TE: rnd−1_family−17−HELITRON
consensus size: 2963bp; fragments: 803; full length: 1 (>=2666.7bp)

divergence to consensus (%)
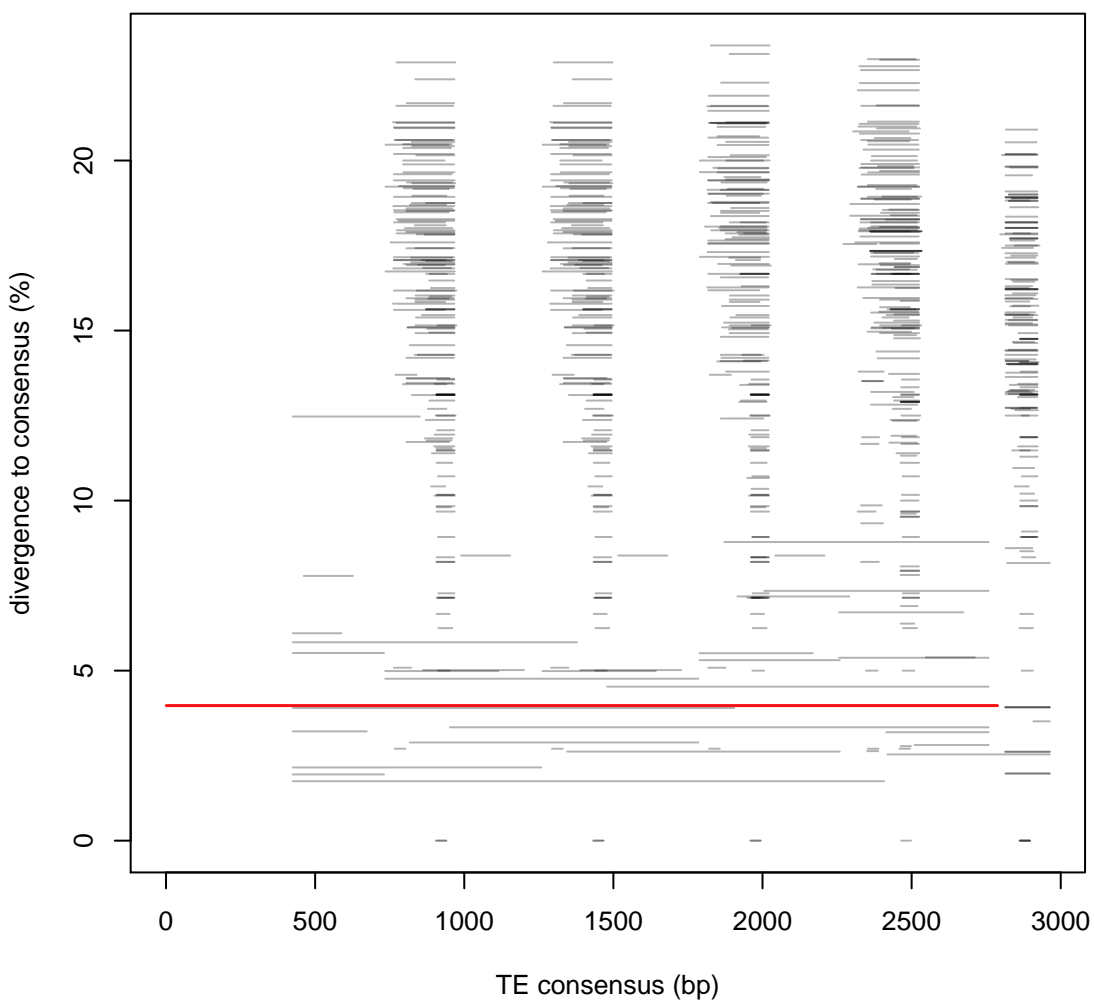
TE consensus (bp)

TE consensus genomic coverage

coverage (bp)
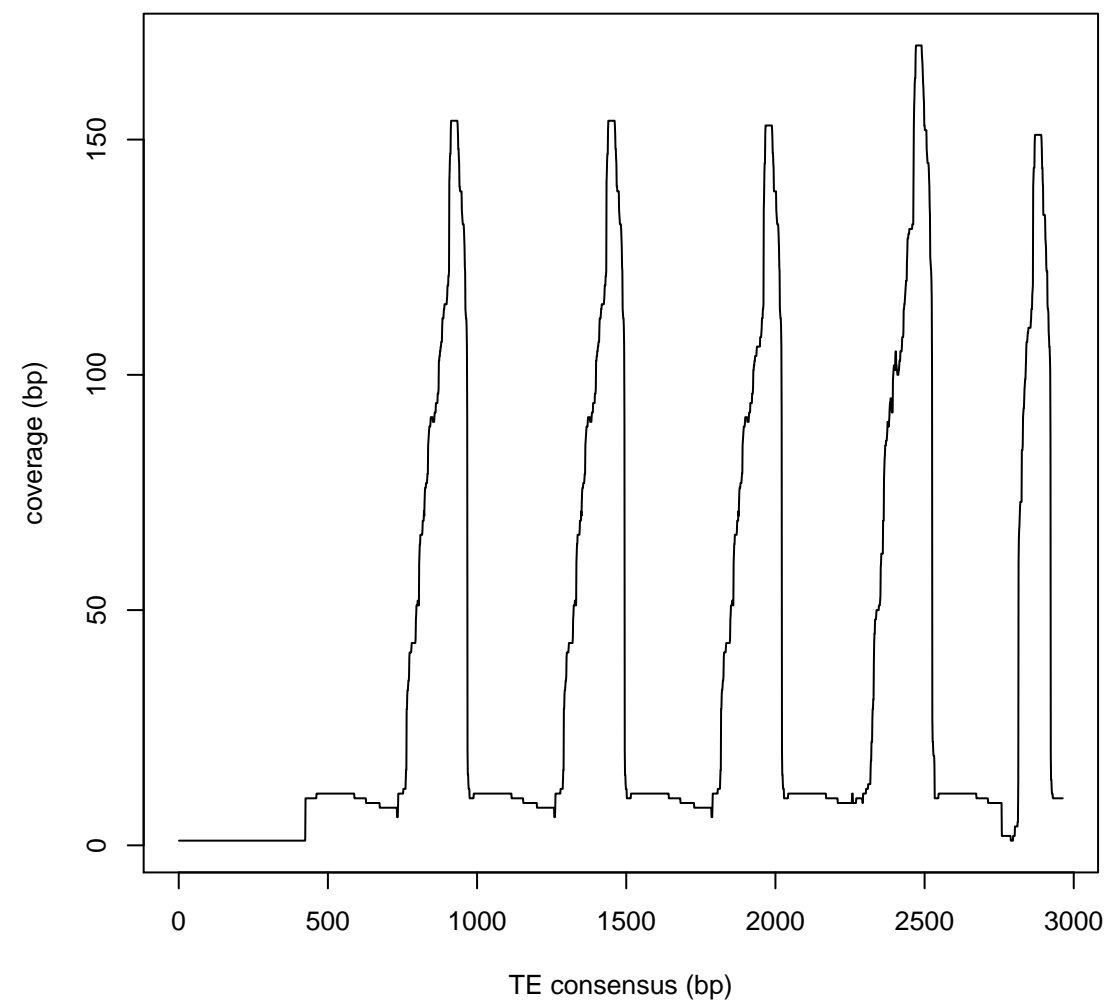
TE consensus (bp)

TE consensus self dotplot (blastn)

rnd−1_family−17−HELITRON (bp)

rnd−1_family−17−HELITRON (bp)
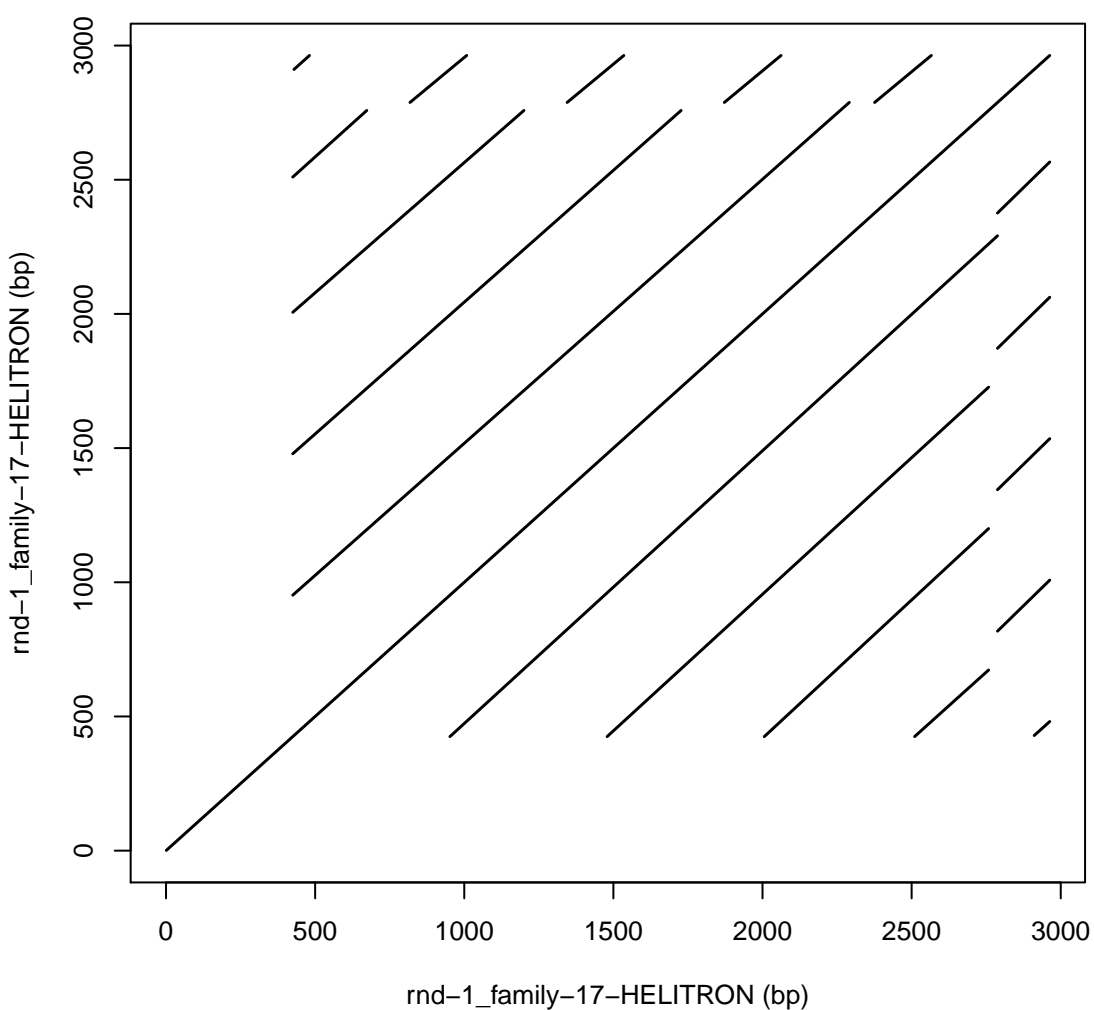
TE consensus structure and protein hits

no orf >400 bp detected

rnd−1_family−17−HELITRON (bp)