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Supplemental Information

Mitochondrial Preprotein Translocase

of Trypanosomatids Has a Bacterial Origin

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Supplemental Inventory

Figure S1, related to Figure 1

Figure S2, related to Figure 2

Figure S3, related to Figure 3

Figure S4, related to Conclusion

1
 Trypanosoma brucei
 Trypanosoma cruzi
 Leishmania braziliensis
 Leishmania major
 Serratia proteamaculans
 Yersinia pseudotuberculosis
 Escherichia coli
 Salmonella enterica
 Dickeya zeae

 121
 Trypanosoma brucei
 Trypanosoma cruzi
 Leishmania braziliensis
 Leishmania major
 Serratia proteamaculans
 Yersinia pseudotuberculosis
 Escherichia coli
 Salmonella enterica
 Dickeya zeae

 241
 Trypanosoma brucei
 Trypanosoma cruzi
 Leishmania braziliensis
 Leishmania major
 Serratia proteamaculans
 Yersinia pseudotuberculosis
 Escherichia coli
 Salmonella enterica
 Dickeya zeae

 261
 Trypanosoma brucei
 Trypanosoma cruzi
 Leishmania braziliensis
 Leishmania major
 Serratia proteamaculans
 Yersinia pseudotuberculosis
 Escherichia coli
 Salmonella enterica
 Dickeya zeae

 481
 Trypanosoma brucei
 Trypanosoma cruzi
 Leishmania braziliensis
 Leishmania major
 Serratia proteamaculans
 Yersinia pseudotuberculosis
 Escherichia coli
 Salmonella enterica
 Dickeya zeae

 601
 Trypanosoma brucei
 Trypanosoma cruzi
 Leishmania braziliensis
 Leishmania major
 Serratia proteamaculans
 Yersinia pseudotuberculosis
 Escherichia coli
 Salmonella enterica
 Dickeya zeae

 617
 Trypanosoma brucei
 Trypanosoma cruzi
 Leishmania braziliensis
 Leishmania major
 Serratia proteamaculans
 Yersinia pseudotuberculosis
 Escherichia coli
 Salmonella enterica
 Dickeya zeae

Figure S1.

Figure S1. Multiple Sequence Alignment of ATOM Homologs from Trypanosomatides and YtfM-like Proteins from Bacteria

Analysis was performed using CLUSTAL W (1.83). GI of sequences are 70831434 (*Trypanosoma brucei*), 71659630 (*Trypanosoma cruzi* strain CL Brener), 154345277 (*Leishmania braziliensis*), 72549827 (*Leishmania major* strain Friedlin), 157368706 (*Serratia proteamaculans*), 153948759 (*Yersinia pseudotuberculosis*), 209398307 (*Escherichia coli*), 198243763 (*Salmonella enterica*), 251788425 (*Dickeya zeae*). Colours indicate regions of high (red) and low (blue) homology.

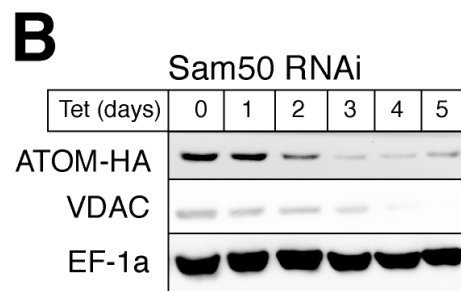
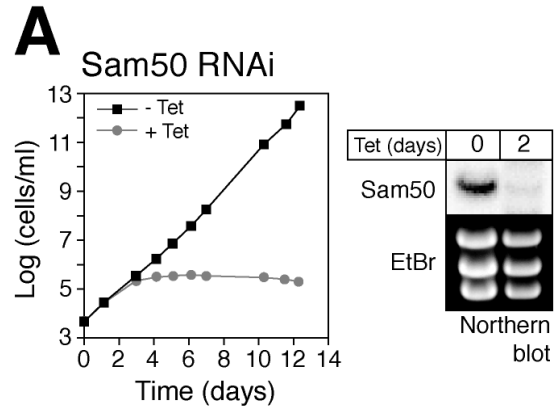


Figure S2. In Vivo Assembly of ATOM Requires Sam50

(A) Growth curve of uninduced and tet-induced Sam50 RNAi cell line. Northern blot indicates efficient ablation of Sam50 mRNA in induced cells. The ethidium bromide (EtBr) stained region of the gel depicting the rRNAs serves as a loading control.

(B) Levels of HA-tagged ATOM (ATOM-HA) and VDAC in total cellular extracts rapidly decline during tet-induction of Sam50 RNAi cells, whereas the levels of elongation factor 1a (EF-1a) are not affected.

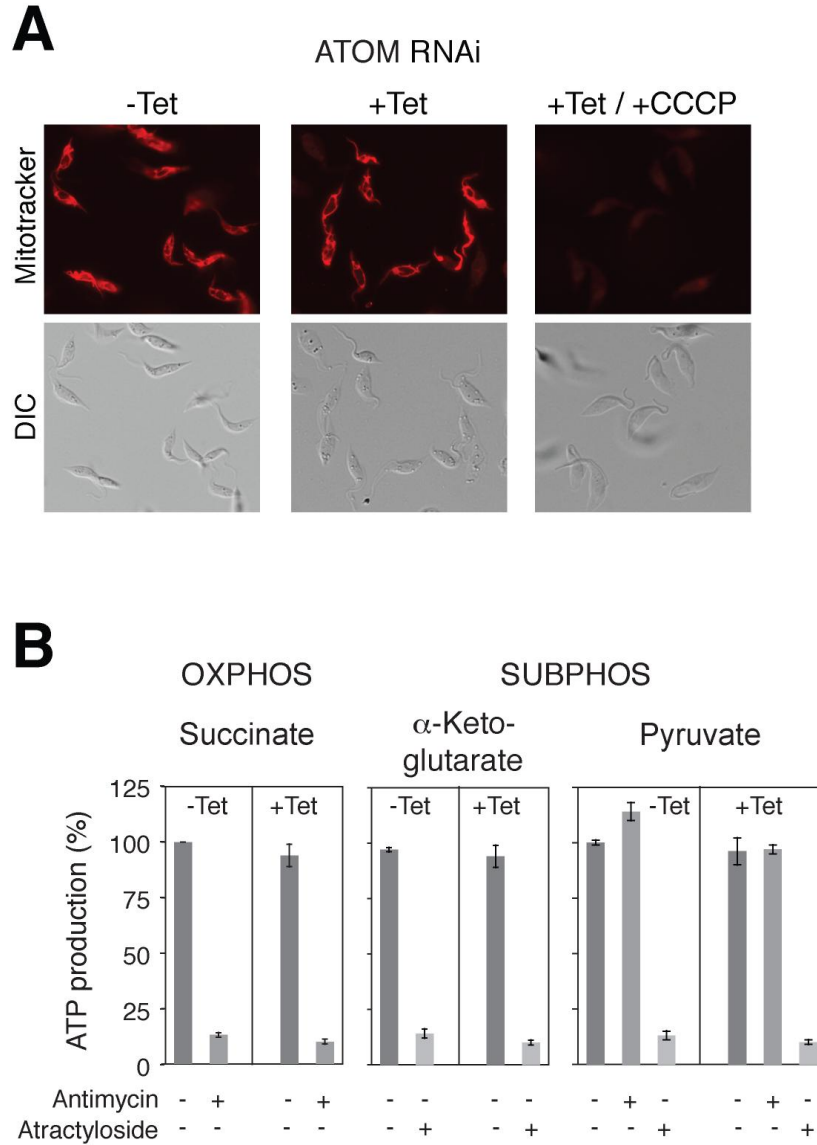


Figure S3. RNAi of ATOM Does Not Induce a General Mitochondrial Dysfunction

(A) Mitotracker staining shows that ATOM RNAi cells (+Tet, 48 hours) have an intact membrane potential. CCCP, carbonyl cyanide m-chlorophenylhydrazone; DIC, differential interference contrast microscopy.

(B) Mitochondrial oxidative (OXPHOS) and mitochondrial substrate level phosphorylation (SUBPHOS) is not affected in induced ATOM RNAi cells (+Tet, 48 hours).

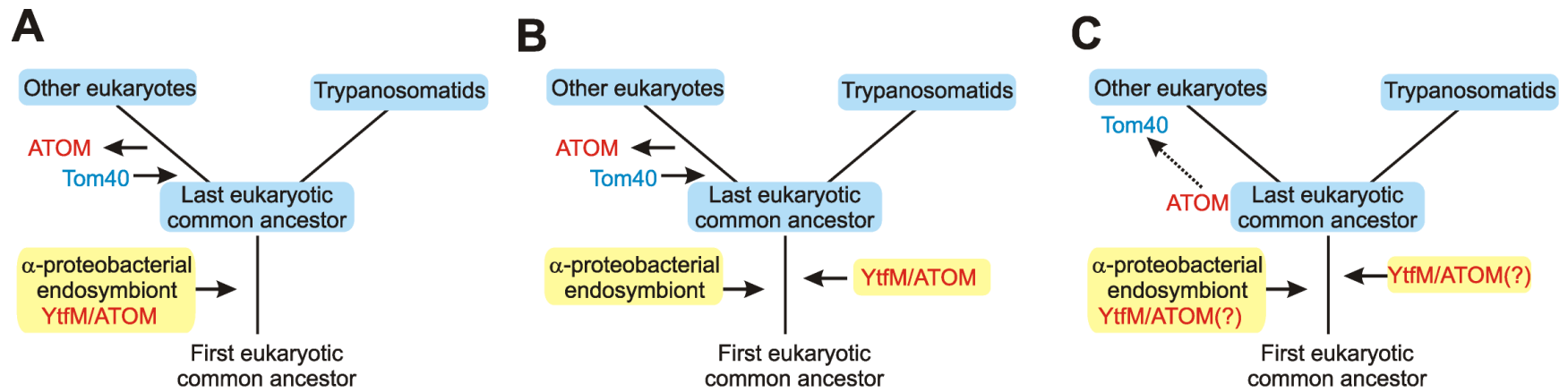


Figure S4. Models for the Evolution of the Mitochondrial Outer Membrane Protein Translocase

(A) YtfM/ATOM-type bacterial protein exporter but not Tom40 were present in the original endosymbiont. The bacterial exporter, adapted to function in reverse, was commandeered for mitochondrial protein import in the last eukaryotic common ancestor and has been retained in the line leading to the trypanosomatids. Tom40 evolved after the ancestor of trypanosomatids diverged from the rest of the eukaryotes. The ATOM in the main branch of eukaryotes was subsequently lost.

(B) As A but ATOM was acquired by horizontal gene transfer and not by the original endosymbiotic event.

(C) ATOM, either acquired by the endosymbiotic event or by horizontal gene transfer, evolved into Tom40 after the trypanosomatids split from all other eukaryotes. Yellow and blue indicate bacterial and eukaryotic evolutionary origins, respectively.