

## SUPPLEMENTARY MATERIAL No.7

## Characterization of the mRNA untranslated regions [UTR] of the *Trypanosoma cruzi* LYT1 isoforms derived by alternative *trans*-splicing

**Suppl. 7.** Multiple alignment of a segment of 3' UTR-II sequence from *T. cruzi* isolates listed in Table 1 and those sequences obtained in this study from 058PUJ (GenBank ID: KU973678) and D.A. (GenBank ID: KU973679) isolates. Sequences were aligned with CLUSTAL Omega [1.2.4] program. Numbers on the right correspond to the nucleotide position in the sequence. An asterisk means that nucleotides are identical in all sequences show in the alignment. The motifs of RNA are indicated in bold. The polymorphisms present in the RNA motifs are shown in red letters.

JR_cl4	GGAGGUACGAUGCGAGAAGAAGAAGAAAAAAAAAAAAGAAAGA	286
Dm28c	GGAGGUACGAUGCGAGAAGAAGAAGAAGAAG-AAAAAAAAGAAAGA	287
Sylvio X10/1	GGAGGUACGAUGCGAGAAGAAGAAGAAAAAAAAAAGAAAGA	283
KU973678.1	GGAGGUACGAUGCGAGAAGAAGAAGAAGAAG-AAAAAAAAGAAAGA	289
KU973679.1	GGAGGUACGAUGCGAGAAGAAGAAGAAGAAG-AAAAAAAAGAAAGA	289
CLBrenerEL	GGAGGUACAAUGCGAGAAGAAGAAGAAGAAG-AAAAA-AGAAAAAAAAAGAAAGAAG	289
Esmeraldo	GGAAGUACAAUGCGAGAAGAAGAAGAAGAAG-AAAGGAAAAAAAAAA	291
Y	GGAAGUACAAUGCGAGAAGAAGAAGAAGAAGAAA-GAAAAAAAAAA	293
CLBrenerNEL	GGAGGUACAAUGCGAGAAGAAGAAGAAGAAG-AAAAA-AGAAAAAAAAAA	289
CLBrener	GGGAAGUCAAUGCCGAGAAGAAGAAGAAGAAGAAGAAAAAAAA	298
Tula.C12	GGAAGUACAAUGCGAGAAGAAGAAGAAGAAG-AAG-GAAAAAAAAAA	295
Marinkellei	AGAAGUACAAUGCGAUAAGAAAAAAAGGAA-AAUAA	261
JR_cl4	AAUGACGUUCGAGCGUAGUUAAGCAUACCCUUUUGAGUGCACUGAACAGAUAAACAAAC	346
Dm28c	AAUGACGUUCGAGCGUAGUUAAGCAUACCCUUUUGAGUGCACUGAACAGAUAAACAAAC	347
Sylvio_X10/1	AAUGACGUUCGAGCGUAGUUAAGCAUACCCUUUUGAGUGCACUGAACAGAUAAACAAAC	343
KU973678.1	AAUGACGUUCGAGCGUAGUUAAGCAUACCCUUUUGAGUGCACUGAACAGAUAAACAAAC	349
KU973679.1	AAUGACGUUCGAGCCUAGUUAAGCAUACCCUUUUGAGUGCACUGAACAGAUAAACAAAC	349
CLBrenerEL	AAUGACGUUCGAGCGUAGUUAAGCAUACCCUUGAGUACACUGAACAGAUAAACAAACA	347
Esmeraldo	AAUGACGUUCGAGCGUGAGCAUAAGCAUACCCUUGAGUACACUGAACAGAUAAACAAGCA	349
Y	AAUGACGUUCGAGCGUGGUUAAGCAUACCCUUGAGGACACUGAACAGAUAAACAAGCA	351
CLBrenerNEL	AAUGACGUUCGAGCGUAGUUAAGCAUACCCUUGAGUACACUGAACAGAUAAACAAACA	347
CLBrener	AAUGACGUUCGACCGUGGUAAGCAUACCCCUUGAGUCCUGGACAGAUUAAACAAGC	354
Tula.Cl2	AAUGACGUUCGAGCGUGGUUAAGCAUACCCUUGAGUACACUGAACAGAUAAACAAGCA	353
Marinkellei	CGUUCGAGCCUAGUUAAGCACACUCUUGAGUUCACUGAACAGAUAAACAAGCA	314