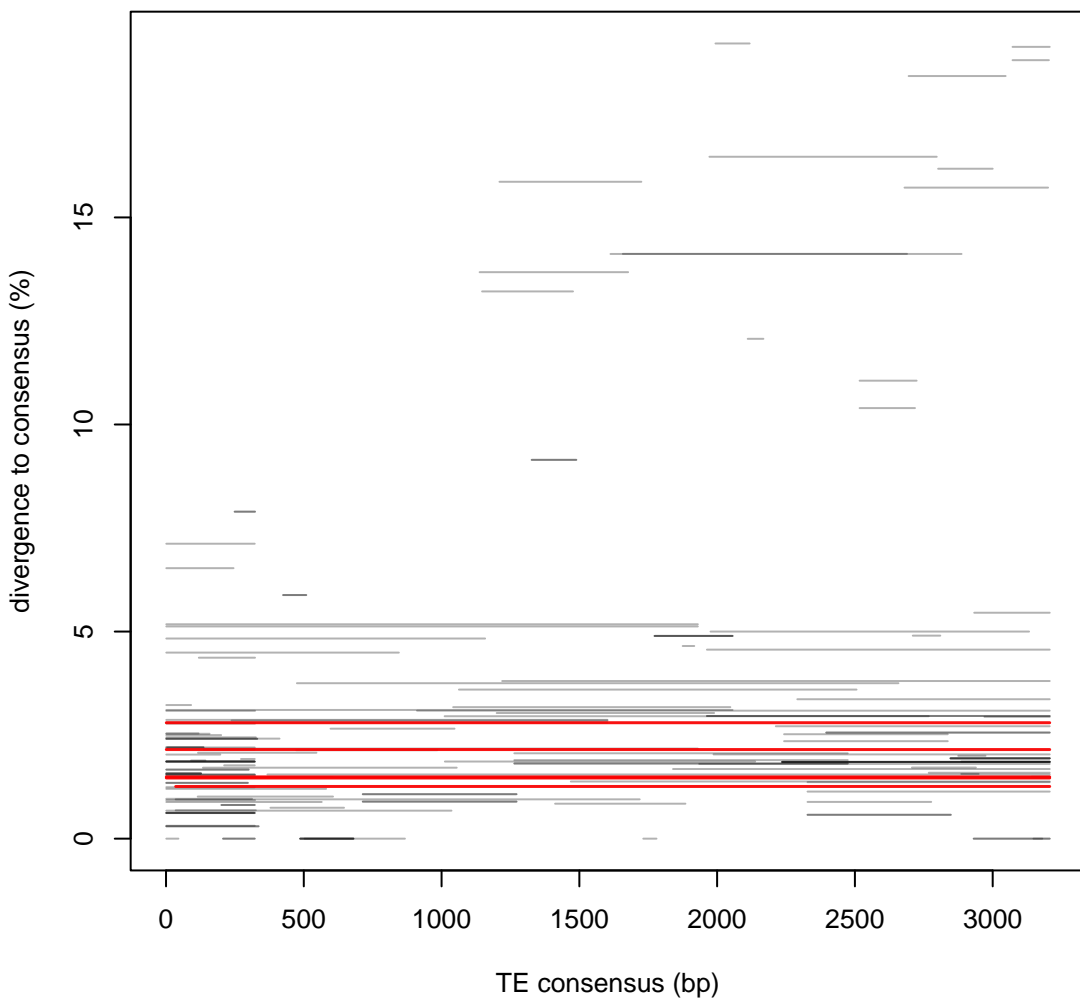
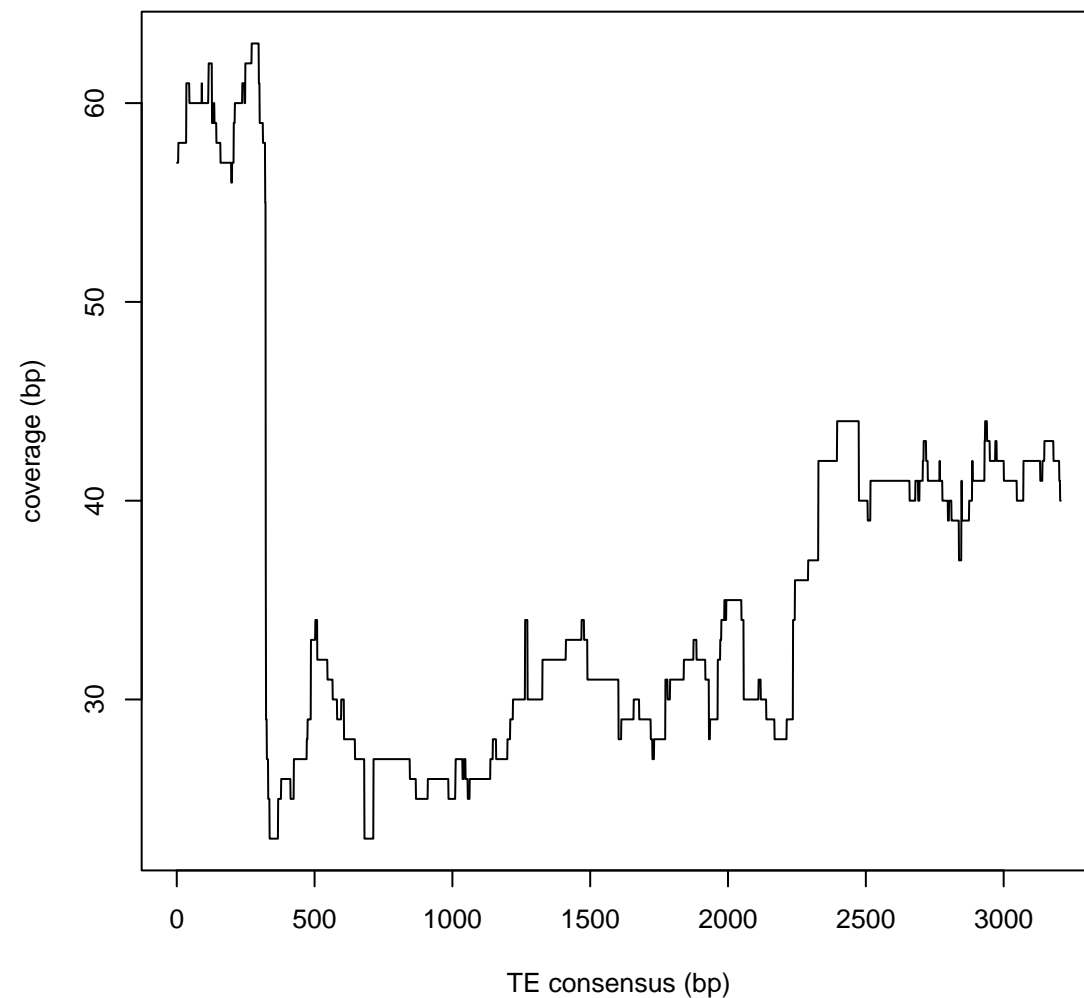


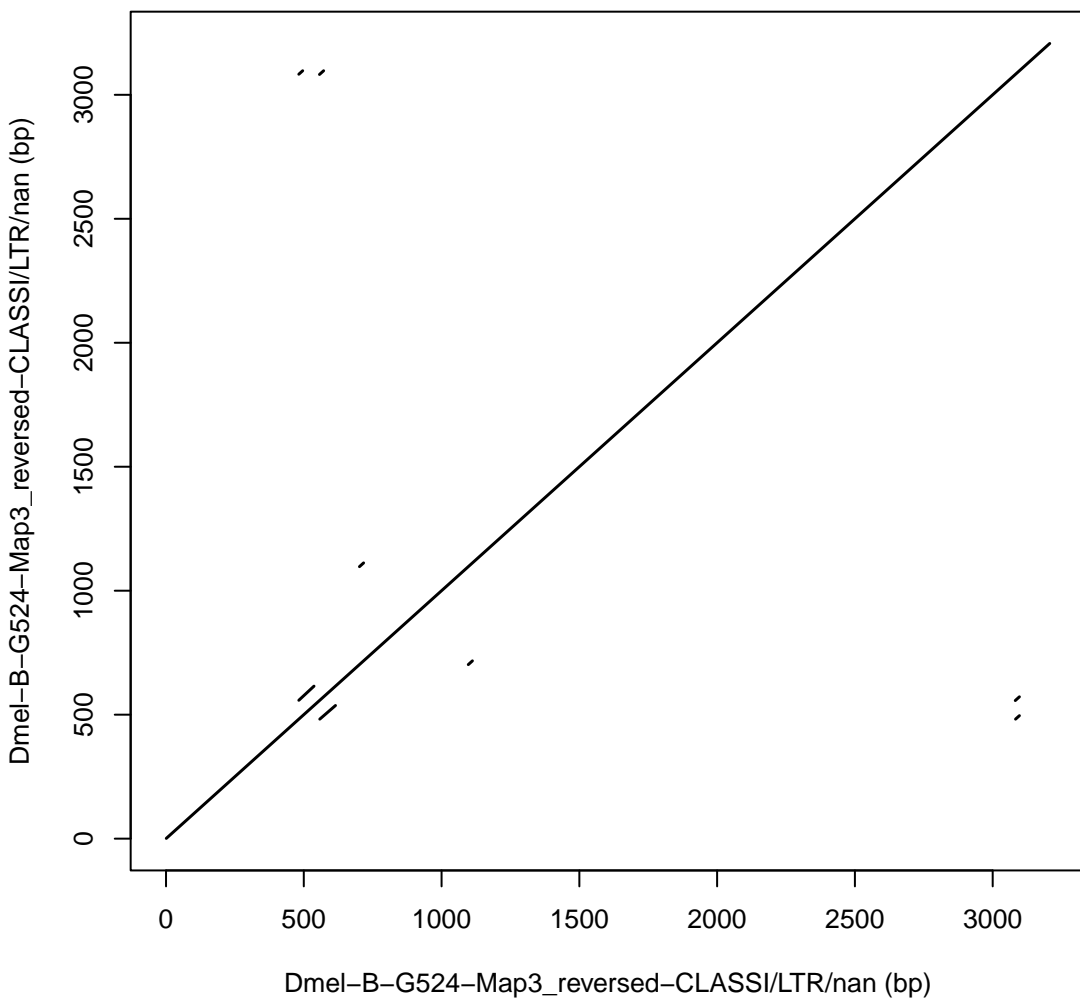
TE: Dmel-B-G524-Map3_reversed-CLASSI/LTR/nan
consensus size: 3207bp; fragments: 168; full length: 5 (>=2886.3bp)



TE consensus genomic coverage



TE consensus self dotplot (blastn)



TE consensus structure and protein hits

