Supporting Information

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Table 1. Prevalence of cn mutations in treatment-experienced patients

Mutation	No. of sequences containing a cn mutation* (%)	No. of sequences containing both a cn mutation and one or more TAM (%)	Probability of having a cn mutation with one or more TAM†
E312Q	16/1667 (1)	11/16 (69)	$P = 0.20$
G335C	7/1221 (0.6)	4/7 (57)	$P = 0.61$
G335D	16/1221 (1.3)	6/16 (38)	$P = 0.95$
N348I	39/1022 (3.8)	29/39 (74)	$P = 0.0098$
A360V	51/991 (5.1)	44/51 (86)	$P = 0.000001$
A360I	2/991 (0.2)	2/2 (100)	$P = 0.30$
V365I	35/987 (3.5)	25/35 (71)	$P = 0.035$
A376S	51/972 (5.2)	26/51 (51)	$P = 0.78$
Total	217/972‡ (21)	147/217 (68)	$P = 0.000013$

*Data were obtained from the Stanford HIV Drug Resistance Database.

†Two proportions tests were preformed by comparing the number of cn mutations with at least 1 TAM (e.g., 11 for E312Q) to the total number of sequences containing at least 1 TAM (537 of 972), against the number of cn mutations without a TAM (e.g., five for E312Q) to the total number of sequences without a TAM (435 of 972).

‡A total of 972 sequences were used because the number analyzable sequences decreases as the sequence is extended toward the RNase H domain.