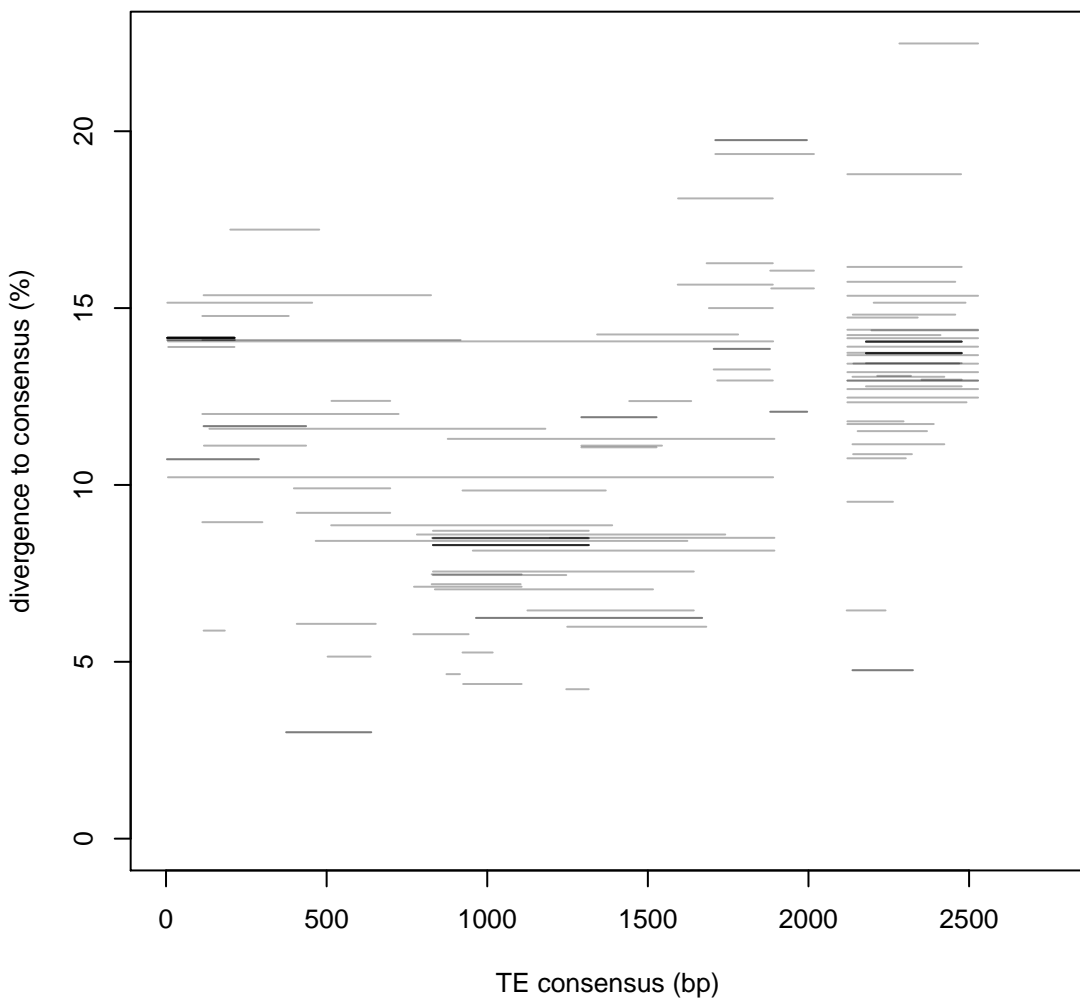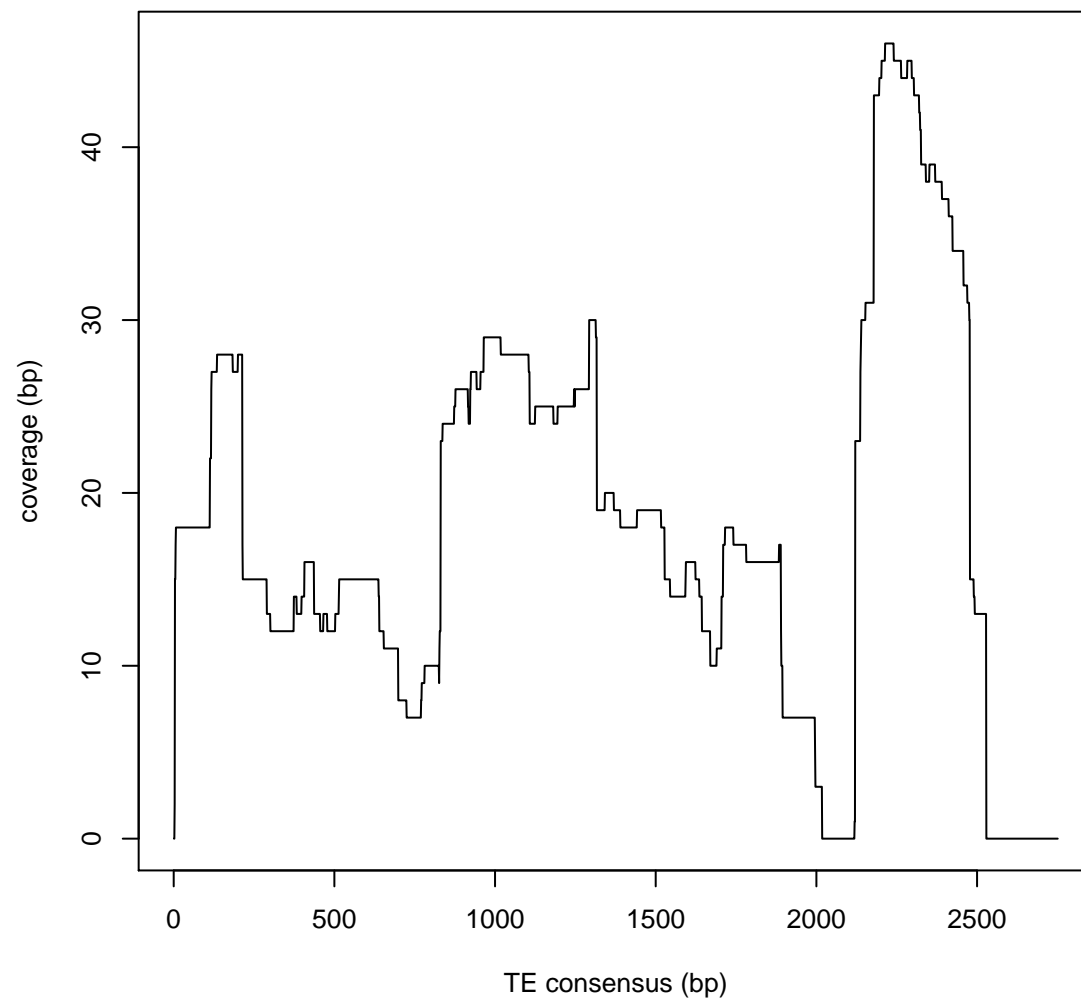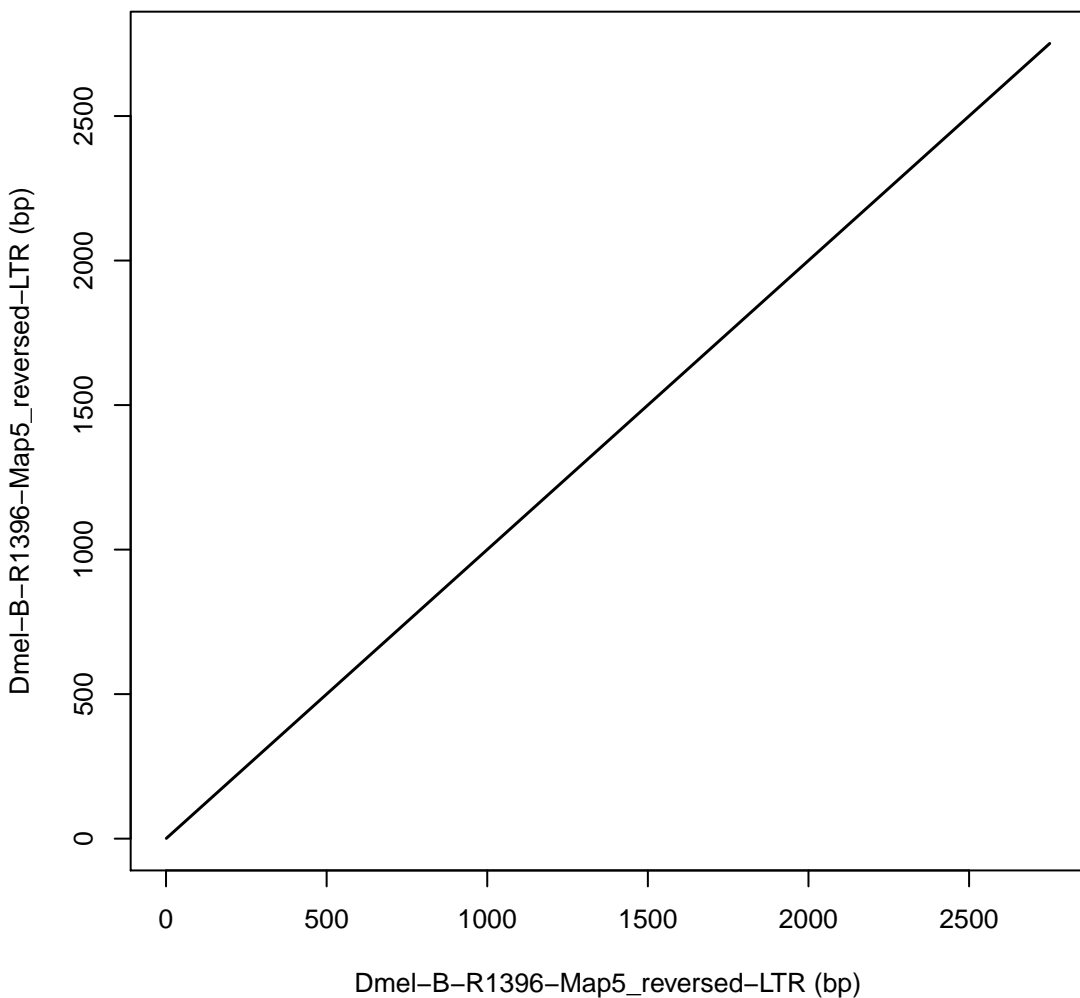**TE: Dmel-B-R1396-Map5_reversed-LTR**
consensus size: 2751bp; fragments: 137; full length: 0 (>=2475.9bp)

TE consensus genomic coverage

TE consensus self dotplot (blastn)

TE consensus structure and protein hits

BEL1_DV_pol LTR/Pao