

Table 4. Characteristics of silent variants of *Borrelia hermsii* HS1

VARIANT	FAMILY	FAMSIZE	PLASMID	STRAND	UHSID	DHSDIST	SCORE	ASFRQ	DNAFRQ	EXPOBS	FREQCL
1	<i>vsp</i>	20	6	0	0.74	42	3	0.177	0.082	1	2
2	<i>vsp</i>	20	6	0	0.84	43	3	0.627	0.219	1	3
3	<i>vsp</i>	20	7	0	0.82	9884	2	0.176	0.014	1	2
4	$\delta$ - <i>vlp</i>	9	7	0	0.30	10659	1	0.141	0.027	1	2
5	$\gamma$ - <i>vlp</i>	13	1	1	0.26	10851	1	0.016	0.000	1	1
6	<i>vsp</i>	20	2	0	0.80	43	3	0.170	0.097	1	2
7	$\alpha$ - <i>vlp</i>	7	2	0	0.93	43	3	0.891	0.146	1	3
8	<i>vsp</i>	20	4	0	0.34	2003	1	0.053	0.000	1	1
9	$\beta$ - <i>vlp</i>	8	6	1	0.99	18183	2	0.051	0.000	1	1
10	$\beta$ - <i>vlp</i>	8	7	0	0.39	16403	1	0.026	0.000	1	1
11	<i>vsp</i>	20	4	0	0.88	2881	2	0.140	0.000	1	1
12	$\beta$ - <i>vlp</i>	8	8	0	0.92	8412	2	0.162	0.000	1	1
13	<i>vsp</i>	20	1	0	0.94	8002	2	0.294	0.014	1	2
14	$\beta$ - <i>vlp</i>	8	8	0	0.98	79	3	0.091	0.041	1	2
16	$\delta$ - <i>vlp</i>	9	3	0	0.62	4446	2	0.134	0.027	1	2
17	$\delta$ - <i>vlp</i>	9	9	0	0.82	80	3	0.605	0.125	1	3
18	$\alpha$ - <i>vlp</i>	7	7	0	0.80	117	3	0.169	0.274	1	3
19	$\gamma$ - <i>vlp</i>	13	1	1	0.26	6152	1	0.039	0.000	1	1
21	$\alpha$ - <i>vlp</i>	7	3	0	0.99	65	3	0.210	0.014	1	2
22	<i>vsp</i>	20	4	0	0.74	43	3	0.038	0.000	1	1
23	$\delta$ - <i>vlp</i>	9	4	1	0.97	10184	2	0.021	0.014	1	2
24	<i>vsp</i>	20	6	0	0.92	42	3	0.371	0.233	1	3
25	$\alpha$ - <i>vlp</i>	7	3	0	0.23	3599	1	.	0.000	1	1
27	<i>vsp</i>	20	6	0	0.74	3436	2	.	0.041	1	2
28	<i>vsp</i>	20	1	0	0.79	5690	2	.	.	0	1
30	<i>vsp</i>	20	3	0	0.84	6067	2	.	.	0	1
32	$\beta$ - <i>vlp</i>	8	4	0	0.74	7754	2	.	.	0	1
34	$\beta$ - <i>vlp</i>	8	3	0	0.41	65	2	.	.	0	1
36	$\delta$ - <i>vlp</i>	9	1	0	0.75	8771	2	.	.	0	1
37	$\gamma$ - <i>vlp</i>	13	6	0	0.38	10958	1	.	.	0	1
39	$\gamma$ - <i>vlp</i>	13	1	1	0.23	3062	1	.	.	0	1
42	$\delta$ - <i>vlp</i>	9	4	0	0.80	41	3	.	0.014	1	2
43	$\gamma$ - <i>vlp</i>	13	7	0	0.62	11892	2	.	.	0	1
44	$\alpha$ - <i>vlp</i>	7	6	1	0.97	13778	2	.	.	0	1
46	$\beta$ - <i>vlp</i>	8	6	1	0.95	16957	2	.	0.027	1	2
48	$\gamma$ - <i>vlp</i>	13	4	0	0.99	780	2	.	.	0	1
49	$\gamma$ - <i>vlp</i>	13	6	1	0.98	19365	2	.	.	0	1
53	$\gamma$ - <i>vlp</i>	13	8	1	0.25	10260	1	.	.	0	1
54	$\gamma$ - <i>vlp</i>	13	8	0	0.90	7254	2	.	.	0	1
56	$\delta$ - <i>vlp</i>	9	7	0	0.59	15288	1	.	.	0	1
58	<i>vsp</i>	20	4	0	0.31	43	2	.	0.014	1	2
59	<i>vsp</i>	20	6	1	0.57	13013	1	.	.	0	1
61	$\delta$ - <i>vlp</i>	9	5	0	0.93	15641	2	.	.	0	1
62	$\alpha$ - <i>vlp</i>	7	5	0	0.84	14390	2	.	.	0	1
63	<i>vsp</i>	20	5	0	0.62	12340	2	.	.	0	1
64	$\gamma$ - <i>vlp</i>	13	5	0	0.23	11099	1	.	.	0	1
65	$\gamma$ - <i>vlp</i>	13	8	0	0.59	18489	1	.	.	0	1
66	<i>vsp</i>	20	8	1	0.86	3353	2	.	.	0	1
68	<i>vsp</i>	20	7	0	0.76	2715	2	.	.	0	1
69	<i>vsp</i>	20	7	0	0.36	17701	1	.	.	0	1
70	$\alpha$ - <i>vlp</i>	7	7	0	0.31	14013	1	.	.	0	1
71	$\beta$ - <i>vlp</i>	8	7	0	0.41	12901	1	.	.	0	1
72	<i>vsp</i>	20	6	0	0.43	12119	1	.	.	0	1
73	$\gamma$ - <i>vlp</i>	13	3	0	0.25	3350	1	.	.	0	1
75	<i>vsp</i>	20	8	0	0.64	446	1	.	.	0	1
76	$\delta$ - <i>vlp</i>	9	8	1	0.89	9095	2	.	.	0	1
77	$\gamma$ - <i>vlp</i>	13	8	0	0.34	9639	1	.	.	0	1

VARIANT: *vsp* or *vlp* gene conferring serotype identity (Supplementary Figure 1).

FAMILY: *vsp* gene family or  $\alpha$ -*vlp*,  $\beta$ -*vlp*,  $\gamma$ -*vlp*, or  $\delta$ -*vlp* gene sub-families<sup>17</sup>.

FAMSIZE: Number of genes in gene family or sub-family<sup>17</sup>.

PLASMID: Location of gene on 9 plasmid sequence contigs; the expression plasmid is 1.

STRAND: Same (= 0) or opposite (=1) orientation as the next downstream DHS element.

UHSID: % nucleotide (nt) identity with the 61 nts of UHS region.

DHSDIST: nt from gene stop codon to nearest downstream DHS or fragment end.

SCORE: 1=UHSID <0.6 and log<sub>10</sub> DHS ≥2.5; 2=UHSID ≥0.6 or DHS <2.5; 3= UHSID ≥0.6 and DHS <2.5.

ASFRQ: Frequency per immunocompetent mouse of serotype in first relapse by antisera typing (Table S1).

DNAFRQ: Frequency per immunocompetent mouse serotype in first relapse by DNA sequence typing.

EXPOBS: Expression of *vsp* or *vlp* variant gene observed (=1) or not observed (=0).

FREQCL: Frequency class 3 = ASFRQ ≥0.35 and/or DNAFRQ ≥0.2; class 2 = ASFRQ ≥0.2 and/or DNAFRQ >0; class 3 = ASFRQ <0.2 and DNAFRQ = 0, or EXPOBS = 0.