TE: rnd-1_family-30-RC/Helitron TE consensus genomic coverage consensus size: 603bp; fragments: 815; full length: 1 (>=542.7bp) divergence to consensus (%) coverage (bp) TE consensus (bp) TE consensus (bp) TE consensus self dotplot (blastn) TE consensus structure and protein hits rnd-1_family-30-RC/Helitron (bp) no orf >400 bp detected rnd-1_family-30-RC/Helitron (bp) rnd-1_family-30-RC/Helitron (bp)