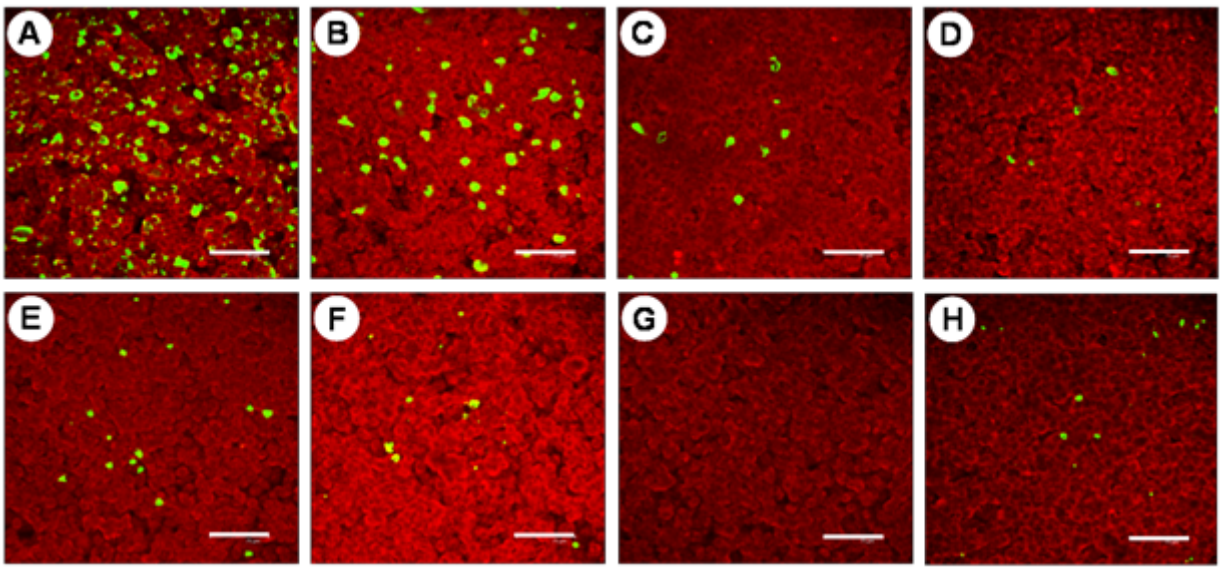
Supplement 1. Primer sequences for quantitative real-time RT-PCR

cDNA target	**Sequence (5' → 3')** [a]	**Accession no.** [b] **or reference**	**Annealing temp.**
GAPDH	**F:** GTCAGCAATGCATCGTGCA	(5)	54 °C
	R:GGCATGGACAGTGGTCATAAGA		
IFN-γ	**F:** CCCGATGAACGACTTGAGAAT	(10)	56 °C
	R: AGACTGGCTCCTTTTCCTTTTG		
iNOS	**F:** GAACAGCCAGCTCATCCGATA	(5)	54 °C
	R: CCCAAGCTCAATGCACAACTT		
IL-1β	**F:** CAGCCAGAAAGTGAGGCTCAA	NM_204524	57 °C
	R: CGCTCATCACACACGACATGTA		
IL-4	**F:** TGACATCCAGGGAGAGGTTTCC	(35)	54 °C
	R: GCTGGCTCTCCCAAACAATTGT		
IL-6	**F:** TTCGACGAGGAGAAATGCCT	NM_204628	56 °C
	R: CGACGTTCTGCTTTTCGCTAT		
IL-8	**F:** AAGGCACTTATGGCCAAGGCT	(10)	55 °C
(CXCL-8)	**R:** ACCGATGTGGAAGGTGGAAGA		
IL-10	**F:** AGGAGACGTTCGAGAAGATGGAT	NM_001004414	56 °C
	R: TCACTTCCTCCTCCTCATCAGC		
IL-12β	**F:** TGGTCCACGCTTTGCAGAT	(5)	54 °C
(p40)	**R:** AAGGTTAAGGCGTGGCTTCTTA		
IL-15	**F:** CGCAATGTATATTCCCGATCCA	NM_204571	56 °C
	R: TTTTCTGACTCTCCGGCCTTC		
IL-17α	**F:** GCTGGATGCCTAACCCAAAA	NM_204460	56 °C
	R: TCGATCCTGTAATCCCATGGA		

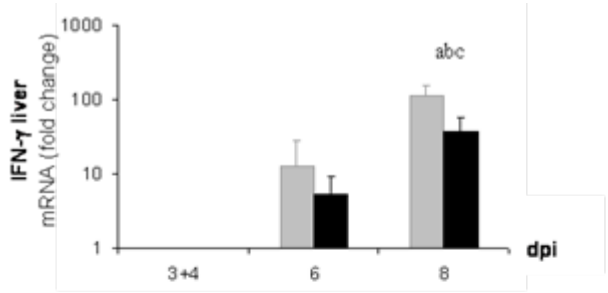
IL-18	**F:** TCTGGCAGTGGAATGTACTTCG	(5)	54 °C
	R: CCATTTTCCCATGCTCTTTCTC		
IL-22	**F:** CTACACCTTGGCTGAAATGGC	NM_001199614	56 °C
	R: TTCATCATGTAGCAGCGGTTG		
LITAF	**F:** GCTGTTCTATGACCGCCCAGTT	(5)	56 °C
	R: AACAACCAGCTATGCACCCCA		
MIP-1β	**F:** TCCTGCTGCTTCACCTACATCT	(5)	59 °C
(CCL4L1)	**R:** ATGAACACAACACCAGCATGAG		
TLR-4	**F:** TTCAAGGTGCCACATCCATACA	(35)	56 °C
	R: AGCGACGTTAAGCCATGGAAG		
XCL1	**F:** AGGAAGCGTTGCAAGTCAGTCA	(10)	56 °C
	R: GCAGACTGCACCCATTTCTGTT		
16S rRNA	**F:** CTTGTACACACCGCCCGTC	(21)	58 °C
	R: GCCCAACCTAGTCAAACCGTC		
cpaf	**F:** CGCACCCTGAGCATCGTTA	(21)	57 °C
	R: AAGACAAAACCCCCAGCTCCT		
ftsW	**F:** TTGTTCCCTGCGTCGCTATC	(21)	57 °C
	R: AAAAGCTATTACGGCTGCGGA		
groEL	**F:** CAACAGGTAGCAGAATCCGGA	(21)	58 °C
	R: CTCTTCGCTGATAAGTTGGCAA		
incA	**F:** CATGTGGAGGAAAGTCGCG	(21)	58 °C
	R: CCCTGATCTGCCGTTTCTGT		
ompA	**F:** GCATTATTGTTTGCCGCTAC;	L39020	56 °C
	R: ATCACCTGAAGCACCTTCCCA		

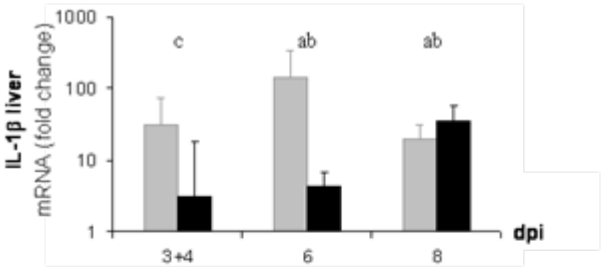
[a] Forward primer (F); reverse primer (R)

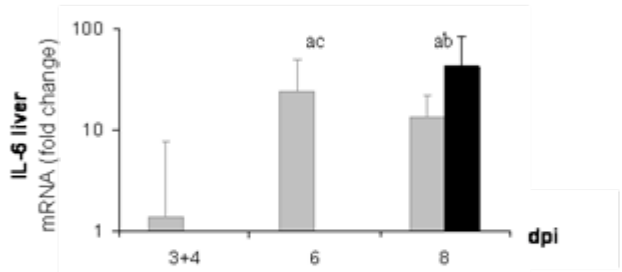
[b] denotes NCBI acc. no. of source sequence

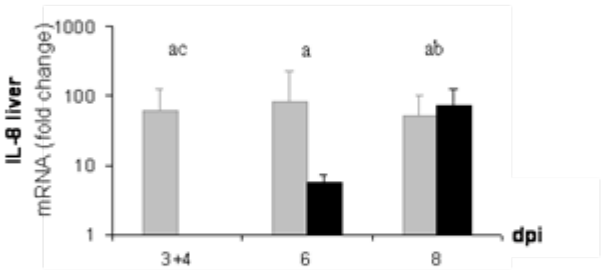


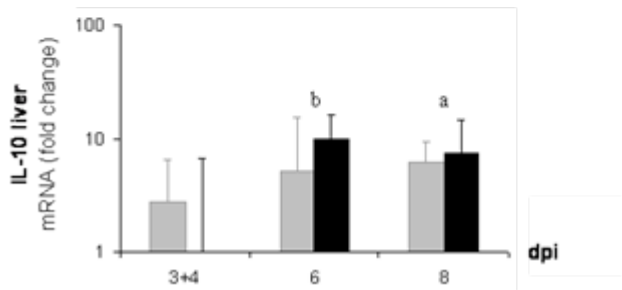
Supplement 2:
Representative confocal laser-scanning micrographs showing recovery of *C. psittaci* and *C. abortus* from infected tissues (CAM and liver), at 44 h of culture in BGM cells (chlamydiae in green, BGM cytoplasm in red, bar = 75 µm).
A-D: recovery of *C. psittaci*, **A:** from CAM at 4 dpi, **B:** from CAM at 8 dpi, **C:** from liver at 4 dpi, **D:** from liver at 8 dpi,
E-H: recovery of *C. abortus*,
E: from CAM at 4 dpi, **F:** from CAM at 8 dpi, **G:** from liver at 4 dpi, **H:** from liver at 8 dpi

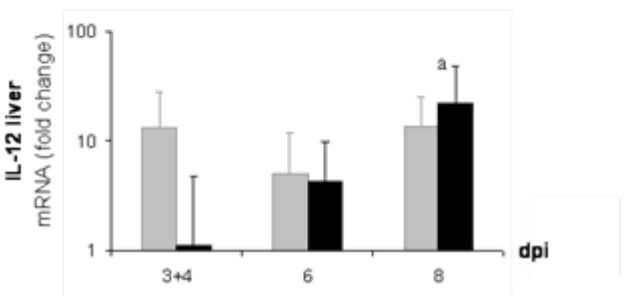


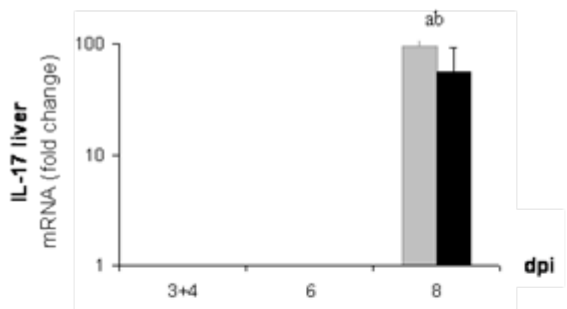


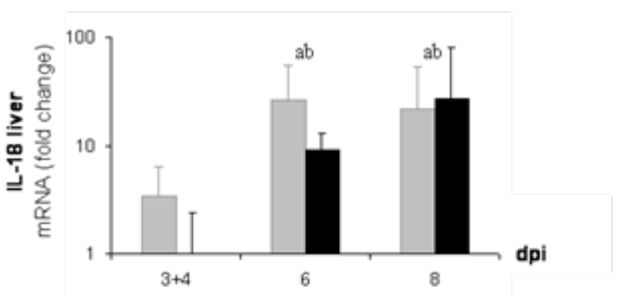


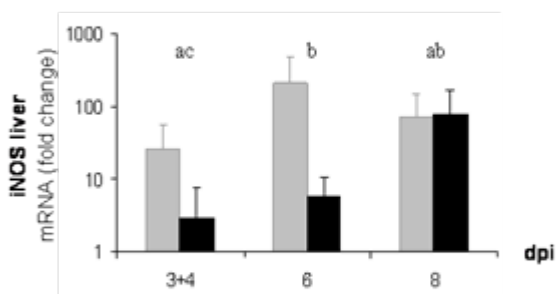


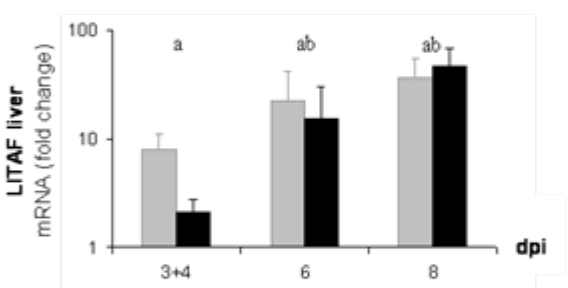


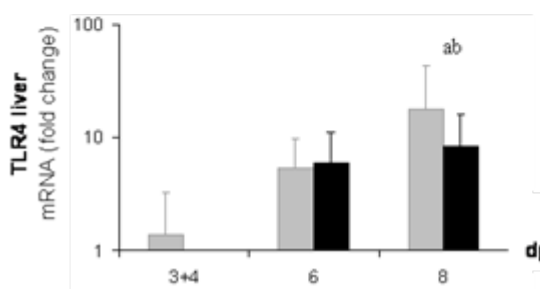












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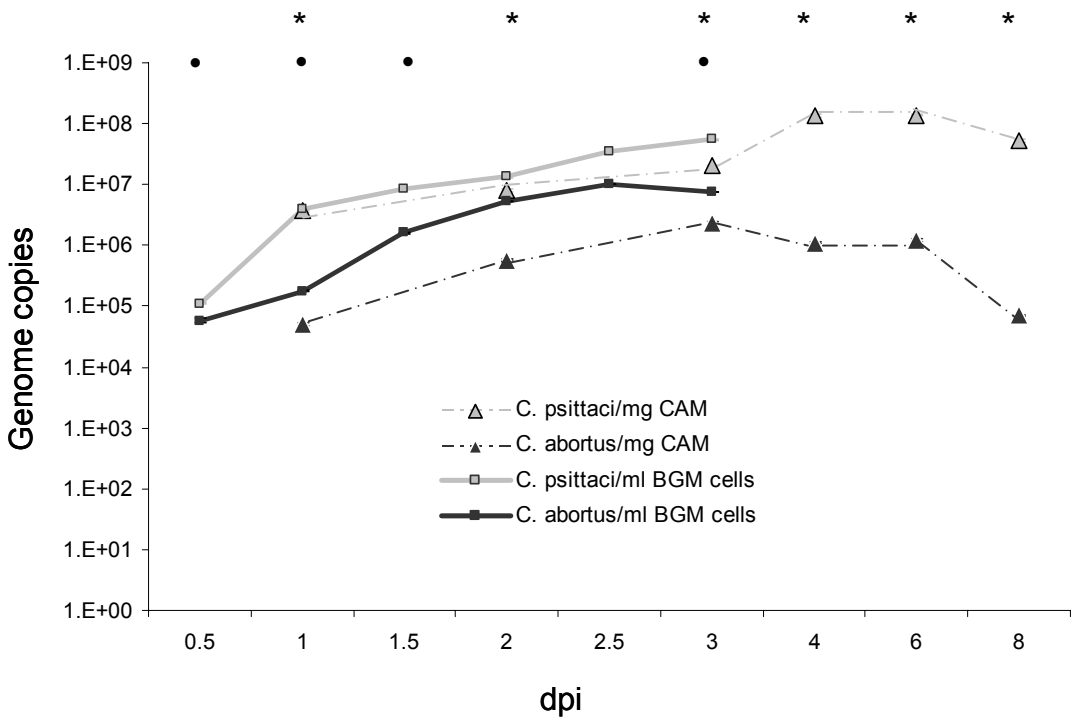
Supplement 3

Supplement 3:
Relative quantification of mRNA expression levels of several immune genes in embryonic liver after infection with *C. psittaci* (■) and *C. abortus* (■) compared to mock infection.
[a, b, c] Means are significantly different ($P \leq 0.05$)
a: *C. psittaci* vs. mock; **b:** *C. abortus* vs. mock; **c:** *C. psittaci* vs. *C. abortus*



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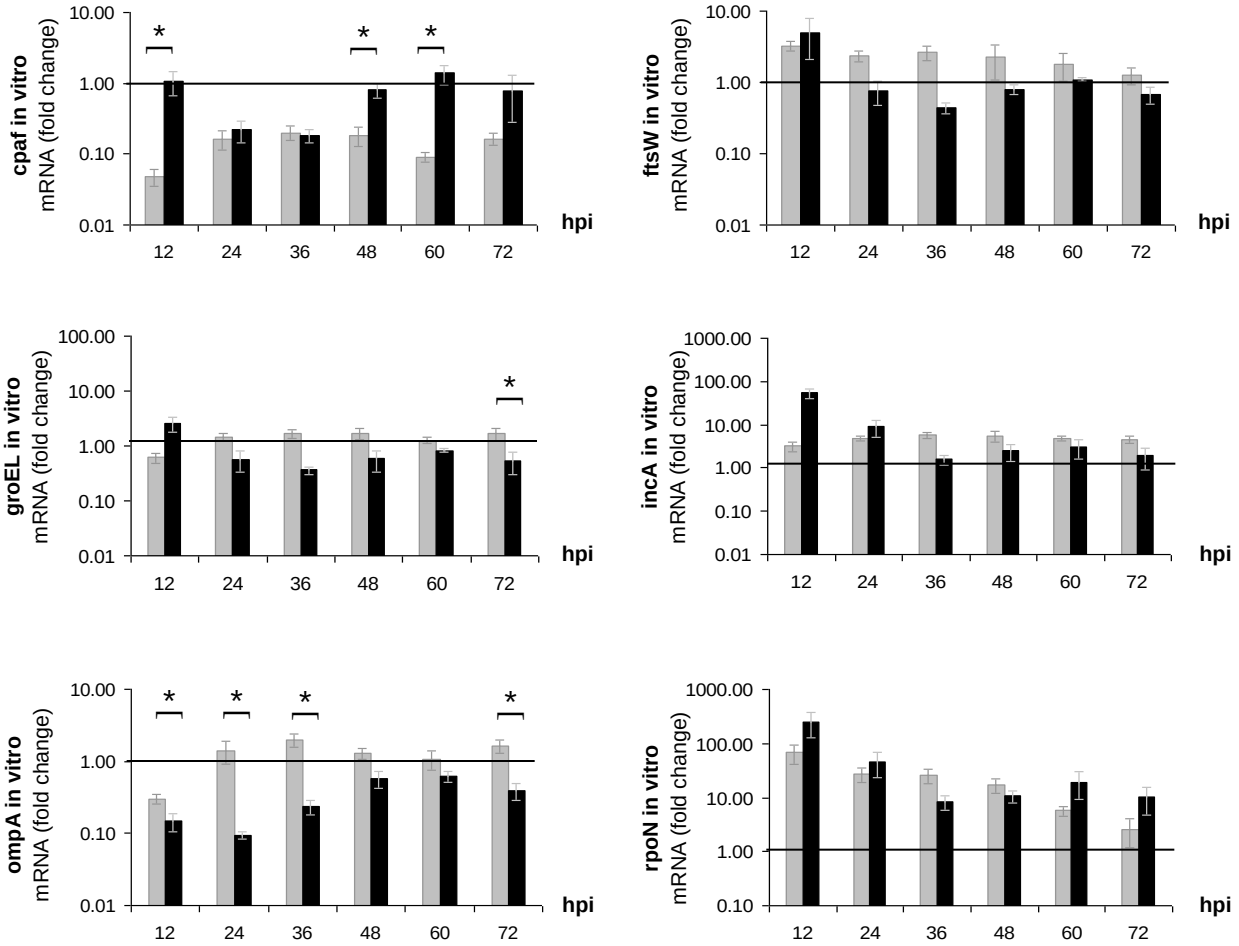
Supplement 4:

Quantitative growth curves for *C. psittaci* DC15 and *C. abortus* S26/3 in CAM of embryonated chicken eggs and BGM cell culture. Genome copies in cell culture were calculated per ml cell suspension, and copy numbers in CAM were calculated per mg tissue.

*; • Medians are significantly different ($P \leq 0.05$) between *C. psittaci*- and *C. abortus*-infected CAM-tissue (*) or *C. psittaci*- and *C. abortus*-infected BGM cell culture (•)(calculated by Mann-Whitney U-test).



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Supplement 5:

mRNA expression levels of essential genes of *C. psittaci* (■) and *C. abortus* (■) in BGM cell culture. Data are presented as fold-changes compared to chlamydial inocula prior to administration.

; * Means are significantly different (*$P \leq 0.05$; ** $P \leq 0.01$) between *C. psittaci*- and *C. abortus*-infected cells (calculated by Mann-Whitney U-test).