Table S5: SNPs distinguishing clade 1 and 2 within host shift virus dataset across the concatenated genes.

Gene	N			P		G							L													
Position (nt)	129	297	639	1503	2179	3027	3057	3084	3204	3976	4173	4327	5163	5577	5598	6312	6729	7050	8166	8223	8430	8457	8984	10111	10335	10524
Position (aa)	43	99	213	50	276	57	67	76	116	378	439	491	244	382	389	627	766	873	1245	1264	1333	1342	1518	1894	1968	2031
Clade 1 nt	CTA	AAA	TTT	CCT	CTA	CTT	GTT	AAC	GCG	GTG	CTT	CGC	CTT	CTG	GTT	AGA	ATC	GTT	TCT	ATC	CAG	AAA	ACG	AGC	ATT	AAC
Clade 1 aa	Leu	Lys	Phe	Pro	Leu	Leu	Val	Asn	Ala	Val	Leu	Arg	Leu	Leu	Val	Arg	Ile	Val	Ser	Ile	Gln	Lys	Thr	Ser	Ile	Asn
Clade 2 nt	CTG	AAG	TTC	CCC	TTA	CTC	GTC	AAT	GCA	ATG	CTC	AGC	CTC	CTT	GTC	AGG	ATA	GTC	TCC	ATT	CAA	AAG	ATG	GGC	ATC	AAT
Clade 2 aa	*	*	*	*	*	*	*	*	*	Met	*	Ser	*	*	*	*	*	*	*	*	*	*	Met	Gly	*	*

Positions (nt) relate to concatenated sequences.
Positions (aa) relate to the individual protein residues.
Synonymous changes are indicated by *, non-synonymous changes are underlined.