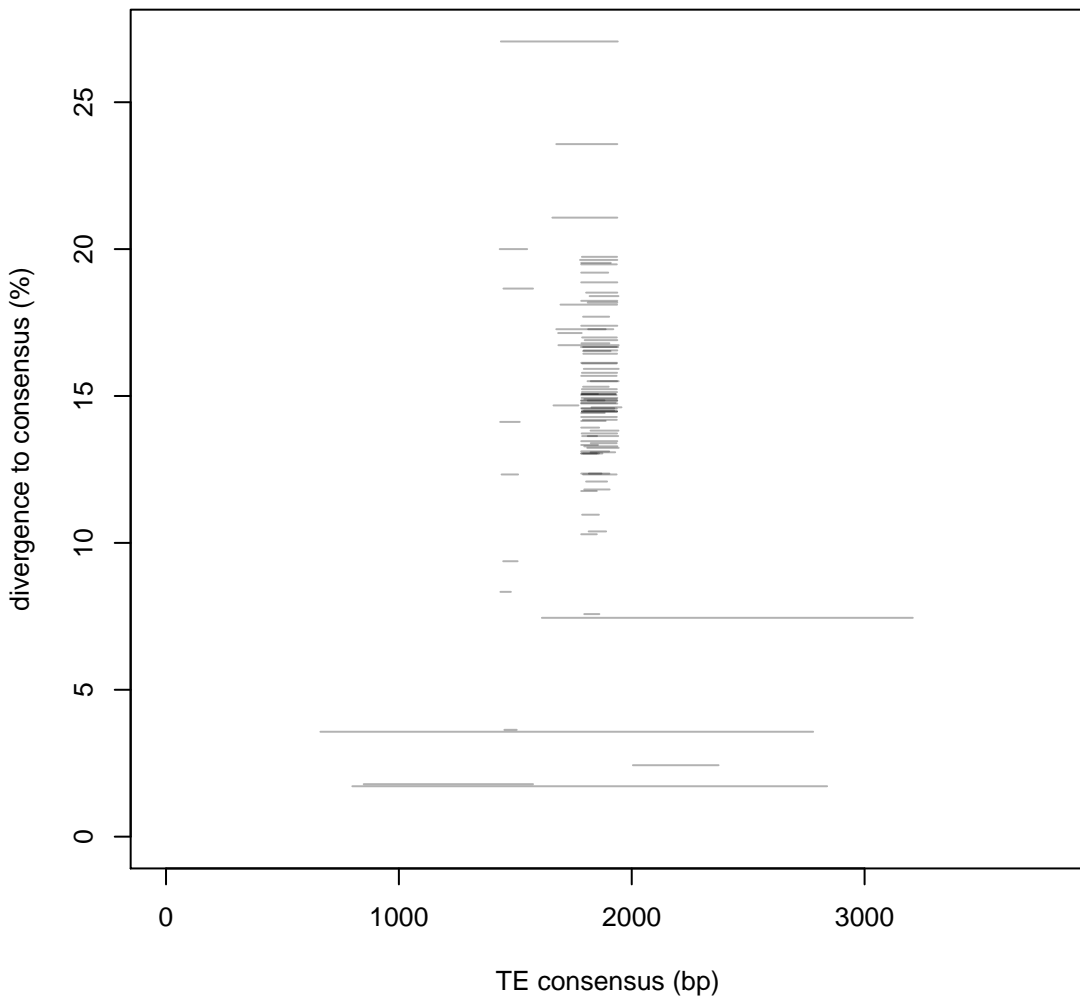
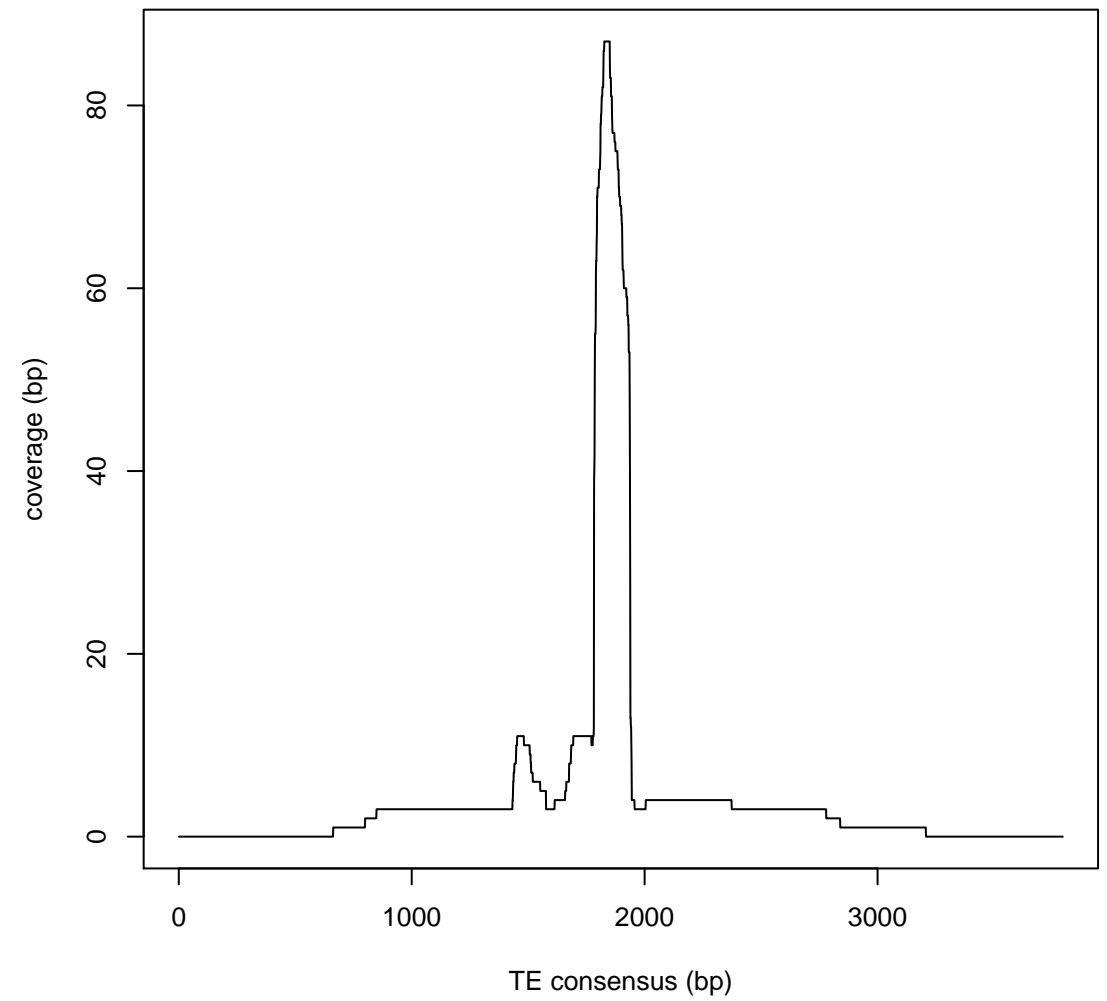


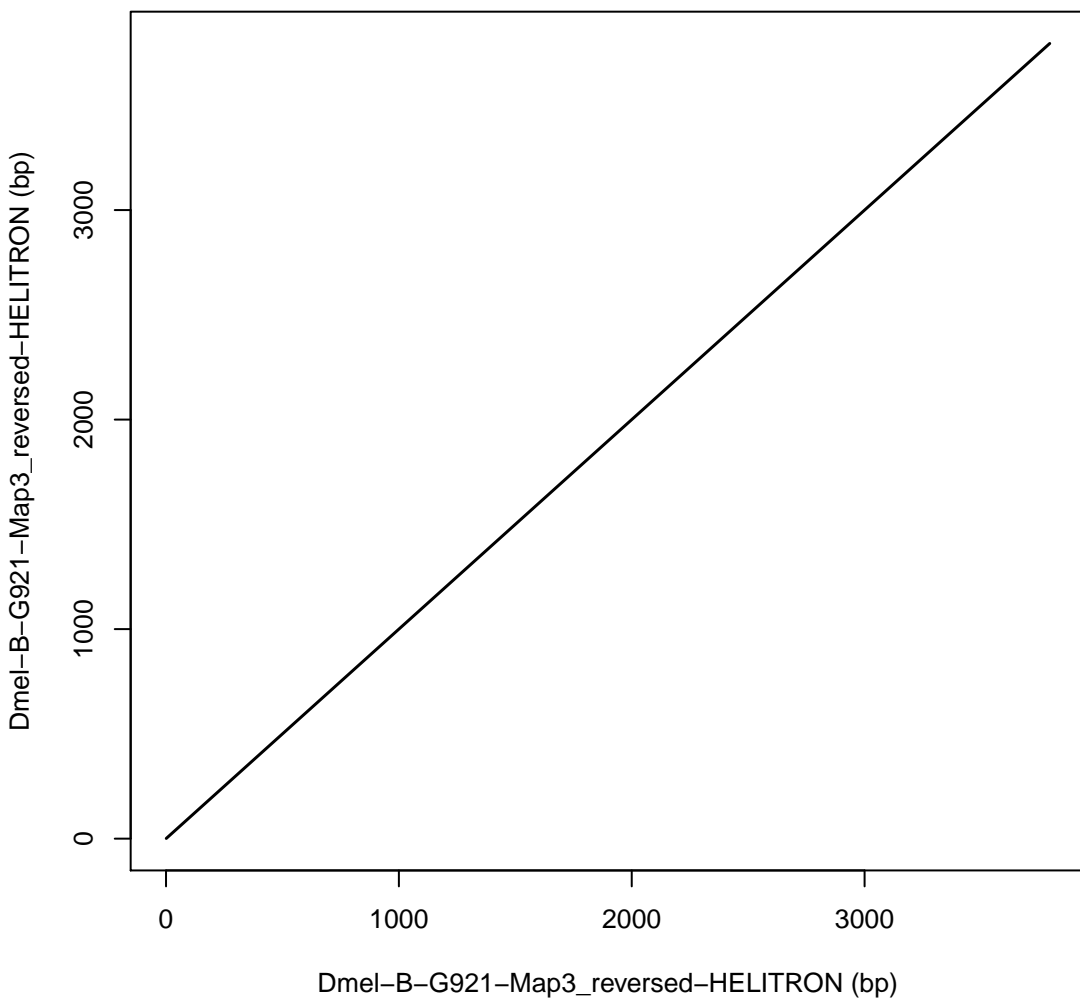
TE: Dmel-B-G921-Map3_reversed-HELITRON
consensus size: 3795bp; fragments: 98; full length: 0 (>=3415.5bp)



TE consensus genomic coverage



TE consensus self dotplot (blastn)



TE consensus structure and protein hits

