TE: Dmel−B−R1587−Map3−CLASSII/Helitron/nan
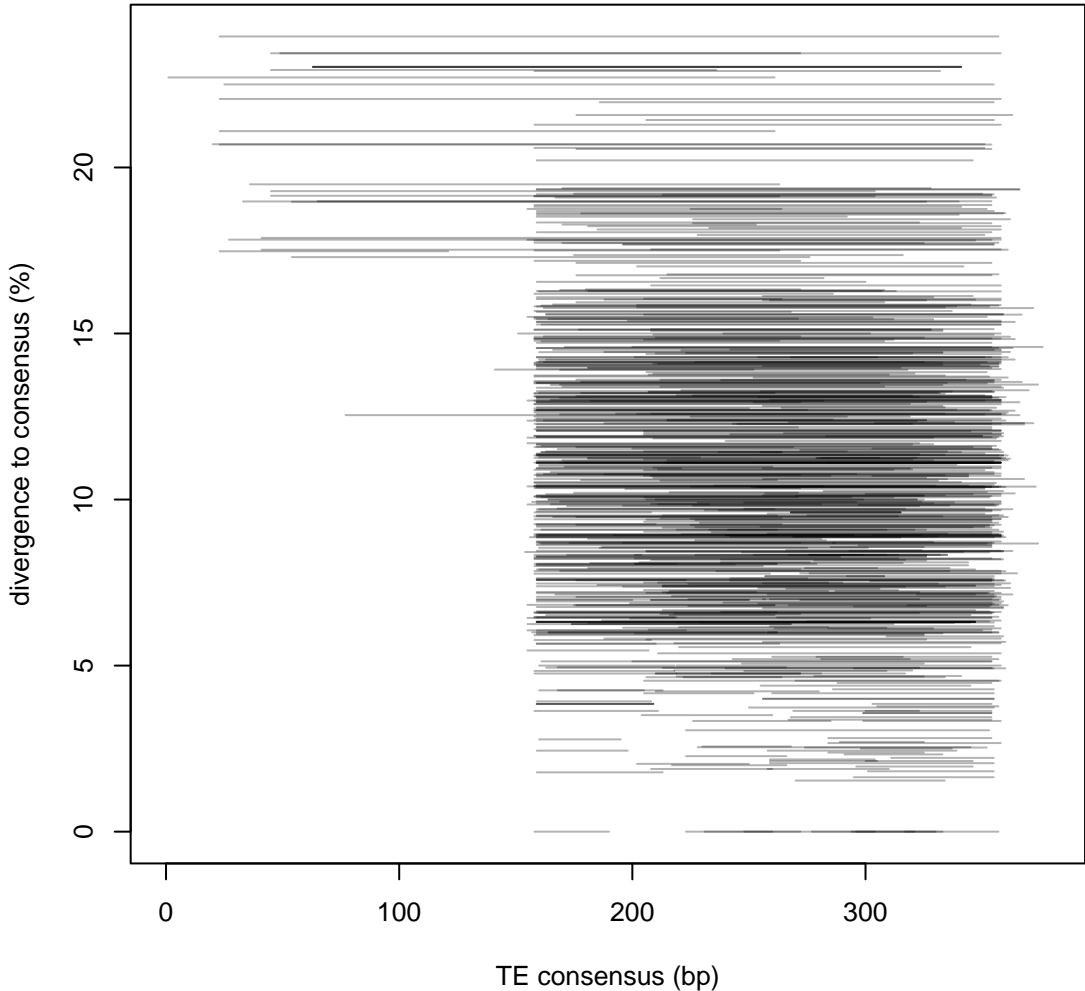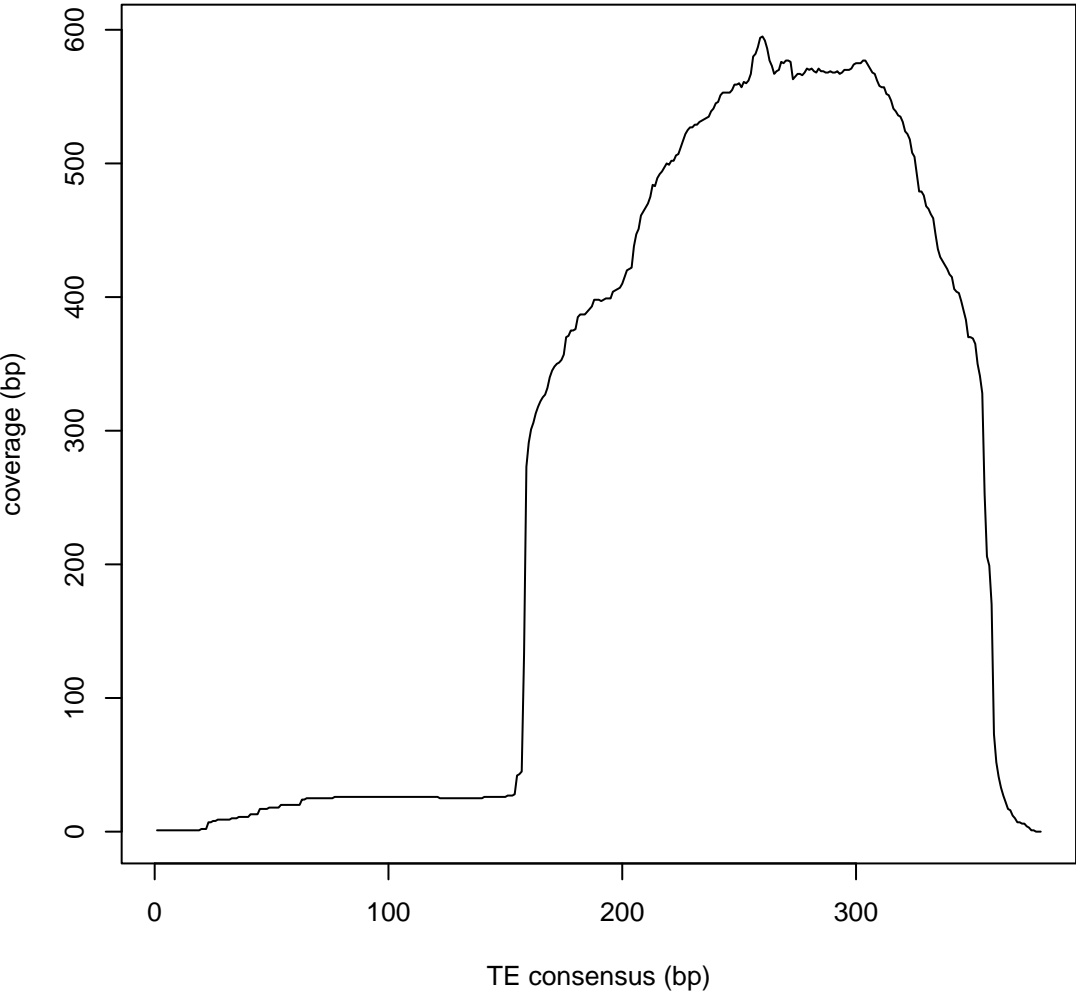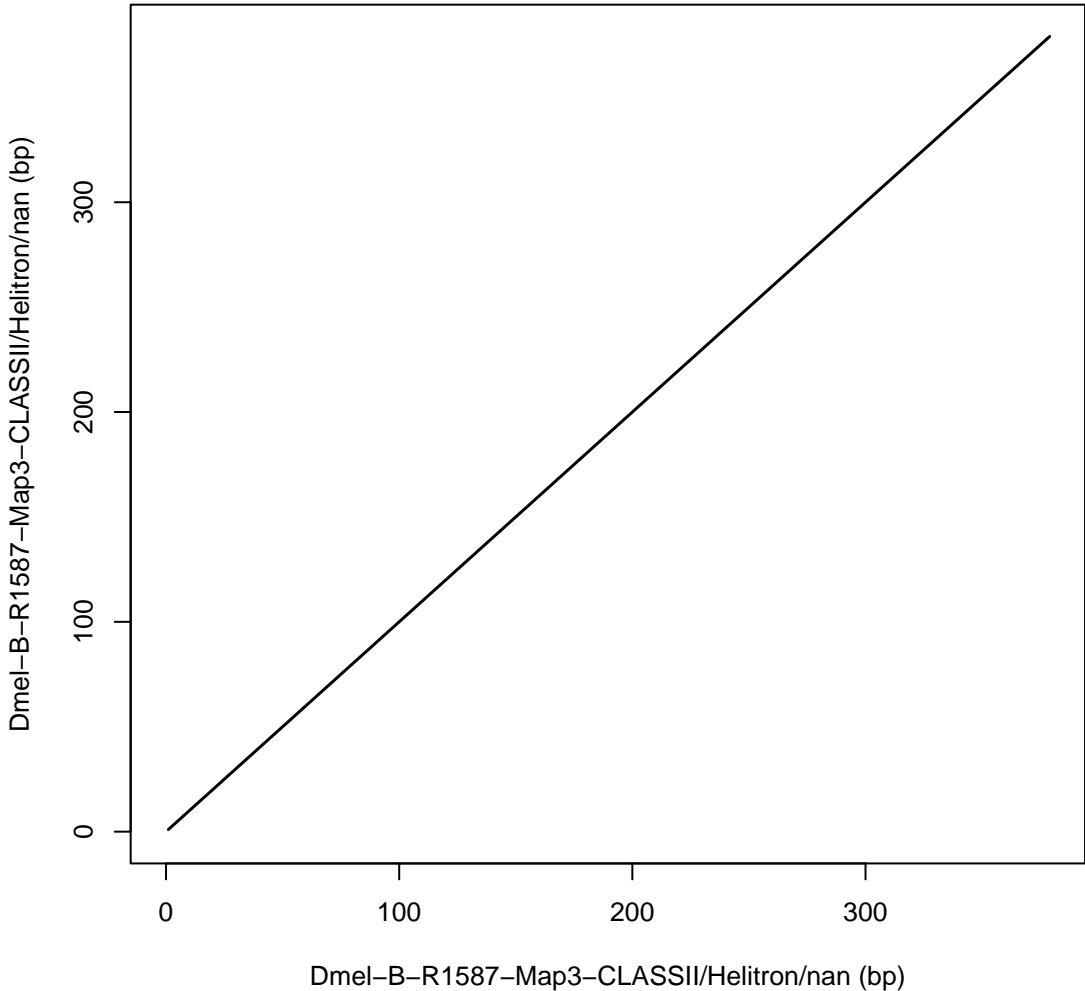consensus size: 379bp; fragments: 723; full length: 0 (>=341.1bp)

divergence to consensus (%)

TE consensus (bp)

TE consensus genomic coverage

coverage (bp)

TE consensus (bp)

TE consensus self dotplot (blastn)

Dmel−B−R1587−Map3−CLASSII/Helitron/nan (bp)

Dmel−B−R1587−Map3−CLASSII/Helitron/nan (bp)

TE consensus structure and protein hits

no orf >400 bp detected

Dmel−B−R1587−Map3−CLASSII/Helitron/nan (bp)