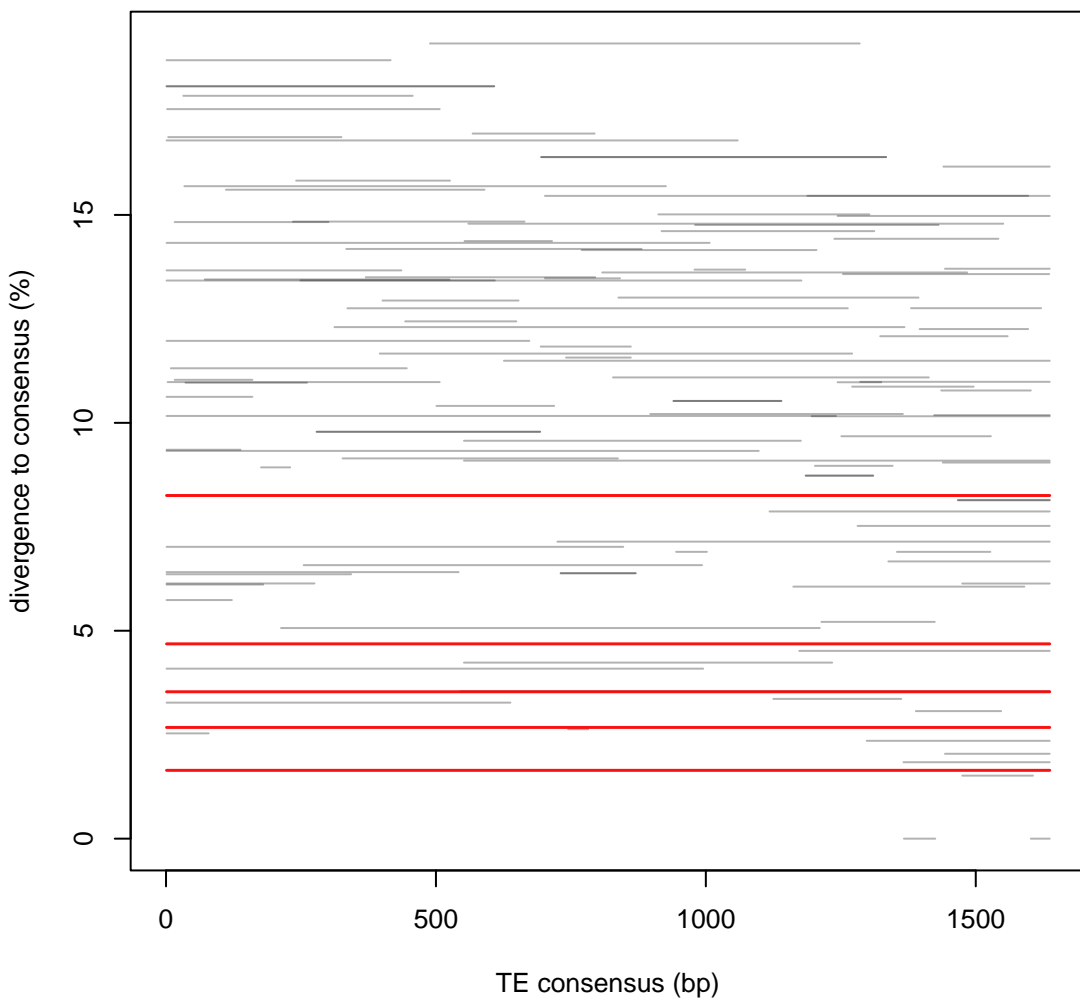
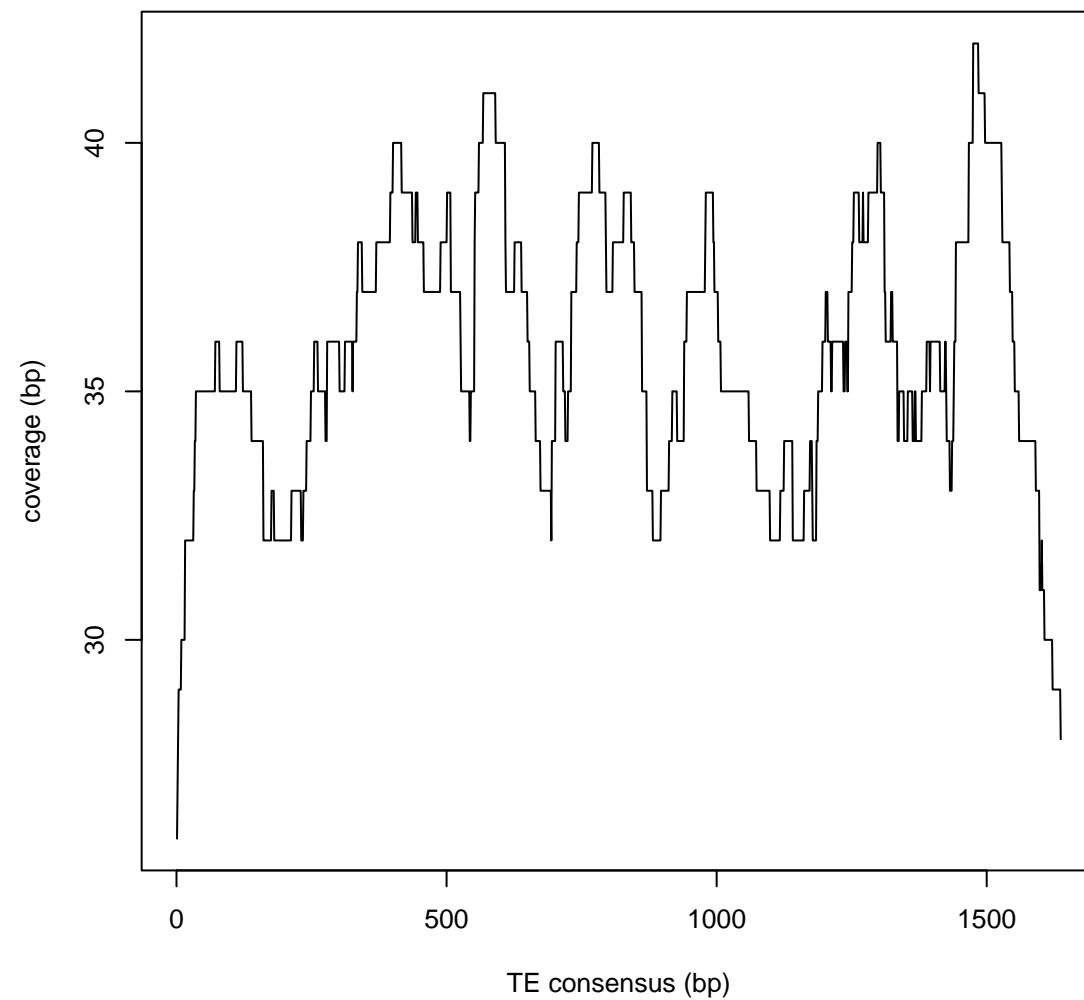


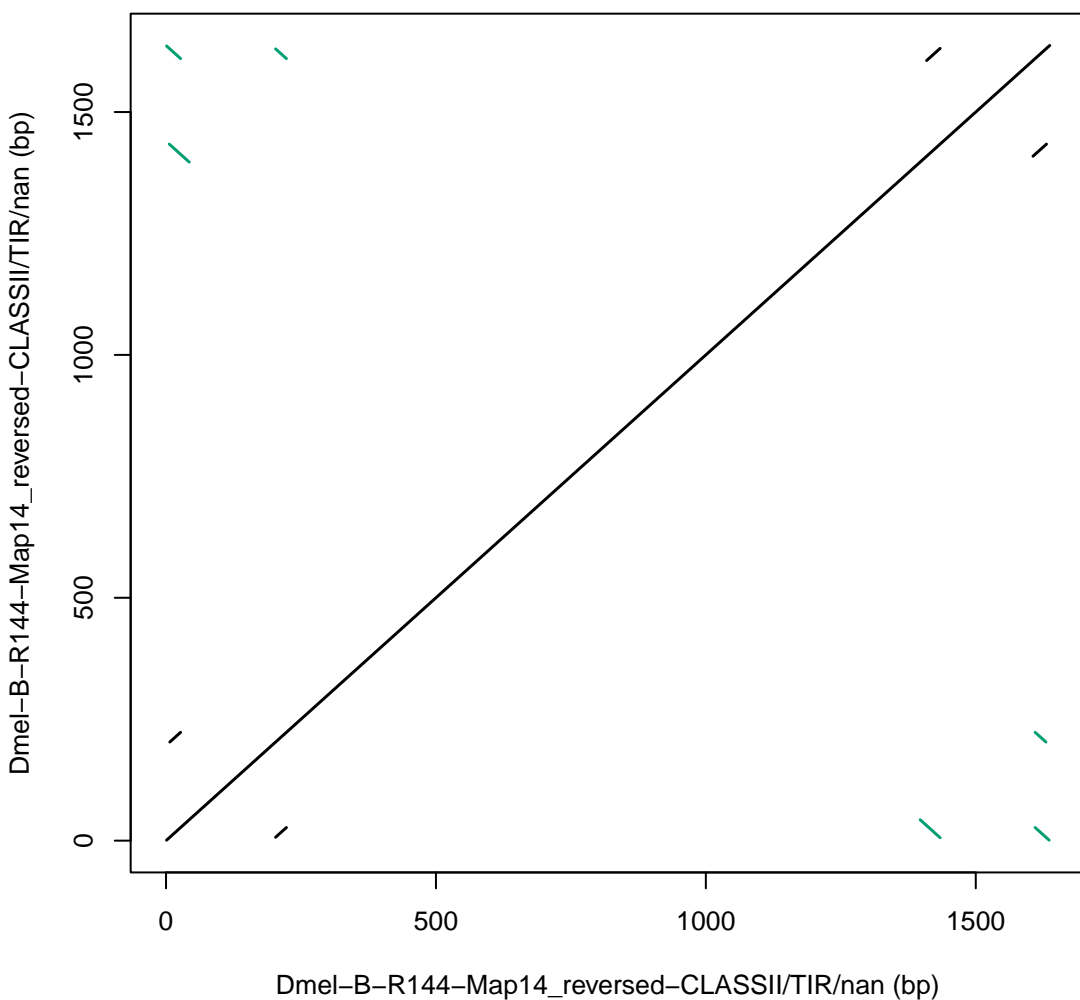
TE: Dmel-B-R144-Map14_reversed-CLASSII/TIR/nan
consensus size: 1637bp; fragments: 123; full length: 5 (≥ 1473.3 bp)



TE consensus genomic coverage



TE consensus self dotplot (blastn)



TE consensus structure and protein hits

