

Table S3: Mutation assay: deep sequence

❖ Sample A: Control original NL4-3 viral total RNA

❖ Sample B: aptamer-stick-siRNA treated mouse J483

When condition: threshold = 1, true (1), mutation >1%

Tat/rev domain (yellow): 4 mutation above 1%

HIV-1 envelop signal domain (grey): 1 mutation above 1%

Gp120 domain (pink) : 6 mutation above 2%

Gp41 domain (blue): 5 mutation above 1%

pos	Ref	B Mutation	A reference	Mutation%	Low	Fold	mutation_coverage	Quality	balance	threshold	indel	True/False
5821	G	T	A	2.03%	1	3.77	25406	high	yes	1	no	1
5837	C	T	A	2.40%	1	2.02	33366	high	yes	1	no	1
6078	A	T	C	4.10%	1	3.97	357	high	yes	1	no	1
6138	C	A	T	1.90%	1	2.15	103	high	yes	1	no	1
6232	G	T	A	2.70%	1	2.54	241	high	yes	1	no	1
6625	G	C	T	3.10%	1	2.38	1897	high	yes	1	no	1
6757	T	G	A	2.29%	1	2.26	2135	high	yes	1	no	1
6874	G	T	A	2.76%	1	2.90	3458	high	yes	1	no	1
6921	C	T	A	5.72%	1	4.31	6342	high	yes	1	no	1
7410	C	T	A	2.91%	1	2.64	1174	high	yes	1	no	1
7651	G	A	T	2.11%	1	2.51	528	high	yes	1	no	1
7829	G	A	T	1.88%	1	2.76	367	high	yes	1	no	1
8026	C	A	T	2.05%	1	2.52	1585	high	yes	1	no	1
8035	T	C	G	4.99%	1	3.77	4397	high	yes	1	no	1
8041	T	A	G	10.34%	1	4.31	9547	high	yes	1	no	1
8291	G	T	A	1.70%	1	2.97	2903	high	yes	1	no	1

Tat/rev site I domain:
5982-6008

Gp120 domain:
6320...7747 nt

Gp41 domain:
7796...8782 nt