

	Panout RYGGGAGAA
Protoch.naegleriophila	AACCTCGGAACAGCATTTGAAACTACATCTCTCGAGGGTAGGCGGAGAAA
Ca.Protoch.amoebophila	AACCTCGGAACAGCATTTGAAACTACATCTCTAGAGGGTAGGCGGAGAAA
Parach.acanthamoebae	AACCTCGGAACAGCATTTGACACTATATTTCTTGAGGGTAGGCGGAGAAA
Ca.Metachlamydia	AACCCCGGAACAGCATTTGAAACTCCATTTCTAGAGGGTAGGCGGAGAAA
Ca.Mesoch.elodeae	AACCTCGGAACAGCATTTGAAACTCCCTTTCTAGAGGGTAGGCGGAGAAA
Ca.Rubidus.massiliensis	AACCTCGGAGCTGCATAGGAACTTCTGTCTAGAGGGTAGGCGGAGAAA
Neoch.hartmannellae	AACCCCGGAACAGCATTTGAAACTCCCTTTCTTGAGGGTAGACGGAGAAA
Can.Fritschea_bemisiae	AACCTCGAAGCTGCATTTGAAACTGCTTGTCTAGAGGGTAGACGGAGAAA
Ca.Fritschea_eriococci	AACCTCGAAGCTGCATTTGAAACTGCTTGTCTAGAGGTAGACGGAGAAA
Ca.Syngnamydia	AACCTCGAAGCTGCATTTGAAACTATTTGTCTTGAGGGTAGACGGAGAAA
Ca.Neptunoch.vexilliferae	AACCTCGAAGCTGCATTTGAAACTACTAATCTTGAGGGTAGACGGAGAAA
Ca.Syngnamydia_venezia	AACCTCGAAGCTGCATTTAAACTACTGATCTTGAGGGTAGACGAAGAAA
Simkania_negevensis	AACCTCGGAGCTGCATTTGAAACTACTTATCTTGAGGGTAGACGGAGAAA
Rhabdoch.crassificans	AACCTCGGAGCCGCATTTGAAACTGCAATCTTGAGGAATGGCGGAGGAA
Ca.Rhabdoch.porcellionis	AACCTTTGGAGCCGCATTTGAAACTGCAATCTTGAGGGTAGCGGAGGAA
Ca.Renich.lutjani	AACCCCGGAGCTGCATTTAAACTATATTTATAGAGGGTAGCGGAGGAAA
Waddlia_sp.G817	AACCCCGGAACCTGCGTTTGAAGTATATTTCTTGAGGCAAGCGGAGAAA
Waddlia_chondrophila	AACCCCGGAACCTGCGTTTGAAGTATATTTCTAGAGGCAAGCGGAGAAA
Estrella	AACCTCAGGGCGGCACCTGAAACTATTTGTCTAGAGGGTAGGCGGAGAAA
Criblamydia_sequanensis	AACCTCGGAACGGCACTCGAAACTGTGTTTCTAGAGGTAGAGGAGAAA
Ch.sanzinia	AACCCCAAGTCAGCACTTAATACTGCTTTTCTAGAGGTAGATGGAGAAA
Ch.ibidis	AACCTCCAAACAGGCATCTAATACTATCTTTCTAGAGGTAGATGGAGAAA
Ch.pneumoniaeAR39	AACCCCAAGTCAGCATTTAAACTATCTTTCTAGAGGTAGATGGGAGAAA
Ch.pecorum	AACCTCAAGTCGGCATCTAATACTATCTTTCTAGAGGTGGATGGAGAAA
Ch.felis_strain	AACCCCAAAATCGGCATCTAATACTATCTTTCTAGAGGTAGATGGAGAAA
Ch.caviae	AACCCCAAGCCAGCATCTAATACTATCTTTCTAGAGGGTAGATGGAGAAA
Ch.psittaci	AACCCCAAGCCAGCATCTAATACTATCTTTCTTGAGGGTAGATGGAGAAA
Ch.gallinacea_08-1274/3	AACCTCAAGCCGGCATCTAATACTATCTTTCTAGAGGGTAGATGGAGAAA
Ch.avium_strain	AACCTTAAGTCAGCATCTAATACTATCTTTCTAGAGGGTAGATGGAGAAA
Ch.suis	AACCCGAATCGGCATCTGATACTATTTTTCTAGAGGGTAGATGGAGAAA
Ch.muridarum	AACCCCGAATCGGCATCTAAACTATTTTTCTAGAGGGTAGATGGAGAAA
Ch.trachomatis	AACCCCGAGTCGGCATCTAATACTATTTTTCTAGAGGTAGATGGAGAAA
Ca.Amphibiich.	AACCTCAAGTCAGCATCTAATACTGCCTATCTAGAGGACAGATGGAGAAA
Ca.Amphibiich.ranarum_strain	AACCTCAAGTCAGCATCTAATACTATCTATCTAGAGGACAGACGGAGAAA
Ca.Clavochl.salmonicola	AACCCCGAACAGGCATCTAAACTGTATTTCTAGAGGTGGGAGGAGAAA
Ca.Similich.latridicola	ATCTCCGGA-CTGCATACAAAACCTGCTCAGCTAGAGTATAAGAGGGGAAA
Ch.bacterium_clone	ATCTTCGGA-CTGCATACAAAACCTGCTTGACTAGAGTGAAGAGGGGAAA
Ca.Similich.labri	ATCTCCGGA-CTGCATACAAAACCTGTTGAGCTAGAGCATAAGAGGGGAAA
Ch.bacterium_CF280911-8	ATCTCCGGA-TCGCATACAAAACCTGCTTGACTAGAGTGAATAGGGGAAA
Ca.Piscichl._salmonis	ACCCCCAGG-CTGCTTCCAAAACCTGCTAGACTAGAGTTCAAGAGGGGAAA
	* * ** * *** * *** * * *
	RYGGGAGAA

	Panout RNGGAATTCCA
Protoch.naegleriophila	ACGGAATTCACAAAGTAGC-GGTGAAA-TGCGTAGATATGTGGAAGAACA
Ca.Protoch.amoebophila	ACGGAATTCACAAAGTAGC-GGTGAAA-TGCGTAGATATGTGGAAGAACA
Parach.acanthamoebae	ACGGAATTCACATGTAGC-GGTGAAA-TGCGTAGATATGTGGAAGAACA
Ca.Metachlamydia	ACGGAATTCACAAAGTAGC-GGTGAAA-TGCGTAGATATGTGGAAGAACA
Ca.Mesoch.elodeae	ACGGAATTCACAAAGTAGC-GGTGAAA-TGCGTAGATATGTGGAAGAACA
Ca.Rubidus.massiliensis	ATGGAATTCACAAAGTAGC-GGTGAAA-TGCGTAGATATGTGGAAGAACA
Neoch.hartmannellae	ATGGAATTCACAAAGTAGC-GGTGAAA-TGCGTAGATATGTGGAAGAACA
Can.Fritschea_bemisiae	ACGGAATTCCAAGGTAGC-GGTGAAA-TGCGTAGATATTTGGAAGAACA
Ca.Fritschea_eriococci	ACGGAATTCCAAGGTAGC-GGTGAAA-TGCGTAGATATTTGGAAGAACA
Ca.Syngnamydia	ACGGAATTCCAAGGTAGC-GGTGAAA-TGCGTAGATATTTGGAAGAACA
Ca.Neptunoch.vexilliferae	ACGGAATTCCAAGGTAGC-GGTGAAA-TGCGTAGATATTTGGAAGAACA
Ca.Syngnamydia_venezia	ATGGAATTCCAAGGTAGC-GGTGAAA-TGCGTAGATATTTGGAAGAACA
Simkania_negevensis	ACGGAATTCACGTGTAGC-GGTGAAA-TGCGTAGATATGTGGAAGAACA
Rhabdoch.crassificans	ACGGAATTCACGTGTAGC-GGTGAAA-TGCTTAGATATGTGGAAGAACA
Ca.Rhabdoch.porcellionis	ACGGAATTCACGTGTAGC-GGTGAAA-TGCGTAGATATGTGGAAGAACA
Ca.Renich.lutjani	ATGGAATTCACGTGTAGC-GGTGAAA-TGCGTAGAAATGTGGAAGAACA
Waddlia_sp.G817	ACGGAATTCACATGTAGC-GGTGAAA-TGCGTAGATATGTGGAAGAACA
Waddlia_chondrophila	ACGGAATTCCTCATGTTGCCGGTGAAATGCGTAGATATTTGGAAGAACA
Estrella	ACGGAATTCACAAAGTAGC-GGTGAAA-TGCGTAGATATGTGGAAGAACA
Criblamydia_sequanensis	ATGGAATTCACAAAGTAGC-GGTGAAA-TGCGTAGATATGTGGAAGAACA
Ch.sanzinia	AGGGAATTCACATGTAGC-GGTGAAA-TGCGTAGATATGTGGAAGAACA
Ch.ibidis	AGGGAATTCACGTGTAGC-GGTGAAA-TGCGTAGATATGTGGAAGAACA
Ch.pneumoniaeAR39	AGGGAATTCACGTGTAGC-GGTGAAA-TGCGTAGATATGTGGAAGAACA
Ch.pecorum	AGGGAATTCACGTGTAGC-GGTGAAA-TGCGTAGATATGTGGAAGAACA
Ch.felis_strain	AGGGAATTCACGTGTAGC-GGTGAAA-TGCGTAGATATGTGGAAGAACA
Ch.caviae	AGGGAATTCACGTGTAGC-GGTGAAA-TGCGTAGATATGTGGAAGAACA
Ch.psittaci	AGGGAATTCACGTGTAGC-GGTGAAA-TGCGTAGATATGTGGAAGAACA
Ch.gallinacea_08-1274/3	AGGGAATTCACGTGTAGC-GGTGAAA-TGCGTAGATATGTGGAAGAACA
Ch.avium_strain	AGGGAATTCACGTGTAGC-GGTGAAA-TGCGTAGATATGTGGAAGAACA
Ch.suis	AGGGAATTCACGTGTAGC-GGTGAAA-TGCGTAGATATGTGGAAGAACA

AGGGAATTTACAGTGTAGC -GGTGAAA -TGCGTAGATATGTGGAAGAACA
AGGGAATTTACAGTGTAGC -GGTGAAA -TGCGTAGATATGTGGAAGAACA
AGGGAATTCACAGTGTAGC -GGTGAAA -TGCGTAGATATGTGGAAGAACA
AGGGAATTCACATGTAGC -GGTGAAA -TGCGTAGATATGTGGAAGAACA
AGGGAATTCACAGTGTAGC -GGTGAAA -TGCGTAGATATGTGGAAGAACA
GCGGAATTCACAAGTAGC -GGTGAAA -TGCGTAGATATGTGGAGGAACA
GCGGAATTCACAAGTAGC -GGTGAAA -TGCGTAGATATGTGGAGGAACA
GCGGAATTCACAAGTAGC -GGTGAAA -TGCGTAGATATGTGGAGGAACA
GCGGAATTCACAAGTAGC -GGTGAAA -TGCGTAGATATGTGGAGGAACA
ATGGAATTCACAAGTAGC -GGTGAAA -TGCGTAGATATGTGGAGGAACA

***** *

RN GGAATTCCA

Panin

GTGGCGAAGGCGCTTTC

[illegible]

GTGGCGAAGGCGCTTTTC

[illegible]

Protocn.naegleriophila
 Ca.Protocn.amoebophila
 Parach.acanthamoebae
 Ca.Metach.
 Ca.Mesoch.elodeae
 Ca.Rubidus.massiliensis
 Neoch.hartmannellae
 Can.Fritschea.bemisiae
 Ca.Fritschea.ericoccci
 Ca.Syngnamydia
 Ca.Neptunoch.vexilliferae
 Ca.Syngnamydia.venezia
 Simkania.negevensis
 Rhabdoch.crassificans
 Ca.Rhabdoch.porcellionis
 Ca.Renich.lutjani
 Waddlia.sp.G817
 Waddlia.chondrophila
 Estrella
 Criblamydia.sequanensis
 Ch.sanzinia
 Ch.ibidis
 Ch.pneumoniaeAR39
 Ch.pecorum
 Ch.felis_strain
 Ch.caviae
 Ch.psittaci
 Ch.gallinacea_08-1274/3
 Ch.avium_strain
 Ch.suis
 Ch.muridarum
 Ch.trachomatis
 Ca.Amphibiich.
 Ca.Amphibiich.ranarum_strain
 Ca.Clavochl.salmonicola
 Ca.Similich.latridicola
 Ch.bacterium_clone
 Ca.Similich.labri
 Ch.bacterium_CF280911-8
 Ca.Piscichl.salmonis

GTATAGGGG-ATCAAAACAGGATTAGATACCTGGTAGTCCTTAACGTAAAC
GC-AAGGGGAGCAAAACAGGATTAGATACCTGGTAGTCCTTGCCGTA AAC
GC-AAGGGGAGCAAAACAGGATTAGATACCTGGTAGTCCTTGCCGTA AAC
GC-AAGGGGAGCAAAACAGGATTAGATACCTGGTAGTCCTTGCCGTA AAC
GC-AAGGGGAGCAAAACAGGATTAGATACCTGGTAGTCCTTGCCGTA AAC
GC-AAGGGGAGCAAAACAGGATTAGATACCTGGTAGTCCTTGCCGTA AAC
GC-AAGGGGAGCAAAACAGGATTAGATACCTGGTAGTCCTTGCCGTA AAC
GC-AAGGGGAGCAAAACAGGATTAGATACCTGGTAGTCCTTGCCGTA AAC
GC-AAGGGGAGCAAAACAGGATTAGATACCTGGTAGTCCTTGCCGTA AAC
GC-AAGGGGAGCAAAACAGGATTAGATACCTGGTAGTCCTTGCCGTA AAC
GC-AAGGGGAGCAAAACAGGATTAGATACCTGGTAGTCCTTGCCGTA AAC
GC-AAGGGGAGCAAAACAGGATTAGATACCTGGTAGTCCTTGCCGTA AAC
GCATGGGG-AGCAAAACAGGATTAGATACCTGGTAGTCCTTGCCGTA AAC
GCATGGGG-AGCAAAACAGGATTAGATACCTGGTAGTCCTTGCCGTA AAC
GCATGGGG-AGCAAAACAGGATTAGATACCTGGTAGTCCTTGCCGTA AAC
GCATGGGG-AGCAAAACAGGATTAGATACCTGGTAGTCCTTGCCGTA AAC
GCAAGGGG-AGCAAAACAGGATTAGATACCTGGTAGTCCTTGCCGTA AAC
* * * * * * * * * * * * * * *

[illegible]

GCGTTAAGTATACCGCCTGGGGAGTAGCTCGCAAGGCTGAAACTCAAAA
GCGTTAAGTATACCGCTGGGGAGTAGCTCGCAAGGCTGAAACTCAAAA
GCGTTAAGTATACCGCTGGGGAGTAGCTCGCAAGGCTGAAACTCAAAA
GCGATAAGTATACCGCCTGGGGAGTAGCTCGCAAGGCTGAAACTCAAAA
GCGATAAGTATACCGCTGGGGAGTAGCTCGCAAGGCTGAAACTCAAAA
GCGATAAGTATACCGCTGGGGAGTAGCTCGCAAGGCTGAAACTCAAAA
GCGATAAGTATACCGCCTGAGGAGTAGCTCGCAAGGCTGAAACTCAAAA
GCGTTAAGTATGCCACTGAGGAGTAGCCGCCGAAGGCTGAAACTCAAAA
GCGTTAAGTATGCCACTGAGGAGTAGCCGCCGAAGGCTGAAACTCAAAA


```

122E AGCAAGGGGAGCAAACAGGATTAGATACCCTGGTAGTCCTTGCCCTAAACATGATA
85E AGCAAGGGGAGCAAACAGGATTAGATACCCTGGTAGTCCTTGCCCTAAACATGATA
20E AGCAAGGGGAGCAAACAGGATTAGATACCCTGGTAGTCCTTGCCCTAAACGATGCATA
1E AGCAAGGGGAGCAAACAGGATTAGATACCCTGGTAGTCCTTGCCCTAAACGATGCATA
52E AGCAAGGGGAGCAAACAGGATTAGATACCCTGGTAGTCCTTGCCCTAAACGATGCATA
10E AGCAAGGGGAGCAAACAGGATTAGATACCCTGGTAGTCCTTGCCCTAAACGATGCATA
38E AGCAAGGGGAGCAAACAGGATTAGATACCCTGGTAGTCCTTGCCCTAAACGATGCATA
42E AGCAAGGGGAGCAAACAGGATTAGATACCCTGGTAGTCCTTGCCCTAAACGATGCATA
48E AGCAAGGGGAGCAAACAGGATTAGATACCCTGGTAGTCCTTGCCCTAAACGATGCATA
6E AGCAAGGGGAGCAAACAGGATTAGATACCCTGGTAGTCCTTGCCCTAAACGATGCATA
7E AGCAAGGGGAGCAAACAGGATTAGATACCCTGGTAGTCCTTGCCCTAAACGATGCATA
8E AGCAAGGGGAGCAAACAGGATTAGATACCCTGGTAGTCCTTGCCCTAAACGATGCATA
123E AGCAAGGGGAGCAAACAGGATTAGATACCCTGGTAGTCCTTGCCCTAAACGATGCATA
28E AGCAAGGGGAGCAAACAGGATTAGATACCCTGGTAGTCCTTGCCCTAAACGATGCATA
11E AGCAAGGGGAGCAAACAGGATTAGATACCCTGGTAGTCCTTGCCCTAAACGATGCATA
120E AGCAAGGGGAGCAAACAGGATTAGATACCCTGGTAGTCCTTGCCCTAAACGATGCATA
18E AGCAAGGGGAGCAAACAGGATTAGATACCCTGGTAGTCCTTGCCCTAAACGATGCATA
24E AGCAAGGGGAGCAAACAGGATTAGATACCCTGGTAGTCCTTGCCCTAAACGATGCATA
39E AGCAAGGGGAGCAAACAGGATTAGATACCCTGGTAGTCCTTGCCCTAAACGATGCATA
32E AGCAAGGGGAGCAAACAGGATTAGATACCCTGGTAGTCCTTGCCCTAAACGATGCATA
33E AGCAAGGGGAGCAAACAGGATTAGATACCCTGGTAGTCCTTGCCCTAAACGATGCATA
21E AGCAAGGGGAGCAAACAGGATTAGATACCCTGGTAGTCCTTGCCCTAAACGATGCATA
15E AGCAAGGGGAGCAAACAGGATTAGATACCCTGGTAGTCCTTGCCCTAAACGATGCATA
14E AGCAAGGGGAGCAAACAGGATTAGATACCCTGGTAGTCCTTGCCCTAAACGATGCATA
142E AGCAAGGGGAGCAAACAGGATTAGATACCCTGGTAGTCCTTGCCCTAAACGATGCATA
46E AGCAAGGGGAGCAAACAGGATTAGATACCCTGGTAGTCCTTGCCCTAAACGATGCATA
126E AGCAAGGGGAGCAAACAGGATTAGATACCCTGGTAGTCCTTGCCCTAAACGATGCATA
C.pneumoniae_AR39
** *****

```

Figure S3. Alignment of panNPCR 58 nt sequences from blood. Polymorphic sites are red shadowed. "Chlamydia-related bacteria" are grey shadowed

Table S1. Sputum sample data.

Number	Sample	Age	Gender	NPCR 461 bp	mtDNA	NPCR 121 bp	5x2x5 panNPCR
1	DS	27	F	+	+	+	+
2	MŠ	24	F	-	+	-	-
3	BŠ	24	F	-	+	-	-
4	MS	27	M	-	+	-	-
5	PS	60	M	+	+	+	+
6	MR	24	M	+	+	+	+
7	2SP	24	F	-	+	+	+
8	3SP	25	F	-	+	-	-
9	4SP	27	F	-	+	-	-
10	5SP	28	M	+	+	+	nd
11	6SP	55	F	-	+	-	+ CRB
12	7SP	58	F	-	+	-	-
13	10SP	27	F	+	+	+	nd
14	11SP	60	F	-	+	-	-
15	17SP	28	F	-	+	-	-
16	18SP	30	M	+	+	+	nd
17	20SP	26	F	+	+	+	nd
18	21SP	27	F	+	+	+	nd
19	27SP	22	F	-	+	-	+ CRB
20	28SP	55	M	-	+	+	nd
21	29SP	35	M	-	+	-	-
22	30SP	53	M	-	+	-	-
23	33SP	23	Ž	+	+	+	nd
24	34SP	27	M	-	+	-	-

25	37SP	49	Ž	-	+	-	-
26	38SP	49	M	-	+	-	-
27	39SP	22	F	-	+	-	-
28	41SP	65	M	-	+	-	-
29	44SP	65	M	-	+	-	-
30	45SP	31	M	+	+	+	nd
31	48SP	53	F	-	+	-	-
32	49SP	72	M	-	+	-	-
33	52SP	29	F	-	+	-	-
34	54SP	22	F	-	+	-	-
35	58SP	26	M	-	+	-	+ CRB
36	60SP	22	M	-	+	-	-
37	61SP	26	F	-	+	-	-
38	64SP	23	F	-	+	-	-
39	66SP	20	F	-	+	-	+ CRB
40	67SP	20	F	-	+	+	+
41	68SP	26	F	-	+	-	-
42	69SP	40	F	-	+	-	-
43	70SP	31	M	-	+	-	-
44	1002	41	M	-	+	-	-
45	3001	25	M	-	+	-	+
46	3002	25	M	-	+	+	nd
47	3003	25	M	-	+	+	nd
48	3004	24	M	-	+	-	-
49	3005	25	M	-	+	-	-
50	3006	22	M	-	+	-	-
51	3007	28	F	-	+	-	-
52	3008	30	M	-	+	-	-
53	3009	20	M	-	+	-	-
54	3010	22	M	-	+	-	-
55	3011	26	M	-	+	-	-
56	3012	21	M	-	+	-	-
57	3013	28	M	-	+	-	-
58	3014	22	M	+	+	+	nd
59	3015	27	M	-	+	-	-
60	3016	27	M	+	+	+	+
61	3017	30	M	-	+	-	-
62	3018	21	M	-	+	-	-
63	3019	30	M	-	+	-	-
64	3020	30	M	-	+	-	-
65	3021	19	M	-	+	-	+ CRB
66	3022	21	M	-	+	+	+
67	3023	24	M	-	+	-	-
68	3024	24	M	-	+	-	-
69	3025	24	M	-	+	-	-
70	3026	22	M	-	+	-	+ CRB
71	3027	21	M	-	+	-	-
72	3028	26	M	-	+	-	-
73	3029	24	M	-	+	-	-

74	3030	23	F	-	+	-	-
75	3031	26	M	-	+	+	nd
76	3032	21	M	-	+	-	-
77	3033	30	M	-	+	-	+ CRB
78	5002	63	F	-	+	-	-
79	5003	57	F	-	+	-	-
80	5004	51	M	-	+	-	-
81	5005	77	M	-	+	+	+
82	5006	74	F	-	+	-	-
83	5007	66	M	-	+	-	-
84	5008	51	F	-	+	-	-
85	5009	66	F	-	+	+	nd
86	2CHP	24	M	-	+	-	+
87	3CHP	60	F	-	+	-	-
88	4CHP	41	F	-	+	-	-
89	5CHP	59	M	-	+	-	-
90	7CHP	77	M	-	+	+	+
91	9CHP	63	F	-	+	-	-
92	11CHP	29	M	-	+	-	+
93	13CHP	44	F	-	+	+	nd
94	14CHP	47	M	-	+	+	+
95	15CHP	47	M	-	+	-	-
96	16CHP	26	F	-	+	+	nd
97	18CHP	28	M	-	+	+	nd
98	19CHP	25	M	-	+	-	+
99	20CHP	53	F	-	+	-	-
100	21CHP	42	F	-	+	-	+
101	23CHP	27	M	-	+	-	+
102	24CHP	33	F	-	+	-	+
103	27CHP	48	M	-	+	-	-
104	29CHP	44	F	-	+	-	-
105	30CHP	55	F	-	+	-	-
106	31CHP	66	M	-	+	-	+
107	33CHP	69	M	-	+	-	-
108	36CHP	62	F	-	+	-	+
109	37CHP	67	M	-	+	-	-
110	38CHP	43	M	-	+	-	-
111	39CHP	39	F	-	+	-	-
112	41CHP	61	F	-	+	+	+
113	45CHP	16	F	-	+	+	nd
114	48CHP	37	M	-	+	+	nd
115	49CHP	37	F	-	+	+	+
116	52CHP	30	M	-	+	-	+ CRB
117	53CHP	55	F	-	+	-	-
118	57CHP	43	F	+	+	+	+ CRB
119	58CHP	67	F	-	+	+	nd
120	60CHP	22	M	-	+	+	nd
121	62CHP	60	M	-	+	-	-
122	63CHP	27	F	-	+	-	-

123	64CHP	24	F	-	+	-	+ ^{CRB}
124	71CHP	28	M	-	+	+	nd
125	73CHP	33	M	-	+*	-	+
126	74CHP	56	F	-	+	-	+ ^{CRB}
127	76CHP	29	M	-	+	-	-
128	77CHP	33	M	-	+*	-	-
129	78CHP	60	F	-	+	+	nd
130	80CHP	34	M	-	+*	-	-
131	81SP	38	F	-	+	-	+ ^{CRB}
132	84CHP	60	F	-	+	+	nd
133	85CHP	61	M	-	+	-	-
134	88CHP	49	M	-	+	-	-
135	91CHP	37	F	-	+	-	-
136	92CHP	43	M	-	+*	-	-
137	93CHP	70	F	-	+	+	nd
138	96CHP	45	F	-	+	-	-
139	97CHP	27	F	-	+*	+	nd
140	98CHP	44	F	-	+*	-	+
141	101CHP	25	F	-	+	-	+
142	102CHP	26	M	-	+*	-	-
143	105CHP	34	F	-	+	-	-
144	107CHP	23	F	-	+*	-	-
145	108CHP	25	F	-	+	-	-
146	109CHP	52	F	-	+	-	+ ^{CRB}
147	110CHP	58	M	-	+	-	+
148	111CHP	-	M	-	+	+	+
149	28CHP	32	M	-	- ^e	nd	nd
150	34CHP	33	M	-	+	+ ^x	-
151	35CHP	32	F	-	+	+ ^x	+ ^x
152	70CHP	25	F	-	- ^e	nd	nd
153	75CHP	29	F	-	+	+ ^x	+ ^x
154	94CHP	45	M	-	+*	+ ^x	+ ^x
155	95CHP	36	F	-	- ^e	nd	nd
156	104CHP	49	M	-	+	+ ^x	+ ^x

M male; F; F Female; *1023 bp mtDNA amplicon absent, but 250 bp present; nd not determined; ^e excluded from further analysis due to the DNA degradation. ^x not included due to low PCR yield (DNA was not sequenced or provided unreadable sequence); CRB - DNA sequence from *Chlamydia*-related bacteria”.

Table S2. ELISA vs panNPCR in blood

Number	Sample	Gender	Age	IgM	IgG	IgA	mtDNA	5x2x5 panNPCR	Free DNA
1.	1E	M	87	-	+/-10.1	11.8	+	+ ^C	+
2.	2E	F	43	-	-	-	+	-	nd
3.	3E	M	56	-	+/-10.1	-	+	-	nd
4.	4E	F	70	-	+/-10.7	-	+	+	nd
5.	5E	F	86	-	-	-	+	-	-
6.	6E	M	53	-	+/-8.6	-	+	+ ^C	-

7.	7E	F	35	-	+/-10.9	-	+	+ ^C	-
8.	8E	F	43	+13.5	-	-	+	+ ^C	-
9.	10E	F	11	-	-	-	+	-	nd
10.	11E	F	28	-	+/-10.6	-	+	+ ^{CRB}	nd
11.	12E	F	52	-	-	-	+	-	nd
12.	13E	M	43	-	+12.7	-	+	-	nd
13.	14E	F	39	+/-11.5	-	-	+	+ ^{CRB}	+
14.	15E	F	29	+12	-	-	+	+ ^{CRB}	nd
15.	16E	M	56	-	+/-8.7	-	+	-	nd
16.	17E	F	54	-	+/-9	-	+	-	nd
17.	18E	M	73	-	+/-9.8	-	+	+ ^{CRB}	nd
18.	19E	F	67	-	+/-11	+/-8.5	+	-	nd
19.	20E	M	62	-	-	-	+	+ ^C	nd
20.	21E	F	28	-	-	-	+	+ ^{CRB}	nd
21.	22E	F	73	-	+/-9.9	-	+	-	nd
22.	23E	F	64	-	-	-	+	-	nd
23.	24E	M	64	+15.4	+/-8.9	-	+	+ ^{CRB}	+
24.	25E	F	47	-	-	-	+	-	nd
25.	26E	M	40	-	+/-9.9	-	+	-	nd
26.	27E	F	66	-	-	-	+	-	nd
27.	28E	M	30	-	-	-	+*	+ ^{CRB}	nd
28.	29E	F	65	-	-	-	+*		nd
29.	30E	F	69	-	-	-	+	-	nd
30.	31E	F	60	-	-	+/-11.3	+	-	nd
31.	32E	M	42	+17.5	-	-	+	+ ^{CRB}	+
32.	33E	F	41	+/-8.9	-	-	+	+ ^{CRB}	-
33.	35E	F	81	-	-	+/-11.5	+*	-	nd
34.	36E	F	43	-	+/-9.5	-	+	-	nd
35.	38E	F	44	+/-8.8	-	-	+	+ ^C	-
36.	39E	M	46	-	-	-	+	+ ^{CRB}	nd
37.	41E	M	26	-	-	+/-9.8	+	-	nd
38.	42E	F	36	-	-	-	+	+ ^C	nd
39.	43E	F	38	-	-	-	+	-	nd
40.	44E	F	45	-	+13.1	-	+*	-	nd
41.	45E	F	41	-	-	-	+	-	nd
42.	46E	M	59	-	+12	-	+*	+ ^{CRB}	nd
43.	47E	M	10	-	-	-	+*	-	nd
44.	48E	F	52	-	-	-	+	+ ^C	nd
45.	49E	M	17	-	-	-	+	-	nd
46.	50E	F	35	-	-	-	+	-	nd
47.	51E	F	10	-	-	-	+	-	nd
48.	52E	F	37	-	+/-10.8	-	+	+ ^C	nd
49.	53E	F	50	-	+13.2	-	+	-	nd
50.	54E	F	75	-	-	-	+	-	nd
51.	55E	F	90	-	+14.2	+25	+	-	nd
52.	56E	F	42	-	-	-	+	-	nd

53.	57E	F	31	-	+12.2	-	+	-	nd
54.	58E	M	43	-	-	-	+	-	nd
55.	59E	F	5	-	-	-	+	+	nd
56.	60E	F	79	-	+/-11	-	+	-	nd
57.	66E	M	87	-	+12.9	-	+	-	nd
58.	67E	F	67	-	+12.2	-	+	-	nd
59.	69E	M	35	-	+12.7	-	+	-	nd
60.	70E	M	64	-	+/-10.7	-	+	-	nd
61.	71E	M	67	-	+14.8	+12.3	+	-	nd
62.	72E	F	66	-	+/-8.7	-	+	+	nd
63.	73E	M	48	-	+13.2	-	+	-	nd
64.	74E	F	66	-	+22.3	+12	+	-	nd
65.	75E	M	59	-	+23.8	+33.2	+	-	nd
66.	76E	F	37	-	-	-	+	-	nd
67.	77E	F	45	-	-	-	+	-	nd
68.	78E	F	39	-	+12.5	-	+	+	nd
69.	79E	F	31	-	+/-10	+14.3	+	+	nd
70.	84E	F	39	-	+13.4	-	+	+	nd
71.	85E	F	43	-	-	+14.7	+	+ ^{CRB}	nd
72.	86E	M	64	-	+24.8	+12.8	+	-	nd
73.	88E	M	36	-	-	+/-9.4	+	-	nd
74.	89E	F	82	-	-	-	+	-	nd
75.	90E	F	62	-	+/-8.5	+20	+	-	nd
76.	95E	F	17	+/-10.7	-	-	+	-	nd
77.	115E	F	50	+19	+12.5	-	+	-	nd
78.	116E	M	31	+/-10.1	-	-	+	-	nd
79.	120E	F	40	+/-11.5	+14.2	-	+	+ ^{CRB}	nd
80.	122E	F	73	+/-9	+14.5	-	+	+ ^{CRB}	nd
81.	123E	F	68	+/-10	+/-11.3	-	+	+ ^{CRB}	nd
82.	124E	F	70	-	+20.7	-	+	-	nd
83.	125E	M	46	-	+17.5	-	+	-	nd
84.	126E	M	34	+12.8	+/-10.1	-	+	+ ^{CRB}	nd
85.	127E	M	35	-	+19.9	+/-9.9	+	-	nd
86.	130E	M	72	-	+16.3	-	+	-	nd
87.	131E	F	8	+/-10.1	-	-	+	-	nd
88.	132E	F	39	-	+16.1	-	+	-	nd
89.	137E	F	66	-	+22.7	-	+	-	nd
90.	142E	M	46	+/-10.3	-	-	+	+ ^{CRB}	nd
91.	143E	F	34	-	+15.5	-	+	+	nd
92.	151E	F	26	+/-10.3	-	-	+	-	nd
93.	152E	F	66	+/-10.3	-	-	+	-	nd
94.	153E	M	47	+/-10.3	-	-	+	-	nd

M male; F female; ELISA IgA, IgM, IgG: Cut-off: 10; Grey zone: 8,5-11,5; Negative: <8,5; Positive: >11,5. C - DNA sequence from the genus *Chlamydia*, CRB - DNA sequence from *Chlamydia*-related bacteria". *1023 bp mtDNA amplicon absent, but 250 bp present; nd - not determined; 4E, 59E, 72E, 78E, 79E, 84E, 143E were not sequenced.