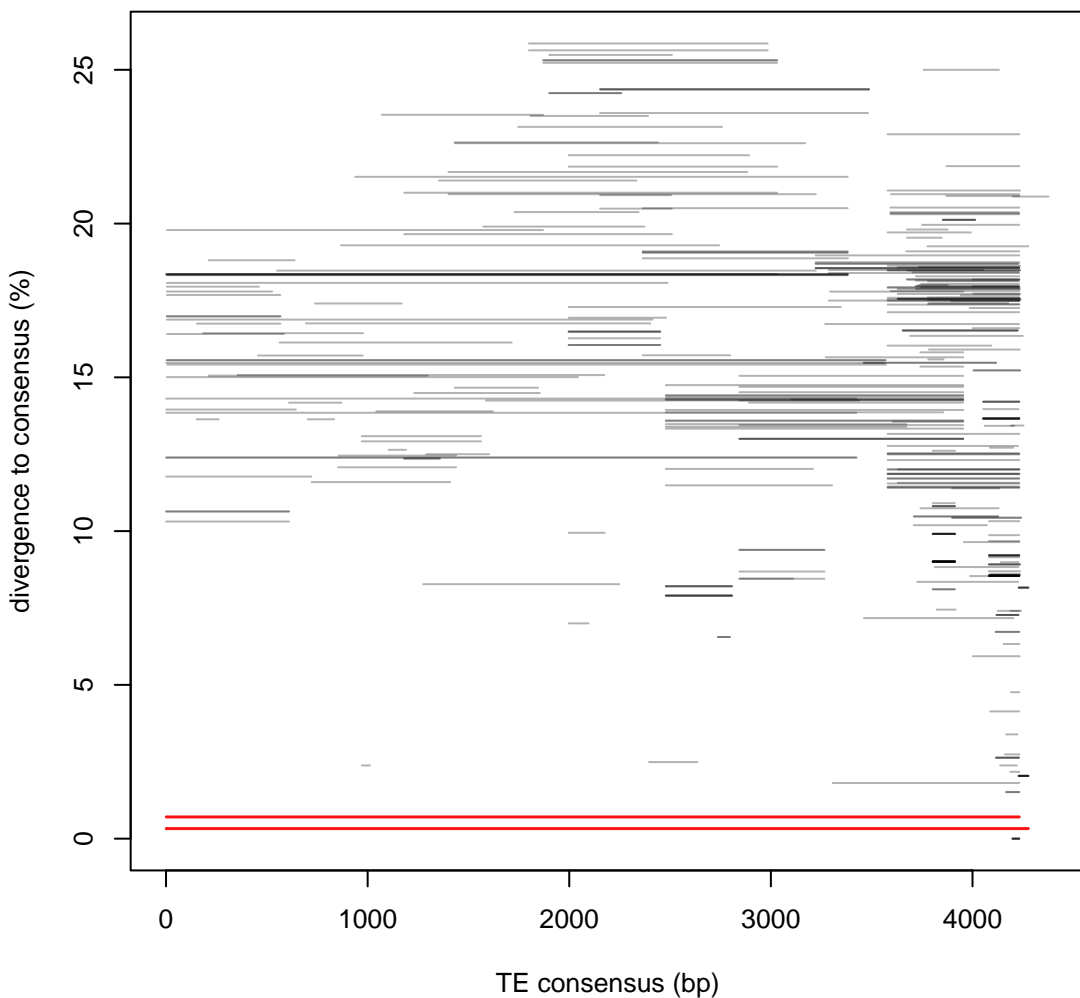
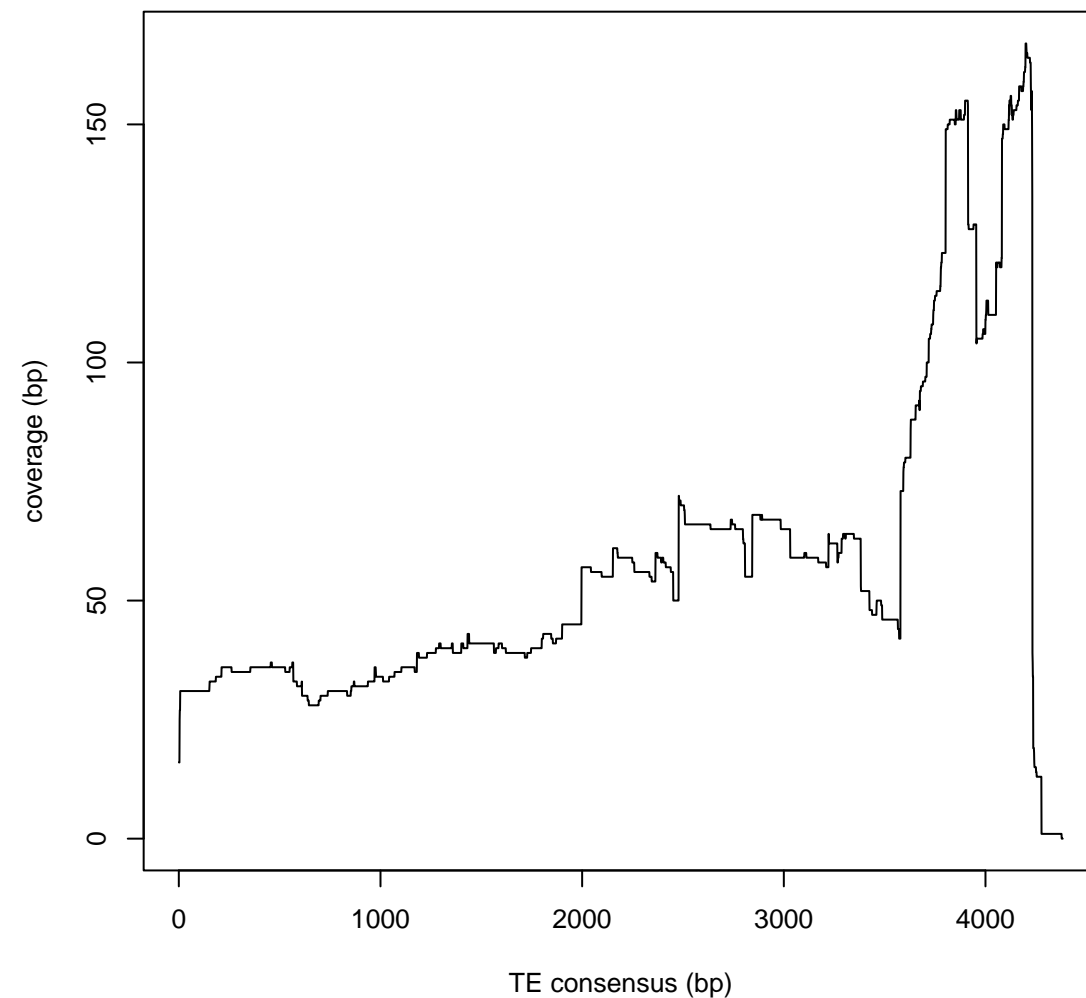


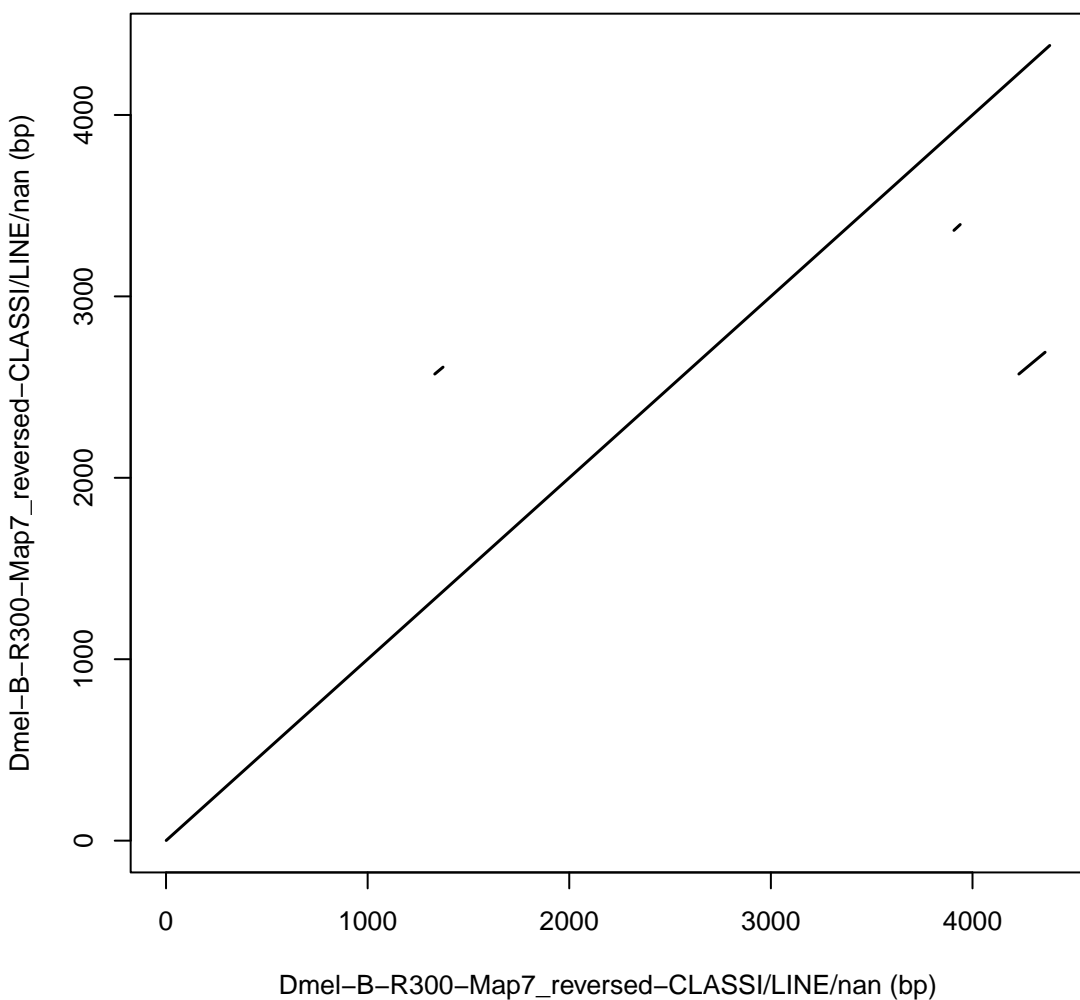
TE: Dmel-B-R300-Map7_reversed-CLASSI/LINE/nan
consensus size: 4383bp; fragments: 371; full length: 2 (≥ 3944.7 bp)



TE consensus genomic coverage



TE consensus self dotplot (blastn)



TE consensus structure and protein hits

