TE: Dmel-B-G522-Map3-CLASSII/TIR/nan
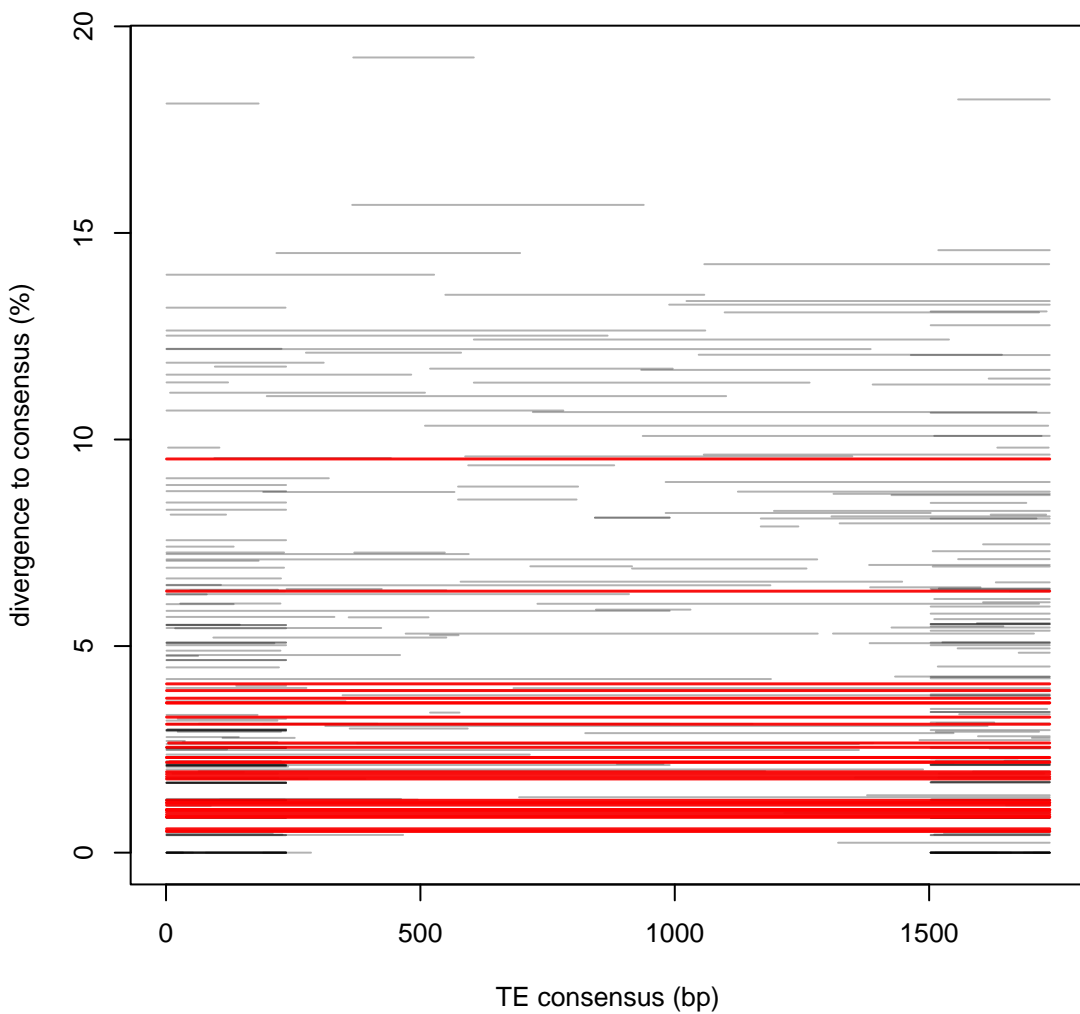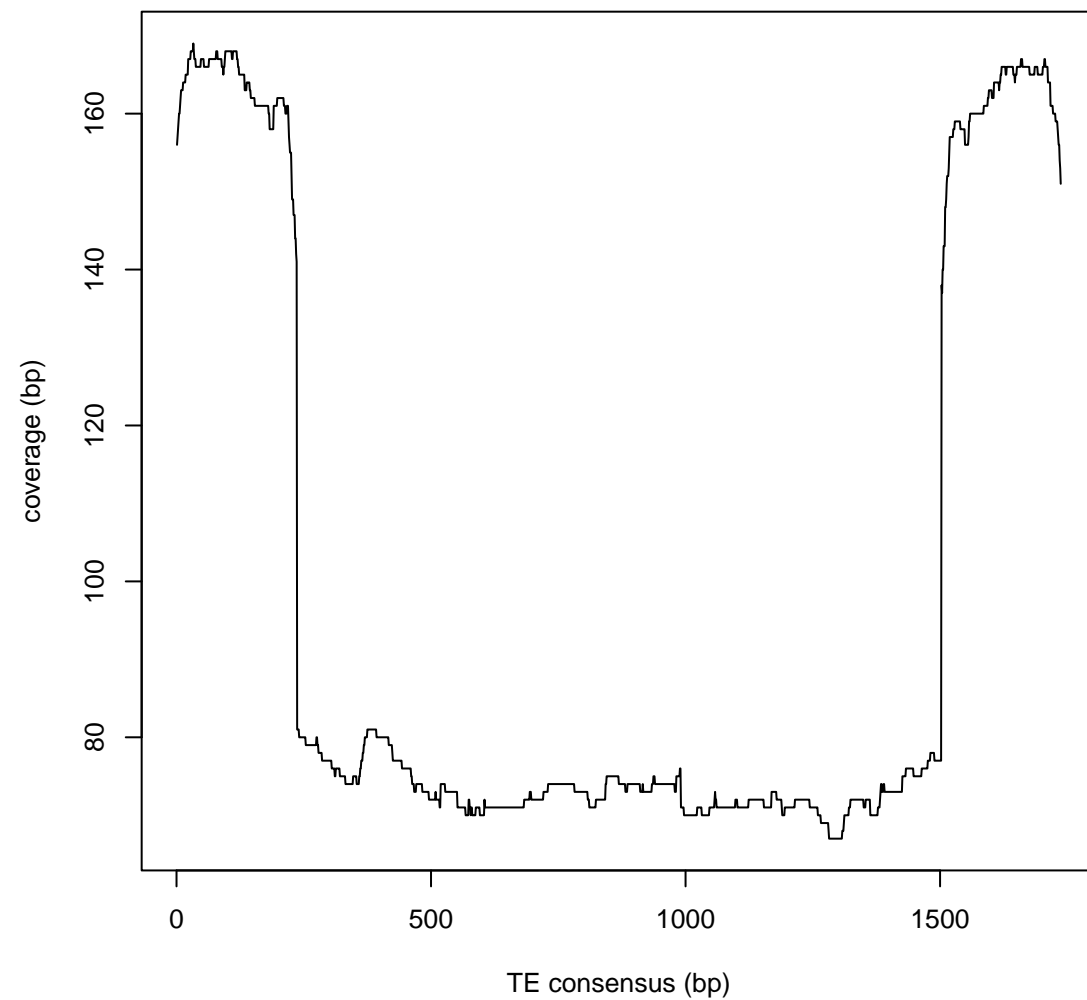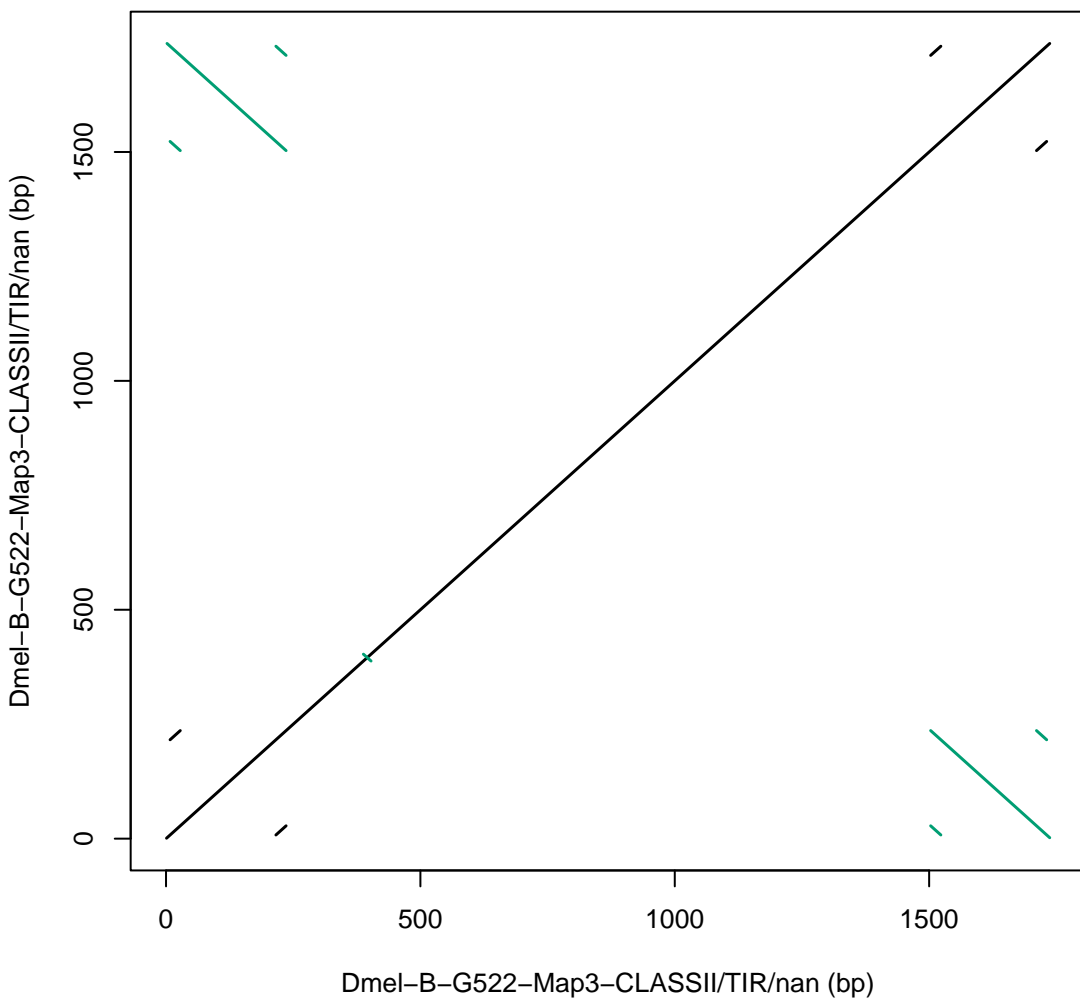**consensus size: 1737bp; fragments: 356; full length: 35 (>=1563.3bp)**

TE consensus genomic coverage

TE consensus self dotplot (blastn)

TE consensus structure and protein hits

Mariner-18_SIn_tp TIR/TcMar-Tc1