TE: rnd–1_family–117–TIR/P
consensus size: 2223bp; fragments: 1801; full length: 0 (>=2000.7bp)

divergence to consensus (%)

TE consensus (bp)

TE consensus genomic coverage

coverage (bp)
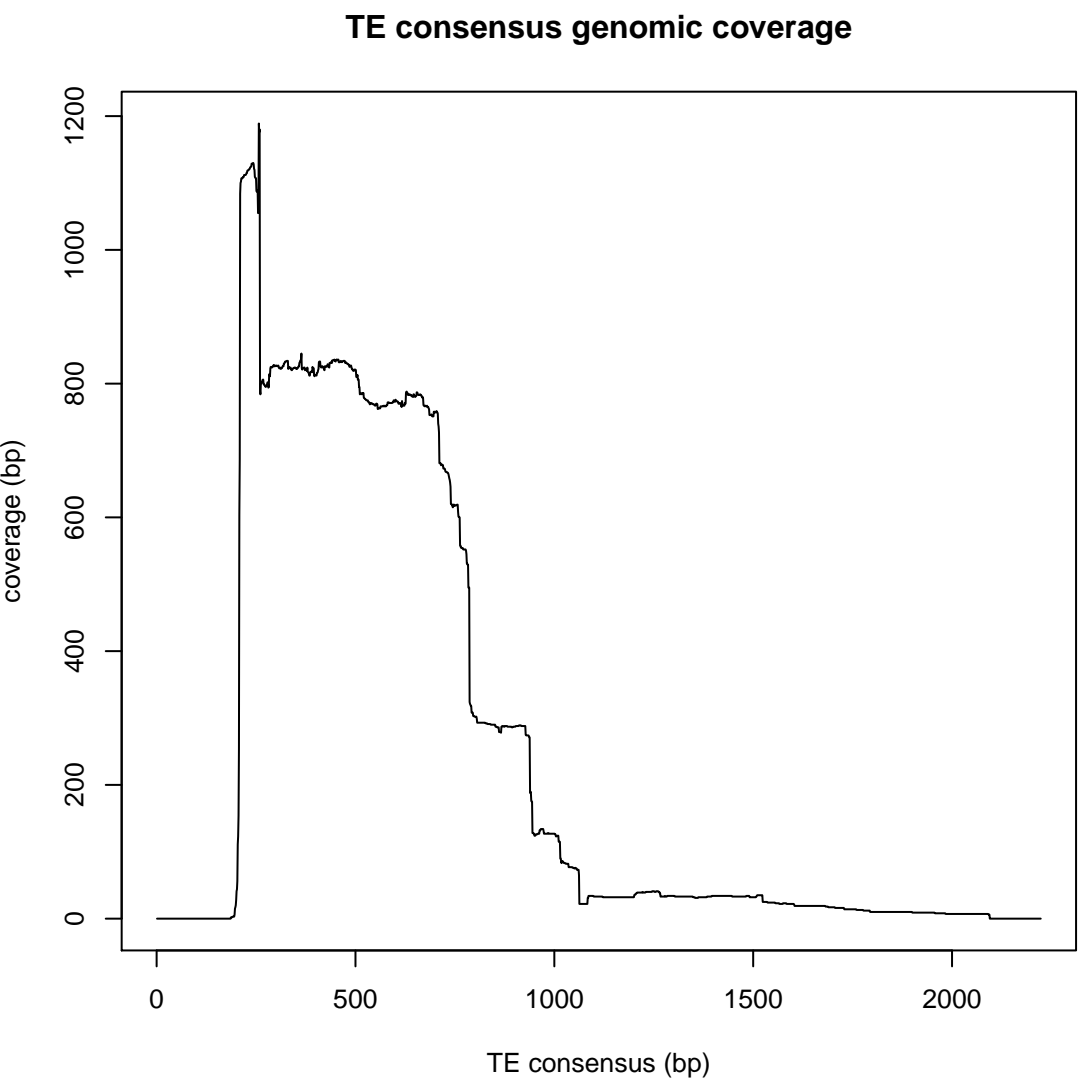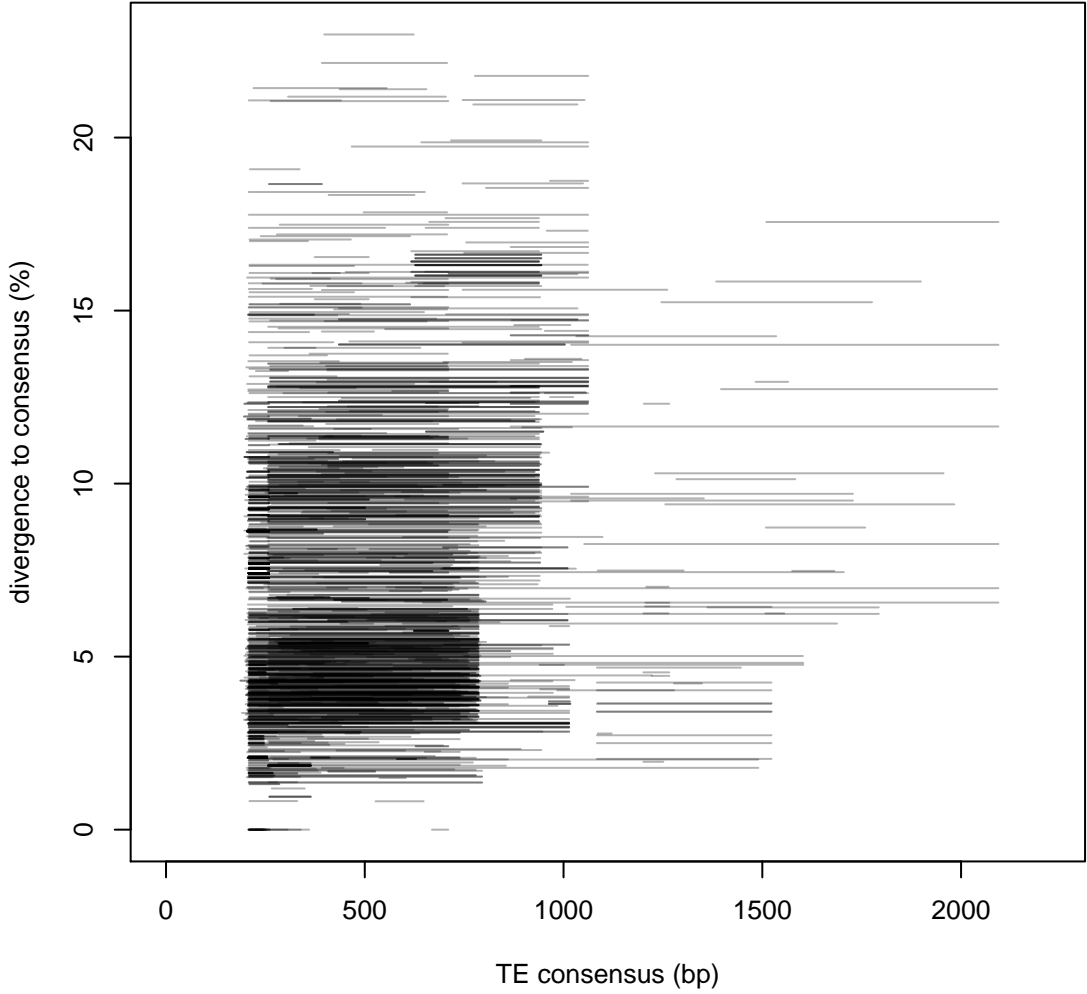
TE consensus (bp)

TE consensus self dotplot (blastn)

rnd–1_family–117–TIR/P (bp)

rnd–1_family–117–TIR/P (bp)
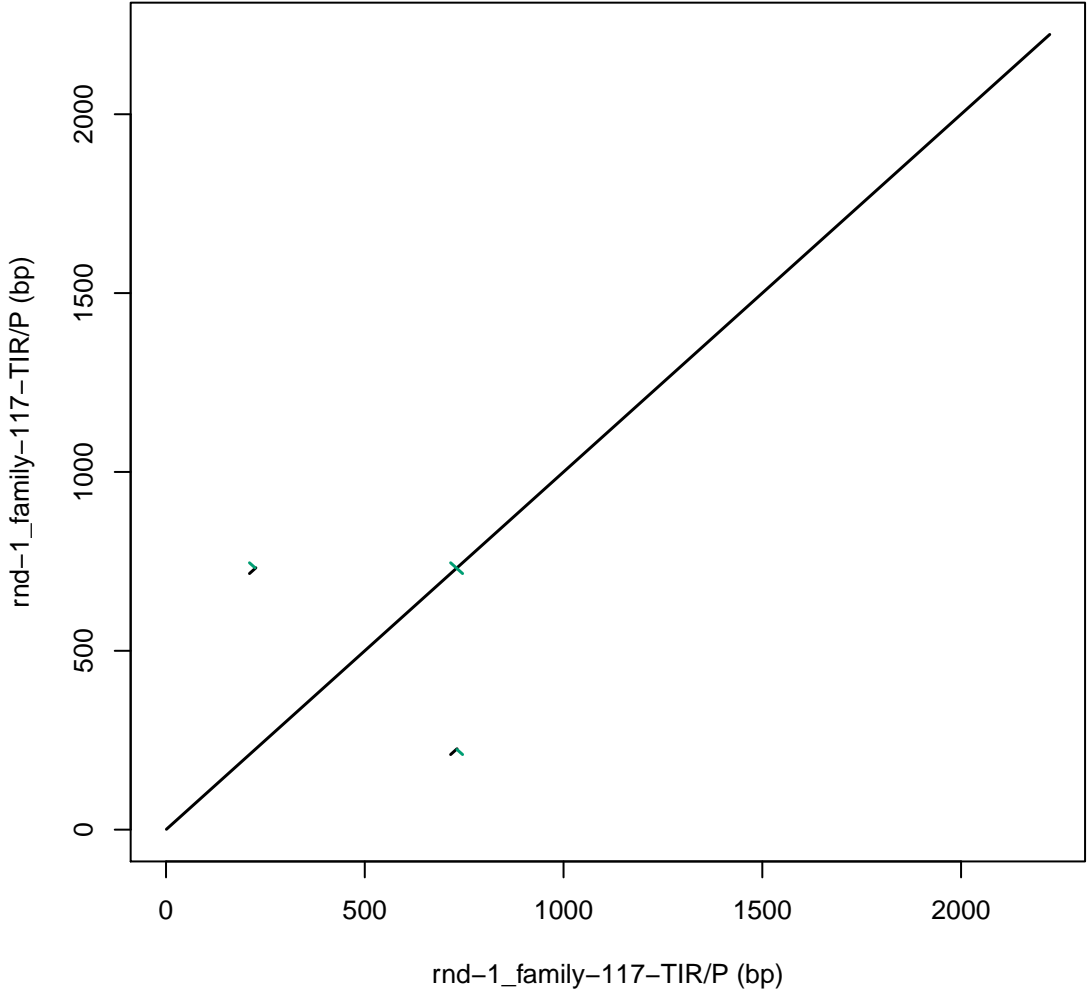
TE consensus structure and protein hits

no orf >400 bp detected

rnd–1_family–117–TIR/P (bp)