Figure S1. Quantification of the burden of _Pneumocystis_. _dhfr_ gene levels were evaluated by qPCR. Data were determined using interpolation of each Ct in a calibration curve. Data were expressed as mean±SD and were adjusted to 100 ng of total genomic DNA for each sample. All data was analyzed by ANOVA. ns = non-significant; **** = p<0.0001.