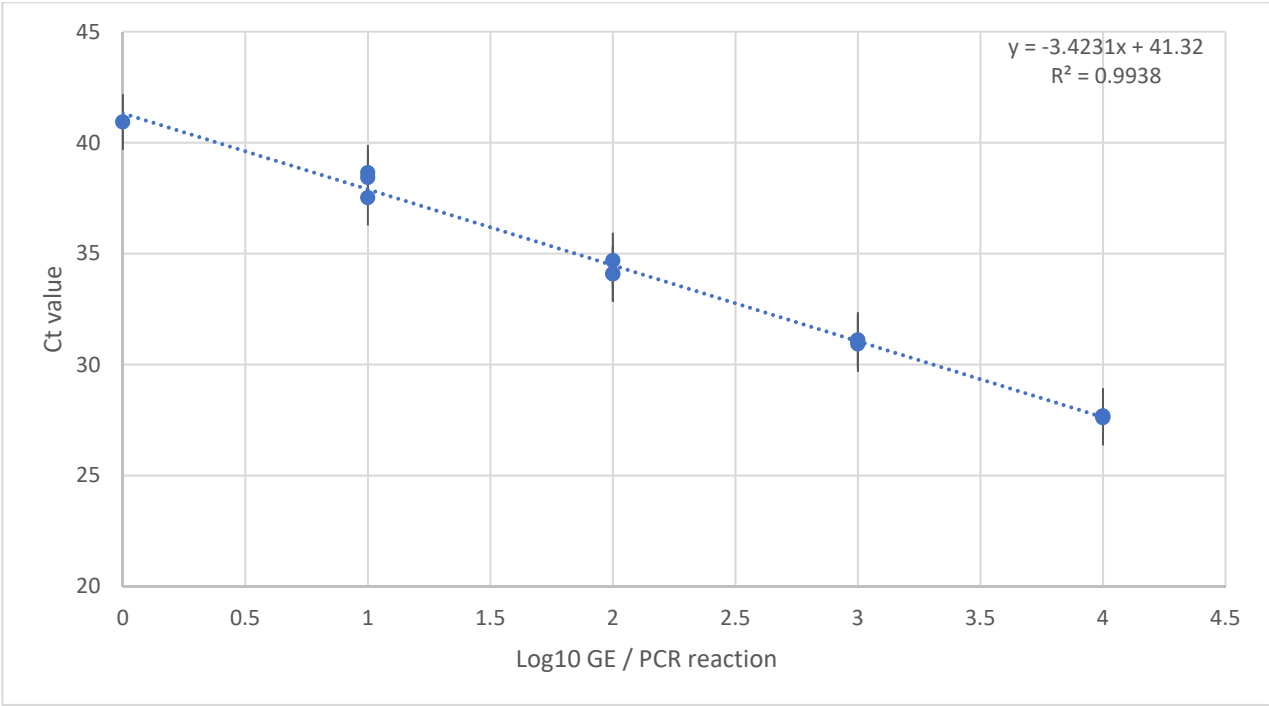


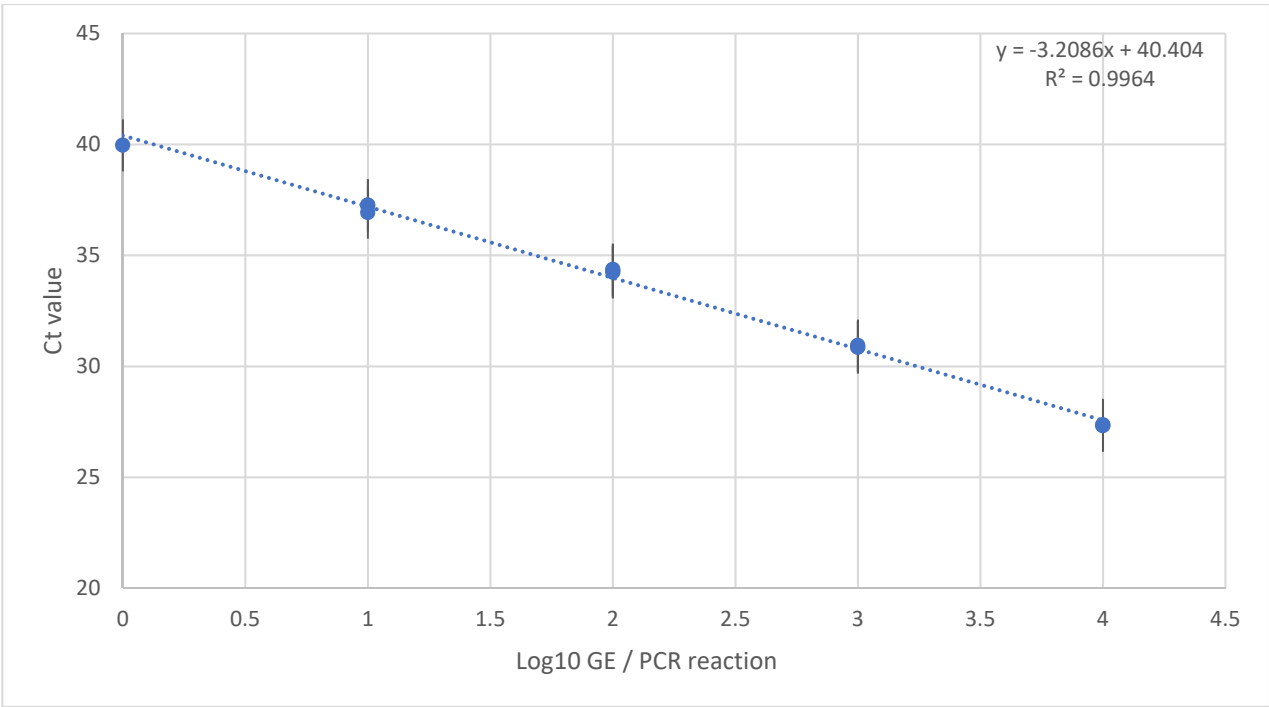
**Table S1.** *Chlamydia* species used to test the specificity of the *enoA*-based *C. psittaci* and *enoA*-based *C. abortus* rtPCRs. Origin of the strains/field isolates: <sup>a</sup>CHU Amiens, France; <sup>b</sup>INRAE Tours, France; <sup>c</sup>Anses Maisons-Alfort, France; <sup>d</sup>Faculty of Veterinary Medicine–Aristotle University of Thessaloniki, Greece; <sup>e</sup>Friedrich-Loeffler-Institut, Germany; <sup>f</sup>vaccine strain; <sup>g</sup>Istituto Zooprofilattico Sperimentale delle Venezie.

Species	Strains/field isolates	<i>C. psittaci</i> rtPCR	<i>C. abortus</i> rtPCR
<i>C. psittaci</i>	Loth <sup>a</sup> , VS1 <sup>b</sup> , L2A <sup>b</sup> , CP3 <sup>b</sup> , GR9 <sup>b</sup> , TT3 <sup>b</sup> , NJ1 <sup>b</sup> , Cal 10 <sup>b</sup> , 13-2791_BC-038 <sup>c</sup> , 13-2791_BC-065 <sup>c</sup>	<b>Positive</b>	Negative
<i>C. abortus</i>	1B <sup>b</sup> , 1H <sup>b</sup> , 1H77 <sup>b</sup> , AB1 <sup>b</sup> , AB2 <sup>b</sup> , AB4 <sup>b</sup> , AB7 <sup>b</sup> , AB7b <sup>b</sup> , AB13 <sup>b</sup> , iC1 <sup>b</sup> , AC1 <sup>b</sup> , POS <sup>d</sup> , LLG <sup>d</sup>	Negative	<b>Positive</b>
Avian <i>C. abortus</i>	15-49D/3 (PS2) <sup>e</sup> , 15-58D/44 (1V) <sup>e</sup> , 15-48D/9 (PS2) <sup>e</sup> , 15-70D/24 (PS1) <sup>e</sup>	Negative	<b>Positive</b>
<i>C. pecorum</i>	iB3 <sup>b</sup> , iB4 <sup>b</sup> , iC3 <sup>b</sup> , iC4 <sup>b</sup>	Negative	Negative
<i>C. felis</i>	Dohycat <sup>f</sup>	Negative	Negative
<i>C. caviae</i>	GPIC <sup>b</sup>	Negative	Negative
<i>C. trachomatis</i>	MRC1 <sup>b</sup>	Negative	Negative
<i>C. gallinacea</i>	08-1274/3 <sup>c</sup>	Negative	Negative
<i>C. avium</i>	10-743/SC13 <sup>c</sup>	Negative	Negative
<i>C. ibidis</i>	10-3098 <sup>c</sup>	Negative	Negative
<i>C. suis</i>	21 <sup>g</sup> , MS06 <sup>g</sup>	Negative	Negative

(A). *C. psittaci enoA* rtPCR



(B). *C. abortus enoA* rtPCR



**Figure S1. Real-time PCR sensitivity test to detect the genomic DNA from *C. psittaci* Loth isolate (A) and *C. abortus* S26/3strain (B).** DNA was extracted and serially diluted. The titre of the genome equivalent (GE) was estimated from the Ct value based on the calibration curve from serial 10-fold dilutions of purified DNA extracted from cell culture containing defined numbers of GE of Loth *C. psittaci* isolate (A) and S26/3 *C. abortus* strain (B). Each dilution was subjected to real-time PCR analysis in triplicate. Y axis corresponds to Ct value and X axis corresponds to Log10 GE/PCR reaction (i.e. 2 µL). (A). *C. psittaci* parameters: the R<sup>2</sup> linearity value from the linear regression is 0.994.  $y = -3.42x + 41.32$  and efficiency= 95.94%%. (B). *C. abortus* parameters: the R<sup>2</sup> linearity value from the linear regression is 0.996.  $y = -3.21x + 40.40$  and efficiency= 104.96%.