

S1 Table. Oligonucleotides used for the ultra deep pyrosequencing analysis of HCV p0 subjected to three passages in the absence or presence of 400 µM favipiravir.

Primer Name	Sequence (5'-3') ^a	Sense	Position ^b	Tm (°C)
RT Oligonucleotide (5'-3')				
NS5A NakedT6R	ACTCAAAGGGTTGATTGGCAAC	-	7747-7726	53
Amplicon 1 Oligonucleotides (5'-3')				
13NS5A T1F	GTTGTA AAAACGACGGCCAGT AAACCACGTCGCCCCTACTCAC	+	6130-6151	58,6
13NS5A T1R	CACAGGAAACAGCTATGACC AGGCGGACATTGCCAGAGAT	-	6474-6455	53,8
Amplicon 2 Oligonucleotides (5'-3')				
13NS5A T2F	GTTGTA AAAACGACGGCCAGT TGACCACGCGCTGCCCTTGC	+	6426-6445	60
13NS5A T2R	CACAGGAAACAGCTATGACC AGACCTCATCCCGGAAAAACG	-	6788-6768	54,4
Amplicon 4 Oligonucleotides (5'-3')				
13NS5A T4F	GTTGTA AAAACGACGGCCAGT ACATCACGGCGGAGACTGC	+	6891-6909	55,4
13NS5A T4R	CACAGGAAACAGCTATGACC AACGGTGGGCGGTTGGTAATC	-	7273-7253	56,3
MID 10 Oligonucleotide (5'-3')				
AFw10M13	CGTATCGCCTCCCTCGCGCCA <i>T</i>CAGTCTCTATGCG GTTGTA AAAACGACGGCCAGT	+	-	60
BRv10M13	CTATGCGCCTTGCCAGCCCGC <i>T</i>CAGTCTCTATGCG CACAGGAAACAGCTATGACC	-	-	60
MID 11 Oligonucleotide (5'-3')				
AFw11M13	CGTATCGCCTCCCTCGCGCCA <i>T</i>CAGTGATACGTCT GTTGTA AAAACGACGGCCAGT	+	-	60
BRv11M13	CTATGCGCCTTGCCAGCCCGC <i>T</i>CAGTGATACGTCT CACAGGAAACAGCTATGACC	-	-	60

^aNucleotides in bold indicate the HCV-specific sequence; boxed nucleotides indicate universal M13 oligonucleotide. Nucleotides TCAG in italics indicate the sequencing key; these are the first four nucleotide to be sequenced and are located immediately downstream from the oligonucleotides A and B (supplier nomenclature, standard letters in the sequences); the underlined nucleotides indicate Roche's Validated Multiplex Identifiers (MID). MIDs 10 and 11 (in primers termed AFw and BRv in the first column) have been used to amplify HCV p0 passaged three times in the absence and presence of favipiravir, respectively.

^bAccording to JFH-1 (accession number #AB047639)