

Supplemental Table 2 . Replicative Capacities for associating mutations within the protease and NC-p1 and p1-p6 cleavage sites

Protease Mutations	Gag	P-P	P-A	Mean P-P	Mean P-A	Median P-P	Median P-A	Std dev P-P	Std dev P-A	p-value
D30N	A431	4	118	32.9	46.0	27.3	39.0	24.7	38.3	1.0E+00
	K436	3	120	30.4	45.3	38.7	35.2	16.5	38.3	1.0E+00
	I437	8	114	26.6	46.8	29.2	39.5	23.4	38.5	1.0E+00
	L449	8	111	49.6	44.1	48.0	34.9	26.5	38.8	1.0E+00
	S451	32	84	35.3	49.1	32.6	39.5	29.5	40.8	1.0E+00
	R452	7	111	43.1	45.2	59.2	34.9	34.1	38.4	1.0E+00
	P453	39	70	45.0	42.8	38.6	37.1	36.8	34.1	1.0E+00
D30N/N88D	A431	122	852	65.1	70.3	61.2	61.2	43.3	48.4	1.0E+00
	K436	14	954	69.6	69.7	64.3	61.7	54.1	47.2	1.0E+00
	I437	80	882	73.9	69.5	56.8	62.0	55.4	46.6	1.0E+00
	L449	296	649	68.4	70.0	61.2	61.7	47.1	47.3	1.0E+00
	S451	272	622	70.2	68.3	63.7	59.0	46.5	48.7	1.0E+00
	R452	124	808	64.8	70.0	57.4	62.0	46.9	47.0	1.0E+00
	P453	590	312	70.9	65.4	61.3	60.7	48.5	43.6	1.0E+00
D30N/N88D/L90M	K436	37	125	64.9	75.1	67.2	70.6	30.4	49.3	1.0E+00
	I437	4	163	55.1	73.7	57.2	68.1	44.0	46.7	1.0E+00
	L449	19	146	80.3	72.1	77.8	68.0	58.4	45.2	1.0E+00
	S451	67	93	72.0	70.2	69.4	59.7	41.9	48.4	1.0E+00
	R452	44	110	64.9	73.9	56.9	68.0	40.8	47.6	1.0E+00
	P453	27	128	55.3	72.5	45.0	70.7	38.4	45.1	1.0E+00
	A431	103	55	67.6	76.3	54.1	70.6	46.4	46.4	1.0E+00
I50L	A431	58	81	32.9	29.6	26.0	23.2	29.2	25.0	1.0E+00
	K436	14	123	19.8	30.6	10.3	25.9	30.3	24.8	1.0E+00
	I437	13	135	28.1	30.7	23.3	58.0	26.4	48.0	1.0E+00
	L449	26	124	25.4	32.6	27.2	24.0	19.5	27.7	1.0E+00
	S451	16	128	28.9	31.6	20.2	25.8	21.8	27.2	1.0E+00
	R452	5	148	45.3	30.4	47.9	23.3	29.4	26.3	1.0E+00
	P453	40	112	27.2	32.2	22.4	25.4	22.2	27.8	1.0E+00

I50V	A431	56	485	37.4	50.9	33.5	45.2	30.7	37.2	4.3E-01
	K436	60	455	55.8	48.6	53.5	43.3	36.3	37.0	1.0E+00
	I437	104	428	49.7	49.3	47.4	43.2	34.8	37.1	1.0E+00
	L449	181	336	46.7	50.2	36.2	44.9	38.6	33.3	1.0E+00
	S451	79	449	51.5	48.9	45.1	43.4	37.6	36.7	1.0E+00
	R452	47	468	47.5	49.3	43.4	43.6	30.8	35.7	1.0E+00
	P453	295	195	49.3	49.5	43.9	37.9	34.1	42.2	1.0E+00
V82A	A431	1775	1636	37.9	46.8	31.3	38.6	30.5	35.6	3.1E-11
	K436	372	2952	41.6	41.9	33.6	33.7	33.3	33.1	1.0E+00
	I437	635	2698	42.4	41.5	36.0	33.1	32.7	33.4	1.0E+00
	L449	321	3041	40.1	42.1	32.5	34.0	32.8	33.2	1.0E+00
	S451	487	2831	44.4	41.5	37.0	33.3	33.5	33.2	1.0E+00
	R452	75	3404	36.1	42.3	29.6	34.5	32.6	33.3	1.0E+00
P453	759	2495	38.9	43.4	32.0	35.5	31.8	33.8	8.1E-02	
V82A/L90M	A431	871	1039	38.8	46.9	32.2	39.0	30.5	35.6	1.3E-04
	K436	227	1628	43.7	42.9	36.2	34.7	33.7	33.3	1.0E+00
	I437	378	1475	43.1	42.7	36.4	34.2	33.3	33.6	1.0E+00
	L449	179	1690	40.1	43.2	32.4	35.6	31.6	33.4	1.0E+00
	S451	247	1605	45.9	42.3	37.0	34.7	33.8	33.3	1.0E+00
	R452	55	1884	34.0	43.4	29.5	35.9	32.1	33.5	1.0E+00
	P453	465	1343	38.6	45.1	32.5	36.9	30.3	34.6	6.6E-02
N88D	A431	138	954	59.4	67.5	53.7	57.0	44.0	48.5	1.0E+00
	K436	15	1068	66.1	66.5	50.2	57.2	54.0	47.6	1.0E+00
	I437	87	989	69.5	66.4	54.6	57.7	55.3	47.1	1.0E+00
	L449	320	739	65.7	66.4	57.6	56.7	47.4	47.8	1.0E+00
	S451	295	709	68.4	64.0	59.7	53.2	46.0	48.9	1.0E+00
	R452	136	910	63.1	66.6	55.0	57.4	47.1	47.5	1.0E+00
	P453	646	361	68.3	61.7	57.6	56.5	49.3	43.0	1.0E+00

N88D/L90M	A431	48	181	54.3	63.8	55.9	50.6	34.4	48.8	1.0E+00
	K436	4	229	55.1	62.4	57.2	50.6	44.0	47.1	1.0E+00
	I437	24	204	67.8	61.9	48.8	50.8	57.5	45.9	1.0E+00
	L449	86	139	64.4	57.8	59.4	46.3	44.4	47.0	1.0E+00
	S451	56	162	59.7	60.4	51.8	48.2	41.0	47.6	1.0E+00
	R452	32	188	51.4	60.8	44.6	50.8	38.8	45.6	1.0E+00
	P453	134	86	60.4	62.0	46.3	54.0	47.1	45.3	1.0E+00
I84V	A431	1957	1703	39.2	44.9	31.8	36.8	31.3	35.0	1.6E-04
	K436	229	3514	35.7	42.5	28.3	34.7	29.3	33.6	1.5E-01
	I437	495	3290	43.1	41.8	37.2	33.7	31.7	33.5	1.0E+00
	L449	1276	2354	43.5	40.2	35.3	33.0	34.3	32.3	6.5E-01
	S451	703	2970	42.5	41.4	33.2	34.1	35.1	32.5	1.0E+00
	R452	649	3063	35.6	43.4	26.9	35.7	30.3	33.8	6.6E-07
I84V/L90M	P453	2948	684	41.7	42.3	33.9	34.7	33.3	33.3	1.0E+00
	A431	1439	1262	39.9	44.0	32.4	36.2	31.5	34.0	2.8E-01
	K436	167	2607	35.5	42.4	27.6	34.9	28.5	33.1	6.3E-01
	I437	347	2454	40.9	42.1	35.5	34.4	30.4	33.2	1.0E+00
	L449	837	1843	43.5	40.5	35.6	33.2	33.1	32.4	1.0E+00
	S451	491	2230	42.0	41.5	33.8	34.2	34.0	32.3	1.0E+00
	R452	517	2226	35.1	43.6	26.7	36.3	28.2	33.4	9.1E-06
L90M	P453	2255	444	41.0	45.2	33.7	36.1	32.2	34.9	1.0E+00
	A431	602	2220	36.7	60.6	27.6	49.8	32.1	46.7	<10.0E-12
	K436	189	2584	47.7	56.1	35.4	44.7	40.1	45.2	1.0E+00
	I437	305	2481	44.4	56.7	36.0	45.3	36.1	45.9	3.9E-03
	L449	297	2494	48.4	56.6	39.5	45.0	39.5	45.5	8.7E-01
	S451	330	2419	56.0	54.7	42.8	43.9	45.5	44.4	1.0E+00
	R452	50	2795	47.0	55.7	37.2	44.3	35.7	44.9	1.0E+00
P453	722	1902	49.9	57.3	38.5	46.5	42.6	45.5	2.8E-03	

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