TE: ltr−1_family−38−LTR/Copia
consensus size: 2104bp; fragments: 12; full length: 0 (>=1893.6bp)

divergence to consensus (%)

TE consensus (bp)

TE consensus genomic coverage

coverage (bp)

TE consensus (bp)

TE consensus self dotplot (blastn)

ltr−1_family−38−LTR/Copia (bp)

ltr−1_family−38−LTR/Copia (bp)

TE consensus structure and protein hits

no orf >400 bp detected

ltr−1_family−38−LTR/Copia (bp)