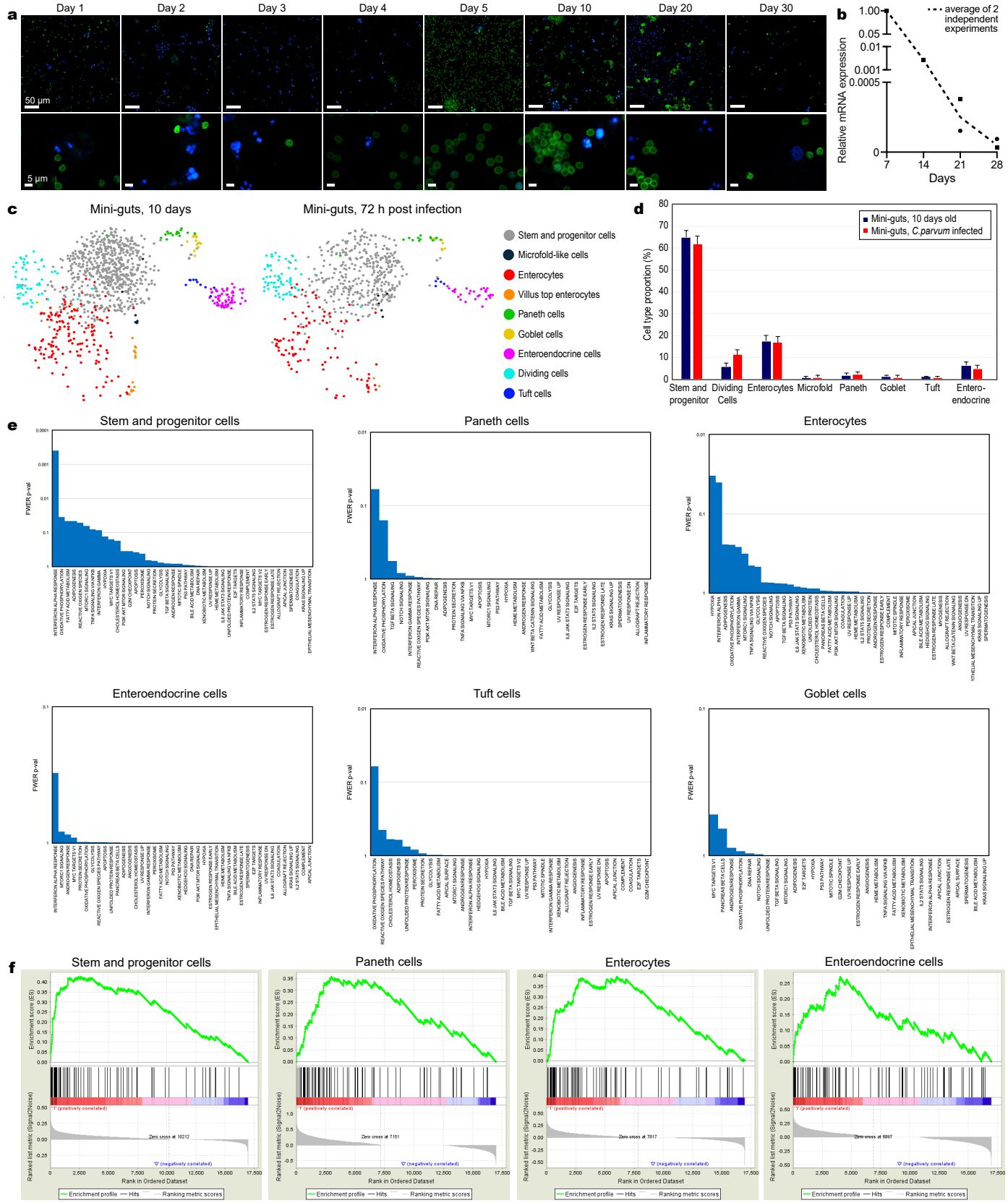

Supplementary Figure 3: Gene expression analyses in mini-gut tubes infected with *C. parvum*. **a**, Fluorescence imaging of oocysts produced de novo in the mini-gut tubes over the course of one month. Crypta-Glo (green) and DAPI (blue) labelling oocyst shells and nuclei, respectively, are shown. Mini-gut tubes were infected with sporozoites and perfused once a day to collect the media from the lumen for detection and quantification of newborn oocysts via immunostaining. **b**, Time-course analysis of *C. parvum* 18S ribosomal RNA expression (measured by RT-qPCR) in infected human small intestinal organoids expanded over several passages (n=2 biologically independent experiments). Organoids were mechanically passaged every 7 days. **c**, Key intestinal epithelial cell types for infected and non-infected mini-guts. **d**, Infected and non-infected mini-guts (at 72 h) exhibited similar cell populations and proportions of cell types. Error bars: 95% confidence intervals as estimated from the theoretical sampling error. **e**, Gene set enrichment analysis for the MSigDB hallmark pathways between infected and control mini-guts by cell type. Family wise error rates (FWER), intrinsically accounting for multiple testing for the 50 MSigDB hallmark gene sets, were computed empirically by comparison to a null-distribution constructed from 10 000 phenotype permutations, with n (individual profiled cells in control / *C. parvum* infected mini-guts) = 625/378 (ISC+TA), 19/15 (Paneth), 169/102 (Enterocytes), 61/30 (Enteroendocrine), 10/5 (Tuft), 14/6 (Goblet). The interferon alpha response stands out in all cell types for which there is sufficient statistical power for accurate testing (i.e. except Tuft and Goblet cells). **f**, Interferon alpha pathway gene enrichment by cell type, highlighting that all epithelial cell types respond to the pathogen, rather than only a subset of specialized cells.