S3 Table. Mutations, corresponding amino acid substitutions and point accepted mutation (PAM) of the NS5A-coding region in the mutant spectra HCV p0 subjected to three passages in the presence of favipiravir (T-705) 400 μM analyzed by ultra deep pyrosequencing[a].

Amplicon A1			Amplicon A2			Amplicon A4		
Mutation[b]	Amino acid substitution[c]	PAM 250	Mutation[b]	Amino acid Substitution[c]	PAM 250	Mutation[b]	Amino acid Substitution[c]	PAM 250
A6158G[d]	T225A[d]	1	A6452G	N62D	2	C6919U	-	-
G6160A[d]	-	-	C6469U	-	-	C6942U	S225F	-3
G6166A[d]	-	-	C6469A	-	-	U6943C	-	-
U6169C[d]	-	-	C6473A	L69M	4	C6952U	-	-
C6187U[d]	-	-	G6486A	R73K	3	C6955U	-	-
U6196C[d]	-	-	C6505U	-	-	G6959U	V231L	2
C6218U[d]	-	-	G6523A	-	-	G6974A	A236T	1
A6220G[d]	-	-	G6526A	-	-	G6989A	A241T	1
G6225A[d]	R247K[d]	3	A6527G	T87A	1	C6999U	T244I	0
A6226G[d]	-	-	C6529U	-	-	A7001G	T245A	1
A6242G[d]	I253V[d]	4	G6559A	-	-	C7003U	-	-
C6246U[d]	T254I[d]	0	C6562U	-	-	G7008A	S247N	1
G6250A[d]	-	-	G6565A	-	-	C7015U	-	-
A6260G[d]	I259V[d]	4	C6575U	P103S	1	U7016C	Y250H	0
C6268U[d]	-	-	C6577U	-	-	A7020G	D251G	1
C6298U	-	-	A6578G	T104A	1	A7026G	D253G	1
A6319G	-	-	A6582G	N105S	1	C7033U	-	-
C6335U	-	-	G6625A	-	-	A7049G	M261V	2
G6337A	-	-	A6632G	T122A	1	A7053C	E262A	0
A6338G	T24A	1	G6637A	-	-	G7064A	A266T	1
A6338U	T24S	1	G6646A	-	-	G7069A	-	-
C6340U	-	-	A6661G	-	-	A7074G	E269G	0
U6343C	-	-	C6665U	-	-	G7075A	-	-
C6373U	-	-	U6679C	-	-	C7077U	P270L	-3
C6379U	-	-	G6682A	-	-	G7081A	-	-
G6410A	A48T	1	U6692A	C142S	0	U7098C	L277P	-3

C6411U	**A48V**	0		C6694U	**-**	-		U7105C	**-**	-
A6452G	**N62D**	2		C6707U	**P147S**	1		G7111A	**-**	-
A6453C	**N62T**	0		G6739A	**-**	-		U7116C	**M283T**	-1
C6454A	**N62K**	1		C6742U	**-**	-		C7119U	**A284V**	0
				G6747A	**R160K**	3		G7124A	**E286K**	0
				C6753U	**A162V**	0		A7125G	**E286G**	0
				G6766A	**-**	-		G7129A	**-**	-
				C6767U	**P167S**	1		G7133A	**D289N**	2
								A7134G	**D289G**	1
								U7137C	**L290P**	-3
								G7141A	**-**	-
								C7142U	**P292S**	1
								C7144U	**-**	-
								U7145C	**S293P**	1
								A7148G	**I294V**	4
								U7149C	**I294T**	0
								A7150G	**I294M**	2
								C7151U	**P295S**	1
								C7152U	**P295L**	-3
								U7154C	**S296P**	1
								C7155U	**S296L**	-3
								A7158G	**E297G**	0
								G7159C	**E297D**	3
								U7160C	**C298R**	-4
								U7164C	**M299T**	-1
								G7165A	**M299I**	2
								C7166U	**L300F**	2
								C7169U	**P301S**	1
								A7172G	**R302G**	-3
								G7173A	**R302K**	3
								G7178A	**G304R**	-3
								G7179A	**G304E**	0

						U7183C	-	-
						A7215G	**D316G**	1
						U7217C	**Y317H**	0
						A7218G	**Y317C**	0
						G7225A	-	-
						G7240C	-	-
Different mutations[e]	**30**		**Different mutations**[e]	**34**		**Different mutations**[e]	**64**	
Synonymous (%)[f]	**18 (60)**		**Synonymous (%)**[f]	**21 (61.8)**		**Synonymous (%)**[f]	**18 (28.1)**	
Non-synonymous (%)[f]	**12 (40)**		**Non-synonymous (%)**[f]	**13 (38.2)**		**Non-synonymous (%)**[f]	**46 (71.9)**	

[a]The population analyzed correspond to passage 3 of the infections described in Fig. 1 and Table 1 of the main text.

[b]The HCV genome residue numbering corresponds to the JFH-1 genome (accession number #AB047639).

[c]Amino acid residues (single letter code) are numbered from N- to the C-terminus of NS5A.

[d]Mutations (and deduced amino acid substitutions) at the NS4B-coding region.

[e]Number of different mutations found comparing the sequence of each individual clone with the consensus sequence.

[f]Number of different synonymous and non-synonymous mutations; their percentage is indicated in parenthesis.