Supplemental Table 1. Average number of secondary mutations

Gag	Protease Profile	Mean P-P	Mean P-A	PP - PA	P-value
A431	D30N	4.6	2.0	2.6	1.7E-03
	D30N/N88D	5.4	3.8	1.6	0.0E+00
	I50L	5.5	3.5	2.0	1.5E-10
	I50V	7.8	6.8	1.0	4.7E-04
	V82A	6.7	6.5	0.3	3.8E-04
	V82A/L90M	7.5	7.5	0.1	1.9E-01
	I84V	7.3	6.6	0.8	0.0E+00
	I84V/L90M	7.7	7.0	0.7	0.0E+00
	N88D	5.5	3.9	1.6	0.0E+00
	N88D/L90M	7.3	5.9	1.5	4.0E-08
	L90M	6.8	4.0	2.8	0.0E+00
K436	D30N	1.6	2.2	-0.6	2.5E-01
	D30N/N88D	4.3	4.0	0.3	1.8E-01
	I50L	5.4	4.2	1.1	2.6E-02
	I50V	7.4	6.9	0.5	1.4E-01
	V82A	6.5	6.6	-0.1	2.4E-01
	V82A/L90M	7.3	7.5	-0.2	4.4E-02
	I84V	7.1	6.9	0.1	1.0E-01
	I84V/L90M	7.5	7.4	0.2	1.2E-01
	N88D	4.3	4.1	0.2	2.1E-01
	N88D/L90M	5.4	6.2	-0.8	3.2E-01
	L90M	5.9	4.4	1.4	2.2E-16
I437	D30N	1.9	2.1	-0.2	6.4E-01
	D30N/N88D	4.3	4.0	0.3	2.5E-01
	I50L	4.8	4.2	0.6	3.3E-01
	I50V	7.8	6.7	1.1	3.8E-07
	V82A	7.0	6.5	0.4	1.7E-08
	V82A/L90M	7.7	7.4	0.3	2.7E-03
	I84V	7.2	7.0	0.2	7.0E-05
	I84V/L90M	7.8	7.3	0.5	4.1E-08
	N88D	4.5	4.1	0.4	1.1E-01
	N88D/L90M	6.6	6.1	0.5	1.8E-01
	L90M	6.1	4.4	1.8	0.0E+00

L449	D30N	2.4	2.1	0.2	8.2E-01
	D30N/N88D	4.2	3.9	0.3	3.0E-01
	I50L	3.8	4.3	-0.5	1.1E-01
	I50V	6.5	7.2	-0.7	4.2E-06
	V82A	7.1	6.5	0.6	1.3E-08
	V82A/L90M	8.1	7.4	0.7	1.7E-09
	I84V	6.7	7.1	-0.4	1.8E-08
	I84V/L90M	7.4	7.3	0.0	5.7E-01
	N88D	4.3	4.0	0.3	7.9E-02
	N88D/L90M	6.3	6.0	0.3	1.4E-01
	L90M	5.2	4.5	0.7	7.2E-07
S451	D30N	2.3	2.1	0.2	7.0E-01
	D30N/N88D	4.0	4.1	-0.1	3.1E-01
	I50L	3.9	4.3	-0.4	2.6E-01
	I50V	7.4	6.9	0.5	3.0E-02
	V82A	6.5	6.6	-0.1	8.3E-01
	V82A/L90M	7.7	7.5	0.2	6.0E-03
	I84V	6.8	7.0	-0.1	2.8E-02
	I84V/L90M	7.3	7.4	-0.1	1.5E-01
	N88D	4.0	4.2	-0.2	9.2E-02
	N88D/L90M	6.1	6.2	-0.1	9.2E-01
	L90M	4.8	4.6	0.3	2.2E-02
R452	D30N	2.7	2.1	0.6	4.8E-01
	D30N/N88D	4.4	4.0	0.4	4.2E-03
	I50L	4.9	4.2	0.6	3.5E-01
	I50V	7.4	6.9	0.5	1.1E-01
	V82A	7.4	6.6	0.8	1.2E-04
	V82A/L90M	7.9	7.5	0.4	4.2E-02
	I84V	7.4	6.9	0.5	7.7E-12
	I84V/L90M	7.7	7.3	0.4	3.0E-07
	N88D	4.4	4.1	0.4	1.4E-02
	N88D/L90M	6.4	6.1	0.3	3.2E-01
	L90M	5.6	4.5	1.0	3.1E-03
P453	D30N	2.4	2.1	0.3	4.7E-01
	D30N/N88D	4.1	4.0	0.1	8.9E-02
	I50L	4.0	4.3	-0.3	3.4E-01
	I50V	6.9	6.9	0.0	9.8E-01
	V82A	7.0	6.5	0.6	2.0E-13
	V82A/L90M	7.8	7.4	0.4	4.4E-07
	I84V	7.0	7.0	0.0	8.9E-01
	I84V/L90M	7.4	7.4	0.0	6.4E-01
	N88D	4.2	4.1	0.1	2.5E-01
	N88D/L90M	6.4	5.8	0.6	2.1E-02
	L90M	5.3	4.3	1.0	0.0E+00

P-P -- Samples with specified mutations present in both the protease and the cleavage site
P-A -- Samples with specified mutations present in the protease but absent the in cleavage site
p-values < 0.05 are significant

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