TE: Dmel-B-G1021-Map15_s_1_s_2-CLASSI/LTR/TRIM TE consensus genomic coverage consensus size: 8242bp; fragments: 19286; full length: 13 (>=7417.8bp) divergence to consensus (%) coverage (bp) TE consensus (bp) TE consensus (bp) TE consensus self dotplot (blastn) TE consensus structure and protein hits Dmel-B-G1021-Map15_s_1_s_2-CLASSI/LTR/TRIM (bp) no orf >400 bp detected

Dmel-B-G1021-Map15_s_1_s_2-CLASSI/LTR/TRIM (bp)

Dmel-B-G1021-Map15_s_1_s_2-CLASSI/LTR/TRIM (bp)