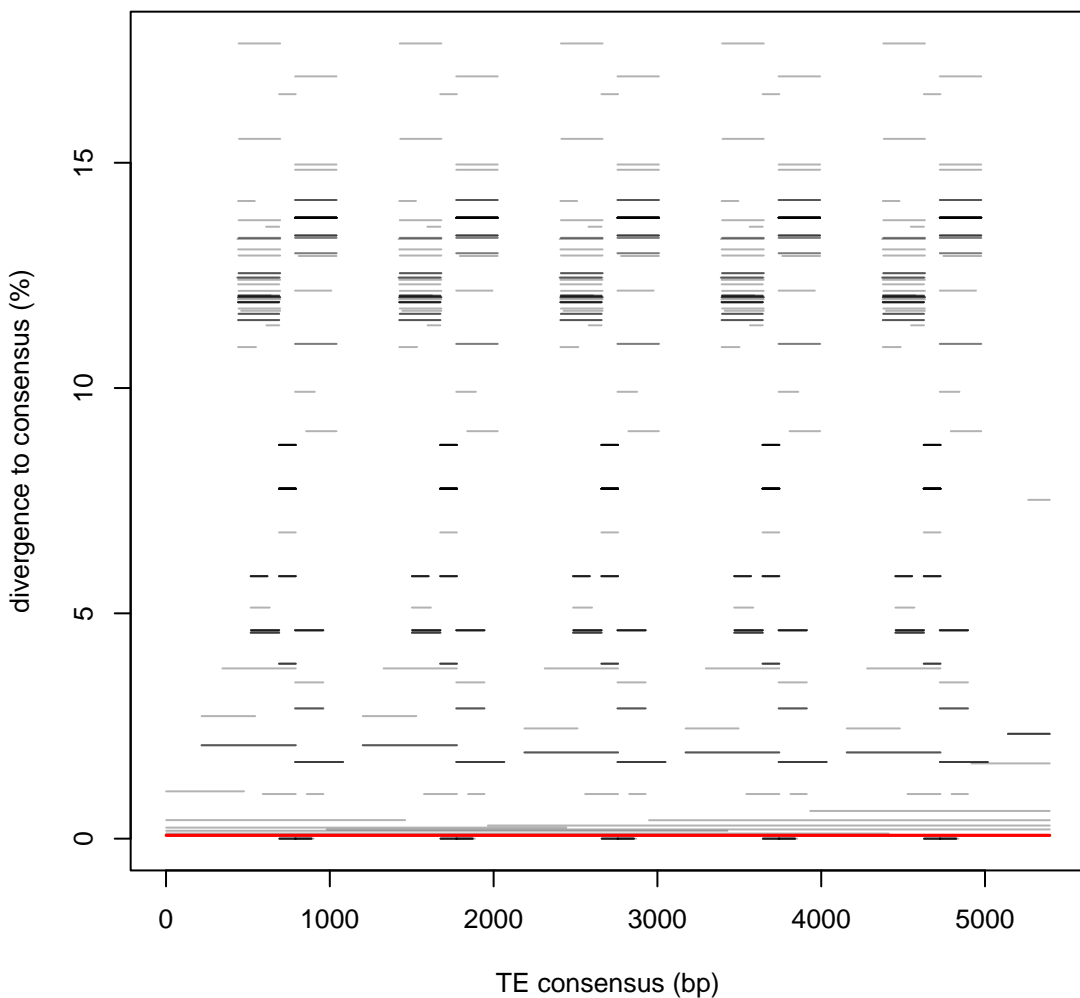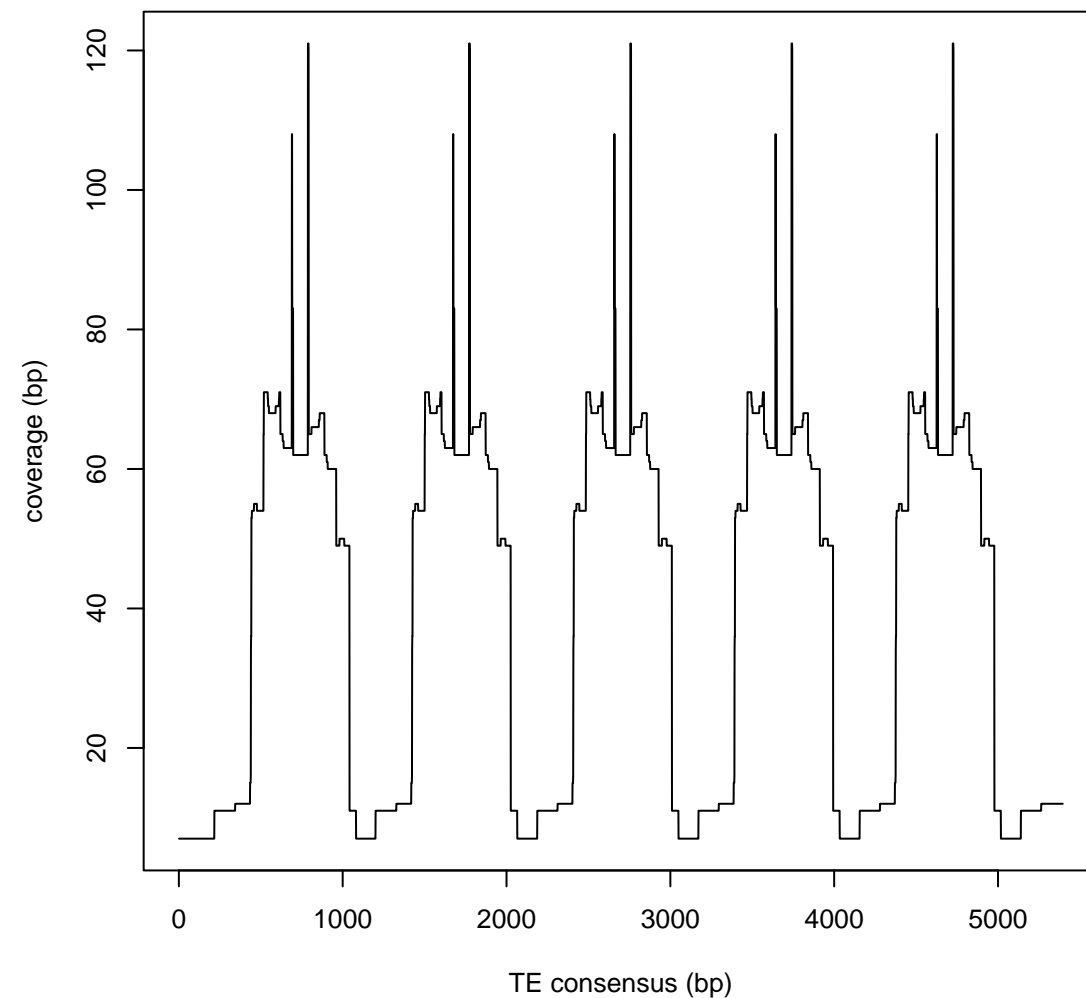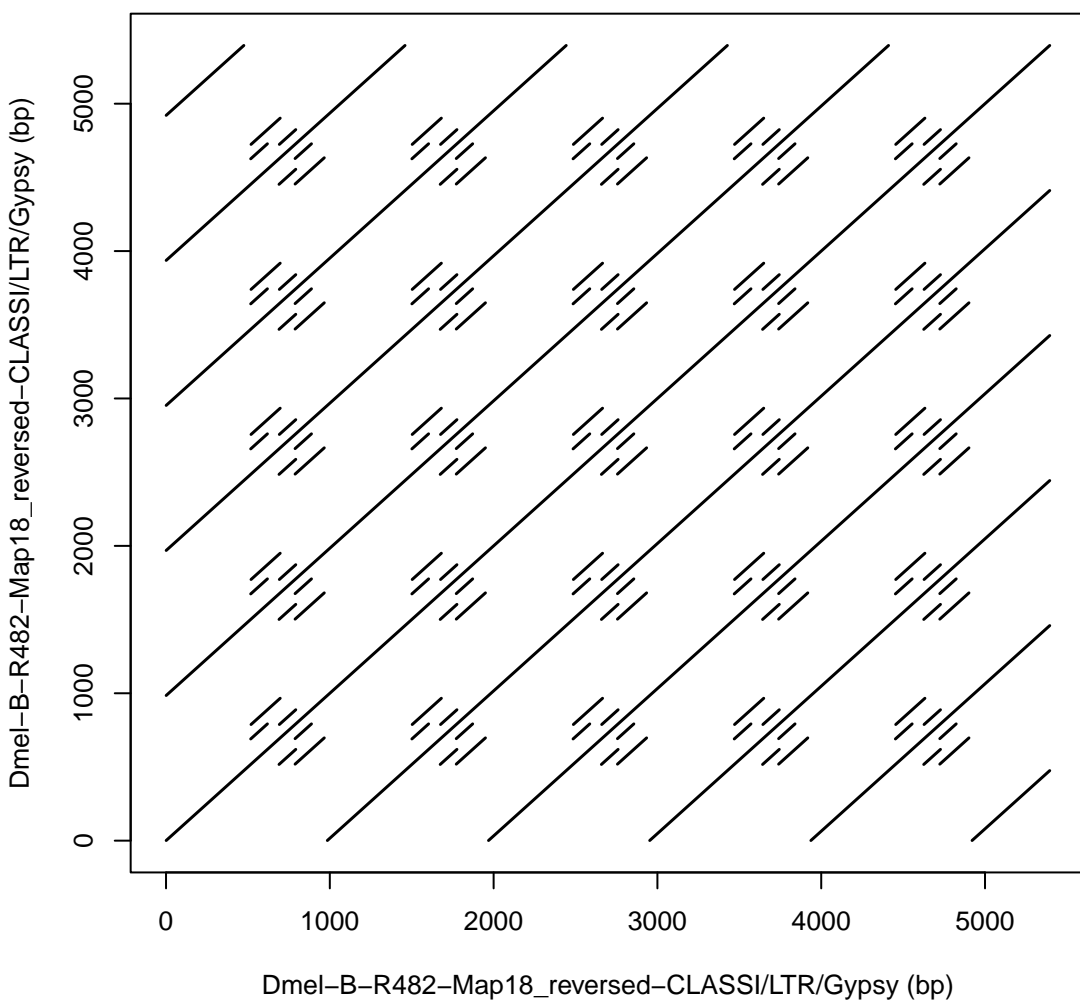## TE: Dmel−B−R482−Map18_reversed−CLASSI/LTR/Gypsy
consensus size: 5395bp; fragments: 922; full length: 2 (>=4855.5bp)

TE consensus genomic coverage

TE consensus self dotplot (blastn)

TE consensus structure and protein hits

no orf >400 bp detected