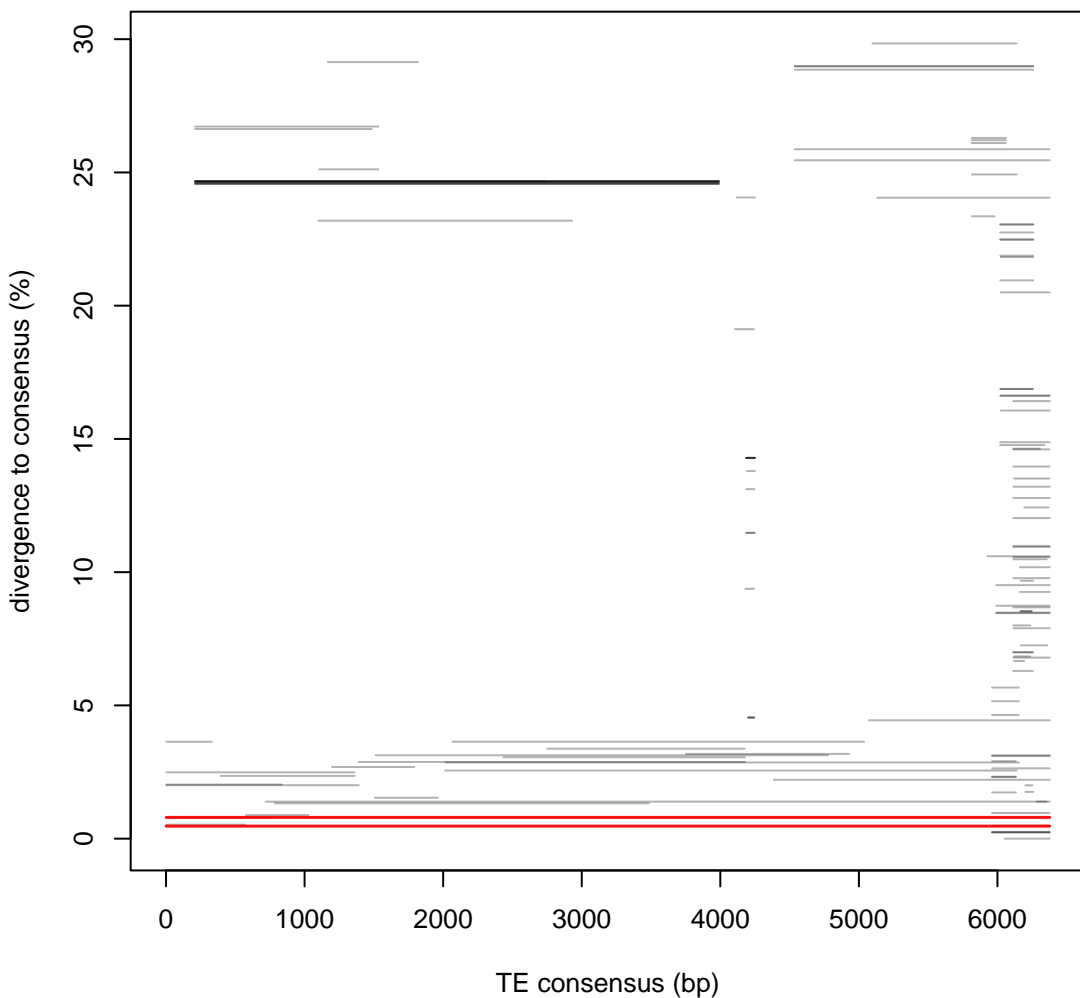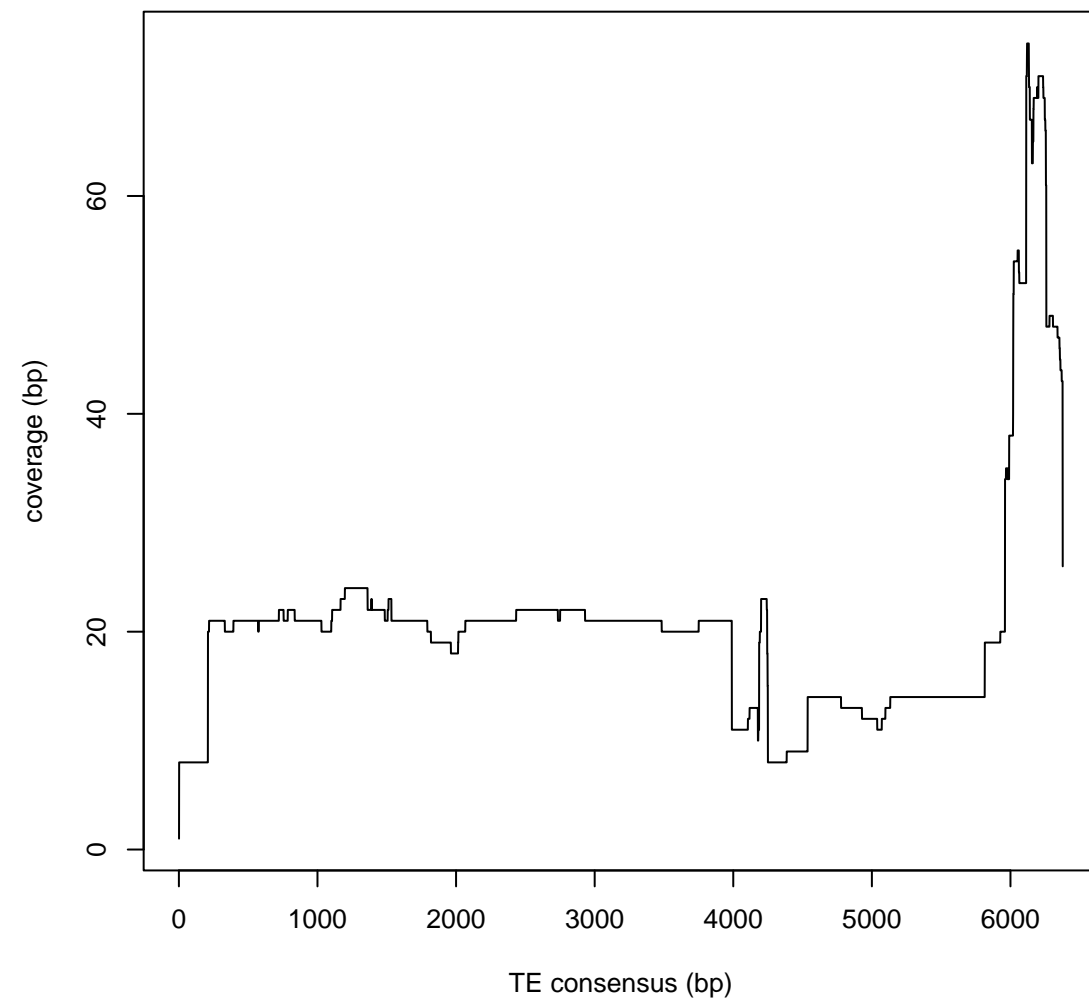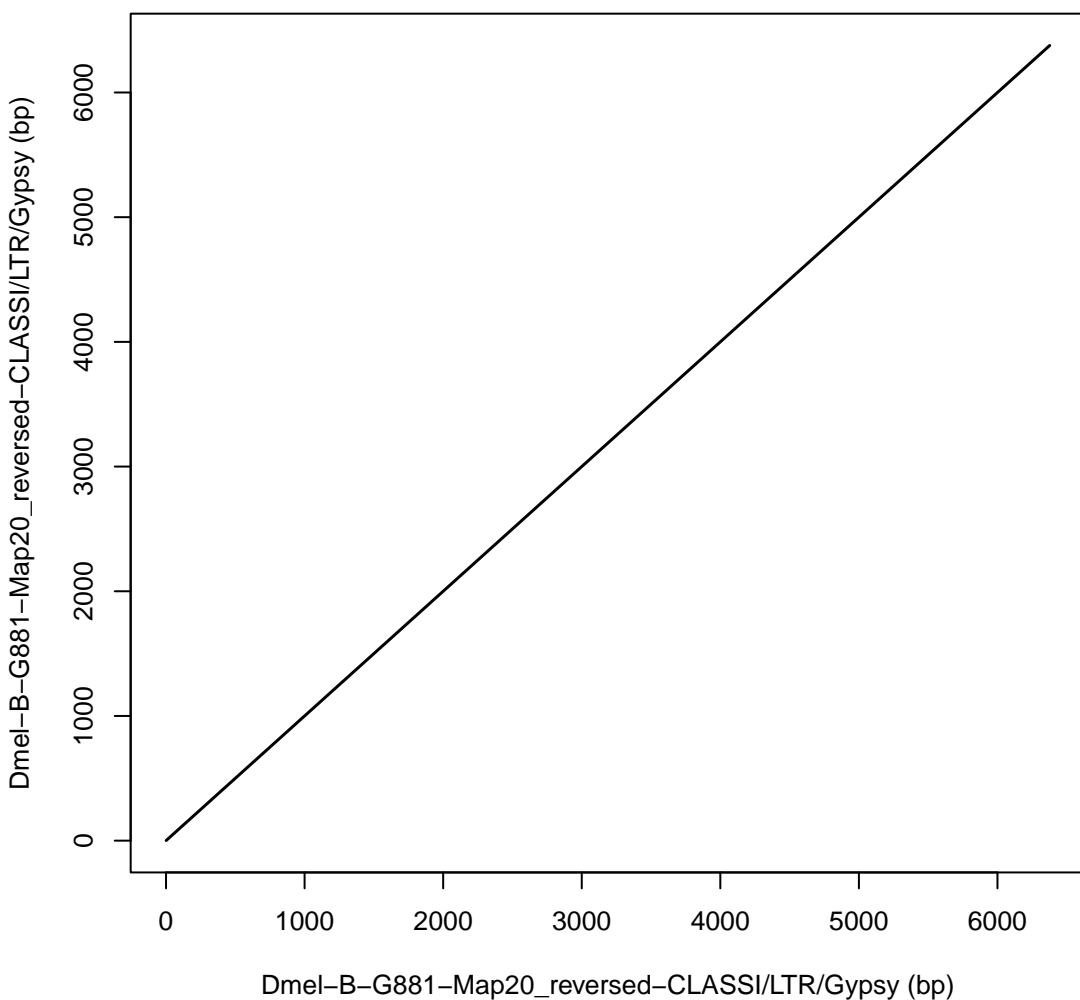## TE: Dmel−B−G881−Map20_reversed−CLASSI/LTR/Gypsy
consensus size: 6377bp; fragments: 136; full length: 2 (>=5739.3bp)

TE consensus genomic coverage

TE consensus self dotplot (blastn)

TE consensus structure and protein hits