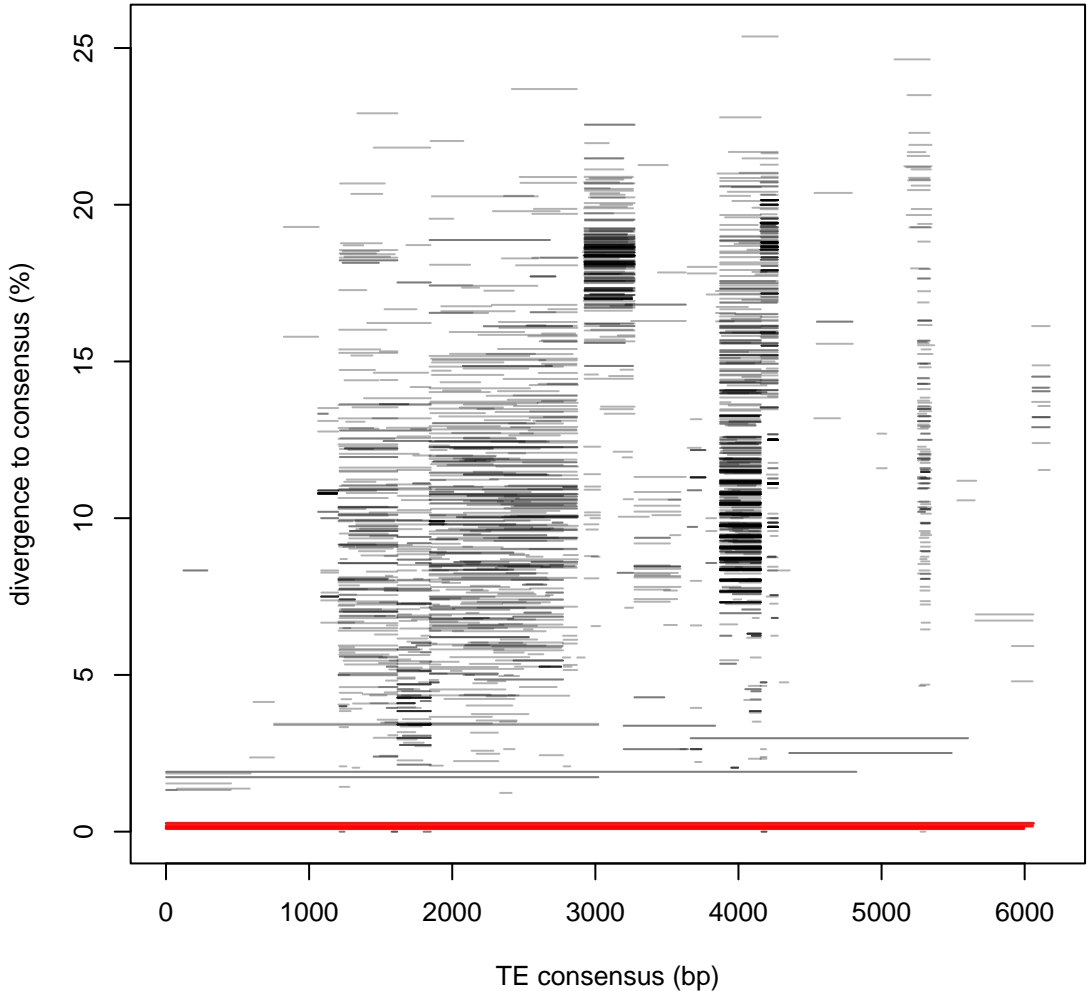
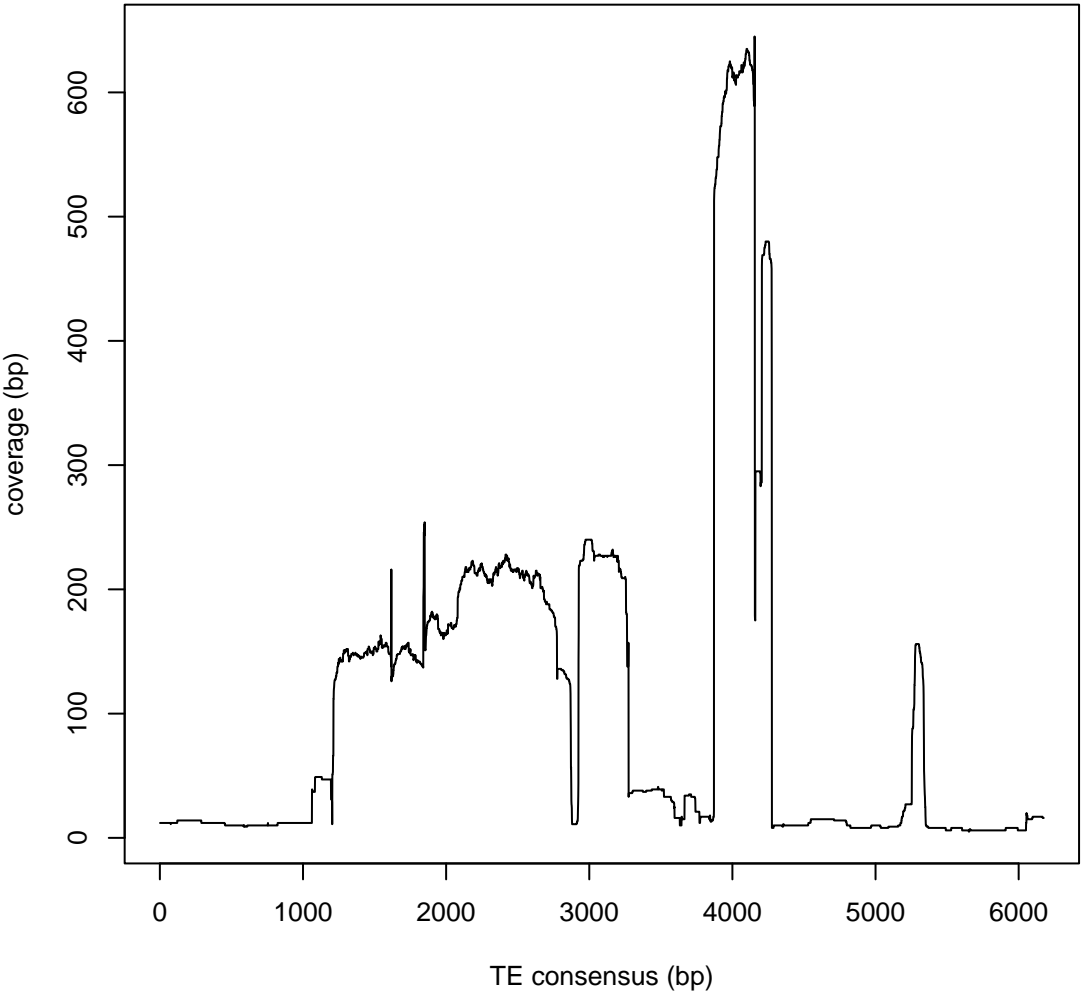


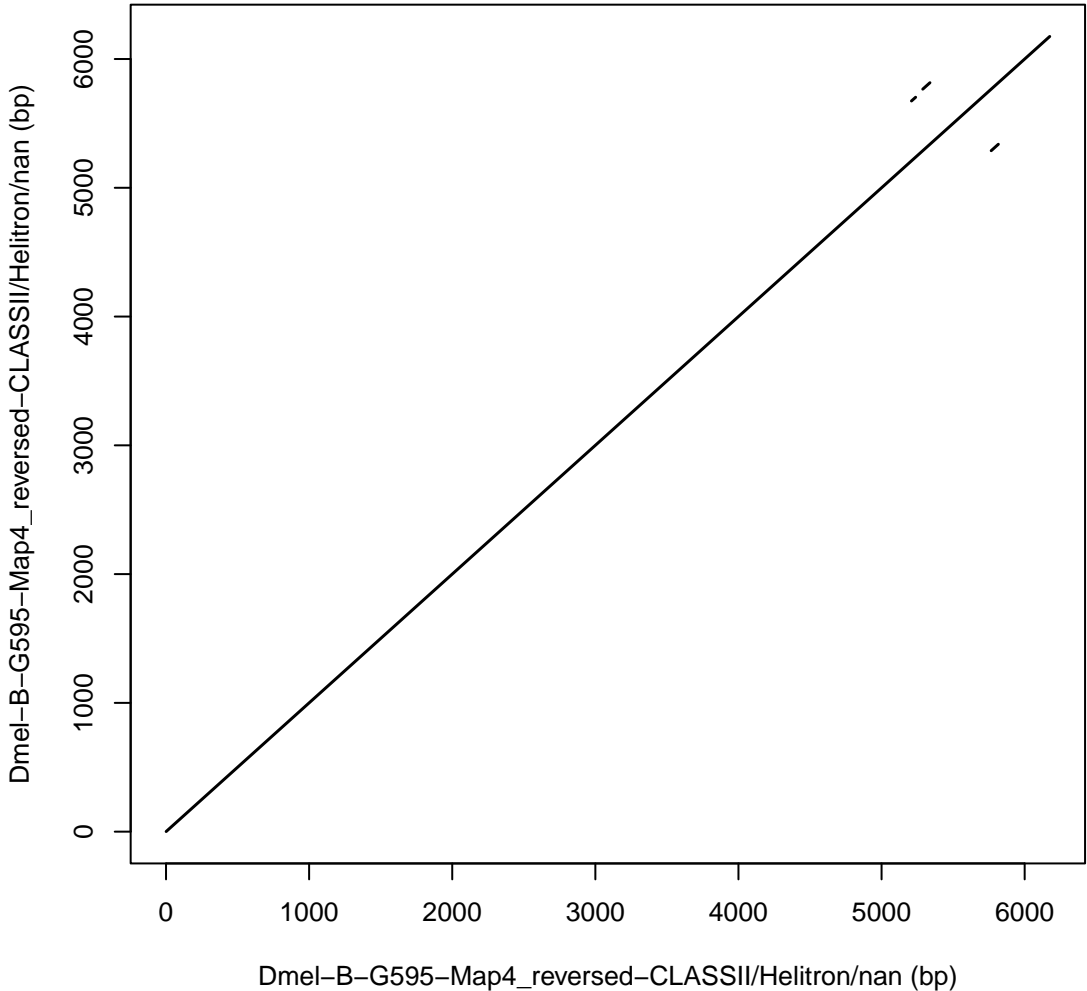
TE: Dmel-B-G595-Map4_reversed-CLASSII/Helitron/nan
consensus size: 6175bp; fragments: 2444; full length: 4 (>=5557.5bp)



TE consensus genomic coverage



TE consensus self dotplot (blastn)



TE consensus structure and protein hits

