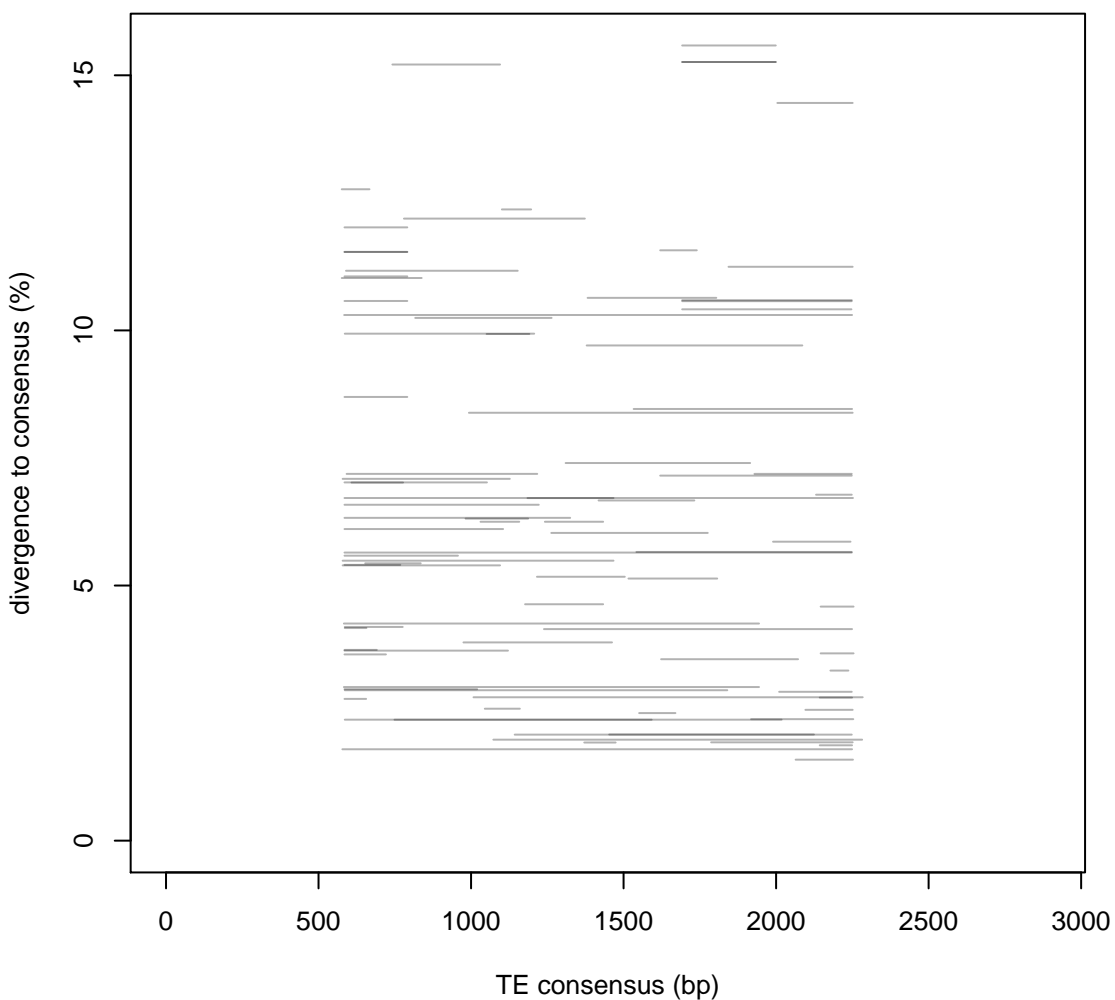
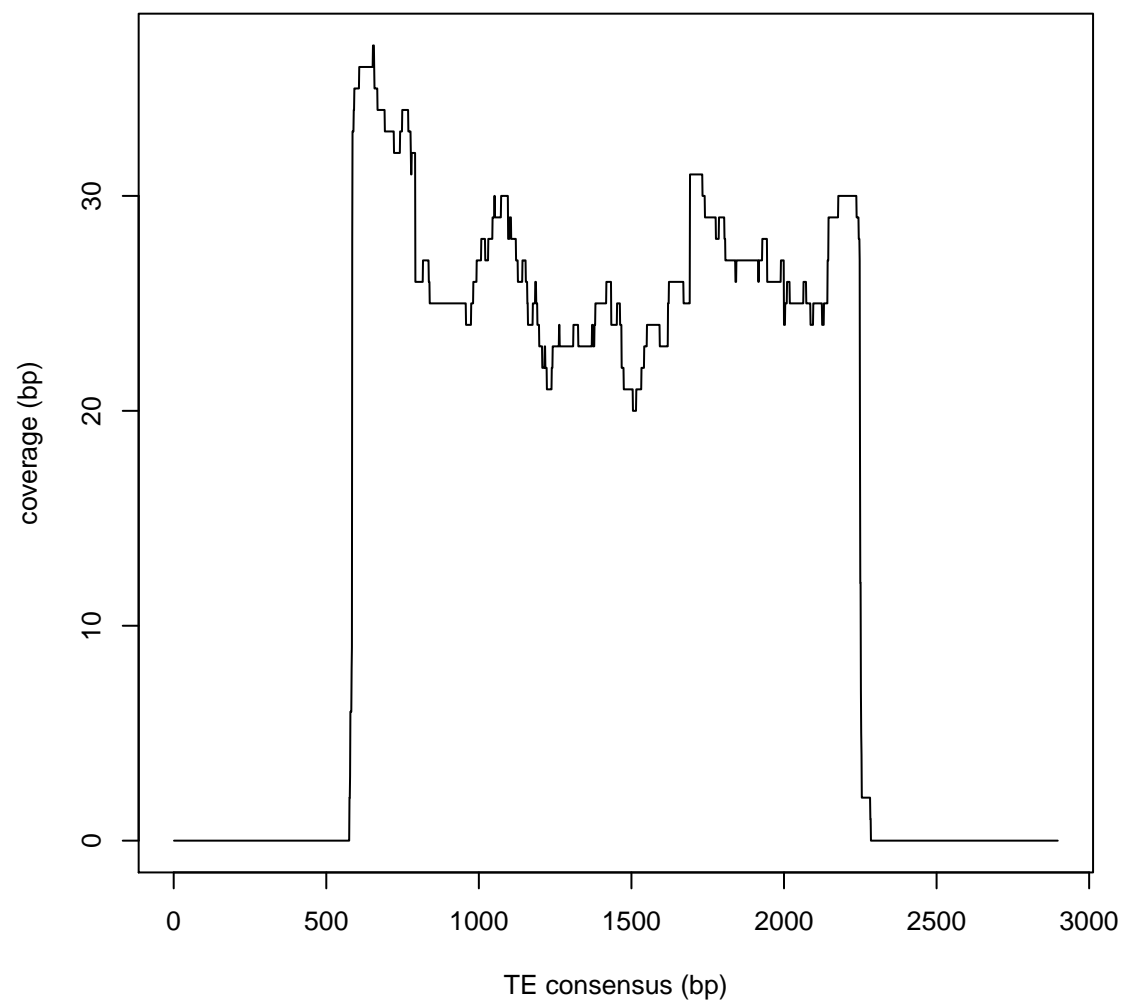


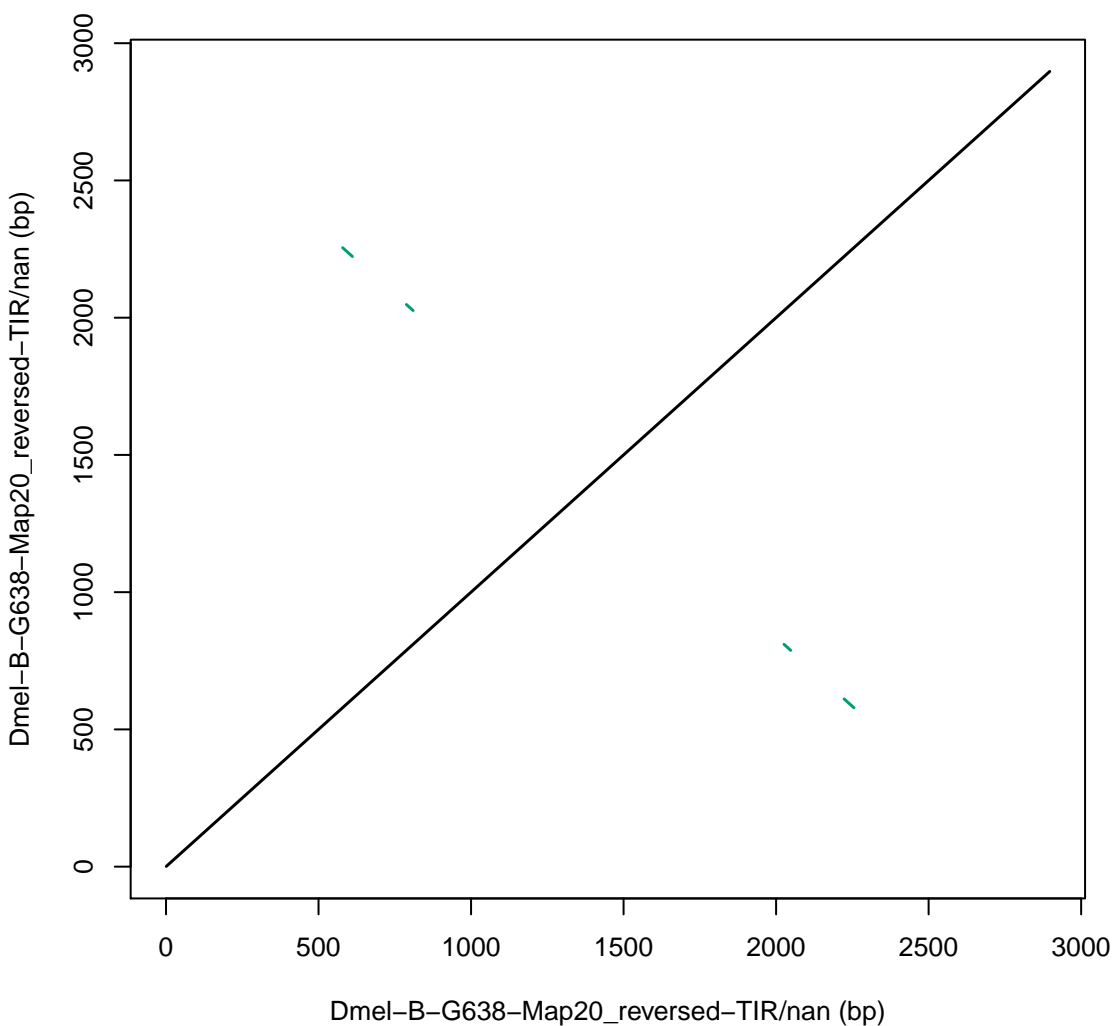
TE: Dmel-B-G638-Map20\_reversed-TIR/nan  
consensus size: 2897bp; fragments: 91; full length: 0 (>=2607.3bp)



TE consensus genomic coverage



TE consensus self dotplot (blastn)



TE consensus structure and protein hits

