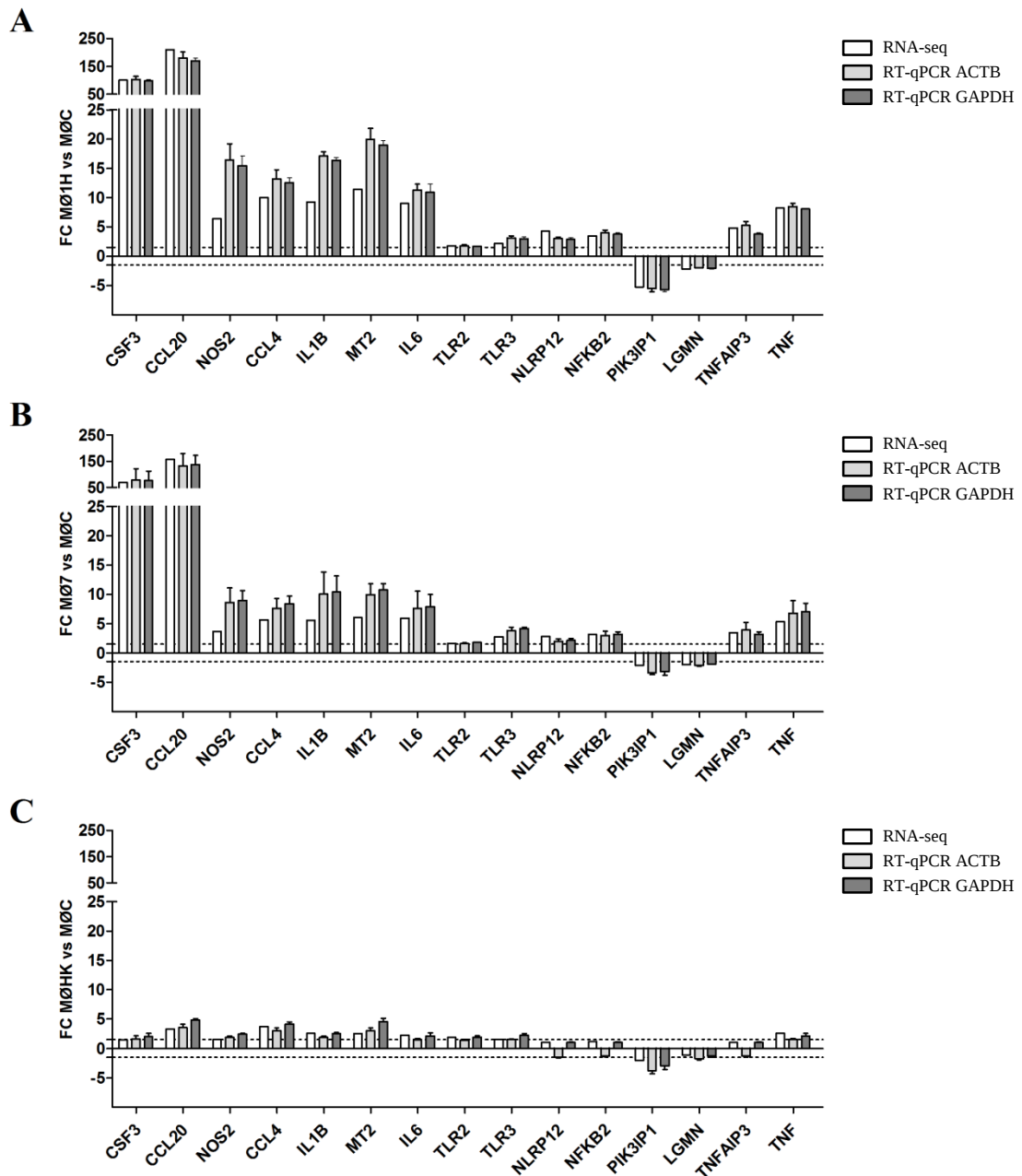




Additional file 8: Figure S1. Transcriptomic validation of RNA-seq analysis by RT-qPCR. Fold changes (FC) in gene expression of *Bos taurus* genes in the comparisons between (A) Nc-Spain1H-infected macrophages (MØ1H) versus non-infected macrophages (MØC), (B) Nc-Spain7-infected macrophages (MØ7) versus MØC, and (C) macrophages inoculated with heat-killed *N. caninum* tachyzoites (MØHK) versus MØC. Gene expression was measured by quantitative real-time PCR (RT-qPCR) and normalized with housekeeping Actin beta (ACTB) and Glyceralde-3-phosphate dehydrogenase (GAPDH). All the differentially expressed genes (FC ≥ 1.5 , delimited by a discontinuous line) showed similar expression profile for both techniques and similar FC for the two housekeepings. Lack of correlation was only observed for three genes expressed by MØHK with FC < 1.5 and normalized with ACTB.