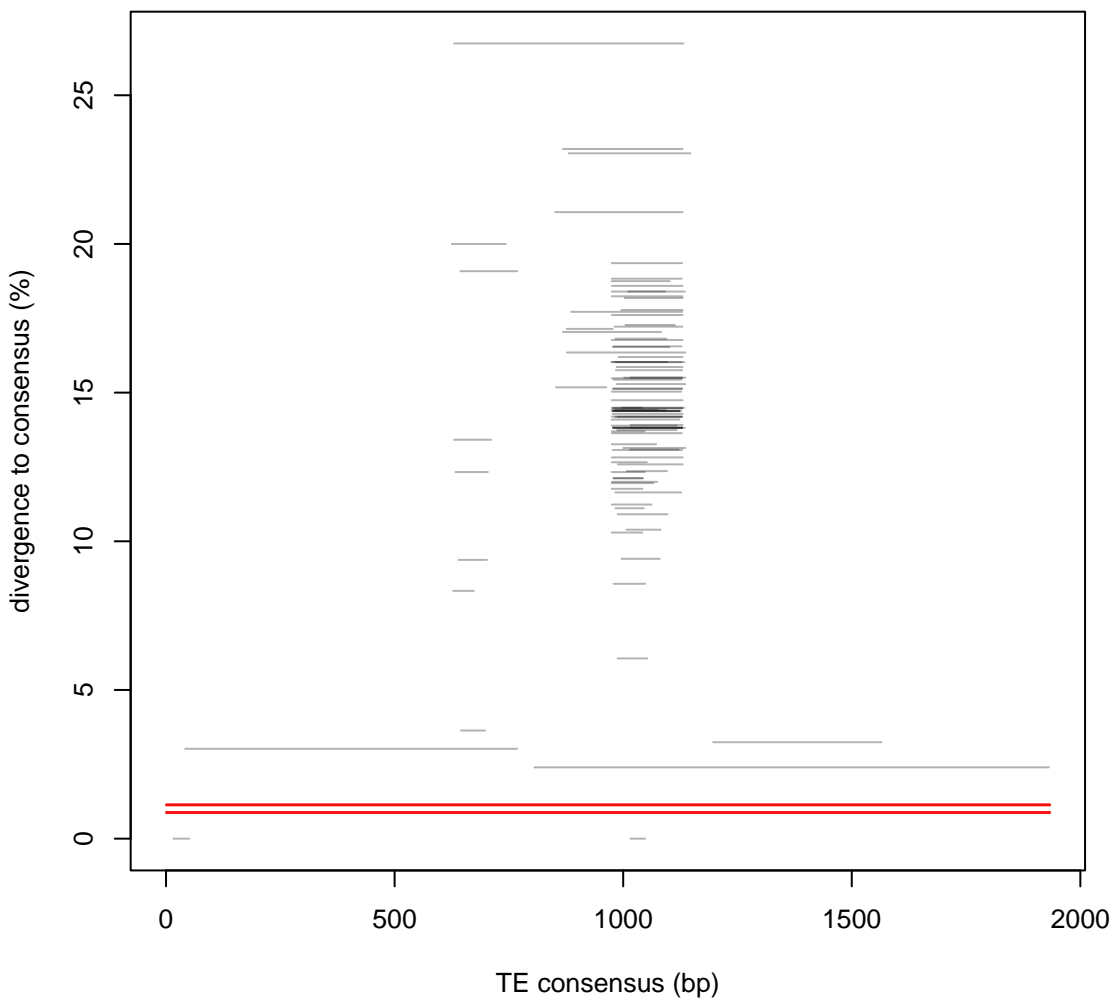
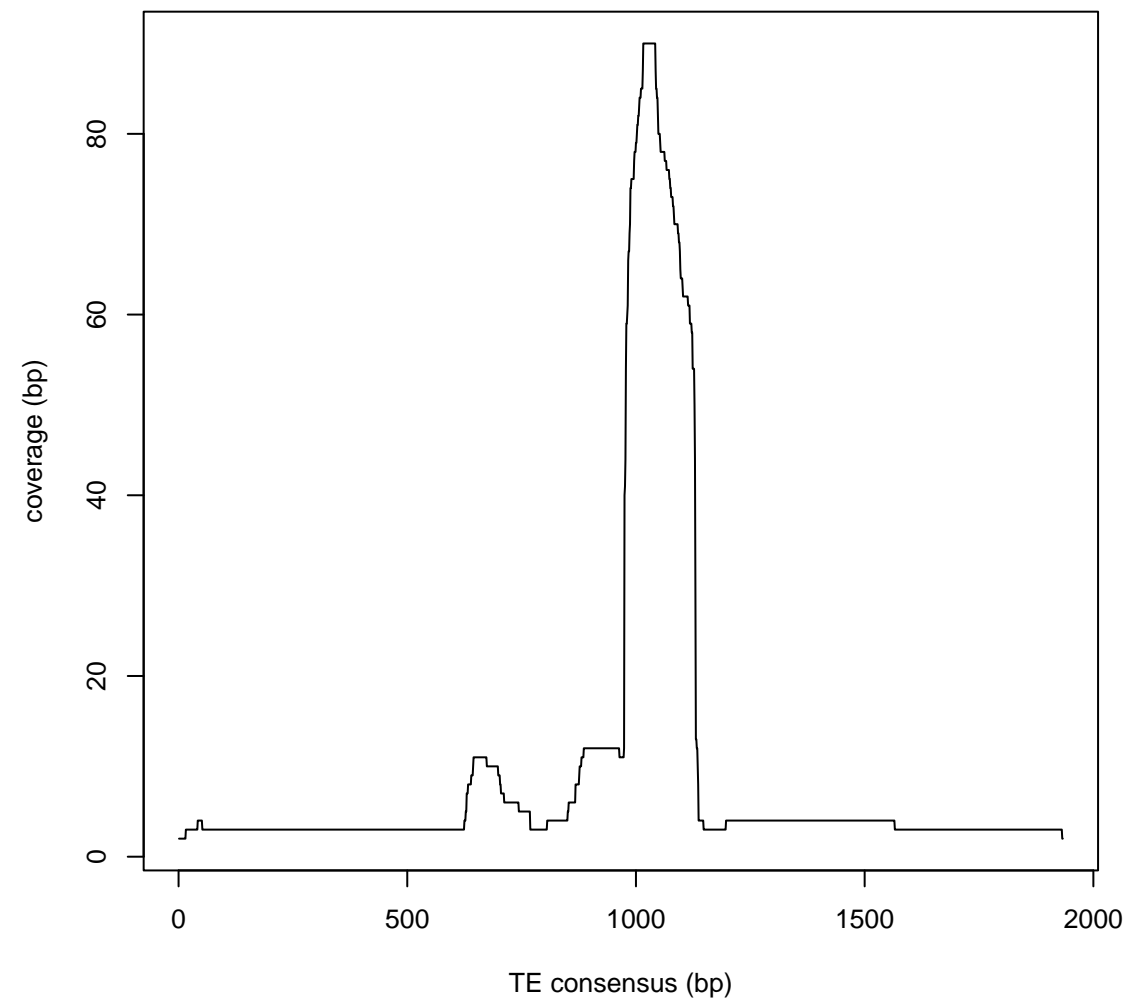


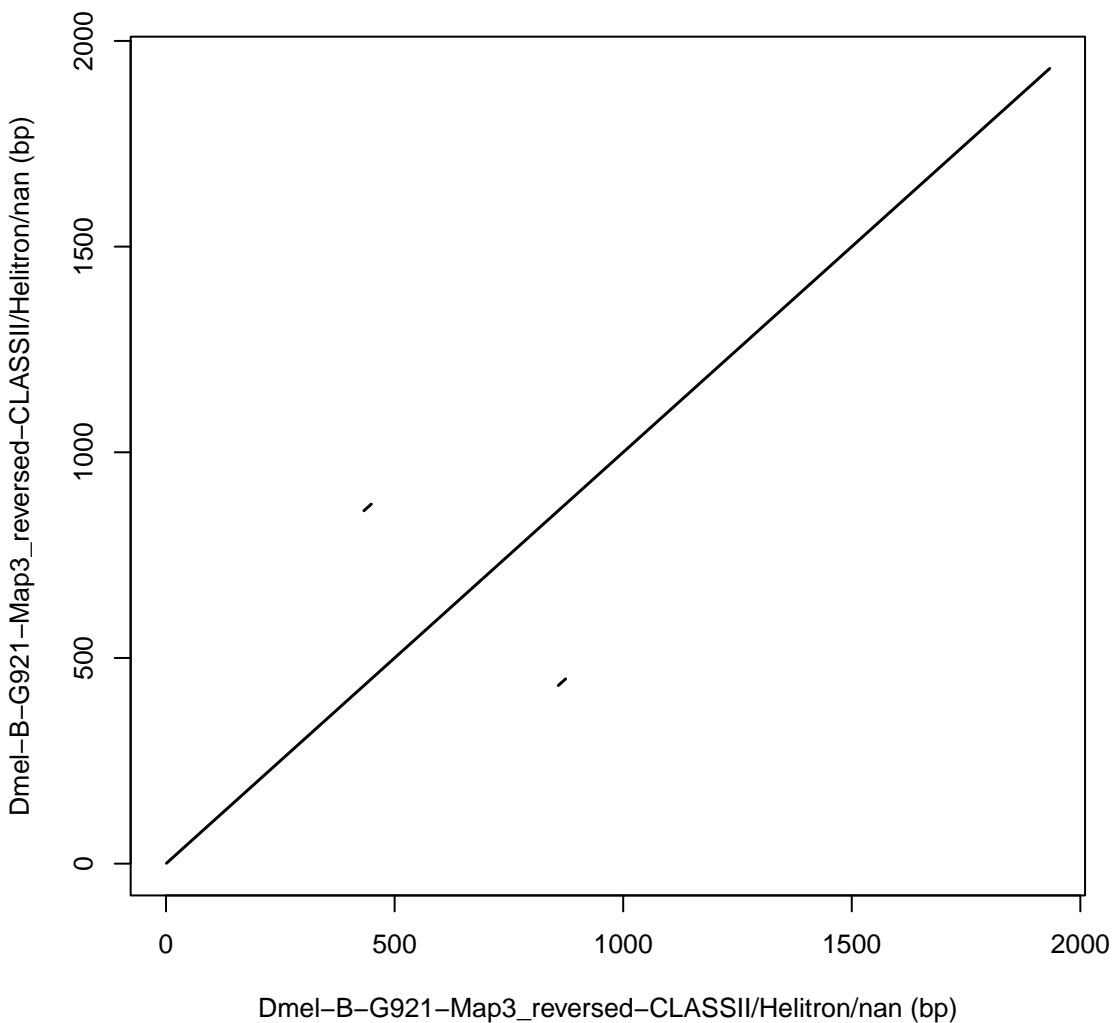
TE: Dmel-B-G921-Map3_reversed-CLASSII/Helitron/nan
consensus size: 1933bp; fragments: 102; full length: 2 (≥ 1739.7 bp)



TE consensus genomic coverage



TE consensus self dotplot (blastn)



TE consensus structure and protein hits

