

Supplemental Table 3. Association between protease mutations and mutations within the NC-p1 and p1-p6 cleavage sites.

Gag Residue (Cleavage Site)	Gag Mutation	Protease Mutations	P-P %	A-P %	P-P	P-A	A-P	A-A	Chi2	p-value
A431 (NC-p1)	A > V	D30N	3	19	4	141	6589	28134	23.7	1.9E-02
		D30N/N88D	12	19	133	975	6460	27300	35.1	5.2E-05
		D30N/N88D/L90M	21	19	40	149	6434	27141	0.4	1.0E+00
		I50L	40	19	64	95	6738	29150	46.3	1.7E-07
		I50V	10	19	63	538	7092	29576	29.3	1.0E-03
		V82A	52	15	1986	1844	4722	26984	3046.1	<10.0E-12
		V82A/L90M	45	17	969	1167	5614	26624	1009.0	<10.0E-12
		I84V	53	14	2161	1921	4456	26551	3504.2	<10.0E-12
		I84V/L90M	53	16	1582	1429	4914	26030	2381.3	<10.0E-12
		N88D	12	19	149	1085	6447	27288	38.1	1.1E-05
		N88D/L90M	20	19	51	210	6426	27167	0.0	1.0E+00
L90M	21	19	669	2487	5805	24803	9.1	1.0E+00		
K436 (NC-p1)	K > R	D30N	3	6	5	140	2008	32160	1.1	1.0E+00
		D30N/N88D	2	6	17	1078	1996	31222	37.3	1.7E-05
		D30N/N88D/L90M	3	6	5	187	1970	31042	3.3	1.0E+00
		I50L	10	6	16	142	2066	33324	4.5	1.0E+00
		I50V	12	6	67	505	2121	34155	33.7	1.1E-04
		V82A	11	5	416	3314	1641	29609	208.6	<10.0E-12
		V82A/L90M	12	6	252	1822	1764	29977	149.8	<10.0E-12
		I84V	6	6	263	3913	1765	28594	1.5	1.0E+00
		I84V/L90M	6	6	192	2902	1795	28511	0.4	1.0E+00
		N88D	1	6	18	1200	2000	31195	43.2	8.3E-07
		N88D/L90M	2	6	5	258	1972	31057	7.0	1.0E+00
L90M	7	6	213	2885	1762	28344	5.1	1.0E+00		

I437 (NC-p1)	I > V	D30N	6	9	9	136	3246	31062	1.4	1.0E+00
		D30N/N88D	8	9	87	1005	3168	30193	2.7	1.0E+00
		D30N/N88D/L90M	12	10	22	169	3160	29989	0.7	1.0E+00
		I50L	8	9	14	156	3369	32135	0.2	1.0E+00
		I50V	19	9	115	476	3432	32957	66.3	6.5E-12
		V82A	19	8	709	3033	2619	28779	437.4	<10.0E-12
		V82A/L90M	20	9	423	1653	2828	29062	296.9	<10.0E-12
		I84V	13	9	543	3673	2730	27739	66.1	7.1E-12
		I84V/L90M	12	9	381	2736	2817	27608	28.5	1.6E-03
		N88D	8	9	94	1120	3165	30172	4.0	1.0E+00
		N88D/L90M	10	10	27	232	3158	30009	0.1	1.0E+00
L90M	11	9	336	2784	2846	27374	5.8	1.0E+00		
L449 (p1-p6)	L > F	D30N	7	15	10	132	5240	28699	7.0	1.0E+00
		D30N/N88D	32	15	339	728	4911	28103	225.1	<10.0E-12
		D30N/N88D/L90M	41	15	76	110	5053	27758	89.4	<10.0E-12
		I50L	17	15	30	143	5414	29600	0.3	1.0E+00
		I50V	35	15	200	371	5404	30590	171.9	<10.0E-12
		V82A	10	16	364	3410	5014	25944	109.8	<10.0E-12
		V82A/L90M	10	16	200	1890	5045	26460	61.3	8.2E-11
		I84V	35	13	1416	2634	3880	26359	1337.9	<10.0E-12
		I84V/L90M	31	14	936	2053	4231	25960	617.9	<10.0E-12
		N88D	31	15	365	824	4899	28090	220.0	<10.0E-12
		N88D/L90M	38	15	96	160	5046	27780	93.1	<10.0E-12
L90M	10	16	328	2800	4801	25068	66.9	4.7E-12		
S451 (p1-p6)	S > N	D30N	26	17	36	102	5571	27130	7.3	1.0E+00
		D30N/N88D	30	17	299	710	5308	26522	115.1	<10.0E-12
		D30N/N88D/L90M	28	17	50	127	5413	26201	14.5	1.2E-02
		I50L	11	17	19	148	5776	28044	3.4	1.0E+00
		I50V	15	17	88	497	5893	28827	1.4	1.0E+00
		V82A	15	17	553	3174	5156	24606	14.3	1.0E+00
		V82A/L90M	14	17	282	1788	5273	25041	19.1	2.0E-01
		I84V	19	17	795	3309	4858	24084	16.8	7.0E-01
		I84V/L90M	18	17	560	2477	4944	23991	3.4	1.0E+00
		N88D	29	17	322	804	5310	26496	107.8	<10.0E-12
		N88D/L90M	25	17	62	183	5424	26204	10.8	1.0E+00
L90M	12	18	373	2696	5090	23632	60.0	1.6E-10		

R452 (p1-p6)	R > S	D30N	6	4	9	131	1420	33353	1.4	1.0E+00
		D30N/N88D	13	4	139	920	1290	32564	224.6	<10.0E-12
		D30N/N88D/L90M	17	4	31	150	1367	32242	74.2	<10.0E-12
		I50L	4	4	7	169	1474	34478	0.0	1.0E+00
		I50V	9	4	54	518	1455	35497	42.8	1.0E-06
		V82A	2	4	87	3808	1365	30345	37.5	1.5E-05
		V82A/L90M	3	4	64	2096	1354	30905	7.5	1.0E+00
		I84V	17	2	724	3419	711	30287	2146.6	<10.0E-12
		I84V/L90M	19	3	576	2483	826	30102	1833.7	<10.0E-12
		N88D	13	4	151	1030	1286	32545	231.8	<10.0E-12
		N88D/L90M	14	4	36	215	1369	32257	63.6	2.6E-11
L90M	2	4	53	3125	1345	29267	53.3	4.9E-09		
P453 (p1-p6)	P > L	D30N	33	31	42	86	10127	22916	0.2	1.0E+00
		D30N/N88D	66	30	671	351	9498	22651	605.9	<10.0E-12
		D30N/N88D/L90M	65	31	119	65	9830	22127	96.9	<10.0E-12
		I50L	26	31	45	130	10490	23407	2.0	1.0E+00
		I50V	60	30	326	217	10574	24269	219.7	<10.0E-12
		V82A	24	32	861	2788	9526	20609	97.8	<10.0E-12
		V82A/L90M	26	31	531	1484	9612	21071	21.6	5.5E-02
		I84V	81	24	3266	784	6975	22319	5397.7	<10.0E-12
		I84V/L90M	83	26	2507	503	7502	21778	4241.0	<10.0E-12
		N88D	64	29	731	403	9467	22657	629.2	<10.0E-12
		N88D/L90M	61	31	152	99	9823	22144	102.3	<10.0E-12
L90M	27	31	797	2127	9152	20065	20.4	1.1E-01		

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