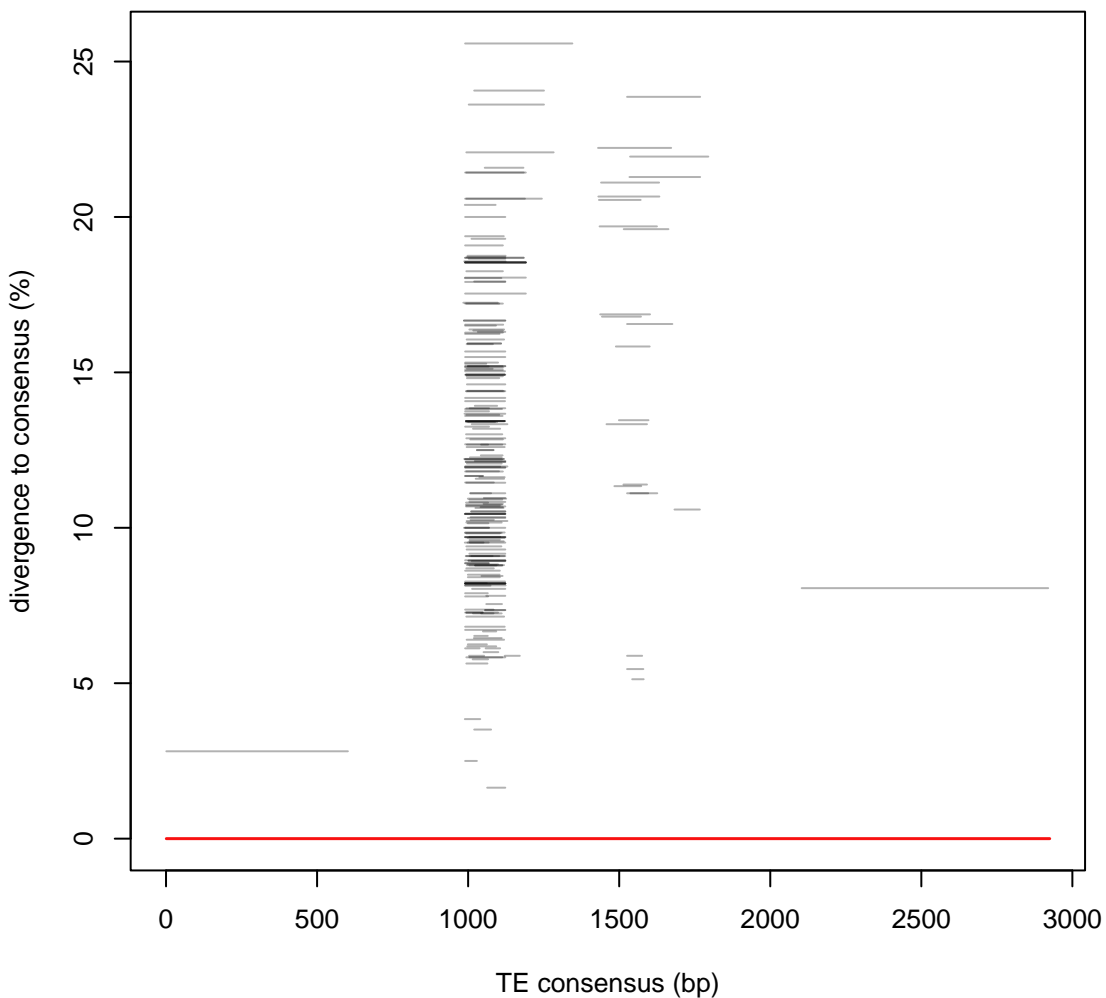
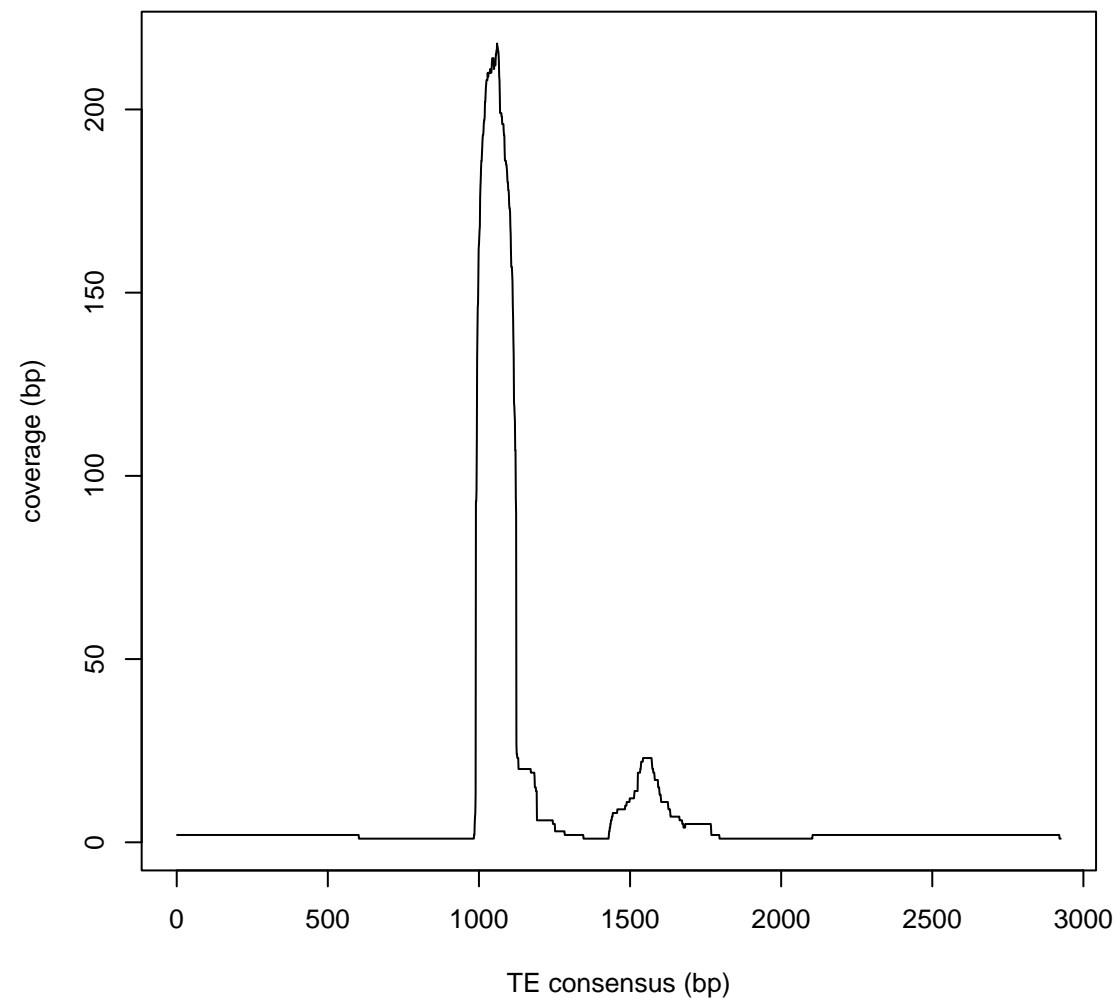


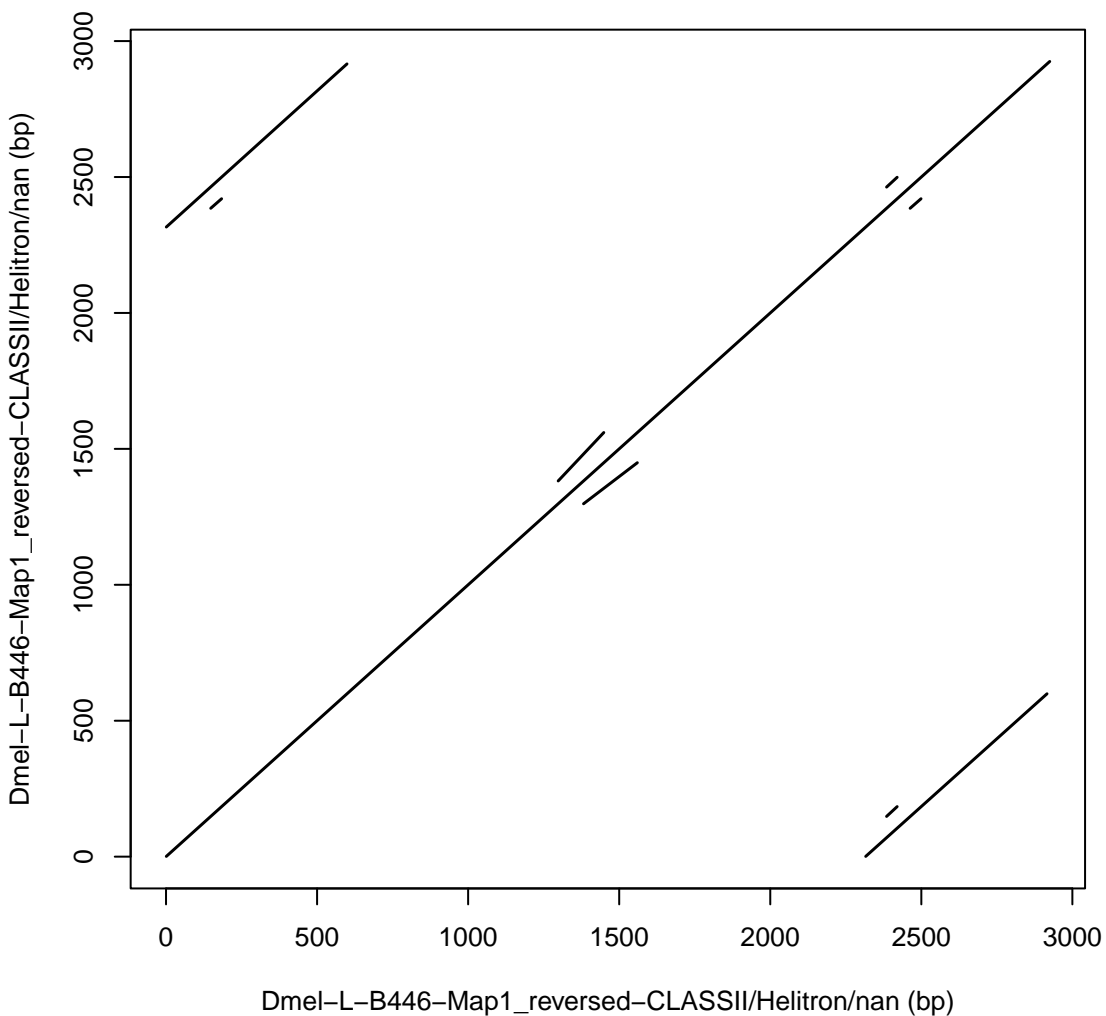
TE: Dmel-L-B446-Map1_reversed-CLASSII/Helitron/nan
consensus size: 2925bp; fragments: 254; full length: 1 (>=2632.5bp)



TE consensus genomic coverage



TE consensus self dotplot (blastn)



TE consensus structure and protein hits

