

Supplementary materials

Name	GGGATTGGGGGGTACAGTGCAGGG	Pct	Count
cluster 0	70.03%	4430
cluster 1A.....	9.8%	620
cluster 2A	4.41%	279
cluster 3A.....	2.97%	188
cluster 4T.....	1.77%	112
cluster 5A.....	1.5%	95
cluster 6C.....	0.87%	55
cluster 7C.....A	0.68%	43
cluster 8A.....A	0.63%	40
cluster 9A.....	0.6%	38
cluster 10AC.....	0.33%	21
cluster 11T.....	0.28%	18
cluster 12AC...T.....	0.28%	18
cluster 13G.....	0.27%	17
cluster 14AC..T.....	0.27%	17
cluster 15C.....	0.25%	16
cluster 16A..T.....	0.24%	15
cluster 17R.....	0.24%	15
cluster 18R.....	0.24%	15
cluster 19T.....	0.22%	14
cluster 20T.....A	0.22%	14
cluster 21A.....A	0.17%	11
cluster 22Y.....	0.14%	9
cluster 23A..T.....	0.13%	8
cluster 24R.....	0.11%	7
cluster 25AA.....	0.09%	6
cluster 26T.....	0.09%	6
cluster 27G.....	0.09%	6
cluster 28C.....	0.08%	5
cluster 29	..A.....	0.08%	5
cluster 30A...C.....	0.08%	5
cluster 31C.....	0.08%	5
cluster 32A.....A	0.06%	4
cluster 33AT..T.....	0.06%	4
cluster 34AT...T.....	0.06%	4
cluster 35R.....	0.05%	3
cluster 36C.....	0.05%	3
cluster 37AC..T.C.....	0.05%	3
cluster 38	...C.....	0.05%	3
cluster 39R.....A	0.05%	3
cluster 40A.....C.....	0.05%	3
cluster 41A....T.....	0.05%	3
cluster 42C.....	0.03%	2
cluster 43T.....A	0.03%	2
cluster 44AA...C.....	0.03%	2
cluster 45C.....	0.03%	2
cluster 46A.....A	0.03%	2
cluster 47A.....C.....	0.03%	2
cluster 48A.A.....	0.03%	2
cluster 49AA.....A	0.03%	2
cluster 50A.....R	0.03%	2
cluster 51T.....	0.03%	2

Figure S1 - Los Alamos Database. Region of the HIV-1 genome corresponding to the TaqMan probe.

Clusters with frequently occurring single mutations are highlighted in a frame.

Name	GGGATTGGGGGTACAGTGCAGGG	Pct	Count
cluster 0	81.03%	974
cluster 1A.....	6.07%	73
cluster 2A.....	2.41%	29
cluster 3A.....	2.16%	26
cluster 4C.....	1.25%	15
cluster 5T.....	0.75%	9
cluster 6T.....	0.58%	7
cluster 7A.....	0.42%	5
cluster 8R.....	0.42%	5
cluster 9R.....	0.42%	5
cluster 10Y.....	0.42%	5
cluster 11A.....A	0.42%	5
cluster 12C.....	0.33%	4
cluster 13R.....	0.33%	4
cluster 14AA.....A	0.25%	3
cluster 15Y.....	0.17%	2
cluster 16A.....A	0.17%	2
cluster 17AC.....	0.17%	2
cluster 18R.....	0.17%	2
cluster 19A.....	0.08%	1
cluster 20G.....G.....	0.08%	1
cluster 21T.....	0.08%	1
cluster 22W.....	0.08%	1
cluster 23N.....	0.08%	1
cluster 24A...T.....	0.08%	1
cluster 25G.....	0.08%	1
cluster 26C.....	0.08%	1
cluster 27R.....R	0.08%	1
cluster 28C...T.....	0.08%	1
cluster 29	.RK.....WA.R...S...A	0.08%	1
cluster 30R...S.....	0.08%	1
cluster 31G.....	0.08%	1
cluster 32	.A.....	0.08%	1
cluster 33G.....	0.08%	1
cluster 34	R.....A.....	0.08%	1
cluster 35R...C.....	0.08%	1
cluster 36	.R.....	0.08%	1
cluster 37K.....	0.08%	1
cluster 38A...W.....	0.08%	1
cluster 39T.TA.AG.A.TG.A.AA.	0.08%	1
cluster 40AC...T.....	0.08%	1
cluster 41A.....	0.08%	1
cluster 42A...C.....	0.08%	1
cluster 43A...T.....	0.08%	1

Figure S2 - NCBI Database (Russian isolates). Region of the HIV-1 genome corresponding to the TaqMan probe.

Clusters with frequently occurring single mutations are highlighted in a frame.



	3'  5'		
Name	CAGCAGTACAAATGGCAGTATTCATYCACA	Pct(%)	Count
cluster 0	73.07	4624
cluster 1G.....	6.62	419
cluster 2G.....	3.05	193
cluster 3G.....	1.96	124
cluster 4C.....	1.6	101
cluster 5T.....	1.44	91
cluster 6TG.....	1.02	64
cluster 7A.....	0.82	52
cluster 8C.....	0.68	43
cluster 9G.....	0.47	30
cluster 10G.....	0.41	26
cluster 11T.....	0.4	25
cluster 12C.....	0.34	22
cluster 13T.....	0.34	21
cluster 14	...T.....	0.32	20
cluster 15	.G.....	0.31	20
cluster 16	...G.....	0.3	19
cluster 17G.....G.....	0.29	18
cluster 18T.....	0.26	17
cluster 19T.....	0.26	17
cluster 20C.....	0.22	14
cluster 21G..G.....	0.19	12
cluster 22G.....A.....	0.17	11
cluster 23	.T.....	0.17	11
cluster 24R.....	0.15	10
cluster 25GC.....	0.13	8
cluster 26R.....	0.11	7
cluster 27Y.....	0.11	7
cluster 28R.....	0.11	7
cluster 29T.....	0.11	7
cluster 30G.....G.....	0.11	7
cluster 31G.....C.....	0.1	6
cluster 32C.....	0.08	5
cluster 33G.....G..T.....	0.08	5
cluster 34A.....	0.08	5
cluster 35R.....	0.08	5
cluster 36A.....	0.08	5
cluster 37	.R.....	0.08	5
cluster 38T.....	0.08	5
cluster 39	...C.....	0.07	4
cluster 40A.....	0.07	4
cluster 41	.C.....	0.07	4
cluster 42Y.....	0.07	4
cluster 43C..TG.....	0.06	4
cluster 44G.....	0.05	3
cluster 45G.....	0.05	3
cluster 46T.....	0.05	3
cluster 47	.G.....G.....	0.05	3
cluster 48C.....	0.05	3
cluster 49G.....C.....	0.05	3
cluster 50G.....C.....	0.05	3
cluster 51	...A.....	0.05	3
cluster 52M.....	0.05	3
cluster 53W.....	0.05	3
cluster 54	.A.....	0.05	3
cluster 55G.....G.....	0.05	3
cluster 56G.....G.....	0.05	3
cluster 57G.....T.....	0.05	3
cluster 58T..G.....	0.05	3
cluster 59G.....TG.....	0.05	3
cluster 60T.....TG.....	0.05	3
cluster 61	.W.....	0.04	2

Figure S3 - Los Alamos Database. Region of the HIV-1 genome corresponding to the forward primer.

3'  5'

Name	CAGCAGTACAAATGGCAGTATTCATYCACA	Pct	Count
cluster 0	76.36	921
cluster 1G.....	6.97	84
cluster 2G.....	1.74	21
cluster 3T.....	1.32	16
cluster 4G.....	1.08	13
cluster 5	...G.....	1.0	12
cluster 6R.....	0.99	12
cluster 7G.....	0.83	10
cluster 8A.....	0.83	10
cluster 9R.....	0.83	10
cluster 10C.....	0.75	9
cluster 11R.....	0.5	6
cluster 12	...C.....	0.41	5
cluster 13	...T.....	0.33	4
cluster 14C.....	0.33	4
cluster 15Y.....	0.33	4
cluster 16	.G.....	0.25	3
cluster 17TG.....	0.25	3
cluster 18W.....	0.17	2
cluster 19C.....	0.17	2
cluster 20R.....	0.17	2
cluster 21T.....G..C.....	0.17	2
cluster 22T.....	0.17	2
cluster 23G.....T.....	0.17	2
cluster 24	...R.....	0.17	2
cluster 25T.....	0.17	2
cluster 26	...T.....	0.17	2
cluster 27W.....	0.17	2
cluster 28	...T....TG....T....T...C..	0.08	1
cluster 29W.....	0.08	1
cluster 30	.W.....	0.08	1
cluster 31	...G..C.....	0.08	1
cluster 32T.....	0.08	1
cluster 33R.....	0.08	1
cluster 34G.....	0.08	1
cluster 35	...C...G.....	0.08	1
cluster 36	...AC.....	0.08	1
cluster 37	.R.....	0.08	1
cluster 38R.T.....	0.08	1
cluster 39G.....A.....	0.08	1
cluster 40	.T.....	0.08	1
cluster 41MA.....	0.08	1
cluster 42	...R.....	0.08	1
cluster 43	...T.....T.....	0.08	1
cluster 44R.....	0.08	1
cluster 45W.....	0.08	1
cluster 46G....A.....	0.08	1
cluster 47R.....M.....	0.08	1
cluster 48T.....	0.08	1
cluster 49	Y.....	0.08	1
cluster 50C..T.....	0.08	1
cluster 51M.....	0.08	1
cluster 52	...G.....G.....	0.08	1
cluster 53	.G..G.....	0.08	1
cluster 54M.....	0.08	1
cluster 55Y.....	0.08	1
cluster 56G..G.....	0.08	1
cluster 57G.....M...	0.08	1
cluster 58R..G.....	0.08	1
cluster 59	...G.....S...	0.08	1
cluster 60	...M.....	0.08	1
cluster 61R..R.....	0.08	1

Figure S4 - NCBI Database (Russian isolates). Region of the HIV-1 genome corresponding to the forward primer.

	3'←	5'		
Name	TGGAAAGGTGAAGGGCAGTRGTAATACAGG	Pct(%)	Count	
cluster 0A.	62.13	3929	
cluster 1	13.36	845	
cluster 2C.....A.	4.36	276	
cluster 3G.....A.	4.13	261	
cluster 4A.....A.	2.17	137	
cluster 5G.....A.	1.83	116	
cluster 6T..A.	1.61	102	
cluster 7C.....A.	1.05	66	
cluster 8G..A.....C.....A.	0.65	41	
cluster 9G.....	0.57	36	
cluster 10G.....	0.55	35	
cluster 11T.....A.	0.34	21	
cluster 12A.....	0.31	20	
cluster 13AC	0.30	19	
cluster 14C.....	0.27	17	
cluster 15A.....C.....A.	0.19	12	
cluster 16A.....G.....A.	0.17	11	
cluster 17R.....	0.16	10	
cluster 18C..A.	0.16	10	
cluster 19G..A.....A.	0.16	10	
cluster 20A.....C..A.	0.16	10	
cluster 21T.....	0.14	9	
cluster 22T.....A.	0.13	8	
cluster 23G.....G.....A.	0.13	8	
cluster 24R.....A.	0.13	8	
cluster 25T.....A.	0.13	8	
cluster 26AT	0.12	8	
cluster 27A.....A.	0.11	7	
cluster 28C.....	0.11	7	
cluster 29C.....A.	0.11	7	
cluster 30A.A.	0.09	6	
cluster 31G.....A.	0.09	6	
cluster 32C.....A.	0.09	6	
cluster 33G.....C.....A.	0.08	5	
cluster 34	...G.....A.	0.08	5	
cluster 35C.....	0.07	4	
cluster 36A.....A.	0.07	4	
cluster 37A.....	0.06	4	
cluster 38	C.....A.	0.06	4	
cluster 39G.....A.	0.06	4	
cluster 40M.....A.	0.06	4	
cluster 41R.....A.	0.06	4	
cluster 42T.....	0.06	4	
cluster 43G.....AC	0.06	4	
cluster 44G..A.....T.....A.	0.06	4	
cluster 45G.....A.	0.05	3	
cluster 46W.....A.	0.05	3	
cluster 47T.....	0.05	3	
cluster 48A.....A.	0.05	3	
cluster 49G..T..A.	0.05	3	
cluster 50R.....A.	0.05	3	
cluster 51T.....C.....A.	0.05	3	
cluster 52T.....A.	0.05	3	
cluster 53M..A.	0.05	3	
cluster 54R..A.....C.....A.	0.05	3	
cluster 55G.....C.....A.	0.05	3	
cluster 56	...G.....A.	0.05	3	
cluster 57C.....C.....A.	0.04	2	
cluster 58A.....	0.03	2	
cluster 59A..G.....	0.03	2	
cluster 60	W.....A.	0.03	2	
cluster 61T.....A.	0.03	2	

Figure S5 - Los Alamos Database. Region of the HIV-1 genome corresponding to the reverse primer.

	3' ← 5'		
Name	TGGAAAGGTGAAGGGGCAGTRGTAATACAGG	Pct	Count
cluster 0	76.52	896
cluster 1A.	12.64	148
cluster 2G.....	3.08	36
cluster 3G.....	1.28	15
cluster 4G.....A.	1.11	13
cluster 5G.....A.	0.34	4
cluster 6A.....	0.34	4
cluster 7R.....	0.34	4
cluster 8C.....	0.26	3
cluster 9C.....	0.26	3
cluster 10A.....	0.26	3
cluster 11R.....	0.26	3
cluster 12R.....	0.18	2
cluster 13	...G.....	0.17	2
cluster 14T....	0.17	2
cluster 15Y.....	0.17	2
cluster 16C....A.	0.17	2
cluster 17T..A.	0.17	2
cluster 18R.....	0.17	2
cluster 19G.G.....A.	0.09	1
cluster 20A..G.....A.	0.09	1
cluster 21	..A.....	0.09	1
cluster 22G.....	0.09	1
cluster 23K.....	0.09	1
cluster 24M....	0.09	1
cluster 25M.....	0.09	1
cluster 26K.....	0.09	1
cluster 27C.....	0.09	1
cluster 28R.K.....	0.09	1
cluster 29GA.	0.09	1
cluster 30T.....	0.09	1
cluster 31GMK....	0.09	1
cluster 32M..A.	0.09	1
cluster 33R.....R.	0.09	1
cluster 34C.G..A.	0.09	1
cluster 35T.....A.	0.09	1
cluster 36R.....A.	0.09	1
cluster 37R....A.	0.09	1
cluster 38	...G.....G.....	0.09	1
cluster 39C....	0.09	1
cluster 40	..R.....RR	0.09	1
cluster 41C.G...G.....	0.09	1
cluster 42A.....AA	0.09	1
cluster 43AC	0.09	1

Figure S6 - NCBI Database (Russian isolates). Region of the HIV-1 genome corresponding to the reverse primer.

Table S1. Quantitative results obtained in Real-Time PCR and digital PCR for DNA constructs

	ddPCR/Bla		PCR/HIV		
Name	Copies/ml	Copies/ml, mean	Copies/ml	Copies/ml, mean	HIV PCR Copies/ml, mean / <u>BLA</u> <u>ddPCR Copies/ml, mean</u>
mut 1	1.96E+04	2.21E+04	296	233	0.01
	2.48E+04		112		
	2.18E+04		291		
mut 2	2.16E+04	2.41E+04	1.34E+04	1.33E+04	0.55
	2.50E+04		1.28E+04		
	2.56E+04		1.37E+04		
			1.23E+04	1.22E+04	0.51
			1.35E+04		
			1.11E+04		
			1.24E+04	1.17E+04	0.49
			1.20E+04		
			1.08E+04		
			1.19E+04	1.22E+04	0.50
mut 3	2.58E+04	2.48E+04	1.27E+04	1.34E+04	0.54
	2.10E+04		1.38E+04		
	2.76E+04		1.36E+04		
			1.53E+04	1.45E+04	0.59
			1.32E+04		
			1.52E+04		
			1.66E+04	1.53E+04	0.62
			1.45E+04		
			1.48E+04		
			1.32E+04	1.30E+04	0.52
mut 4	2.96E+04	2.60E+04	8.56E+03	9.18E+03	0.35
	2.12E+04		1.09E+04		
	2.72E+04		8.32E+03		
			8.15E+03	9.55E+03	0.37
			9.94E+03		
			1.07E+04		
			1.03E+04	8.96E+03	0.34
			8.26E+03		
			8.45E+03		
			8.82E+03	7.50E+03	0.29
mut 5	2.78E+04	2.43E+04	2.54E+04	2.63E+04	1.08
	2.38E+04		2.55E+04		
	2.12E+04		2.82E+04		
			3.54E+04	3.31E+04	1.36
			3.13E+04		
			3.26E+04		
			2.88E+04	2.79E+04	1.15

			2.61E+04		
			2.90E+04		
			2.65E+04	2.65E+04	1.09
			2.47E+04		
			2.85E+04		
mut 6	2.10E+04	2.44E+04	3.54E+04	3.12E+04	1.28
	2.68E+04		2.71E+04		
	2.54E+04		3.17E+04		
			3.48E+04	3.20E+04	1.31
			3.08E+04		
			3.05E+04		
			2.84E+04	3.07E+04	1.26
			3.56E+04		
			2.87E+04		
			2.92E+04	2.75E+04	1.13
			2.52E+04		
			2.83E+04		
mut 7	3.12E+04	2.87E+04	3.35E+04	3.04E+04	1.06
	2.76E+04		2.88E+04		
	2.72E+04		2.90E+04		
			3.49E+04	3.59E+04	1.25
			3.81E+04		
			3.47E+04		
			3.06E+04	3.17E+04	1.11
			2.87E+04		
			3.63E+04		
			2.69E+04	2.57E+04	0.89
			2.74E+04		
			2.30E+04		
mut 8	2.82E+04	2.77E+04	9.53E+03	1.04E+04	0.38
	2.90E+04		1.17E+04		
	2.60E+04		1.02E+04		
			1.10E+04	1.14E+04	0.41
			1.12E+04		
			1.22E+04		
			1.20E+04	1.21E+04	0.44
			1.29E+04		
			1.15E+04		
			1.17E+04	1.05E+04	0.38
			8.26E+03		
			1.21E+04		
K+	2.84E+04	3.11E+04	2.81E+04	2.40E+04	0.77
	3.20E+04		2.36E+04		
	3.30E+04		2.10E+04		
			2.43E+04	3.17E+04	1.02
			4.63E+04		
			2.83E+04		
			1.88E+04	2.50E+04	0.80
			2.08E+04		
			3.98E+04		
			2.24E+04	2.16E+04	0.70

			2.23E+04		
			2.03E+04		