

S1 Table. Variant alleles of the single-locus variants (SLVs) found within *C. abortus* clonal complex and comparison with LLG singleton clone (ST30).

ST of ancestor clone	ST of SLV	Variant locus in SLV	Ancestral allele	SLV allele	No of nucleotide differences	Other clones containing SLV allele	Amino acid change ^a
19	86	<i>hemN</i>	4	14	1	ST25	Syn
19	87	<i>hemN</i>	4	21	1	None	A-T ^b
19	29	<i>fumC</i>	5	18	1	None	Syn
86	25	<i>gatA</i>	5	18	1	None	Syn
comparison with ST30 (singleton clone)		Variant locus in singleton	ST19 allele	Singleton allele		Other clones containing singleton allele	
		<i>gatA</i>	5	13	1	ST36*	G-D ^c
		<i>oppA</i>	8	18	1	None	Syn
		<i>gidA</i>	8	19	1	None	Syn
		<i>enoA</i>	8	16	2	None	G-E ^d
		<i>fumC</i>	5	17	3 ^e	None	Syn

^a Residue in ST19 is given first. Syn, synonymous change

^b Amino-acid Thr (T) at the position 115 is unique among all chlamydial *hemN*-encoded protein alleles (S2A.b Fig)

^c Amino-acid Gly (G) characterizing *C. abortus* clonal complex is unique among all chlamydial *gatA*-encoded protein alleles at the conserved position 125 (S2B.b Fig)

^d Amino-acid Glu (E) is unique among all chlamydial *enoA*-encoded protein alleles at the conserved position 106 (S2D.b Fig)

^e Residue T at position 243 of *fumC*_17 harbouring in the LLG singleton is unique among all chlamydial *fumC* alleles (S2C.b Fig)

* ST36 corresponds to the variant *C. psittaci* 84/2334 strain previously proposed belonging to *C. abortus* [22]