TE: Dmel-B-R235-Map4\_reversed-LTR TE consensus genomic coverage consensus size: 2692bp; fragments: 62; full length: 2 (>=2422.8bp) divergence to consensus (%) coverage (bp) TE consensus (bp) TE consensus (bp) TE consensus self dotplot (blastn) TE consensus structure and protein hits Dmel-B-R235-Map4\_reversed-LTR (bp) no orf >400 bp detected 

Dmel-B-R235-Map4\_reversed-LTR (bp)

Dmel-B-R235-Map4\_reversed-LTR (bp)