Table S 1. Nature and position of variants between P78 and P0.

						P78-1c		P78-2c		P78-1s		P78-2s	
#	Position on KHV-J Reference	Reference Sequence	Alternate Sequence	Type of Variation	Predicted ORF	Allele Freq – Reference	Allele Freq – Alternate	Allele Freq – Reference	Allele Freq – Alternate	Allele Freq – Reference	Allele Freq – Alternate	Allele Freq – Reference	Allele Freq – Alternate
1	17848	C	G	missense variant	KHVJ011	0.80	0.20	0.75	0.25	0.76	0.24	0.72	0.28
2	17849	G	A	missense variant	KHVJ011	0.80	0.20	0.74	0.26	0.78	0.22	0.73	0.27
3	17850	C	G	synonymous variant	KHVJ011	0.80	0.20	0.74	0.26	0.79	0.21	0.74	0.26
4	26023	G	A	missense variant	KHVJ019	0.56	0.44	0.60	0.40	0.55	0.45	0.54	0.46
5	34507	T	TC	frameshift variant	KHVJ024	0.62	0.38	0.65	0.35	0.63	0.37	0.62	0.38
6	83069	C	CCGAAGCAGCCGAAGCAGCCGAAGCAGA	inframe insertion	KHVJ055	0.78	0.22	0.85	0.15	0.72	0.28	0.79	0.21
7	124200	AGGGG	A	intergenic variant	KHVJ075-KHVJ076	0.38	0.63	0.40	0.60	0.62	0.38	0.31	0.69
8	138300	C	A	missense variant	KHVJ082	0.00	1.00	0.00	1.00	0.00	1.00	0.00	1.00
9	154881	G	T	synonymous variant	KHVJ093	0.82	0.18	0.85	0.15	0.86	0.14	0.83	0.17
10	157768	C	A	missense variant	KHVJ095	0.10	0.90	0.08	0.92	0.11	0.89	0.09	0.91
11	187878	GTCT	G	inframe deletion	KHVJ111	0.87	0.13	0.91	0.09	0.87	0.13	0.90	0.10

12	193352	G	A	missense variant	KHVJ113/ KHVJ114	0.66	0.34	0.63	0.37	0.60	0.40	0.65	0.35
13	209653	A	T	missense variant	KHVJ125	0.65	0.35	0.62	0.38	0.56	0.44	0.55	0.45
14	223325	A	C	missense variant	KHVJ138	0.00	1.00	0.00	1.00	0.00	1.00	0.00	1.00
15	256979	C	T	missense variant	KHVJ159	0.00	1.00	0.00	1.00	0.00	1.00	0.00	1.00
16	257090	C	T	missense variant	KHVJ159	0.00	1.00	0.00	1.00	0.00	1.00	0.00	1.00
17	258111	C	T	intergenic variant	KHVJ159-KHVJ160	0.26	0.74	0.27	0.73	0.32	0.68	0.36	0.64
18	259695	CG	C	frameshift variant	KHVJ160	0.69	0.31	0.73	0.27	0.67	0.33	0.67	0.33
19	269057	TTCC	T	inframe deletion	KHVJ166	0.66	0.34	0.59	0.41	0.61	0.39	0.45	0.55
20	270260	AGAGGC AGAG	A	inframe deletion	KHVJ166/ KHVJ167	0.73	0.27	0.71	0.29	0.71	0.29	0.72	0.28
21	272753	T	TGGTGGA AGGTTGA ACATGGT GGACAC. TGGTGGA AGGTTGA ACATGGT GGACAC GGTGGA AGGTTGA ACATGGT GGACAC	frameshift variant	KHVJ169	0.59	0.41	0.28	0.72	0.50	0.50	0.38	0.62

All variations located in the terminal repeats appear only once. Predicted ORFs were deduced from the genome annotation of KHV-J (AP008984). Missense variant indicates a nucleotide substitution that modifies the amino acid; synonymous variant denotes a nucleotide substitution that does not modify the amino acid; frameshift variant indicates

an insertion or a deletion that changes the reading frame; intergenic variant points to a mutation located between two predicted open reading frames. When more than two variants co-occur at a single position, only the frequency of the most abundant alternate (from all replicates) is indicated. Only variations <100 bp were listed.

Table S 2. Nature and position of variants between P99 and P0.

						P99-1c		P99-2c	
#	Position on KHV-J Reference	Reference Sequence	Alternate Sequence	Type of Variation	Predicted ORF	Allele Freq – Reference	Allele Freq – Alternate	Allele Freq – Reference	Allele Freq – Alternate
1	7090	C	CA	intergenic variant	KHVJ04-KHVJ05	0.00	1.00	0.00	1.00
2	7300	C	A	missense variant	KHVJ05	0.00	1.00	0.00	1.00
3	8635	GAGCACC	G	inframe deletion	KHVJ06	0.00	1.00	0.00	1.00
4	8926	G	T	missense variant	KHVJ06	0.00	1.00	0.00	1.00
5	8963	GC	G	frameshift variant	KHVJ06	0.00	1.00	0.00	1.00
6	9201	G	A	missense variant	KHVJ06	0.00	1.00	0.00	1.00
7	9709	T	C	missense variant	KHVJ06	0.00	1.00	0.00	1.00
8	11333	A	ATC	intergenic variant	KHVJ06-KHVJ07	0.00	1.00	0.03	0.97
9	22308	AAATTAGGGCTAG	A	intergenic variant	KHVJ015-KHVJ016	0.84	0.16	0.00	1.00
10	23622	T	C	synonymous variant	KHVJ017	0.88	0.12	0.82	0.18
11	24969	C	CCAA	inframe insertion	KHVJ018	0.88	0.12	0.90	0.10
12	31414	ACT	A	frameshift variant	KHVJ023	0.66	0.34	0.86	0.14

13	37042	C	CTGT	inframe insertion	KHVJ026	0.90	0.10	0.70	0.30
14	51203	G	GACA	intergenic variant	KHVJ037-KHVJ038	0.01	0.99	0.89	0.11
15	62988	CT	C	intergenic variant	KHVJ049-KHVJ050	0.00	1.00	0.00	1.00
16	83669	G	C	missense variant	KHVJ056	0.74	0.26	0.01	0.99
17	85005	TG	T	intergenic variant	KHVJ057-KHVJ058	0.71	0.29	0.65	0.35
18	104329	C	T	missense variant	KHVJ070	0.87	0.13	0.73	0.27
19	104341	T	C	missense variant	KHVJ070	0.84	0.16	0.84	0.16
20	104472	T	G	missense variant	KHVJ070	0.79	0.21	0.81	0.19
21	105490	C	T	missense variant	KHVJ070	0.68	0.32	0.73	0.27
22	112097	C	G	missense variant	KHVJ071	0.84	0.16	0.68	0.32
23	124125	CTT	C	intergenic variant	KHVJ075-KHVJ076	0.16	0.84	0.76	0.24
24	124140	GT	G	intergenic variant	KHVJ075-KHVJ076	0.14	0.86	0.10	0.90
25	124200	AGGGGGG	A.AG	intergenic variant	KHVJ075-KHVJ076	0.06	0.65	0.11	0.89
26	138300	C	A	missense variant	KHVJ082	0.00	1.00	0.08	0.64
27	151633	GT	G	intergenic variant	KHVJ090-KHVJ091	0.90	0.10	0.00	1.00
28	151649	T	TA	intergenic variant	KHVJ090-KHVJ091	0.90	0.10	0.89	0.11

29	151780	G	GTGA	intergenic variant	KHVJ090-KHVJ091	0.89	0.11	0.88	0.12
30	152587	G	A	missense variant	KHVJ091	0.84	0.16	0.87	0.13
31	158882	C	G	missense variant	KHVJ096	0.78	0.22	0.90	0.10
32	159828	G	T	missense variant	KHVJ096	0.00	1.00	0.79	0.21
33	187878	GTCT	G	inframe deletion	KHVJ111	0.22	0.78	0.00	1.00
34	205798	ACTT	A	inframe deletion	KHVJ123	0.34	0.66	0.14	0.86
35	216278	T	TCAACAGCAG	inframe insertion	KHVJ131	0.00	1.00	0.29	0.71
36	223325	A	C	missense variant	KHVJ138	0.00	1.00	0.00	1.00
37	226260	A	C	missense variant	KHVJ140	0.00	1.00	0.00	1.00
38	230658	C	A	missense variant	KHVJ144	0.00	1.00	0.00	1.00
39	247692	G	C	synonymous variant	KHVJ153	0.03	0.97	0.00	1.00
40	253848	C	CGCT	inframe insertion	KHVJ157	0.00	1.00	0.03	0.97
41	257090	C	T	missense variant	KHVJ159	0.00	1.00	0.00	1.00
42	258111	C	T	intergenic variant	KHVJ159-KHVJ160	0.00	1.00	0.00	1.00
43	265700	TTGC	T	inframe insertion	KHVJ165	0.87	0.13	0.00	1.00
44	269057	TTCCTCC	T	inframe insertion	KHVJ166	0.00	1.00	0.84	0.16

45	269368	T	C	missense variant	KHVJ166	0.16	0.84	0.01	0.99
46	270260	A	AGAGGCAGAG	inframe insertion	KHVJ166/KHVJ167	0.06	0.94	0.15	0.85
47	270518	C	CT	frameshift variant	KHVJ166/KHVJ167	0.10	0.90	0.03	0.97
48	270520	G	GCCCTT	frameshift variant	KHVJ166/KHVJ167	0.09	0.91	0.15	0.85
49	270562	C	T	missense variant	KHVJ166/KHVJ167	0.01	0.99	0.14	0.86
50	270749	C	CACAGACT	intergenic variant	KHVJ167-KHVJ168	0.07	0.93	0.03	0.97
51	270789	A	AGC	intergenic variant	KHVJ167-KHVJ168	0.14	0.86	0.05	0.95
52	270792	CT	C	intergenic variant	KHVJ167-KHVJ168	0.14	0.86	0.14	0.86
53	270796	AGC	A	intergenic variant	KHVJ167-KHVJ168	0.12	0.88	0.14	0.86
54	270801	C	CT	intergenic variant	KHVJ167-KHVJ168	0.11	0.89	0.14	0.86
55	270911	GACAGAGACACAAGACAGAC	G	intergenic variant	KHVJ167-KHVJ168	0.00	1.00	0.16	0.84
56	271009	C	CAA	intergenic variant	KHVJ167-KHVJ168	0.00	1.00	0.00	1.00
57	271715	TTCAGTGTCCTCC	T	inframe deletion	KHVJ168	0.68	0.32	0.00	1.00
58	274370	AATC	A	intergenic variant	KHVJ170-KHVJ171	0.25	0.75	0.67	0.33

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