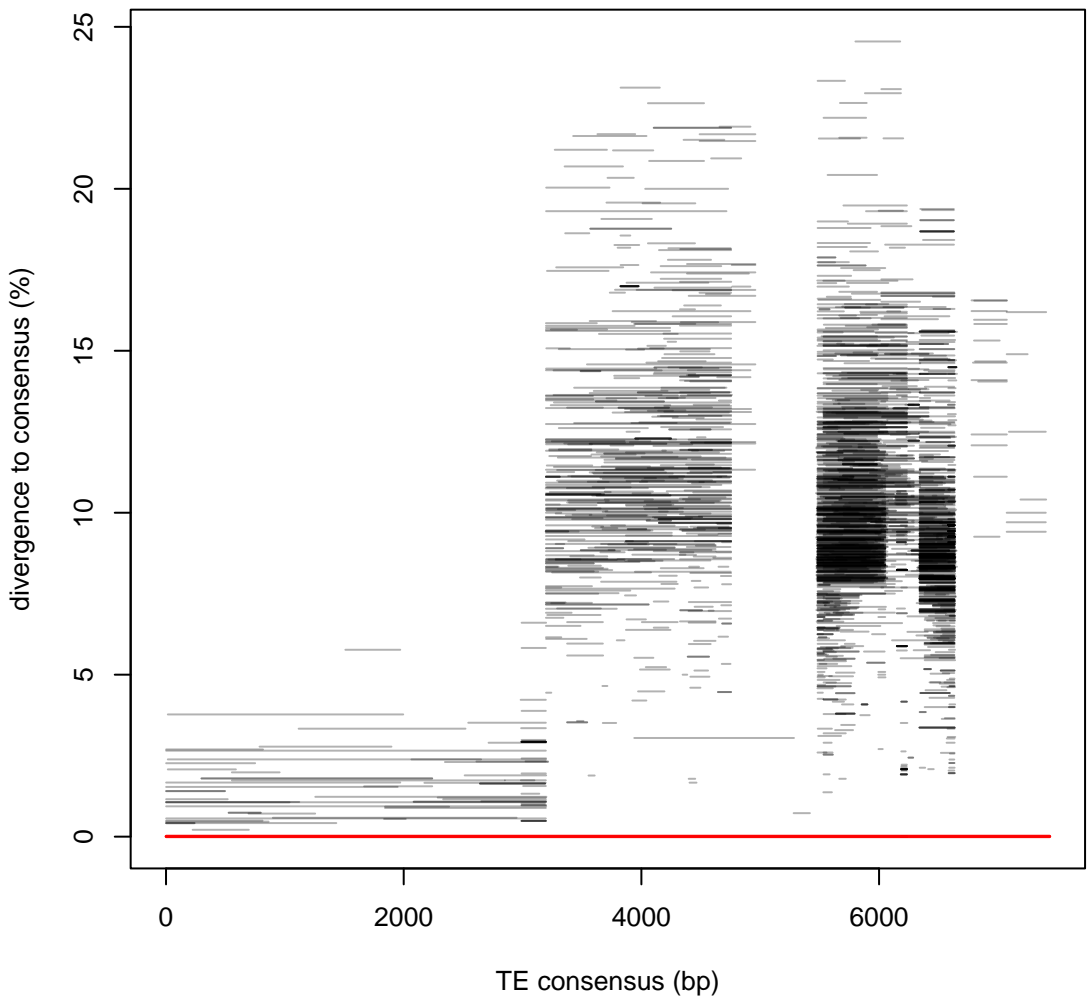
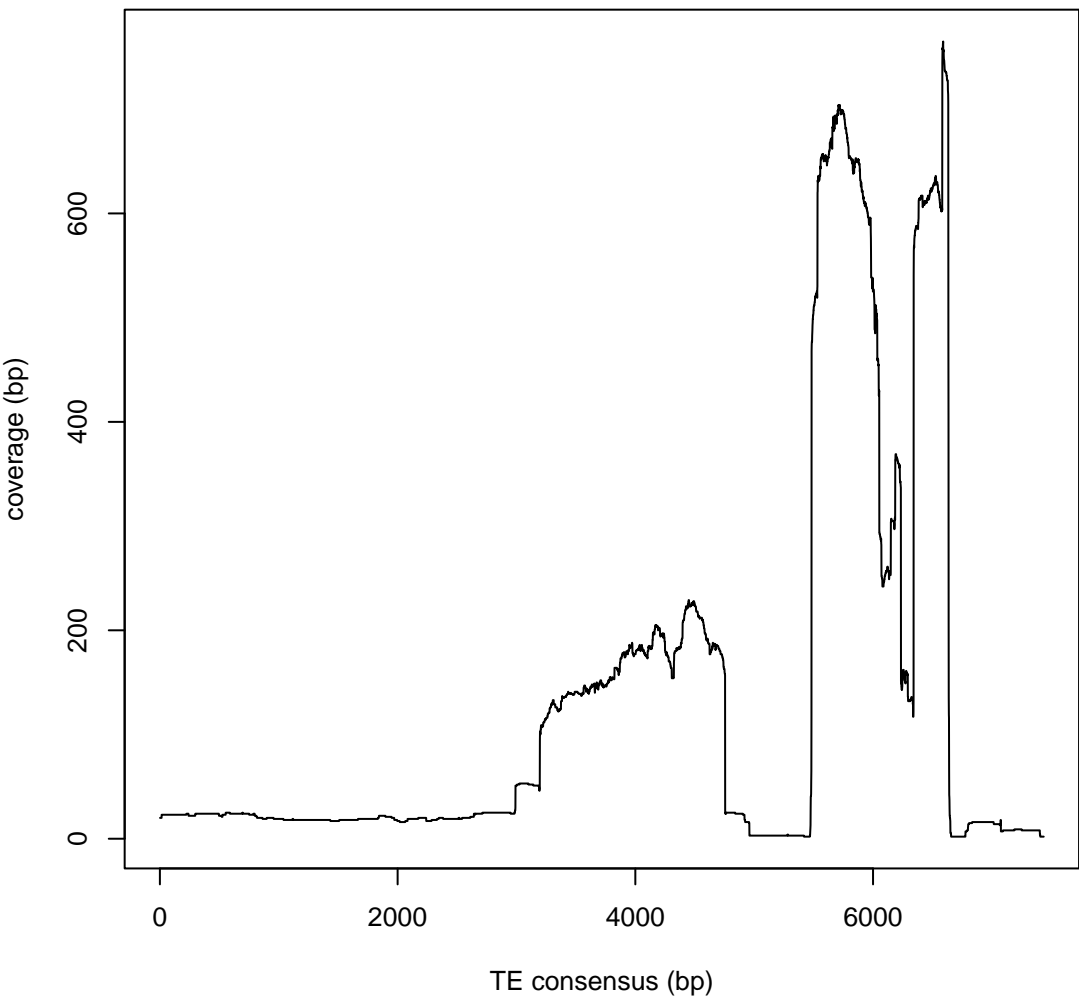


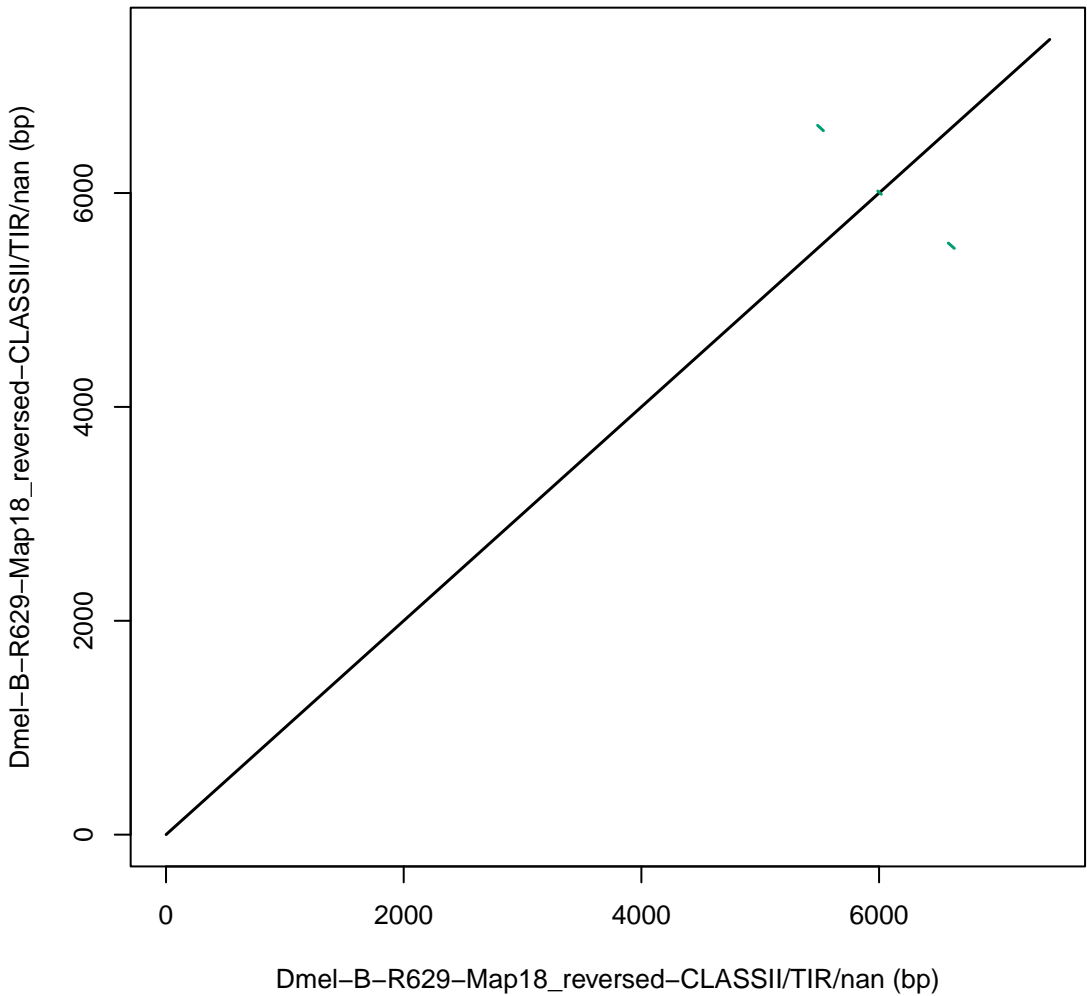
TE: Dmel-B-R629-Map18_reversed-CLASSII/TIR/nan
consensus size: 7436bp; fragments: 2616; full length: 2 (>=6692.4bp)



TE consensus genomic coverage



TE consensus self dotplot (blastn)



TE consensus structure and protein hits

