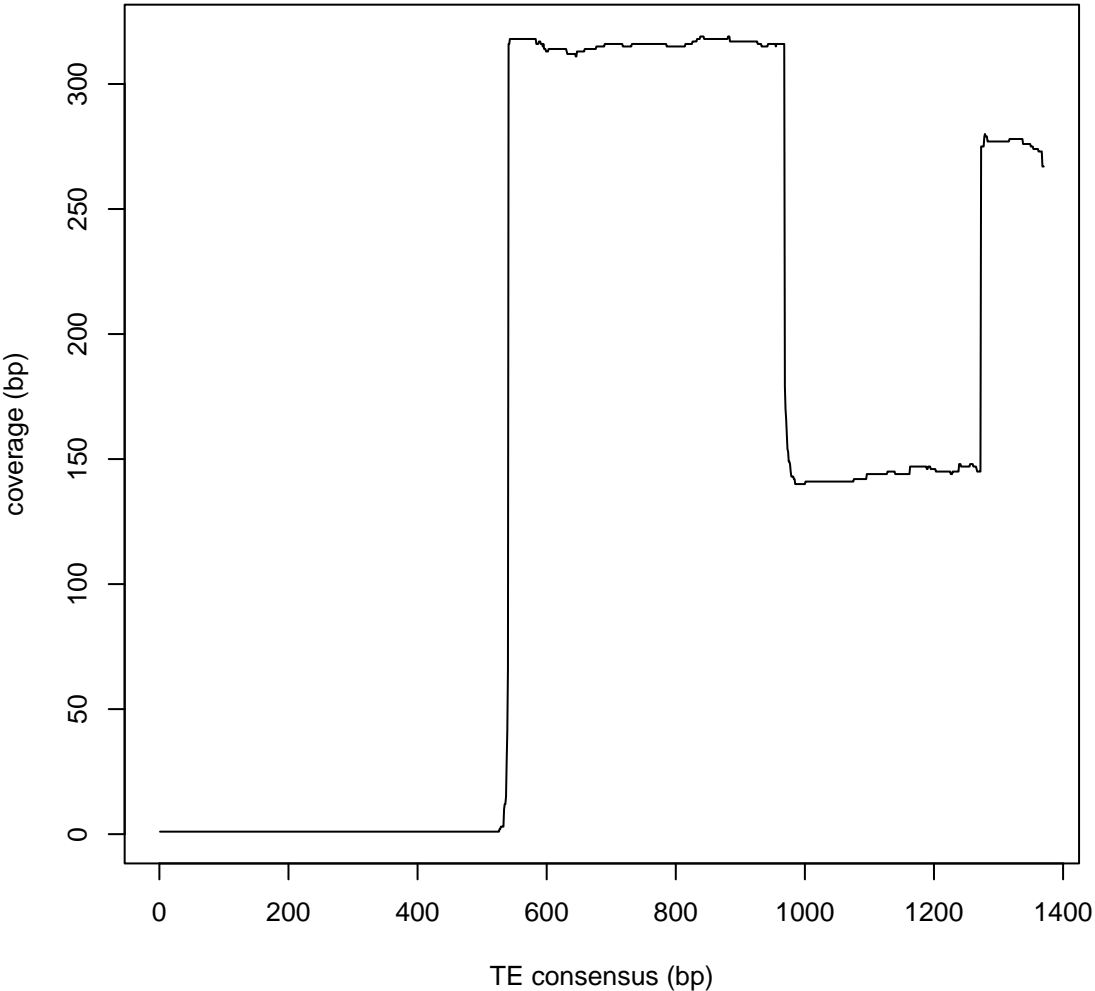


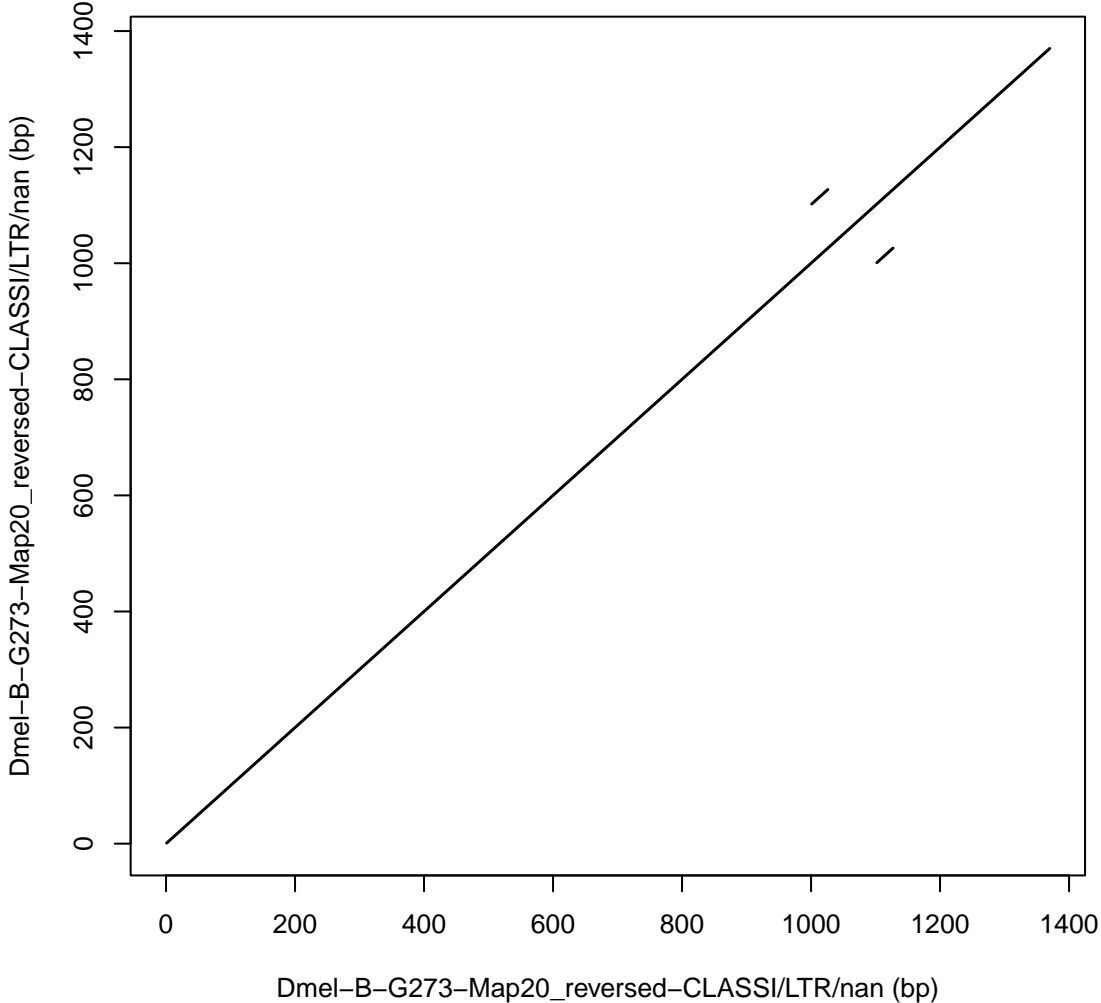
TE: Dmel-B-G273-Map20_reversed-CLASSI/LTR/nan
consensus size: 1370bp; fragments: 484; full length: 1 (>=1233bp)



TE consensus genomic coverage



TE consensus self dotplot (blastn)



TE consensus structure and protein hits

