Figure S2

Before batch adjustment

L. major

A

L. amazonensis

B

metac
amast4
amast24
amast48
amast72

After batch adjustment

L. major

C

L. amazonensis
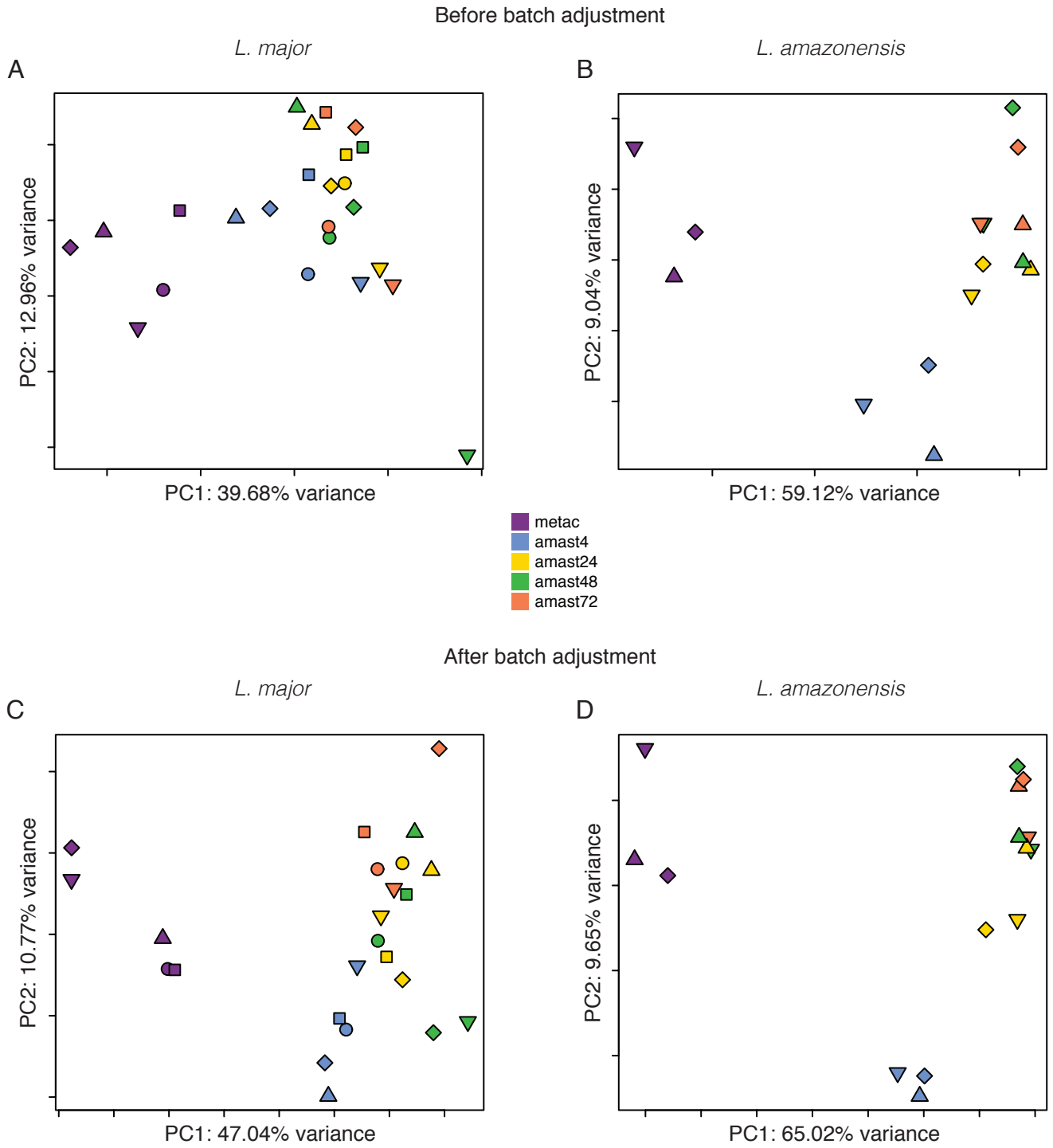
D

Figure S2. Global gene expression profiles of *Leishmania* parasites before and after batch adjustment. RNA-seq was carried out on human macrophages infected with *L. major* or *L. amazonensis* at 4, 24, 48, and 72 hpi as well as on the metacyclic promastigotes used for the infection. Principal component analysis (PCA) plots are shown for *L. major* (**A**, **C**) and *L. amazonensis* (**B**, **D**) transcriptomes over the course of the experiment both before (**A**, **B**) and after (**C**, **D**) including experimental batch as a covariate in the statistical model. The first two principal components are shown on the X and Y axes, respectively, with the proportion of total variance explained by the PC indicated. Each experimental sample is represented as a single point with color indicating sample type/timepoint and shape indicating experimental batch. Samples are named according to sample type ("metac" for metacyclic promastigotes or "amast" for intracellular amastigotes) and time point (4, 24, 48, or 72 hpi). All analyses were performed after filtering out non- and lowly-expressed genes and quantile normalization.