Supplementary data for:

RAB11 FUNCTION IN *TRYPANOSOMA BRUCEI*; IDENTIFICATION OF CONSERVED AND NOVEL INTERACTION PARTNERS

Carme Gabernet-Castello, Kelly N. DuBois, Camus Nimmo and Mark C. Field

Department of Pathology, University of Cambridge, Tennis Court Road, Cambridge, CB2 1QP, UK Running title: Conservation and novelty of Rab11 functions

Address correspondence to: Mark C. Field, Department of Pathology, University of Cambridge, Tennis Court Road, Cambridge, CB2 1QP, UK. Telephone: + 44 (0)1223-333734; Email: mcf34@cam.ac.uk.

Supplementary figure legends

Table S1: Accession numbers for members of the family of Rab11-interacting proteins (FIPs) as retrieved by BLAST analysis and HMM searches of selected genomes. See materials and methods for details of sources of data.

Table S2: Accession numbers for TbAZI1 homologues retrieved from selected genomes. See materials and methods for details of sources of data.

Figure S1: Costaining of trypanosomes for Sec15 and Rab5A. Bloodstream form parasites expressing YFP tagged TbSec15 were fixed and prepared for immunofluorescence analysis using anti-GFP antibody. Location of YFP-TbSec15 compared to location of early endosomes by immunostaining of Rab5A. Left panels, YFP-TbSec15 (green, white arrows), center panels, rabbit polyclonal anti-Rab5A (red). DNA was visualized with DAPI (blue, right panels, merge). Scale bar 2μm.

Figure S2: BD-Rab11QL is expressed in *S. cerevisiae.* AH109 yeast cells transformed with pGBKT7-Rab11QL were grown to mid-log phase. Yeast total cell lysates were fractionated by SDS-PAGE and analysed by Western blotting for expression of Rab11Q66L fused to the binding domain in the yeast two hybrid system, Rab11 antibody was used at a dilution of 1:2000.

Figure S3: Identification of two novel Rab11-interacting proteins by yeast two hybrid screen of a *T. brucei* **genomic library.** Panel A and B: Multiple sequence alignments of RBP74 and TbAZI1 against other kinetoplastid sequences and against the human AZI1 sequence were generated by ClustalW and drawn with ESPRIPT (90). Amino acidic sequences were obtained from geneDB and ncbi. Accession numbers are Tb927.5.1640 and Tc00.1047053506315.80 for RBP74 in *T. brucei* and the *T. cruzi* orthologue; Tb09.211.4830, Tc00.1047053510761.4 and LmF35.1650 for TbAZI1 in *T. brucei* and the orthologues in *T. cruzi* and *L. major*. Strictly conserved residues are in black, boxed residues designate 75% in conservation levels. Underlined are the library fragments of RBP74 and TbAZI1 as returned from the yeast two-hybrid screen.

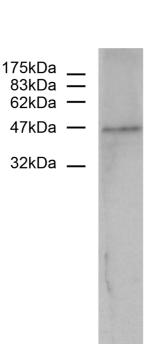
Figure S4: RBP74 RNAi. Panel A: Growth curves of uninduced and induced RBP74 RNAi in triplicate cultures. Panel B: Quantitative real time PCR assay for RBP74 mRNA levels in uninduced and induced RBP74 RNAi cultures. Tubulin was used as a standard. Panel C: ConA and transferrin uptake upon RBP74 knockdown as measured by FACS. Closed bars indicate uninduced cells, open bars indicate induced cells. Panel D: Transferrin recycling in the RBP74 RNAi cell line.

Figure S5: Rab11 is not affected upon TbAZI1 knockdown. Rab11 localization and levels in induced RBP74 RNAi cells (upper panels) and TbAZI1 RNAi cells (lower panels) as measured by immunofluorescence (left panels) and Western blotting (right panels). Scale bars are 2µm.

Figure S6: ConA and transferrin uptake and recycling are not affected by RNAi of TbAZI1. Endocytosis was analysed by measuring ConA (mainly VSG) and transferrin (ESAG6/7-mediated) uptake

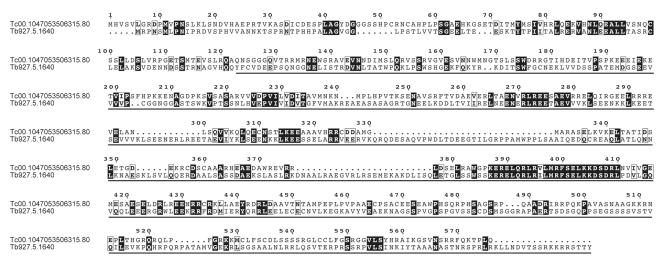
by FACS in uninduced (closed bars) and induced (open bars) TbAZI1 RNAi cells (upper histogram). Transferrin recycling was measured by FACS in TbAZI1 uninduced (solid line) and induced cells (dotted line) (lower graph).

Figure S7: TbAZI1 knockdown does not produce any defects in the staining of the flagellum attachment zone nor in the structure of the paraflagellar rod as visualized by immunofluorescence analysis. Uninduced and induced TbAZI1 RNAi cells were stained for the component A of the paraflagellar rod (PFRA) with L8C4 antibody (upper panels) or the flagellum attachment zone antibody L3B2 (bottom panels). Left, merge of PFR-A or FAZ (red) and DAPI fluorescence (blue); right, phase contrast. Scale bars are 2um.

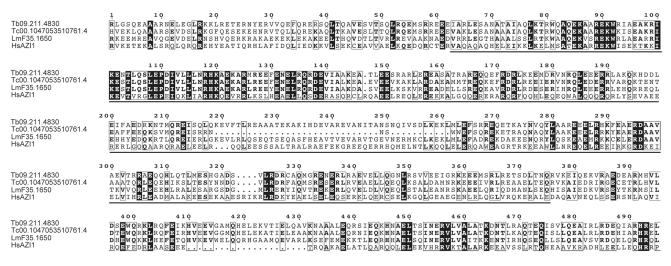


BD-Rab11QL









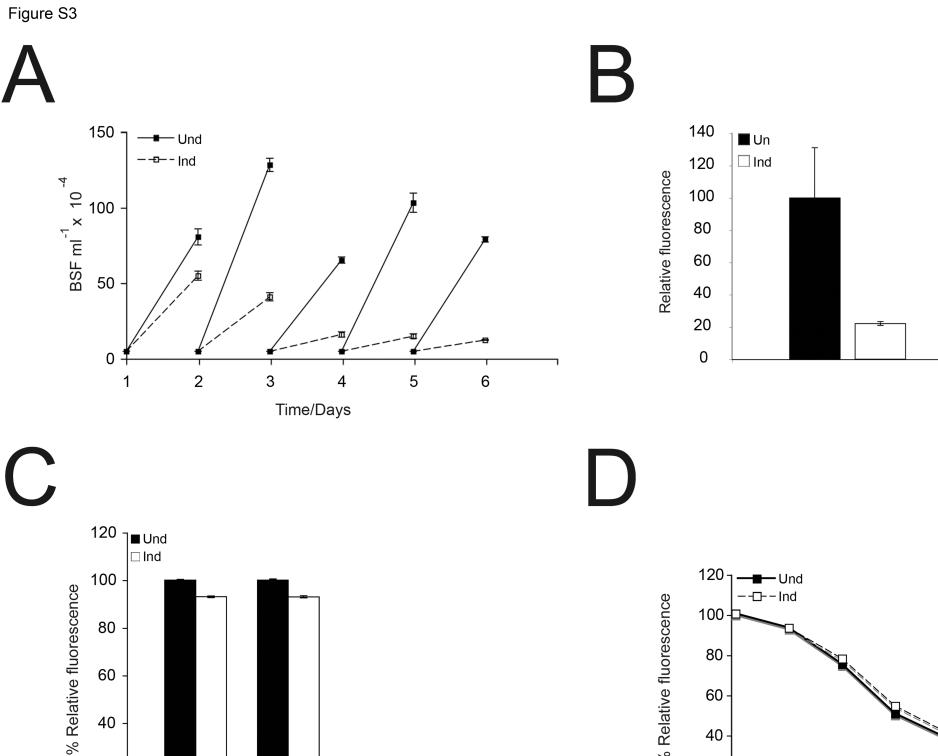
40

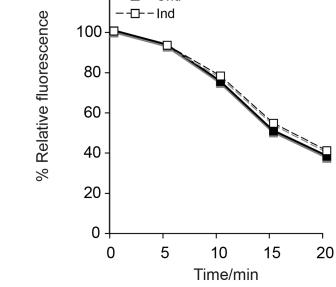
20

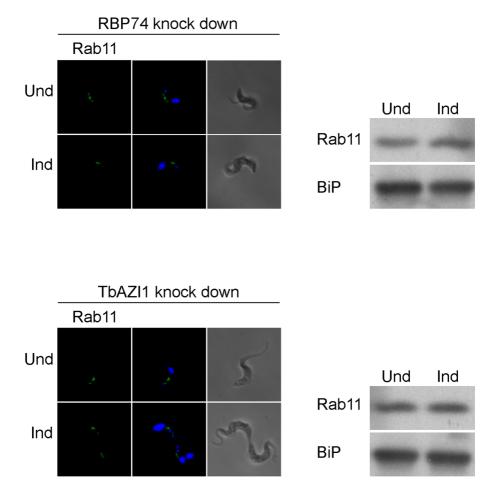
0

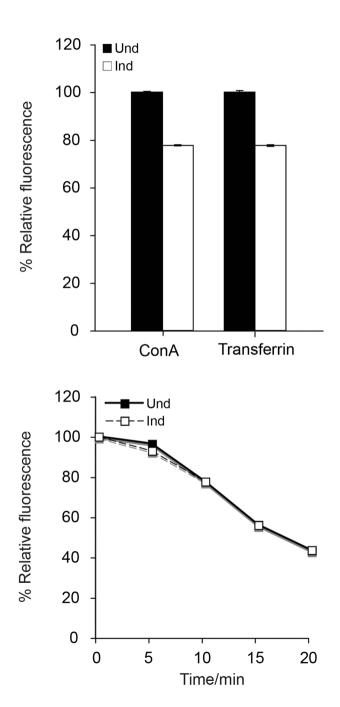
ConA

Transferrin









TbAZI1 knock down PFR Phase Und Ind TbAZI1 knock down **FAZ** Phase Und

Ind

Table S1: FIP family of Rab11 interacting proteins; organisms and access						
		H. sapiens	D. melanogaster	C. elegans		
Class I	FIP1	NP_079427	Rip11-PA	Y39F10B.1a		
	FIP2	NP_055719				
	FIP5/Rip11	NP_056285				
Class II	FIP3	NP_055515	Nuf-PA	Q20813		
	FIP4	NP_116321				
_	RAB6IP2	NP_829883	BrpD	CE28392		
		_	•			

on numbers	
N. vectensis	M. brevicollis
>jgi Nemve1 244614 estExt_fgenesh1_pg.C_1280020	>jgi Monbr1 35581 estExt_fgenesh1
	>jgi Monbr1 33287 estExt_fgenesh2
	>jgi Monbr1 10784 fgenesh1_pg.sca

Table 32. Organis	ms and accession numbers for AZI	Thomologues	
Lineage	Taxon	Accession number	
Metazoa	Homo sapiens	NP_055799.2	
	Drosophila melanogaster	CG1625-PA	
	Caenorhabditis elegans	-	
	Nematostella vectensis	jgi Nemve1 245298 estExt_fgenesh1_pg.C_1540001	
Fungi	Batrachochytrium dendrobatidis	BDEG_03563.1	
	Saccharomyces cerevisiae	-	
	Cryptococcus neoformans	-	
Amoebozoa	Dictyostelium discoideum	-	
	Entamoeba histolytica	-	
Plantae	Arabidopsis thaliana	-	
	Chlamydomonas reinhardtii	jgi Chlre3 148926 Chlre2_kg.scaffold_23000076	
	Ostreococcus tauri	-	
	Cyanidioschyzon merolae	-	
	Thalassiosira pseudonana	-	
	Phytophthora ramorum	>jgi Phyra1_1 80449 fgenesh1_pg.C_scaffold_49000055	
Chromalveolata	Paramecium tetraurelia	>GSPATP00027365001	
	Plasmodium falciparum	-	
	Toxoplasma gondii	20.m03921	
	Eimeria tenella	GLIMMERHMM190_V3.0.1_PHASES00000215796	
	Cryptosporidium parvum	-	
	Theileria parva	-	
	Tetrahymena thermophila	3720.m00056	
Kinetoplastida	Trypanosoma brucei	Tb09.211.4830	
	Trypanosoma cruzi	Tc00.1047053510761.4	
	Leishmania major	LmjF35.1650	
	Naegleria gruberi	-	
	Trichomonas vaginalis	-	