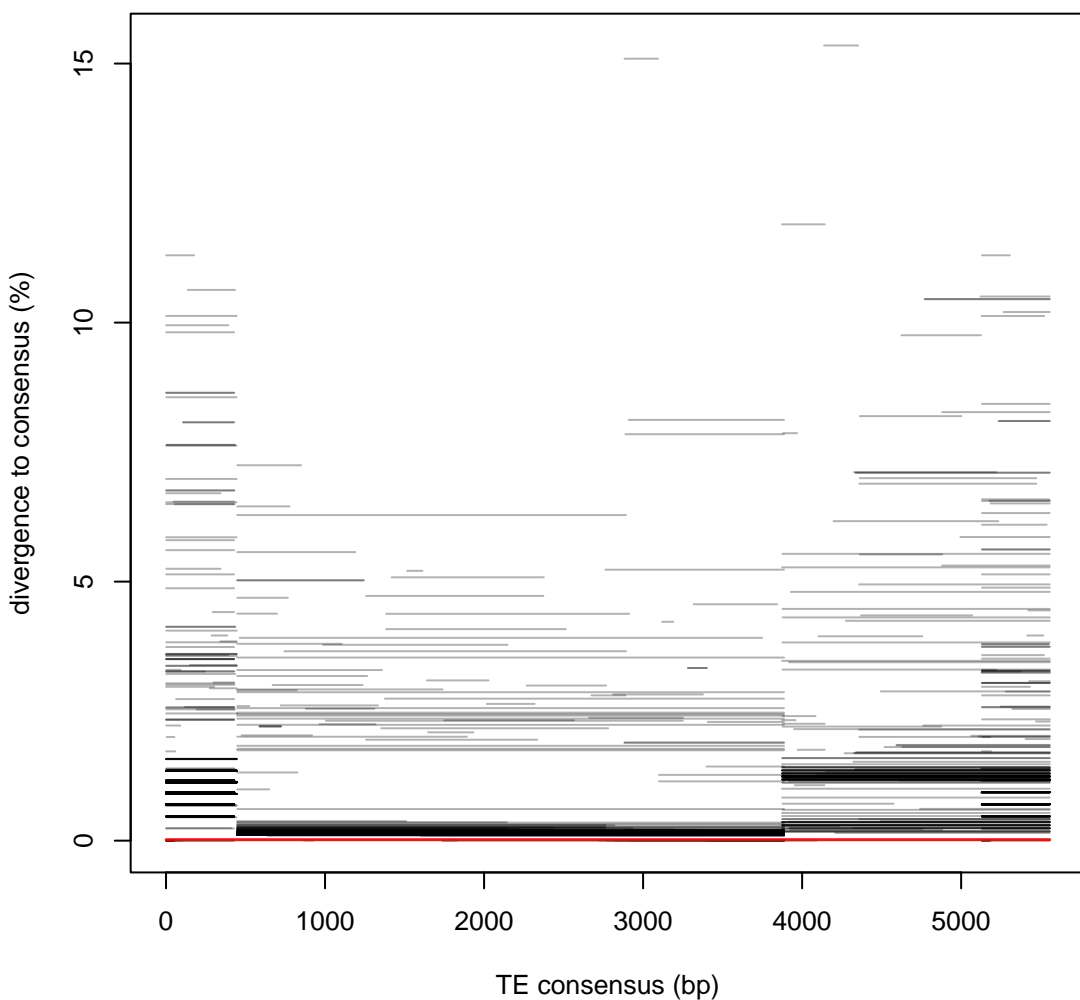
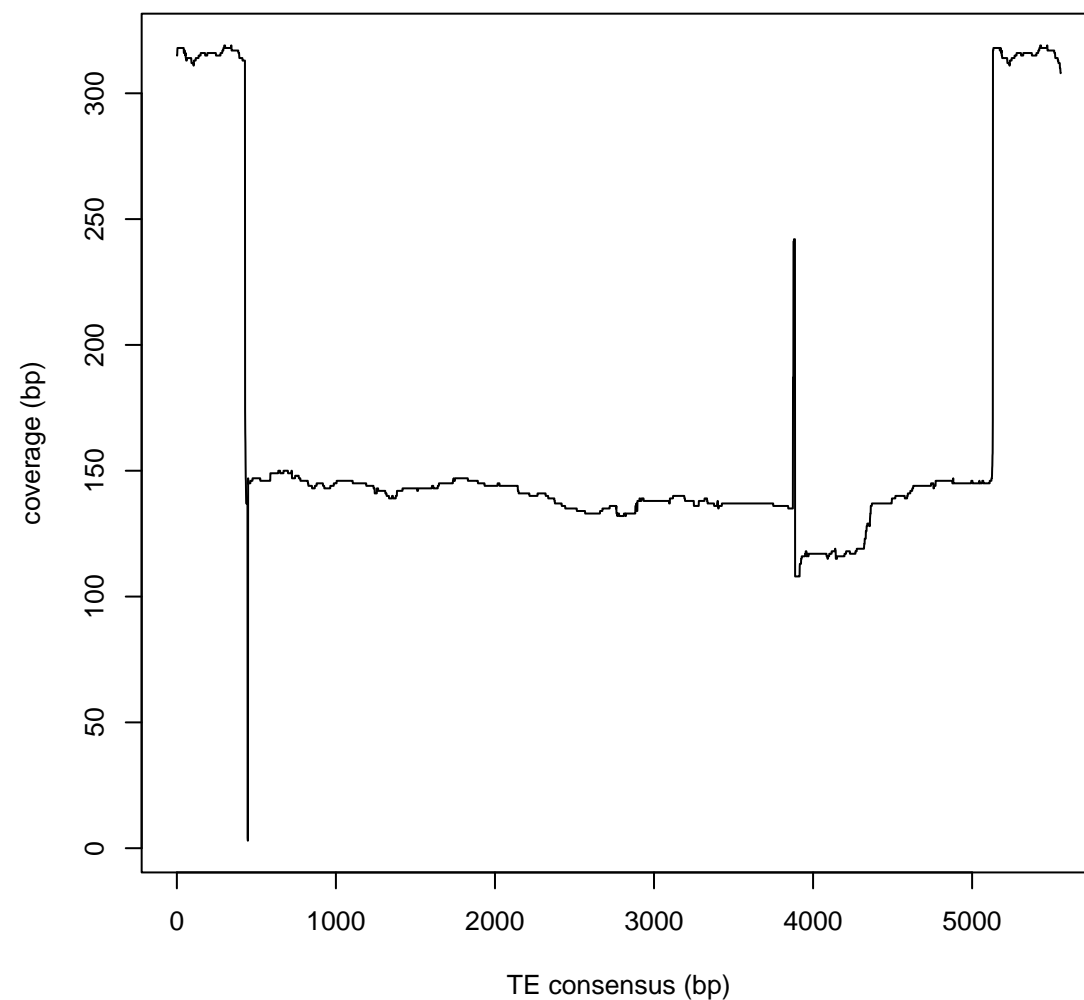


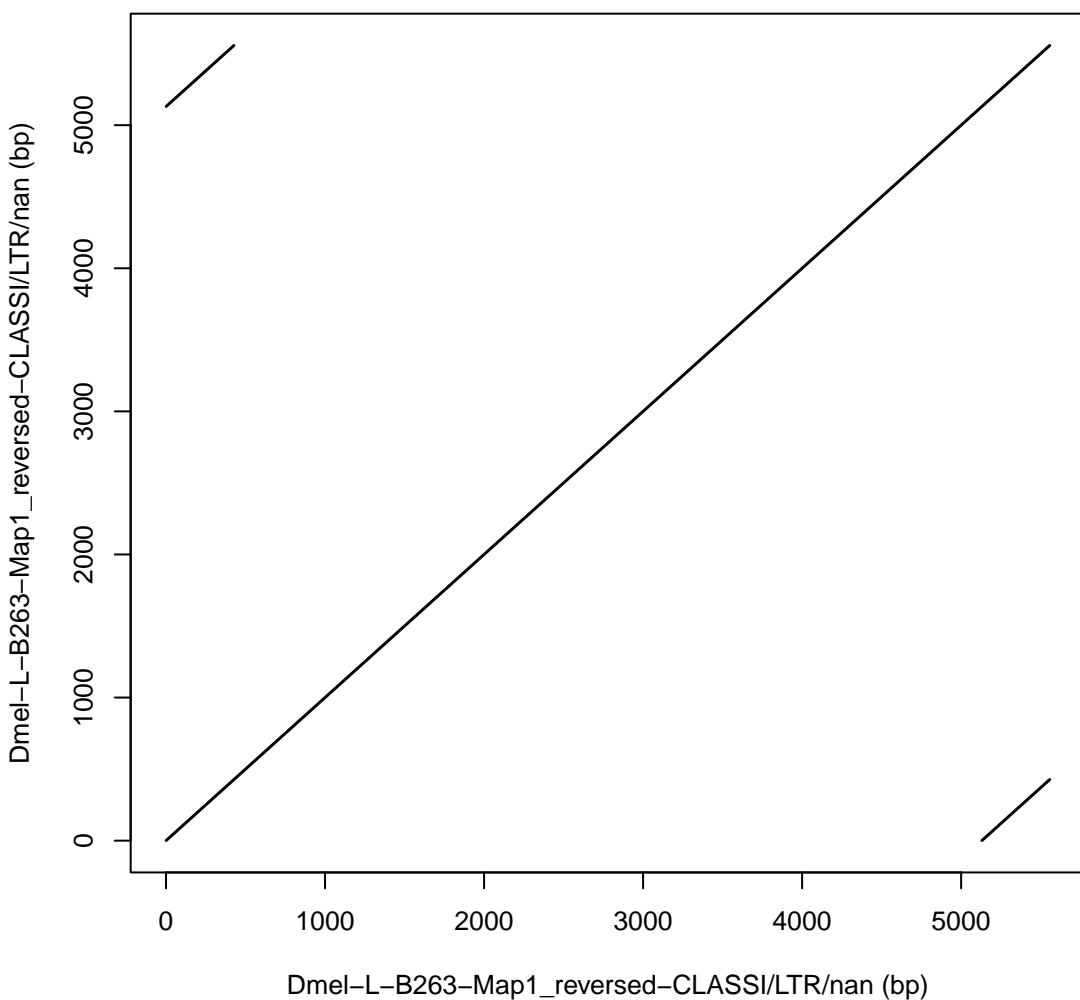
TE: Dmel-L-B263-Map1_reversed-CLASSI/LTR/nan
consensus size: 5557bp; fragments: 884; full length: 1 (>=5001.3bp)



TE consensus genomic coverage



TE consensus self dotplot (blastn)



TE consensus structure and protein hits

