TE: Dmel-B-R10-Map3-CLASSII/Helitron/nan TE consensus genomic coverage consensus size: 4613bp; fragments: 395; full length: 2 (>=4151.7bp) divergence to consensus (%) coverage (bp) TE consensus (bp) TE consensus (bp) TE consensus self dotplot (blastn) TE consensus structure and protein hits Dmel-B-R10-Map3-CLASSII/Helitron/nan (bp) Gypsy2_pol LTR/Gypsy BEL-599_AA_pol LTI Dmel-B-R10-Map3-CLASSII/Helitron/nan (bp) Dmel-B-R10-Map3-CLASSII/Helitron/nan (bp)