

Supplementary material for Purser and Norris (2000) *Proc. Natl. Acad. Sci. USA* **97** (25), 13865-13870.

**Table 3.** Primer sequences, amplicon coordinates, and  $T_m$  information for specific PCR amplification of *Borrelia burgdorferi* B31 plasmids

Plasmid	Primer	Sequence	Amplicon coordinates	Corresponding gene(s)	$T_m$ , °C*
cp9	F-4568	5' GGA CTG GTA TTT ACT CCG GCT GAT AGA GC 3'	6372-6650	BBC10 rev protein ( <i>rev</i> ) (6808-6284)	64.3
	R-4569	5' CCT TAA TGA TGA GGC CGA TGA AGT TGC 3'			62.0
cp26	F-4536	5' ATA GCC CAT TCC AGA CAT TAA ACC GCC T 3'	14001-14394	BBB17 <i>guaB</i> (15107-13896)	73.0
	R-4537	5' AGT TCC CCA AAT AAC AGC AAT CTG CGA 3'			72.9
cp32-1	F-4571	5' ACG ATA GGG TAA TAT CAA AAA AGG 3'	21583-22054	BBP33 conserved hypothetical protein (21510-22115)	53.1
	R-4572	5' AGT TCA TCT AAT AAA AAT CCC GTG 3'			53.5
cp32-2 and cp32-7†	F-4577	5' GGA ATG TAT TAA TTG ATA ATT CAG 3'	20986-21360	BBO32 plasmid partition protein, putative (20766-21512)	47.7
	R-4578	5' GCG AAC TAA ATA GTG CCT TAT GGG 3'			58.0
cp32-3	F-4529	5' GCA AGT TCC CAC GAT AAC ACA CCC GTA T 3'	26897-27416	<i>ospG-bapA</i> (26708-27295, 27410-27916)	73.7
	R-4530	5' TTT TCA TAT CCC CTC CTA GCT TTA TTG CC 3'			70.1
cp32-6	F-4575	5' GAC TTT ACA TAG TAT AAA TGC TTT TGG 3'	21008-21281	BBM32 plasmid partition protein, putative (20721-21467)	53.5
	R-4576	5' TCT CGT TAT TAT AAA ATA AGT AGG 3'			48.0
cp32-8	F-4579	5' GAA GAT TTA AAC AAA AAA ATT GCG 3'	21376-21610	BBL32 plasmid partition protein, putative (20740-21477), BBL33 hypothetical protein (21467-21556), BBL34 conserved hypothetical protein (21540-22097)	50.7

Plasmid	Primer	Sequence	Amplicon coordinates	Corresponding gene(s)	$T_m$ , °C*
	R-4580	5' GTA ATC ACT TCT TTT TTA CCA TCG 3'			52.9
cp32-9	F-4581	5' TAT CAA AAA AGT GCT GTT TTA TAG 3'	21473-21721	BBN32 plasmid partition protein, putative (20817-21569), BBN33 conserved hypothetical protein (21614-22171)	50.2
	R-4582	5' TAA TCT CAA ATA TTC TTC TTT ATG 3'			46.2
lp17	F-4507	5' ACT GCA ATC TGC CCA AGC TAC ATA ATC T 3'	7657-7939	BBD12 hypothetical protein-BBD13 hypothetical protein ( <i>Bb</i> ) (7752-7624, 7787-8110)	69.7
	R-4508	5' AAG GTA AGG ACG GTT GTC TAC ATG GAT T 3'			68.7
lp21	F-4562	5' TGT GGT TGC TAA AAC CCA AGC GT 3'	14905-15520	BBU06 conserved hypothetical protein-BBU07 conserved hypothetical protein (14633-15232, 15349-15810)	63.1
	R-4563	5' TTG TTT CTA ATT GCT CTG AAT TGC ATC C 3'			58.8
lp25	F-4511	5' AGA ATT ATG TCG GTG GCG TTG T 3'	14663-14921	BBE21.1 transposase-related protein, pseudogene ( <i>Bb</i> ) 14767-14893	66.3
	R-4484	5' ATT AAA GCC GCC TTT TCC TTG GT 3'			68.1
lp25 (secondary site)	F-4596	5' TTG CTG CCA TTT CTC ACT TGG TAA 3'	9783-9959	BBE16 hypothetical protein (10187-9570)	65.0
	R-4597	5' ATA AAA GCG ACA GGT TAT CGT GCA G 3'			64.6

Plasmid	Primer	Sequence	Amplicon coordinates	Corresponding gene(s)	$T_m$ , °C*
lp28-1	F-4340	5' CGG GGA TCC AGC CAA GTT GCT GAT AAG GAC GAC CC 3'	(149 bp)	<i>vlsE</i> upstream conserved region	71.9
	R-4084	5' ACG GCA GTT CCA ACA GAA CCT GTA CTA TCT 3'			64.6
lp28-1 (secondary site)	F-4598	5' TTC TGA TGG CAC TGA GCA AAC CA 3'	1309-1457	BBF01 Erp D protein, putative (47-1462)	67.3
	R-4599	5' AAC CCT TTA CAC TTT CTT CGA TTG CGC T 3'			69.2
lp28-2	F-4523	5' CCC TCA TCA AGT TTT TCC ATG TGT TTT T 3'	13824-14276	BBG17 hypothetical protein (14341-13511)	69.7
	R-4524	5' AGG TGG CCT TTC CGA GCT TGT ACC TTA C 3'			73.2
lp28-3	F-4534	5' AAC ACT ATC TTA AAT GTC CCC CAC AA 3'	11570-11901	BBH17 hypothetical protein (11837-12025)	66.0
	R-4535	5' GTG GAA GAG TGG TTA TGG TCA ATT TT 3'			65.7
lp28-4	F-4525	5' TCA CCT CAG CTA ATC TAT TTA TCG ACA C 3'	9005-9219	putative noncoding region	65.1
	R-4526	5' AAG CGC GGA GTT TTC GGC TG 3'			72.4
lp36	F-4518	5' TTC TTA TCC CTG ACT TTC ACT TTT GAG G 3'	7247-7627	BBK12 hypothetical protein (7335-8030)	67.7
	R-4519	5' TCC TTT ACT TCT ATG TTT TTA CTT TCC TTG GT 3'			66.0
lp38	F-4505	5' AGC A/GGC AGA ACA AAA CAT GCA AAA ACT G 3'	6541-6668	BBJ09 <i>ospD</i> (6089-6859)	71.8
	R-4506	5' TCC AAG CTA TTT CTA CGG CCT CTT TAG C 3'			70.0
lp54	F-4538	5' GCA AAA TGT TAG CAG CCT TGA CGA GAA A 3'	9446-9554	BBA15 <i>ospA</i> (9393-10211)	72.5
	R-4539	5' TAG ATC GTA CTT GCC GTC TTT GTT TTT T 3'			67.8
lp56	F-4566	5' ACT ATT AAG ACG AGC AAT AAA AAG TCC A 3'	42929-43524	BBQ67 adenine specific DNA methyltransferase (43732-40439)	57.7
	R-4567	5' GAC GAA GCA AAG AAG GAT TTG GAT CAC C 3'			62.4

\*As calculated based on the nearest-neighbor thermodynamic parameter set of Allawi and SantaLucia (1) and a coefficient of 12.0 for the salt dependence.

†This primer set does not distinguish between cp32-2 and cp32-7.

Reference:

1. Allawi, H. T. & SantaLucia, J., Jr. (1997) *Biochemistry* **36**, 10581--10594.