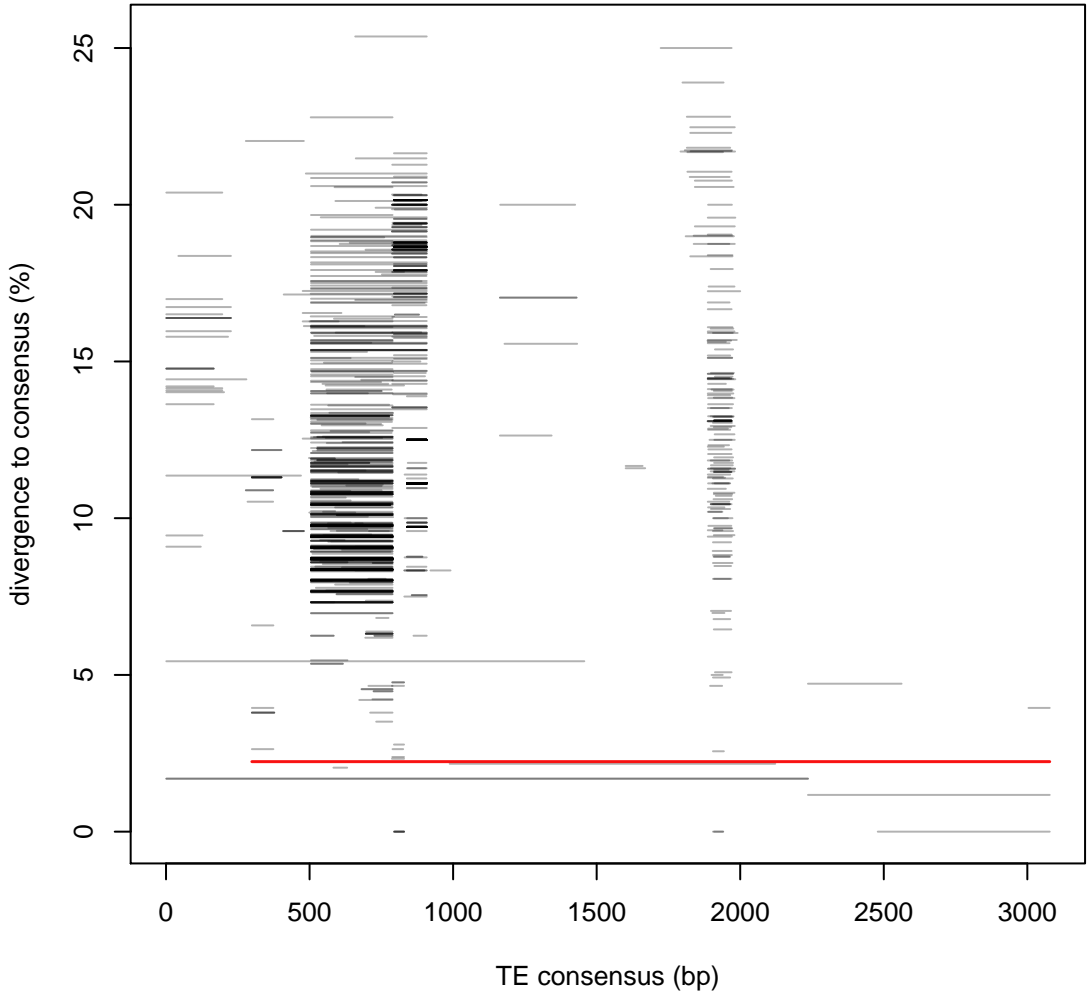
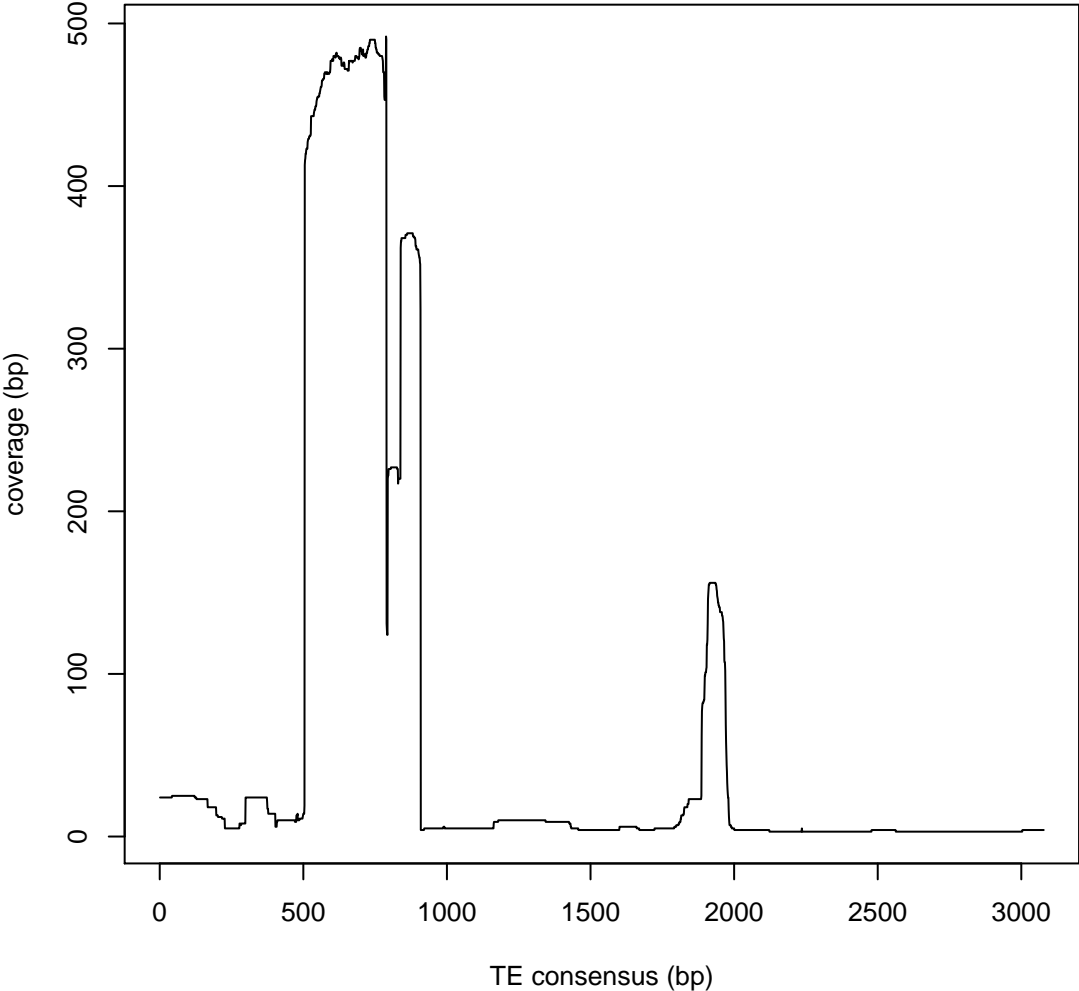


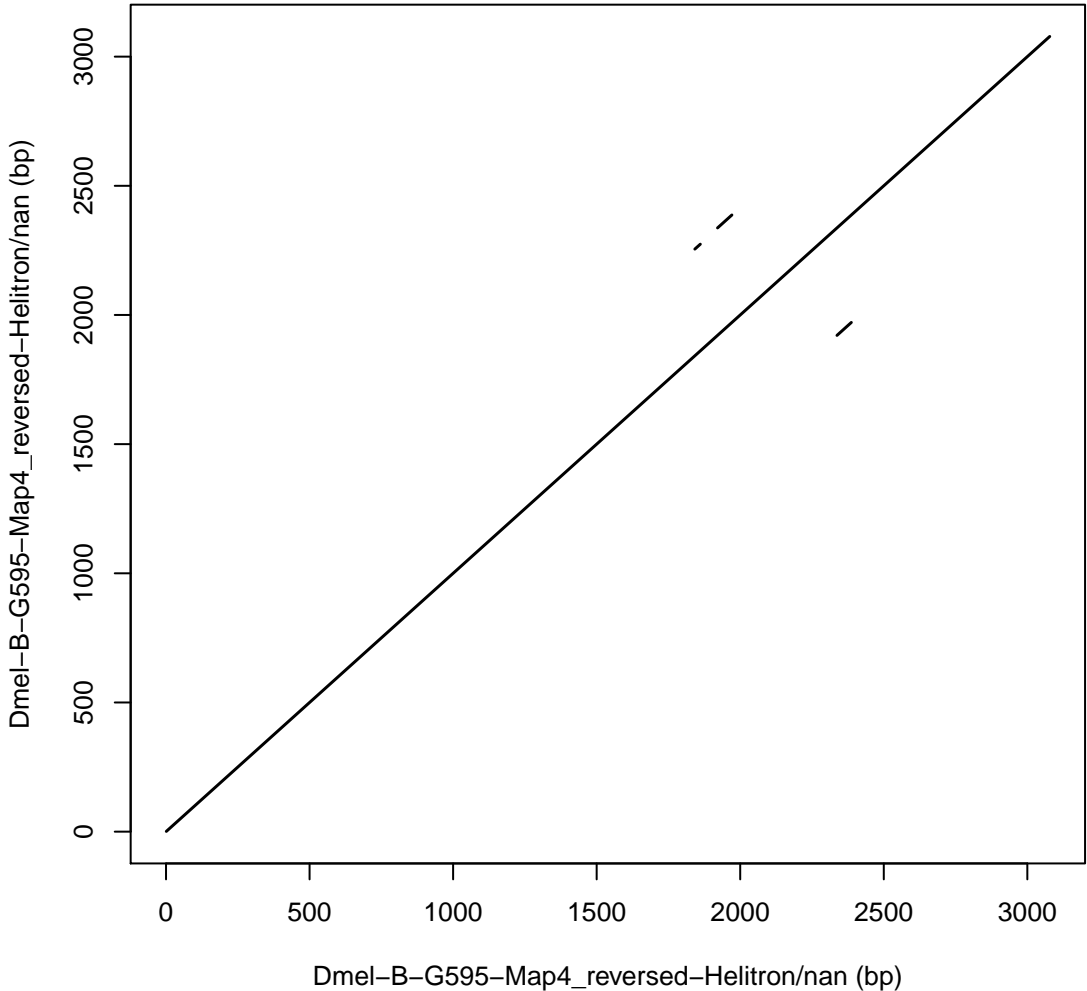
TE: Dmel-B-G595-Map4_reversed-Helitron/nan
consensus size: 3078bp; fragments: 1056; full length: 1 (>=2770.2bp)



TE consensus genomic coverage



TE consensus self dotplot (blastn)



TE consensus structure and protein hits

