

**Supplementary information for:**

**The single ENTH domain protein of trypanosomes; functional and evolutionary relationship with the epsins**

Carne Gabernet-Castello, Joel B. Dacks and Mark C. Field\*

Department of Pathology, University of Cambridge, Tennis Court Road, Cambridge, CB2 1QP, UK

**\*Corresponding author:** Telephone; + 44 (0)1223-333734, email; mcf34@cam.ac.uk, skype; mfield34

**Legends to supplementary figures and tables**

**Table S1: Accessions for Epsin and EpsinR candidates retrieved from various databases and as used in the phylogenetic analysis.** See methods for sources of these data.

**Figure S1: Phylogenetic analysis of Epsin/EpsinR families.** The topologies generated from three different algorithms are shown; A; MrBayes, B; RaxML and C; PhyML. In each case numbers against the internodes indicate statistical support, either posterior probability (A) or bootstrap values (B and C).

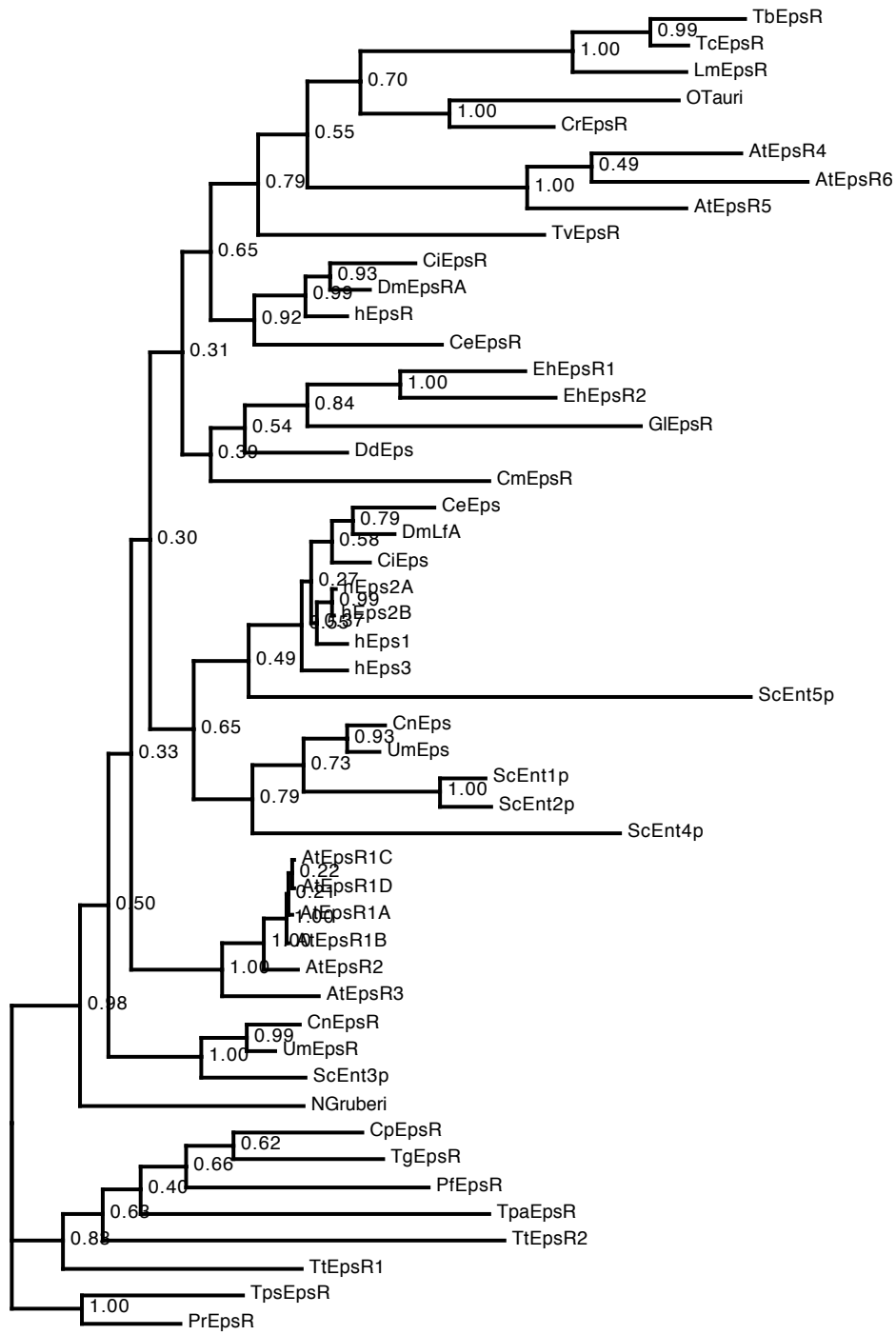
**Figure S2: TbEpsinR antibody verification.** BSF cell lysate and purified recombinant GST-TbEpsinR from *E.coli* were fractionated by SDS-PAGE in duplicate, and analysed by Western blotting with anti-TbEpsinR antibody (left panels), or anti-TbEpsinR antibody pre-incubated with recombinant purified GST-TbEpsinR (right panels). Note that the signal is lost when the antibody is preincubated with the recombinant protein.

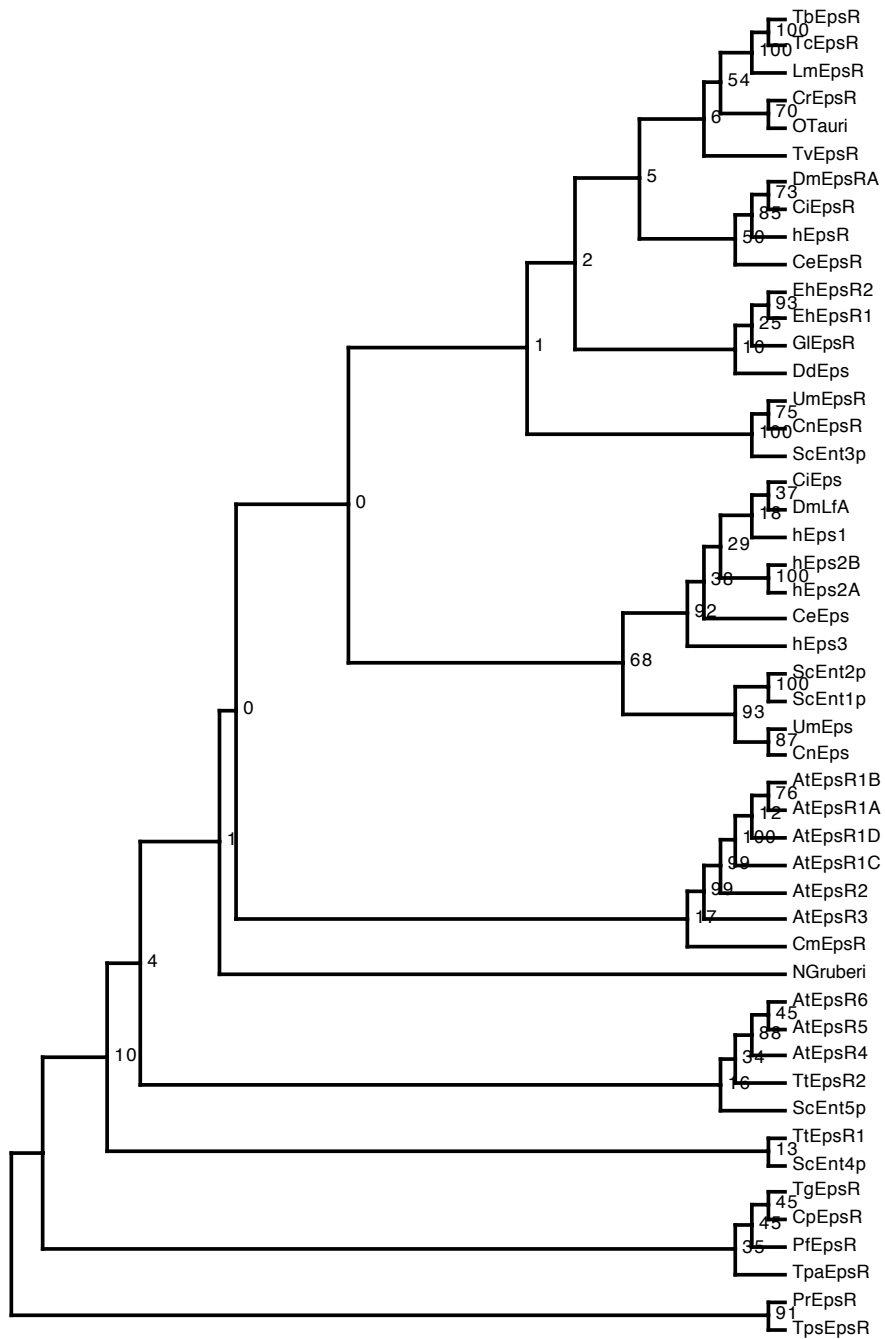
**Figure S3: Absence of morphological abnormalities following TbRab5A RNAi.** Cells were induced for RNAi of TbRab5A as described in methods. Cells were prepared for thin section transmission EM as described (25). Scale bars are 2 $\mu$ m (panel A) and 5 $\mu$ m (panels B - D). Apart from the apparent compression of internal membrane-bound compartments, there is no evidence for proliferation, enlargement or other abnormal endosomal structures under these conditions.

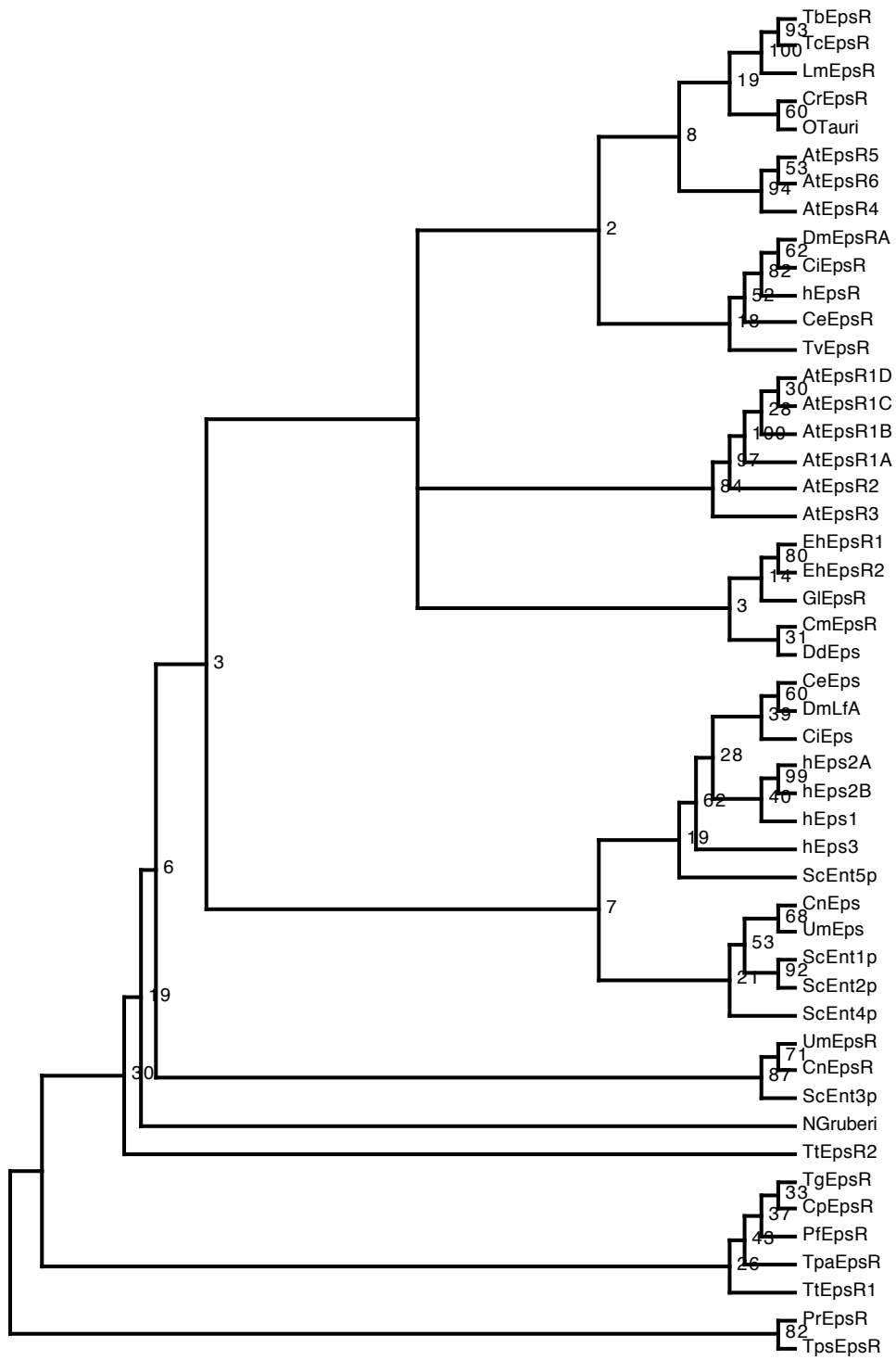
**Figure S4: TbEpsinR expression levels in TbRab5A RNAi cells.** TbRab5A RNAi was induced in cells with 1 $\mu$ g ml<sup>-1</sup> tetracycline for 24h and whole cell lysates analyzed by Western blotting for TbEpsinR and TbRab5A. TbBiP was used as a loading control. Histograms show quantitation of total protein, filled bars are expression levels in uninduced cells and open bars levels in induced cells.

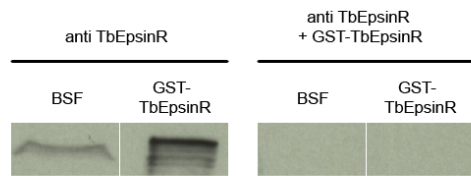
**Figure S5: Cell-cycle analysis of TbEpsinR knockdown cells.** p2T7•TbEpsinR cells were induced for 24h with tetracycline, fixed with 4% paraformaldehyde and stained with DAPI. Panel A: To determine position in the cell-cycle, the numbers of nuclei and kinetoplasts per cell were counted for at least 200 cells for uninduced and induced cultures. Panel B: Light microscopy was used to determine incidence of cells with abnormal morphologies and cells presenting the Big Eye phenotype; at least 200 cells were counted.

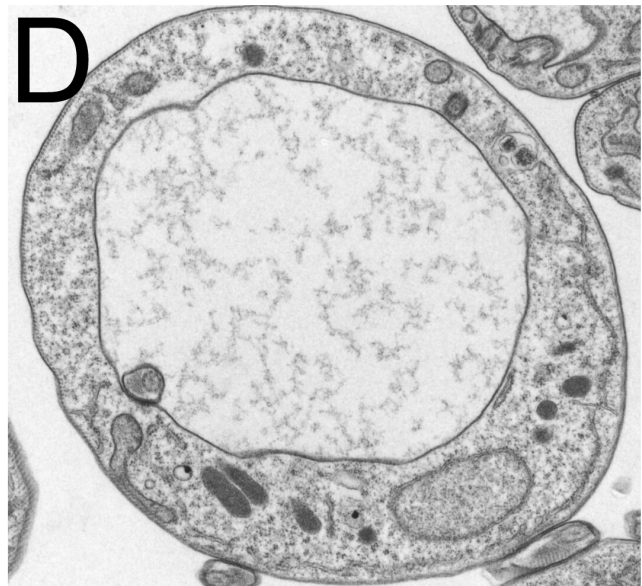
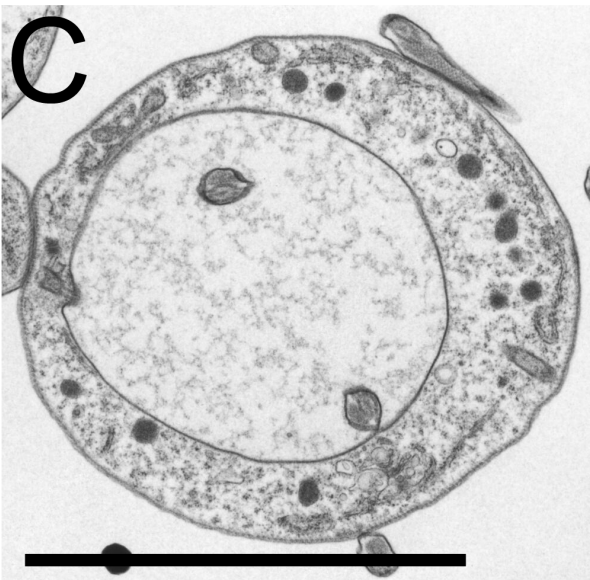
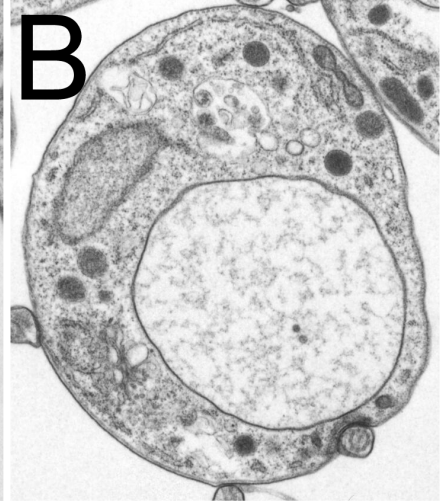
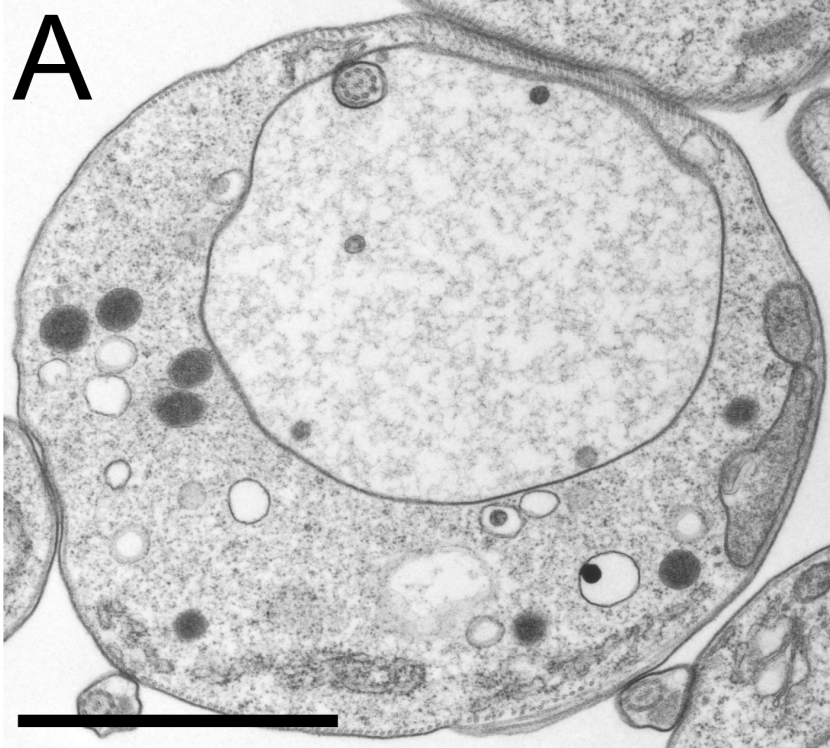
**Figure S6: TbEpsinR protein copy number.** Lysates of 10<sup>7</sup> BSF cells, and aliquots of purified GST-TbEpsinR equivalent to 10<sup>11</sup>, 10<sup>12</sup> and 10<sup>13</sup> copies of recombinant protein, estimated based on protein concentration, were analyzed by Western blotting with anti-TbEpsinR antibody. The TbEpsinR copy number in BSF was estimated to be between 10<sup>4</sup> and 10<sup>5</sup> copies per cell.

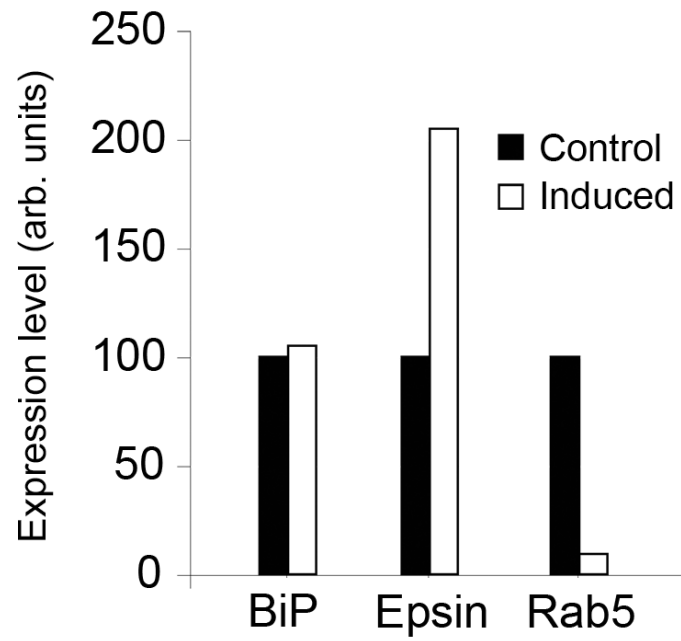
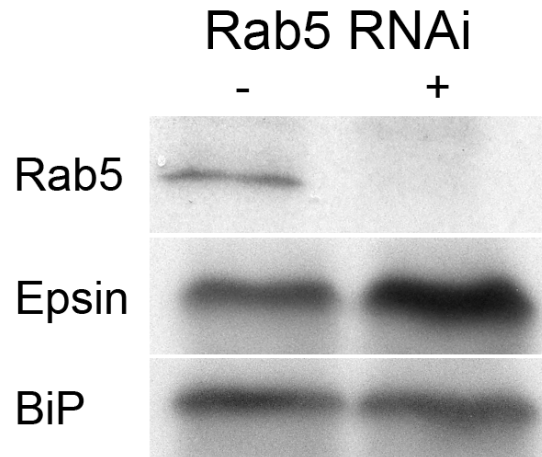






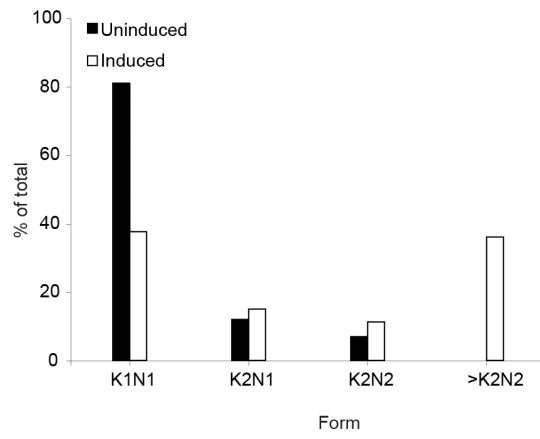








# A



# B

