

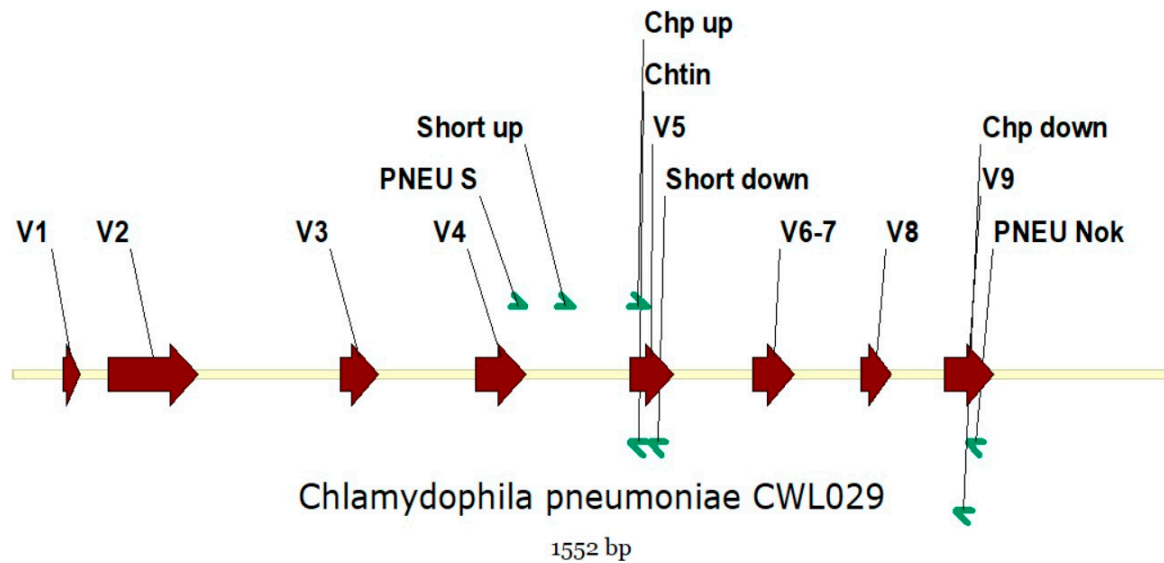
Alignment statistics for match #1

Score	Expect	Identities	Gaps	Strand
441 bits(488)	2e-122	819/1190 (69%)	28/1190 (2%)	Plus/Minus
Query 1	ATGAAAAAACTCTTAAAGTCGGCGTTATTATCCGCCGCATTTGCTGGTTCTGTCGGCTCC	60		
Sbjct 785542	ATGAAAAAACTCTTGAAATCGGTATTAGTATTTGCCGC-TTTGA--GTTCTGCTTCCTCC	785486		
Query 61	TTACAAGCCTTGCTGTAGGGAACCTTCTGATCCAAGCTTATTAATTGATGGTACAATA	120		
Sbjct 785485	TTGCAAGCTCTGCCTGTGGGGAATCCTGCTGAACCAAGCCTTATGATCGACGGAATTCTG	785426		
Query 121	TGGGAAGGTGCTGCAGGAGATCCTTGCGATCCTTGCGCTACTTGGTGCGACGCTATTAGC	180		
Sbjct 785425	TGGGAAGGTTTCGGCGGAGATCCTTGCGATCCTTGCACTTGGTGTGACGCTATCAGC	785366		
Query 181	TTACGTGCTGGATTTTACGGAGACTATGTTTTCGACCGTATCTTAAAAGTAGATGCACCT	240		
Sbjct 785365	ATGCGTATGGGTTACTATGGTGACTTTGTTTTCGACCGTGTGTTTGAACAGATGTGAAT	785306		
Query 241	AAAACATTTTCTATGGGAGCCAAGCCTACTGGATCCGC-----TGCTGCAAACTATACT	294		
Sbjct 785305	AAAGAATTCCAAATGGGTGACAAGCCTACAAGTACTACAGGCAATGCTACAGCTCCAACC	785246		
Query 295	ACTGCCGTAGATAGACCTAACCCGGCCTACAATAAGCATTTACACGATGCAGAGTGGTTC	354		
Sbjct 785245	ACTCTTACAGCAAGAGAGAATCCTGCTTACGGCCGACATATGCAGGATGCTGAGATGTTT	785186		
Query 355	ACTAATGCAGGCTTCATTGCCTTAAACATTTGGGATCGCTTTGATGTTTTCTGTACTTTA	414		
Sbjct 785185	ACAAATGCCGCTTGCATGGCATTGAATATTGGGATCGCTTTGATGTATTCTGTACACTA	785126		
Query 415	GGAGCTTCTAATGGTTACATTAGAGGAACTCTACAGCGTTCAATCTCGTTGGTTTATTC	474		
Sbjct 785125	GGAGCCTCTAGCGGATACCTTAAAGGAACTCTGCTTCTTTCAATTTAGTTGGATTGTTT	785066		
Query 475	GGAGTTAAAGGTACT-----ACTGTAAATGCAAATGAACTACCAAACGTTTCTTTAAGT	528		
Sbjct 785065	GGAGATAATGAAATCAAAGCACGGTCAAAACGAATTCTGTACCAAATATGAGCTTAGAT	785006		
Query 529	AACGGAGTTGTTGAACTTTACACAGACACCTCTTCTCTTGGAGCGTAGGCGCTCGTGGA	588		
Sbjct 785005	CAATCTGTTGTTGAACTTTACACAGATACTGCCTTCTCTTGGAGCGTGGGCGCTCGAGCA	784946		
Query 589	GCCTTATGGGAATGCGGTTGTGCAACTTTGGGAGCTGAATTCCAATATGCACAGTCCAAA	648		
Sbjct 784945	GCCTTGTGGGAGTGCGGATGTGCGACTTTAGGGGCTTCTTTCCAATACGCTCAATCTAAA	784886		
Query 649	CCTAAAGTTGAAGAACTTAATGTGATCTGTAACGTATCGCAATTCTCTGTAAACAAACCC	708		
Sbjct 784885	CCTAAAGTCGAAGAATTAAACGTTCTCTGTAACGCAGCTGAGTTTACTATCAATAAGCCT	784826		
Query 709	AAGGGCTATAAAGGCGTTGCTTTCCC-CTTGCCAACAGACGCTGGCGTAGCAACAGCTAC	767		
Sbjct 784825	AAAGGATATGTAGGGCAAGAATTCCCTCTTGCACTCATA-GCAGGAACTGATGCAGCGAC	784767		
Query 768	TGGAACAAAGTCTGCGACCATCAATTATCATGAATGGCAAGTAGGAGCCTCTCTATCTTA	827		
Sbjct 784766	GGGCACTAAAGATGCCTCTATTGATTACCATGAGTGGCAAGCAAGTTTAGCTCTCTCTTA	784707		
Query 828	CAGACT-AAACTCTTTAGTGCCATACATTGGAGTACAATGGTCTCGAGCAACTTTTGATG	886		
Sbjct 784706	CAGATTGAATATGTTCACT-CCCTACATTGGAGTTAAATGGTCTCGAGCAAGTTTGATG	784648		
Query 887	CTGATAACATCCGCATTGCTCAGCCAAAACCTACAGC--TGTTTTAACTTAACTGC	944		
Sbjct 784647	CCGATACGATTTCGTATAGCCAGCCAAAATCAGCTACAGCTATCTTTGATACT--ACCAC	784590		
Query 945	ATGGAACCCCTTCT-TTACTAGGAAATGCCACAGCATTGTCTACTACTGA--TTCGTTCT	1000		
Sbjct 784589	GCTTAACCCAACTATTGCT-GGAGCTGGCGATGTGAAAGCTAGCGCAGAGGGTCAGCTCG	784531		
Query 1001	CAGACTTCATGCAAAATTGTTTCCTGTGATCAACAAGTTTAAATCTAGAAAAGCTTGTG	1060		
Sbjct 784530	GAGATACCATGCAAAATCGTCTCCTTGCAATTGAACAAGATGAAATCTAGAAAATCTTGCG	784471		

<i>C.abortus</i>	AATTCGATGCAACGCGAAGAACCTTACCTGGGCTTGACATGTATTTGACCGCGGCAGAAA
<i>C.psittaci</i>	AATTCGATGCAACGCGAAGAACCTTACCTGGGCTTGACATGTATTTGACCGCGGCAGAAA
<i>C.pneumoniae</i>	AATTCGATGCAACGCGAAGGACCTTACCTGGACTTGACATGTATTTGACAACTGTAGAAA
<i>C.trachomatis</i>	AATTCGATGCAACGCGAAGGACCTTACCTGGGTTTGACATGTATATGACCGCGGCAGAAA
<i>E.coli</i>	AATTCGATGCAACGCGAAGAACCTTACCTGGTCTTGACATCCACGGAAGT-TTTCAGAGA
<i>Shigella</i>	AATTCGATGCAACGCGAAGAACCTTACCTGGTCTTGACATCCACAGAACC-TTGTAGAGA
<i>Yersinia</i>	AATTCGATGCAACGCGAAGAACCTTACCTGGTCTTGACATCCACAGAACC-TTCCAGAGA
<i>Salmonella</i>	AATTCGATGCAACGCGAAGAACCTTACCTGGTCTTGACATCCAGAGAACC-TGGCAGAGA
<i>C.jejuni</i>	AATTCGAAGATACGCGAAGAACCTTACCTGGGCTTGATATCCTAAGAACC-TTATAGAGA
	***** * ***** ***** ** * ** *
<i>C.abortus</i>	TGTC--GTTTTT---CGCAAGGACAGATACACAGGTGCTGTCATGGCTGTCGTCAGCTCG
<i>C.psittaci</i>	TGTC--GTTTTT---CGCAAGGACAGATACACAGGTGCTGTCATGGCTGTCGTCAGCTCG
<i>C.pneumoniae</i>	TACA--GCTTTC---CGCAAGGACAGATACACAGGTGCTGTCATGGCTGTCGTCAGCTCG
<i>C.trachomatis</i>	TGTC--GTTTTT---CACAAGGCATATACACAGGTGCTGTCATGGCTGTCGTCAGCTCG
<i>E.coli</i>	TGAGAATGTGCC---TTCGGGAACCGTGAGACAGGTGCTGTCATGGCTGTCGTCAGCTCG
<i>Shigella</i>	TACGAGGGTGCC---TTCGGGAACCTGTGAGACAGGTGCTGTCATGGCTGTCGTCAGCTCG
<i>Yersinia</i>	TGGATTGGTGCC---TTCGGGAACCTGTGAGACAGGTGCTGTCATGGCTGTCGTCAGCTCG
<i>Salmonella</i>	TGCCGGGGTGCC---TTCGGGAACCTGTGAGACAGGTGCTGTCATGGCTGTCGTCAGCTCG
<i>C.jejuni</i>	TATGAGGGTGCTAGCTTGCTAGAACCTTAGAGACAGGTGCTGCACGGCTGTCGTCAGCTCG
	* * * * *
<i>C.abortus</i>	TGCCGTGAGGTGTTGGGTTAAGTCCCGCAACGAGCGCAACCCTTATCGTTAGTTGCCAAC
<i>C.psittaci</i>	TGCCGTGAGGTGTTGGGTTAAGTCCCGCAACGAGCGCAACCCTTATCGTTAGTTGCCAAC
<i>C.pneumoniae</i>	TGCCGTGAGGTGTTGGGTTAAGTCCCGCAACGAGCGCAACCCTTATCGTTAGTTGCCAGC
<i>C.trachomatis</i>	TGCCGTGAGGTGTTGGGTTAAGTCCCGCAACGAGCGCAACCCTTATCGTTAGTTGCCAGC
<i>E.coli</i>	TGTTGTGAAATGTTGGGTTAAGTCCCGCAACGAGCGCAACCCTTATCCTTTGTTGCCAGC
<i>Shigella</i>	TGTTGTGAAATGTTGGGTTAAGTCCCGCAACGAGCGCAACCCTTATCCTTTGTTGCCAGC
<i>Yersinia</i>	TGTTGTGAAATGTTGGGTTAAGTCCCGCAACGAGCGCAACCCTTATCCTTTGTTGCCAGC
<i>Salmonella</i>	TGTTGTGAAATGTTGGGTTAAGTCCCGCAACGAGCGCAACCCTTATCCTTTGTTGCCAGC
<i>C.jejuni</i>	TGTCGTGAGATGTTGGGTTAAGTCCCGCAACGAGCGCAACCACGTATTTAGTTGCTAAC
	** **** ***** * ** ***** *
<i>C.abortus</i>	ACTTAGGGTGGGAACCTCTAACGAGACTGCCTGGGTAAACCAGGAGGAAGGCGAGGATGAC
<i>C.psittaci</i>	ACTTAGGGTGGGAACCTCTAACGAGACTGCCTGGGTAAACCAGGAGGAAGGCGAGGATGAC
<i>C.pneumoniae</i>	ACTTAGGGTGGGAACCTCTAACGAGACTGCCTGGGTAAACCAGGAGGAAGGCGAGGATGAC
<i>C.trachomatis</i>	ACTTAGGGTGGGAACCTCTAACGAGACTGCCTGGGTAAACCAGGAGGAAGGCGAGGATGAC
<i>E.coli</i>	GGTCCGGCCGGGAACCTCAAAGGAGACTGCCAGTGATAAACTGGAGGAAGGTGGGGATGAC
<i>Shigella</i>	GGTCCGGCCGGGAACCTCAAAGGAGACTGCCAGTGATAAACTGGAGGAAGGTGGGGATGAC
<i>Yersinia</i>	GGTCCGGCCGGGAACCTCAAAGGAGACTGCCAGTGATAAACTGGAGGAAGGTGGGGATGAC
<i>Salmonella</i>	GGTTCGGCCGGGAACCTCAAAGGAGACTGCCGGTGATAAACCGGAGGAAGGTGGGGATGAC
<i>C.jejuni</i>	GGTTCGGCCGAGCACTCTAAATAGACTGCCTTCG-TAAGGAGGAGGAAGGTGTGGACGAC
	* ** * * * * * * * * * * * * * * * * *
<i>C.abortus</i>	GTCAAGTCAGCATGGCCCTTATGCCCAGGGCTACACACGTGCTACAATGGCCAGTACAGA
<i>C.psittaci</i>	GTCAAGTCAGCATGGCCCTTATGCCCAGGGCTACACACGTGCTACAATGGCCAGTACAGA
<i>C.pneumoniae</i>	GTCAAGTCAGCATGGCCCTTATGTCCAGGGCGACACACGTGCTACAATGGTTAGTACAGA
<i>C.trachomatis</i>	GTCAAGTCAGCATGGCCCTTATGCCCAGGGCGACACACGTGCTACAATGGCCAGTACAGA
<i>E.coli</i>	GTCAAGTCATCATGGCCCTTACGACCAGGGCTACACACGTGCTACAATGGCGCATACAAA
<i>Shigella</i>	GTCAAGTCATCATGGCCCTTACGACCAGGGCTACACACGTGCTACAATGGCGCATACAAA
<i>Yersinia</i>	GTCAAGTCATCATGGCCCTTACGACCAGGGCTACACACGTGCTACAATGGCGCATACAAA
<i>Salmonella</i>	GTCAAGTCATCATGGCCCTTACGACCAGGGCTACACACGTGCTACAATGGCGCATACAAA
<i>C.jejuni</i>	GTCAAGTCATCATGGCCCTTATGCCCAGGGCGACACACGTGCTACAATGGCATATACAA
	***** ***** * ***** ***** *****
<i>C.abortus</i>	AGGTAGC AATATCGCAAGATGGAGCAAATCT - CAAAGCTGGCCCC AGTTCGGATTGTAG
<i>C.psittaci</i>	AGGTAGC AATATCGTGAGATGGAGCAAATCT - CAAAGCTGGCCCC AGTTCGGATTGTAG
<i>C.pneumoniae</i>	AGGTAGC AAGATCGTGAGATGGAGCAAATCT - AAAAGCTAGCCCC AGTTCGGATTGTAG
<i>C.trachomatis</i>	AGGTGGC AAGATCGCGAGATGGAGCAAATCT - CAAAGCTGGCCCC AGTTCGGATTGTAG
<i>E.coli</i>	GAGAAGCGACCTCGCGAGAGCAAGCGGACCTCATAAAGTGCGTCGTAGTCCGGATTGGAG
<i>Shigella</i>	GAGAAGCGACCTCGCGAGAGCAAGCGGACCTCATAAAGTGCGTCGTAGTCCGGATTGGAG
<i>Yersinia</i>	GAGAAGCGAACTCGCGAGAGCAAGCGGACCTCATAAAGTGCGTCGTAGTCCGGATTGGAG
<i>Salmonella</i>	GAGAAGCGACCTCGCGAGAGCAAGCGGACCTCATAAAGTGCGTCGTAGTCCGGATTGGAG
<i>C.jejuni</i>	GAGACGCAATACCGGAGGTGGAGCAAATCTA-TAAAAATATGTCCAGTTTCGATTGTTT
	* ** * * * * * * * * * * * * * * * * *

A.





B.

Figure S2 Design of primers specific for four chlamydial species infecting humans. Reference sequences: *Chlamydia abortus* GN6 CP021996.1; *Chlamydia psittaci* 84/55 CP003790; *Chlamydia pneumoniae* TW-183 AE009440.1; *Chlamydia trachomatis* C/TW-3 CP006945.1; *E.coli* ECOUW87; *Shigella dysenteriae* CP061527.1; *Yersinia sp.* EU555393; *Salmonella enterica* CP045958.1; *Campylobacter jejuni* ATCC 35925 CP020045.1. **A.** Outer primers are in red letters and yellow shadowed; Inner primers are marked in blue; degenerate positions are grey shadowed. **B.** Location of the primers on the 16S rRNA gene. PNEU S pos. 676-686; PNEU Nok pos. 1280-1301; Chp up pos. 826-850; Chp down pos. 1264-1286; Short down pos. 854-874; Short up pos. 729-750; Chtinok pos. 826-850.

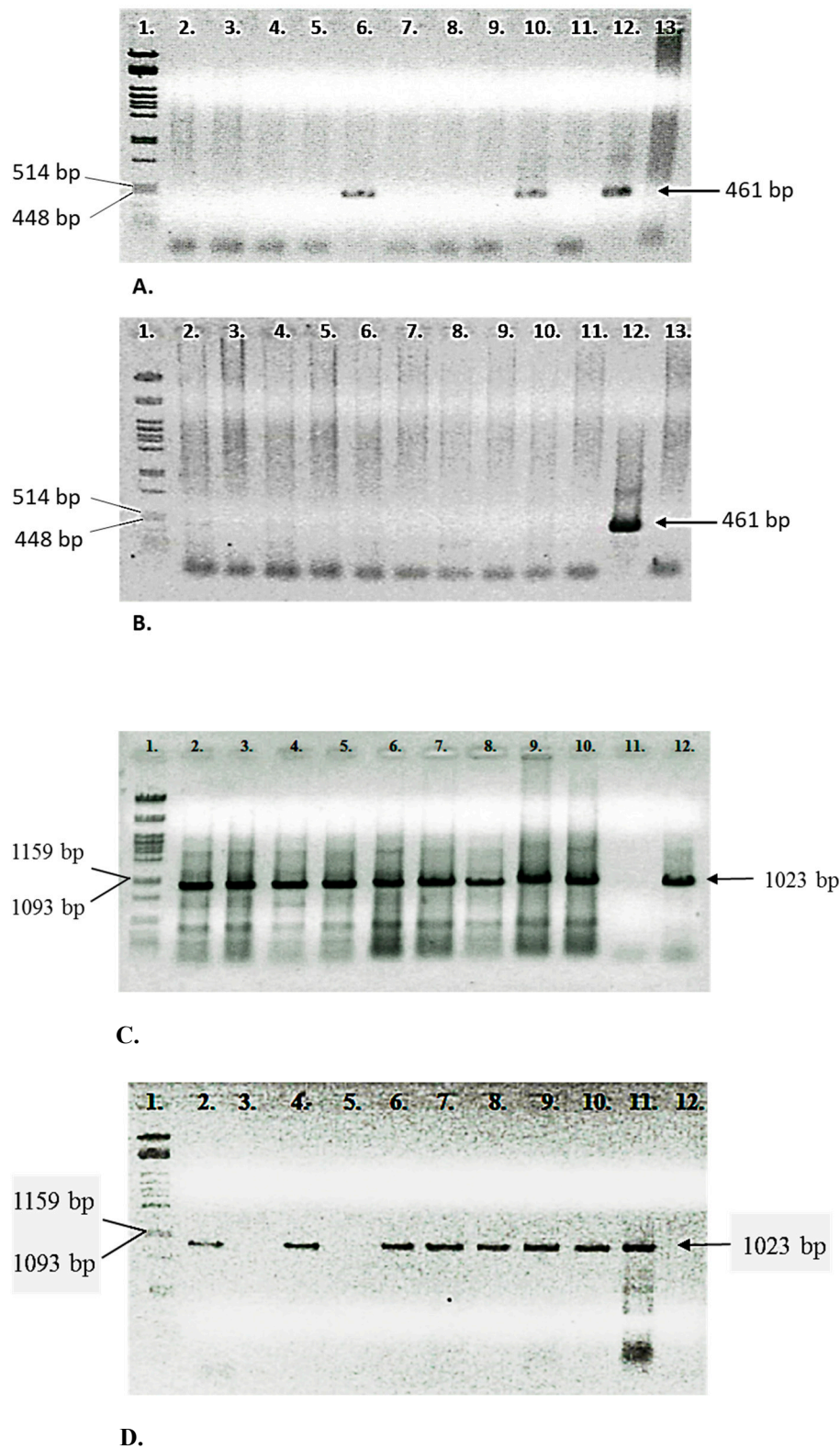


Figure S3 Amplification and DNA degradation during 1 year of storage at -20°C. Lanes: 1. λ /*Pst*I size marker, 2. 3SP, 3. NC, 4. 4SP, 5. NC, 6. 5SP, 7. NC, 8. 6SP, 9. NC, 10. 33SP, 11/12 positive and negative control (NC). **A. B.** Chp up/Chp down primers. Size of PCR product is 461 bp. **A.** Fresh DNA preps. **B.** After 1 year of storage at -20°C. **C. D.** MT for/MT rev primers. Size of PCR product is 1023 bp. **C.** Fresh DNA preps. **D.** After 1 year of storage at -20°C.

>DS

AGCAAGGGGAGCAAACAGGATTAGATACCCTGGTAGTCCTTGCCGTAAACGATCCATACTTG
ATGTGGATGGTCTCAAA

>MR

AGCAAGGGGAGCAAACAGGATTAGATACCCTGGTAGTCCTTGCCGTAAACGATCCATACTTG
ATGTGGATGRTCTCAAA

>2SP

AGCAAGGGGAGCAAACAGGATTRGATACCCTGGTAGTCCTTGCCGTAAACGATCCATACTTG
ATGTGGATGGTCTCAAA

>10SP

AGCAAGGGGAGCAAACAGGATTAGATACCCTGGTAGTCCTTGCCGTAAACGATCCATACTTG
ATGTGGATGGTCTCAAA

>18SP

AGCAAGGGGAGCAAACAGGATTAGATACCCTGGTAGTCCTTGCCGTAAACGATCCATACTTG
ATGTGGATGGTCTCAAA

>21SP

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ATGTGGATGGTCTCAAA

>28SP

AGCAAGGGGAGCAAACAGGATTAGATACCCTGGTAGTCCTTGCCGTAAACGATCCATACTTG
ATGTGGATGGTCTCAAA

>33SP

AGCAAGGGGAGCAAACAGGATTAGATACCCTGGTAGTCCTTGCCGTAAACGATCCATACTTG
ATGTGGATGGTCTCAAA

>45SP

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ATGTGGATGGTCTCAAA

>67SP

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ATGTGGATGGTCTCAAA

>3002

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ATGTGGATGGTCTCAAA

>3003

AGCAAGGGGAGCAAACAGGATTAGATACCCTGGTAGTCCTTGCCGTAAACGATCCATACTTG
ATGTGGATGGTCTCAAA

>3014

AGCAAGGGGAGCAAACAGGATTAGATACCCTGGTAGTCCTTGCCGTAAACGATCCATACTTG
ATGTGGATGGTCTCAAA

>3016

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>3022

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ATGTGGATGGTCTCAAA

>3031

AGCAAGGGGAGCAAACAGGATTAGATACCCTGGTAGTCCTTGCCGTAAACGATCCATACTTG
ATGTGGATGGTCTCAAA

>5005

AGCAAGGGGAGCAAACAGGATTAGATACCCTGGTAGTCCTTGCCGTAAACGATCCATACTTG
ATGTGGATGGTCTCAAA

>5009

AGCAAGGGGAGCAAACAGGATTAGATACCCTGGTAGTCCTTGCCGTAAACGATCCATACTTG
ATGTGGATGGTCTCAAA

>7CHP

AGCAAGGGGAGCAAACAGGATTGGATACCCTGGTAGTCCTTGCCGTAAACGATCCATACTTG
ATGTGGATGGTCTCAAA

>13CHP

AGCAAGGGGAGCAAACAGGATTAGATACCCTGGTAGTCCTTGCCGTAAACGATCCATACTTG
ATGTGGATGGTCTCAAA

>14CHP

AGCAAGGGGAGCAAACAGGAATAGATACCCTGGTAGTCCTTGCCGTAAACGATCCATACTTG
ATGTGGATGGTCTCAAA

>16CHP

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ATGTGGATGGTCTCAAA

>18CHP

AGCAAGGGGAGCAAACAGGATTAGATACCCTGGTAGTCCTTGCCGTAAACGATCCATACTTG
ATGTGGATGGTCTCAAA

>28CHP

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>41CHP

AGCAAGGGGAGCAAACAGGATTAGATACCCTGGTAGTCCTTGCCGTAAACGATCCATACTTG
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>45CHP

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>97CHP

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ATGTGGATGGTCTCAAA

>111CHP

AGCAAGGGGAGCAAACAGGATTAGATACCCTGGTAGTCCTTGCCGTAAACGATCCATACTTG
ATGTGGATGGTCTCAAA

>*C. trachomatis*

AGCAAGGGGAGCAAACAGGATTAGATACCCTGGTAGTCCTTGCCGTAAACGATGCATACTTG
ATGTGGATGGTCTCAA

>*C. pneumoniae*

AGCAAGGGGAGCAAACAGGATTAGATACCCTGGTAGTCCTTGCCGTAAACGATGCATACTTG
ATGTGGATGGTCTCAA

>*C. psittaci*

AGCAAGGGGAGCAAACAGGATTAGATACCCTGGTAGTCCTTGCCGTAAACGATGCATACTTG
ATGTGGATAGTCTCAA

>C. *abortus*

AGCAAGGGGAGCAAACAGGATTAGATACCCTGGTAGTCCTTGCCGTAAACGATGCATACTTG
ATGTGGATAGTCTCAA

A.

>DS

TATGCCGCCTGAGGAGTACACTCGCAAGGGTGAAACTCAAAAGAATTGACGGGGGGCCCGCA
CAAGCAGTGGAGCATGTGGTTTAATTCGATGCAACGCGAAGGACCTTACCTGGACTTGACAT
GTATTTGACAACTGTAGAAATACAGCTTTCCGCAAGGACAGATACACAGGTGCTGCATGGCT
GTCGTCAGCTCGTGCCGTGAGGTGTTGGGTAAAGTCCCGCAACGAGCGCAACCCTTATCGTTA
GTTGCCAGCACTTAGGGTGGGAACTCTAACGAGACTGCCTGGGTAAACCAGGAGGAAGGCGA
GGATGACGTCAAGTCAGCATGGCCCTTATGTCCAGGGCGACACACGTGCTACAATGGTTAGT
ACAGAAGGTAGCAAGATC

>MR

TATGCCGCCTGAGGAGTACACTCGCAAGGGTGAAACTCAAAAGAATTGACGGGGGGCCCGCA
CAAGCAGTGGAGCATGTGGTTTAATTCGATGCAACGCGAAGGACCTTACCTGGACTTGACAT
GTATTTGACAACTGTAGAAATACAGCTTTCCGCAAGGACAGATACACAGGTGCTGCATGGCT
GTCGTCAGCTCGTGCCGTGAGGTGTTGGGTAAAGTCCCGCAACGAGCGCAACCCTTATCGTTA
GTTGCCAGCACTTAGGGTGGGAACTCTAACGAGACTGCCTGGGTAAACCAGGAGGAAGGCGA
GGATGACGTCAAGTCAGCATGGCCCTTATGTCCAGGGCGACACACGTGCTACAATGGTTAGT
ACAGAAGGTAGCAAGATC

>PS

TATGCCGCCTGAGGAGTACACTCGCAAGGGTGAAACTCAAAAGAATTGACGGGGGGCCCGCA
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GTTGCCAGCACTTAGGGTGGGAACTCTAACGAGACTGCCTGGGTAAACCAGGAGGAAGGCGA
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GTCGTCAGCTCGTGCCGTGAGGTGTTGGGTAAAGTCCCGCAACGAGCGCAACCCTTATCGTTA
GTTGCCAGCACTTAGGGTGGGAACTCTAACGAGACTGCCTGGGTAAACCAGGAGGAAGGCGA
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ACAGAAGGTAGCAAGATC

>10SP

TATGCCGCCTGAGGAGTACACTCGCAAGGGTGAAACTCAAAAGAATTGACGGGGGGCCCGCA
CAAGCAGTGGAGCATGTGGTTTAATTCGATGCAACGCGAAGGACCTTACCTGGACTTGACAT
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GGATGACGTCAAGTCAGCATGGCCCTTATGTCCAGGGCGACACACGTGCTACAATGGTTAGT
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>18SP

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>21SP

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GTATTTGACAACTGTAGAAATACAGCTTTCCGCAAGGACAGATACACAGGTGCTGCATGGCT
GTCGTCAGCTCGYGCCGTGAGGTGTTGGGTAAAGTCCCGCAACGAGCGCAACCCTTATCGTTA
GTTGCCAGCACTTAGGGTGGGAACTCTAACGAGACTGCCTGGGTAAACCAGGGGAAGGCGAG
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AGAAGGTAGCAAGATC

>33SP

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GTTGCCARCACTTAGGGTGGGAACTCTAACGAGACTGCCTGGGTAAACCAGGAGGAAGGCGA
GGATGACGTCAAGTCAGCATGGCCCTTATGTCCAGGGCGACACACGTGCTACAATGGTTAGT
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>45SP

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GTTGCCAGCACTTAGGGTGGGAACTCTAACGAGACTGCCTGGGTAAACCAGGAGGAAGGCGA
GGATGACGTCAAGTCAGCATGGCCCTTATGTCCAGGGCGACACACGTGCTACAATGGTTAGT
ACAGAAGGTAGCAAGATC

>3014

TACTCAAGAATTGGACGGGCGTGTTCCGCACAAGCAGTGGAGCATGTGGTTTAATTTCGATGCA
ACGCGAAGAACCCTTACCCAGGCTCGAAATGCAAAGGCAATCAACAGAGATGTTGAGTTCCGC
AAGGACTTTTGTATAGGTGCTGCATGGCTGTCGTCAGCTCGTGCCGTGAGGTGTTGGGTAAAGT
CCCGCAACGAGCGCAACCCTTATCGTTAGTTGCCAACATTTTAGGTGGGAACTCTAACGAGAC
TGCTGGGTAAACCAGGAGGAAGGTGAGGATGACGTCAAGTCCGCATGGCCCTTATGTCTGG

GGCTACACACGTGCTACAATGGTCGGTACAGAAGGCAGCAAGATCGTGAGATGGAGCAAAT
CA

>3016

TATGCCGCCTGAGGAGTACACTCGCAAGGGTGAAACTCAAAAGAATTGACGGGGGGCCCGCA
CAAGCAGTGGAGCATGTGGTTTAATTCGATGCAACGCGAAGGACCTTACCTGGACTTGACAT
GTATTTGACAACTGTAGAAATACAGCTTTCCGCAAGGACAGATACACAGGTGCTGCATGGCT
GTCGTCAGCTCGTGCCGTGAGGTGTTGGGTAAAGTCCCGCAACGAGCGCAACCCTTATCGTTA
GTTGCCAGCACTTAGGGTGGGAACCTCTAACGAGACTGCCTGGGTAAACCAGGAGGAAGGCGA
GGATGACGTCAAGTCAGCATGGCCCTTATGTCCAGGGCGACACACGTGCTACAATGGTTAGT
ACAGAAGGTAGCAAGATC

>57CHP

TGGGGAGTACGCTCGCAAGGGTGAAACTCAAAAGAATTGACGGGGGGCCCGCACAAAGCAGTG
GAGCATGTGGTTTAATTCGATGCAACGCGAAGAACCTTACCCAGGCTCGAAATGCAAAGGCA
ATCAACAGAGATGTTGAGTTCCGAAAGGACTTTTGTATAGGTGCTGCATGGCTGTCGTCAGCT
CGTGCCGTGAGGTGTTGGGTAAAGTCCCGCAACGAGCGCAACCCTTATCGTTAGTTGCCAACA
CGCAAGGTGGGGACTCTAACGAGACTGCCTAGGTAAACCTAGGAGGAAGGTGAGGATGACGT
CAAGTCCGCATGGCCTTTATGTCTGGGGCTACACA

B.

Figure S4 A. Sequences of 79 nt SNPCR products, **B.** sequences of 346 nt of SNPCR product amplified from sputa.

CLUSTAL X (1.81) multiple sequence alignment

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14. CHP      AGCAAGGGGAGCAAAACAGGAATTAGATACCCTGGTAGTCCTTGCCGTAAACGATCCATACT
60. CHP      AGCAAGGGGAGCAAAACAGGATTAGATACCCTGGTAGTCCTTGCCGTAAACGATCCATACT
2. SP        AGCAAGGGGAGCAAAACAGGATTGATACCCTGGTAGTCCTTGCCGTAAACGATCCATACT
7. CHP       AGCAAGGGGAGCAAAACAGGATTGGATACCCTGGTAGTCCTTGCCGTAAACGATCCATACT
MR           AGCAAGGGGAGCAAAACAGGATTAGATACCCTGGTAGTCCTTGCCGTAAACGATCCATACT
111. CHP     AGCAAGGGGAGCAAAACAGGATTAGATACCCTGGTAGTCCTTGCCGTAAACGATCCATACT
97. CHP      AGCAAGGGGAGCAAAACAGGATTAGATACCCTGGTAGTCCTTGCCGTAAACGATCCATACT
93. CHP      AGCAAGGGGAGCAAAACAGGATTAGATACCCTGGTAGTCCTTGCCGTAAACGATCCATACT
84. CHP      AGCAAGGGGAGCAAAACAGGATTAGATACCCTGGTAGTCCTTGCCGTAAACGATCCATACT
78. CHP      AGCAAGGGGAGCAAAACAGGATTAGATACCCTGGTAGTCCTTGCCGTAAACGATCCATACT
71. CHP      AGCAAGGGGAGCAAAACAGGATTAGATACCCTGGTAGTCCTTGCCGTAAACGATCCATACT
58. CHP      AGCAAGGGGAGCAAAACAGGATTAGATACCCTGGTAGTCCTTGCCGTAAACGATCCATACT
49. CHP      AGCAAGGGGAGCAAAACAGGATTAGATACCCTGGTAGTCCTTGCCGTAAACGATCCATACT
48. CHP      AGCAAGGGGAGCAAAACAGGATTAGATACCCTGGTAGTCCTTGCCGTAAACGATCCATACT
45. CHP      AGCAAGGGGAGCAAAACAGGATTAGATACCCTGGTAGTCCTTGCCGTAAACGATCCATACT
41. CHP      AGCAAGGGGAGCAAAACAGGATTAGATACCCTGGTAGTCCTTGCCGTAAACGATCCATACT
28. CHP      AGCAAGGGGAGCAAAACAGGATTAGATACCCTGGTAGTCCTTGCCGTAAACGATCCATACT
18. CHP      AGCAAGGGGAGCAAAACAGGATTAGATACCCTGGTAGTCCTTGCCGTAAACGATCCATACT
16. CHP      AGCAAGGGGAGCAAAACAGGATTAGATACCCTGGTAGTCCTTGCCGTAAACGATCCATACT
13. CHP      AGCAAGGGGAGCAAAACAGGATTAGATACCCTGGTAGTCCTTGCCGTAAACGATCCATACT
5009. SP     AGCAAGGGGAGCAAAACAGGATTAGATACCCTGGTAGTCCTTGCCGTAAACGATCCATACT
5005. SP     AGCAAGGGGAGCAAAACAGGATTAGATACCCTGGTAGTCCTTGCCGTAAACGATCCATACT
3031. SP     AGCAAGGGGAGCAAAACAGGATTAGATACCCTGGTAGTCCTTGCCGTAAACGATCCATACT
3022. SP     AGCAAGGGGAGCAAAACAGGATTAGATACCCTGGTAGTCCTTGCCGTAAACGATCCATACT
3016. SP     AGCAAGGGGAGCAAAACAGGATTAGATACCCTGGTAGTCCTTGCCGTAAACGATCCATACT
3014. SP     AGCAAGGGGAGCAAAACAGGATTAGATACCCTGGTAGTCCTTGCCGTAAACGATCCATACT
3003. SP     AGCAAGGGGAGCAAAACAGGATTAGATACCCTGGTAGTCCTTGCCGTAAACGATCCATACT
3002. SP     AGCAAGGGGAGCAAAACAGGATTAGATACCCTGGTAGTCCTTGCCGTAAACGATCCATACT
67. SP       AGCAAGGGGAGCAAAACAGGATTAGATACCCTGGTAGTCCTTGCCGTAAACGATCCATACT
45. SP       AGCAAGGGGAGCAAAACAGGATTAGATACCCTGGTAGTCCTTGCCGTAAACGATCCATACT
33. SP       AGCAAGGGGAGCAAAACAGGATTAGATACCCTGGTAGTCCTTGCCGTAAACGATCCATACT
28. SP       AGCAAGGGGAGCAAAACAGGATTAGATACCCTGGTAGTCCTTGCCGTAAACGATCCATACT
21. SP       AGCAAGGGGAGCAAAACAGGATTAGATACCCTGGTAGTCCTTGCCGTAAACGATCCATACT
18. SP       AGCAAGGGGAGCAAAACAGGATTAGATACCCTGGTAGTCCTTGCCGTAAACGATCCATACT
10. SP       AGCAAGGGGAGCAAAACAGGATTAGATACCCTGGTAGTCCTTGCCGTAAACGATCCATACT
DS           AGCAAGGGGAGCAAAACAGGATTAGATACCCTGGTAGTCCTTGCCGTAAACGATCCATACT
C. trachomatis AGCAAGGGGAGCAAAACAGGATTAGATACCCTGGTAGTCCTTGCCGTAAACGATGCATACT
C. pneumoniae  AGCAAGGGGAGCAAAACAGGATTAGATACCCTGGTAGTCCTTGCCGTAAACGATGCATACT
C. psittaci    AGCAAGGGGAGCAAAACAGGATTAGATACCCTGGTAGTCCTTGCCGTAAACGATGCATACT
C. abortus     AGCAAGGGGAGCAAAACAGGATTAGATACCCTGGTAGTCCTTGCCGTAAACGATGCATACT
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14. CHP      TGATGTGGATGGTCTCAAA
60. CHP      TGATGTGGATGGTCTCAAA
2. SP        TGATGTGGATGGTCTCAAA
7. CHP       TGATGTGGATGGTCTCAAA
MR           TGATGTGGATGRTCTCAAA
111. CHP     TGATGTGGATGGTCTCAAA
97. CHP      TGATGTGGATGGTCTCAAA
93. CHP      TGATGTGGATGGTCTCAAA
84. CHP      TGATGTGGATGGTCTCAAA
78. CHP      TGATGTGGATGGTCTCAAA
71. CHP      TGATGTGGATGGTCTCAAA
58. CHP      TGATGTGGATGGTCTCAAA
49. CHP      TGATGTGGATGGTCTCAAA
48. CHP      TGATGTGGATGGTCTCAAA
45. CHP      TGATGTGGATGGTCTCAAA
41. CHP      TGATGTGGATGGTCTCAAA
28. CHP      TGATGTGGATGGTCTCAAA
18. CHP      TGATGTGGATGGTCTCAAA
16. CHP      TGATGTGGATGGTCTCAAA
13. CHP      TGATGTGGATGGTCTCAAA
5009. SP     TGATGTGGATGGTCTCAAA
5005. SP     TGATGTGGATGGTCTCAAA
3031. SP     TGATGTGGATGGTCTCAAA
3022. SP     TGATGTGGATGGTCTCAAA
3016. SP     TGATGTGGATGGTCTCAAA
3014. SP     TGATGTGGATGGTCTCAAA
3003. SP     TGATGTGGATGGTCTCAAA
3002. SP     TGATGTGGATGGTCTCAAA
67. SP       TGATGTGGATGGTCTCAAA
45. SP       TGATGTGGATGGTCTCAAA
33. SP       TGATGTGGATGGTCTCAAA
28. SP       TGATGTGGATGGTCTCAAA
21. SP       TGATGTGGATGGTCTCAAA
18. SP       TGATGTGGATGGTCTCAAA
10. SP       TGATGTGGATGGTCTCAAA
DS           TGATGTGGATGGTCTCAAA
C. trachomatis  TGATGTGGATGGTCTCAAA
C. pneumoniae  TGATGTGGATGGTCTCAAA
C. psittaci     TGATGTGGATAGTCTCAAA
C. abortus     TGATGTGGATAGTCTCAAA
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Figure S5 Alignment of SNPCR sequences. Polymorphic sites are grey shadowed.

TABLE S1 Sputum sample data.

Number	Sample	Age	Gender	NPCR 461 bp	NPCR 121 bp	mtDNA 1023 bp	mtDNA 250 bp
1	DS*	27	F	+	+	+	nd
2	MŠ	24	F	-	-	+	nd
3	BŠ	24	F	-	-	+	nd
4	MS	27	M	-	-	+	nd
5	PS*	60	M	+	+	+	nd
6	MR	24	M	+	+	+	nd
7	2SP	24	F	-	+	+	nd
8	3SP	25	F	-	-	+	nd
9	4SP	27	F	-	-	+	nd
10	5SP	28	M	+	+	+	nd
11	6SP	55	F	-	-	+	nd
12	7SP	58	F	-	-	+	nd
13	10SP	27	F	+	+	-	+
14	11SP	60	F	-	-	+	nd
15	17SP	28	F	-	-	+	nd
16	18SP	30	M	+	+	+	nd

17	20SP	26	F	+	+	+	nd
18	21SP	27	F	+	+	+	nd
19	27SP	22	F	-	-	+	nd
20	28SP	55	M	-	+	+	nd
21	29SP	35	M	-	-	+	nd
22	30SP	53	M	-	-	+	nd
23	33SP	23	F	+	+	+	nd
24	34SP	27	M	-	-	+	nd
25	37SP	49	F	-	-	+	nd
26	38SP	49	M	-	-	+	nd
27	39SP	22	F	-	-	+	nd
28	41SP	65	M	-	-	+	nd
29	44SP	65	M	-	-	+	nd
30	45SP*	31	M	+	+	+	nd
31	48SP	53	F	-	-	+	nd
32	49SP	72	M	-	-	+	nd
33	52SP	29	F	-	-	+	nd
34	54SP	22	F	-	-	+	nd
35	58SP	26	M	-	-	+	nd
36	60SP	22	M	-	-	+	nd
37	61SP	26	F	-	-	+	nd
38	64SP	23	F	-	-	+	nd
39	66SP	20	F	-	-	+	nd
40	67SP	20	F	-	+	+	nd
41	68SP	26	F	-	-	+	nd
42	69SP	40	F	-	-	+	nd
43	70SP	31	M	-	-	+	nd
44	1002	41	M	-	-	+	nd
45	3001	25	M	-	-	+	nd
46	3002	25	M	-	+	+	nd
47	3003	25	M	-	+	+	nd
48	3004	24	M	-	-	+	nd
49	3005	25	M	-	-	+	nd
50	3006	22	M	-	-	+	nd
51	3007	28	F	-	-	+	nd
52	3008	30	M	-	-	+	nd
53	3009	20	M	-	-	+	nd
54	3010	22	M	-	-	+	nd
55	3011	26	M	-	-	+	nd
56	3012	21	M	-	-	+	nd
57	3013	28	M	-	-	+	nd
58	3014	22	M	+	+	+	nd
59	3015	27	M	-	-	+	nd
60	3016	27	M	+	+	+	nd
61	3017	30	M	-	-	+	nd
62	3018	21	M	-	-	+	nd
63	3019	30	M	-	-	+	nd
64	3020	30	M	-	-	+	nd
65	3021	19	M	-	-	+	nd

66	3022	21	M	-	+	+	nd
67	3023	24	M	-	-	+	nd
68	3024	24	M	-	-	+	nd
69	3025	24	M	-	-	-	+
70	3026	22	M	-	-	+	nd
71	3027	21	M	-	-	-	+
72	3028	26	M	-	-	+	nd
73	3029	24	M	-	-	+	nd
74	3030	23	F	-	-	+	nd
75	3031	26	M	-	+	+	nd
76	3032	21	M	-	-	+	nd
77	3033	30	M	-	-	+	nd
78	5002	63	F	-	-	+	nd
79	5003	57	F	-	-	+	nd
80	5004	51	M	-	-	+	nd
81	5005	77	M	-	+	+	nd
82	5006	74	F	-	-	+	nd
83	5007	66	M	-	-	+	nd
84	5008	51	F	-	-	+	nd
85	5009	66	F	-	+	+	nd
86	2CHP	24	M	-	-	-	+
87	3CHP	60	F	-	-	+	nd
88	4CHP	41	F	-	-	-	+
89	5CHP	59	M	-	-	-	+
90	7CHP	77	M	-	+	+	nd
91	9CHP	63	F	-	-	+	nd
92	11CHP	29	M	-	-	+	nd
93	13CHP	44	F	-	+	-	+
94	14CHP	47	M	-	+	+	nd
95	15CHP	47	M	-	-	-	+
96	16CHP	26	F	-	+	+	nd
97	18CHP	28	M	-	+	+	nd
98	19CHP	25	M	-	-	+	nd
99	20CHP	53	F	-	-	+	nd
100	21CHP	42	F	-	-	-	+
101	23CHP	27	M	-	-	+	nd
102	24CHP	33	F	-	-	+	nd
103	27CHP	48	M	-	-	+	nd
104	29CHP	44	F	-	-	+	nd
105	30CHP	55	F	-	-	+	nd
106	31CHP	66	M	-	-	+	nd
107	33CHP	69	M	-	-	+	nd
108	36CHP	62	F	-	-	+	nd
109	37CHP	67	M	-	-	-	+
110	38CHP	43	M	-	-	+	nd
111	39CHP	39	F	-	-	+	nd
112	41CHP	61	F	-	+	+	nd
113	45CHP	16	F	-	+	+	nd
114	48CHP	37	M	-	+	+	nd

115	49CHP	37	F	-	+	+	nd
116	52CHP	30	M	-	-	-	+
117	53CHP	55	F	-	-	+	nd
118	57CHP	43	F	+	+	+	nd
119	58CHP	67	F	-	+	+	nd
120	60CHP	22	M	-	+	-	+
121	62CHP	60	M	-	-	+	nd
122	63CHP	27	F	-	-	+	nd
123	64CHP	24	F	-	-	+	nd
124	71CHP	28	M	-	+	+	nd
125	73CHP	33	M	-	-	-	+
126	74CHP	56	F	-	-	+	nd
127	76CHP	29	M	-	-	+	nd
128	77CHP	33	M	-	-	-	+
129	78CHP	60	F	-	+	+	nd
130	80CHP	34	M	-	-	-	+
131	81CHP	38	F	-	-	+	nd
132	84CHP	60	F	-	+	+	nd
133	85CHP	61	M	-	-	+	nd
134	88CHP	49	M	-	-	+	nd
135	91CHP	37	F	-	-	+	nd
136	92CHP	43	M	-	-	-	+
137	93CHP	70	F	-	+	+	nd
138	96CHP	45	F	-	-	+	nd
139	97CHP	27	F	-	+	-	+
140	98CHP	44	F	-	-	-	+
141	101CHP	25	F	-	-	+	nd
142	102CHP	26	M	-	-	-	+
143	105CHP	34	F	-	-	+	nd
144	107CHP	23	F	-	-	-	+
145	108CHP	25	F	-	-	+	nd
146	109CHP	52	F	-	-	+	nd
147	110CHP	58	M	-	-	+	nd
148	111CHP	-	M	-	+	+	nd
149	1080*	24	M	+	-	+	nd
150	1082*	47	F	-	+	+	nd
151	1089*	65	F	-	+	+	nd
152	1096*	41	F	-	+	+	nd
153	1779*	33	F	-	+	+	nd
154	1788*	38	F	-	+	+	nd
155	1803*	52	M	-	+	+	nd
156	1828*	49	F	-	+	+	nd
157	1838*	42	M	-	+	+	nd

* positive or threshold IgG or IgA; nd – non determined