TE: Dmel−B−R1564−Map5_reversed−CLASSI/LINE/nan
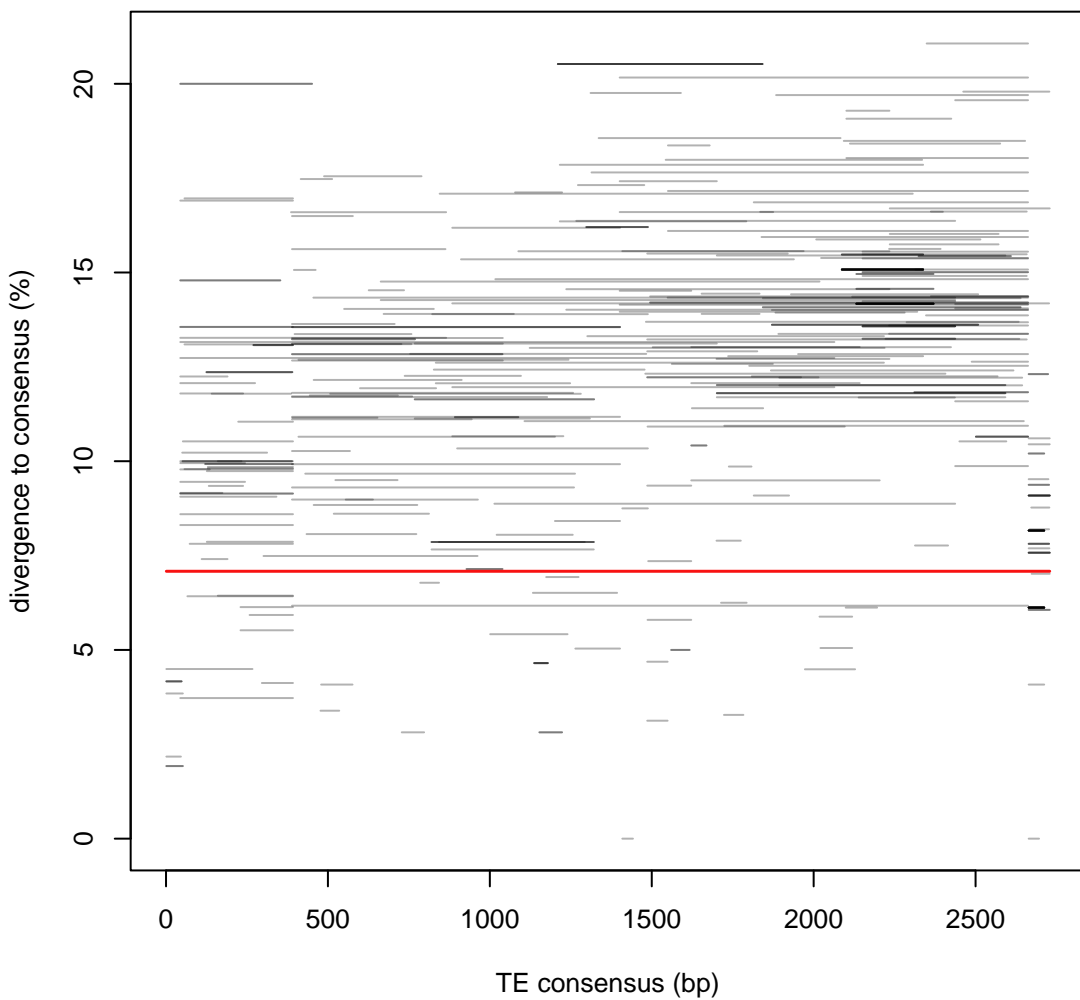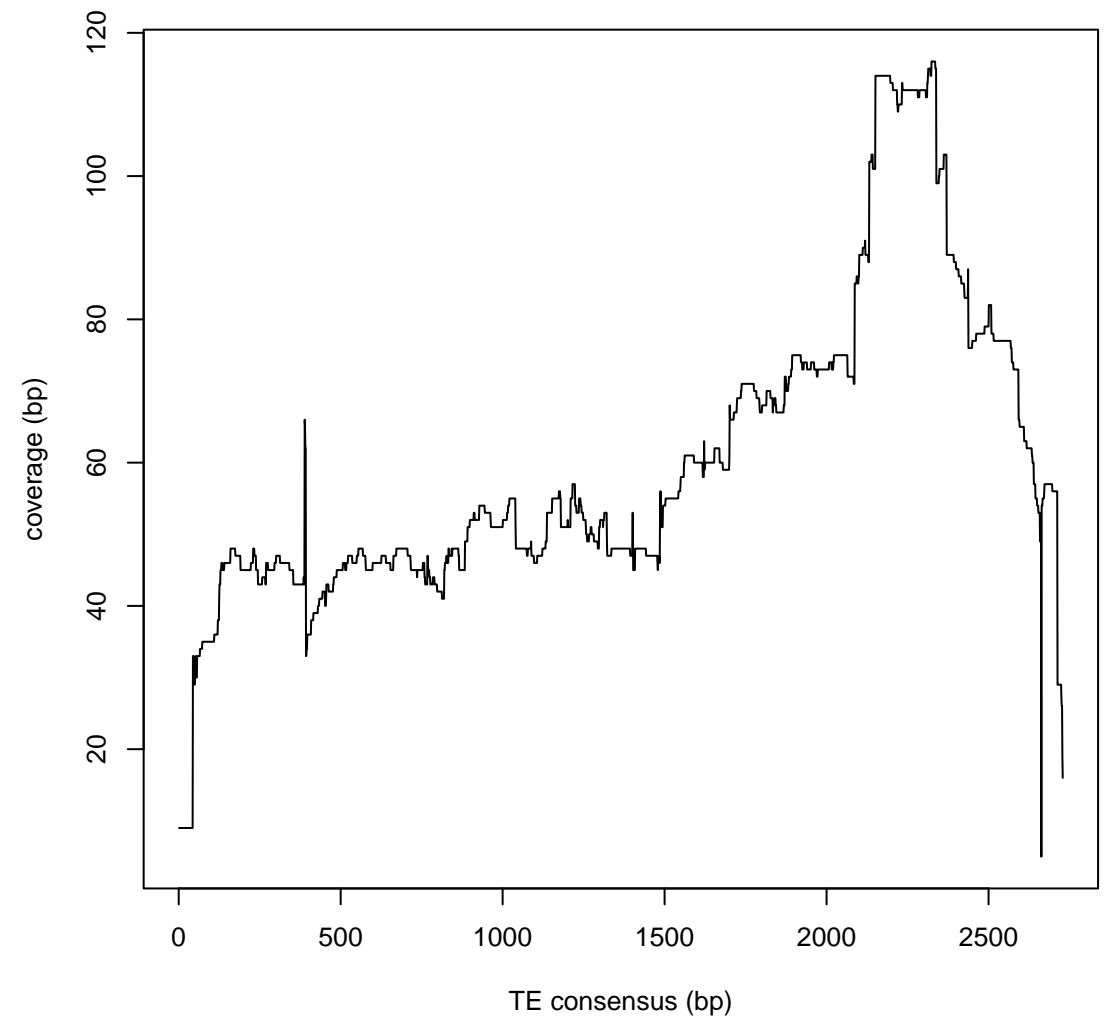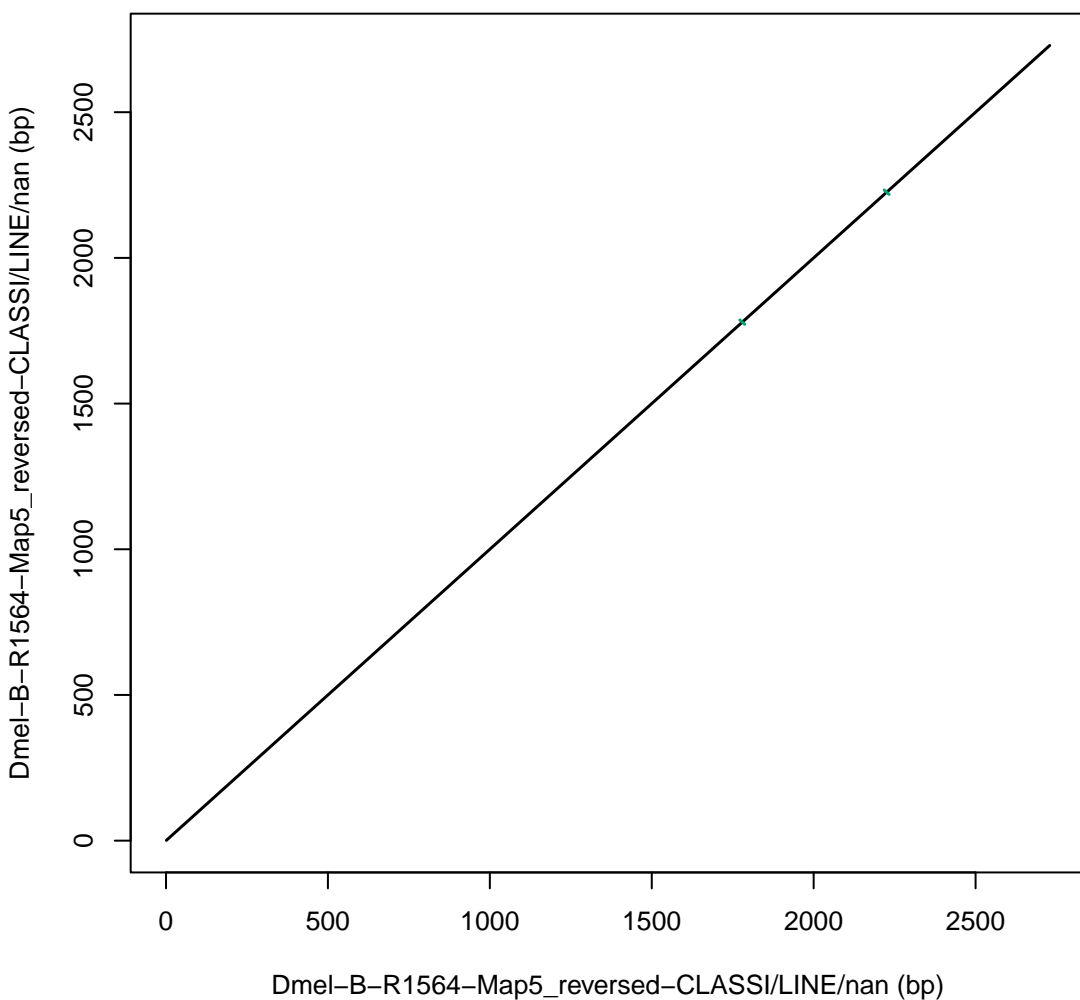**consensus size: 2729bp; fragments: 391; full length: 1 (>=2456.1bp)**

divergence to consensus (%)

TE consensus (bp)

TE consensus genomic coverage

coverage (bp)

TE consensus (bp)

TE consensus self dotplot (blastn)

Dmel−B−R1564−Map5_reversed−CLASSI/LINE/nan (bp)

Dmel−B−R1564−Map5_reversed−CLASSI/LINE/nan (bp)

TE consensus structure and protein hits

3_CQ_pol LINE/R1−LOA

R1−4_AP_pol LINE/R1

LOA_pol LINE/R1−LOA

LOA−8_AAe_pol LINE/R1−LO

Dmel−B−R1564−Map5_reversed−CLASSI/LINE/nan (bp)