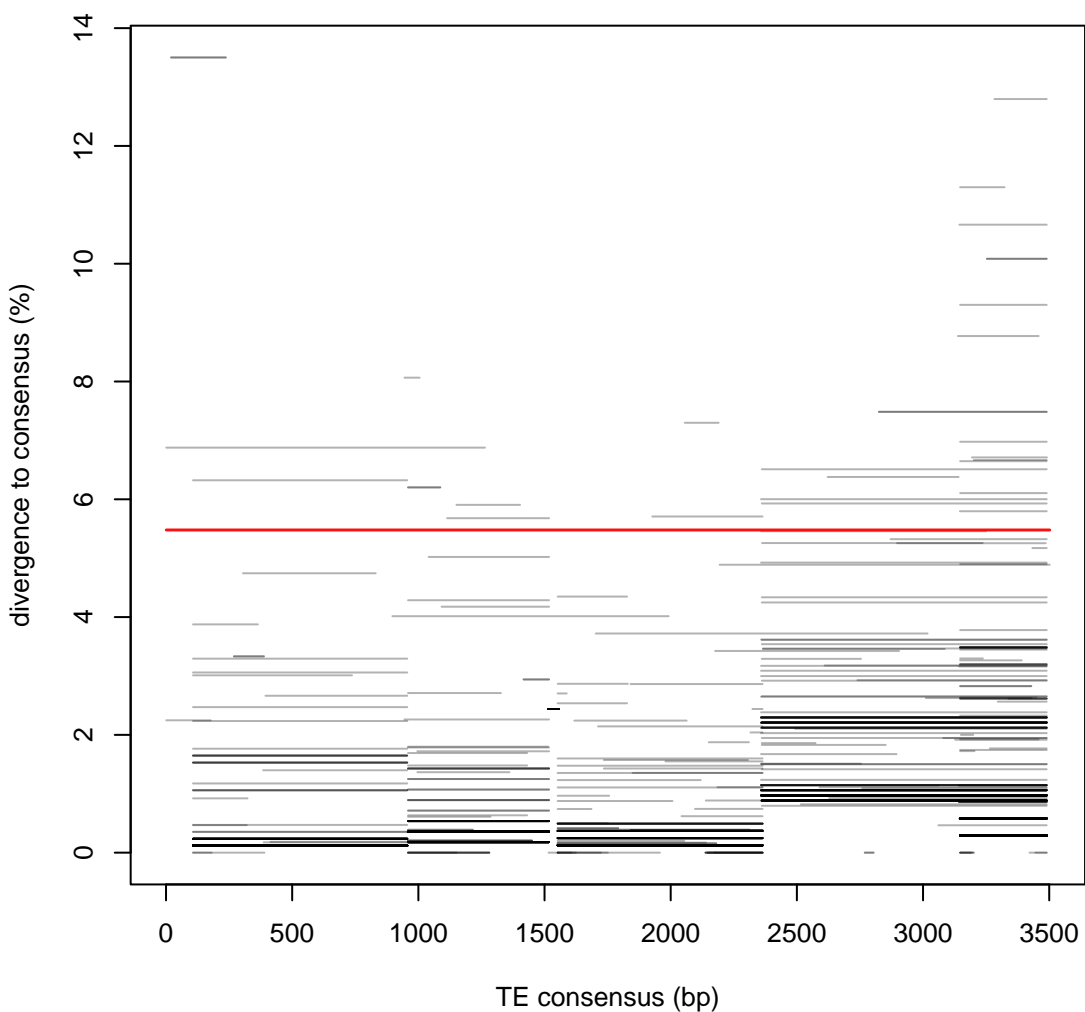
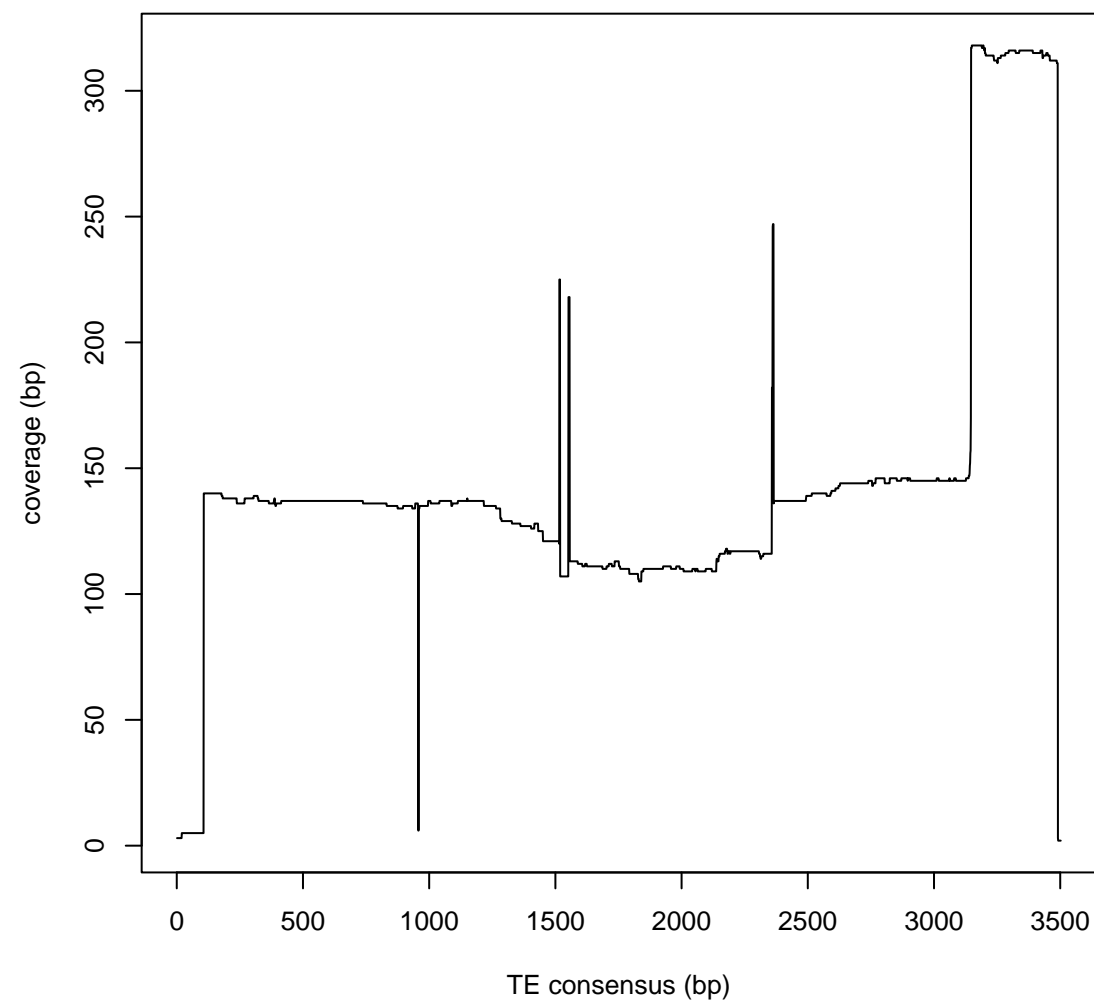


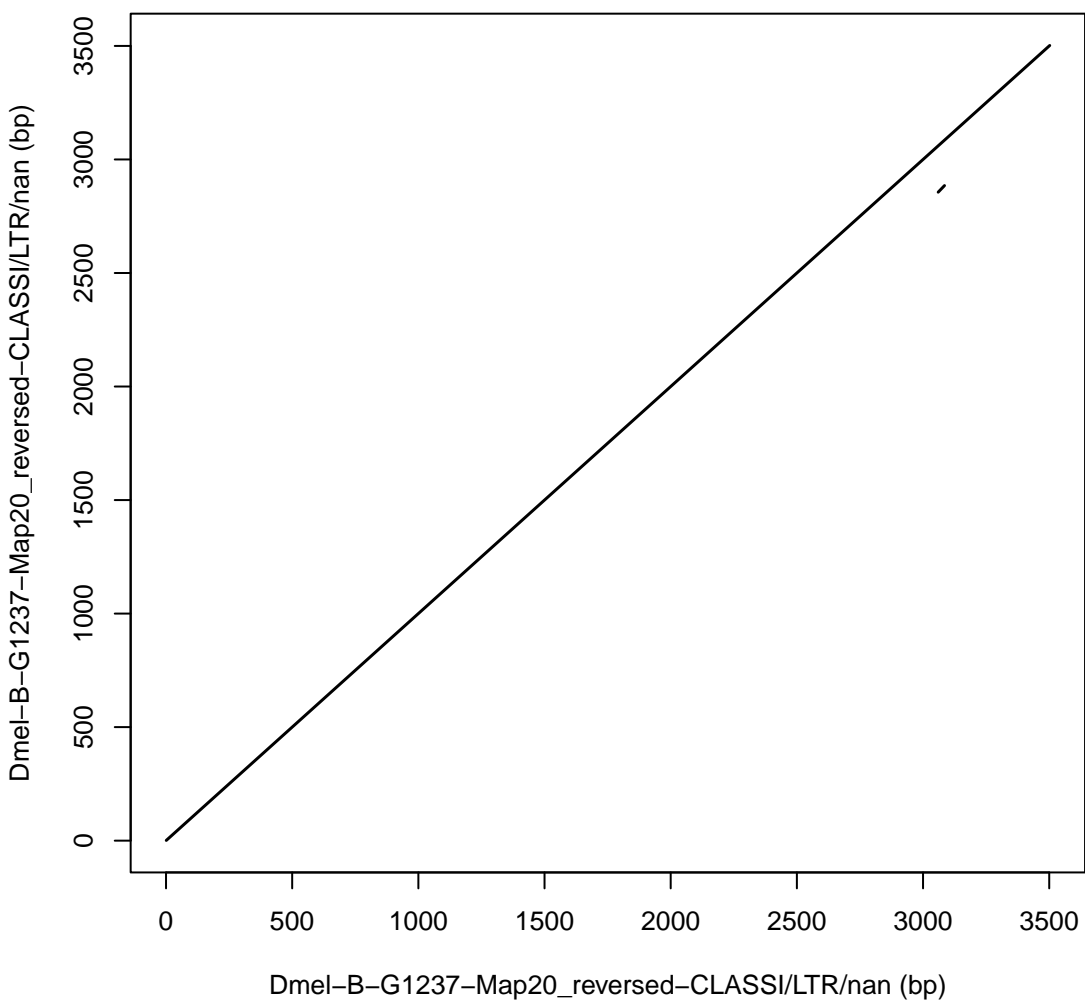
TE: Dmel-B-G1237-Map20\_reversed-CLASSI/LTR/nan  
consensus size: 3502bp; fragments: 870; full length: 1 (>=3151.8bp)



TE consensus genomic coverage



TE consensus self dotplot (blastn)



TE consensus structure and protein hits

