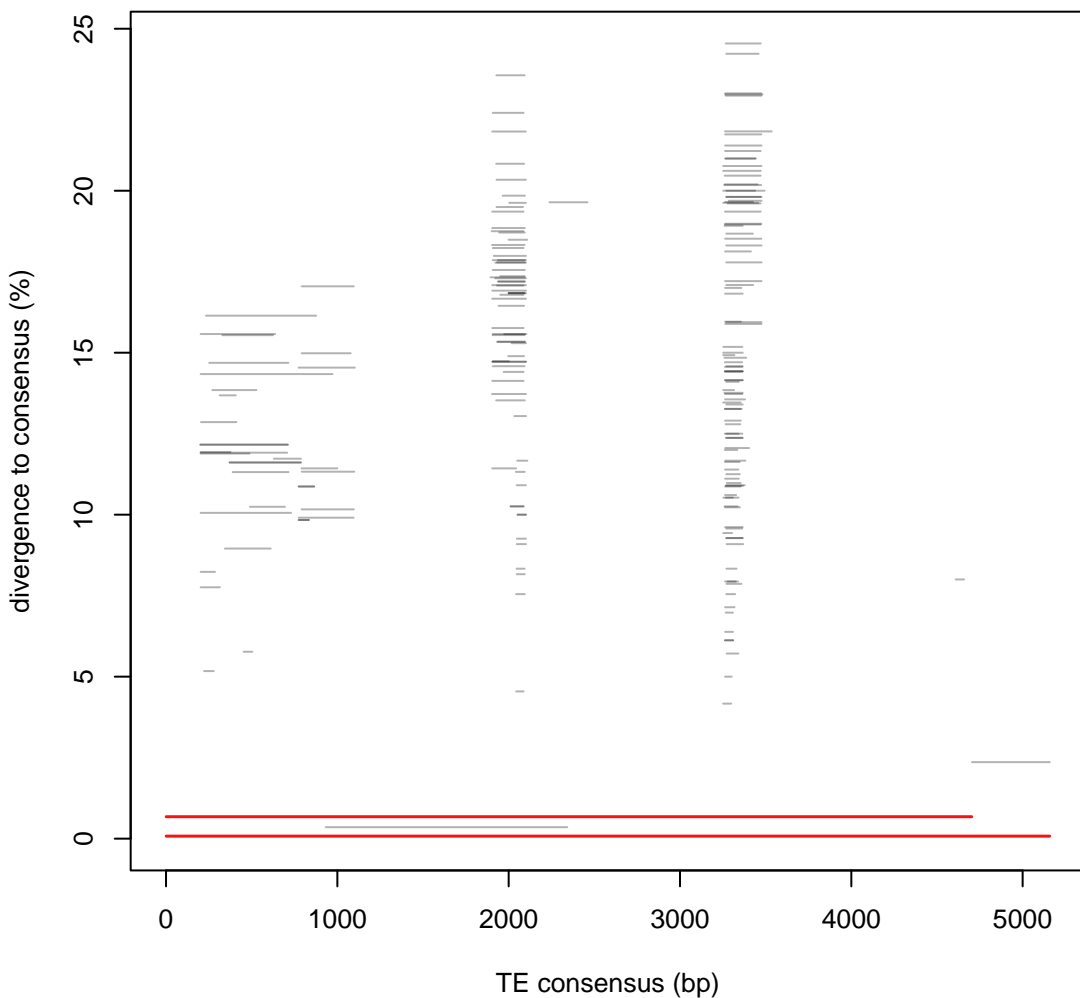
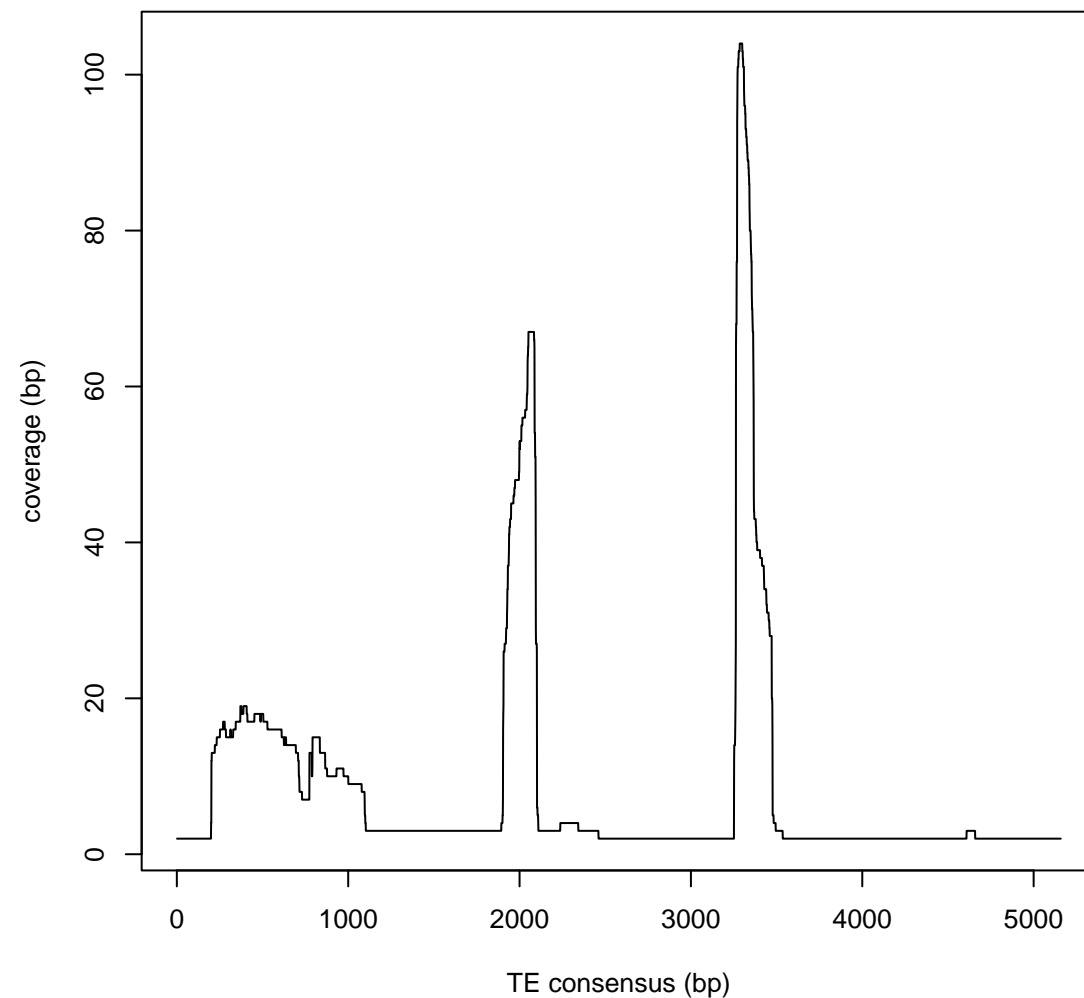


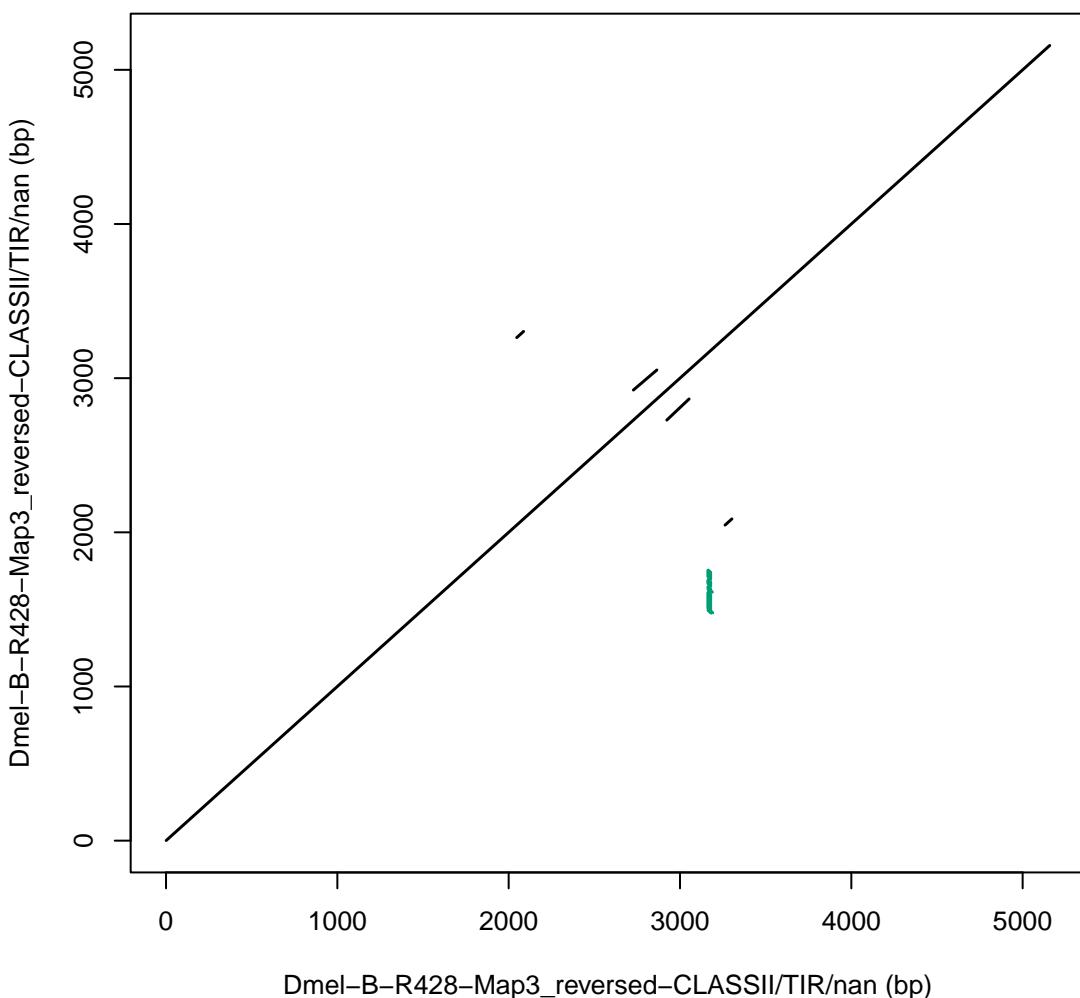
TE: Dmel-B-R428-Map3_reversed-CLASSII/TIR/nan
consensus size: 5158bp; fragments: 209; full length: 2 (>=4642.2bp)



TE consensus genomic coverage



TE consensus self dotplot (blastn)



TE consensus structure and protein hits

