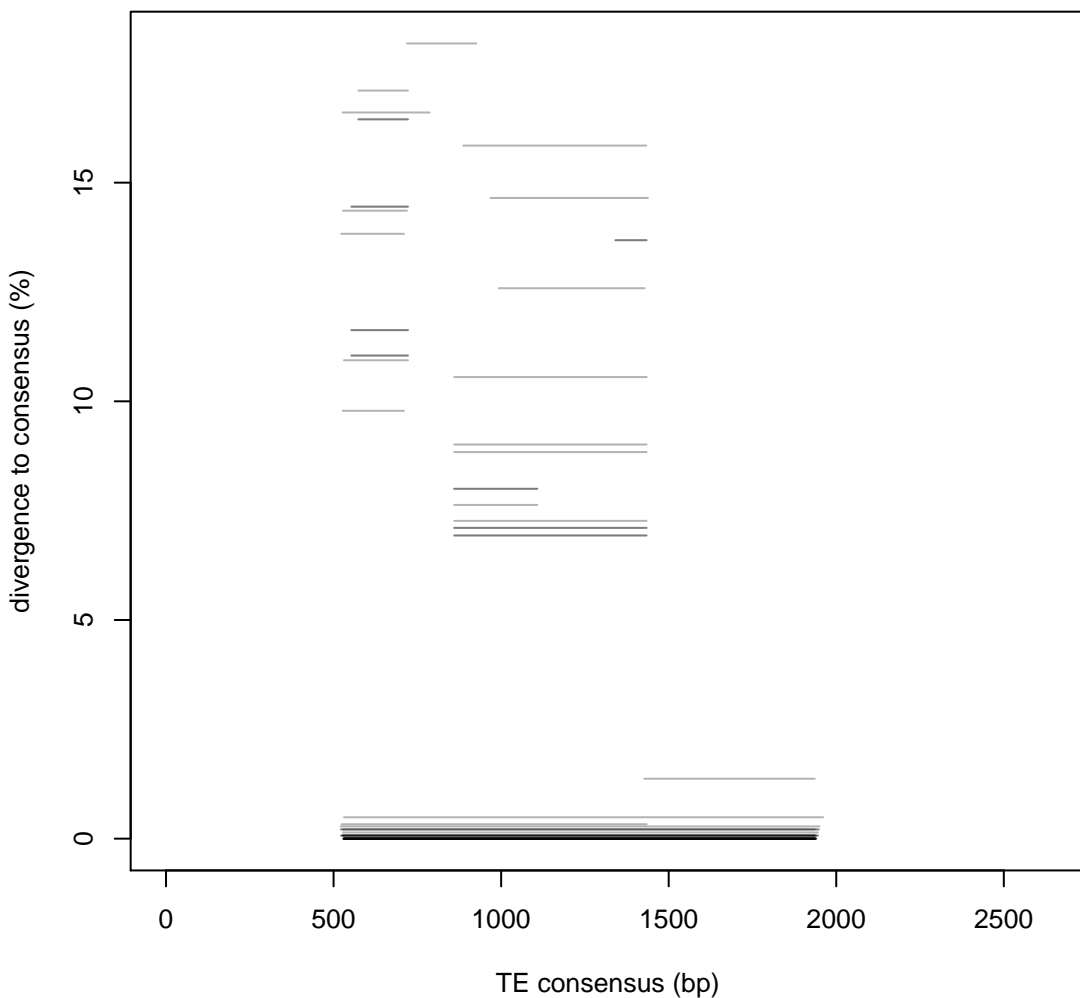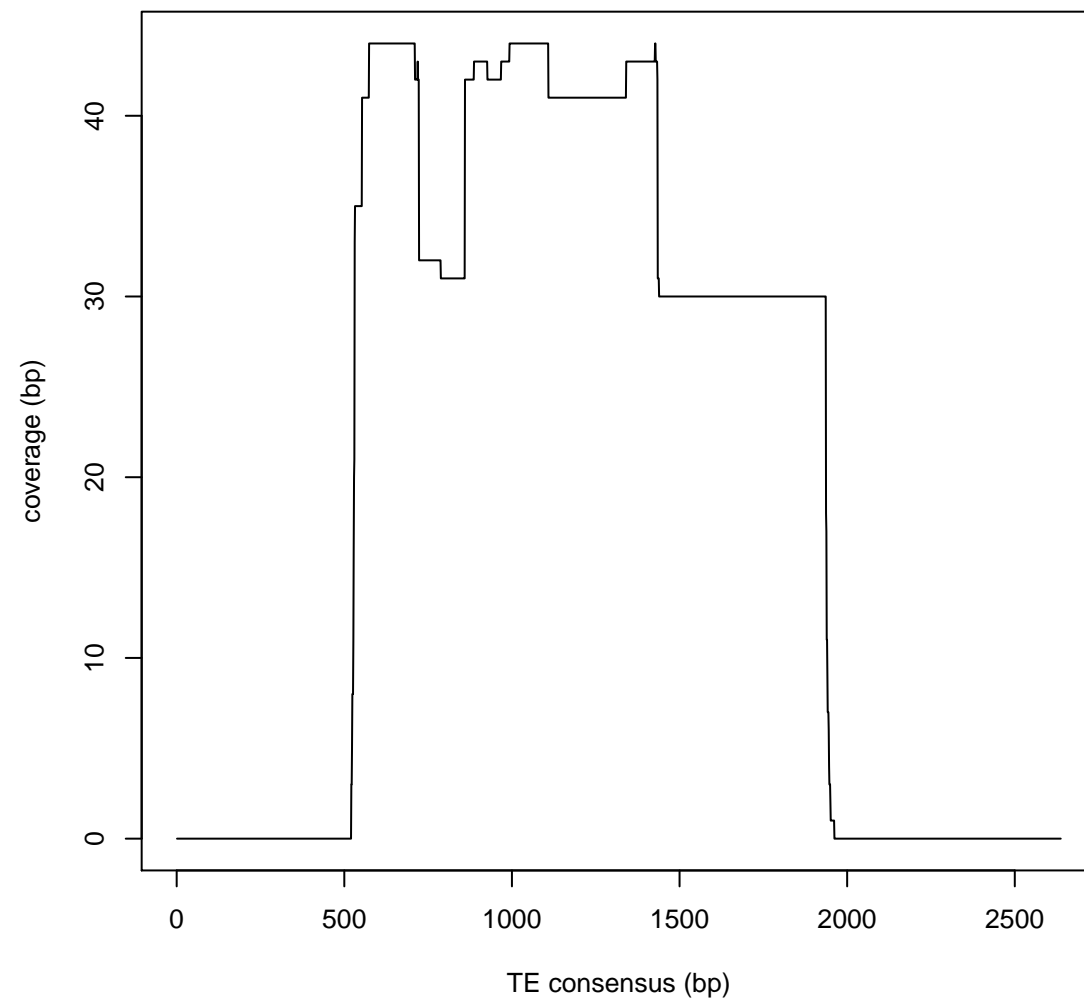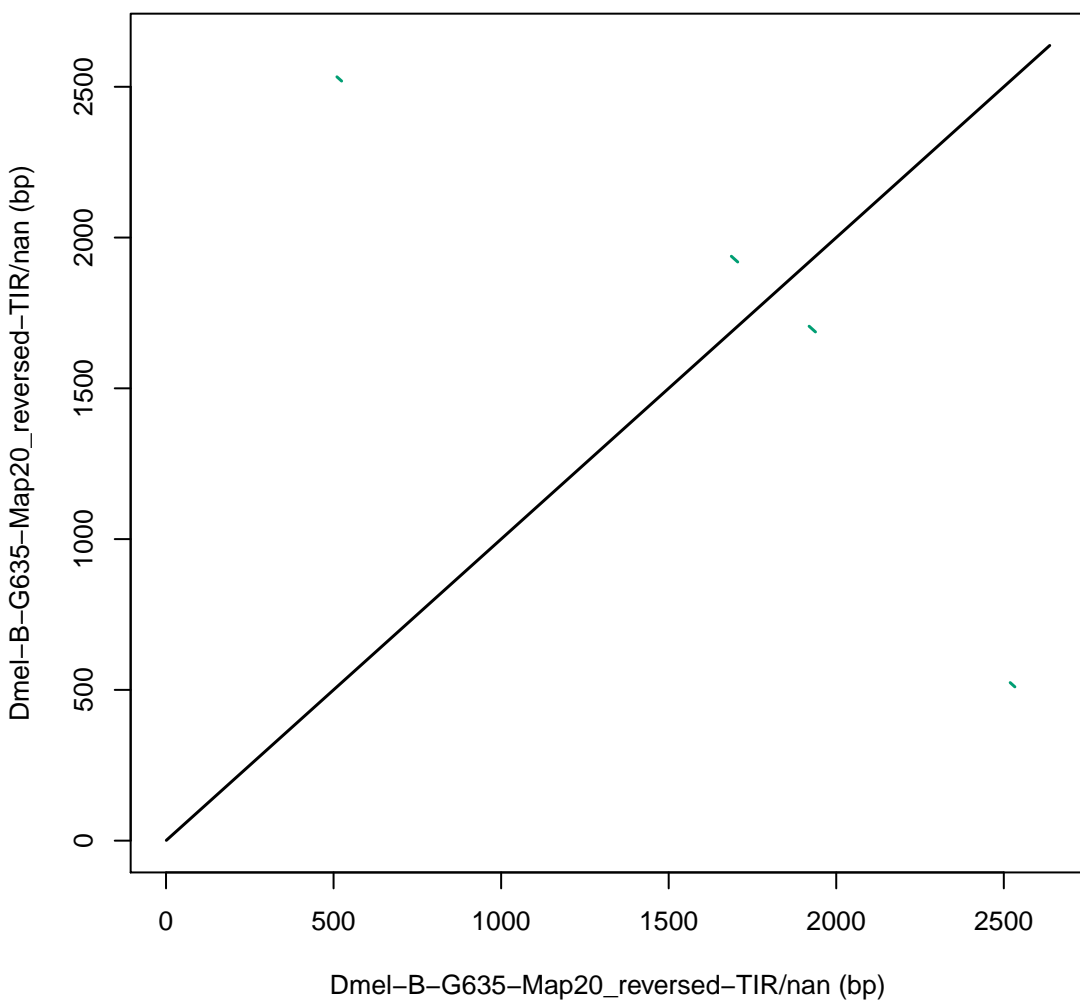**TE: Dmel−B−G635−Map20_reversed−TIR/nan**
consensus size: 2637bp; fragments: 62; full length: 0 (>=2373.3bp)

TE consensus genomic coverage

TE consensus self dotplot (blastn)

TE consensus structure and protein hits

Zator−1_HM TIR/Zator

UN−Hobo_tp TIR/hAT−hobo