

## SUPPLEMENTARY MATERIAL No.5

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

**Suppl. 5.** The location of the *LYT1* UTRs sequences in the genomic sequence of the CL-Brener (GenBank ID: AF320626.1) strain of *T. cruzi*. The trans-splicing signals: the acceptor dinucleotide AG and polypyrimidine tracts are underlined and in bold. The ATG and TGA codons are highlighted in blue. The delimitation of the 5´ UTRs and 3´ UTR-I are shown in gray, and that of the 3´ UTR-II is underlined.

AGTCCTTTGCTTTTTTTTTTTAACCTGTAAGTTTCATGTAAAATGAAAAATGCGGAAACCAAAAGGTATG GAATTACGGCGTATGTATGTCATCCACTTCCCATCCCCTTTACGTGTTTTCGCAACTTGCCCTTTTGCTCT AAAGCCGCAGCATTAGTAGCACCCACAGCAGACACGCCGACGTGCCGCGGGGCTGCCATTGCGAATA ACTTT<mark>ARC</mark>GGACGTGCCGGCCCCCGTGAGGGCGTTGGAAGATCAACGGAGATGCCGGCTGCTGGACCGAC GGGGTCTCAAAGAAGTCAAACGCAACGGGAGGTGAAAGCGTCACAAGACGCCGACGCGGCGGCCATTAGT AGTTATTTCCAGTCCGAATTGGTGACATCTCAGTCGCACGAGGGTGTGTCTCCTCTGGCAAAGACTAGGG TGGGAAGGGGACCCCAAACAGCGAGTGCTGCAGGATTTGCCAGCGATGCACGCGGAGGGACAAAAC CAGCACGGTAGAGAGGGTGACAAGGGTGTTTCCGTGAAGATGGACTCCCCTGGTCGCGTACAGGTGCTGG AGCAAATGTTGCTACACCTGGCTGCATTGAACAGACAGCTAGAATTAGAACTTATAGAAACGCGACGGGA ACTGACGATGTACAAGCAGCTTTTACCTGATGTGCAGCCCAGACCGAGGCCCATGCTTTGTCTCAGGAG CATCACAAAGCGAATAGTGCTGCTCCGCCACTGATGTCAGATGAGAGGCGACGACAGATGCTCTTCACAG GGCAACAACAACAGCAACAGTGGAAGATCTGCATGGCGGTATTAGCGGGTGGGAAACGGCAGCGAG GAGAATGCGCTATGGTTACGAGGAGGGGGGGGGGGCGCCCTTTCAGATGGTGAGGGCCGTCCACGTTGC GCAGGTCGTATGGGCTCCCCGAAGAGATTCCTTTCAACACACCGCCTCGAAGCAGCAGCAGGAACCATCGGA ACCCTCACGCTGCTAACGGGACAAATGGCAATAGTCATGTTCCCCATTCGTCCAGACAAAAAAAGTCACCC GACAAGAGGAGCTGCTGTAACTTCCGTACCGTTGGCGGCGTCCGCAACCAATCGCCGAGGTCGTTCCATG CGACAACATACCCGACCCCGCGGACCTTCTCATCTTTTCGAACGCCTCGACGCTGAGGATGCAATTGATA TGCTGGAGACCTTGAAGCTCTCTCTCATGTATCGCTGCAACCACTCGCATCATCGATCAACAGAAGGAGA TGTTGTGCGCCCGCCGCAAGCCCCGGAAAGGCACGCGGTCTGTTGCACCACCACCACCACCACCGTCC ATGTTATCATCGTCACAAAGAAAGCTTGCCGCCGCAGTTGCTGGAGCGCCGGCATGCAGCGTCTCAGCAC GACACGGAAGGAACCATGGCGTTTCTGCGGTGGGAGATCCGTCAAGGGGCAATCGAGTTTCAGAAACAGC TCGCATAGCTCATGCTCCTTCTTTTGGGGGGAAGAAATGCGCGCGGGCCTAACCCAACTCCATTTCTCT TCCCCTTCCAGAAGGGCTACGCCGATGAAAAAAGACACGCCATTGTCACGTGGTCAAGCGGCTGGAGTAG GATATTGGAGCAGCTTGAAAACATGCTGGCAGCTGAT<mark>TGA</mark>AGTCTTTGGCATTAGGGATGACAATCATAG TCGTTTTGCAGCTTCGTTGAGGTTGGTACATTCTGAGAATTGTATCTGCACAGGGTGCAGTGATACACAC ACACACACACATACAAATACATGTACACTTATGTTGTTTGCTATCTACCAGGAGGGGTGAGGAGTGAG TGGAAATGAGCAAGCGGTGAAAGTTTTCTTCCTCACAGTCTTCCGGCGACGCGAAGAGCAGGAGAATGG CCGTGGTAAGCATACCCCTTGAGTCCTGGACAGATTAAACAAGCCCCAGGGTCAGAAAAATGAAACCGGG ATTGAAAAAAAAAAAAAAATTTCCCCCAGAGGAGAAGTTTGAAAAAA