

A

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XP_001682355.1 -----CDLNDTWEDVLTAFNDCLK-GESTWSCHCLDG 31
XP_814406.1 -----MACDLDTEWVECMGEFKEFIGKTGNPWCYTCG 34
XP_844906.1 -----MLCALDDTWADCLDEFKALSSGTWKCESLAG 34
NP_001118295.1 --MQSVREDEDSSSPIHHDSTSSSIPSGDNNSVWADVSPLLSAACSDLQEGE-LINGDN 57
sp|Q5VZE5|NAA35_HUMAN MVMKASVDDDDSGWEL-----SMPEKMEKSNNTNWVDITQDFEACRELKGE-LLHDKL 53
NP_579858.1 MVMKAAVDDDDASGWEL-----NVPEKMEKSSTSWVDITQDFEDACRELKGE-LLHDKL 53
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XP_001682355.1 IDKEVILSAPEIMDPKTDSGFNCEEI---YLSHLLKTEEVPS----AATVSTEAALLD 83
XP_814406.1 VEKETMLSAPEVMDAKTDPGCGYGSI---CSLNCLLKDGITIPS----AATLTG-EALLD 85
XP_844906.1 VDKEAMLSAPEVMDAKTDPGCGYAQI---RSLNDLLAKGDIPS----AATLQG-QELLD 85
NP_001118295.1 FNLFAAMSALEIMDPKMDSGMVSTFYF----IDEAIESGFAPVPISSDSTVN-VQSIID 111
sp|Q5VZE5|NAA35_HUMAN FGLFEAMSAIEMMDPKMDAGMIGNQVNRKVLNFEQAIKDGTIK----IKDLT-LPELIG 107
NP_579858.1 FGLFEAMSAIEMMDPKMDAGMIGNQVNRKVLNFEQAIVKDGITIK----IKDLS-LPELIG 107
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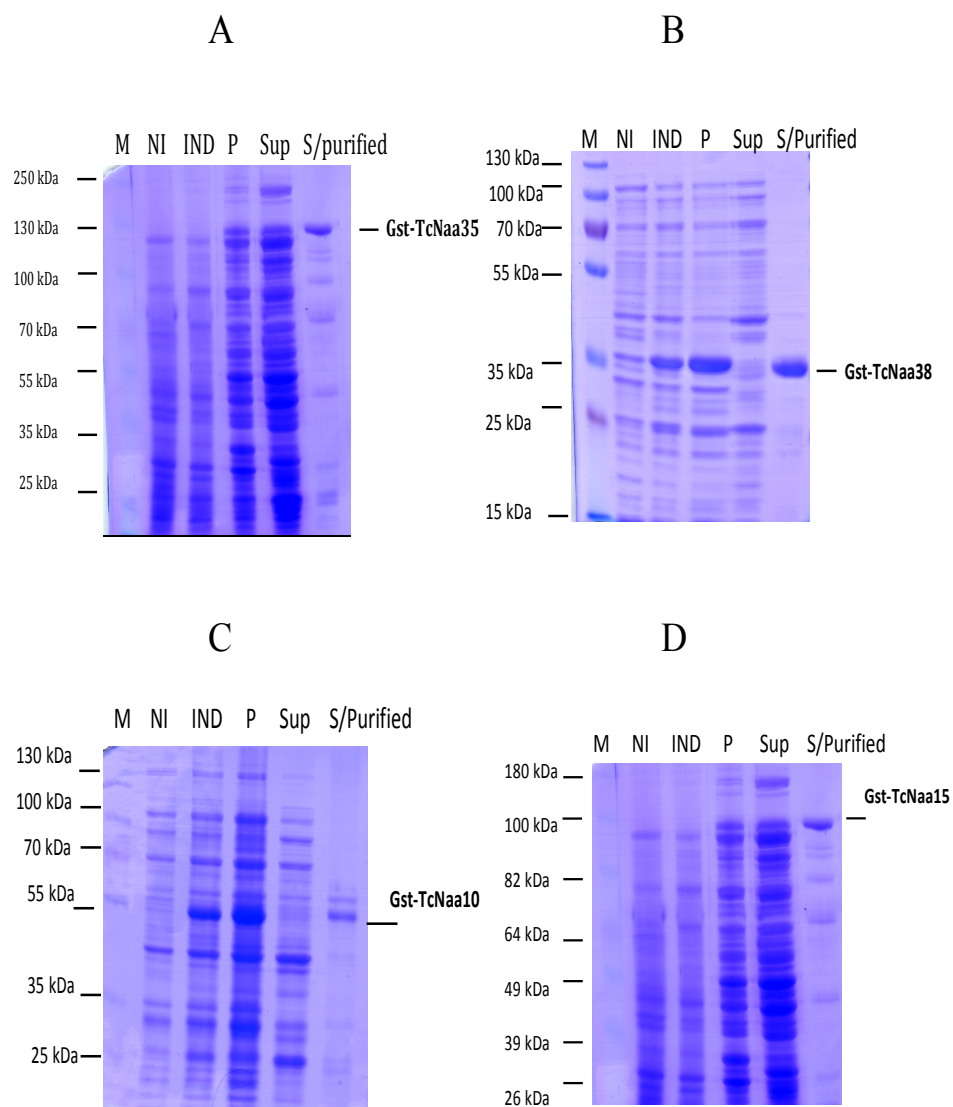
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XP_814406.1 VMDLIHLKELNYLQGFSLTSGCLEFYSYFFCMDLLKEQNLTYTYCRALARCIDLTRAVM 145
XP_844906.1 VMDLILAKELQYLQGFSLTSGCLAFYFFKMDLLKEQNPVLHAYCRGVVTVIVLRAVM 145
NP_001118295.1 IMDHLLACEATWHMGHSLAQTVFSCIVLVRPERTSSQ-ALLHSYCRVIRATCRAVSVSV 170
sp|Q5VZE5|NAA35_HUMAN IMDTCFCCLITWLEGHSLAQTVFTCLYIHNPDFIEDP-AM-KAFALGILKICDIAREKVN 165
NP_579858.1 IMDTCFCCLITWLEGHSLAQTVFTCLYIHNPDFIEDP-AM-KAFALGILKICDIAREKVN 165
: ** : * : * : * : * : * : * : * : * : *
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B

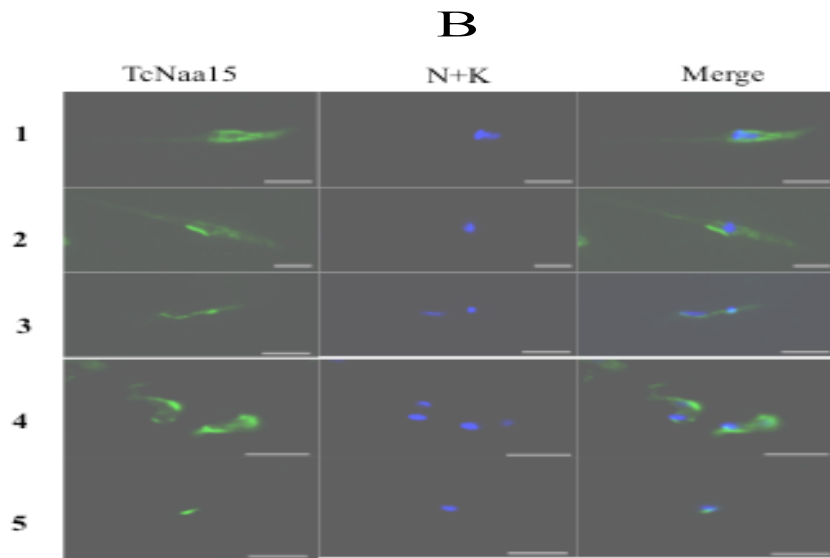
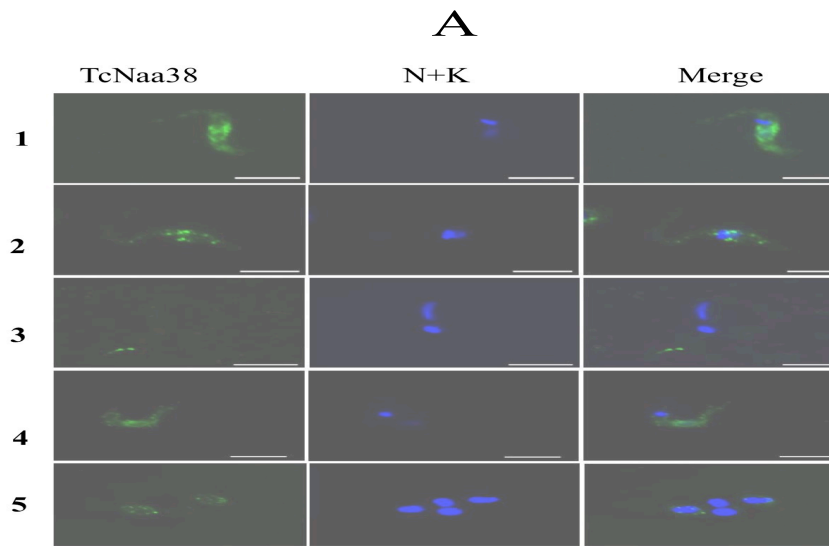
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XP_003722006.1 MGKYTMLHNINKVLCVMLDDGRVTVTGKLLVDFDKHMNVVLGDAVEERPQSKMAEE----- 55
XP_808107.1 MGRESMLHNINRTRLRIVLIDGRELTGKLLVYDRHMNVVLGDATESREETKKMKEA----- 55
XP_951644.1 MGHQNMMLHNINRTRLRVTLDGREMTGKMLLFDKFMNVVLADTVETRKEKKMKDA----- 55
: : : * * * * : : * : * : * . * . : :

NP_010946.3 SKDGTTLNIKVEKRVLGLTILRGEQILSTVV----- 82
NP_001317040.1 -----SAGEPRVLGLAMVPGHHIVSIEV----- 74
XP_003722006.1 -----GVSSKRQLGLILLRGEHVSVTVMKDSENGGSGAVAN-----FGGAPKLAK 101
XP_808107.1 -----GISPQRSLGLVLLRGVHVIVSVNLGASENNGDGEGKTKGQPANFEKAPRAKV 107
XP_951644.1 -----GISPQRKLGMIILLRGEYVVAVSVLKD-----VSEDKAQPANFESATREKL 101
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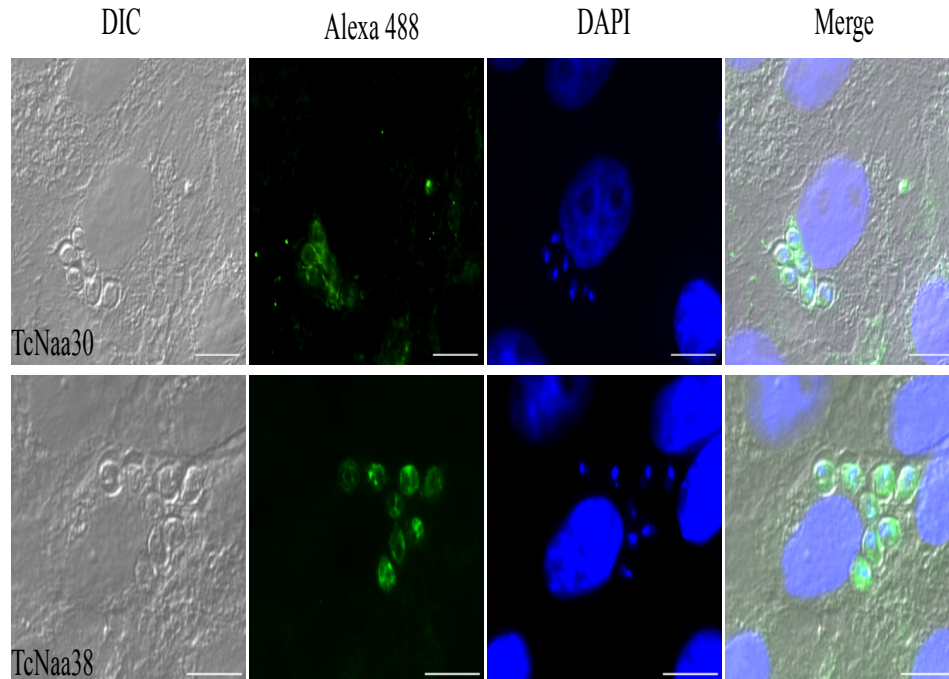

C; Comparison of TcNaa10 sequence with selected eukaryotes. The over lined indicates the consensus sequence RXXGXA for NatA, where acetyl –CoA binds. The two arrows indicate the active sites and a symbol ‡ is the predicated possible lysine auto acetylation site. Used sequences in the alignment are: Yeast (NP_011877.1), Human (NP_003482.1), *Leishmania major* (XP_001681770.1), *T. cruzi* (XP_817467.1) and *T. brucei* (XP_828529.1). **D**; TcNaa15 sequence comparison with putative homologues from other species. Polypeptides used in the alignment are: *Leishmania major* (XP_001686706.1), *T. cruzi* (XP_807954.1), *T. brucei* (XP_822811.1), Human (NP_476516.1 and Yeast (END60314.1. * Indicates residues, which are highly conserved.



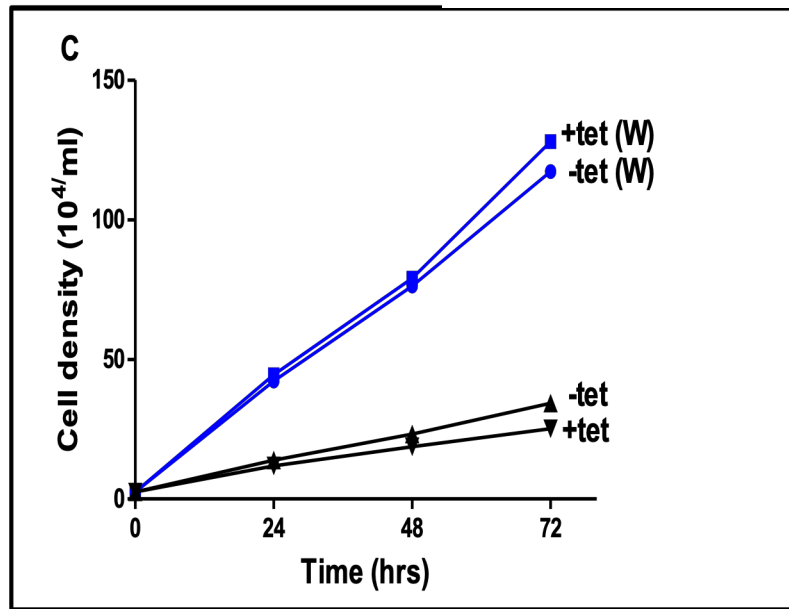
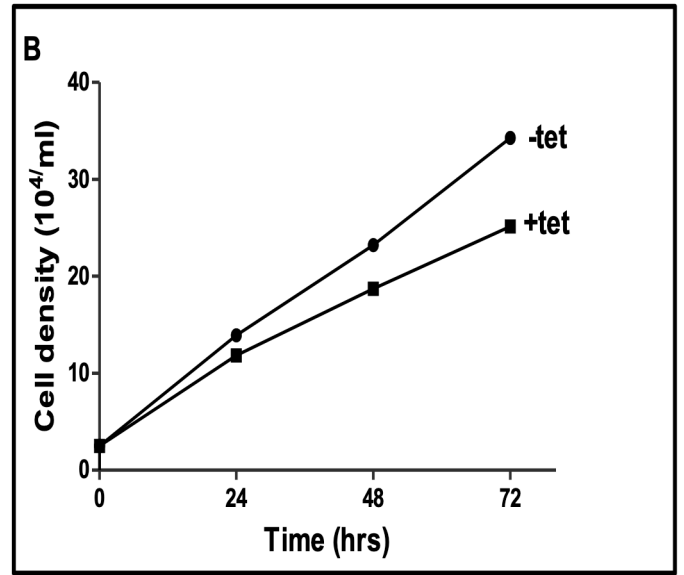
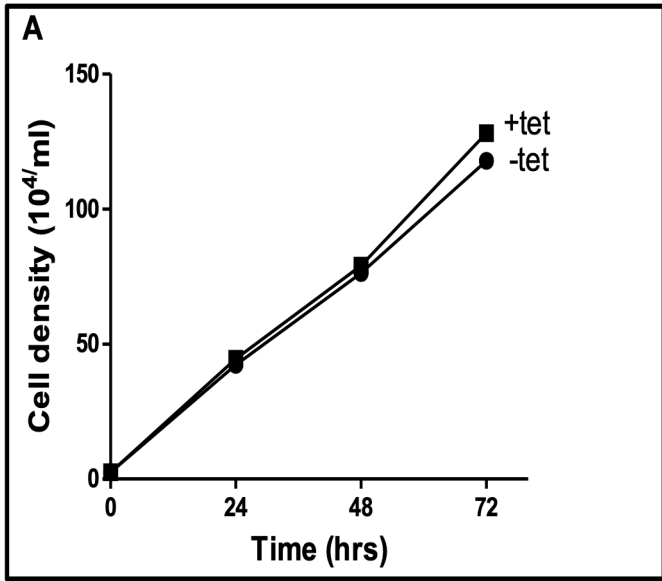
Supplementary Figure 2: Recombinant protein production and analysis on 10 % SDS-PAGE. **A;** Recombinant GST-TcNaa35. **B;** GST-TcNaa38. **C;** GST-TcNaa10 and **D;** GST-TcNaa15. Samples loaded in the different lanes are as follows, Lane1; Molecular mass in kDa. Lane 2; Non-induced (NI). Lane 3; Induced (IND), Lane 4; Pellet (P). Lane 5; Supernatant (Sup). Lane 6; Semi Purified (S/Purified).

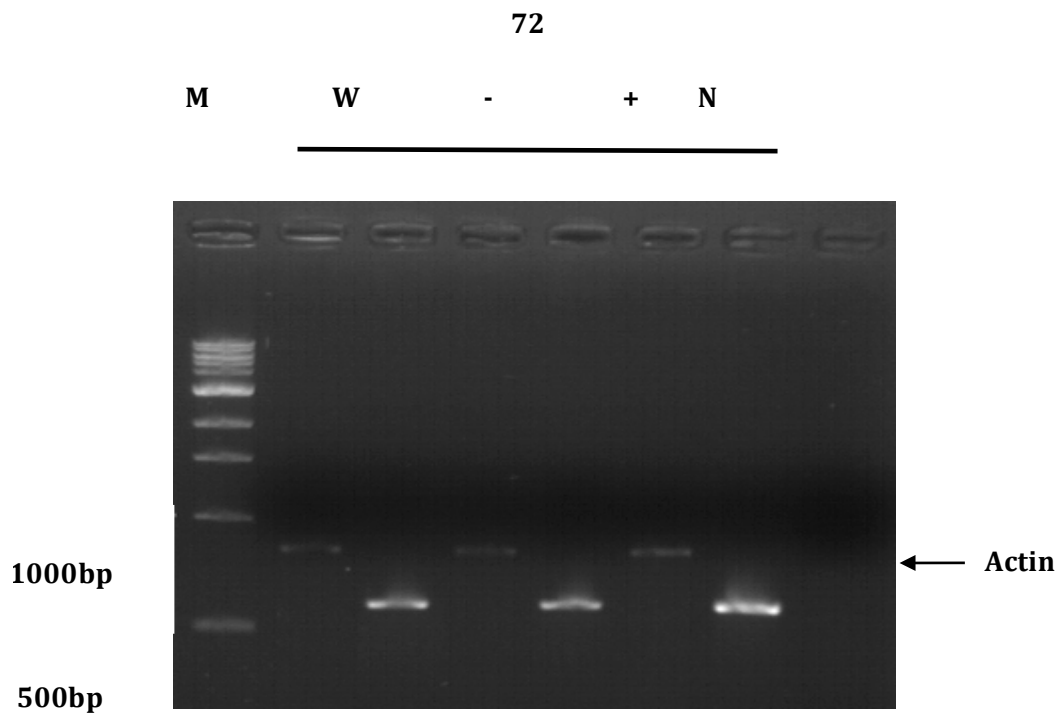
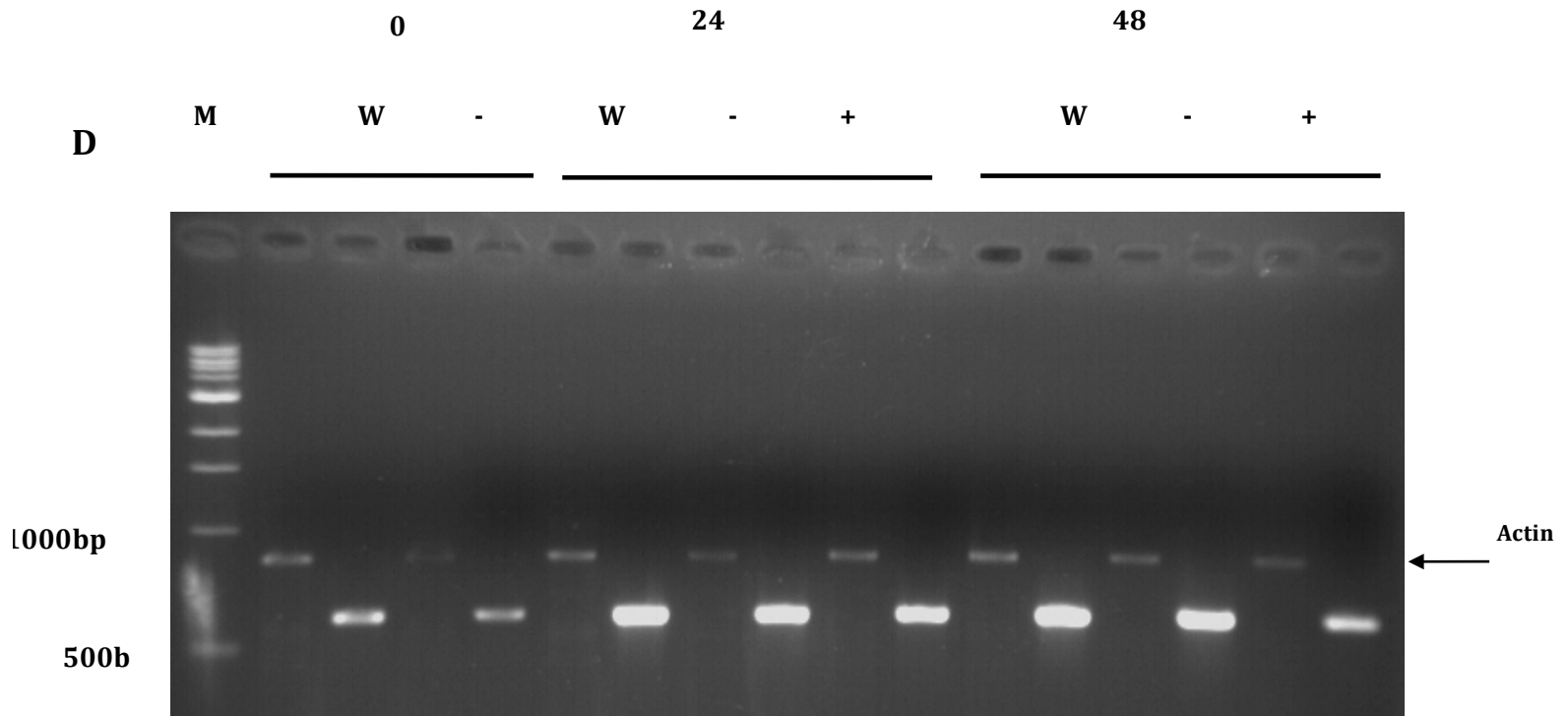


Supplementary Figure 3: Localization of TcNaa38 and TcNaa15. Number 1 to 5 denotes, Midlog epimastigotes, Stationary epimastigotes, Metacyclic trypomastigotes, Trypomastigotes, and Amastigotes, respectively. *T. cruzi* four developmental stages were immunolabelled with, **A**; anti-TcNaa38 and **B**; anti-TcNaa15. The nucleus and kinetoplast were visualized using DAPI stain (N+K), scale bars = 5 μ m.



Supplementary Figure 4: Localization of TcNaa30 and TcNaa38 in internal amastigotes. Parasites were allowed to invade Vero cells and divide. Cells were immunolabelled with anti - TcNaa30 and anti- TcNaa38 (green) and counter labeled with DAPI (blue) to visualize the nucleus and kinetoplast, scale bars = 10 μ M.





Supplementary Figure 5: Phenotype of the knock down of putative *T. brucei* Naa30 by RNAi showing growth curves and mRNA level, **A;** Wild type, **B;** Transfected, **C;** The parasite growth of the transfectants compared to that of the wild type (blue). Cells at a density of 2.5×10^4 /ml were grown in the absence (-**Tet**) or presence (+**Tet**) of tetracycline (100ng/ml) over a period of 72h. The result is a representative of the mean parasite growth of *T. b. brucei* 427 obtained from three independent experiments. **D;** Gene expression analysis of wild type (W), non-induced (-) and induced (+) cells using Reverse Transcriptase PCR. The products were separated on a 2% agarose gel alongside a 1kb DNA ladder and visualized using ethidium bromide staining. Shown is day 0-48h and day 72h post-RNAi induction. Actin (700bp) was amplified as an internal control alongside NatC catalytic subunit (573bp). The cell densities used for Day 0, 24, 48 and 72h from which RNA was isolated were 1×10^5 /ml; 2.73×10^5 /ml; 3.75×10^5 /ml and 4.7×10^5 /ml, respectively.