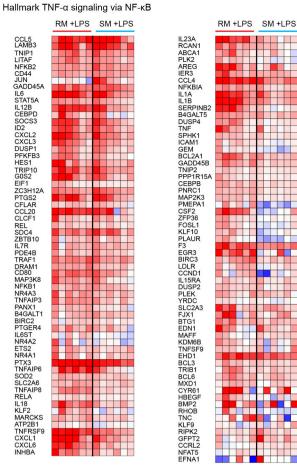
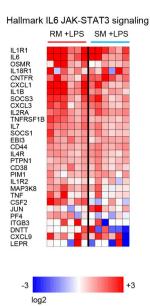
a





b

Extended Data Figure 9 | LPS-mediated induction of TNF and IL-6 inflammatory signalling is globally attenuated in *C. atys.* a, b, Data shown are the leading-edge genes depicted in Fig. 3f, g (GSEA plots), for TNF-signalling genes (a) and IL-6-signalling genes (b). Values are the log<sub>2</sub>-transformed difference between LPS-treated and untreated samples for each individual animal. Genes selected are the combination of leading-edge/core-enriched genes for *M. mulatta* and *C. atys* GSEA analyses for

each pathway. The gene sets selected for enrichment testing were obtained from the MSIGDB database hallmark collection are denoted at the top of each panel. Genes were organized using hierarchical clustering with Spearman dissimilarity and average linkage to estimate distance between genes and clusters, respectively. The colour scale at the bottom denotes the maximum and minimum on a  $\log_2$  scale. For animal study source data, see Supplementary Table 2.