

Supplementary Table S5. Branch site analyses of HCV phylogenies. *p* values were FDR corrected to account for the number of tested branches. The non structural region was divided into two sub regions (Reg1 and Reg2) based on the presence of a recombination breakpoint.

Region	Branch	BUSTED <i>p</i> value (FDR correction)	MA vs MA1 <i>p</i> value (FDR correction)	Selected Sites (both methods)	Selected Sites BUSTED	Selected Sites BEB
E1/E2						
	GT1	0.710 (0.71)	0.057 (0.057)	-	-	-
	GT1_GT4	0.064 (0.072)	1.98x10-06 (3.57x10-6)	-	-	3
	GT1_GT4_GT5	0.018 (0.023)	0.020 (0.022)	1	1	3
	GT2	8.34x10-5 (2.50x10-4)	1.12x10-6 (3.36x10-6)	12	13	15
	GT2_GT7	1.66x10-3 (3.10x10-3)	6.35x10-5 (8.16x10-5)	6	10	8
	GT2_GT3_GT7	1.75x10-5 (7.88x10-5)	3.98x10-7 (1.79x10-6)	4	7	6
	GT3	1.72x10-3 (3.10x10-3)	3.47x10-7 (1.79x10-6)	1	4	5
	GT4	0.012 (0.018)	1.72x10-6 (3.57x10-6)	0	2	5
	GT6	7.04x10-7 (6.34x10-6)	2.77x10-6 (4.16x10-6)	9	14	11
NS Reg1						
	GT1	3.03x10-3 (7.18x10-3)	2.05x10-10 (6.15x10-10)	1	1	9
	GT1_GT4	3.19x10-3 (7.18x10-3)	3.73x10-05 (4.80x10-5)	1	2	2
	GT2	0.067 (0.10)	7.66x10-05 (8.62x10-5)	-	-	3
	GT2_GT7	0.033 (0.059)	1.01x10-17 (9.09x10-17)	-	-	6
	GT2_GT3_GT7	1.96x10-3 (7.18x10-3)	2.97x10-8 (6.68x10-8)	6	8	7
	GT3	1 (1)	1.79x10-11 (8.06x10-11)	-	-	12
	GT4	0.975 (1)	3.68x10-4 (3.68x10-4)	-	-	5
	GT5_GT6	2.56x10-3 (7.18x10-3)	2.17x10-5 (3.26x10-5)	4	4	4
	GT6	0.088 (0.11)	3.19x10-7 (5.74x10-7)	-	-	5
NS Reg2						
	GT1	5.17x10-9 (1.16x10-8)	1.79x10-24 (1.61x10-23)	7	9	16
	GT1_GT4	2.55x10-4 (2.55x10-4)	1.01x10-9 (1.01x10-9)	4	4	4
	GT1_GT4_GT5	1.09x10-5 (1.23x10-5)	5.61x10-10 (6.31x10-10)	1	3	1
	GT2	9.66x10-9 (1.74x10-8)	2.54x10-23 (1.14x10-22)	9	14	15
	GT2_GT7	8.31x10-11 (2.49x10-10)	2.32x10-20 (6.96x10-20)	12	15	14
	GT3	3.04x10-8 (3.91x10-8)	4.86x10-10 (6.25x10-10)	7	13	13
	GT3_GT6	2.40x10-8 (3.60x10-8)	2.14x10-12 (3.21x10-12)	7	11	7
	GT4	1.12x10-11 (5.04x10-11)	4.79x10-19 (8.62x10-19)	8	15	12
	GT6	1.39x10-13 (1.25x10-12)	2.58x10-19 (5.81x10-19)	11	19	19

GT, genotype; NS, non structural region.