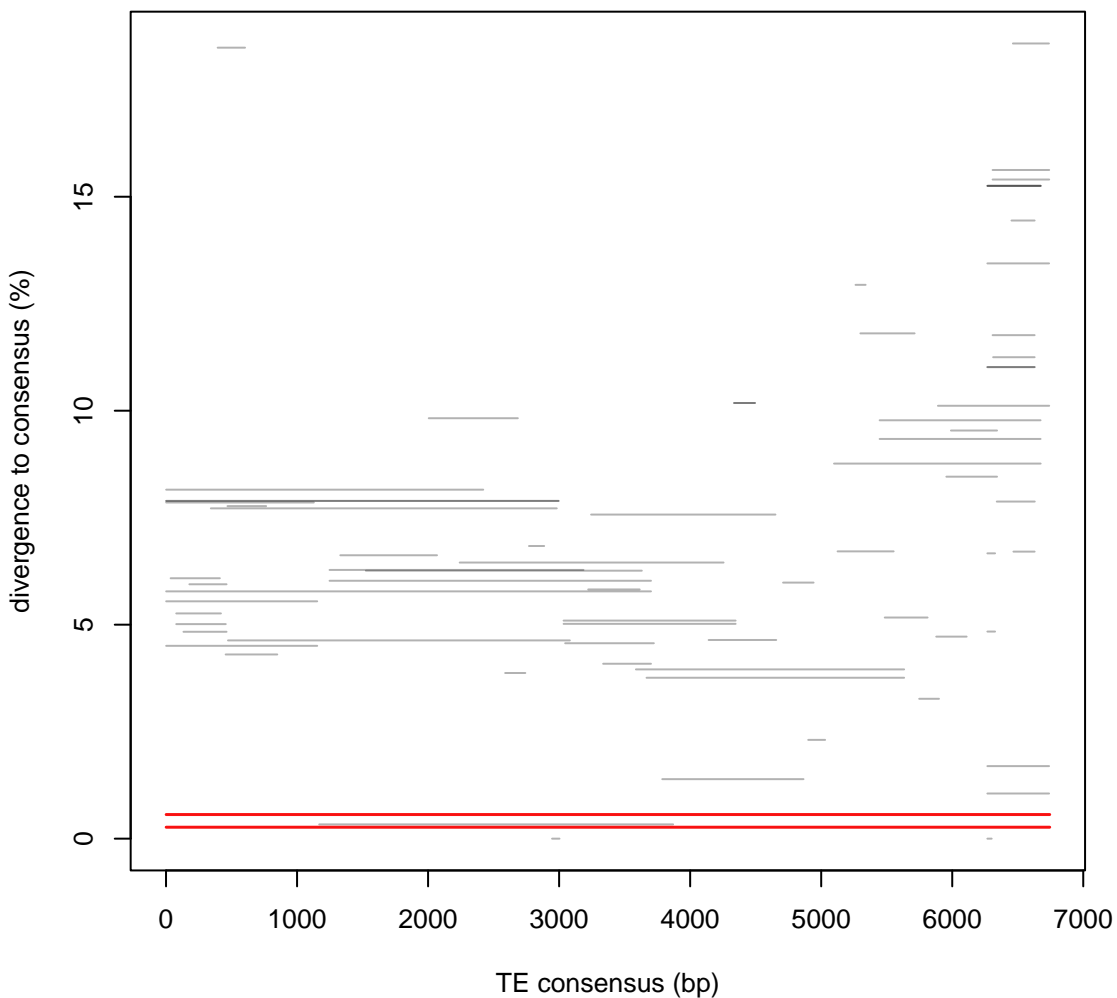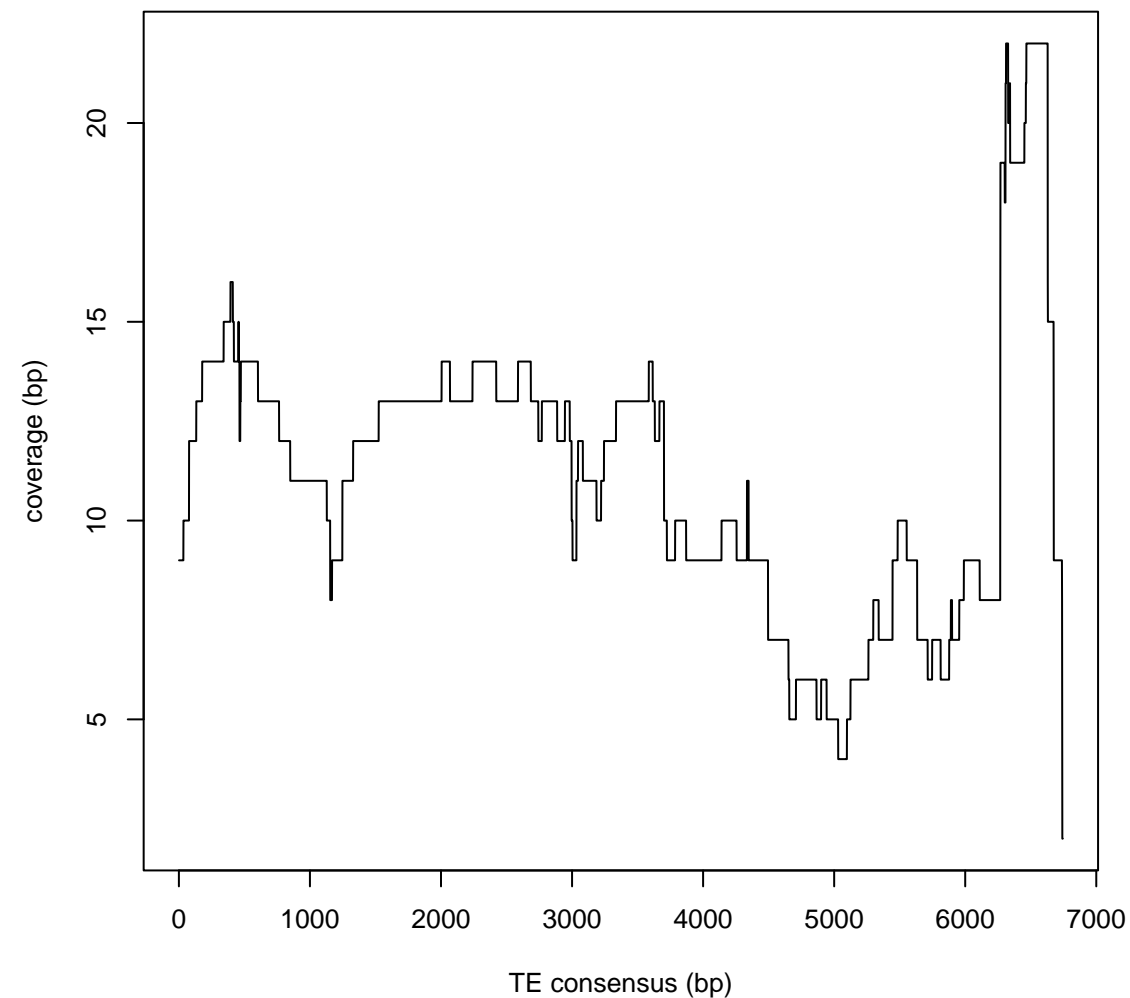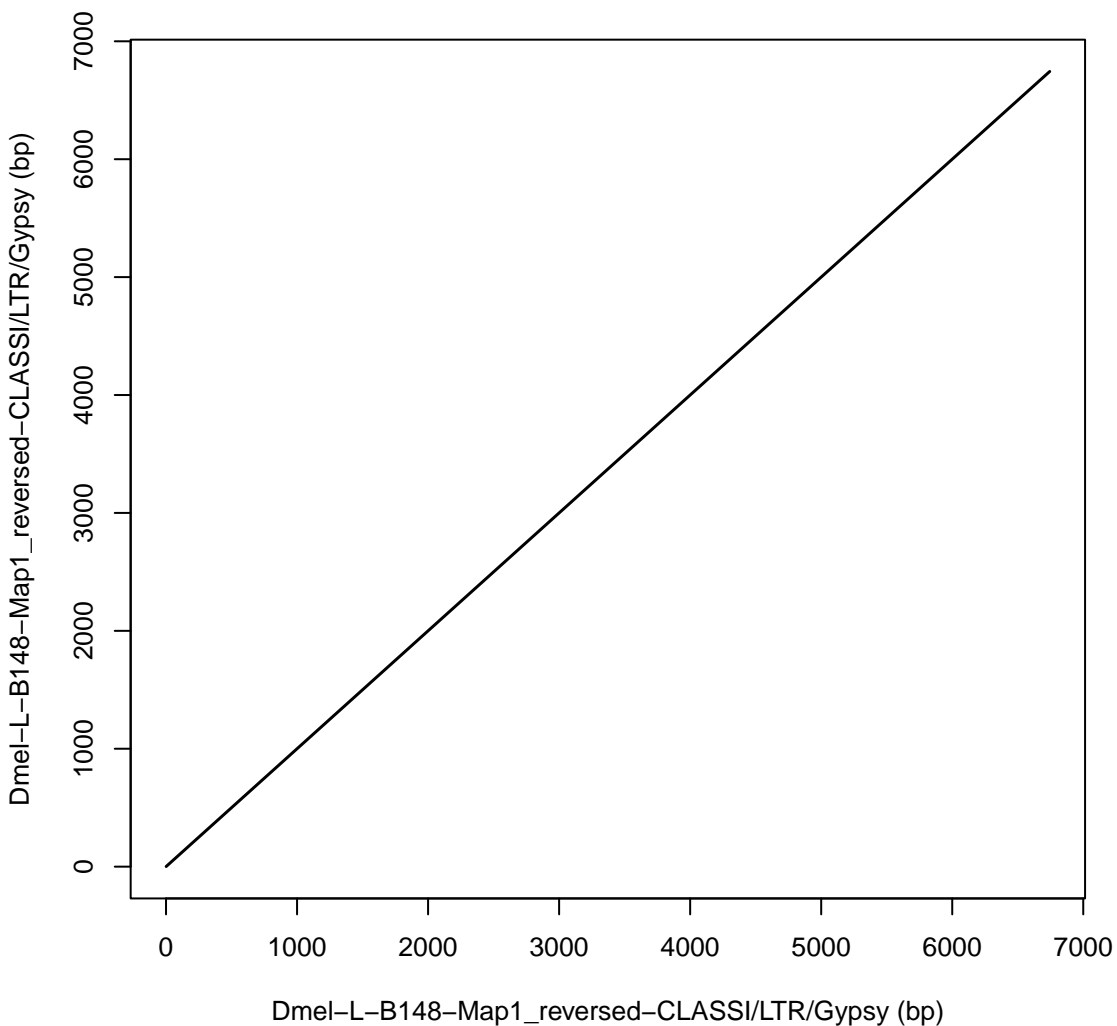**TE: Dmel−L−B148−Map1_reversed−CLASSI/LTR/Gypsy**
consensus size: 6744bp; fragments: 74; full length: 2 (>=6069.6bp)

TE consensus genomic coverage

TE consensus self dotplot (blastn)

TE consensus structure and protein hits