**Legends to Supplementary Figures**

**Fig. S1.** Restriction endonuclease analysis of *T. musculi* kDNA. (A) Kinetoplast DNA from *T. musculi* is resolved on a 1.0% agarose gel. (B) Restriction endonuclease digestion of *T. musculi* kDNA as analyzed on a 1.0% agarose gel. (C) Computer simulated virtual restriction patterns derived from the complete *T. musculi* maxicircle with the same set of restriction enzymes from (B). Asterisks indicate >4.0 kb-long bands identified both in (B) and (C), and a triangle indicates the band (~5 kb) only present in (B). The marker is DL10000 (Takara, China).

**Fig. S2.** The assembly contigs in *T. musculi.* Themaxicircle is drawn in a linear form, starting from the *12S rRNA* gene. Regions covered by raw reads and the assembly contigs are shown below in green and overlaps at each end are colored in blue.

**Fig. S3.** PCR amplification of *T. musculi* maxicircle DNA using twelve pairs of primers, fragments are analyzed on a 1.0 % agarose gel. The marker is DL10000 (Takara, China). The information on the primers has been summarized in Table S1.

**Fig. S4.** Dot plot comparative analysis of the coding region of *T. musculi* compared with the coding region of *T. lewisi* (A), *T. cruzi* (B) and *T. brucei* (C), respectively. Diagonal lines indicate that the DNA sequences of two compared species are homologous in the corresponding regions (allow 10% indels, 25% mutations and e-value < 1 × 10-5 in alignment). The break regions in seen in the *T. musculi* vs. other Trypanosomatidae species are due to the insertions and deletions in *T. musculi* which are, respectively, marked by blue and orange ellipses.

**Fig. S5.** Circos plots that compare the maxicircles of two species, (A) *T. musculi* (left sequence) and *T. lewisi* (right sequence); (B) *T. musculi* (left sequence) and *T. cruzi* (right sequence); (C) *T. musculi* (left sequence) and *T. brucei* (right sequence). Ribbons inside the circle connect homologous regions (>300 bp), and the colors represent the percent of sequence identity in the range [70%; 100%] in the order yellow, green, and blue. Sequence identity was calculated using BLAST. Recently developed primers (TM1-2 and TL1-3) for distinguishing *T. musculi* and *T. lewisi* were indicated (Hong *et al.*, 2017).

**Fig. S6.** GC percentage graphs of the maxicircle coding regions of *T. brucei* (A)and *T. musculi* (B). The regions where percentage GC content value lie above the dashed lines may likely have RNA editing. Window size is 100 bp.

**Fig. S7.** Diagram of the repeated elements (α, α’, β, β’, γ, γ’, σ) identified by dot plot analysis of DRII.

**Fig. S8.** Circos plots that compare the maxicircles from three *T. cruzi* strains. (A) *T. cruzi* TCC (left sequence) and *T. cruzi* Dm28c(right sequence); (B) *T. cruzi* TCC (left sequence) and *T. cruzi* Y(right sequence); (C) *T. cruzi* Dm28c(left sequence) and *T. cruzi* Y (right sequence). Ribbons inside the circle connect homologous regions (>300 bp), and the colors represent the percent of sequence identity in the range [70%; 100%] in the order yellow, green, and blue. Sequence identity was calculated using BLAST.