Summary of main features of potentially encoding *TATE* copies

***Scaffold/contig*_position**	**ORF1 Position Domain**	**ORF2 Position Domain**	**ORF3 Position Domain**	**Repeats Basic structure size, identity**
B. saltans				
CYKH01000290.1_1157-6382		1-5226 DNA_BRE_C RVT_1		5’ →A1→A2 3’ →B1→B2 A: 73 bp, 99%; B: 161 bp, 81%
CYKH01000240.1_371-4765		1-4395 DNA_BRE_C RVT_1		5’ – absent 3’ – absent
C. fasciculata				
CfaC1_16_593910-598902	1-1225 N	1269-3471 DNA_BRE_C	2960-4994 RT_like DNA_pol3	5’ – absent 3’ – absent
C. mellificae				
MDUD01001032.1_377-5156	1-987 N	1338-3360 DNA_BRE_C	3389-5156 RT_like RNase	5’ →A1 3’ →A2 A: 357 bp, 100% B: missing data
S. culicis				
AUXH01000761.1_1187-6266	1-840 N	933-3987 Atrophin-1	3566-6266 RT_like	5’ →A1 3’ →A2 A: 346 bp, 99%
Lep. pyrrhocoris				
LpyrH10_03_995010-1005122	1-1095 N	674-3938 DNA_BRE_C	3151-5869 N	5’ – absent 3’ – absent
LpyrH10_45_4163-13642	1-1200 N	1623-3486 DNA_BRE_C	2732-5318 RT_like dnaA	5’ – absent 3’ – absent
LpyrH10_10_418649-428385	1-1014 N	969-3291 DNA_BRE_C	3317-5138 RT_like	5’ – absent 3’ – absent
L. braziliensis				
LbrM.11_536345-553559	1-1218 N	1311-4259 DNA_BRE_C	Interrupted ORF	5’ →A1 3’ →B1→A2→B2 A: 381 bp, 96% B: 294 bp, 99%
LbrM.30_1128659-1142875	1-1218 N	1311-4245 DNA_BRE_C	3356-6218 RT_like RNase	5’ A1→B1→A2 3’ →C→B2 A: 375 bp, 98% B: 637 bp, 94% C: 293 bp, 98%
LbrM.20.2_676198-690033	1-1218 N	1311-4260 DNA_BRE_C SPOR	3371-5837 RT_like RNase GcrA	5’ ←A1 3’ ←A2 A: 71 bp, 100%
LbrM.34_19966225-2010719	1-3642 DNA_BRE_C SPOR		2754-5616 RT_like RNase	5’ →A1 3’ →A2 A: 382 bp, 89%
T. theileri				
NBCO01000006.1_199922-210051	1-1104 N	1281-3762 DNA_BRE_C	3014-5981 RT_like	5’ →A1 3’ →A2 A: 91 bp, 100%

Note: The position in the scaffold/contig refers to the position of the copy in the scaffold (first nucleotide of ORF 1 to the last nucleotide of ORF3). The position of the ORFs refers to their position within the copy, starting with the first position of the ORF1. Different repetitions are represented by different letters (A, B, C). The positions (5' or 3' end) of the repeat fragments are indicated and the fragments are represented in order. The size and identity of repeats are indicated. The presence of protein domains is indicated; N - no predicted domain;