TE: rnd−1_family−263−LTR/GYPSY
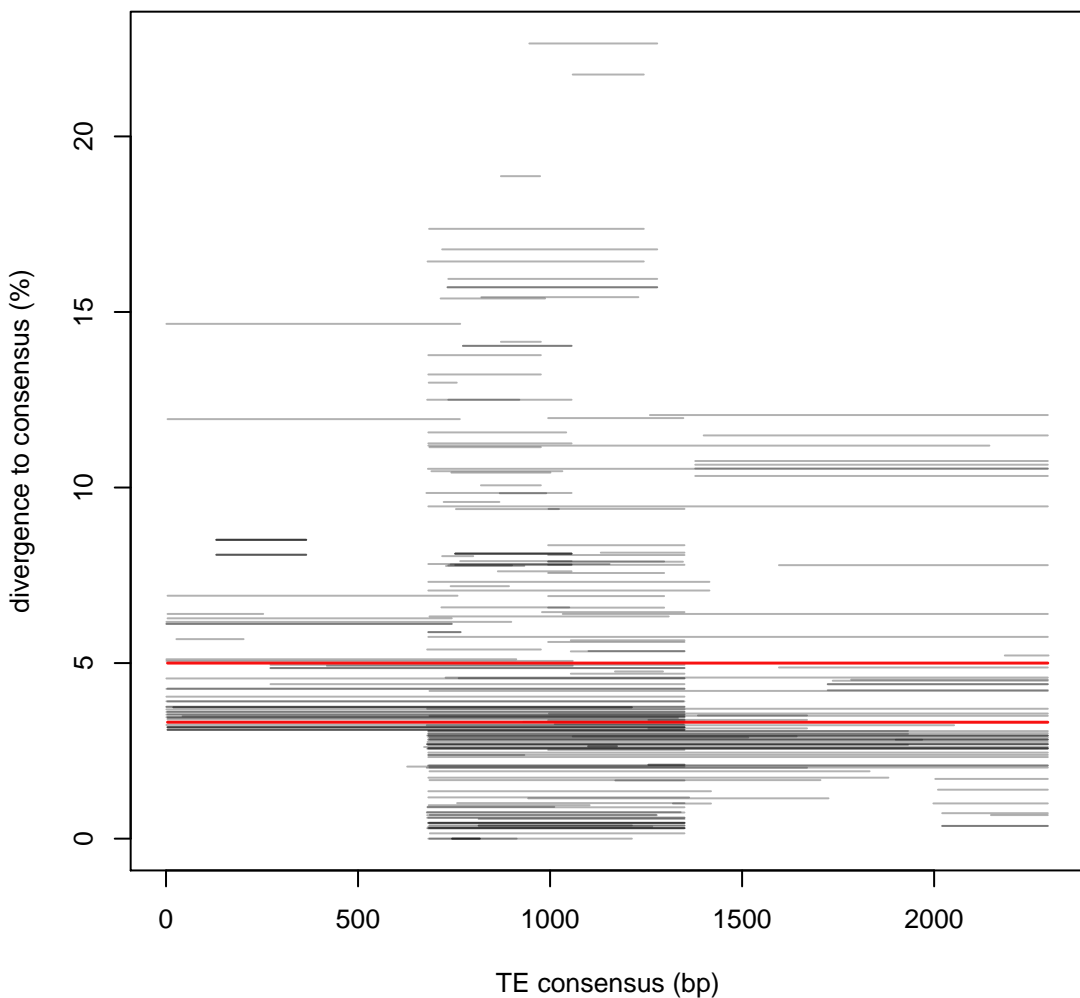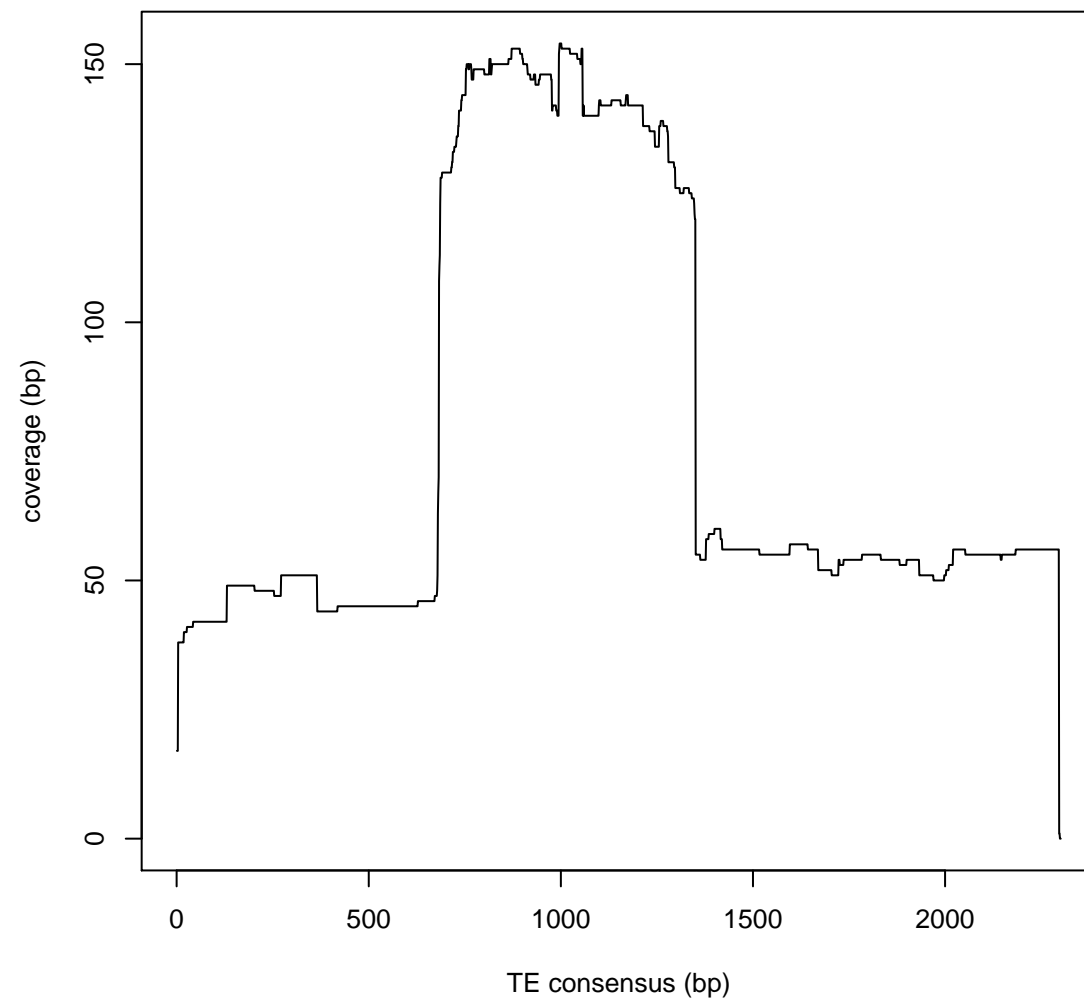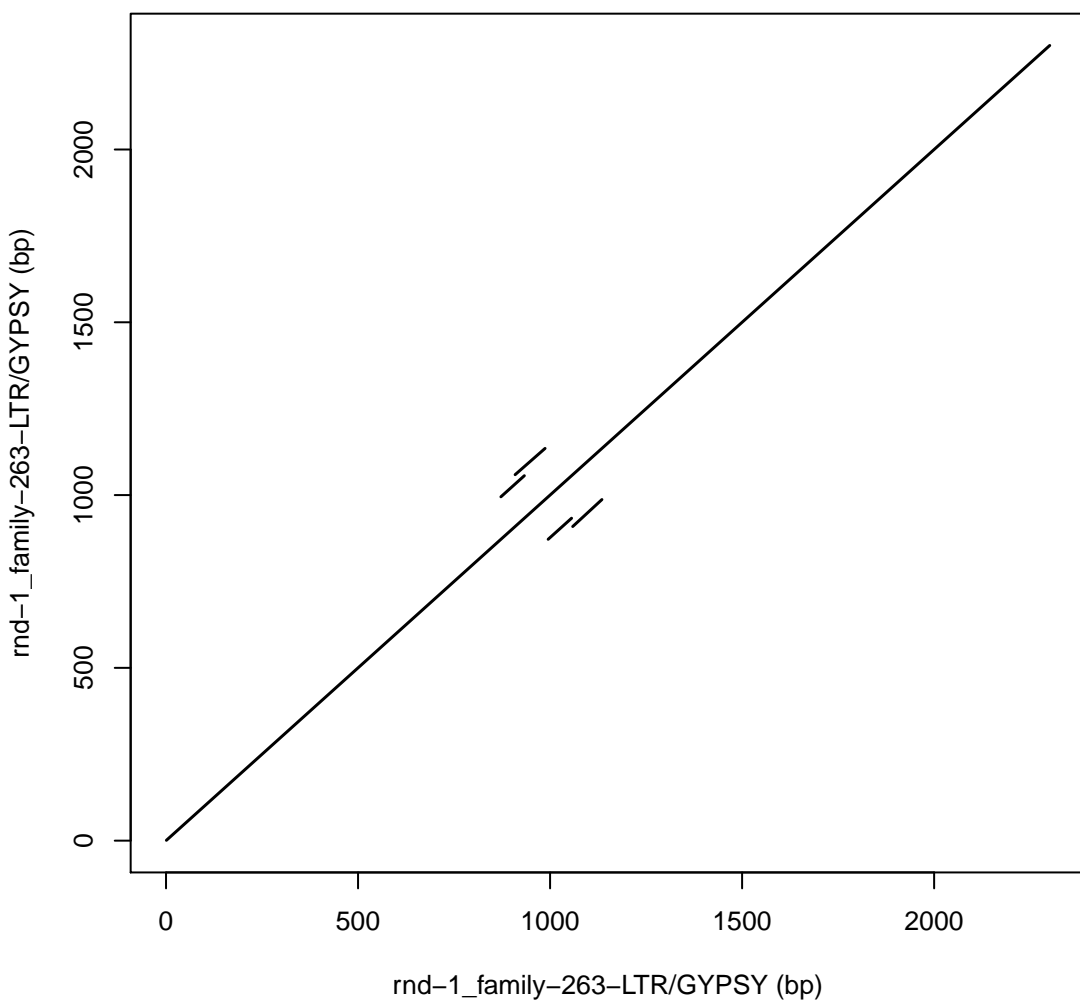**consensus size: 2301bp; fragments: 235; full length: 2 (>=2070.9bp)**

TE consensus (bp)

divergence to consensus (%)

TE consensus genomic coverage

coverage (bp)

TE consensus (bp)

TE consensus self dotplot (blastn)

rnd−1_family−263−LTR/GYPSY (bp)

rnd−1_family−263−LTR/GYPSY (bp)

TE consensus structure and protein hits

no orf >400 bp detected

rnd−1_family−263−LTR/GYPSY (bp)