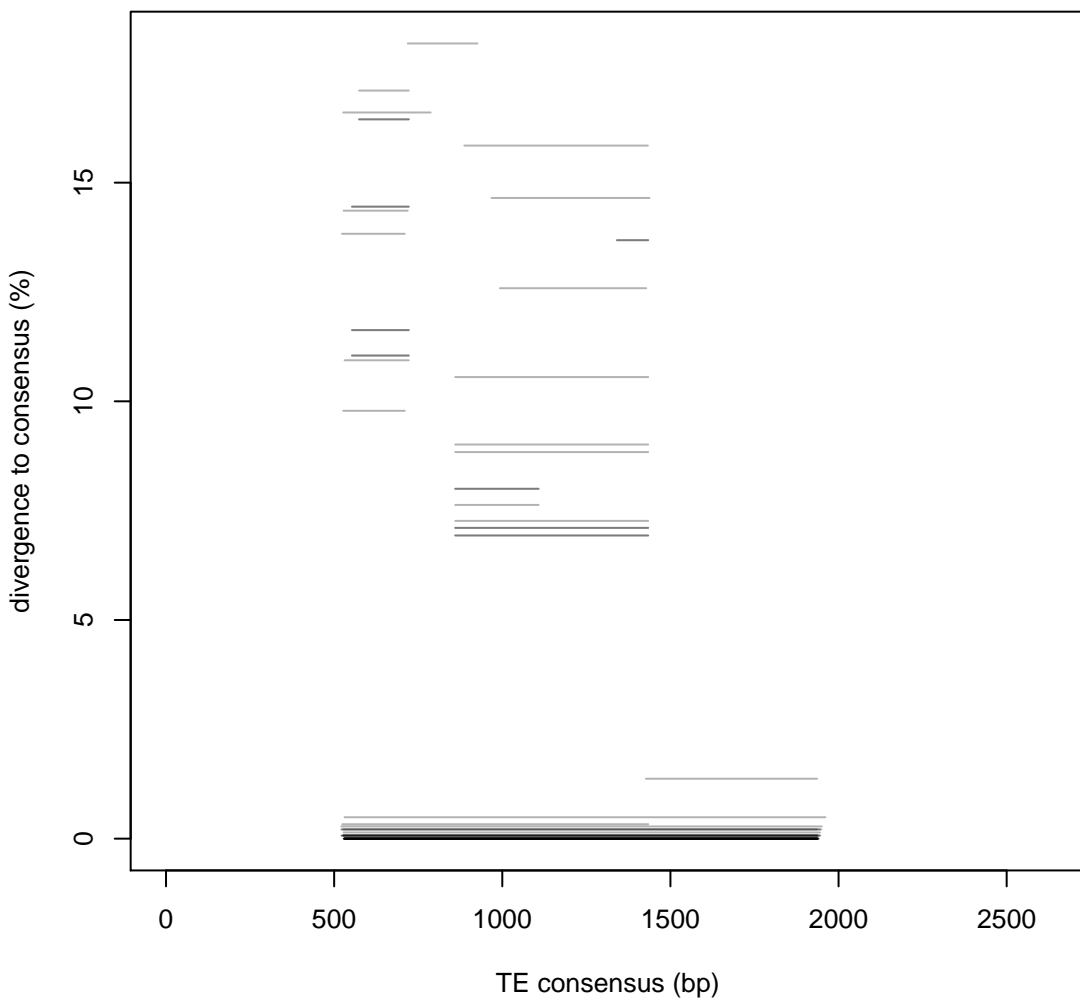
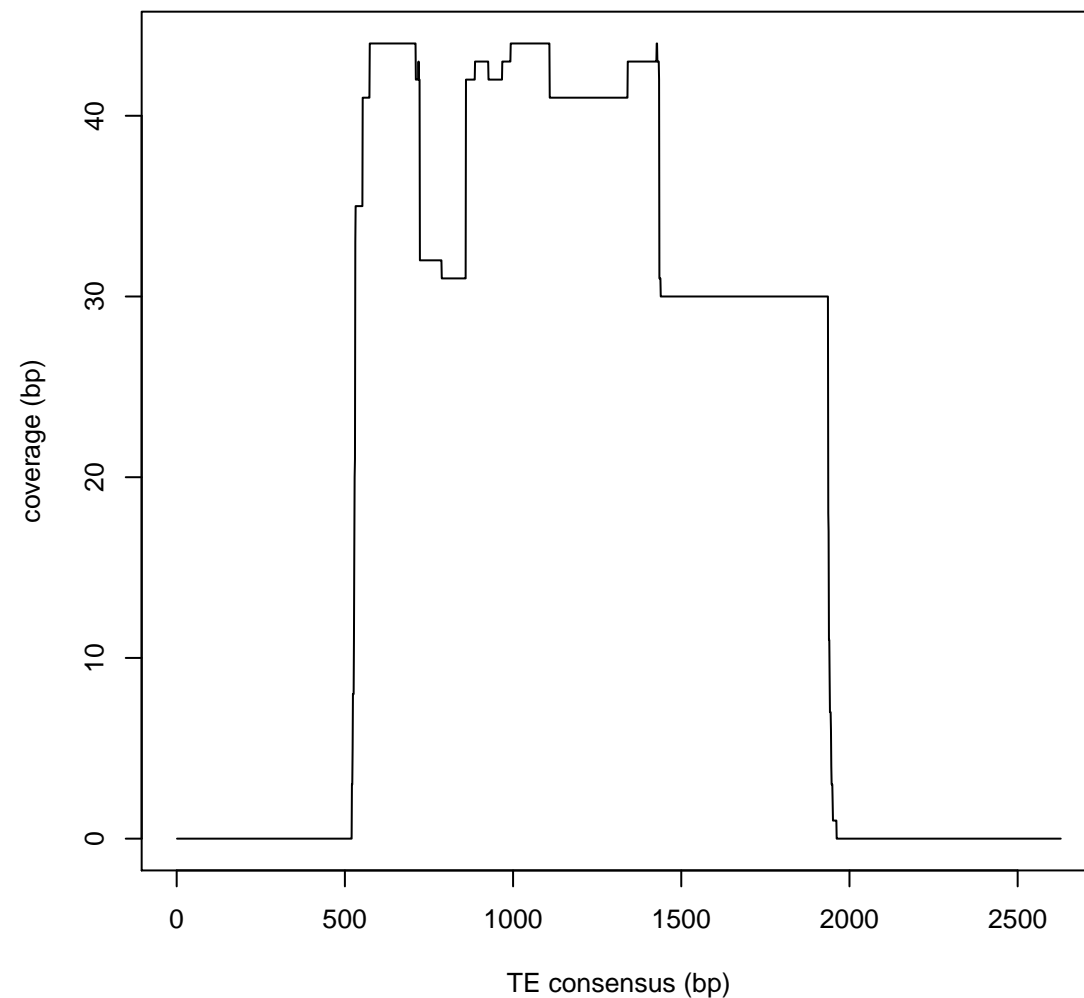


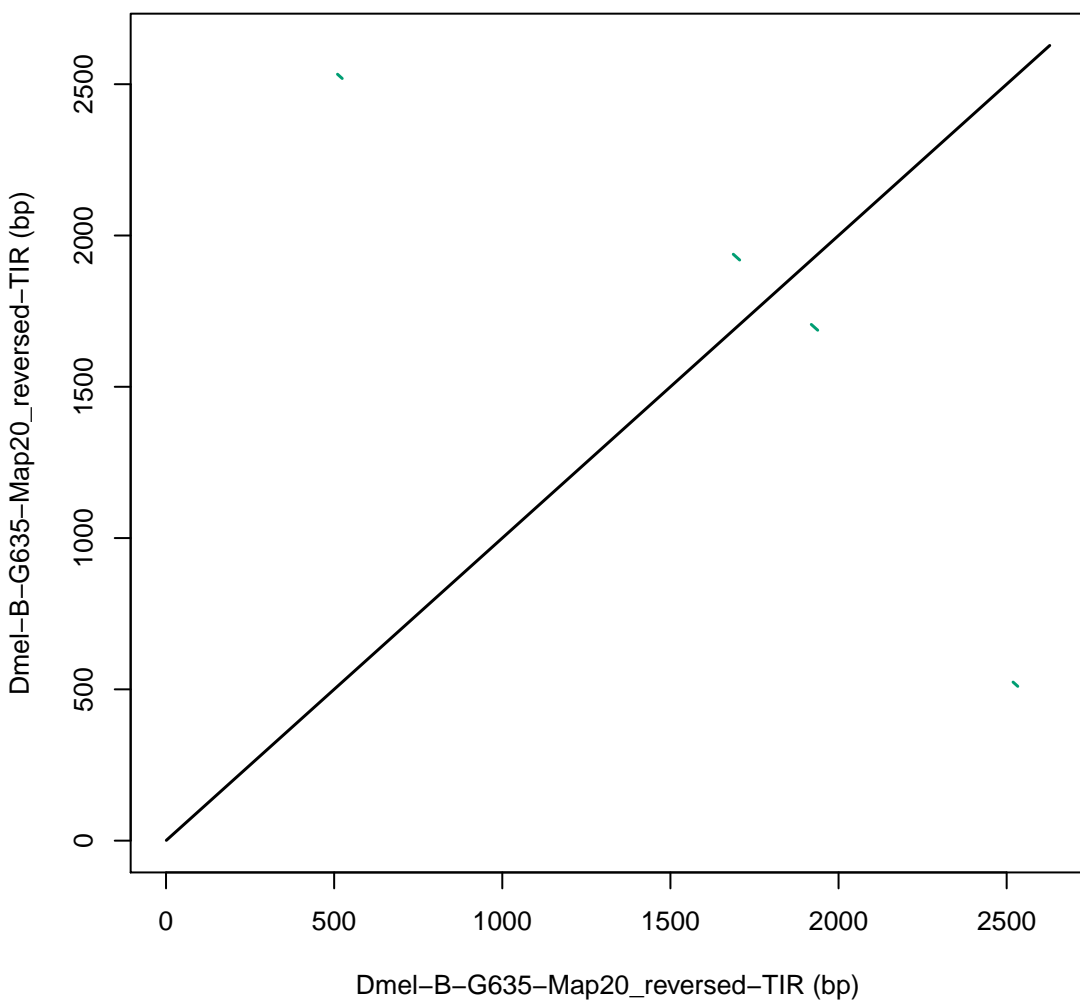
TE: Dmel-B-G635-Map20_reversed-TIR
consensus size: 2628bp; fragments: 62; full length: 0 (>=2365.2bp)



TE consensus genomic coverage



TE consensus self dotplot (blastn)



TE consensus structure and protein hits

