

# Supplementary Materials

**Table S1.** Treatment recommendations for each HCV genotype, according to the most recent guidelines [15]. All approved interferon-containing and interferon-free regimens are listed in the table, with the respective HCV genotype in which they can be administered. For the same treatment regimen, the duration of therapy and whether or not ribavirin (RBV) needs to be added to the regimen, can still differ between different genotypes.

	<b>Regimen</b>	<b>Genotype</b>
<b>IFN-free</b>	Sofosbuvir + RBV	2 + 3
	Sofosbuvir/Ledipasvir (+ RBV)	1 + 4 + 5 + 6
	Ombitasvir/Paritaprevir/Ritonavir + Dasabuvir (+ RBV)	1
	Sofosbuvir + Simeprevir (+ RBV)	1 + 4
	Sofosbuvir + Daclatasvir (+ RBV)	All
	Ombitasvir/Paritaprevir/r (+ RBV)	4
<b>IFN-containing</b>	PegIFN- $\alpha$ + RBV + Sofosbuvir	All
	PegIFN- $\alpha$ + RBV + Simeprevir	1 + 4

**Table S2.** Within-genotype nucleotide diversity estimates (%) for all six HCV genotypes. Nucleotide diversity is given for each of the genetic regions encoding the ten viral proteins separately, and also for the full genome (excluding UTR). IQR or interquartile range gives a set of values between the 25th percentile (Q1) and the 75th percentile (Q3).

%	Core Genetic Region	E1 Genetic Region	E2 Genetic Region	p7 Genetic Region	NS2 Genetic Region	NS3 Genetic Region	NS4A Genetic Region	NS4B Genetic Region	NS5A Genetic Region	NS5B Genetic Region	Full-Genome (Excluding UTR)
HCV1	6.34	17.23	21.51	17.3	18.95	14.16	10.97	14.7	17.56	12	13.53
HCV2	8.63	18.63	18.76	18.55	18.38	14.45	15.76	13.36	17.19	11.65	14.51
HCV3	8.81	16.5	19.35	17.14	16.43	13.99	13.34	14.45	16.55	11.78	14.59
HCV4	9.11	23.79	25.75	26.71	28.32	19.17	20.25	19.57	24.02	16.74	20
HCV5	7.99	17.4	17.45	16.8	17.96	12.35	12.89	14.7	15.17	12.04	13.97
HCV6	12.63	28.93	26.52	34.49	27.91	21.38	22.98	22.87	27.51	20.35	23.37
<b>Median</b>	<b>8.72</b>	<b>18.02</b>	<b>20.43</b>	<b>17.93</b>	<b>18.67</b>	<b>14.31</b>	<b>14.55</b>	<b>14.7</b>	<b>17.38</b>	<b>12.02</b>	<b>14.55</b>
<b>IQR (Q1-Q3)</b>	<b>8.15–9.04</b>	<b>17.27–22.50</b>	<b>18.91–24.69</b>	<b>17.18–24.67</b>	<b>18.07–25.67</b>	<b>1.03–17.99</b>	<b>13.00–19.13</b>	<b>14.51–18.35</b>	<b>16.71–22.41</b>	<b>11.84–15.57</b>	<b>14.11–18.65</b>

**Table S3.** Within-genotype amino acid diversity estimates (%) for all six HCV genotypes. Amino acid diversity is given for each of the ten proteins separately, and also for the overall polyprotein. IQR or interquartile range gives a set of values between the 25th percentile (Q1) and the 75th percentile (Q3).

%	Core	E1	E2	p7	NS2	NS3	NS4A	NS4B	NS5A	NS5B	Full-Genome Polyprotein
HCV1	2	15	19.01	14.19	15.85	5.31	7	7.04	14.42	7.5	8.71
HCV2	4.52	17.17	13.87	15.47	15.42	5.66	10.21	4.61	14.78	8.18	9.6
HCV3	4.2	13.98	17.45	14.18	10.92	6	5.08	6.97	12.06	7.63	9.48
HCV4	3	17.66	19.85	23.36	24.11	6.75	11.26	7.29	17.56	10.58	12.17
HCV5	5.82	14.16	13.95	18.03	15.58	5.46	6.84	9.2	12.46	7.98	9.82
HCV6	5.33	25.45	20.91	33.94	21.22	8.78	13.54	13.02	21.57	13.48	15.67
<b>Median</b>	<b>4.36</b>	<b>16.09</b>	<b>18.23</b>	<b>16.75</b>	<b>15.72</b>	<b>5.83</b>	<b>8.61</b>	<b>7.17</b>	<b>14.60</b>	<b>8.08</b>	<b>9.71</b>
<b>IQR (Q1-Q3)</b>	<b>2.13–3.3</b>	<b>14.37–17.54</b>	<b>14.83–19.64</b>	<b>14.51–22.03</b>	<b>15.46–19.88</b>	<b>5.51–6.56</b>	<b>6.88–11.00</b>	<b>6.99–8.72</b>	<b>12.95–16.87</b>	<b>7.72–9.98</b>	<b>9.51–11.58</b>

**Table S4.** HCV inter-genotype genomic diversity (%). Inter-genotype pairwise nucleotide diversity (upper triangle) and amino acid diversity (bottom triangle) at the genome level.

		<b>NUCLEOTIDE DIVERSITY (%)</b>					
		<b>HCV1</b>	<b>HCV2</b>	<b>HCV3</b>	<b>HCV4</b>	<b>HCV5</b>	<b>HCV6</b>
<b>AMINO ACID DIVERSITY (%)</b>	<b>HCV1</b>	-	33.66	32.28	29.03	30.85	31.29
	<b>HCV2</b>	28.42	-	35.46	33.77	34.36	34.5
	<b>HCV3</b>	25.02	29.87	-	32.39	32.79	32.92
	<b>HCV4</b>	21.06	28.36	24.98	-	31.09	31.18
	<b>HCV5</b>	23.42	29.62	26.25	24.12	-	31.93
	<b>HCV6</b>	23.77	28.87	25.57	25.57	24.63	-

**Table S5.** Nucleotide alignment of the H77 (NC\_004102) reference sequence with the consensus of all six HCV genotypes. For each genotype, a consensus alignment was obtained, based on the most frequently occurring nucleotides in the respective datasets. Consensus nucleotides indicated in bold, highlight positions that display a different consensus nucleotide compared to reference sequence H77.

	1	10	20	30	40	50	60	70	79																																																																			
H77 (NC_004102)	A	T	G	A	G	C	A	C	G	A	A	T	C	T	A	A	C	C	T	C	A	A	A	A	A	C	C	A	A	A	C	G	T	A	A	C	C	A	A	C	C	A	A	C	C	G	T	C	G	C	C	C	A	C	A	G	G	A	C	G	T	C	A	A	G	T	T	C	C	C	G	G	T	G		
HCV1	A	T	G	A	G	C	A	C	G	A	A	T	C	T	A	A	C	C	T	C	A	A	A	A	A	C	C	A	A	A	C	G	T	A	A	C	C	A	A	C	C	A	A	C	C	G	T	C	G	C	C	C	A	C	A	G	G	A	C	G	T	C	A	A	G	T	T	C	C	C	G	G	T	G		
HCV2	A	T	G	A	G	C	A	C	A	A	A	T	C	T	A	A	C	C	T	C	A	A	A	A	A	C	C	A	A	A	A	G	A	A	C	A	C	A	A	C	C	G	C	C	C	C	C	A	C	A	G	G	A	C	G	T	C	A	A	G	T	T	C	C	C	G	G	T	G							
HCV3	A	T	G	A	G	C	A	C	A	<b>A</b>	C	T	T	C	T	A	A	C	C	T	C	A	A	A	A	A	C	C	A	A	A	A	A	G	A	A	C	A	C	C	A	C	C	A	T	C	C	G	T	C	G	C	C	C	A	C	A	G	G	A	C	G	T	C	A	A	G	T	T	C	C	C	G	G	T	G
HCV4	A	T	G	A	G	C	A	C	G	A	A	T	C	T	A	A	C	C	T	C	A	A	A	A	A	C	C	A	A	A	C	G	T	A	A	C	C	A	A	C	C	A	A	C	C	G	C	C	C	C	C	<b>A</b>	T	G	G	A	C	G	T	T	A	A	G	T	T	C	C	C	G	G	T	G				
HCV5	A	T	G	A	G	C	A	C	G	A	A	T	C	T	A	A	C	C	T	C	A	A	A	A	A	C	C	A	A	A	A	G	A	A	C	A	C	A	A	C	C	G	C	C	C	C	C	A	C	A	G	G	A	C	G	T	C	A	A	G	T	T	C	C	C	G	G	T	G							
HCV6	A	T	G	A	G	C	A	C	A	<b>A</b>	C	T	T	C	C	A	A	A	C	C	C	C	A	A	A	A	C	C	A	A	A	A	G	A	A	C	A	C	A	A	C	C	G	C	C	C	C	A	T	G	G	A	C	G	T	C	A	A	G	T	T	C	C	C	G	G	T	G								
	80	90	100	110	120	130	140	150	158																																																																			
H77 (NC_004102)	G	C	G	T	C	A	G	A	T	C	G	T	T	G	G	T	G	G	A	G	T	T	A	C	T	T	G	T	T	G	C	C	G	C	G	C	A	G	G	G	G	C	C	T	A	G	A	T	T	G	G	T	G	T	G	C	G	C	G	A	C	G	A	G	G	A	A	G	A	C	T	T	C			
HCV1	G	C	G	T	C	A	G	A	T	C	G	T	T	G	G	T	G	G	A	G	T	T	A	C	T	T	G	T	T	G	C	C	G	C	G	C	A	G	G	G	G	C	C	T	A	G	A	T	T	G	G	T	G	T	G	C	G	C	G	A	C	G	A	G	G	A	A	G	A	C	T	T	C			
HCV2	G	C	G	C	C	A	G	A	T	C	G	T	T	G	G	C	G	A	G	T	T	A	C	T	T	G	C	T	G	C	C	G	C	G	C	A	G	G	G	C	C	C	C	A	G	G	T	T	G	G	T	G	T	G	C	G	C	G	A	C	A	A	G	A	A	G	A	C	T	T	C					
HCV3	G	C	G	G	A	C	A	G	A	T	C	G	T	T	G	G	T	G	A	T	A	C	G	T	T	G	C	C	G	C	G	C	A	G	G	G	C	C	C	A	C	G	A	T	T	G	G	T	G	T	G	C	G	C	G	A	C	G	C	G	T	A	A	A	C	T	T	C								
HCV4	G	T	G	C	C	A	G	A	T	C	G	T	T	G	G	C	G	A	G	T	T	A	C	T	T	G	T	T	G	C	C	G	C	A	G	G	G	C	C	C	C	A	G	G	T	T	G	G	T	G	T	G	C	G	C	G	A	C	T	C	G	G	A	A	G	A	C	T	T	C						
HCV5	G	T	G	T	C	A	G	A	T	C	G	T	T	G	G	T	G	A	G	T	T	A	C	T	T	G	T	T	G	C	C	G	C	A	G	G	G	C	C	C	T	A	G	G	T	T	G	G	T	G	T	G	C	G	C	G	A	C	T	C	G	G	A	A	G	A	C	T	T	C						
HCV6	G	C	G	T	C	A	G	A	T	C	G	T	T	G	G	T	G	A	G	T	T	A	C	T	T	G	T	T	G	C	C	G	C	A	G	G	G	C	C	C	C	C	C	C	A	T	T	G	G	T	G	T	G	C	G	C	G	A	C	G	A	G	G	A	A	G	A	C	T	T	C					

Table S5. Cont.

	159	170	180	190	200	210	220	230	237		
H77 (NC_004102)	CGAGCGGT	TCGCAACCT	CGAGGT	AGACGT	CAGCCT	ATCCCCA	AAGGCACGT	CGGCCCG	AGGGCAGG	ACCTGGGCT	CAGCCC
HCV1	CGAGCGGT	TCGCAACCT	CGAGGT	AGACGT	CAGCCT	ATCCCCA	AAGGCT	CGTCCGCC	CGAGGGC	AGGACCT	GGGCTCAGCCC
HCV2	CGAGCGAT	CCCAGCCG	CGTGGG	AGACGCC	AGCCCAT	CCCCGAA	AAGATCGG	CGCTCCAC	CCGGCAAG	TCTGGGG	AAAAGCCA
HCV3	TGAACGGT	CACAGCCT	CGCGG	ACGGCG	ACAGCCT	ATCCCCA	AAGGCG	CGTCCG	AGCGAAGG	CCGGTCT	GGGCTCAGCCC
HCV4	GGAGCGGT	TCGCAACCT	CGTGGG	AGGCGCCA	AACTAT	CCCCAAGG	CGCGCC	AGCCGAG	GGCAGGT	CTGGGCT	CAGCCC
HCV5	AGAACGGT	TCGCAACCC	CGTGG	ACGGCG	CCAGCCT	ATCCCCA	AAGGCG	CCAAACCC	ACGGGCC	GGTCTGGG	GTTAAACCC
HCV6	CGAACGAT	CCCAGCCC	AGAGGC	AGGCGCC	AGCCTAT	ACCAAAGG	CGCGCC	AGCCCAC	GGGCCG	CACTGGGCT	CAGCCC
	238	250	260	270	280	290	300	310	316		
H77 (NC_004102)	GGGTACCCT	TGGCCCT	CTATGG	CAATG	AGGGT	TGCGGGT	GGGCGGG	ATGGCT	CCTGTCT	CCCCGT	GGCTCTCGGCCTA
HCV1	GGGTACCCT	TGGCCCT	CTATGG	CAATG	AGGGT	TGCGGGT	GGGCGGG	ATGGCT	CCTGTCT	CCCCGT	GGCTCTCGGCCTA
HCV2	GGATATCCT	TGGCCCT	GTACGG	AAACG	AGGGCT	TGCGGT	GGGCAGG	TGGTCT	CCTGTCCCC	CGGGTCT	CGTCCTA
HCV3	GGGTACCCT	TGGCCCT	CTATGG	TAAACG	AGGGCT	TGCGGT	GGGCAGG	TGGTCT	CCTGTCCCC	ACGGCT	CCCCGTCCAT
HCV4	GGGTACCCT	TGGCCT	TTACGG	CAATG	AGGGT	TGCGGT	GGGCAGG	ATGGCT	CCTGTAC	CCCCG	CGGCTCTCGGCCGT
HCV5	GGGTACCCT	TGGCCCT	TTACGG	CAATG	AGGGCT	TGCGGT	GGGCAGG	TGGTCT	CCTCCCC	CGGGTCT	CGGCCTA
HCV6	GGTTACCCT	TGGCCCT	TTATGG	AAACG	AGGGCT	TGCGGT	GGGCAGG	TGGTCT	CCTGTCCCC	CGGGT	CCCCGCCAA
	317	330	340	350	360	370	380	390	395		
H77 (NC_004102)	GCTGGGG	CCCCAC	AGACCCC	GGCGT	AGGTC	CGCAAT	TTGGGTA	AAGGCAT	CGATACC	CTTACGT	GCGGCTTCGCCGA
HCV1	GTTGGGG	CCCCAC	AGACCCC	GGCGT	AGGTC	CGCAAT	TTGGGTA	AAGGCAT	CGATACC	CTTACGT	GCGGCTTCGCCGA
HCV2	CTTGGGG	CCCCACT	GACCCC	GGCAT	AGATC	ACGCAAT	TTGGGTA	AAGGCAT	CGATACC	ATTACGT	TGGTTTTGCCGA
HCV3	CTTGGGG	CCCCAA	TGACCCC	GGCGA	AAGTCC	CGCAAT	TTGGGTA	AAGTCA	TCGATACC	CTTACGT	GCGGATTGCCGA
HCV4	CTTGGGG	CCCCAA	TGATCCC	GGCGG	AGGTC	CGCAAT	TTGGGTA	AAGTCA	TCGATACC	CTTACGT	GCGGCTTCGCCGA
HCV5	ATTGGGG	CCCCAA	TGACCCC	GGCGA	AAATC	CGCAAT	TTGGGTA	AAGTCA	TCGATACC	CTTACGT	GCGGATTGCCGA
HCV6	ATTGGGG	CCCCAA	TGACCCC	GGCGA	AAGTCC	CGCAAT	TTGGGTA	AAGTCA	TCGATACC	CTTACGT	GCGGCTTCGCCGA

Table S5. Cont.

	396	400	410	420	430	440	450	460	470	474
H77 (NC_004102)	CCTCATGGGGTACATACCGCTCGTCGGCGCCCCCTTTGGAGGCGCTGCCAGGGCCCTGGCGCATGGCGTCCGGGTTCTG									
HCV1	CCTCATGGGGTACATTCCGCTCGTCGGCGCCCCCTTTGGAGGCGCTGCCAGGGCCCTGGCGCATGGCGTCCGGGTTCTG									
HCV2	CCTCATGGGGTACATCCCTGTCGTTGGCGCCCCGGTTGGAGGCGCTGCCAGAGCTCTGGCACACGGTGTAGGGTCTG									
HCV3	CCTCATGGGGTACATCCCGCTCGTCGGCGCTCCCGTAGGAGGCGCTCGCAAGAGCCCTCGCGCATGGCGTGAGGGCCCTT									
HCV4	CCTCATGGGATACATCCCGCTCGTAGGCGCCCCCGTGGGTGGCGCTGCCAGGGCCCTGGCGCATGGCGTCAGGGCTGTG									
HCV5	CCTCATGGGGTACATCCCGCTCGTAGGCGGCCCGTTGGGGGCGTCGCAAGGGCTCTCGCACACGGTGTGAGGGTTCTT									
HCV6	TCTCATGGGGTACATCCCGCTCGTAGGCGCGCCATTGGGCGGGCTCGCGGGCTGCCCTCGCACATGGTGTGAGGGCAATC									
	475	480	490	500	510	520	530	540	550	553
H77 (NC_004102)	GAAGACGGCGTGAACATATGCAACAGGGAACCTTCTGGTTGCTCTTTCTCTATCTTCCTTCTGGCCCTGCTCTTTGCC									
HCV1	GAAGACGGCGTGAACATATGCAACAGGGAATCTTCTGGTTGCTCTTTCTCTATCTTCCTTCTGGCCCTGCTCTTTGCC									
HCV2	GAGGACGGGATAAATTATGCAACAGGGAATCTACCCGGTTGCTCTTTTTCTATCTTCTTGCTTCTTCTGTCGTGCA									
HCV3	GAAGACGGGATAAATTCGCAACAGGGAACCTTGCCCGTTGCTCCTTTCTATCTTCCTTCTTGCTCTGTTCTCTTCTGCT									
HCV4	GAGGACGGGATCAATTATGCAACAGGGAATCTTCCCGTTGCTCTTTCTCTATCTTCCTTCTGGCACTTCTCTCGTGCC									
HCV5	GAGGACGGGGTAAACTATGCAACAGGGAATTTGCCCGTTGCTCTTTCTCTATCTTTATCCTTGCACTTCTTTCGTGCC									
HCV6	GAGGACGGGATCAATTATGCAACAGGGAATCTTCCCGTTGCTCTTTCTCTATCTTCCTTCTGGCACTACTCTCGTGCC									
	554	560	570	580	590	600	610	620	632	
H77 (NC_004102)	TGACTGTGCCCGCTTCAGCCTACCAAGTGCGCAATCCTCGGGGCTTTACCATGTCACCAATGATTGCCCTAACTCGAG									
HCV1	TGACCGTGCCCGCTTCAGCCTACCAAGTGCGCAACTCCTCGGGGCTTTACCATGTCACCAATGATTGCCCTAACTCGAG									
HCV2	TCACAGTGCCAGTGTCTGCAGTGGAAGTCAGGAACATCAGTTCTAGCTACTAGGCCACTAATGATTGCTCGAACAACAG									
HCV3	TAATTCATCCAGCAGCTAGTCTAGAGTGGCGGAATACGCTCTGGCCTCTACGTCCTTACCAACGACTGTTCCAACAGCAG									
HCV4	TGACTGTCCCCGCTCGGCTGTGCACTATCGCAACGCTCGGGGCACTACCACATCACCAATGACTGCCCCGAATCCAG									
HCV5	TGACCGTCCCGGCTCTGCAGTTCCCTACCGAAATGCCTCTGGGGTTATCATGTCACCAATGATTGCCCAACTCTTC									
HCV6	TCACAACGCCAGCCTCGGCAGTCCACTACGGCAACACCACTGGGATATACCATCTCACCAATGACTGCCCCAACTCCAG									



Table S5. Cont.

	870	880	890	900	910	920	930	940	948
H77 (NC_004102)	GTTTACCTTCTCTCCCAGGCGCCACTGGACGACGCAAGACTGCAATTGTTCTATCTATCCCGGCCATATAACGGGTTCAT								
HCV1	GTTTACCTTCTCTCCCAGGCGCCACTGGACGACGCAAGACTGCAATTGTTCTATCTATCCCGGCCATATAACGGGTTCAC								
HCV2	<b>TTTCATAGTATCGCCACAACACCACAACCTTCACCCAAGAGTGCAACTGTTCCATCTACCAAGGTCACATCACCGGCCAC</b>								
HCV3	<b>CTTCACGTTCAGACCTCGTCGCCATCAAACGGTCCAGACCTGTAAGTCTACTGTACCCAGGCCATCTTACAGGACAT</b>								
HCV4	GTTTACCTTCCAGCCGCGCCGCGCCACTGGACCACCCAGGACTGCAATTGTTCCATCTACTGGCCACATCACAGGCCAC								
HCV5	GTTTACCTTATAGGCCTCGCCAGCATACTACGGTGCAGGACTGCAACTGTTCCATTACAGTGGCCATATCACCGGCCAC								
HCV6	<b>TTTCACCTTCCGACCCCGCCGCGCCATCAGACCGTGCAAGACTGCAACTGCTCCATCTATACAGGCCACGTCACCGGCCAC</b>								
	949	960	970	980	990	1000	1010	1020	1027
H77 (NC_004102)	CGCATGGCATGGGATATGATGATGAACTGGTCCCCTACGGCAGCGTTGGTGGTAGCTCAGCTGCTCCGGATCCCACAAG								
HCV1	CGCATGGCATGGGATATGATGATGAACTGGTCCCCTACAACGGCGCTGGTAGTAGCTCAGCTGCTCCGGATCCCACAAG								
HCV2	CGCATGGCATGGGACATGATGATGAACTGGTCACCAACTCTTACCATGATCCTGGCCTACGCTGCTCGTGTCTCTGAGC								
HCV3	CGAATGGCTTGGGATATGATGATGAACTGGTCCCCGCTGTGGGTATGGTGGTGGCGCACGTCCTGCGGTTGCCCCAGA								
HCV4	<b>GTTTACCTTCCAGCCGCGCCGCGCCACTGGACCACCCAGGACTGCAATTGTTCCATCTACTGGCCACATCACAGGCCAC</b>								
HCV5	CGGATGGCATGGGACATGATGATGAACTGGTACCTACGACAGCCTTGCTGATGGCCAGTTGTTACGGATTCCCCAGG								
HCV6	<b>AGGATGGCTTGGGACATGATGATGAACTGGTACCCACAGCCACTTATGTCCTCTCTAGCGTCCTGAGAGTACCTCAGA</b>								
	1028	1040	1050	1060	1070	1080	1090	1100	1106
H77 (NC_004102)	CCATCATGGACATGATCGCTGGTGCTCACTGGGGAGTCTGGCGGGCATAGCGTATTCTCCATGGTGGGGAAGTGGGC								
HCV1	CCATCTTGGACATGATCGCTGGTGCCCACTGGGGAGTCTGGCGGGCATAGCGTATTCTCCATGGTGGGGAAGTGGGC								
HCV2	<b>TCGTCTTGAATCATCTTCGGCGGCCACTGGGGTGTGATGTTTGGCTTGGCCTACTTCTCCATGCAGGGAGCGTGGGC</b>								
HCV3	CCTTGTTCGACATAATAGCCGGGGCCCAATTGGGGCATCTTGGCGGGCCTAGCCTATTACTCCATGCAGGGCAACTGGGC								
HCV4	CCCTGGTTGACATGCTCGCGGGCGGCCACTGGGGCGTCTGGCTGGCATGGCGTTCTTACAGCATGCAGGCCAATTGGGC								
HCV5	<b>TGGTCATTGACATCATTGCCGGGGGCCACTGGGGGTCTTGTTCGCCCGCCGATACTTCGCGTCAACGGCTAACTGGGC</b>								
HCV6	<b>TGCTCCTGAGATGTTACTTGGTGGCCATTGGGGCGTCTAGGTGCCGTGGTGTACTTCAGTATGGTGGGCAACTGGGC</b>								











Table S5. Cont.

	2055	2060	2070	2080	2090	2100	2110	2120	2130	2133
H77 (NC_004102)	GTCCACCGGCCTCATCCACCTCCACCAGAACATTGTGGACGTGCAGTACTTGTACGGGGTAGGGTCAAGCATCGCGTCC									
HCV1	GTCCACCGGCCTCATCCACCTCCACCAGAACATCGTGGACGTGCAATACTTGTACGGGGTGGGGTCAAGCATTGTGTCC									
HCV2	ATCTACTGGCCTATTGCACCTCCACCAAAACATCGTGGACGTGCAGTACCTCTATGGACTTTCTCCGGCTATACAAGA									
HCV3	GTCAACAGGTCTAATACACCTCCACCAAAACATCGTGGATGTCCAATACCTTTATGGTGTGGATCTGGCATGGTGGGA									
HCV4	CTCGACTGGCTTGATCCACCTCCACCAGAACATCGTGGACGTCCAGTACCTTTACGGTGTGGGTCCGCGGTGGTGTCA									
HCV5	TAGCACTGGCCTCATACTTACATCAGAATATAGTAGACACCAGTACCTTTACGGCCTGAGCTCCAGCATCGTCTCG									
HCV6	ATCAACTGGCCTCATCCACCTGCACCAGAACATAGTGGACGTGCAGTACCTCTACGGAGTCTCCTCGAGCATCGTCTCG									
	2134	2140	2150	2160	2170	2180	2190	2200	2212	
H77 (NC_004102)	TGGGCCATTAAGTGGGAGTACGTGTTCTCCTGTTCTCCTGCTTGCAGACGCGCGCTGCTCCTGCTTGTGGATGA									
HCV1	TGGGCCATCAAGTGGGAGTACGTGTTCTCCTGTTCTCCTGCTTGCAGACGCGCGCTGCTCCTGCTTGTGGATGA									
HCV2	TACATCGTGAAGTGGGAGTGGGTGGTCCTCTTTCTGCTGTTGGCAGACGCCAGGGTCTGTGCATGCCTTTGGATGC									
HCV3	TGGGCGTTGAAATGGGAGTTCGTATCCTCGTTTTCTCCTCCTAGCAGACGCACGCGTGTGCGTTGCCCTTTGGCTGA									
HCV4	TGGGCTCTCAAGTGGGAGTACGTTGTGCTTGCCTCCTGCTGCTCGCAGACGCCAGGGTCTGTGCGTGCCTGTGGATGA									
HCV5	TGGGCCGTTAAGTGGGAGTACATAGTGTGGCCTTTTACTACTTGTGATGCCGTATCTGTACTTGCCTGTGGATCA									
HCV6	TGGGCAGTGAAGTGGGAGTACGTTGTCTGGTGTTCCTGGTGTGGCAGATGCTCGCATTTGTGCGTGTCTGTGGTTGA									
	2213	2220	2230	2240	2250	2260	2270	2280	2291	
H77 (NC_004102)	TGTTACTCATATCCCAAGCGGAGGCGGCTTTGGAGAACCTCGTAATACTCAATGCAGCATCCCTGGCCGGGACGCACGG									
HCV1	TGTTACTCATATCCCAAGCGGAGGCGGCTTTGGAGAACCTCGTGGTACTCAATGCAGCATCCCTGGCCGGGACGCACGG									
HCV2	TCATCATACTGGGCCAAGCCGAGGCGGCGCTTGAGAAGCTCATCATCTTGCCTCCGCTAGCGCTGCTAGTGCCAATGG									
HCV3	TGCTGATGATATCACAAGCAGAAGCAGCCTTGAGAACCTTGTACGCTGAACGCCGTCGCTGCTGCCGGGACACATGG									
HCV4	TGCTGCTGGTGTGCGAGGTTGAGGCAGCCCTGGCCAACTGATTACCATCAATGCTGTTTACGCCGCTGGCACTCACGG									
HCV5	TGCTCCTAGTTTGTGAGGCTGAAGCAGCCCTGGAGAACGTATTGCTCTAAACGCGGCTGCGGCCGCGGGACTCATGG									
HCV6	TGCTGCTCGTAGGCCAAGCTGAGGCAGCACTGGAGAACCTTATCGTCTCAACGCGGCCTTGCCGCCAGCACTCACGG									

















Table S5. Cont.

	3929	3940	3950	3960	3970	3980	3990	4000	4005
H77 (NC_004102)	ATGACATAATAATTTGTGACGAGTGCCACTCCACGGATGCCACATCCATCTTGGGCATCGGCACTGTCCTTGACCAA								
HCV1	ATGACATAATAATTTGTGACGAGTGCCACTCCACGGATGCCACATCCATCTTGGGCATCGGCACTGTCCTTGACCAA								
HCV2	ATGACATCATCATATGCGATGAATGCCATT <b>CAGTGGACGCTACTACCATCCTTGGCATTGGAACAGTCCTTGACCAG</b>								
HCV3	ATGAT <b>GTGATT</b> ATCTGTGATGAATGTCATG <b>CCCAAGACGCTACTAGCATATTGGGTATAGGCACGGTCTTAGATCAG</b>								
HCV4	ATGACATCATCATCTGTGACGAGTGCCATTCCACTGAT <b>TCCACAACGATCCTTGGCATAGGCACGGTCTTGACCAA</b>								
HCV5	ATGAC <b>GTGAT</b> CATATGCGACGAGTGCCATT <b>CCCAGGACGCTACCACCATCCTTGGGATAGGCACAGTCCTTGACCAG</b>								
HCV6	ATGACATCATCATCTGTGACGAGTGCCACT <b>CAACAGACCCTACCACGGTCTTGGGCATAGGCACGGTTCTCGACCAG</b>								
	4006	4010	4020	4030	4040	4050	4060	4070	4082
H77 (NC_004102)	GCAGAGACTGCGGGGGCGAGACTGGTTGTGCTCGCCACTGCTACCCCTCCGGGCTCCGTCACTGTGTCCCATCCTAA								
HCV1	GCAGAGACTGCGGGGGCGAGACTGGTCGTGCTCGCCACCGCTACCCCTCCGGGCTCCGTCACCGTGCCCCATCCTAA								
HCV2	GCTGAGACCGCAGGTG <b>TCAGGCTAGTGGTTTTGCCACAGCCACGCCTCCCGGTACGGTGACA</b> ACTCCCCACACCAA								
HCV3	GCTGAGACGGCTGGGGTGAGGCTG <b>ACGGTTTTAGCGACAGCA</b> ACTCCCCAGGCAGCATCACTGTGCCACATTCTAA								
HCV4	GCGGAGACCGCTGGAGCGCGCCTTGTCTGCTCGCGACCGCCACGCCACCAGGGTCGGTGACA <b>ACCCCCATCCCAA</b>								
HCV5	GCAGAGACGGCTGGAGCTAGGCTCGTCT <b>TGGCCACGGCCACTCCCCCGGCAGTGTGACA</b> ACGCCCCACCCCAA								
HCV6	GCGGAGACTGCCGGAGTGCGCCT <b>ACTGTGCTCGAACAGCAACGCCGCTGGTTCTGTCACTGTCCCCATCCTAA</b>								
	4083	4090	4100	4110	4120	4130	4140	4150	4159
H77 (NC_004102)	CATCGAGGAGGTTGCTCTGTCCACCACCGGAGAGATCCCTTTTACGGCAAGGCTATCCCCCTCGAGGTGATCAAGG								
HCV1	CATCGAGGAGGTTGCTCTGTCCACCACCGGAGAGATCCCTTTTACGGCAAGGCTATCCCCCTCGAGG <b>CAATCAAGG</b>								
HCV2	CATAGAGGAGGTGGCCCTCGG <b>T</b> CATAGGGGCGAGATCCCTTTTATGGCAAGGCTATCCCC <b>TAGCTTACATCAAGG</b>								
HCV3	CATCGAAGAAGTGGCCCTGGGCT <b>CTGA</b> AGGTGAGATCCCTTTCTACGGTAAGGCTATACCGATAGCCCTGCTCAAGG								
HCV4	CATAGAGGAGGTGGCCCTGCCGACGACGGGAGAGATACCCTTCTACGGCAGGGCGATCCCCCTAGCTGTCATCAAGG								
HCV5	CATCGAGGAGGTGGCCCTGCCT <b>TCGGAGGGGGAAAT</b> CCCCCTTCTACGGCAGGGCCATCCCCCTTGCTCTTATAAAGG								
HCV6	CATA <b>ACAGAGACAGCCCTCCCTACTACGGGAGAAAT</b> ACCCTTTTATGGGAAGGCAATCCCCCTTGAGT <b>ACATCAAAG</b>								











Table S5. Cont.

	5078	5090	5100	5110	5120	5130	5140	5153	
H77 (NC_004102)	CAATTATACCTGACAGGGAGGTTCTCTACCAGGAGTTCGATGAGATGGAAGAGTGCTCTCAGCACTTACCGTACAT								
HCV1	CAATCATACCTGACAGGGAAGTCCTCTACCGGGAGTTCGATGAGATGGAAGAGTGCTCTCAGCACCTACCGTACAT								
HCV2	<b>TTGTGGCCCCTGACAAGGAAGTCCTATATGAGGCCTTTGATGAGATGGAAGAATGCGCCTCCAAAGCCGCCCTCAT</b>								
HCV3	CACTCGTTCCAGACAAAGAGGTGTTGTATCAACAATACGATGAGATGGAGGAGTGCTCGCAAGCCGCCCATATAT								
HCV4	CCGTCATCCCCGACCGAGAGGTGCTCTACCAACAGTTTGACGAGATGGAGGAGTGCTCCAAGCACCTTCCACTAGT								
HCV5	CCATCATTCCCGACAGGGAGGTGCTATACCAGCAATTTGATGAGATGGAGGAGTGCTCGGCCTCCCTGCCCTATAT								
HCV6	CTGTTGTCCCTGATCGGGAGGTCTTGTACCAACAATTTGACGAGATGGAGGAGTGCTCTAGGCACATCCCCTACCT								
	5154	5160	5170	5180	5190	5200	5210	5220	5229
H77 (NC_004102)	CGAGCAAGGGATGATGCTCGCTGAGCAGTTCAAGCAGAAGGCCCTCGGCCTCCTGCAGACCGCGTCCCGCCAAGCA								
HCV1	CGAGCAAGGGATGATGCTCGCCGAGCAGTTCAAGCAGAAGGCCCTCGGCCTCCTGCAGACCGCGTCCCGCCAGGCA								
HCV2	<b>TGAGGAAGGGCAGCGGATGGCGGAGATGCTCAAGTCCAAGATACAAGGCCTCCTACAACAGGCCACAAAACAGGCC</b>								
HCV3	CGAACAAGCTCAGGTAATAGCCCACCAGTTCAAGGAGAAAGTCCTTGGATTGCTGCAGCGAGCCACCCAACAACAA								
HCV4	CGAGCACGGCCTGCAACTGGCAGAGCAATTCAAACAGAAGGCCCTCGGCGTGCTGAACATCGCCGGCAAGCAGGCC								
HCV5	<b>GGACGAGGCACGTGCCATTGCCGGGCAATTCAAGGAGAAAGTGCTCGGCCTCATTGGCACGGCCGGCCAGAAAGCT</b>								
HCV6	CGCTGAGGGCCAGCAGATAGCCGAACAGTTCAAACAAAAGGTGCTCGGTCTCATCCAGACCACCGCCAAGCAGGCA								
	5230	5240	5250	5260	5270	5280	5290	5300	5305
H77 (NC_004102)	GAGGTTATCACCCCTGCTGTCCAGACCAACTGGCAGAAACTCGAGGTCTTCTGGGCGAAGCACATGTGGAATTTCA								
HCV1	GAGGTTATCGCCCCTGCTGTCCAGACCAACTGGCAAAAAGCTCGAGGCCTTCTGGGCGAAGCATATGTGGAACTTCA								
HCV2	<b>CAAGACATACAGCCAGCCATACAGTCATCATGGCCCAAGCTTGAACAATTTGGGCCAAACACATGTGGAACTTCA</b>								
HCV3	<b>GCTGTCAATTGAGCCCATAGTAGCTACCAACTGGCAAAAAGCTTGGAGGCCTTCTGGCACAAGCATATGTGGAATTTG</b>								
HCV4	<b>CAGGAGGCAGCACCAGTGGTCCAGTCCAACCTTGGCCAAGCTTGAACAGTTCTGGGCAAAGCACATGTGGAACTTCA</b>								
HCV5	<b>GAAACTCTGAAACCGGCAGCCACGTCTATGTGGAGCAGGGCCGAGCAGTTCTGGGCAAACACATGTGGAACTTTG</b>								
HCV6	<b>GAAGAACTGAAGCCTGCTGTCCATTCCGCGTGGCCTAAGCTTGAGCAGTTTGGCAGAAACACATGTGGAACTTTG</b>								

Table S5. Cont.

	5306	5310	5320	5330	5340	5350	5360	5370	5381
H77 (NC_004102)	TCAGTGGGATACAATACTTGGCGGGCCTGTCAACGCTGCCTGGTAACCCCGCCATTGCTTCATTGATGGCTTTTAC								
HCV1	TCAGTGGGATACAATACTTGGCGGGCCTGTCAACGCTGCCTGGTAACCCCGCCATTGCATCATTGATGGCTTTTAC								
HCV2	TCAGTGGCATAACAGTACCTGGCGGGACTCTCCACCCTACCGGGAAATCCCGCAGTGGCATCAATGATGGCTTTTAC								
HCV3	TGAGTGGGATCCAGTACCTAGCAGGCCTCTCCACTTTGCCTGGCAACCCCTGCTGTGGCGTCTCTTATGGCGTTTAC								
HCV4	TCAGCGGCATCCAATACCTTGGCCGGTGTGCCACCTTGCCCGGCAACCCCTGCCATTGCTTCCCTCATGTCCTTAC								
HCV5	TCAGTGGGATCCAATACCTAGCTGGCCTTTCGACCTTGCCCGGCAATCCCGCCGTGGCCACGTTGATGTCCTTAC								
HCV6	TCAGCGGGATTGAGTACCTGGCGGGCTTATCCACCCTGCCCGGCAACCCAGCTGTGGCATCCCTCATGTCATTCTC								
	5382	5390	5400	5410	5420	5430	5440	5450	5457
H77 (NC_004102)	AGCTGCCGTCACCAGCCCACTAACCCTGGCCAAACCCTCCTCTTCAACATATTGGGGGGGTGGGTGGCTGCCAG								
HCV1	AGCTGCTGTCACCAGCCCACTAACCCTAGCCAAACCCTCCTCTTCAACATCTTGGGGGGGTGGGTGGCTGCCAG								
HCV2	CGCCGCACTGACTAGCCCACTATCCACCAGCACCACCATCCTCTTGAACATCATGGGGGGATGGTTGGCCTCCCAG								
HCV3	TGCTTCAGTCACCAGTCCCCTGACGACCAACCAAACTATGTTTTTAACATACTCGGGGGGTGGGTGCTACCCAT								
HCV4	CGCCGCTGTCACCAGCCCCCTGACCACCAACAAACCCTCCTCTTCAACATCTTAGGAGGGTGGGTGGCCTCGCAG								
HCV5	CGCCGCGGTGACCTCCCCCTTACAACACAACAGACCCTCCTCTTAAATATTCTAGGAGGGTGGGTGGCCTCACAG								
HCV6	AGCGTCGCTGACCAGCCCACTGACCCTTCTCAGACCCTCCTCCTCAACATCTTAGGGGGGTGGGTAGCCTCCCAA								
	5458	5470	5480	5490	5500	5510	5520	5533	
H77 (NC_004102)	CTCGCCGCCCCCGGTGCCGCTACCGCCTTTGTGGGCGCTGGCTTAGCTGGCGCCGCCATCGGCAGCGTTGGACTGG								
HCV1	CTCGCCGCCCCCGGTGCCGCTACCGCCTTTGTGGGCGCTGGCTTAGCTGGCGCCGCCATCGGCAGTGTGGACTGG								
HCV2	ATTGCCCCCTGCCGGGGCCACTGGCTTCGTTGTCAGTGGTCTAGTGGGGGCGGCCGTCGGAAGCATAGGCCTGG								
HCV3	TTGGCAGGGCCCCAGAGCTCTTCCGATTCGTGGTAAGCGGCTTGCCCGGCGCTGCCATAGGGGGTATAGGCCTGG								
HCV4	ATCGCGACCCCCACGGCCTCTACGGCTTTTGTGCTGAGCGGCCTCGCGGGGGCTGCGGTTGGCAGTGTGGGCCTGG								
HCV5	ATCGCGCACCCACGGCCGCACTGCGTTCGTGTTAGTGAATGGCCGGGGCCGAGTCGGTAGCATCGGGTTGG								
HCV6	CTGGCTACCCCCCGCGTCTACAGCTTTTGTGGTGGAGCGGCCTAGCAGGCGCCGCGGTGGGAAGCATTGGGCTCG								



Table S5. Cont.

	5762	5770	5780	5790	5800	5810	5820	5830	5837
H77 (NC_004102)	CCTTCGCCTCCCGGGGAACCATGTTTCCCCACGCACTACGTGCCGGAGAGCGATGCAGCCGCCCGCTCACTGC								
HCV1	CCTTCGCCTCCCGGGGAACCATGTTTCCCCACGCACTACGTGCCGGAGAGCGATGCAGCTGCCCGCTCACTGC								
HCV2	CCTTTGCCTCCAGAGGAAACCATGTTGCCCTACCCACTACGTGGCGGAGTCTGACGCCTCGCAGCGCGTGACGCA								
HCV3	CATTTCGCATCCCGGGGCAACCACGTCTACCAACGCACTATGTTCCCGAGAGCGATGCTGCAGCGAGGGTCACCGC								
HCV4	CGTTTCGCATCGCGAGGCAATCACGTGTCTCCACGCACTACGTCCCCGAGACCGACGCAGCGGCCCGCTGACTGC								
HCV5	CGTTTCGCTCCCGGGGCAATCATGTGTCTCCGACACACTACGTGCCCGAGACGGACGCGTCGGCCAAAGTCACGCA								
HCV6	CCTTTGCCTCAAGGGGCAACCACGTGTCCCCACGCACTACGTGCCTGAGACTGACGCGTCACGGAAAGTGACTAA								
	5838	5850	5860	5870	5880	5890	5900	5913	
H77 (NC_004102)	CATACTCAGCAGCCTCACTGTAACCCAGCTCCTGAGGCGACTGCATCAGTGGATAAGCTCGGAGTGTACCACTCCA								
HCV1	CATACTCAGCAGCCTCACTGTACCCAGCTCCTGAGGCGACTGCACCAGTGGATAAGCTCGGAGTGCACCACTCCA								
HCV2	GGTGCTAAGCTCACTCACAATTACCAGTTACTTAGGAGACTACATACCTGGATCACTGAAGATTGCCAGTCCCA								
HCV3	ATTGCTGAGTTCTCTAACTGTACAAAGTCTGCTCCGGCGGTTGCACCAGTGGATCAATGAAGACTACCCAAGTCTT								
HCV4	CATACTATCATCCCTGACTGTGACATCCCTTCTCAGACGCCTCCACAAGTGGATCAATGAGGACTGCTCCACTCCC								
HCV5	GCTGCTCAGTCCCTCACAGTAACATCTCTTCTGAAGAGGCTCCATACATGGATCGGTGAGGACTACTCCACGCCC								
HCV6	CATACTCAGTTCCCTTACCATCACCAGCCTACTCCGTAAGTTACATCAGTGGATCAATGAAGACTGGTCCACCCCT								
	5914	5920	5930	5940	5950	5960	5970	5980	5989
H77 (NC_004102)	TGCTCCGGTTCCTGGCTAAGGGACATCTGGGACTGGATATGCGAGGTGCTGAGCGACTTAAAGACCTGGCTGAAAG								
HCV1	TGCTCCGGTTCCTGGCTAAGGGACATCTGGGACTGGATATGCGAGGTGCTGAGCGACTTAAAGACCTGGCTAAAGG								
HCV2	TGCTCGGGTCTTGGCTCCGGGACATTTGGGATTGGGTTTGTTCCATCCTCACAGACTTAAAGAACTGGCTGTCTT								
HCV3	TGCAGCGCGGATTGGCTGCGTACCATCTGGGACTGGGTTTGCACGGTGTGTCCGACTTCAAGACATGGCTCTCTG								
HCV4	TGTGACTCATCTTGGCTGTGGGAGATCTGGGACTGGGTCTGCACCGTACTGAGTGACTTCAAGACGTGGCTCAAGG								
HCV5	TGTGATGGCACATGGCTTAGGGCCATTTGGGACTGGGTCTGCACGGCACTGACAGACTTCAAAGCCTGGCTGCAGG								
HCV6	TGCTCTACCTCATGGTTGCGCGACATCTGGGACTGGGTGTGTACTGTGCTATCTGACTTCAAACCTGGCTCAAAG								

Table S5. Cont.

	5990	6000	6010	6020	6030	6040	6050	6060	6065
H77 (NC_004102)	CCAAGCTCATGCCACA	AACTGCCTGGGATTCC	CTTTGTGTCCTGCCAG	CGCGGGTATAGGGGG	TCTGGCGAGGAGA				
HCV1	CCAAGCTCATGCCACA	AACTGCCTGGGATCCC	CTTTGTGTCCTGCCA	ACGCGGGTATAGGG	GGGTCTGGCGAGGG				
HCV2	CAAAATTGCTCCCCA	AAATGCCCGGCCCTT	CCCTTCATCTCTTG	CCAAAAGGGATACAG	GGGTGTGTGGGCTG				
HCV3	CTAAGATCATGCCAG	CGCTCCCTGGGCTG	CCCTTCATTTCTGT	CAAAAGGGATACAAG	GGCGTGTGGCGGGG				
HCV4	CTAAGCTACTGCCCG	CATGCCCGCATCCC	CTTCTCTCTGCCAA	AAGGGGTACAAGGG	GGGAGTGGCGGGG				
HCV5	CAAACTCCTCCCGC	AACTCCCGGAGTG	CCCTTCTCTCATG	CCAGAGGGGTACA	AAGGTGTGTGGCG				
HCV6	CCAAACTTGTCCCAC	CCCTGCCCGGGTCC	CCCTTCTCTCGTG	CCAAACGGGGATA	CAGGGGAGTCTGG				
	6066	6070	6080	6090	6100	6110	6120	6130	6141
H77 (NC_004102)	CGGCATTATGCACAC	TGCTGCCACTGTGG	AGCTGAGATCACTG	GACATGTCAAAAAC	CGGGACGATGAGG				
HCV1	CGGCATCATGCACAC	TGCTGCCACTGTGG	AGCTGAGATCACTG	GACATGTCAAAAAC	CGGGACGATGAGG				
HCV2	GGGAATCATGACTAC	TGCTGGTCCATGCC	GAGCAAACATCTCG	GGCCATGTCCGCAT	GGGCACCATGAAA				
HCV3	CGGTGTGATGTCAAC	ACGCTGTCTTGGC	GGGCATCAATAACC	GGTCATGTGAAGA	ATGGGTCCATGCG				
HCV4	CGGGGTAATGCACAC	CACATGCCCTTGCG	GCGCAGAGCTGGC	CGCCACATCAAAA	ACGGCTCGATGAG				
HCV5	TGGAGTGAATTCCAC	CAAGTGTCCGTGCG	GAGCGACGATATCT	GCCACGTGAAGA	ACGGAACCATGAG				
HCV6	CGGGGTGTGCCACAC	CCTGCACCTGCGGG	GCCGAGATAGCTG	GCCACGTCAAAA	ACGGGACCATGA				
	6142	6150	6160	6170	6180	6190	6200	6210	6217
H77 (NC_004102)	GGTCCTAGGACCTGC	CAGGAACATGTGG	AGTGGGACGTTCCC	CATTAACGCCTAC	ACCACGGGCCCTG				
HCV1	GGTCCTAAGACCTGC	CAGGAACATGTGG	AGTGGGACCTTCCC	CATCAACGCCTAC	ACCACGGGCCCTG				
HCV2	GGCCCGAAGACCTG	CTTGAACATGTGG	CAGGGGACCTTCCC	CATCAATTGTTAC	ACAGAAGGGCCTT				
HCV3	GGGCCGCGCACATG	TGCTAACATGTGG	CACGGTACTTTCCC	CATCAATGAGTAC	ACCACCGGACCC				
HCV4	GGGCCCAAGACCTG	CAGCAACACCTGG	CATGGGACCTTCCC	CATCAATGCTTAC	ACCACAGGCCCC				
HCV5	GGCCCGAAGATGTG	CAGTAACACCTGG	CACGGAACCTTCCC	AATCAACGCCACA	ACAACAGGGCCC				
HCV6	GGGCCCGGACATGC	CAGCAACATCTGG	CACGGCACTTTCCC	CATCAATGCCACC	ACGACCGGCCCT				

Table S5. Cont.

	6218	6230	6240	6250	6260	6270	6280	6293	
H77 (NC_004102)	TTCCTGCGCCGAACTATAAGTTCGCGCTGTGGAGGGTGTCTGCAGAGGAATACGTGGAGATAAGGCCGGGTGGGGGA								
HCV1	TTCCTGCGCCGAACTATAACGTTTCGCGCTGTGGAGGGTGTCTGCAGAGGAATACGTGGAGATAAGGCCGGGTGGGGGA								
HCV2	<b>A</b> ACCCCTCCTAATTACAAG <b>ACC</b> GCAATTTGGAGGGTGG <b>CAGCGT</b> CGGAGTACGTTGAGGT <b>CACGCAGCATGGCTC</b>								
HCV3	<b>G</b> CCCAT <b>CAC</b> CCAACT <b>A</b> CACT <b>CG</b> CGCACTATGGCGCGTGGCTGCC <b>AACAGCT</b> ACGTTGAGGT <b>G</b> CGCCGGTGGGGGA								
HCV4	TCC <b>AG</b> CGCCGAACTACAAGTTCGCGCTGTGGAGGGTGTCCGCGGAGGAATACGTGGAGGT <b>T</b> CGCAGAGTGGGTGA								
HCV5	<b>C</b> CCCGGCTCCCAACTACAAGTTCGCCTTGTGGAGGGT <b>AGG</b> CGCTGCGGACTACGCGGAGGT <b>G</b> CGCCCGTAGGGGA								
HCV6	TCC <b>AG</b> CGCCCAACTACAAG <b>AGG</b> GCTCTTTGGAGGGTATCCGCTGAGGAGTACGTTGAGGTACGGAGGGTGGGCGA								
	6294	6300	6310	6320	6330	6340	6350	6360	6369
H77 (NC_004102)	CTTCCACTACGTATCGGGTATGACTACTGACAATCTTAAATGCCCGTGCCAGATCCCATCGCCCCGAATTTTTCACA								
HCV1	CTTCCACTACGT <b>G</b> ACGGGCATGACTACTGACAACCTTAAATGCCCGTGCCAG <b>G</b> TCCCATCGCCCCGAATTTTTCACA								
HCV2	<b>T</b> TTCTCGTACGTAACGGGG <b>T</b> TAAACCAGTGACAACCTTAA <b>AGG</b> TCCCTTGCCAGGTACCAGCTCCAGAGTTCTTCTCT								
HCV3	CTTCCATTACATTACGGGGG <b>CC</b> CACAGAAGATGAGCTCAAGTGTCCGTGCCA <b>AGT</b> GCCGGCTGCTGAGTTCTTACT								
HCV4	<b>T</b> TTCCATTATGT <b>C</b> ACGGGGTGAC <b>ACA</b> AGATAACATCAAGTGCCCTGCCAGGT <b>TC</b> TGCCCTGAGTTCTTCACT								
HCV5	CT <b>ACC</b> ACTACATTACGGGGGTGAC <b>AC</b> AGGACAATCTGAAGTGTCCCTGCCAGGT <b>ACC</b> ATCTCCAGAGTTCTTACG								
HCV6	CT <b>G</b> CCACTACGT <b>G</b> GT <b>AG</b> GGGTCACTGCTGACGACCTGAAATGCCCATGCCAGGT <b>GC</b> CTGCTCCTGAGTTCTTCACT								
	6370	6380	6390	6400	6410	6420	6430	6440	6445
H77 (NC_004102)	GAATTGGACGGGGTGCGCCTACATAGGTTTGCGCCCCCTTGCAAGCCCTTGCTGCGGGAGGAGGTATCATT <b>C</b> AGAG								
HCV1	GAATTGGACGGGGTGCGCCTGCATAGGTT <b>CG</b> CGCCCCCTTGCAAGCCCTTGCTGCGGGAGGAGGTCTCATT <b>C</b> AGAG								
HCV2	<b>T</b> GGGTGGACGGGGTG <b>CAA</b> ATAC <b>CCG</b> ATT <b>CG</b> CCCCACT <b>CC</b> AGGTCCCTTCTTTCGGGATGAGGTA <b>AC</b> GTT <b>C</b> ACCG								
HCV3	GAAGTGGATGGGGTGAGACT <b>CC</b> ACCGTTACGCCCTCCATGTAAGCCCTGTTGAGGGATGAGAT <b>C</b> ACTTTCAT <b>G</b> G								
HCV4	GAGGTGGACGGCGT <b>C</b> AGGCTAC <b>CCG</b> CC <b>AC</b> GCCCC <b>TG</b> CGTGCAAGCCCTGCTGAGGGACGAAGT <b>G</b> ACCTT <b>C</b> ACCG								
HCV5	GAGCTGGACGGCGTGAGGATT <b>C</b> ACCGCTTCGCGCCACCCTGCAACCCCTCCTAAGGGAGGAGGTTACTT <b>T</b> CTCCG								
HCV6	GAGGTTGATGGCGTGAGGATA <b>C</b> ACCGTT <b>AC</b> GCGCCACCCTGCAAGCCCTGCTGAGGGACGAAGT <b>G</b> ACCTT <b>T</b> CTCTG								

Table S5. Cont.

	6446	6450	6460	6470	6480	6490	6500	6510	6521
H77 (NC_004102)	TAGGACTCCACGAGTACCCGGTGGGGTCGCAATTACCTTGCGAGCCCCGAACCGGACGTAGCCGTGTTGACGTCCAT								
HCV1	TAGGACTCCACGAGTACCCGGTGGGGTCGCAATTACCTTGCGAGCCCCGAACCGGACGTGGCCGTGTTGACGTCCAT								
HCV2	TAGGCCTCAATTCCTTTGTGGTCCGGCTCTCAGCTCCCTTGTGACCCTGAGCCGGACACCGAGGTATTGGCCTCCAT								
HCV3	TAGGGTTGAATTCCTACGCGATAGGATCTCAACTCCCCTGTGAGCCCCGAACCAGATGTTTCTGTGCTGACCTCGAT								
HCV4	TGGGCCTCAACACGTTTGTGGTGGGGTCCCAGCTCCCCTGCGAGCCAGAGCCAGACGTGGCCGTGTTAACATCCAT								
HCV5	TGGGGCTGCACTCCTACGTGGTGGGGTCCCAACTACCCTGTGAGCCAGAACCTGATGTGACCGTCCTGACGTCAAT								
HCV6	TGGGTCTCTCCACCTACGCCGTAGGGTCGCAGCTCCCTTGCAGCCAGAGCCAGACGTGATGGTTCGTACATCAAT								
	6522	6530	6540	6550	6560	6570	6580	6590	6597
H77 (NC_004102)	GCTCACTGATCCCTCCCATATAACAGCAGAGGGCGGCCGGGAGAAGGTTGGCGAGAGGGTCACCCCTTCTATGGCC								
HCV1	GCTCACTGATCCCTCCACATAACAGCAGAGGGCGGCTAGGAGAAGGTTGGCGAGGGGGTCACCCCTTCTTTGGCC								
HCV2	GCTGACAGACCCGTCCACATCACGGCGGAGGCGGCAGCCAGGCGATTGGCCAGGGGATCTCCCCCTTACAGGCC								
HCV3	GTTGAGAGACCCCTTCCCATATCACCGCCGAGACGGCAGCGCGCCGCTTGC GCGCGGGTCCCTCCATCAGAGGCA								
HCV4	GCTGACAGACCCATCCACATCACCGCGGAGACGGCGCGCCGAGGCTGGCCAGGGGGTCACCGCCCTCGTTGGCC								
HCV5	GCTGTGACACCCGTGCCACATCACGGCAGAGACGGCCAAGCGCAGGCTAGATCGAGGGTCTCCGCCCTCTTGCT								
HCV6	GCTGACAGACCCCTCACACATCACCGCAGAGGCGGCAGCACGGCGCCTGGCGAGGGGGTCCCCCTCCCTGGCC								
	6598	6610	6620	6630	6640	6650	6660	6673	
H77 (NC_004102)	AGCTCCTCGGCCAGCCAGCTGTCCGCTCCATCTCTCAAGGCAACTTGACCCCAACCATGACTCCCCTGACGCCG								
HCV1	AGCTCCTCGGCTAGCCAGCTGTCTGCTCCATCTCTCAAGGCAACTTGACCCCAACCATGACTCCCCTGACGCCG								
HCV2	AGCTCCTCAGCGAGCCAGCTCTCCGCCCCGTCTTGAAGGCTACCTGTACCACCCATAAGATGGCATATGATTGTG								
HCV3	AGCTCATCCGCCAGCCAACTATCAGCTCCGTCGTTGAAGGCCACTTGCCAGACGCATAGGCCTCATCCAGACGCTG								
HCV4	AGCTCCTCGGCTAGCCAGCTTCCGCCCCATCCCTCAAAGCCACATGCACCGCCCACCAGACTCCCCTGGCGCTG								
HCV5	AGCTCCTCGGCCAGTCAGCTCTCGCCCCCTCCCTCAAGGCTACCTGCACTACACACCACCCAGACGCAGACCTCA								
HCV6	AGCTCATCGGCCAGCCAGCTGTCAGACCCGTCCTGAAGGCCACATGCACAACGGACCACCCGGACGCGGAACTGA								





Table S5. Cont.

	6902	6910	6920	6930	6940	6950	6960	6970	6977
H77 (NC_004102)	GGAAAAAGCCTGACTACGAACCACCTGTGGTCCATGGCTGCCCGCTACCACCTCCACGGTCCCCCTCTGTGCCTCC								
HCV1	GGAAAAAGCCGGACTACGAACCACCTGTGGTCCATGGCTGCCACTT---CCTCCACAGTCCCCTCTGTGCCTCC								
HCV2	GGAAGAGGCCGGACTATGAACCACCCACTGTCTAGGCTGTGCCCTC---CCCACACCTCAAGCGCCAGTGCCCCC								
HCV3	GGAAAGCACCGGATTATGTACCACCAACTGTCCATGGATGCGCCTTA---CCACGGGGCGCTCCACCGGTGCCTCC								
HCV4	GGAAGCAACCGGACTACGAACCTCCGGTCTCAGGGTGCGCCCTG---CCCAGTAAGCCGCCCCCGTTCTCTCC								
HCV5	GGAAGCGGCCGGATTATGACCCCCCCCAGGTGTCAGGCTGCCCGCTA---CCTGCGGGCCTCCCGCCTGTCCCGCC								
HCV6	GGAAGACGCCCGAATACGAGCCTCCAGTGGTGTCTGGGTGTGCCCTG---CCACCTAAACCGACTCCAATTCCTCC								
	6978	6990	7000	7010	7020	7030	7040	7053	
H77 (NC_004102)	GCCTCGAAAAAGCGTACGGTGGTCTCACCGAATCAACCCTATCTACTGCCTTGGCCGAGCTTGCCACCAAAAAGT								
HCV1	GCCTCGGAAGAAGCGG---GTGGTCTCACCGAATCAACCGTATCTACTGCCTTGGCCGAGCTTGCCACCAAGAGC								
HCV2	ACCTCGGAGGCGCCGC--AAAGTCTGACTCAGGACAATGTGGAGGGGGTCTCAGGGAGATGGCCGACAAAGTG								
HCV3	CCCTCGGAGGAAAAGA---ATCCAGCTGGATGGTCCAATGTGTCCGCGGCGCTAGCTGCGCTAGCGGAAAAATCA								
HCV4	CCCCAGGAGGAAGCGG--GTCGTGCTCTCCGAGTCCAACGTCTCAGACGCCTTGGCGGACTTGGCAGCGAAGTCC								
HCV5	TCCGCGGAGGAAGAGGAAGATGGAACCTATCTGACTCTACCGTGTCCCAAGTCATGGCCGACTTGGCGCACGCCAGG								
HCV6	ACCGAGGAGGAAGAGGCTGCACCTGGATGAGTCCACGGTCTCACACGCCTTGGCGCAGCTGGCCGAGAAGACGTTT								
	7054	7060	7070	7080	7090	7100	7110	7120	7129
H77 (NC_004102)	TTTGGCAGCTCCTCAACTTCCGGCATTACGGGCGACAATACGACAACATCCTCTGAGCCCGCCCCTTCTGGCTGCC								
HCV1	TTTGGC---TCCTCAACTTCCGGCATTACGGGCGACAATACGACAACATCCTCTGAGCCCGCCTCCTCTGGCTGC-								
HCV2	TTCAGC---CGCGACTCCGGCCATTCCACCGGGGAGGACACCGGAGGGGACACCGGCCAGGACCCCCCTGAGGAG-								
HCV3	TTCCCGTCCGAAGAGAATAGCTCATCTCAGGGGTCGACACACAGTCCAGCACTACTTCCAAGGTGCCCCCTTCT-								
HCV4	TTTGGCCAGCCGGACTCCGATTCCGGGGCAGGCCTCACCACCCCAACTGAGACTTCTGACCCAGACCCCATCATT-								
HCV5	TTCAAGGCCCATCCATTGAAGGCCAGGATTCTGCGTTGGGCACTGGCAGCCAACCCGATTTCAGGGCCTGAGGAA-								
HCV6	CCGGAGACTGCCCCAGCAGCCAGTGCAGACTCGGGACTAGCAACTACCAGTGCCGCTGCAGCGGCCCCAGCAGCA-								





Table S5. Cont.

	7586	7590	7600	7610	7620	7630	7640	7650	7661
H77 (NC_004102)	GCCATGCCAGAAAGGCCGTAGCCACATCAACTCCGTGTGGAAAGACCTTCTGGAAGACAGTGTAACACCAATAGA								
HCV1	GCCATGCCAGAAAGGCCGTAAACCACATCAACTCCGTGTGGAAAGACCTTCTGGAAGACAGTGTAACACCAATAGA								
HCV2	GCTTATCCAGGAGGGCCGTTAACCACATCCGGTCCGTGTGGGAGGACCTCCTGGAAGACCAACATACACCAATTGA								
HCV3	CCTTGTCCAGCAAGGCCATTAACCAGATCCGCTCCGTCTGGGAGGACTTGCTGGAAGACACCACAACCTCCAATTCC								
HCV4	GCCATTCCCAGCAAGGCCATTAACCACATCAACTCCGTGTGGGAGGACTTGCTGGAAGACAACACTACCCCATTC								
HCV5	CTCTCGACAAGAAAGCCCTTAAGCACATCGAGGGTGTGTGGCAAGACTTACTGGATGACTCTGATACCCCATTGCC								
HCV6	GCCATGCTAGCAAGGCCATTAACCACATCAACTCCGTGTGGGAGGACTTGCTAGAAGACACTGAAACACCAATTCC								
	7662	7670	7680	7690	7700	7710	7720	7730	7737
H77 (NC_004102)	CACTACCATCATGGCCAAGAACGAGGTTTTCTGCGTTCAGCCTGAGAAGGGGGTTCGTAAGCCAGCTCGTCTCATC								
HCV1	CACC---ATCATGGCTAAGAACGAGGTTTTCTGCGTTCAGCCTGAGAAGGGGGTTCGTAAGCCAGCTCGTCTCATC								
HCV2	CACC---ATCATGGCCAAAAATGAGGTGTTCTGTGTTGATCCCACCAAAGGCGGGAAAAAGCCAGCTCGCCTCATC								
HCV3	AACC---ATCATGGCGAAGAACGAGGTGTTTTGTGTGGACCCCGTTAAGGGGGCCGCAAGCCCGCTCGCCTCATT								
HCV4	AACA---ATCATGGCCAAGAATGAGGTCTTCTGTGAAACCAGGAGAAGGGCGGCCGAAAGCCAGCTCGTCTAATC								
HCV5	GACC---ATCATGGCAAAAAACGAGGTGTTTCGAGTGGAGCCGTCCAAGGGGGGAAAGAAGCCAGCACGGCTAATA								
HCV6	TACC---ATCATGGCCAAGAATGAGGTCTTCTGCGTGGATCCGTCGAAGGGGGGACGCAAGCCGGCACGCCTGATC								
	7738	7750	7760	7770	7780	7790	7800	7813	
H77 (NC_004102)	GTGTTCCCCGACCTGGGCGTGCGCGTGTGCGAGAAGATGGCCCTGTACGACGTGGTTAGCAAGTCCCCCTGGCCG								
HCV1	GTGTTCCCCGACCTGGGTGTGCGCGTGTGCGAGAAGATGGCCCTGTACGACGTGGTCAGCAAGTCCCTCTGGCCG								
HCV2	GTATACCCTGACCTGGGGTCAAGGTGTGCGAGAAGATGGCCCTCTATGACATTGCACAAAAGCTTCCCAAGGCAG								
HCV3	GTGTACCCTGACCTGGGGTGTGCGTGTCTGTGAGAAACGCGCCCTATATGACGTGATACAGAAGTTGTCAATTGAGA								
HCV4	GTATACCCGACCTGGGGTGTGCGGTGTGCGAGAAGAGGGCGCTTATGACGTGTCAAAAACTTCCTAAGGCCG								
HCV5	GTCTACCCCGACCTTGAGTCCGCGTCTGCGAGAAGCGGGCATTGTACGACATAGCTCAAAAAGTCCGACAGCCC								
HCV6	GTTTACCCGACCTAGGCGTGTGCGGTGTGCGAGAAGAGGGCCCTATACGACATCACGCGGAAGTTACCACTGGCCG								



**Table S5. Cont.**

	8042	8050	8060	8070	8080	8090	8100	8110	8117
H77 (NC_004102)	TTGGGGGCCCTCTTACCAATTCAAGGGGGGAAAAGTGGGGTACCGCAGGTGCCGCGGAGCGGGCTACTGACAAC								
HCV1	TCGGGGGCCCTCTTACCAATTCAAGGGGGGAGAACTGGGGTATCGCAGGTGCCGCGGAGCGGGCTACTGACGAC								
HCV2	TAGGAGGGCCCATGACAAACAGCAAGGGGCAATCTGCGGTTACAGGCGTTGCCGCGCAAGCGGTGTTTTACCAC								
HCV3	GCGGGGGCCCTATGTTCAACAGCAAGGGGGCCCAGTGTGGTTATCGCCGTTGCCGTGCCAGTGGAGTTCTGCCTAC								
HCV4	TGGGCGGCCCCATGTATAACAGCAAGGGGAGACCTTTGCGGGTATCGGAGATGCCGCGCAAGCGGGCTTACACCAC								
HCV5	GTGGAGGCCCCATGTATAACAGCAAGGGGCAACAATGTGGTTATCGTAGATGCCGCGCCAGCGGGCTTTCACCAC								
HCV6	TTGGTGGCCCCATGTTCAACTCAAAGGGCCAGTCTGTGGTACCGCAGATGCCGCGCCAGTGGGGTGTCCCCAC								
	8118	8130	8140	8150	8160	8170	8180	8193	
H77 (NC_004102)	TAGCTGTGGTAACACCCTCACTTGCTACATCAAGGCCCGGCAGCCTGTCGAGCCGCAGGGCTCCAGGACTGCACC								
HCV1	TAGCTGTGGTAACACCCTCACTTGCTACATCAAGGCCCGGCAGCCTGTCGAGCCGCAGGGCTCCAGGACTGCACC								
HCV2	CAGCATGGGGAACACCATGACATGCTACATCAAAGCCCTTGCAGCATGCAAAGCTGCAGGGATCGTGGACCCCACT								
HCV3	CAGCTTCGGCAACACAATCACTTGTTACATCAAGGCCACAGCGGGTGCAGGGCCGAGGCCTCCGGAACCCGGAC								
HCV4	CAGCTTCGGGAACACACTGACGTGCTATCTTAAGGCCACAGCAGCCACCAGGGCCGAGGCCTAAAGGACTGCACC								
HCV5	TAGTATGGGCAACACCATGACGTGCTACATTAAGGCTTTAGCCTCCTGTAGAGCTGCAAAGCTCCGGGACTGCACG								
HCV6	CAGCATGGGCAACACCATCACATGCTACCTGAAAGCACAGGCCCGCTGCAGGGCAGCCGGCCTCAAGGACTTTGAC								
	8194	8200	8210	8220	8230	8240	8250	8260	8269
H77 (NC_004102)	ATGCTCGTGTGTGGCGACGACTTAGTCGTTATCTGTGAAAGTGGGGGTCCAGGAGGACGCGGCGAGCCTGAGAG								
HCV1	ATGCTCGTGTGTGGCGACGACCTAGTCGTTATCTGTGAAAGTGGGGAGTCCAGGAGGACGCGGCGAGCCTGAGAG								
HCV2	ATGCTGGTGTGTGGAGACGACCTGGTCGTCATCTCAGAGAGCCAAGGGAACGAGGAGGACGAGCGAAACCTGAGAG								
HCV3	TTTCTGTCTGCGGAGATGATCTGGTCGTGGTGGCTGAGAGTGATGGCCTCGAGGAGGATAGAGCAGCCCTGAGAG								
HCV4	ATGCTGGTCTGCGGTGACGACTTAGTCGTTATCGCCGAAAGCGATGGCGTGGAGGAGGACAACCGAGCCCTCGGAG								
HCV5	CTCCTGGTGTGTGGTGACGACCTTGTGGCCATCTGCGAGAGCCAGGGGACACACGAGGATGAAGCGAGCCTGAGAG								
HCV6	ATGTTGGTCTGCGGAGACGATTTGGTGGTCATTTGTGAGAGTGCTGGCGTCCAGGAGGACACTGCTGCCCTGCGAG								







Table S5. Cont.

	8726	8730	8740	8750	8760	8770	8780	8790	8801
H77 (NC_004102)	GAAAACTTGGGGTCCCGCCCTTGCAGCTTGGAGACACCGGGCCCGGAGCGTCCGCGCTAGGCTTCTGTCCAGAGG								
HCV1	GGAAACTTGGGGTCCCGCCCTTGCAGCTTGGAGACACCGGGCCCGGAGTGTCCGCGCTAAGCTTCTGTCCAGAGG								
HCV2	GAAAACTTGGAGCGCCTCCCTTAGAGCGTGGAAAGAGTCGGGGCGCGTGCTGTGAGGGCCTCACTCATCGCCCAG--								
HCV3	GGAAGCTTGGGTGCCCCCCCCTACGAGCTTGGAGACATCGGGCACGAGCAGTGCGCGCCAAGCTTATCGCCCAGGG								
HCV4	GGAAACTTGGGGTACCCCCATTGAGAGCGTGGAGACATCGGGCCCGAGCAGTCCGCGCCAAGCTCATCGCCCAGGG								
HCV5	GGAAGCTTGGGGTACCCCCTTTGGAGAGCTTGGAGACATCGGGCTCGAGCTGTACGCGCTAAGCTCATCGCCCAGGG								
HCV6	GGAAACTTGGGGCACCTCCCTTGGAGAGCCTGGAGACATCGAGCCAGAGCGGTGAGAGCCAAGCTCATTGCCCAGGG								
	8802	8810	8820	8830	8840	8850	8860	8870	8877
H77 (NC_004102)	AGGCAGGGCTGCCATATGTGGCAAGTACCTCTTCAACTGGGCAGTAAGAACAAAGCTCAAACCTCACTCCAATAGCG								
HCV1	AGGCAGGGCTGCCATATGTGGCAAGTACCTCTTCAACTGGGCAGTAAGGACAAAGCTCAAACCTCACTCCAATAGCG								
HCV2	-----								
HCV3	AGGGAAGGCCAAAATATGCGGCCTTTATCTCTTTAATTGGGCGGTACGCACCAAGACCAAACCTCACTCCATTGCCA								
HCV4	AGGGAGAGCCAGAATCTGTGGCATATACCTCTTAACTGGGCGGTAAAAACCAAACCTCAAACCTCACTCCATTGCC								
HCV5	AGGTAGGGCCGCCATCTGCGGCATCTATCTCTTCAACTGGGCGGTGAAGACAAAACGCAAACCTCACTCCATTAGCT								
HCV6	GGGAAAGCCGCTATATGCGGCAAGTACCTCTTCAACTGGGCGGTGAAGACCAAGCTCAAACCTCACTCCATTGCGC								
	8878	8890	8900	8910	8920	8930	8940	8953	
H77 (NC_004102)	GCCGCTGGCCGGCTGGACTTGTCCGGTTGGTTCACGGCTGGCTACAGCGGGGAGACATTTATCACAGCGTGTCTC								
HCV1	GCCGCTGGCCAGCTGGACTTGTCCGGCTGGTTCACGGCTGGCTACAGCGGGGAGACATTTATCACAGCGTGTCTC								
HCV2	-----								
HCV3	GCCGCTGGCCAGTTGGATTTATCCAGCTGGTTTACGGTTGGCGTGGCGGGAAACGACATTTATCACAGCGTGTCC								
HCV4	GCTGCTGCCAAACTCGACTTGTGAGTTGGTTTACGGTGGGCGCCGGCGGGGGGACATTTATCACAGCGTGTCCC								
HCV5	GACGCTGACCGGCTGGACTTGTCCAGCTGGTTCACCGTTGGCGTGGCGGGGGGACATTTATCACAGCATGTCCC								
HCV6	GCCGCGACCAACCTTGACTTGTGAGGCTGGTTCGTGGCAGGCTACAGCGGGGGGACATTTATCACAGCGTGTCCC								

Table S5. Cont.

	8954	8960	8970	8980	8990	9000
H77 (NC_004102)	ATGCCCGGCCCCGCTGGTTCTGGTTTTGCCTACTCCTGCTCGCTGCA					
HCV1	GTGCCCGGCCCCGCTGGTTCTGGTTTTGCCTACTCCTGCTTGCTGCA					
HCV2	-----					
HCV3	GTGCCCGAACCCGCCATTGCTGCTTTGCCTACTCCTACTAAC-GTA					
HCV4	GTGCCCGACCCCGCTATTACTCCTGTGCCTACTCCTACTTCCGTA					
HCV5	GTGCCCGACCCCGCTACTTACTCCTGTGCCTACTCCTACTTAGCGTA					
HCV6	GGGCTCGACCCCGCATATTACTCCTGTGCCTACTCCTACTCACCGTA					

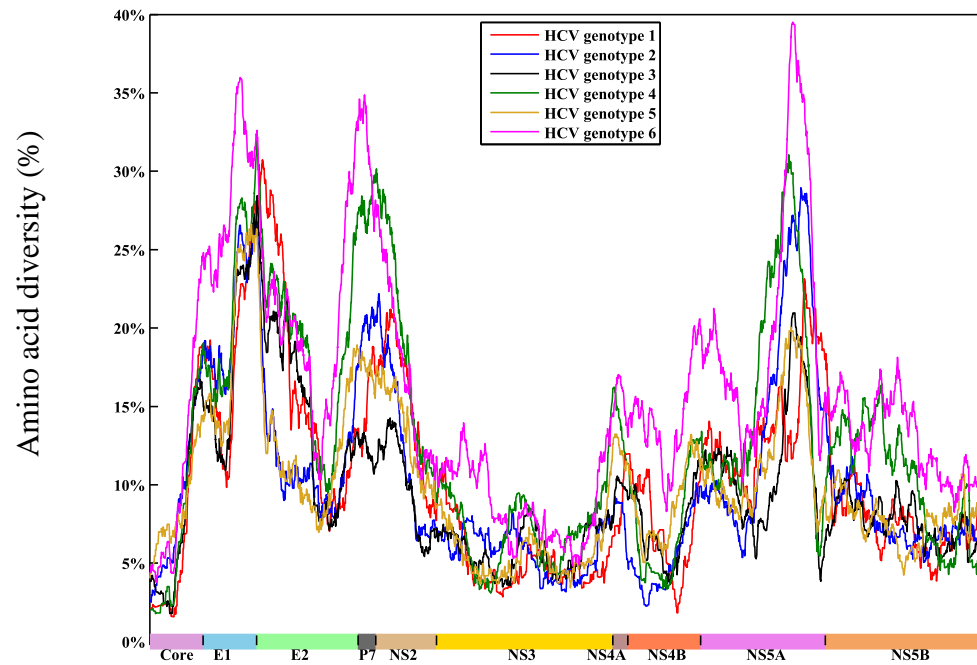


Figure S1. Full-genome sliding window plot for within-genotype amino acid diversity. A sliding window of 100 amino acid positions with a step size of one amino acid was used. The six genotypes were plotted separately in color-coded solid lines.

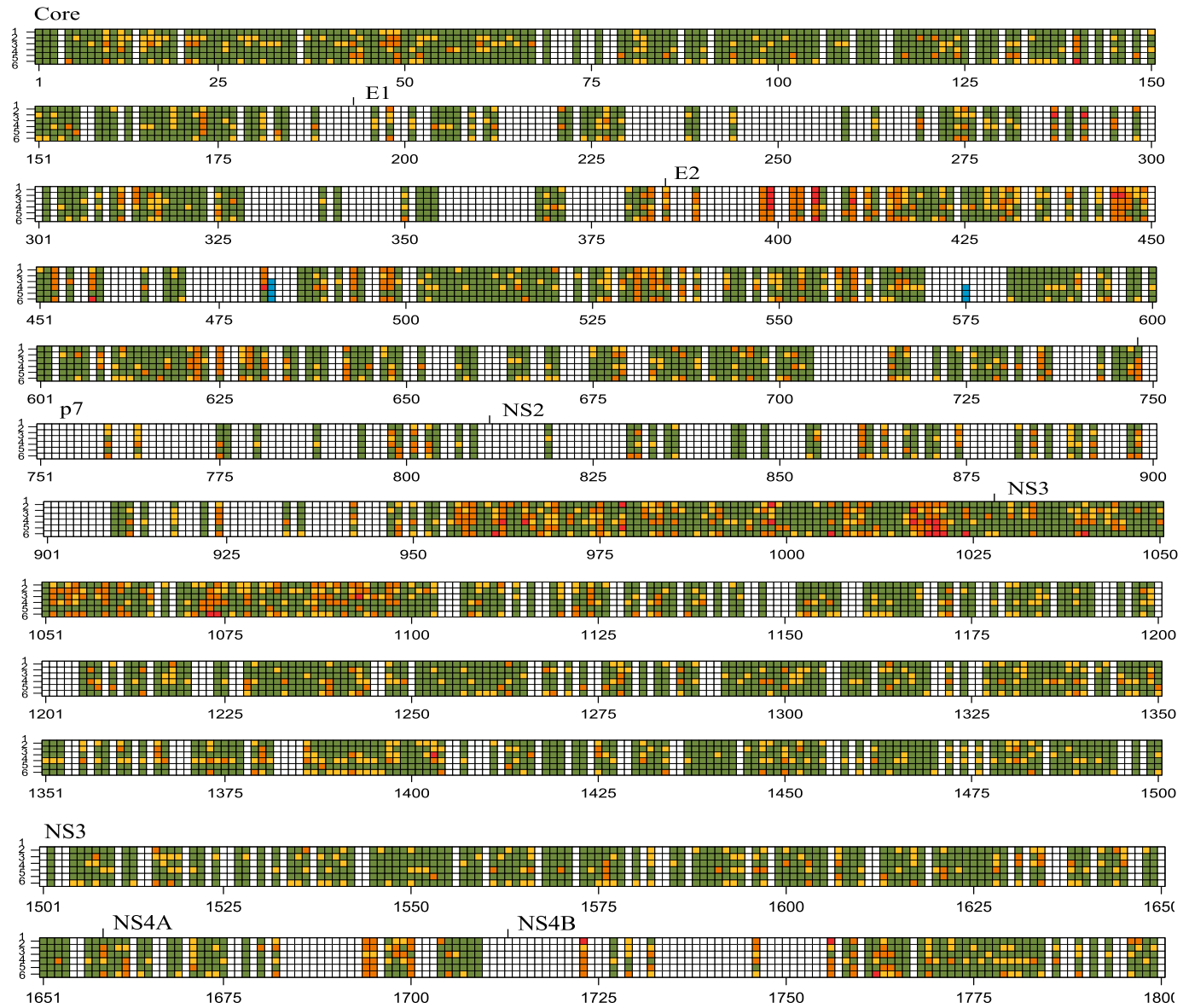
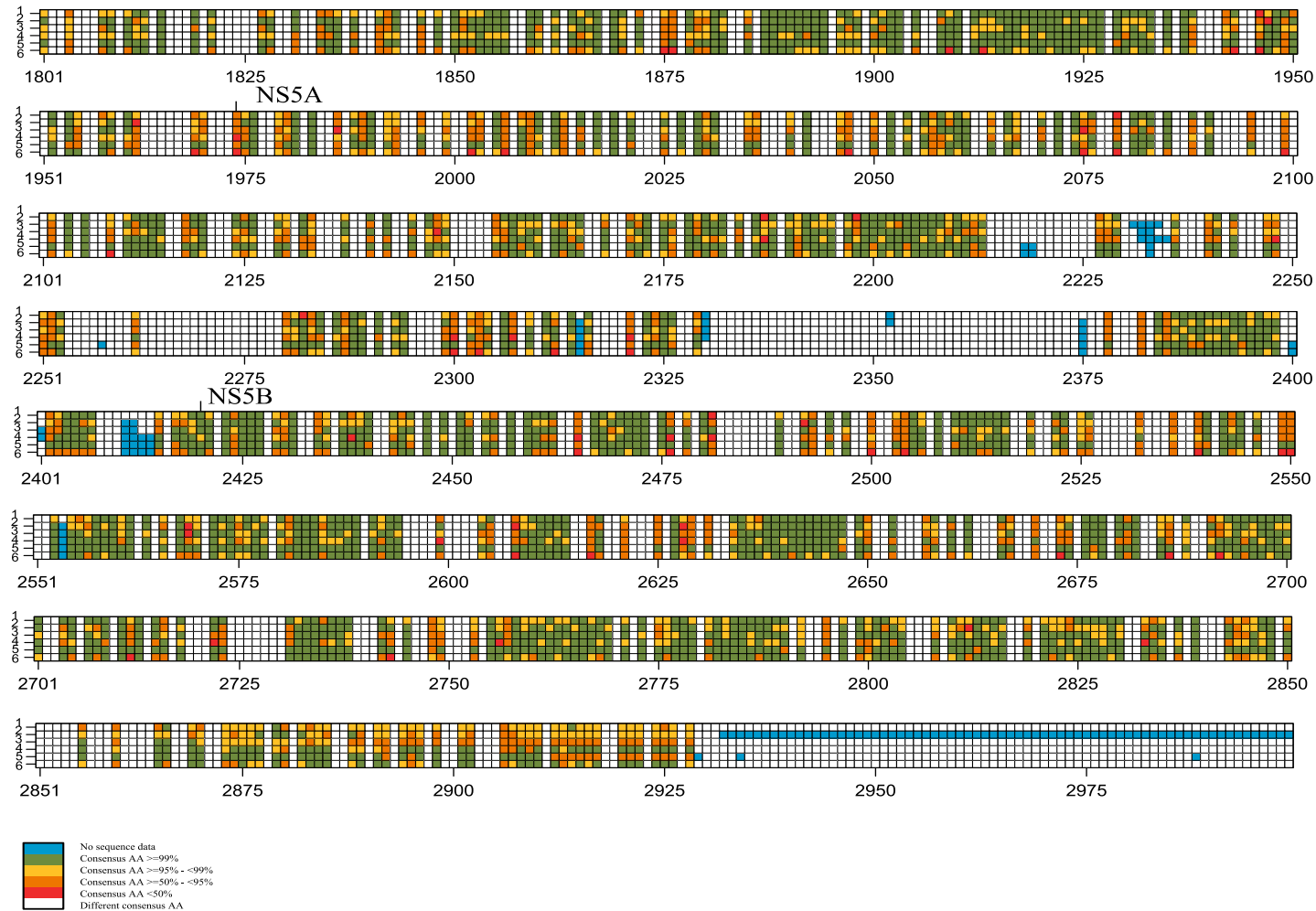


Figure S2. Cont.



**Figure S2.** Discretized frequencies of pan-genotypic consensus positions in the HCV full-genome, on amino acid level. The distribution of positions that shared a consensus amino acid across genotypes 1-6, aligned against the general reference sequence H77, is shown for the whole HCV genome. HCV genotype 1 is placed at the top and each square represents a single position. Positions that shared a consensus amino acid across all six genotypes were colored according to the frequency of the consensus amino acid in the respective genotype (for frequency  $x$ : category  $x < 50\%$  in red,  $50\% \leq x < 95\%$  in orange,  $95\% \leq x < 99\%$  in yellow and  $x \geq 99\%$  in green). Positions with different consensus amino acids were colored white and positions with no sequence data or a deletion were indicated in blue. It can be seen that HCV2 sequences of NS5B are shorter compared to other HCV genotypes.

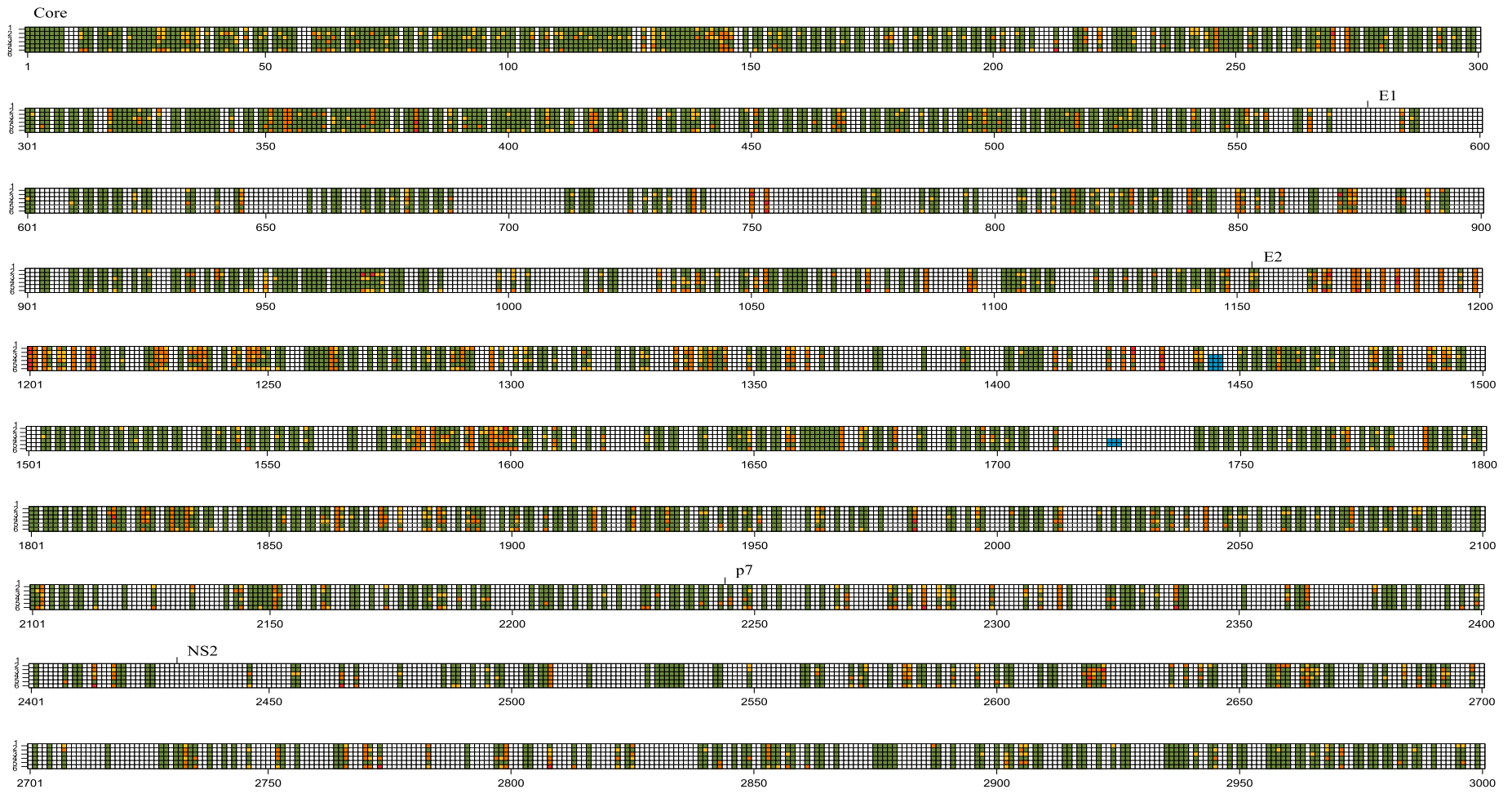


Figure S3. Cont.

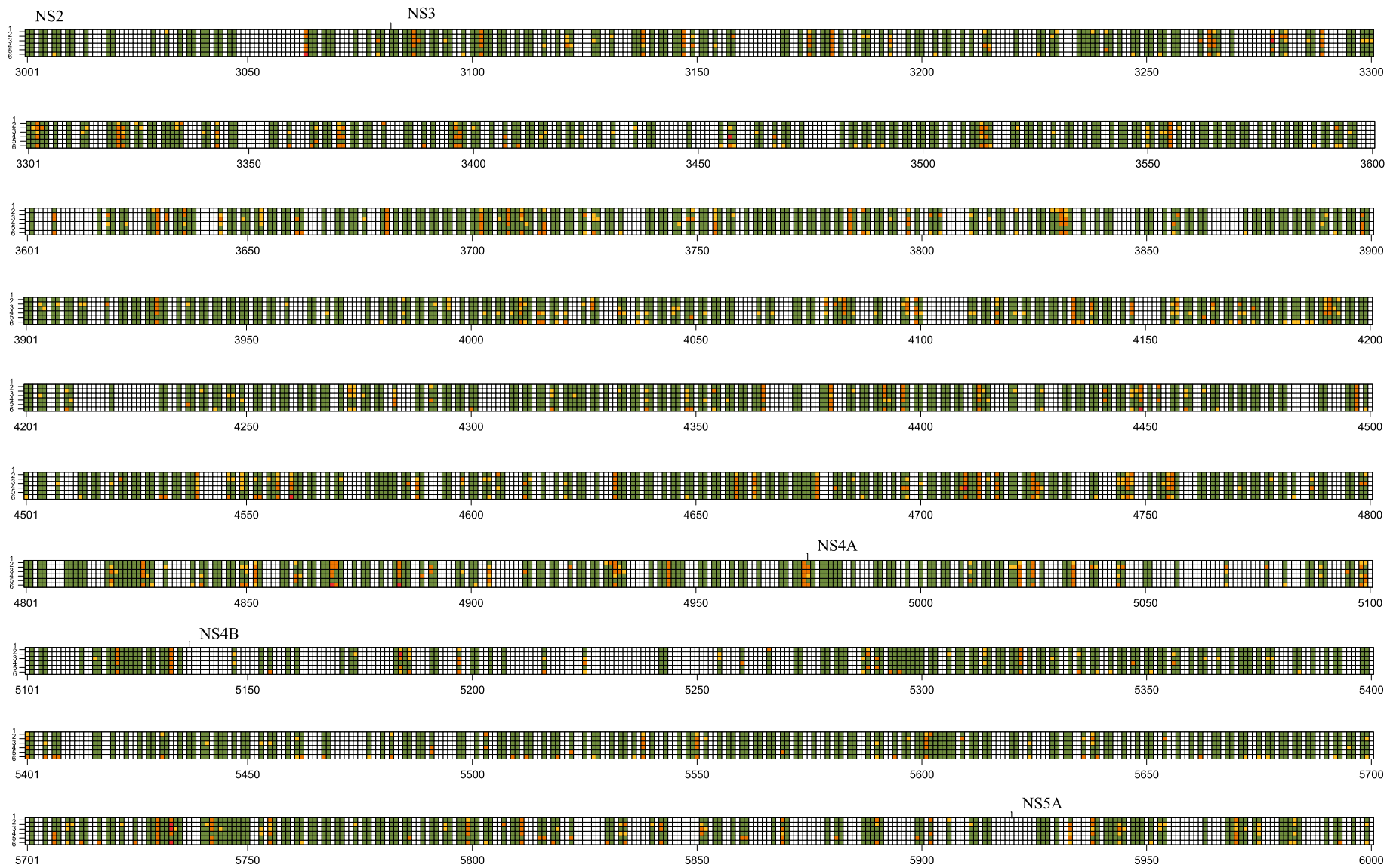
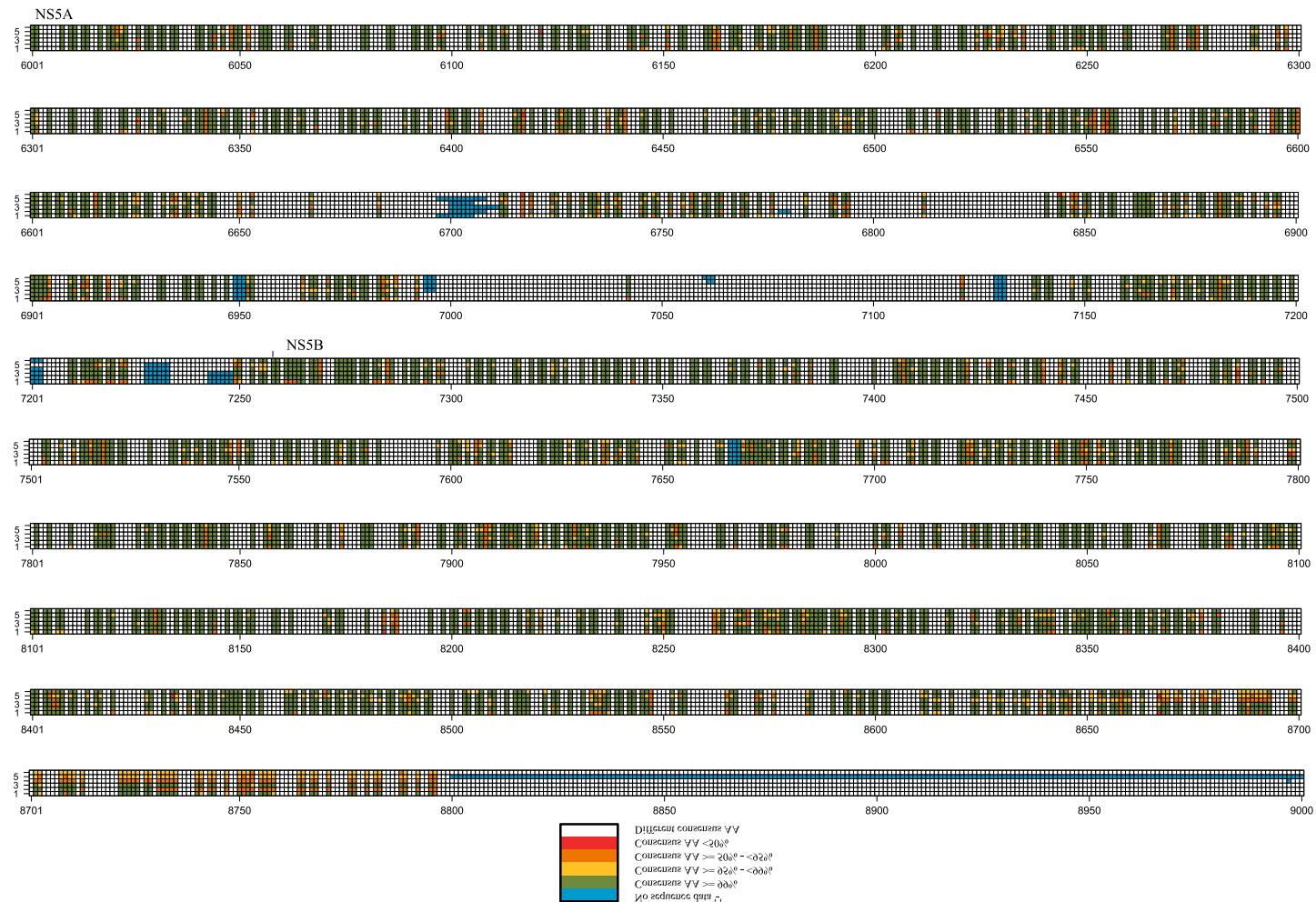


Figure S3. *Cont.*



**Figure S3.** Discretized frequencies of pan-genotypic consensus positions in the HCV full-genome, on nucleotide level. The distribution of positions that shared a consensus nucleotide across genotypes 1–6, aligned against the general reference sequence H77, is shown for the whole HCV genome. Genotype 1 is placed at the top and each square represents a single position. Positions that shared a consensus nucleotide in all six genotypes were colored according to the frequency of the consensus nucleotide in the respective genotype (for frequency  $x$ : category  $x < 50\%$  in red,  $50\% \leq x < 95\%$  in orange,  $95\% \leq x < 99\%$  in yellow and  $x \geq 99\%$  in green). Positions with different consensus nucleotides were colored white and positions with no sequence data or a deletion were indicated in blue. It can be seen that HCV2 sequences of NS5B are shorter compared to other genotypes.

**Table S6.** Amino acid alignment of the H77 (NC\_004102) reference sequence with the consensus of all six HCV genotypes. For each genotype, a consensus alignment was obtained, based on the most frequently occurring amino acids in the respective datasets. Consensus amino acids indicated in bold, highlight positions that display a different consensus amino acid compared to reference sequence H77.

	1	10	20	30	40	50	60	70	80																																																																							
H77 (NC_004102)	M	S	T	N	P	K	P	Q	R	K	T	K	R	N	T	N	R	R	P	Q	D	V	K	F	P	G	G	G	Q	I	V	G	G	V	Y	L	L	P	R	R	G	P	R	L	G	V	R	A	T	R	K	T	S	E	R	S	Q	P	R	G	R	R	Q	I	P	K	A	R	R	P	E	G	R	T	W	A	Q	P	G	
HCV1	M	S	T	N	P	K	P	Q	R	K	T	K	R	N	T	N	R	R	P	Q	D	V	K	F	P	G	G	G	Q	I	V	G	G	V	Y	L	L	P	R	R	G	P	R	L	G	V	R	A	T	R	K	T	S	E	R	S	Q	P	R	G	R	R	Q	I	P	K	A	R	R	P	E	G	R	T	W	A	Q	P	G	
HCV2	M	S	T	N	P	K	P	Q	R	K	T	K	R	N	T	N	R	R	P	Q	D	V	K	F	P	G	G	G	Q	I	V	G	G	V	Y	L	L	P	R	R	G	P	R	L	G	V	R	A	T	R	K	T	S	E	R	S	Q	P	R	G	R	R	Q	I	P	K	D	R	R	S	T	G	K	S	W	G	K	P	G	
HCV3	M	S	T	L	P	K	P	Q	R	K	T	K	R	I	T	N	R	R	P	Q	D	V	K	F	P	G	G	G	Q	I	V	G	G	V	Y	L	L	P	R	R	G	P	R	L	G	V	R	A	T	R	K	T	S	E	R	S	Q	P	R	G	R	R	Q	I	P	K	A	R	R	S	E	G	R	S	W	A	Q	P	G	
HCV4	M	S	T	N	P	K	P	Q	R	K	T	K	R	N	T	N	R	R	P	M	D	V	K	F	P	G	G	G	Q	I	V	G	G	V	Y	L	L	P	R	R	G	P	R	L	G	V	R	A	T	R	K	T	S	E	R	S	Q	P	R	G	R	R	Q	I	P	K	A	R	R	P	E	G	R	S	W	A	Q	P	G	
HCV5	M	S	T	N	P	K	P	Q	R	K	T	K	R	N	T	N	R	R	P	Q	D	V	K	F	P	G	G	G	Q	I	V	G	G	V	Y	L	L	P	R	R	G	P	R	L	G	V	R	A	T	R	K	T	S	E	R	S	Q	P	R	G	R	R	Q	I	P	K	A	R	Q	P	T	G	R	S	W	G	Q	P	G	
HCV6	M	S	T	L	P	K	P	Q	R	K	T	K	R	I	T	N	R	R	P	M	D	V	K	F	P	G	G	G	Q	I	V	G	G	V	Y	L	L	P	R	R	G	P	R	L	G	V	R	A	T	R	K	T	S	E	R	S	Q	P	R	G	R	R	Q	I	P	K	A	R	Q	P	T	G	R	H	W	A	Q	P	G	
Core																																																																																
	81	90	100	110	120	130	140	150	160																																																																							
H77 (NC_004102)	Y	P	W	P	L	Y	G	N	E	G	C	G	W	A	G	W	L	S	P	R	G	S	R	P	S	W	G	P	T	D	P	R	R	R	S	R	N	L	G	K	V	I	D	T	L	T	C	G	F	A	D	L	M	G	Y	I	P	L	V	G	A	P	L	G	G	A	A	R	A	L	A	H	G	V	R	V	L	E		
HCV1	Y	P	W	P	L	Y	G	N	E	G	C	G	W	A	G	W	L	S	P	R	G	S	R	P	S	W	G	P	T	D	P	R	R	R	S	R	N	L	G	K	V	I	D	T	L	T	C	G	F	A	D	L	M	G	Y	I	P	L	V	G	A	P	L	G	G	A	A	R	A	L	A	H	G	V	R	V	L	E		
HCV2	Y	P	W	P	L	Y	G	N	E	G	C	G	W	A	G	W	L	S	P	R	G	S	R	P	T	W	G	P	T	D	P	R	H	R	S	R	N	L	G	K	V	I	D	T	L	T	C	G	F	A	D	L	M	G	Y	I	P	L	V	G	A	P	V	G	G	V	A	R	A	L	A	H	G	V	R	V	L	E		
HCV3	Y	P	W	P	L	Y	G	N	E	G	C	G	W	A	G	W	L	S	P	R	G	S	R	P	S	W	G	P	N	D	P	R	R	R	S	R	N	L	G	K	V	I	D	T	L	T	C	G	F	A	D	L	M	G	Y	I	P	L	V	G	A	P	V	G	G	V	A	R	A	L	A	H	G	V	R	A	L	E		
HCV4	Y	P	W	P	L	Y	G	N	E	G	C	G	W	A	G	W	L	S	P	R	G	S	R	P	S	W	G	P	N	D	P	R	R	R	S	R	N	L	G	K	V	I	D	T	L	T	C	G	F	A	D	L	M	G	Y	I	P	L	V	G	A	P	V	G	G	V	A	R	A	L	A	H	G	V	R	A	L	E		
HCV5	Y	P	W	P	L	Y	A	N	E	G	L	G	W	A	G	W	L	S	P	R	G	S	R	P	N	W	G	P	N	D	P	R	R	K	S	R	N	L	G	K	V	I	D	T	L	T	C	G	F	A	D	L	M	G	Y	I	P	L	V	G	G	P	V	G	G	V	A	R	A	L	A	H	G	V	R	V	L	E		
HCV6	Y	P	W	P	L	Y	G	N	E	G	C	G	W	A	G	W	L	S	P	R	G	S	R	P	H	W	G	P	N	D	P	R	R	R	S	R	N	L	G	K	V	I	D	T	L	T	C	G	L	A	D	L	M	G	Y	I	P	L	V	G	A	P	L	G	G	V	A	A	A	L	A	H	G	V	R	A	L	E		
	16	170	180	190	200	210	220	230	240																																																																							
H77 (NC_004102)	G	V	N	Y	A	T	G	N	L	P	G	C	S	F	S	I	F	L	L	A	L	S	C	L	T	V	P	A	S	A	Y	Q	V	R	N	S	S	G	L	Y	H	V	T	N	D	C	P	N	S	S	I	V	E	A	A	D	A	I	L	H	T	P	G	C	V	P	C	V	R	E	G	N	A	S	R	C	W	V		
HCV1	G	V	N	Y	A	T	G	N	L	P	G	C	S	F	S	I	F	L	L	A	L	S	C	L	T	V	P	A	S	A	Y	Q	V	R	N	S	S	G	L	Y	H	V	T	N	D	C	P	N	S	S	I	V	E	A	A	D	A	I	L	H	T	P	G	C	V	P	C	V	R	E	G	N	S	S	R	C	W	V		
HCV2	G	I	N	Y	A	T	G	N	L	P	G	C	S	F	S	I	F	L	L	A	L	S	C	I	T	V	P	V	S	A	V	E	V	R	N	I	S	S	Y	A	T	N	D	C	S	N	S	I	T	W	Q	L	T	N	A	V	L	H	L	P	G	C	V	P	C	E	N	D	N	G	T	L	R	C	W	I				
HCV3	G	I	N	F	A	T	G	N	L	P	G	C	S	F	S	I	F	L	A	L	F	S	C	L	I	H	P	A	A	S	L	E	W	R	N	T	S	G	L	Y	V	L	T	N	D	C	S	N	S	I	V	E	A	D	D	V	I	L	H	T	P	G	C	V	P	C	V	Q	D	G	N	T	S	T	C	W	T			
HCV4	G	I	N	Y	A	T	G	N	L	P	G	C	S	F	S	I	F	L	L	A	L	S	C	L	T	V	P	A	V	H	Y	R	N	A	S	G	I	Y	H	I	T	N	D	C	P	N	S	S	I	V	E	A	D	H	H	I	L	H	L	P	G	C	V	P	C	V	R	T	G	N	Q	S	R	C	W	V				
HCV5	G	V	N	Y	A	T	G	N	L	P	G	C	S	F	S	I	F	L	L	A	L	S	C	L	T	V	P	A	S	A	V	P	Y	R	N	A	S	G	Y	H	V	T	N	D	C	P	N	S	S	I	V	E	A	D	N	L	I	L	H	A	P	G	C	V	P	C	V	R	E	G	N	V	S	R	C	W	V			
HCV6	G	I	N	Y	A	T	G	N	L	P	G	C	S	F	S	I	F	L	L	A	L	S	C	L	T	V	P	A	S	A	V	H	Y	G	N	S	S	G	Y	H	L	T	N	D	C	P	N	S	S	I	V	E	A	D	A	M	I	L	H	L	P	G	C	V	P	C	V	R	V	G	N	Q	S	R	C	W	H			
Core E1																																																																																
	241	250	260	270	280	290	300	310	320																																																																							
H77 (NC_004102)	A	V	T	P	T	V	A	T	R	D	G	K	L	P	T	Q	L	R	R	H	I	D	L	L	V	G	S	A	T	L	C	S	A	L	Y	V	G	D	L	C	G	S	V	F	L	V	G	Q	L	F	T	F	S	P	R	R	H	W	T	Q	D	C	N	C	S	I	Y	P	G	H	I	T	G	H	R	M	A	W		
HCV1	A	L	T	P	T	V	A	T	R	D	G	K	L	P	T	Q	L	R	R	H	I	D	L	L	V	G	S	A	T	L	C	S	A	L	Y	V	G	D	L	C	G	S	V	F	L	V	G	Q	L	F	T	F	S	P	R	R	H	W	T	Q	D	C	N	C	S	I	Y	P	G	H	I	T	G	H	R	M	A	W		
HCV2	Q	V	T	P	N	V	A	V	K	H	R	G	A	L	T	H	N	L	R	T	H	V	D	M	I	V	M	A	A	T	V	C	S	A	L	Y	V	G	D	V	C	G	A	V	M	I	V	S	Q	A	F	I	V	S	P	Q	R	H	N	F	T	Q	E	C	N	C	S	I	Y	Q	G	H	I	T	G	H	R	M	A	W
HCV3	P	V	T	P	T	V	A	V	R	Y	V	G	A	T	T	A	S	I	R	S	H	V	D	L	L	V	G	A	A	T	M	C	S	A	L	Y	V	G	D	M	C	G	A	V	F	L	V	G	A	F	T	F	R	P	R	R	H	Q	T	V	Q	T	C	N	C	S	L	Y	P	G	H	L	T	G	H	R	M	A	W	
HCV4	A	L	T	P	T	V	A	A	P	Y	L	G	A	P	L	E	S	R	R	H	V	D	L	M	V	G	A	A	T	L	C	S	A	L	Y	V	G	D	L	C	G	A	F	L	V	G	M	F	T	Q	P	R	R	H	W	T	Q	D	C	N	C	S	I	T	G	H	I	T	G	H	R	M	A	W						
HCV5	Q	I	T	P	T	V	S	A	P	S	F	G	A	V	T	A	P	L	R	R	A	V	D	Y	L	A	G	G	A	A	L	C	S	A	L	Y	V	G	D	A	C	G	A	V	F	L	V	G	M	F	T	Y	R	P	R	Q	H	T	T	V	Q	D	C	N	C	S	I	Y	S	G	H	I	T	G	H	R	M	A	W	
HCV6	P	V	S	P	T	L	A	V	P	N	A	S	T	P	A	T	G	F	R	R	H	V	D	L	L	V	G	A	A	V	C	S	A	L	Y	I	G	D	L	C	G	G	V	F	L	V	G	Q	L	F	T	F	R	P	R	R	H	W	T	V	Q	D	C	N	C	S	I	Y	T	G	H	V	T	G	H	R	M	A	W	



Table S6. Cont.

		Core E1								
		321	330	340	350	360	370	380	390	400
H77 (NC_004102)	D	M	M	M	N	W	S	P	T	A
HCV1	D	M	M	M	N	W	S	P	T	A
HCV2	D	M	M	L	N	W	S	P	T	L
HCV3	D	M	M	M	N	W	S	P	A	V
HCV4	D	M	M	M	N	W	S	P	T	T
HCV5	D	M	M	M	N	W	S	P	T	A
HCV6	D	M	M	M	N	W	S	P	T	T
		E1 E2								
		401	410	420	430	440	450	460	470	480
H77 (NC_004102)	G	L	L	T	P	G	A	K	Q	N
HCV1	S	L	F	S	P	G	A	K	Q	N
HCV2	G	L	F	S	P	G	P	Q	N	I
HCV3	S	L	F	S	P	G	A	Q	Q	N
HCV4	S	L	F	T	P	G	S	R	Q	N
HCV5	S	L	F	T	P	G	P	Q	N	L
HCV6	G	L	F	S	P	G	A	K	Q	N
		481	490	500	510	520	530	540	550	560
H77 (NC_004102)	D	E	R	P	Y	C	W	H	Y	P
HCV1	D	Q	R	P	Y	C	W	H	Y	P
HCV2	D	E	D	M	R	C	W	H	Y	P
HCV3	D	R	P	Y	C	W	H	Y	A	P
HCV4	D	R	P	Y	C	W	H	Y	A	P
HCV5	D	K	P	Y	C	W	H	Y	P	R
HCV6	D	R	P	Y	C	W	H	Y	A	P
		561	570	580	590	600	610	620	630	640
H77 (NC_004102)	T	K	V	C	G	A	P	P	C	V
HCV1	T	K	V	C	G	A	P	P	C	V
HCV2	T	K	T	C	G	A	P	P	C	R
HCV3	V	K	T	C	G	A	P	P	C	N
HCV4	T	K	T	C	G	A	P	P	C	S
HCV5	V	K	T	C	G	A	P	P	C	N
HCV6	V	K	T	C	G	A	P	P	C	Q

Table S6. Cont.

		E1 E2									
		641	650	660	670	680	690	700	710	720	
H77 (NC_004102)		EAACNWTRGERCDLEDRDRSELSPLLLSTTQWQVLP	CSFTTLPALSTGLIHLHQ	NIVDVQYLYGVGSSIASWA	IKWEYVV						
HCV1		EAACNWTRGERCDLEDRDRSELSPLLLSTTQWQVLP	CSFTTLPALSTGLIHLHQ	NIVDVQYLYGVGSSIVSWA	IKWEYVV						
HCV2		SAACNFRGDRCRLEDRDRGQQSPLLHSTTEWAVL	PCSFSDLPALSTGLLHLHQ	NIVDVQYLYGLSPA	ITRYIVKWEWVV						
HCV3		TAACNWTRGERCDIEDRDRSEQHPLLHSTTELA	ILPCSFPTMPALSTGLIHLHQ	NIVDVQYLYGVGSGMV	GWALKWEFVI						
HCV4		EAACNWTRGEPGLEHRDRTELSPLLLSTTQWQVLP	CSFTTLPALSTGLIHLHQ	NIVDVQYLYGVGS	AVVSWALKWEYVV						
HCV5		EAACNWTRGERCDLEDRDRAELSPLLHTTTQW	AILPCSFPTPALSTGLIHLHQ	NIVDTQYLYGLSSSIVSWA	VKWEYIV						
HCV6		DAACNWTRGERCELDDRRIEMSPLLFSTTQL	AILPCSFPTMPALSTGLIHLHQ	NIVDVQYLYGVSSSVVSWA	VKWEYVV						
		721	730	740	750	760	770	780	790	800	
H77 (NC_004102)		LLFLLADARVCSCWMLLISQAEAALENLVILNA	ASLAGTHGLVSFLVFFC	FAWYLKGRWVPGAVYAFYGMW	PLLLLL						
HCV1		LLFLLADARVCSCWMLLISQAEAALENLVV	LNASLAGTHGLVSFLVFFC	FAWYLKGRWVPGAAYALYGMW	PLLLLL						
HCV2		LLFLLADARVCACLWMLIILGQAEAALEKLI	LHSASAASANGPLWFFIFIAAWY	LKGRVPLATYSVLGLWS	FLLLV						
HCV3		LVFLLADARVCVALWMLMISQAEAALENLV	TLNAVAAAGTHGIGWYLVAFCA	AHVRGKLVPLVTYSLTGLWS	LALLV						
HCV4		LAFLLADARVCACLWMLLVSQVEAALANLIT	NAASAGTHGFWYAILFICVAWY	VKGRLPAAATYAACGMW	PLLLLL						
HCV5		LAFLLADARICTLWIMLLVCQAEAALENV	VVLNAAAAGTHGFFWGLLVIC	FAWHFKGRLVPGATYLC	LGIWPLLLLL						
HCV6		LAFLVLADARICACWMLLVGQAEAALENL	VLNAAAAGTHGFFWGLLVIC	FAWHFKGRLVPGATYLC	LGIWPLLLLL						
		E2 p7									
		801	810	820	830	840	850	860	870	880	
H77 (NC_004102)		LALPQRAYALDTEVAASCGGVVLVGLMAL	TLSPYKRYISWCMWWLQYFL	TRVEAQLHVWVPP	LNVRGGRDAVILL	MCCV					
HCV1		LALPQRAYALDTEVAASCGGVVLVGLMAL	TLSPYKRYISWCLWWLQYFL	TRAEAQLHVWVPP	LNVRGGRDAVILL	MCCV					
HCV2		LALPQQAYALDAAEQGELGLVLLVIISIF	TLTPAYKILLSRSVWWLSYMLV	LAEAIQQQWVPP	LEARGGRDGII	WAAVIL					
HCV3		LLLQRAYAWSGEDSATLGAGVLALFGFF	TLSPWYKHWIGRLMWWNQYTIC	RCEAALQVWVPP	LAVRGSRDG	VILLTSL					
HCV4		LALPERAYAFDREVAGSLGGGVVLLTIL	TLSPHYKRWLARGIWWLQYFI	ARAEALLHVYVPS	LEVGRPRDS	VIIITALF					
HCV5		LLLPHRALALDSSDGSVGLVLIILTI	FTLTPGYKMMVVLVWVWLQYFI	ARVEAAIHVWVPP	LQVRGGRDAI	IIIMLTCLF					
HCV6		LALPRRAYAMDNEQAASLGALVLLIIT	IFTLSPAYKLLTSFIWVWVQYFI	ARAEAMLHVWVPS	LRVGRGRDA	VILLTCLL					
		p7 NS2									
		881	890	900	910	920	930	940	950	960	
H77 (NC_004102)		HPTLVFDITKLLLAIFGPLWILQASLLK	VPYFVRVQGLLRICALARKI	AGGHYVQMAIIKLGALT	GTYYNHLT	PLRDWA					
HCV1		HPTLVFDITKLLLAIFGPLWILQASLLK	VPYFVRVQGLLRICALARKM	AGGHYVQMAIIKLGALT	GTYYNHLT	PLRDWA					
HCV2		HPRLVFEITKLLAILGPAYLLKASLLR	VPYFVRAHALLRVCTLRVH	LAGARYIQMLLITLGR	WTGTYYIDHLS	PLRDWA					
HCV3		YPSLIFDITKLLIAVLGPLYLIQA	AITTPYFVRAHVLRCLM	LRSVMGGKYFQMIIS	IGRWENTYLYDHL	APLRDWA					
HCV4		HPHLAFDITKYLLAILGPLYLQASLLR	VPYFVRAHALIKICSLVR	GVYQYKQMAL	LKLGALTGTYYIDHL	APLRDWA					
HCV5		HPALGFEITKILLGILGPLYLLQHSL	TCLPYFIRARALLRCLLAK	HLVYQYKVAALLHL	GRLTGTYYIDHL	APLRDWA					
HCV6		HPQLGFEVTKILLALLGPLYLLQYSL	LKVPYFVRAHILLRACML	VRRLAGGKYVQAC	LLRLGAWTGTYYIDHL	APLRDWA					

Table S6. Cont.

	p7 NS2								
	961	970	980	990	1000	1010	1020	1030	1040
H77 (NC_004102)	HNGLRDLAVAVEPVVFSRMETKLITWGADTAACGDIINGLPVSARRGQEILLGPADGMVSKGWRLAPITAYAQQTRGLL								
HCV1	HNGLRDLAVAVEPVVFSRMETKLITWGADTAACGDIINGLPVSARRGQEILLGPADGMVSKGWRLAPITAYAQQTRGLL								
HCV2	HNGLRDLAVAVEPVVFSRMETKLITWGADTAACGDIINGLPVSARRGQEILLGPADGMVSKGWRLAPITAYAQQTRGLL								
HCV3	HNGLRDLAVAVEPVVFSRMETKLITWGADTAACGDIINGLPVSARRGQEILLGPADGMVSKGWRLAPITAYAQQTRGLL								
HCV4	HNGLRDLAVAVEPVVFSRMETKLITWGADTAACGDIINGLPVSARRGQEILLGPADGMVSKGWRLAPITAYAQQTRGLL								
HCV5	HNGLRDLAVAVEPVVFSRMETKLITWGADTAACGDIINGLPVSARRGQEILLGPADGMVSKGWRLAPITAYAQQTRGLL								
HCV6	HNGLRDLAVAVEPVVFSRMETKLITWGADTAACGDIINGLPVSARRGQEILLGPADGMVSKGWRLAPITAYAQQTRGLL								
	NS2 NS3								
	1041	1050	1060	1070	1080	1090	1100	1110	1120
H77 (NC_004102)	GCIITSLTGRDKNQVEGEVQIVSTATQTFLATCINGVCWTVYHGAGTRTIASPKGPVIQMYTNVDQDLVGWPA PQGSRSL								
HCV1	GCIITSLTGRDKNQVEGEVQIVSTAAQTFLATCINGVCWTVYHGAGTRTIASPKGPVIQMYTNVDQDLVGWPA PQGARSL								
HCV2	GCIITSLTGRDKNQVEGEVQIVSTATQSFATCINGVCWTVYHGAGTRTIASPKGPVIQMYTNAEGDLVGWPSPPGTKSL								
HCV3	GCIITSLTGRDKNQVEGEVQIVSTATQTFLATCINGVCWTVYHGAGTRTIASPKGPVIQMYTNVDQDLVGWPA PPGAKSL								
HCV4	GCIITSLTGRDKNQVEGEVQIVSTATQSFLATCINGVCWTVYHGAGTRTIASPKGPVIQMYTNVDQDLVGWPA PPGVKSL								
HCV5	GCIITSLTGRDKNQVEGEVQIVSTATQTFLATCINGVCWTVYHGAGTRTIASPKGPVIQMYTNVDKDLVGWPSPPGTRSL								
HCV6	GCIITSLTGRDKNQVEGEVQIVSTATQSFLATCINGVCWTVYHGAGTRTIASPKGPVIQMYTNVDQDLVGWPA PPGARSL								
	1121	1130	1140	1150	1160	1170	1180	1190	1200
H77 (NC_004102)	TPCTCGSSDLYLVTRHADVIPVRRRGDSRGSLLSPRPISYLKSSGGP LCPAGHAVGLFRAAVCTRGVAKAVDFIPVEN								
HCV1	TPCTCGSSDLYLVTRHADVIPVRRRGDSRGSLLSPRPISYLKSSGGP LCPAGHAVGIFRAAVCTRGVAKAVDFIPVES								
HCV2	DPCTCGAVDLYLVTRNADVIPVRRRKDDRRGALLSPRPLSTLKGSSGGP V LCPRGHAVGLFRAAVCSRGVAKSIDFIPVES								
HCV3	EPCTCGASDLYLVTRDADVIPARRRGDSTASLLSPRPLACLKSSGGP VMCP SGHVAGIFRAAVCTRGVAKALQFIPVET								
HCV4	APCTCGASDLYLVTRHADVVPVRRRGDTRGALLSPRPISYLKSSGGP LCP LGHAVGIFRAAVCTRGVAKAVDFVPVES								
HCV5	TPCTCGASDLYLVTRHADVIPARRRGDTRASLLSPRPISYLKSSGGP VMCP SGHVGVFRAAVCTRGVAKALEFIPVEN								
HCV6	TPCTCGSSDLYLVTRNADVIPARRRGDNRAALLSPRPISYLKSSGGP I LCP SGHVGLFRAAVCTRGVAKSLDFVPVEN								
	1201	1210	1220	1230	1240	1250	1260	1270	1280
H77 (NC_004102)	LETTMRSPVFTDNSSPPAVPQSFQVAHLHAPTGS GKSTKVPAAAYAAQGYKVLV LNPSVAATLGF GAYMSKAHGVDPNIRT								
HCV1	LETTMRSPVFTDNSSPPAVPQSFQVAHLHAPTGS GKSTKVPAAAYAAQGYKVLV LNPSVAATLGF GAYMSKAHGVDPNIRT								
HCV2	LDIATRSPSFS DNSTPPAVPQTYQVGYLHAPTGS GKSTKVPAAAYASQGYKVLV LNPSVAATLGF GAYMSKAHG INPNIRT								
HCV3	LSTQARSFSFS DNSTPPAVPQSYQVGYLHAPTGS GKSTKVPAAAYVAQGYNVLV LNPSVAATLGF GSFMSRAYGIDPNIRT								
HCV4	LETTMRSPVFTDNSTPPAVPQTYQVAHLHAPTGS GKSTKVPAAAYAAQGYKVLV LNPSVAATLGF GAYMSKAHGIDPNIRS								
HCV5	LETTMRSPVFTDNSTPPAVPHEFQVGH LHAPTGS GKSTKVPAAAYAAQGYKVLV LNPSVAATLGF GAYMSRAYGVDPNIRT								
HCV6	METTMRSPSFTDNSTPPAVPQTYQVGYLHAPTGS GKSTKVPAAAYASQGYKVLV LNPSVAATLGF GSYMSQAHGIDPNIRT								

Table S6. Cont.

	NS2 NS3													
	1281	1290	1300	1310	1320	1330	1340	1350	1360					
H77 (NC_004102)	GVRTIT	TGSPIT	YSTY	GKFLAD	GGCSGG	AYDIIIC	DECHSD	ATSILG	IGTVLD	QAETAG	ARLVVL	ATATPP	GSVTV	SHP
HCV1	GVRTIT	TGSPIT	YSTY	GKFLAD	GGCSGG	AYDIIIC	DECHSD	ATSILG	IGTVLD	QAETAG	ARLVVL	ATATPP	GSVTV	PHP
HCV2	GVRTV	TTGDP	ITYSTY	GKFLAD	GGCSAG	AYDIIIC	DECHSD	ATILG	IGTVLD	QAETAG	VRLVVL	ATATPP	GTVTT	PHS
HCV3	GNRTV	TTGAK	LTYSTY	GKFLAD	GGCSGG	AYDVII	CDECHA	QDATS	SILGIG	TVLDQA	ETAGV	RVLTVL	ATATPP	GSITV
HCV4	GVRTIT	TGAPIT	YSTY	GKFLAD	GGCGGG	AYDIIIC	DECHSD	STTIL	GIGTVL	DAETAG	ARLVVL	ATATPP	GSVTT	PHA
HCV5	GVRTV	TGAAIT	YSTY	GKFLAD	GGCSGG	AYDVII	CDECHS	QDATT	ILGIGT	VLDQA	ETAGAR	LVVLAT	ATATPP	GSVTT
HCV6	GVRTIT	TGGAIT	YSTY	GKFLAD	GGCSGG	AYDIIIC	DECHSD	PTTVL	GIGTVL	DAETAG	VRLTVL	ATATPP	GSVTV	PHP
	1361	1370	1380	1390	1400	1410	1420	1430	1440					
H77 (NC_004102)	NIEEVAL	STTGEI	PFYGKA	IPLEVI	KGGRHL	FCHSKK	KCDELA	AKLVAL	GINAVAY	YRGLDV	SVIPTS	GDVVV	VSTDAL	
HCV1	NIEEVAL	STTGEI	PFYGKA	IPLEVI	KGGRHL	FCHSKK	KCDELA	AKLVAL	GINAVAY	YRGLDV	SVIPTS	GDVVV	VATDAL	
HCV2	NIEEVAL	GHEGEI	PFYGKA	IPLA	YIKGGR	HLIFCH	SKKKCD	EALALR	GMGNVA	VAYRGL	DVSVIPT	QGDVVV	VATDAL	
HCV3	NIEEVAL	GSEGEI	PFYGKA	IPAL	LKGGRH	LIFCHS	KKKCD	EALAKL	RMGLNA	VAYRGL	DVSVIPT	TGDVVV	CATDAL	
HCV4	NIEEVAL	PTTGEI	PFYGRA	IPLAL	IKGGRH	LIFCHS	KKKCD	EALAKL	SSLGLN	VAYRGL	DVSVIPT	SGDVVV	CATDAL	
HCV5	NIEEVAL	PSEGEI	PFYGRA	IPLAL	IKGGRH	LIFCHS	KKKCD	EALAKL	TSQGVN	VAYRGL	DVAVIP	ATGDVV	VVCS	
HCV6	NITETA	LPTTGEI	PFYGKA	IPLEYI	KGGRHL	FCHSKK	KCDELA	AKLTS	LGLNAV	AFYRGV	DVSVIPT	SGDVVV	CATDAL	
	1441	1450	1460	1470	1480	1490	1500	1510	1520					
H77 (NC_004102)	MTGFTG	DFDSVI	DCNCT	CVTQ	TVDFSL	DPTFTI	ETTTLP	QDAVSR	TQRRGR	TGRGK	PGIYRF	VAPGER	PSGMF	DSSVLC
HCV1	MTGFTG	DFDSVI	DCNCT	CVTQ	TVDFSL	DPTFTI	ETTTLP	QDAVSR	TQRRGR	TGRGK	PGIYRF	VAPGER	PSGMF	DSSVLC
HCV2	MTGYT	GDFDS	VIDCN	VAVT	QIVDF	SLDPT	FTITTT	QVQDA	VSR	SQRRGR	TGRGR	LGIYR	VSSGER	PSGMF
HCV3	MTGFTG	DFDSVI	DCNVA	VEQY	VDFSL	DPTFSI	ETRTAP	QDAVSR	SQRRGR	TGRGR	LGIYR	VTPGER	PSGMF	DSSVLC
HCV4	MTGFTG	DFDSVI	DCN	SVIQ	TVDFSL	DPTFSI	ETTTVP	QDAVSR	SQRRGR	TGRGR	LGIYR	VTPGER	PSGMF	DTSVLC
HCV5	MTGFTG	DFDSVI	DCN	SAVT	QTVDF	SLDPT	FTIETT	VPQDA	VSR	SQRRGR	TGRGR	HHGIYR	VSSGER	PSGIF
HCV6	MTGFTG	DFDSVI	DCN	VAVT	QVDF	SLDPT	FSIETT	VPQDA	VSR	SQRRGR	TGRGK	PVYRY	VSSGER	PSGMF
	1521	1530	1540	1550	1560	1570	1580	1590	1600					
H77 (NC_004102)	YDAGCA	WYELTP	AETT	VRLRAY	MNTPGL	PVCQD	HLEF	WEGV	FTGLTH	IDA	HFLS	QTKQ	SGEN	FPYL
HCV1	YDAGCA	WYELTP	AETT	VRLRAY	MNTPGL	PVCQD	HLEF	WEGV	FTGLTH	IDA	HFLS	QTKQ	SGEN	FPYL
HCV2	YDAGA	AWYEL	TPAETT	VRLRAY	FNTPL	PVCQD	HLEF	WEAV	FTGLTH	IDA	HFLS	QTKQ	GGEN	FAYL
HCV3	YDAGC	SWYDL	QPAETT	VRLRAY	LSTPL	PVCQD	HLD	FWES	VFTGLTH	IDA	HFLS	QTKQ	QGLN	FSYL
HCV4	YDAGCA	WYELTP	AETT	TRLRAY	FNTPL	PVCQD	HLEF	WESV	FTGLTH	IDA	HFLS	QTKQ	AGDN	YPYL
HCV5	YDAGCA	WYDL	TPAETT	VRLRAY	LNTPL	PVCQD	HLEF	WEGV	FTGLT	IDA	HMLS	QTKQ	GGEN	FPYL
HCV6	YDTGCA	WYELTP	SETT	VRLRAY	LNTPL	PVCQD	HLEF	WEGV	FTGLTH	IDA	HFLS	QTKQ	AGEN	FAYL



Table S6. Cont.

		NS4A NS4B								
		1921	1930	1940	1950	1960	1970	1980	1990	2000
H77 (NC_004102)		ASRGNHVSPTHYVPESDAAARVTAILSSLTVTQLLRRRLHQWISSECTTPCSGSLRDIWDWICEVLSDFKTWLKAKLMPQ								
HCV1		ASRGNHVSPTHYVPESDAAARVTAILSSLTVTQLLRRRLHQWISSECTTPCSGSLRDIWDWICEVLSDFKTWLKAKLMPQ								
HCV2		ASRGNHVAPTHYVAESDASQRVTQLLSSLTITSLRRRLHAWITEDCPVPCSGSLRDIWDWVCSILTDFKNWLSKLLPK								
HCV3		ASRGNHVSPTHYVPESDAAARVTAALLSSLTVTSLRRRLHQWINE <del>D</del> YPSPCSGDWLRTIWDWVCTVLSDFKTWLSAKIMPA								
HCV4		ASRGNHVSPTHYVPESDAAARVTAILSSLTVTSLRRRLHKWINE <del>D</del> CSTPCDSSWLRWEWDWVCTVLSDFKTWLKAKLLPR								
HCV5		ASRGNHVSPTHYVPETDASAKVTQLLSSLTVTSLKRLHTWIGEDYSTPCDGTWLRAIWDWVCTALTDKAWLQAKLLPQ								
HCV6		ASRGNHVSPTHYVPETDASRNV <del>T</del> QILSSLTITSLRKLHQWINE <del>D</del> WSTPCSTSWLRDIWDWVCTVLSDFKTWLKAKLVPS								
		NS4B NS5A								
		2001	2010	2020	2030	2040	2050	2060	2070	2080
H77 (NC_004102)		LPGIPFVSCQRGYRGVWRGDGIMHTRCHCGAEITGHVKNGTMRIVGPRTRCNMWSGTFPINAYTTGPCTPLPAPNYKFAL								
HCV1		LPGIPFVSCQRGYRGVWRGDGIMHTRCHCGAEITGHVKNGTMRIVGPKTCRNMWSGTFPINAYTTGPCTPLPAPNYSFAL								
HCV2		MPGLPFISCQKGYAGVWAGTGIMTRCPCGANISGHV <del>R</del> MGTMKITGPKTCLNLWQGTFFPINCYTEGPCVPKPPNYKTAI								
HCV3		LPGLPFISCQKGYKGVWRGDGVMSTRPCGASITGHVKN <del>G</del> SMRLAGPRTCANMWHGTFPINEYTTGPSTPCSPNYTRAL								
HCV4		MPGIPFLSCQKGYKGEWRGDGVMHTT <del>C</del> PCGAELAGHIKNGSMRIVGPKTCSNTWHGTFPINAYTTGPGVPIAPAPNYKFAL								
HCV5		LPGVPFLSCQRGYKGVWRGDGVN <del>S</del> TKPCGATISGHVKNGTMRIVGPKLCSNTWHGTFPINATTTGPSVPAPAPNYKFAL								
HCV6		LPGIPFLSCQRGYRGVWRGDGVCHTTCTCGAVIAGHVKNGTMKITGPRTCSNTWHGTFPINATTTGPSVPIAPAPNYTRAL								
		2081	2090	2100	2110	2120	2130	2140	2150	2160
H77 (NC_004102)		WRVSAEEYVEIRRVGDFHYVSGM <del>T</del> TDNLKPCQIPSP <del>E</del> FFTEL <del>D</del> GVRLHRFAPPCKPLLR <del>E</del> EV <del>S</del> FRVGLHEYPVGSQ <del>L</del> PC								
HCV1		WRVSAEEYVEIRRVGDFHYVTG <del>M</del> TDNLKPCQVPSP <del>E</del> FFTEL <del>D</del> GVRLHRFAPPCKPLLR <del>E</del> EV <del>S</del> FRVGLHQYYPVGSQ <del>L</del> PC								
HCV2		WRVAASEYVEVTQHGSFSYVTGLTSDNLKVP <del>C</del> QVPAPEFFSWVDGVQIHRFAPTPGPF <del>R</del> DEVTF <del>T</del> VGLNSFVVG <del>S</del> Q <del>L</del> PC								
HCV3		WRVAANSYVEVRRV <del>G</del> DFHYITGATEDELKPCQVPAPEFFTEVDGVRLHRYAPPCKPLLR <del>D</del> EITFMVGLNSYAIG <del>S</del> Q <del>L</del> PC								
HCV4		WRVSAEEYVEVRRV <del>G</del> DFHYVTGVTQDN <del>I</del> KPCQVPAPEFFTEVDGVRLH <del>R</del> HAPPCKPLLR <del>D</del> EVTF <del>S</del> VGLNTFVVG <del>S</del> Q <del>L</del> PC								
HCV5		WRVGAADYAEVRRV <del>G</del> DYHYITGVTQDN <del>L</del> KPCQVPSPEFFTEL <del>D</del> GVRIHRFAPP <del>C</del> NPLLR <del>E</del> EV <del>C</del> FSVGLHSYVVG <del>S</del> Q <del>L</del> PC								
HCV6		WRVSAEEYVEVRRV <del>G</del> D <del>S</del> HYVGV <del>T</del> ADNLKPCQVPAPEFFTEVDGVRIHRFAPPCKPLLR <del>D</del> EVTF <del>S</del> VGLSSYAVG <del>S</del> Q <del>L</del> PC								
		2161	2170	2180	2190	2200	2210	2220	2230	2240
H77 (NC_004102)		EPEPDVAVLTSMLTDP <del>S</del> HITAEEAARRLARGSP <del>S</del> MASSASQLSAPSLKATCTANHDSPDAELIEANLLWRQEMGGNIT								
HCV1		EPEPDVAVLTSMLTDP <del>S</del> HITAEEAARRLARGSP <del>S</del> LASSASQLSAPSLKATCTTNHDS <del>P</del> DAELIEANLLWRQEMGGNIT								
HCV2		DPEPDTEVLASMLTDP <del>S</del> HITAEEAARRLARGSP <del>S</del> QASSASQLSAPSLKATCTTHKMAYDCDMVDANLF---MGGDVT								
HCV3		EPEPDVSVLTSMLRDP <del>S</del> HITAETAARRLARGSP <del>S</del> EASSASQLSAPSLKATCQTHRPH <del>P</del> DAELVDANLLW--EMGSNIT								
HCV4		EPEPDVAVLTSMLTDP <del>S</del> HITAEEAARRLARGSP <del>S</del> LASSASQLSAPSLKATCTAHHDS <del>P</del> GADLIEANLLW---GANAT								
HCV5		EPEPDVTVLTSMLSDPAHITAETAARRLDRGSP <del>S</del> LASSASQLSAPSLKATCTTHH--PDAELIEANLLWR-CMGGNIT								
HCV6		EPEPDVTVVTSMLTDP <del>S</del> HITAETAARRLARGSP <del>S</del> LASSASQLSAPSLKATCTTDH--PDAELIEANLLWR-EMGGNIT								

Table S6. Cont.

		NS4B NS5A									
		2241	2250	2260	2270	2280	2290	2300	2310	2320	
H77 (NC_004102)		RVESENKVVILDSFDPLVAEEDEREVSVP	AEILRKSRRFARALP	VWARPDYNPPLVETWKKPDY	EPPVVHGCPLPPRSP						
HCV1		RVESENKVVILDSFDPLVAEEDEREISVP	AEILRKSRRFPALPI	WARPDYNPPLLETWKKPDY	EPPVVHGCPLPPPKSP						
HCV2		RIESDSKVVILDSLDSMTEVEDDREPSV	PSEYLIPRRKFPPALP	WARPDYNPPVIETWKR	PDYEPPTVLGCAL-PTPQA						
HCV3		RVESETKVVILDSFEPLRAETDDAELSV	AAECFKKPKYPPALPI	WARPDYNPPLDRWKAPDY	VPPTVHGCAL-PRGAP						
HCV4		RVESEDKVVVILDSFEPLVAEPDDREVS	VAAEILRPSKFKFPALPI	WARPDYNPPLVETWKKPDY	DPVVHGCAL-PSKPP						
HCV5		RVEAENKVVILDSFEPL- <b>KA</b> EDDREISV	SADCFRRGPAFPALP	VWARPGYDPPLLETWKR	PDYDPPQVSGCPL-PAGLP						
HCV6		RVESENKVVVILDSFDPLTPEYDDEISV	SAECHIRPRPKFPALPI	WARPDYNPPLLETWKA	PDYEPVVSGCAL-PPKPT						
		2321	2330	2340	2350	2360	2370	2380	2390	2400	
H77 (NC_004102)		PVPPPRKKR-VVLTESTLSTALAE	LATKSF	-SSTSGITGDNTT	SSEPAPSGC	PPDSDVESYSSM	PPLLEGEP	GDPDLS			
HCV1		PVPPPRKKR-VVLTESTVSTALAE	LATKSF	-SSTSGITGDNTT	SSEPASSGC	PPDSDAESYSSM	PPLLEGEP	GDPDLS			
HCV2		PVPPPRRRR-KVLTQDNVEGVL	REMAKVF	S-GDSGHSTGADT	GGDTGQDPPDE	-AASETGSLSSM	PPLLEGEP	DPDLEK			
HCV3		PVPPPRRRR-IQLDGSNVSA	ALAALA	AEKSFSEENSSSG	VDTQSSTTSK	VPPS-GESDSE	SCSSM	PPLLEGEP	DPDLC		
HCV4		PVPPPRRRR-VVLS	ESNVSDALADLA	AKSFGQPES	DSGAGLTTPT	TETSDPDPII	-DKSDDG	SYSSM	PPLLEGEP	DPDLS	
HCV5		PVPPPRRRRKMELSD	STVSQVLADLA	HARFKAP	SGQDSALGT	GSQPDSG	PDE-DDSDA	ASYSSM	PPLLEGEP	DPDLS	
HCV6		PIPPPRRRRHLDESTV	SHALAQ	LAEKVFPES	DPTPSSD	GLSITSG	SPPAPT	-AASDA	ASYSSM	PPLLEGEP	DPDLS
		2401	2410	2420	2430	2440	2450	2460	2470	2480	
H77 (NC_004102)		GSWSTVSSGADTEDVVC	SMSYSWTGALV	TPCAAEEQ	KLPINALS	NLLRHHNL	VYSTTS	RSACQRQ	KKVTFDRL	QVLD	
HCV1		GSWSTVSSAADTEDVVC	SMSYWTGALIT	PCAAEEQ	KLPINALS	NLLRHHNL	VYSTTS	RSACQRQ	KKVTFDRL	QVLD	
HCV2		SSWSTVSDQE--DSV	ICSMSYSWTGALIT	PCGPEEEK	LPIPLNS	LMRFHNK	VYSTTS	RSASLRA	KKVTFDRV	QVLD	
HCV3		-SWSTVSSEE--QSV	VCSMSYSWTGALIT	PCSAEEEK	LPIPLNS	LLRHHNL	VYSTSS	RSASQRQ	KKVTFDRL	QVLD	
HCV4		-SWSTVSSED----	VVCSMSYSWTGALV	TPCAAEE	KLPINPLNS	LLRHHNM	VYATTS	RSATTRQ	KKVTFDRM	QVVD	
HCV5		GSWSTVSEDS----	VVCSMSYSWTGALIT	PCSAEEEK	LPIPLNS	LLRHHNL	VYSTSS	RSASQRQ	KKVTFDRL	QVLD	
HCV6		GSWSTVSEDD----	VVCSMSYSWTGALIT	PCAAEEEK	LPIPLNS	LLRHHNL	VYSTTS	RSASLRA	KKVTFDRV	QVLD	
		NS5A NS5B									
		2481	2490	2500	2510	2520	2530	2540	2550	2560	
H77 (NC_004102)		YQDVLKEVKAAASKV	KANLLS	VVEEACSL	TPPHS	AKSKFGY	GAKDVR	CHARKAV	AHINSV	WKD	
HCV1		YQDVLKEVKAAASKV	KANLLS	VVEEACSL	TPPHS	ARSKFGY	GAKDVR	CHARKAV	NHINSV	WKD	
HCV2		YDVLQDVKRAASKV	SARLLS	VVEEACAL	TPPHS	ARSRYG	FAKEVRS	LSRR	AVNH	IRSV	
HCV3		YKTALKEVKERASR	VKARMLT	IEEACAL	VPPHS	ARSKFGY	SAKDVR	SLSSK	AINQ	IRSV	
HCV4		YHEVLKEIKARASG	VKARLLS	VVEEACDL	TPPHS	ARSKFGY	GAKDVR	SHSRK	AINH	IRSV	
HCV5		YREVVD	EMKRLASKV	KARLLPLEE	ACGLTPPHS	ARSKYGY	GAKEVRS	LDKK	KALH	IEGV	
HCV6		YDVLKEIKLRAS	TQAKLLS	IEEACDL	TPPHS	ARSKFGY	GAKDVR	SHASK	AINH	IRSV	





**Table S6. Cont.**

	NS5A NS5B								
	2881	2890	2900	2910	2920	2930	2940	2950	2960
H77 (NC_004102)	QRLHGLSAFSLHSYSPGEINRVAACLRKLGVPPLRAWRHRARSVRARLLSRGGRAAICGKYLFWAVRTKTKLTPIAAAG								
HCV1	QRLHGLSAFSLHSYSPGEINRVAACLRKLGVPPLRAWRHRARSVRAKLLSRGGRAAICGKYLFWAVRTKTKLTPIAAAS								
HCV2	ERLHGLDAFSLHTYSPHELSRVAATLRKLGAPPLRAWKSRARAVRASLIAQ-----								
HCV3	ERLHGLSAFTLHSYSPVELNRVAGTLRKLGCPPPLRAWRHRARAVRAKLIQGGKAKICGLYLFWAVRTKTKLTPPAAG								
HCV4	QRLHGLSAFTLHGYSPELNRVAGSLRKLGVPPPLRAWRHRARAVRAKLIQGGARICGIYLFWAVKTKLTPLPAAA								
HCV5	QRLHGLSAFSLHSYSPSEINRVASCLRKLGVPPLRAWRHRARAVRAKL-AQGG-AAICGIYLFWAVKTKRKLTPADAD								
HCV6	QRLHGMAAFSLHGYSPELNRVGAACLRKLGAPPLRAWRHRARAVRAKLIQGGKAAICGKYLFWAVKTKLTPLRGAS								
	2961	2970	2980	2990	3000				
H77 (NC_004102)	RLDLSGWFTAGYSGGDIYHSVSHARPRWFWFCLLLAVGV								
HCV1	QLDLSGWFTAGYSGGDIYHSVSRARPRWFWFCLLLAVGV								
HCV2	-----								
HCV3	QLDLSSWFTVGVGGNDIYHSVSRARTRHLLLCLLLTVGV								
HCV4	KLDLSSWFTVGVAGGGDIYHSVSRARPRYLLLCLLLSVG								
HCV5	RLDLSSWFTVGVAGGGDIYHSMSRARPR-LLLCLLLSVG								
HCV6	KLDLSGWFWAGYSGGDIYHSVSRARPRLLLCLLLTVGV								

**Table S7.** Proportion of positions under positive selective pressure for all six HCV genotypes, according to the SLAC and FEL method. For all ten viral proteins, the proportion of positively selected positions (dN/dS ratio > 1, *p*-value < 0.05%) is listed, together with the median and IQR (Q1-Q3) over all six HCV genotypes. For each viral protein both the number of positively selected positions according to SLAC and FEL was listed per individual HCV genotype, with the upper percentage for SLAC and the lower for FEL.

	%	HCV1	HCV2	HCV3	HCV4	HCV5	HCV6	Median (IQR = Q1 - Q3)
Core	SLAC	3.65	0.52	0	0	0	0	0.26 (0-0.52)
	FEL	2.60	0.52	0.52	0	0	1.56	0.52 (0.13-1.3)
E1	SLAC	6.77	0.52	0.52	0.52	0	0	0.52 (0.13-0.52)
	FEL	2.60	1.56	0.52	0	1.04	0.52	0.78 (0.52-1.43)
E2	SLAC	9.37	2.20	1.65	0.38	0	0.83	1.24 (0.83-2.07)
	FEL	6.89	2.20	2.75	1.10	1.93	1.93	2.07 (1.31-2.62)
p7	SLAC	4.76	0	0	0	0	0	0
	FEL	0	0	0	0	0	0	0
NS2	SLAC	3.23	0.46	0	0	0	0	0.23 (0-0.46)
	FEL	1.84	0.92	0	0	0	0	0 (0-0.69)
NS3	SLAC	0.32	0.32	0	0	0	0	0
	FEL	0.16	0.32	0.16	0	0	0	0.08 (0-0.16)
NS4A	SLAC	0	0	0	0	0	0	0
	FEL	0	0	0	0	0	0	0
NS4B	SLAC	0.77	0	0.38	0	0	0	0
	FEL	0.38	0	0.38	0	0	0	0 (0-0.29)
NS5A	SLAC	1.35	0	0.22	0	0	0	0
	FEL	0.67	0	0.22	0	0.22	0.22	0.11 (0-0.22)
NS5B	SLAC	3.37	0.51	0	0	0	0	0
	FEL	3.55	1.18	0.17	0.34	0	0	0.25 (0.04-0.97)
Full-genome	SLAC	3.12	0.53	0.30	0.13	0	0.17	0.23 (0.14-0.47)
	FEL	2.16	0.76	0.53	0.20	0.10	0.40	0.46 (0.13-1.3)

**Table S8.** Positions under positive selective pressure for all six individual HCV genotypes. For the six HCV genotypes, all positively selected positions (dN/dS ratio > 1, *p*-value < 0.05%), according to SLAC are listed, based on the total alignment and the H77 numbering.

HCV genotype 1	Core: 10, 16, 44, 71, 75, 158, 161
	E1: 28, 40, 44, 65, 106, 108, 117, 139, 149, 153-154, 163, 192
	E2: 2-3, 7, 10-12, 15, 18-19, 21-22, 25, 49, 53, 59-62, 78, 80, 91-93, 113-114, 135, 141, 170, 183, 187, 190, 193, 222, 234, 253
	p7: 29, 38, 62
	NS2: 22, 58, 108, 121, 140, 145-146
	NS3: 545, 598
	NS4A: /
	NS4B: 36, 145
	NS5A: 204, 215, 235, 339, 392, 395
	NS5B: 57, 90, 102, 109, 112, 122, 173, 182, 206, 267, 303, 329, 356, 431, 508, 542-543, 548, 563, 582
HCV genotype 2	Core: 71
	E2: 1, 12, 17, 22, 25, 61, 78, 119, 165
	NS2: 125
	NS3: 288, 360
HCV genotype 3	NS5B: 396, 564, 578
	E1: 44
	E2: 81, 113, 158, 179, 197, 343
	NS4B: 167
HCV genotype 4	NS5A: 12
	E2: 1, 14, 33, 51
HCV genotype 5	/
HCV genotype 6	Core: 75
	E2: 4, 17, 60
	NS2: 118