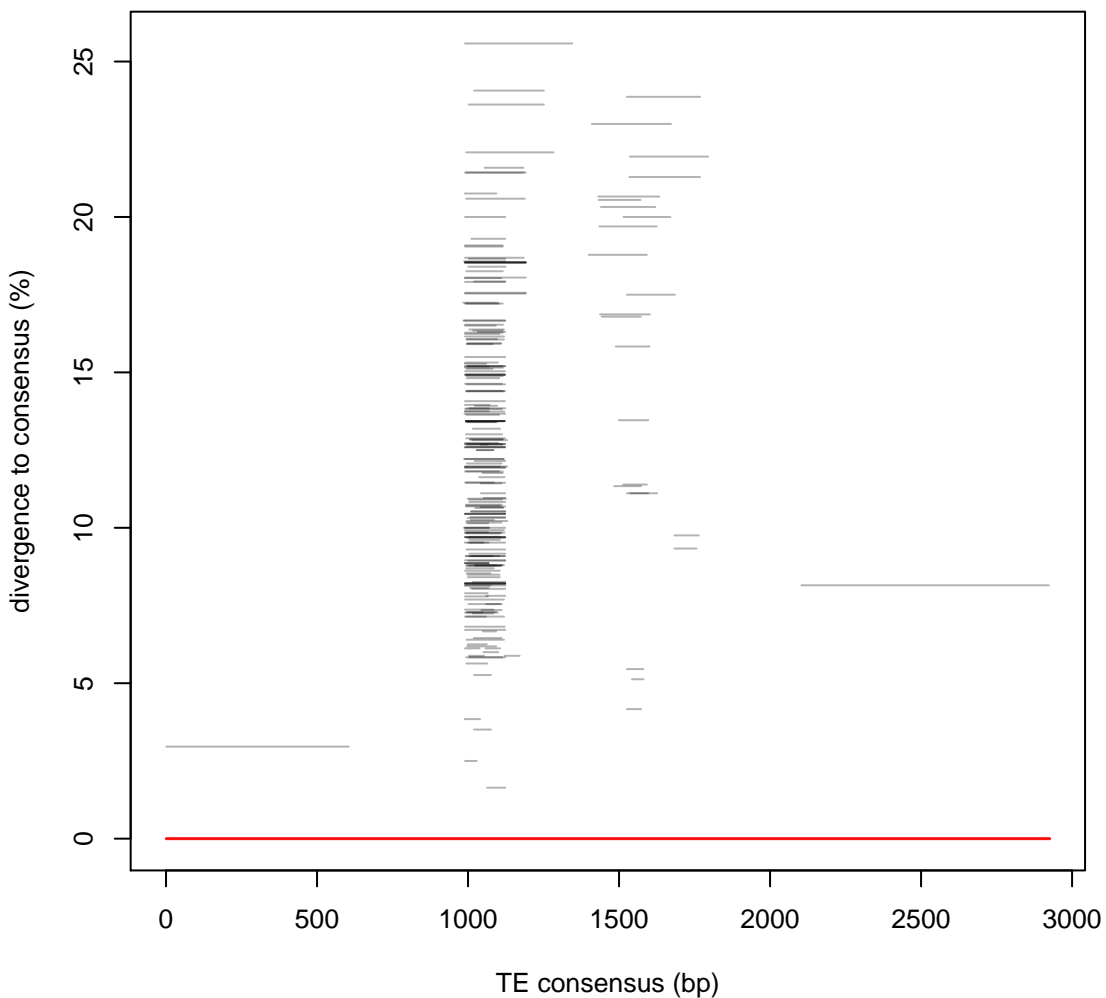
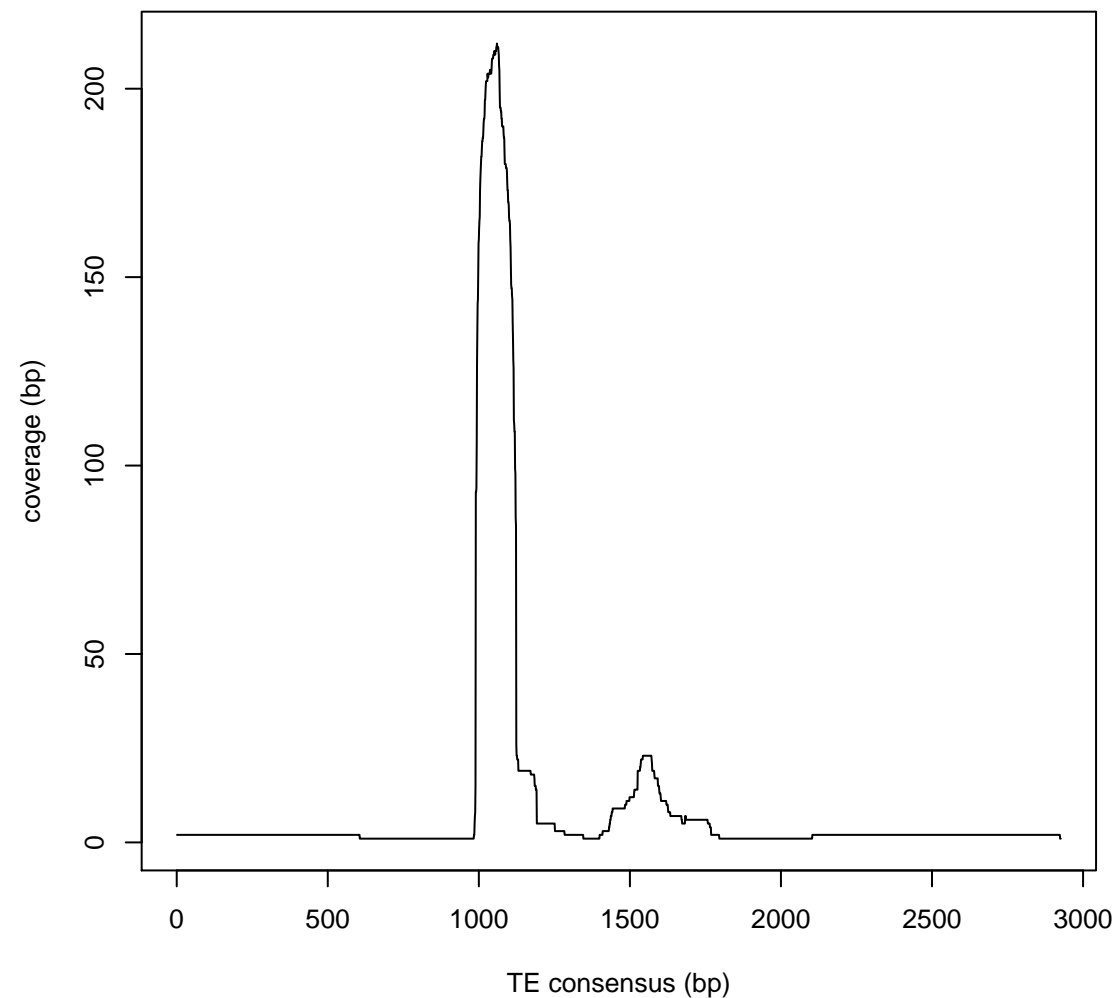


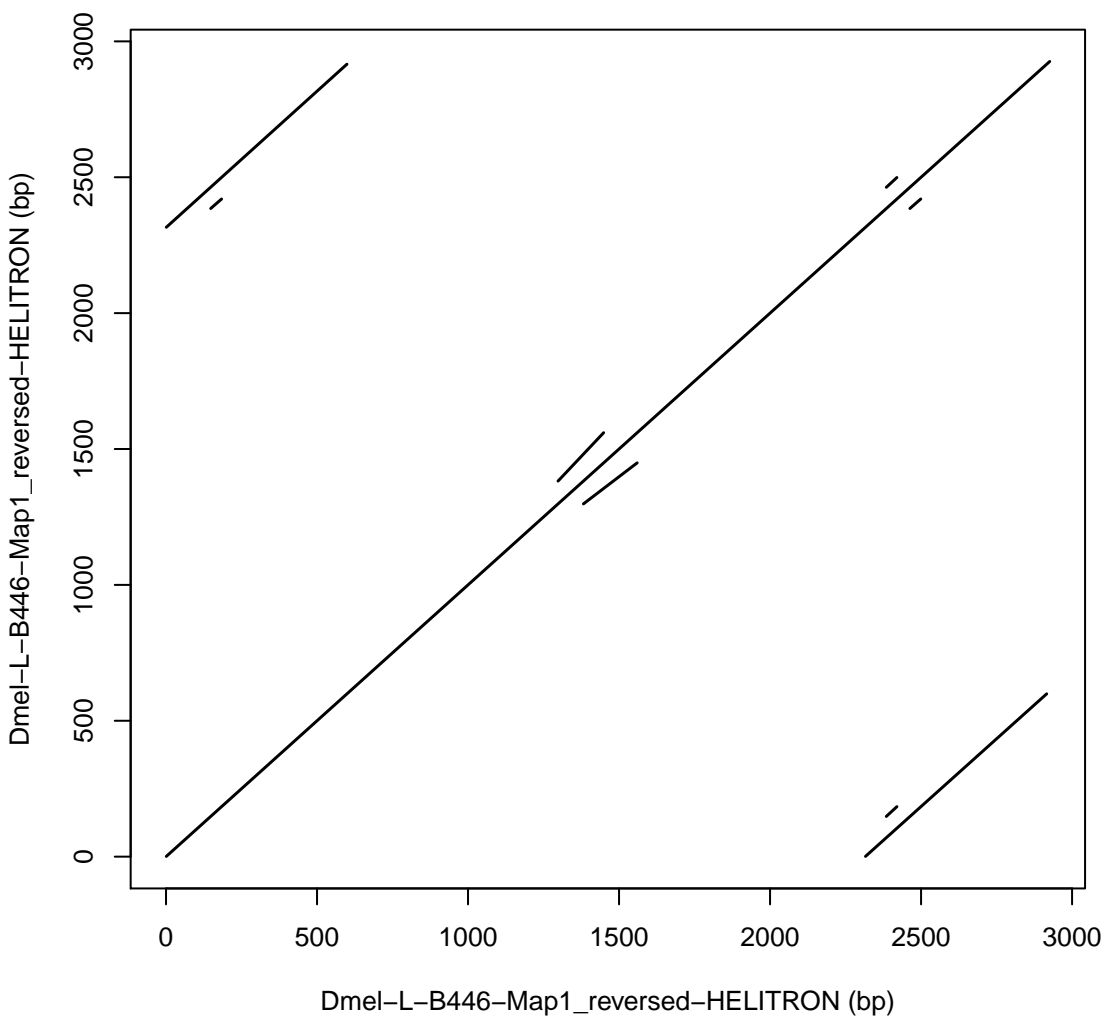
TE: Dmel-L-B446-Map1_reversed-HELITRON
consensus size: 2926bp; fragments: 247; full length: 1 (>=2633.4bp)



TE consensus genomic coverage



TE consensus self dotplot (blastn)



TE consensus structure and protein hits

