TE: rnd-1_family-131-TIR/hAT-Ac TE consensus genomic coverage consensus size: 2976bp; fragments: 272; full length: 15 (>=2678.4bp) 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-131-TIR/hAT-Ac (bp) Ambal-1_FCy_pol LINE/CRE-Am BEL-632_AA_pol LTR/Pao rnd-1_family-131-TIR/hAT-Ac (bp) rnd-1_family-131-TIR/hAT-Ac (bp)