

SUPPLEMENTARY DATA

TABLE S1: GENBANK ACCESSION NUMBERS OF VIRUS SEQUENCES

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chr10	18902718	rs6481583	+
chr15	66957020	rs6494621	+
chr16	27813510	rs6498038	+
chr12	120764559	rs6553	+
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chr12	120878449	rs656933	-
chr14	80457125	rs6574576	+
chr11	100069001	rs6590574	+
chr1	4459129	rs662036	-
chr2	39162037	rs66771682	+
chr1	159883032	rs6682796	+
chr4	115302551	rs66997216	+
chr6	116250092	rs6755	-
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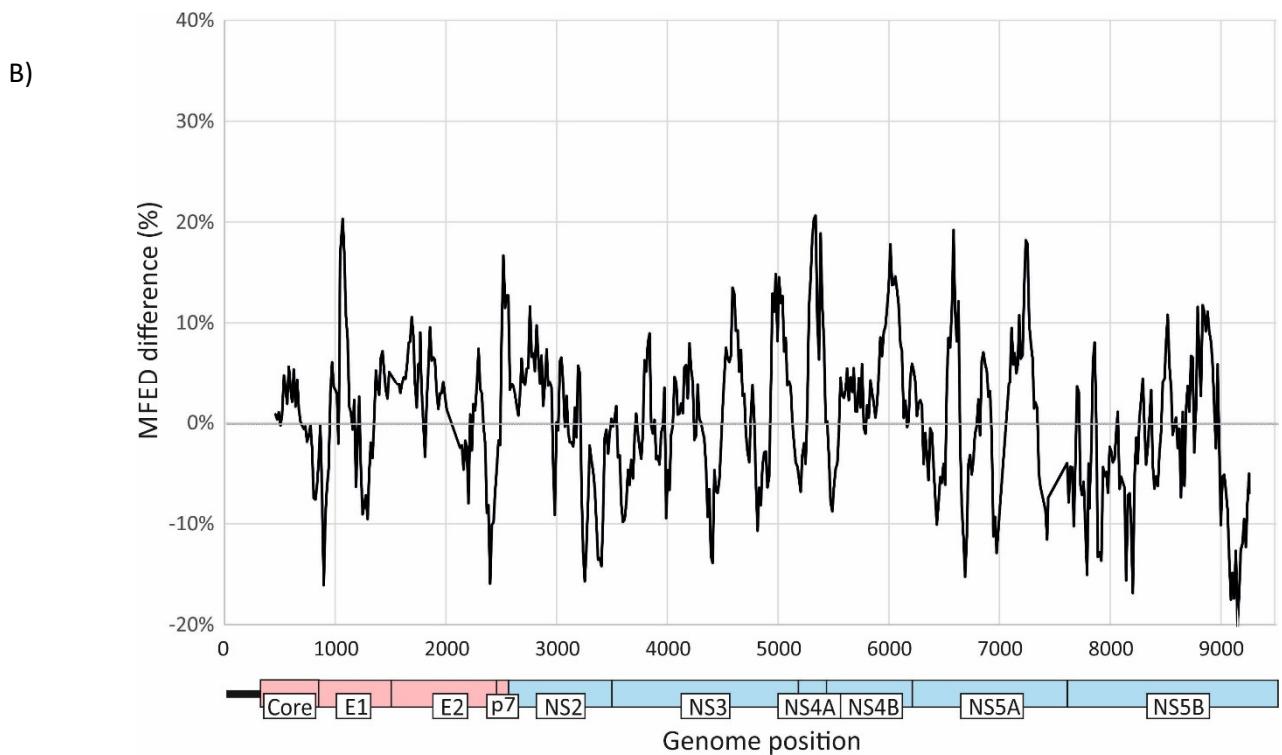
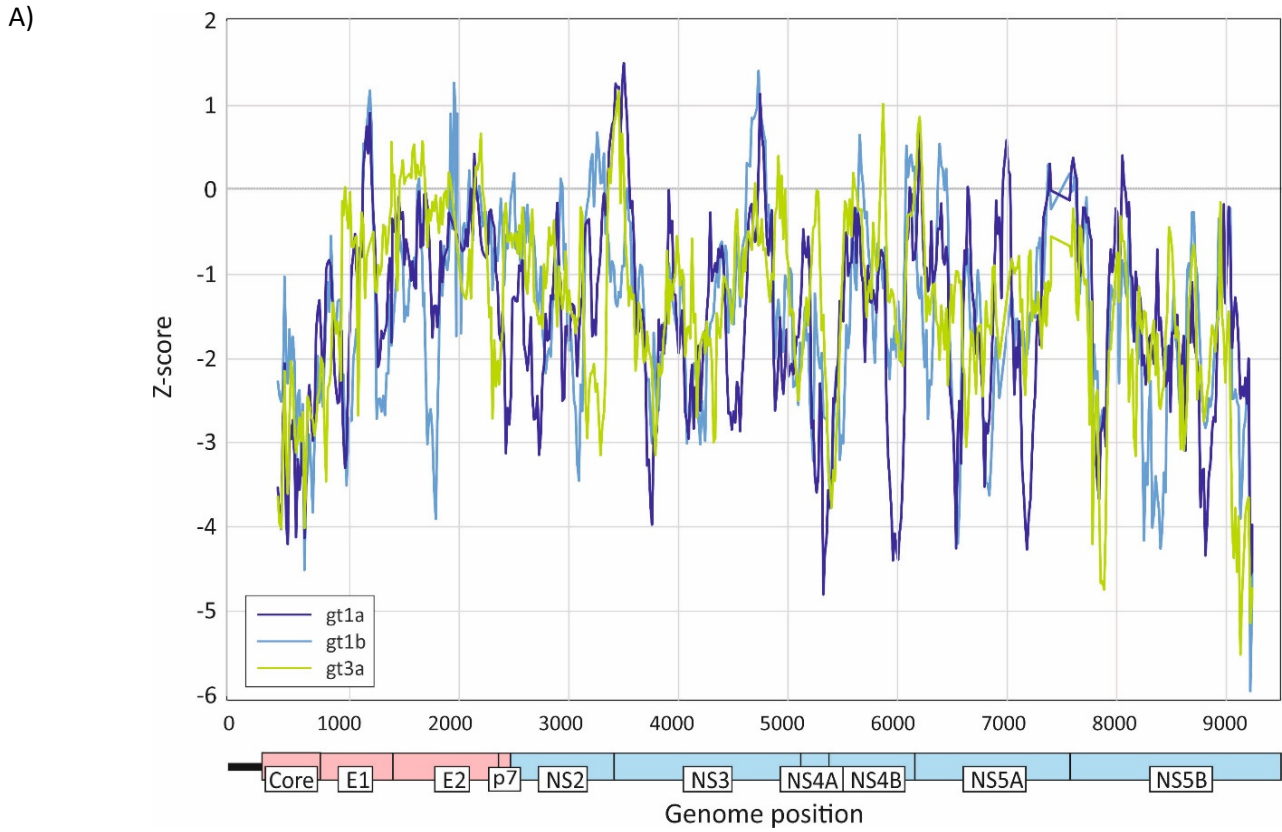
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chr8	70524140	rs7387249	+

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chr7	133120296	rs7777197	+
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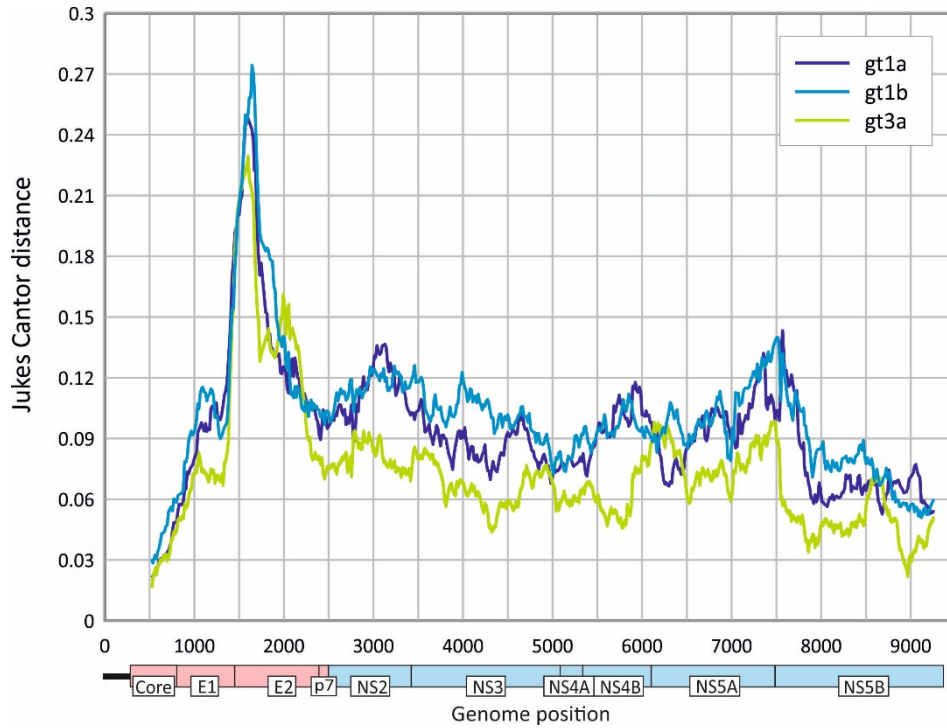
FIGURE S1

GENOME SCANS OF Z-SCORES, MFED DIFFERENCES AND SEQUENCE DIVERGENCE

OF HCV GENOTYPES 1a, 1b AND 3a



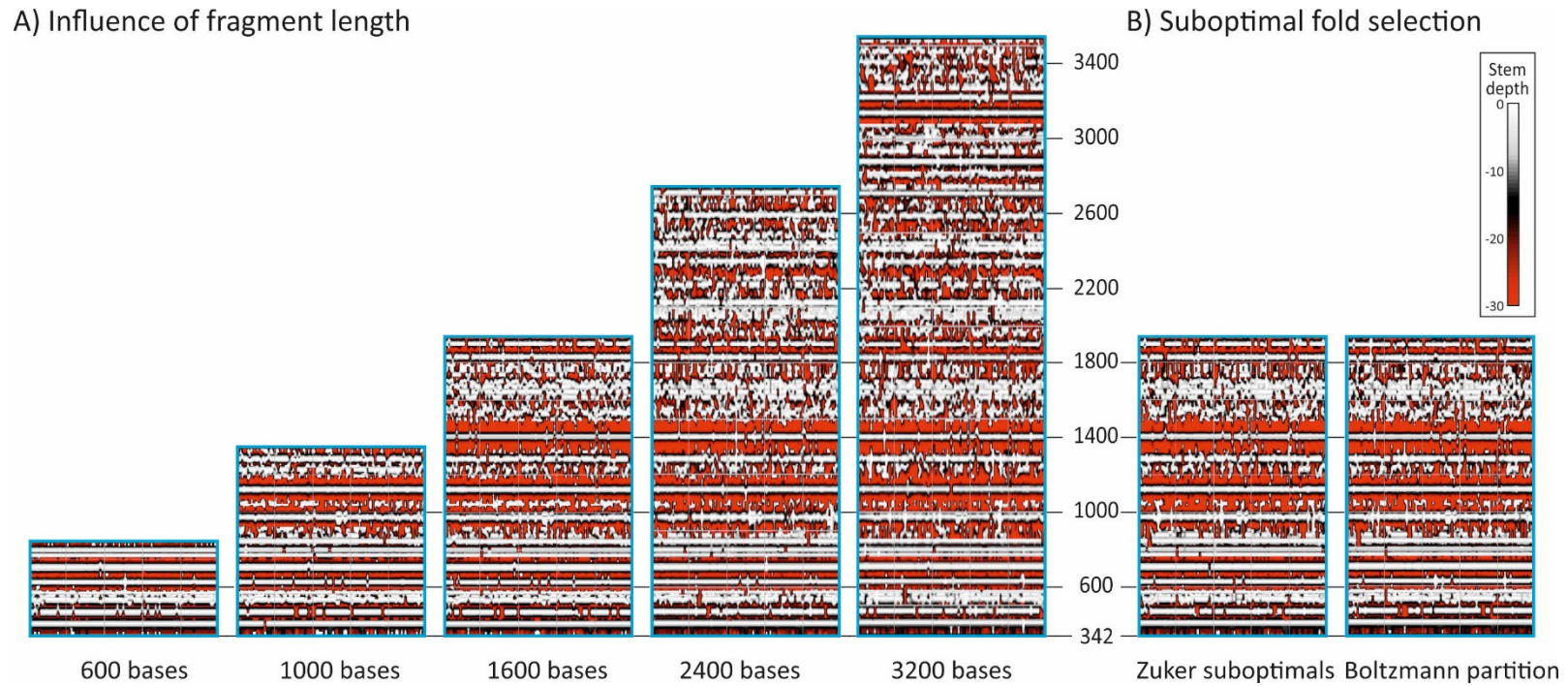
C)



A) Z-scores calculated for consecutive 240 base fragments, incrementing by 15 bases across the HCV coding region (569 fragments). Z-scores represent the position of the MFE of the native sequence within the distribution of MFE values of 49 sequence order randomised controls. Graph lines show mean values of genotypes 1a (n=388), 1b (n=106) and 3a (n=855) sequences plotted by genome position. (B) Differences in MFED values for gt1a and gt3a scanned across the genome. (C) Mean divergence between prototype sequences of genotype 1a (M67463 – H77), 1b (D90208 – HCV-J) and 3a (D17763 – NZL-1) and representative sequences of each genotype sampled from the study population. Mean distances were calculated for 360 fragments incrementing by 15 bases between fragments with Jukes-Cantor correction for multiple substitutions. .

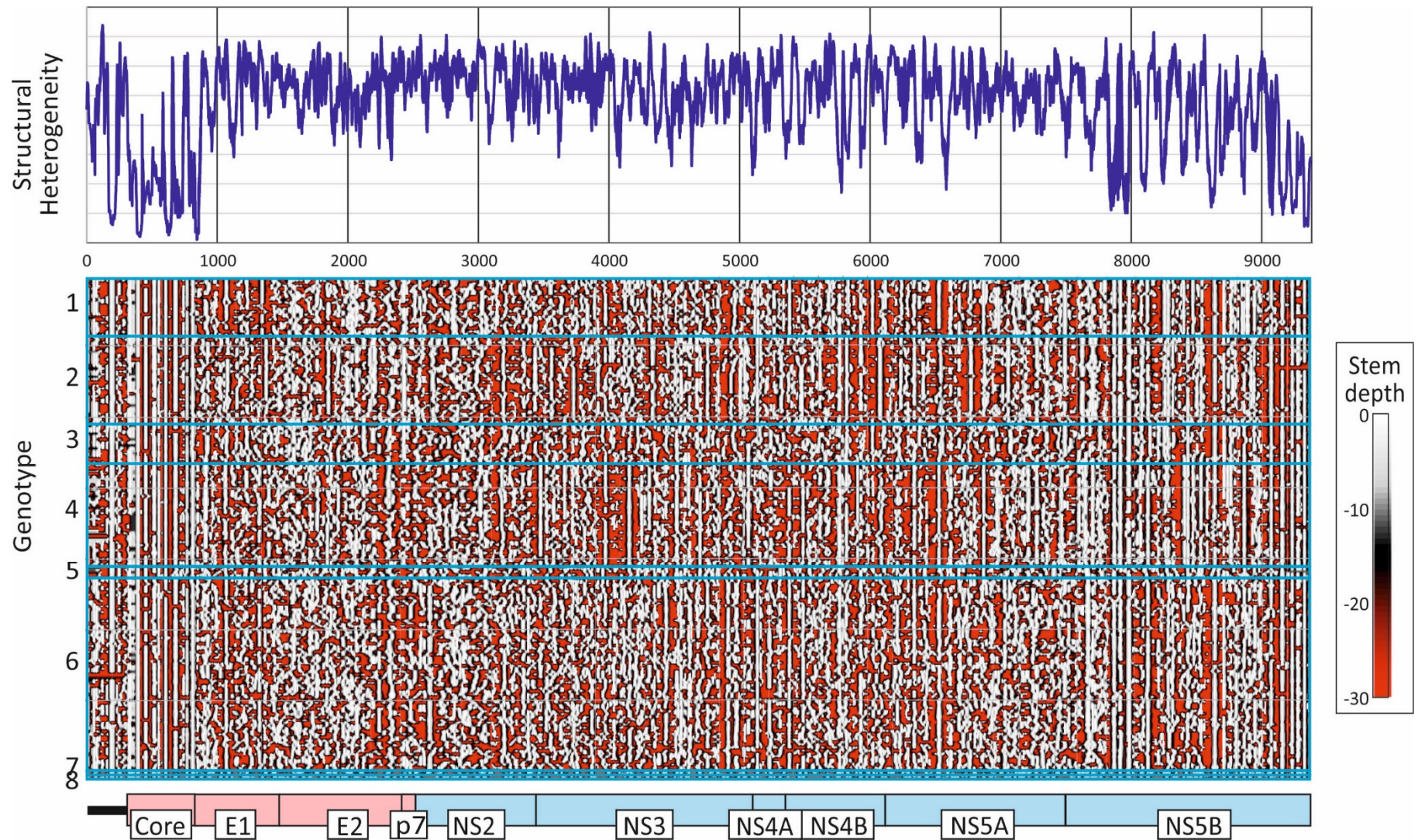
FIGURE S2

INFLUENCE OF SEQUENCE LENGTHS and SUBOPTIMAL SAMPLING METHOD ON CONTOUR PLOT PREDICTIONS



Contour plots of 99 HCV genotype 1b sequences generated using different run parameters. (A) Comparison of contour plots for sequence fragments of lengths 600, 1000, 1600 (as used for other plots presented in the study), 2400 and 3200 bases (approaching the upper bound of sequence length for RNAsubopt). (B) Comparison of the default selection methods for suboptimal folds (those within 5% of the optimum (minimum) MFE (selection of `--deltaEnergy` parameter in RNAsubopt) sd used in the plots shown in Fig. S2A) with alternative methods based on a random selection of Boltzman weights in the partition function (`--stochBT`) and on Zuker sub-optimals (`--zucker`).

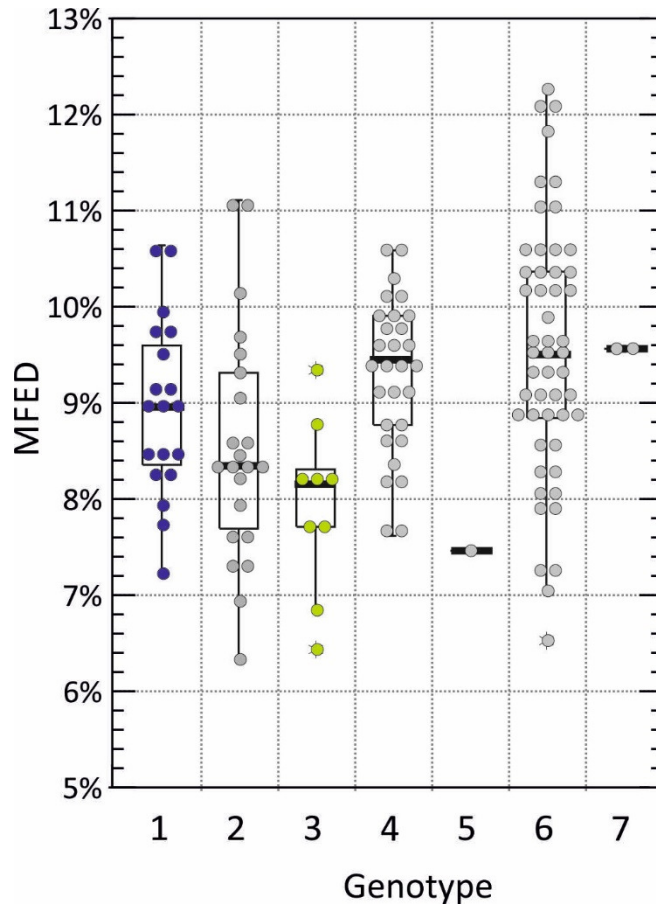
FIG. S3. CONTOUR PLOTS OF PROTOTYPE SEQUENCES OF EACH DIFFERENT GENOTYPE AND SUBTYPE OF HCV



Contour plot of single examples of each currently classified and candidate HCV subtype and genotype (data derived from <https://talk.ictvonline.org/ictv-wikis/flaviviridae/w/sg:flavi/56/hcv-classification>) listed in Table S1; Suppl./ Data.

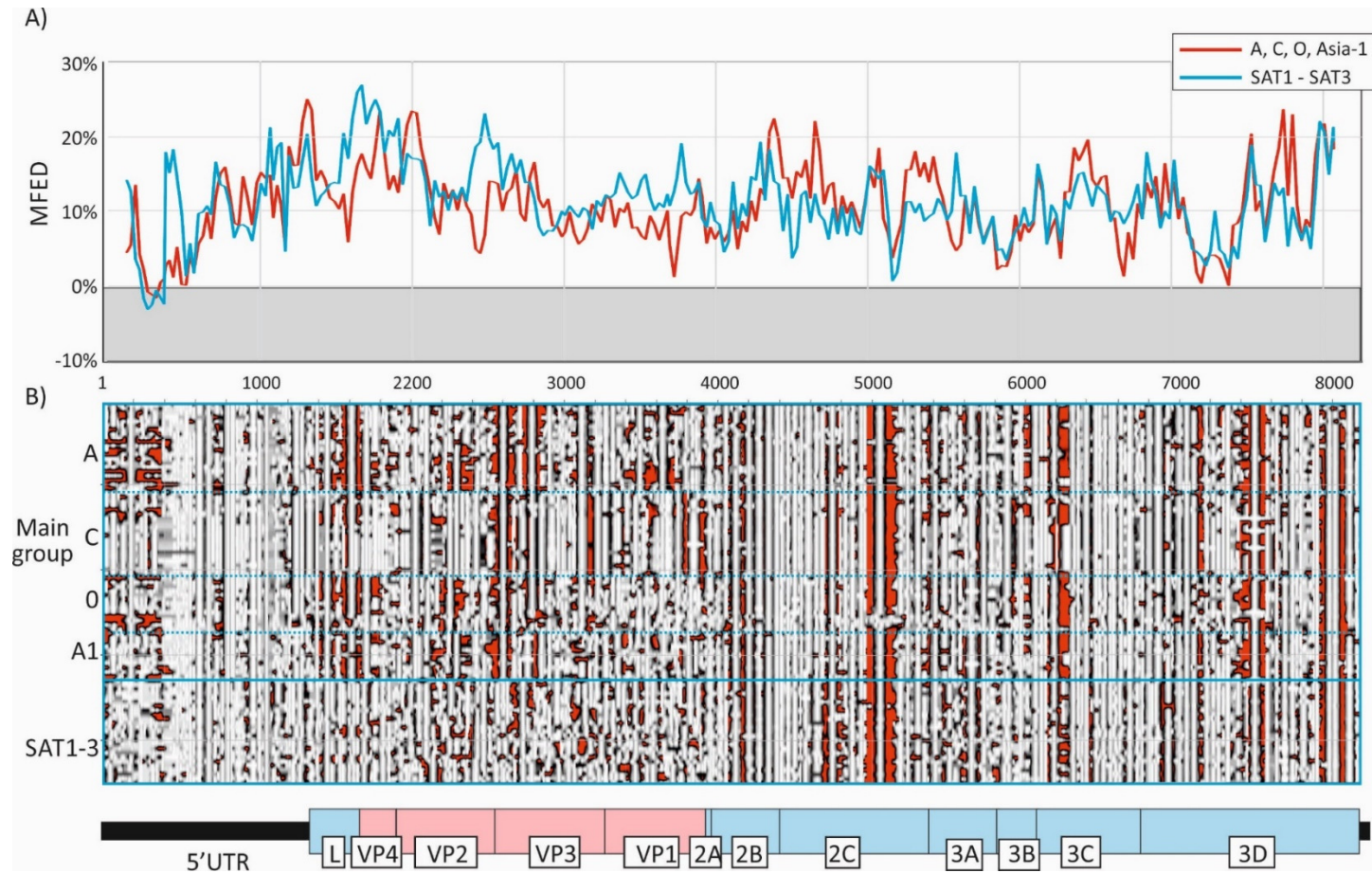
FIGURE S4

MFED VALUES FOR REPRESENTATIVE EXAMPLES OF EACH HCV GENOTYPE / SUBTYPE



Mean values of sequence fragments for individual polyprotein sequences of all classified subtypes for HCV genotypes 1-7 (individual representative sequences for each subtype shown). The box plots show (from the top): 2 standard deviations (SDs) above mean, 1 SD above mean, mean, 1 SD below mean and 2 SDs below mean; stars represent outliers outside this range.

FIG. S5. CONTOUR PLOTS OF DIFFERENT FMDV TYPES



RNA structure prediction in different serotypes of FMDV. (A) MFED scan of the genome of the two FMDV groups using fragment sizes and increments as used for HCV (Fig. 1). (B) Contour plot of representative example sequences of each FMDV type.