



S1.



S2.





































CTR1



KDa 100

63

35

25



Fig5G

WCL

Infected

KDa 100

63

35

25

Uninfected -

GAPDH \_\_\_\_\_ 37

Biotin pull-down

ninfected

CTR1

Infected

1 1.42 200 

-1.31

1.9

Biotin pull-down WCL Uninfected > Uninfected Infected Infected

+ -

KDa 100

63

35 25

37





35

63





-					
	-	-	-		-
				8111	
2					

ATP7A

CTR1

α-Tubulin













FigS4













## Supplementary figures

#### Figure S1.

(A) Representative immunofluorescence image of ATP7A (green), co-stained with Golgi marker GM130 (magenta), in J774A.1 macrophages with no treatment, high copper (100  $\mu$ M Cu) and copper chelated conditions (25  $\mu$ M TTM) treatment for 2 hours. The merged images represent colocalization of ATP7A with GM130. The scale bar represents 5  $\mu$ m. (B) ) Fraction of ATP7A colocalization with GM130 from the above mentioned conditions is plotted. Asterisks indicate values that are significantly different from Basal samples. Sample size of macrophage (n): 13. \*\*\*\*p  $\leq$  0.0001, ns; (Wilcoxon rank-sum test).

# Figure S2. Determination of parasite load and copper content of macrophage upon *Leishmania* infection and *Leishmania*-specific modulation of host ATP7A

(A) Leishmania load was determined by C<sub>t</sub> values of *L.major* kDNA at indicated time points after infection of J774A.1 macrophages and normalised against 3 hour infection. Error bars represent mean  $\pm$  SD of values calculated from three independent experiments. Asterisks indicate values that are significantly different from 3hr Infection samples. \*\*p  $\leq$  0.01, \*\*\*p  $\leq$  0.001, ns; (Student's t test). (B) Measurement of intracellular copper level using ICP-MS at the above mentioned condtions. Error bars represent mean  $\pm$  SD of values calculated from three independent experiments. Asterisks indicate values that are significantly different mean  $\pm$  SD of values calculated from three independent experiments. Asterisks indicate values that are significantly different from Uninfected samples. \*p  $\leq$  0.05, \*\*p  $\leq$  0.01, ns; (Student's t test). (C) Immunoblot of ATP7A of J774A.1 macrophages with and without 3 hour infection and indicated treatment conditions. GAPDH is used as housekeeping control.

## Figure S3. No crossreactivity of host specific antibodies with Leishmania proteins

Immunoblot of ATP7A, CTR1, Clusterin and GAPDH from J774A.1 and *L. major* probed using host specific antibodies, representing lack of crossreactivity of host specific antibodies with *Leishmania* proteins.

## Figure S4. Confirmation of knockdown of host copper regulators via siRNA

Immunoblots of ATP7A, CTR1 and ATOX1 after treatment of J774A.1 macrophages with scrambled siRNA and ATP7A, CTR1 or ATOX1 siRNA respectively, confirming siRNA-mediated knockdowns. GAPDH is used as housekeeping control.

#### Fig S5. CTR1 endocytosis is not triggered by latex phagocytic beads

Immunofluorescence image of CTR1 (green) in J774A.1 macrophage with FluoSpheres<sup>™</sup> Carboxylate-modified Microsphere beads (magenta) confirming absence of endocytosis of CTR1 due to general phagoscytosis triggered by the beads. Macrophage nuclei is stained with DAPI (blue).

# Fig S6. ATP7A and CTR1 of peritoneal macrophages are modulated by *L.major* infection. Optimal treatment of copper and TTM changes mice copper content without side effects, while *Leishmania* infection does not alter expression copper regulators in intestine, brain, spleen and kidney

(A) Immunoblot of ATP7A and CTR1 from thioglycollate elicited peritoneal macrophages from BALB/c mice with or without *L.major* infection for 3 hours. The fold changes of ATP7A and CTR1 glycosylated monomer abundance normalized against housekeeping control  $\alpha$ tubulin have been mentioned. Measurement of (B) whole serum copper of BALB/c mice, (C) Ceruloplasmin level representative of serum bioavailable copper, normalised to that of the untreated mice and (D) Haemoglobin levels, 4 weeks post initiation of respective treatments to simulate different copper conditions. Error bars represent mean  $\pm$  SD of values. Asterisks indicate values that are significantly different from Untreated samples. Sample size (n): 6 for each condition,  $*p \le 0.05$ ,  $***p \le 0.001$ , ns; (Student's t test). (E) Immunoblot of ATP7A and CTR1 from intestine, brain, spleen and kidney of infected and uninfected mice. The fold changes of ATP7A and CTR1 glycosylated monomer abundance normalized against housekeeping control  $\alpha$ -tubulin have been mentioned.

## Fig S7. Uncropped blots

Uncropped blots are indicated to their corresponding figures. The same GAPDH loading control was used for the infected samples in Fiure 2G and Figure 2F. GAPDH loading control is same for Figure 2A and 4E where same conditions were used to check the protein levels of ATP7A and CTR1.

Primer	Primer Sequence (5'- 3')
ATP7AFP	GAAGAGGTCGGACTGCTGTC
ATP7ARP	CCTTAGTAATGCCAACCTGAGAAGC
CTR1FP	CAAGATAGCCCGAGAGGGTC
CTR1RP	GATGTGCAGCACTGTCTGC
COMMD1FP	CAAGATAGCCCGAGAGGGTC
COMMD1RP	GATGTGCAGCACTGTCTGC
ClusterinFP	AGGAAAAGCCGTGCGGAAT
ClusterinBP	GCCTGGAGACATGTGGAGTT
mGAPDHFP	CGTGCCTGGAGAAACC
mGAPDHRP	TGGAAGAGTGGGAGTTGCTGTTG
kDNA_FP	AAGGGTGAACGCCAAAAACG
kDNA_RP	GTTCGGTTAATCCGCGAACG

## Table S2.

Antibody Name	Туре	Catalog Number
Rabbit Anti-ATP7A antibody	Primary	Abcam ab13995
Rabbit Anti-CTR1 antibody	Primary	Abcam ab129067
Rabbit Anti-COMMD1 antibody	Primary	Abcam ab102794
Rabbit Anti Clusterin Beta Chain antibody	Primary	Abcam ab184099
Rabbit Anti-GAPDH antibody	Primary	BioBharati BB-AB0060
Mouse Anti-Lamp1 antibody	Primary	DSHB H4A3
Mouse Anti-alpha 1 Sodium Potassium ATPase antibody	Primary	Abcam ab7671
Rabbit Anti-Tubulin alpha antibody	Primary	Affinity Biosciences AF7010
Anti-rabbit IgG, HRP-linked Antibody	Secondary	CST#7074
Anti-mouse IgG, HRP-linked Antibody	Secondary	CST#7076
Donkey Anti-Rabbit Alexa488	Secondary	Life Technologies A-21206
Donkey Anti-Mouse Alexa568	Secondary	Life Technologies A-11057