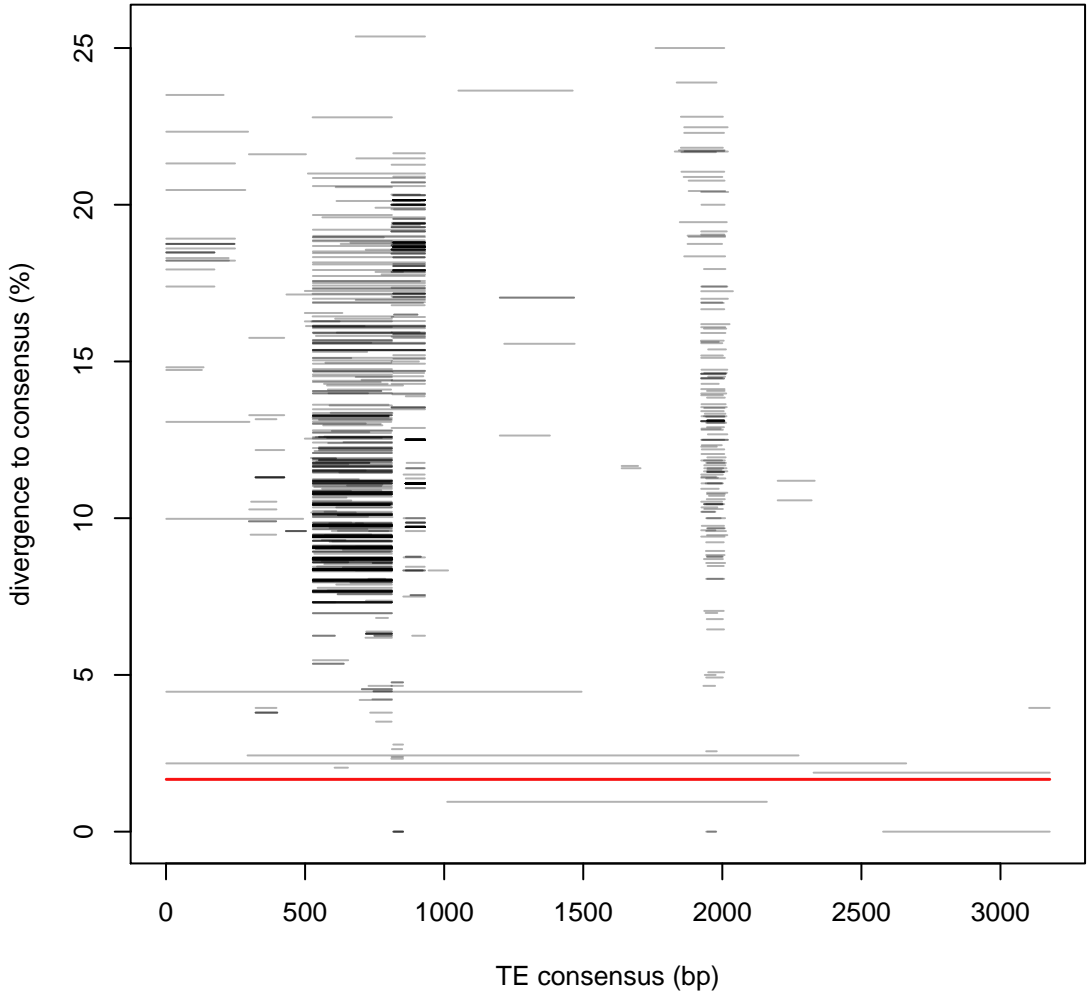
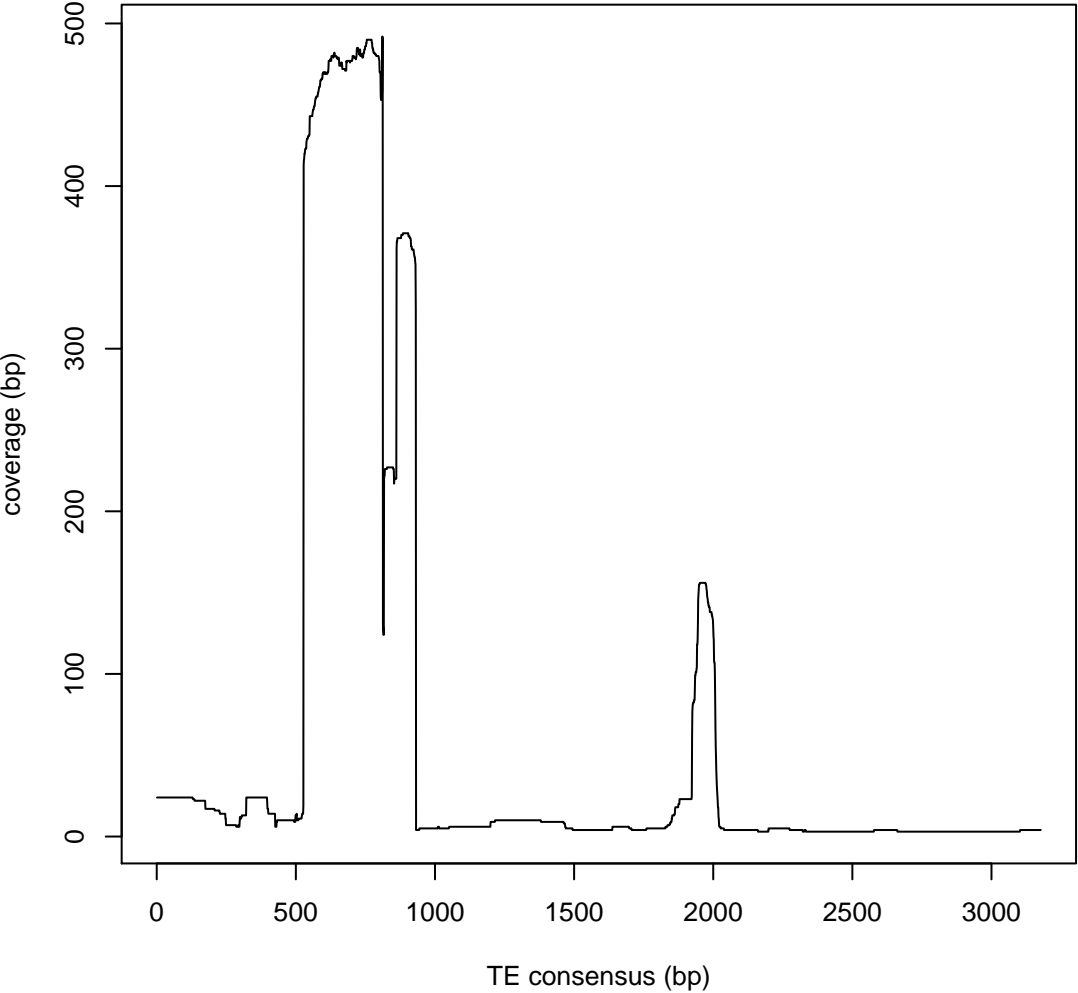


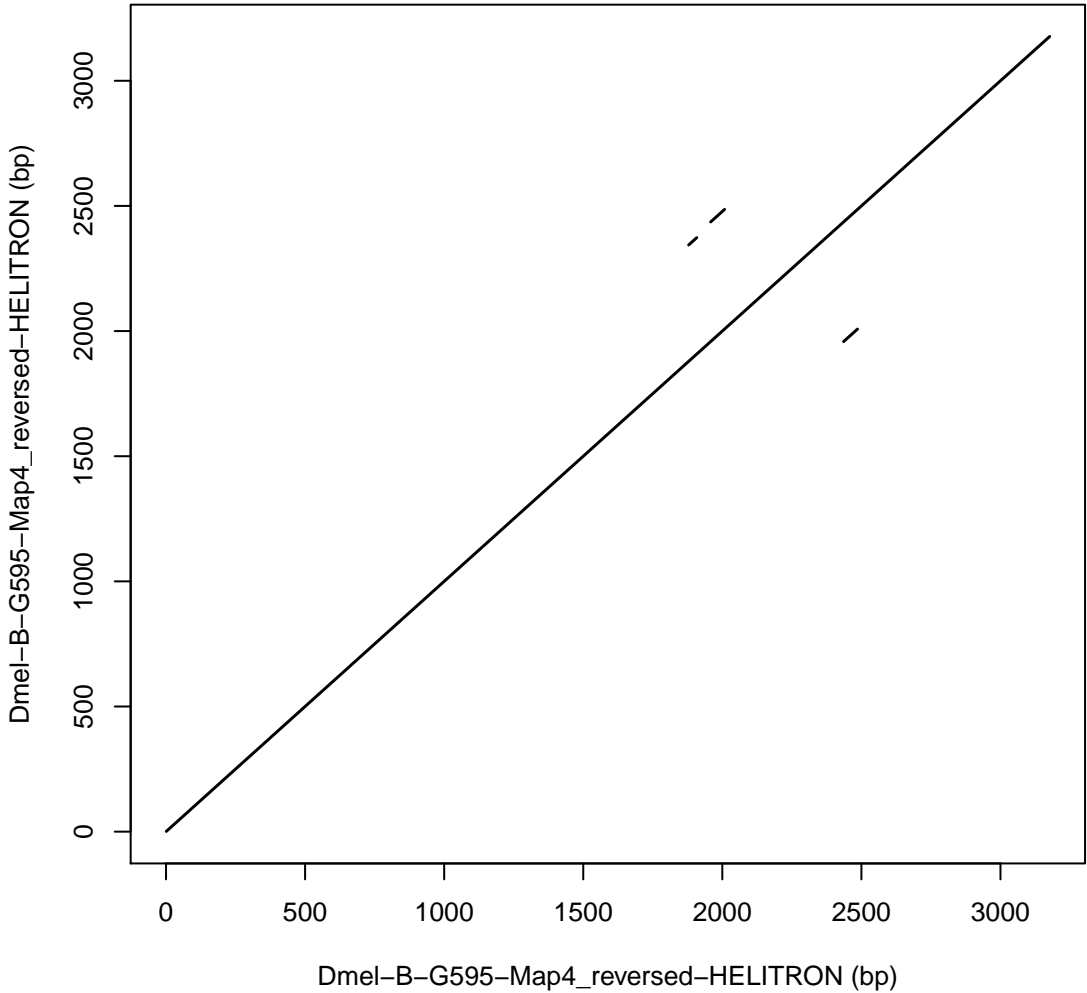
TE: Dmel-B-G595-Map4_reversed-HELITRON
consensus size: 3177bp; fragments: 1056; full length: 1 (>=2859.3bp)



TE consensus genomic coverage



TE consensus self dotplot (blastn)



TE consensus structure and protein hits

