A

```
Tb927.5.810           MSTATSAPVVESMSDTVVCPQLSRHSTSLEELYTIGYNRSHSPSCFSSAGCEEEEGQKNYLAERYKTKLCKNFVQYGTCP  80
TcIL3000.0.37550      MPAALSKPAKMVIMSDGQCEVQSSRSCSLSQSIVPCGSYTGSP---SVAEMDEEGHAKVYLAERYKTKYCNNFVINGACP  77
TvY486_0500320        -MAFDSSSVTSLQSLSAPDVLPPSLSVDKPHFFADYNADFN-------------KHGKTYLAERYKTKLCKNFMELSFCP  66
Tc00.1047053504929.5  --------MTSMHCTLVPTPPPPFYGVCMEDTMSLGYACAS--------GVESDMAAKPYLAERYKTKFCRNYVLTGICP  64
LmxM.34.1040          --------------------MSKNTGSVTEQHKRISHAAGD-----------NNEEEKHILAGRYKTKLCKNYVAKGECP  49

                                  a        b                c        d
Tb927.5.810           YDIRCMFAHGEEELRTAEMNIVDGLVTKDAITSFQKLWHRAVSASSGSKHHSSH-----VANRRGVMTTATTTTTAC---  152
TcIL3000.0.37550      YDTRCMFAHSAEELRTAEMNIADGLITMEAIRRFQRLLHQVTRSSRFARLRPVR-----TSAPWAMVPAASIGPAAMP--  150
TvY486_0500320        YGFICMFAHGEEELRTPKMNYEDGLSTEESIRVFQRMWYKVAFQQQHSAVQN----------SVGFLWPFTCTSLMP---  133
Tc00.1047053504929.5  YQRRCMFAHGDHELRTPEMNIRDGLVTEEAIRLFRRQFLSDICAFDRLRRR-------------GFPAPPYFYHAMC---  128
LmxM.34.1040          YDVRCMFAHGEDELRTSDDNIRDGLVTEEAIKDFQRQQNQAKRRAAFAAARFHNNHDHSHSHNHSHTHNHTVRPVSHRNA  129

Tb927.5.810           -------GSTDAAMHICRRMQRVVAAAAAAVPCGGRRVVS---------GSIRIRGCVRHNPYCHNILPTVSRYYSTMPD  216
TcIL3000.0.37550      ------HAYHDLRQSSAKGICERAGCVAA--------------------ATPMAGVRYTHNPYRCDILPLLSRLYSKLPD  204
TvY486_0500320        ---------PPPYHHHVPYFAQIPVKSTT--------------------SFPPPAARYRHDPYCAEVIPPESRFYSRLPD  184
Tc00.1047053504929.5  -----------VCMSDCG-----VP-----------------------VRMAPAKIYTHNPYKSDIIPLQNRLYSQPPA  168
LmxM.34.1040          YEIEENVESNEVYHNRHRHHNVRLHPQQESVSIPQPQQQQQQQQHEEQFQLQSAVVQYYTHNPYVFDLIPAVARLPPVYHD  209

Tb927.5.810           VFTRPYSKSDSCGNEAITEGNAWTYANEEGNEKETPAMISSGVPELTAWKRFNYVAERSQCTSVPEQNLPCADFAAIKES  296
TcIL3000.0.37550      MFVVPCNRVPDSGSELAQLPEERLSERILDGDE--------TVPAFTERANAQQEQLRCDSDARCHEALFLPESLPSDEP  276
TvY486_0500320        AALDSQEAR-------------------------------NKHCYCSRAQSDNGKEGALCTASPASECFSQFQLTTLQL  232
Tc00.1047053504929.5  LAMMTAAT---------------------------------VMPQYYEEG----TMCRSSCDPSEHQDDFEPCVEIVSSP  211
LmxM.34.1040          VV---------------------------------EEGCWYEEEPAPAQEDYYFPSSDMMMPLVPSLVTQQYLPYPHQQ  255

Tb927.5.810           NNTGGNASCVDVENV--DDAEHSTCSSYGNESGYFCRASRSASCGEQSQSHLKREGNEGRGEGLHMFLSL              364
TcIL3000.0.37550      DVACTPDSGSEEVDG--RVGDRSVCSSTGNESGDVHNSPTYASHFVKG--SLRTVCRGVSEESSHTDLYL              342
TvY486_0500320        QNSENEPQLLPHIRS--DDGDSSLCSSYGSHSGLSRSMSVTNSLAKRS----ESLSTYHEVEVIQ                   291
Tc00.1047053504929.5  RCYACNES---------DDAEPSACSSIGSDSEDNRQSTPCKEYINES---MPSEEVMSGEAALQ                   264
LmxM.34.1040          CGKQFETVASASTYSGEEAMYGHSESSASSVYRSVARCTAAELPSNSDIPAMVMEP                             311
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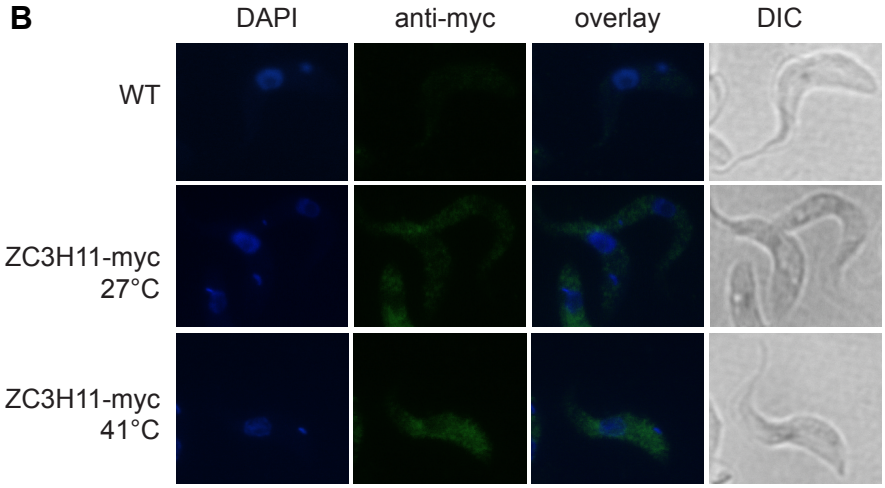
B



Supplementary Figure S1

A. Alignment of amino-acid sequences of selected Kinetoplastid ZC3H11s. The alignment was done using ClustalW (Slow, accurate, Gonnet), in the DNAStar package. Identical amino acids are shadowed in black and conserved amino acids in grey. Groups used were : (DE), (HKR), (AGILV), (NQ), (FWY), (ST), (P), (CM). The CCCH motif is in pink. The codes for conserved residues are listed at the bottom. Arrows indicate clone boundaries: a) N-terminus of the C-terminal fragment used in the tethering assay; b) C terminus of ZC3H11-104 used for RNA-binding assays; c) C terminus of ZC3H11-119 used for RNA-binding assays; d) C-terminus of the N-terminal fragment used in the tethering assay.

B. Location of ZC3H11-myc in procyclic forms. Results are shown for normal cells (not expressing myc-tagged protein) and cells expressing ZC3H11-myc grown at the normal temperature (27°C) or subjected to a one-hour heat shock at 41°C. DIC - differential interference contrast image.