

Appendix Table. Primers used for amplifying and sequencing the 9 intergenic spacers

Spacer name	Spacer position on the genome*	Spacer size (amplicon size, bp)†	Forward primer (5'‐3')	Reverse primer (5'‐3')	Reference
<i>tRNA-Ala/GCA-</i> <i>tRNA-Ile/AUC</i> (S1)	1412349– 1412683	335 (588)	TGCACAGAAAAACCTCACCTT	AGGTCGGAGGTTCAAGTCCT	This study
BH2865724- <i>dut</i> (S2)	1685859– 1686289	431 (602)	GGTTTTGCCACGGGTATT	GGAAGTTCTAACCTTGTCATGG	(31)
<i>DnaJ</i> related protein- <i>cobS</i> (S3)	1828960– 1829320	361 (490)	CAATGGAGGCAACC GTTCTT	GTGATATCGGGTACATTTCAACTG	(31)
<i>pssA</i> - Oxidoreductase (S4)	609654– 610228	575 (709)	GATTTTCTTCCGTGTAGCTTGT	TGTGCGTAAAATCGATTCATG	(31)
<i>carB</i> -Cold shock protein (S5)	1292681– 1293066	386 (509)	AGAAGCTATCGAACACTCACAA	TGAATGAACCGAACCTTAGT	(31)
<i>alr-gcvP</i> (S6)	1431110– 1431442	333 (540)	TCAAAGAGGTGATTGGGTAGAGC	CTGTTCACGTATTGATAATGTTGC	(31)
<i>ftsK</i> - Oxidoreductase (S7)	1799482– 1799984	503 (594)	GCGAACCTTGAGAACTCTGCA	GGGTTTACACCTTCATTGAGATCA	(31)
BH2864883- BH2864884 (S8)	1594026– 1594377	352 (689)	GAAATTCCCTGCTGCAAAGC	GAAAATTGGGGAGGGTGT	This study
<i>acpP2</i> -Malate oxidoreductase (S9)	853898– 854063	166 (296)	CAACTTCACTGATTCTGCGATAA	CGAGGAGTGGTTAATATGACAGCT	(31)

\*Intergenic spacer designations consist of the name of the 5' open reading frame (ORF)—the name of the 3'-ORF. ORFs encoding putative proteins of unknown function have designations beginning with BH and are numbered with reference to the *Bartonella henselae* type strain, Houston-1, genome (GenBank accession no. BX897699).

†The position of the spacers on the genome and spacer sizes were deduced from the genome sequence of *B. henselae* Houston-1. These values may vary among *B. henselae* strains.