TE: Dmel−B−G1630−Map3_reversed−CLASSI/LTR/Gypsy
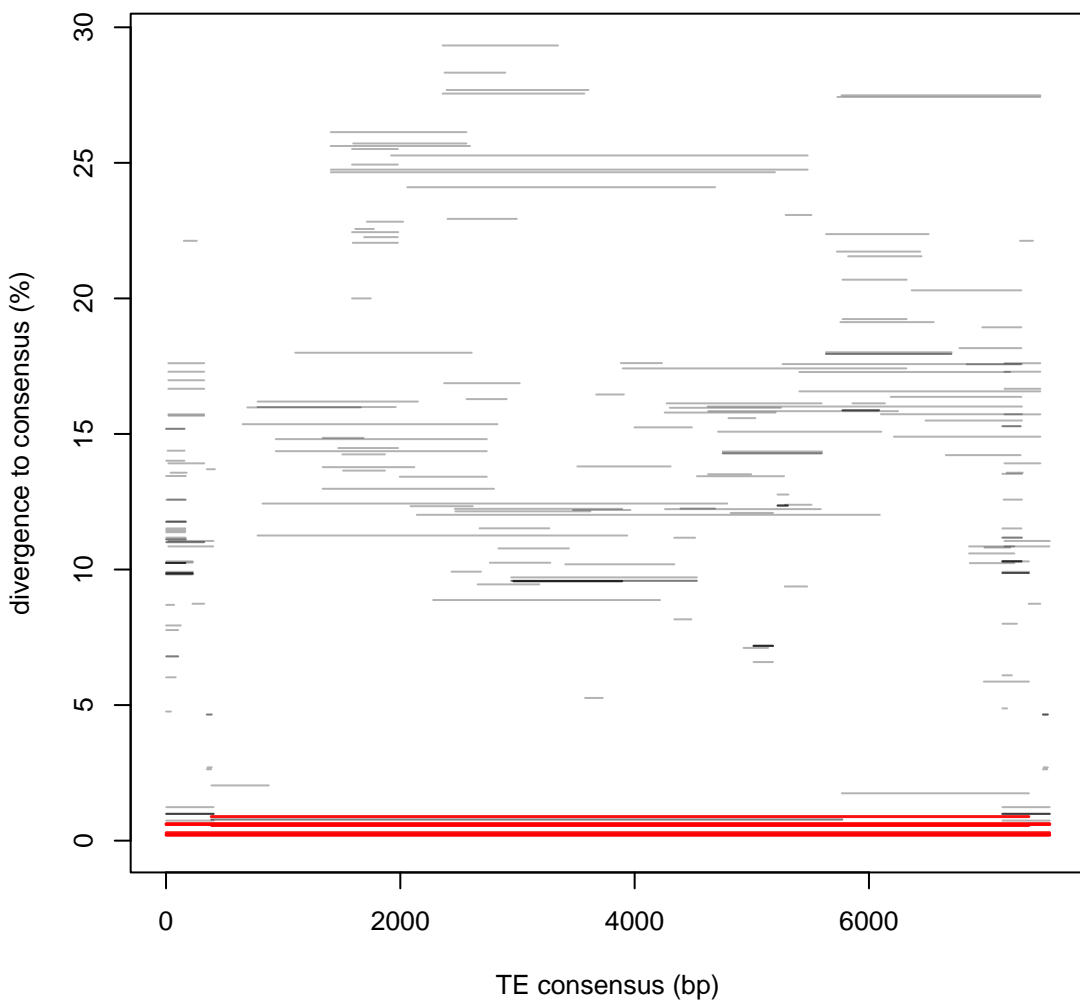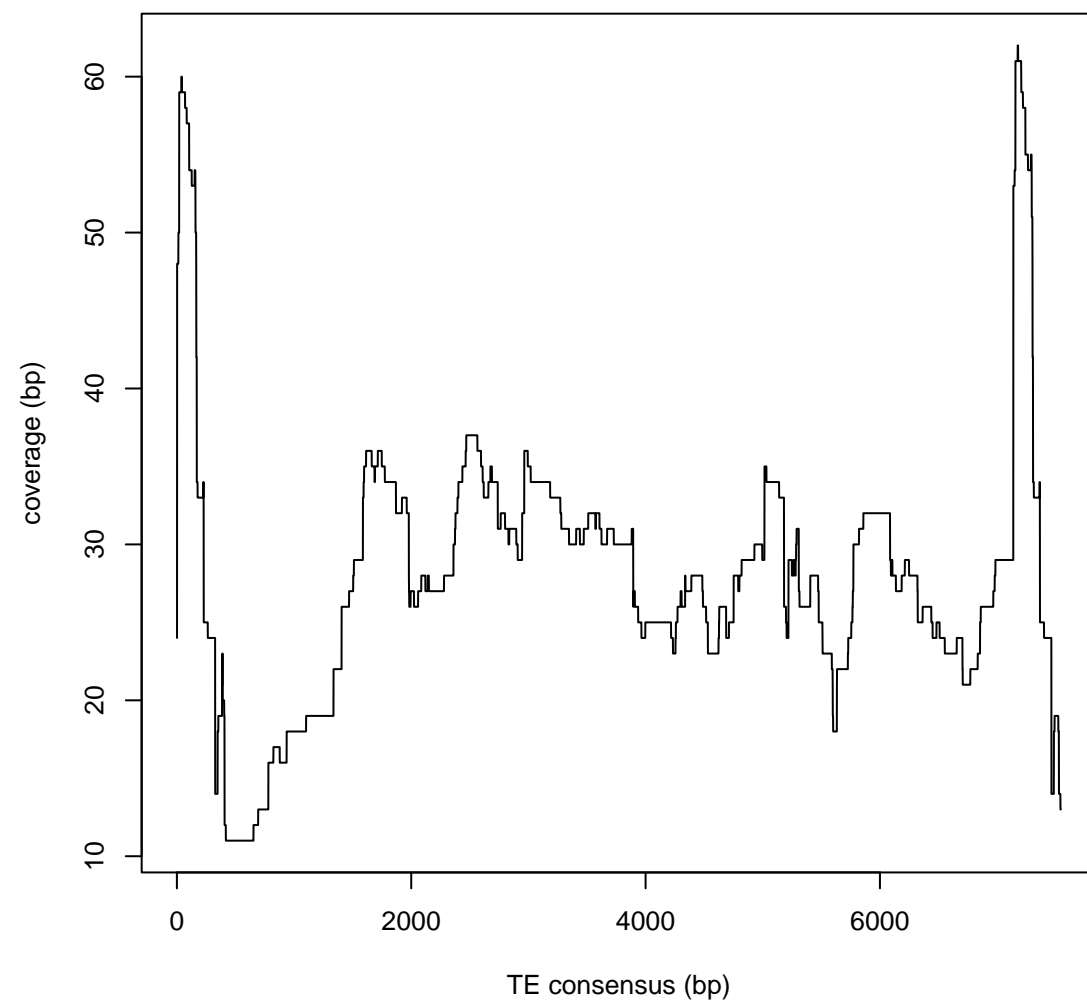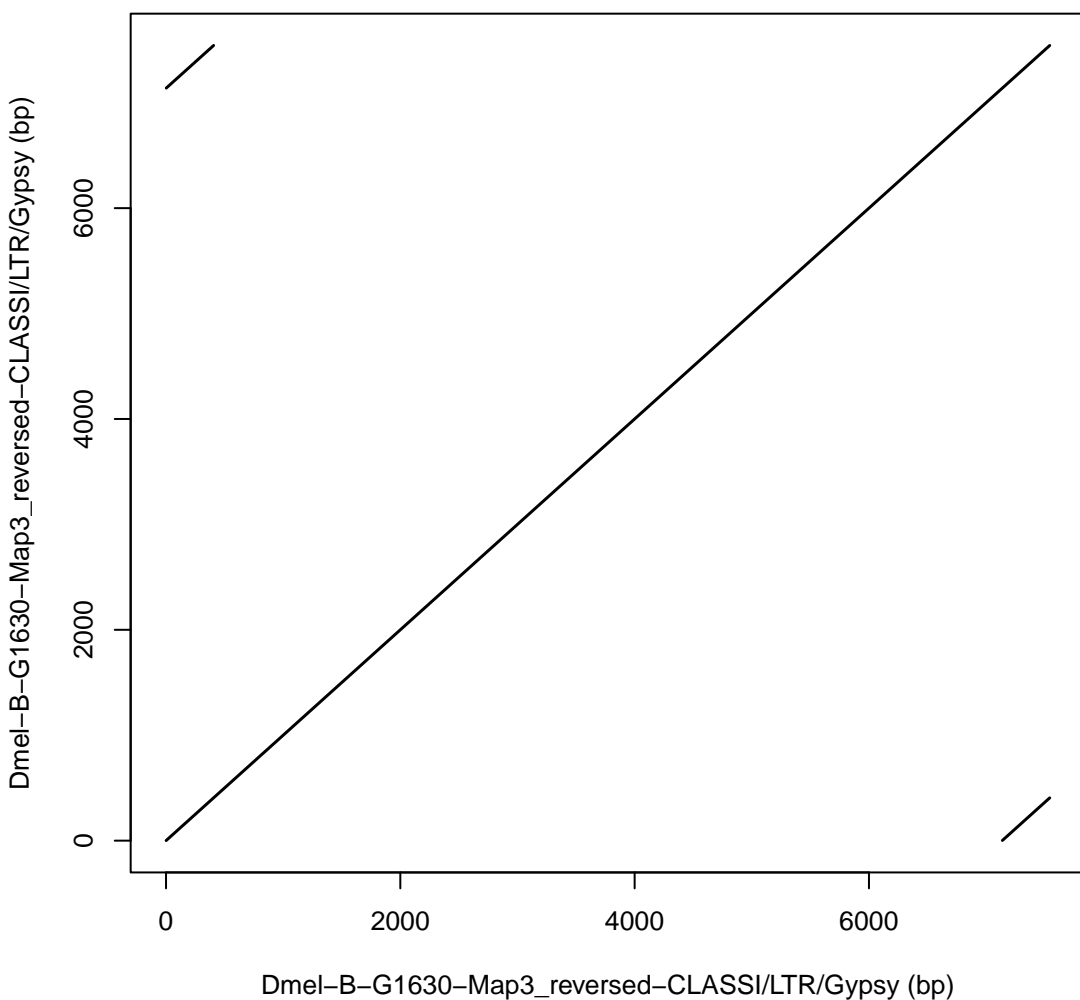consensus size: 7543bp; fragments: 240; full length: 8 (>=6788.7bp)

TE consensus genomic coverage

TE consensus self dotplot (blastn)

TE consensus structure and protein hits

no orf >400 bp detected