Whole Genome HIV-1 Genotyping Report (RUO)

DeepChek® Whole Genome HIV-1 analysis summary

Sample information

Viral Load	
Viral Load Date	
Viral Load Method	
Report id	102-95dbb46f-fbd2-11ed-bd7c-0242ac1f0002

Sample ID	Test 1
Alternative ID	
Sample type	Plasma
Sample date	26/05/2023
Input	

P17, P24, P7, PROT, RT, INT, GP120, GP41 :
HIVWG1_S1_L001_R1_001.fastq.gz
HIVWG1_S1_L001_R2_001.fastq.gz
=> 90.69% of the 3788170 initial reads mapped to HIV organism

Comments

NGS details

Date of sequencing	26/05/2023
NGS Method	DeepChek® Assay (ABL)
Assay version	
Plate ID	
Cartridge S/N	
Reagent expiration date	
Notes	

DeepChek®- analysis details

Sequencing platform	Illumina - MiniSeq
Processing software version	Missing data
Processing started date	26/05/2023 16:35:13
Processing finished date	
Coverage	
Matrix	1→132 (aa)
Capside	1→231 (aa)
Nucleocapsid	1→55 (aa)
Protease	1→99 (aa)
Reverse Transcriptase	1→440 (aa)
Integrase	1→289 (aa)
Glycoprotein 120 (or V3 loop)	1→135,153→511 (aa)
Glycoprotein 41	1→231,236→238,241,243,253,298 (aa)

DeepChek®-HIV software version	2.0
DeepChek®-HIV expert system	2.3
DeepChek®-HIV algorithms version	13.1

HIVDb (9.4 12-2022)

Classification of mutations of interest HIVDb (mutation score ≠ 0)

DeepChek® Whole Genome HIV-1 Drug Resistance Analysis

HIV Nucleoside Reverse Transcriptase Inhibitors

	Algorithm	Sanger	NGS	Threshold
Abacavir	HIVDb	S	S	S
Didanosine	HIVDb	S	S	S
Emtricitabine	HIVDb	S	S	S
Lamivudine	HIVDb	S	S	S
Stavudine	HIVDb	S	S	S
Tenofovir	HIVDb	S	S	S
Zidovudine	HIVDb	S	S	S

HIVDb	
S	Susceptible (S) Potential low-level resistance (PLLR)
I	Low-level resistance (LLR) Intermediate resistant (IR)
R	High-level resistance (HLR)

DeepChek® Whole Genome HIV-1 Drug Resistance Analysis

HIV Non-Nucleoside Reverse Transcriptase Inhibitors

	Algorithm	Sanger	NGS	Threshold
Doravirine	HIVDb	S	S	S
Efavirenz	HIVDb	S	S	S
Etravirine	HIVDb	I	I	I
Nevirapine	HIVDb	I	I	I
Rilpivirine	HIVDb	I	I	I

HIVDb	
S	Susceptible (S) Potential low-level resistance (PLLR)
I	Low-level resistance (LLR) Intermediate resistant (IR)
R	High-level resistance (HLR)

DeepChek® Whole Genome HIV-1 Drug Resistance Analysis

HIV Protease Inhibitors

	Algorithm	Sanger	NGS	Threshold
Atazanavir/r	HIVDb	S	S	S
Darunavir/r	HIVDb	S	S	S
Fosamprenavir/r	HIVDb	S	S	S
Indinavir/r	HIVDb	S	S	S
Lopinavir/r	HIVDb	S	S	S
Nelfinavir	HIVDb	S	S	S
Saquinavir/r	HIVDb	S	S	S
Tipranavir/r	HIVDb	S	S	S

HIVDb	
S	Susceptible (S) Potential low-level resistance (PLLR)
I	Low-level resistance (LLR) Intermediate resistant (IR)
R	High-level resistance (HLR)

DeepChek® Whole Genome HIV-1 Drug Resistance Analysis

HIV Integrase Inhibitors

	Algorithm	Sanger	NGS	Threshold
Bictegravir	HIVDb	S	S	S
Cabotegravir	HIVDb	S	S	I
Dolutegravir	HIVDb	S	S	I
Elvitegravir	HIVDb	S	S	I
Raltegravir	HIVDb	S	S	I

HIVDb	
S	Susceptible (S) Potential low-level resistance (PLLR)
I	Low-level resistance (LLR) Intermediate resistant (IR)
R	High-level resistance (HLR)

DeepChek® Whole Genome HIV-1 Subtyping

Matrix

	Subtype	Similarity (1)
NGS	42_BF	92.05

Capside

	Subtype	Similarity (1)
NGS	B	94.23

Nucleocapsid

	Subtype	Similarity (1)
NGS	B	91.52

Protease

	Subtype	Similarity (1)
NGS	B	93.6

Reverse Transcriptase

	Subtype	Similarity (1)
NGS	B	93.5

Integrase

	Subtype	Similarity (1)
NGS	B	95.6

Glycoprotein 120 (or V3 loop)

	Subtype	Similarity (1)
NGS	B	81.74

Glycoprotein 41

	Subtype	Similarity (1)
NGS	B	90.37

(1) Similarity reflects the percentage of aligned bases that are identical to the closest reference sequence.

Subtyping determination performed through homology testing of a 20% consensus sequence generated from all the reads mapped to this particular region and compared to an updated set of reference sequences.

DeepChek® Whole Genome HIV-1 Mutation Analysis

HIV Matrix mutations

Position	Mutation	Sanger	NGS	Threshold	Prevalence %	Q-Score
8	L→I	✓	✓	✓	94.49	34
9	S→R		✓	✓	6.07	22
18	K→R	✓	✓	✓	70.25	33
26	K→S	✓	✓	✓	89.97	32
30	K→R	✓	✓	✓	95.17	34
38	S→R			✓	3.02	21
58	R→K		✓	✓	11.18	33
76	R→K	✓	✓	✓	95.46	34
84	T→V	✓	✓	✓	92.17	33
91	R→K	✓	✓	✓	94.53	34
93	E→D	✓	✓	✓	94.63	34
95	K→L			✓	3.06	30
	K→R	✓	✓	✓	94.45	33
109	N→D			✓	3.96	32
	N→S		✓	✓	5.72	33
111	S→N			✓	3.16	31
	S→R		✓	✓	5.13	22
	S→del		✓	✓	5.81	
112	K→del		✓	✓	6.67	
113	K→N	✓	✓	✓	89.87	34
114	K→N			✓	4.27	30
116	Q→K	✓	✓	✓	86.8	33
117	Q→insX		✓	✓	5.94	28
118	A→insA	✓	✓	✓	62.29	34
119	A→insX			✓	4.61	26
124	H→N	✓	✓	✓	92.77	34
125	S→N	✓	✓	✓	91.77	34
126	N→S	✓	✓	✓	93.03	33

Subtype B K03455 was used as the reference sequence for the alignment (using BWA v0.7.15 alignment tool).

Mutations of interest based on HIVDb v9.4 (mutation score ≠ 0) (Bold red text)

Insufficient number of sequences to guarantee, at the 99% confidence level, that all mutations with the given threshold frequency have been found at that position.

DeepChek® Whole Genome HIV-1 Mutation Analysis

HIV Capsid mutations

Position	Mutation	Sanger	NGS	Threshold	Prevalence %	Q-Score
6	I→L	✓	✓	✓	93.6	32
12	H→Q			✓	3.23	22
27	V→I	✓	✓	✓	88.07	34
41	S→T	✓	✓	✓	94.89	34
71	E→D	✓	✓	✓	93.34	33
83	V→L		✓	✓	5.73	31
84	H→Q			✓	3.09	21
102	S→R			✓	4.87	21
107	T→S		✓	✓	16	32
109	S→R			✓	3.47	22
120	N→S		✓	✓	13.04	33
121	N→T	✓	✓	✓	77.64	32
166	D→E			✓	3.81	21
168	F→L			✓	3.32	23
200	T→R			✓	4.53	23
	T→S	✓	✓	✓	91.21	33
225	G→R			✓	3.23	21
	G→S	✓	✓	✓	92.37	32

Subtype B K03455 was used as the reference sequence for the alignment (using BWA v0.7.15 alignment tool).

Mutations of interest based on HIVDb v9.4 (mutation score ≠ 0) (Bold red text)

Insufficient number of sequences to guarantee, at the 99% confidence level, that all mutations with the given threshold frequency have been found at that position.

DeepChek® Whole Genome HIV-1 Mutation Analysis

HIV NucleoCapsid mutations

Position	Mutation	Sanger	NGS	Threshold	Prevalence %	Q-Score
1	M→insX			✓	3.01	27
3	R→K	✓	✓	✓	91.6	34
10	R→K	✓	✓	✓	92.72	34
11	K→R	✓	✓	✓	93.29	32
12	I→T	✓	✓	✓	93.03	33
24	T→I	✓	✓	✓	37.68	33
	T→V	✓	✓	✓	55.92	33
41	K→R	✓	✓	✓	60.22	33

Subtype B K03455 was used as the reference sequence for the alignment (using BWA v0.7.15 alignment tool).

Mutations of interest based on HIVDb v9.4 (mutation score ≠ 0) (Bold red text)

Insufficient number of sequences to guarantee, at the 99% confidence level, that all mutations with the given threshold frequency have been found at that position.

DeepChek® Whole Genome HIV-1 Mutation Analysis

HIV Reverse Transcriptase mutations

Position	Mutation	Sanger	NGS	Threshold	Prevalence %	Q-Score
3	S→R			✓	3.73	22
14	P→T			✓	3.12	22
16	M→I			✓	3.05	23
19	P→T			✓	3.08	22
25	P→T			✓	3.43	22
27	T→K			✓	3.32	22
35	V→T	✓	✓	✓	92.45	34
39	T→A	✓	✓	✓	92.16	33
49	K→N			✓	3.34	30
52	P→T			✓	3.97	22
54	N→K			✓	3.67	23
55	P→T			✓	3.17	23
57	N→K			✓	3.39	23
59	P→T			✓	3.06	23
60	V→I	✓	✓	✓	94.56	34
68	S→R			✓	3.45	21
87	F→L			✓	3.05	24
102	K→R			✓	3.2	31
106	**V→I**	✓	✓	✓	89.23	34
122	E→K	✓	✓	✓	94.95	34
123	D→E	✓	✓	✓	93.93	34
135	I→M		✓	✓	12.85	34
	I→T		✓	✓	5.55	32
142	I→V	✓	✓	✓	90.55	32
144	Y→*			✓	3.25	23
162	S→R			✓	4.99	22
175	N→K			✓	3.39	23
177	D→G		✓	✓	18.84	32
179	**V→D**	✓	✓	✓	91.3	33
181	Y→*			✓	3.55	23
195	I→L			✓	3.04	27
211	R→K	✓	✓	✓	91.93	33
214	L→F	✓	✓	✓	91.26	33
221	H→Q			✓	3.07	22
224	E→D			✓	3.29	22
235	H→Q			✓	3.37	22
245	V→K	✓	✓	✓	93.5	34
268	S→R			✓	4.7	22
272	P→A	✓	✓	✓	95.15	33
277	R→K	✓	✓	✓	93.31	34
281	K→R			✓	4.83	33
286	T→A	✓	✓	✓	93.54	32
292	V→I		✓	✓	11.55	33
293	I→V	✓	✓	✓	92.9	33
329	I→L	✓	✓	✓	91.88	33
335	G→R			✓	3.75	22
	G→S	✓	✓	✓	90.49	32

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DeepChek® Whole Genome HIV-1 Mutation Analysis

HIV Reverse Transcriptase mutations

Position	Mutation	Sanger	NGS	Threshold	Prevalence %	Q-Score
339	Y→*			✓	3.02	23
342	Y→*			✓	3.15	23
344	E→D	✓	✓	✓	85.38	33
346	F→Y		✓	✓	5.32	33
356	R→K	✓	✓	✓	94.03	34
359	G→R			✓	3.75	21
	G→S	✓	✓	✓	90.75	33
360	A→N	✓	✓	✓	83.27	33
	A→T		✓	✓	9.5	31
365	V→I	✓	✓	✓	95.08	34
376	T→A	✓	✓	✓	92.41	32
379	S→R			✓	3.17	22
381	V→E			✓	3	23
386	T→I	✓	✓	✓	93.45	33
390	K→R	✓	✓	✓	93.05	34
402	W→*			✓	3.05	28
	W→R			✓	3.36	22
431	K→T	✓	✓	✓	93.58	33
432	E→D		✓	✓	6.89	28
435	V→A		✓	✓	8.09	33
	V→I			✓	3.01	28
	V→L		✓	✓	9.33	32
	V→M	✓	✓	✓	76.29	34

Subtype B K03455 was used as the reference sequence for the alignment (using BWA v0.7.15 alignment tool).

Mutations of interest based on HIVDb v9.4 (mutation score ≠ 0) (Bold red text)

Insufficient number of sequences to guarantee, at the 99% confidence level, that all mutations with the given threshold frequency have been found at that position.

DeepChek® Whole Genome HIV-1 Mutation Analysis

HIV Protease mutations

Position	Mutation	Sanger	NGS	Threshold	Prevalence %	Q-Score
3	V→I	✓	✓	✓	92.63	33
12	T→P	✓	✓	✓	94.77	33
14	K→R	✓	✓	✓	94.14	33
16	G→E	✓	✓	✓	87.92	33
35	E→D	✓	✓	✓	91.09	33
37	S→Y	✓	✓	✓	91.13	34
41	R→K	✓	✓	✓	94.82	34
62	I→V	✓	✓	✓	92.78	33
63	L→A	✓	✓	✓	93.63	33
68	G→E	✓	✓	✓	91.04	34
71	A→T	✓	✓	✓	93.58	34
72	I→V	✓	✓	✓	93.68	34
77	V→I	✓	✓	✓	95.33	34
93	I→L	✓	✓	✓	93.92	33

Subtype B K03455 was used as the reference sequence for the alignment (using BWA v0.7.15 alignment tool).

Mutations of interest based on HIVDb v9.4 (mutation score ≠ 0) (Bold red text)

Insufficient number of sequences to guarantee, at the 99% confidence level, that all mutations with the given threshold frequency have been found at that position.

DeepChek® Whole Genome HIV-1 Mutation Analysis

HIV Integrase mutations

Position	Mutation	Sanger	NGS	Threshold	Prevalence %	Q-Score
10	D→E	✓	✓	✓	93.19	33
17	S→N		✓	✓	11.23	33
24	S→R			✓	4.42	22
39	S→R			✓	3.19	21
57	S→R			✓	4.02	22
72	V→I	✓	✓	✓	93.68	34
81	S→R			✓	4.36	21
101	L→I	✓	✓	✓	94.31	34
112	T→V	✓	✓	✓	85.99	33
119	S→R			✓	3.13	21
123	G→S	✓	✓	✓	93.48	33
124	A→T	✓	✓	✓	93.12	33
127	R→K	✓	✓	✓	93.91	33
132	W→R			✓	3.29	22
136	K→T		✓	✓	9.46	33
144	N→K			✓	3.44	22
147	S→R			✓	4.92	21
184	N→K			✓	3.29	23
195	S→R			✓	4.16	21
201	V→I	✓	✓	✓	93.54	34
206	T→S	✓	✓	✓	91.47	33
222	N→K			✓	3.32	22
223	F→L			✓	4.13	21
225	V→D			✓	3	21
230	**S→R**			✓	3.85	21
232	N→D	✓	✓	✓	89.15	32
	N→E			✓	3.83	21
255	S→R			✓	4.48	22
256	D→E	✓	✓	✓	89.61	33
280	C→R			✓	4.5	22
	C→S	✓	✓	✓	91.09	33
283	S→R			✓	4.93	22

Subtype B K03455 was used as the reference sequence for the alignment (using BWA v0.7.15 alignment tool).

Mutations of interest based on HIVDb v9.4 (mutation score ≠ 0) (Bold red text)

Insufficient number of sequences to guarantee, at the 99% confidence level, that all mutations with the given threshold frequency have been found at that position.

DeepChek® Whole Genome HIV-1 Mutation Analysis

HIV GP120 mutations

Position	Mutation	Sanger	NGS	Threshold	Prevalence %	Q-Score
3	V→A		✓	✓	11.49	31
	V→insRGI		✓	✓	14.57	35
	V→insXXX	✓	✓	✓	59.39	34
4	K→R		✓	✓	6.39	29
5	E→K	✓	✓	✓	88.8	36
	E→insXXX			✓	4.94	33
6	K→N	✓	✓	✓	96.69	35
7	Y→C	✓	✓	✓	76.05	35
10	L→W	✓	✓	✓	97.76	35
15	W→V		✓	✓	7.78	34
	W→insMLN			✓	4.09	33
	W→insXX	✓	✓	✓	81.09	36
16	R→I	✓	✓	✓	87.26	36
	R→insXXX		✓	✓	7.4	34
19	T→M	✓	✓	✓	96.67	35
29	S→K	✓	✓	✓	94.39	34
31	T→E	✓	✓	✓	93.73	34
32	E→D	✓	✓	✓	94.5	34
33	K→N	✓	✓	✓	94.84	34
34	L→M	✓	✓	✓	93.75	34
49	T→A		✓	✓	11.98	30
	T→S	✓	✓	✓	68.31	32
62	D→R			✓	3.47	23
	D→S	✓	✓	✓	92.65	34
65	V→A	✓	✓	✓	94.47	33
72	H→Q			✓	3.32	27
77	T→I	✓	✓	✓	93.92	34
80	N→D		✓	✓	19.15	32
84	V→I			✓	3.68	29
	V→L	✓	✓	✓	93.6	33
85	V→E	✓	✓	✓	21.68	34
	V→G	✓	✓	✓	73.67	33
87	V→E		✓	✓	6.21	32
	V→G	✓	✓	✓	68.55	33
	V→K	✓	✓	✓	20.9	34
92	N→D	✓	✓	✓	92.2	33
96	W→R			✓	3.01	23
99	D→N	✓	✓	✓	94.15	34
105	H→Q		✓	✓	9.73	32
108	I→V	✓	✓	✓	93.37	34
110	S→R			✓	3.34	22
115	S→R			✓	3.77	22
128	S→R	✓	✓	✓	69.57	34
130	K→N	✓	✓	✓	96.91	35
132	T→S	✓	✓	✓	96.56	35
133	D→N	✓	✓	✓	98.88	36

DeepChek® Whole Genome HIV-1 Mutation Analysis

HIV GP120 mutations

Position	Mutation	Sanger	NGS	Threshold	Prevalence %	Q-Score
134	L→V	✓	✓	✓	98.5	35
135	K→N			✓	4.07	24
Fragment between amino acid 136 and 152 could not be amplified						
137	D→V		✓	✓	19.51	29
152	G→A	✓	✓	✓	100	37
160	N→Y	✓	✓	✓	96.92	35
161	I→V	✓	✓	✓	95.88	33
162	S→T	✓	✓	✓	94.93	33
164	S→G	✓	✓	✓	22.82	35
	S→R	✓	✓	✓	73.82	34
165	I→R	✓	✓	✓	96.41	35
166	R→K	✓	✓	✓	96.24	35
167	G→D	✓	✓	✓	95.77	35
168	K→R		✓	✓	16.04	35
169	V→H	✓	✓	✓	93.24	35
170	Q→K	✓	✓	✓	96.17	35
171	K→R			✓	3.32	33
	K→T		✓	✓	6.42	33
175	F→I		✓	✓	15.71	34
	F→L	✓	✓	✓	21.14	34
	F→V	✓	✓	✓	59.2	34
177	Y→N	✓	✓	✓	96.53	35
178	K→A		✓	✓	5.01	31
	K→D	✓	✓	✓	55.56	33
	K→Y	✓	✓	✓	33	34
181	I→L		✓	✓	12.05	34
182	I→V	✓	✓	✓	94.57	34
184	I→insKE	✓	✓	✓	74.91	35
186	N→K	✓	✓	✓	67.05	35
187	D→V	✓	✓	✓	95.28	35
188	T→N	✓	✓	✓	84.45	35
	T→S		✓	✓	12.5	35
189	T→N	✓	✓	✓	96.18	35
190	S→R		✓	✓	5.7	34
192	K→I	✓	✓	✓	96.9	35
201	I→V			✓	3.33	32
208	V→I	✓	✓	✓	94.32	34
209	S→T	✓	✓	✓	91.31	33
216	H→Y	✓	✓	✓	62.91	34
219	A→T	✓	✓	✓	92.58	32
225	I→L	✓	✓	✓	94.4	33
229	N→R	✓	✓	✓	94.8	34
230	N→D		✓	✓	5.17	31
	N→E	✓	✓	✓	90.89	34
231	K→E	✓	✓	✓	93.39	34
232	T→D		✓	✓	10.8	33
	T→N	✓	✓	✓	83.42	34

DeepChek® Whole Genome HIV-1 Mutation Analysis

HIV GP120 mutations

Position	Mutation	Sanger	NGS	Threshold	Prevalence %	Q-Score
234	N→K		✓	✓	5.89	32
238	P→Q		✓	✓	12.34	33
	P→R	✓	✓	✓	84.28	32
252	R→K	✓	✓	✓	22.44	33
264	S→R			✓	4.08	22
268	E→K	✓	✓	✓	93.52	34
270	V→I		✓	✓	6.63	34
275	V→E	✓	✓	✓	92.68	34
281	A→T	✓	✓	✓	85.09	34
283	T→I		✓	✓	10.2	33
	T→V			✓	4.82	33
290	T→E	✓	✓	✓	94.11	34
291	S→T	✓	✓	✓	94.94	35
293	E→K	✓	✓	✓	96.03	35
301	N→I		✓	✓	8.26	32
303	T→A		✓	✓	7.13	34
306	R→S	✓	✓	✓	89.95	35
310	Q→del	✓	✓	✓	97.76	
315	R→A	✓	✓	✓	96.67	34
318	V→Y	✓	✓	✓	95.31	36
319	T→A	✓	✓	✓	96.7	35
320	I→T	✓	✓	✓	93.94	35
321	G→insD	✓	✓	✓	87.26	35
322	K→I	✓	✓	✓	91.8	36
325	N→D	✓	✓	✓	88.36	34
326	M→I	✓	✓	✓	97.57	35
330	H→Q		✓	✓	5.04	31
333	I→L	✓	✓	✓	95.81	35
334	S→R		✓	✓	5.55	32
335	R→K	✓	✓	✓	98.05	35
337	K→D		✓	✓	13.52	34
	K→E	✓	✓	✓	83.72	34
339	N→M		✓	✓	5.12	34
	N→R	✓	✓	✓	90.13	34
340	N→K	✓	✓	✓	41.89	35
	N→R	✓	✓	✓	55.5	35
343	K→E		✓	✓	8.48	35
	K→N	✓	✓	✓	71	35
	K→Q			✓	3.74	35
	K→S		✓	✓	8.46	35
344	Q→L	✓	✓	✓	97.15	35
345	I→V	✓	✓	✓	96.4	35
347	S→E	✓	✓	✓	94.32	35
350	R→K	✓	✓	✓	96.47	36
352	Q→K			✓	3.51	35
353	F→Y			✓	4.34	35

DeepChek® Whole Genome HIV-1 Mutation Analysis

HIV GP120 mutations

Position	Mutation	Sanger	NGS	Threshold	Prevalence %	Q-Score
354	G→del	✓	✓	✓	97.64	
360	I→S	✓	✓	✓	81.28	34
	I→V		✓	✓	10.17	33
362	K→N		✓	✓	12.46	34
	K→S	✓	✓	✓	81.65	34
363	Q→K		✓	✓	12.4	33
	Q→N	✓	✓	✓	82.44	35
375	S→R			✓	3.55	21
389	Q→A			✓	3.5	32
	Q→P		✓	✓	8.7	31
393	S→G	✓	✓	✓	93.12	33
396	F→Y	✓	✓	✓	82.48	36
	F→insX		✓	✓	11.07	35
397	N→L	✓	✓	✓	83.13	37
398	S→A			✓	3.44	33
	S→H			✓	4.12	37
	S→N	✓	✓	✓	84.95	37
399	T→A	✓	✓	✓	82.01	36
400	W→del	✓	✓	✓	96.41	
401	S→I			✓	3.05	34
	S→del	✓	✓	✓	95.57	
402	T→del	✓	✓	✓	95.22	
403	E→del	✓	✓	✓	94.37	
404	G→del	✓	✓	✓	98.02	
405	S→T	✓	✓	✓	83.69	37
	S→del		✓	✓	14.16	
407	N→I	✓	✓	✓	90.43	37
408	T→I			✓	4.55	34
409	E→T			✓	3.75	35
411	S→N	✓	✓	✓	88.61	37
412	D→E	✓	✓	✓	93.87	36
413	T→N	✓	✓	✓	93.34	36
417	P→Q	✓	✓	✓	95.92	34
429	K→G	✓	✓	✓	91.07	32
432	K→R	✓	✓	✓	93	33
439	I→T		✓	✓	7.84	33
440	S→M		✓	✓	8.71	34
	S→Q	✓	✓	✓	82.91	34
442	Q→L	✓	✓	✓	95.3	33
444	R→K	✓	✓	✓	93.88	34
453	L→I	✓	✓	✓	88.77	34
459	G→insX		✓	✓	10.9	34
	G→insXX	✓	✓	✓	70.81	34
460	N→D			✓	4.26	34
	N→K			✓	3.08	32
	N→insX		✓	✓	6.08	34

DeepChek® Whole Genome HIV-1 Mutation Analysis

HIV GP120 mutations

Position	Mutation	Sanger	NGS	Threshold	Prevalence %	Q-Score
461	S→D	✓	✓	✓	31.42	35
	S→G		✓	✓	8.39	34
	S→N		✓	✓	10.33	35
462	N→T	✓	✓	✓	81.94	35
463	N→K		✓	✓	5.08	33
	N→T		✓	✓	9.95	35
464	E→D		✓	✓	10.13	34
	E→G	✓	✓	✓	39.26	34
	E→K	✓	✓	✓	32.71	35
	E→N		✓	✓	13.36	35
465	S→P		✓	✓	7.75	34
	S→T	✓	✓	✓	86.31	35
467	I→V	✓	✓	✓	93.67	33
471	G→A	✓	✓	✓	54.75	33
474	D→N	✓	✓	✓	94.62	34
476	R→K	✓	✓	✓	93.23	34
481	S→R			✓	4.78	22
489	V→I		✓	✓	7.71	33
496	V→I	✓	✓	✓	92.95	34

Subtype B K03455 was used as the reference sequence for the alignment (using BWA v0.7.15 alignment tool).

Mutations of interest based on HIVDb v9.4 (mutation score ≠ 0) (Bold red text)

Insufficient number of sequences to guarantee, at the 99% confidence level, that all mutations with the given threshold frequency have been found at that position.

DeepChek® Whole Genome HIV-1 Mutation Analysis

HIV GP41 mutations

Position	Mutation	Sanger	NGS	Threshold	Prevalence %	Q-Score
8	F→I		✓	✓	8.85	31
	F→L			✓	3.26	25
9	L→I		✓	✓	9.1	32
17	S→R			✓	3.36	21
23	S→L			✓	3.86	32
24	M→I	✓	✓	✓	87.94	33
	M→L		✓	✓	5.74	29
33	L→*		✓	✓	5.66	31
46	R→M	✓	✓	✓	91.77	33
49	E→D	✓	✓	✓	93.2	34
53	H→R	✓	✓	✓	96.66	33
54	L→M	✓	✓	✓	93.9	33
69	I→V	✓	✓	✓	92.59	32
75	Y→F	✓	✓	✓	89.06	33
77	K→Q	✓	✓	✓	93.86	34
96	A→T		✓	✓	16.37	33
101	A→T	✓	✓	✓	93.36	33
102	S→R			✓	3.21	22
104	S→R			✓	3.78	21
108	L→Y	✓	✓	✓	95.53	35
109	E→D	✓	✓	✓	94.31	34
113	N→H	✓	✓	✓	94.46	34
114	H→N	✓	✓	✓	95.95	35
115	T→M	✓	✓	✓	95.87	34
119	E→Q	✓	✓	✓	87.19	34
121	D→E	✓	✓	✓	95.48	34
122	R→K	✓	✓	✓	96	34
125	N→D	✓	✓	✓	94.64	34
128	T→S		✓	✓	17.16	35
129	S→G			✓	3.12	33
	S→N	✓	✓	✓	85.31	34
130	L→I	✓	✓	✓	30.41	35
	L→T		✓	✓	11.11	35
	L→V	✓	✓	✓	51.63	34
132	H→Y	✓	✓	✓	96.51	35
133	S→D	✓	✓	✓	82.83	34
	S→N		✓	✓	11.91	34
137	E→K	✓	✓	✓	95.95	34
147	Q→L	✓	✓	✓	90.22	33
155	W→*			✓	3.01	26
156	A→E			✓	3.22	21
157	S→N	✓	✓	✓	92.08	34
163	N→D		✓	✓	14.72	32
165	T→S		✓	✓	17.25	33
172	K→R		✓	✓	9.81	34
173	L→I	✓	✓	✓	46.41	34
	L→M	✓	✓	✓	45.14	34

DeepChek® Whole Genome HIV-1 Mutation Analysis

HIV GP41 mutations

Position	Mutation	Sanger	NGS	Threshold	Prevalence %	Q-Score
176	M→I		✓	✓	6.36	30
182	V→I	✓	✓	✓	92.66	34
189	A→T	✓	✓	✓	93.98	34
191	L→I	✓	✓	✓	95.2	34
209	H→L			✓	3.88	24
210	L→H			✓	4.48	22
213	P→Q	✓	✓	✓	95.12	34
218	R→G		✓	✓	6.72	27
220	E→G	✓	✓	✓	95.9	32
225	E→G	✓	✓	✓	96.43	33
231	R→S			✓	4.85	21
232	D→G	✓	✓	✓	95.83	32
233	R→T	✓	✓	✓	95.79	33
235	I→T	✓	✓	✓	95.45	32
239	N→H	✓	✓	✓	95.79	33
241	S→F	✓	✓	✓	96.04	33
Fragment between amino acid 244 and 252 could not be amplified						
245	I→V	✓	✓	✓	89.25	33
Fragment between amino acid 254 and 297 could not be amplified						
256	S→R		✓	✓	5.15	23
259	R→H	✓	✓	✓	88.42	33
268	T→A	✓	✓	✓	98.67	33
272	E→G	✓	✓	✓	94.87	32
276	R→Q	✓	✓	✓	97.65	33
277	R→G		✓	✓	5.43	31
281	A→V	✓	✓	✓	96.43	32
285	W→L	✓	✓	✓	95.12	35
287	N→S	✓	✓	✓	93.83	33
299	S→R			✓	4.9	21
Fragment between amino acid 300 and 302 could not be amplified						
301	V→I	✓	✓	✓	98.95	35
306	A→T	✓	✓	✓	96	34
310	A→T	✓	✓	✓	91.3	34
321	V→A	✓	✓	✓	91.23	33
322	V→L			✓	4.24	28
324	G→R	✓	✓	✓	94.39	34
325	A→I	✓	✓	✓	94.39	33
343	I→S	✓	✓	✓	90.91	31
345	L→V	✓	✓	✓	89.32	33

Subtype B K03455 was used as the reference sequence for the alignment (using BWA v0.7.15 alignment tool).

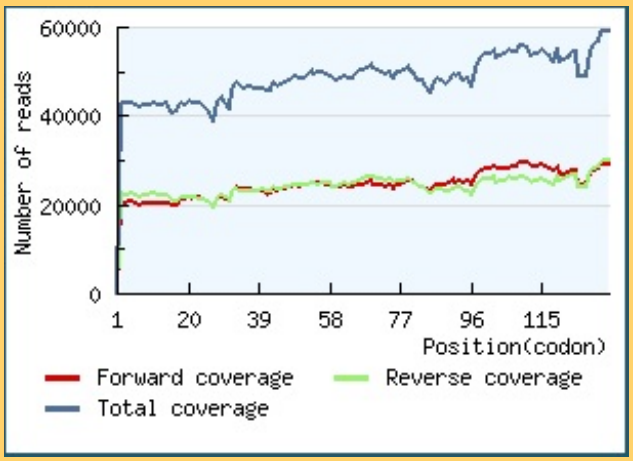
Mutations of interest based on HIVDb v9.4 (mutation score ≠ 0) (Bold red text)

Insufficient number of sequences to guarantee, at the 99% confidence level, that all mutations with the given threshold frequency have been found at that position.

DeepChek® Whole Genome HIV-1 Expert System

Coverage

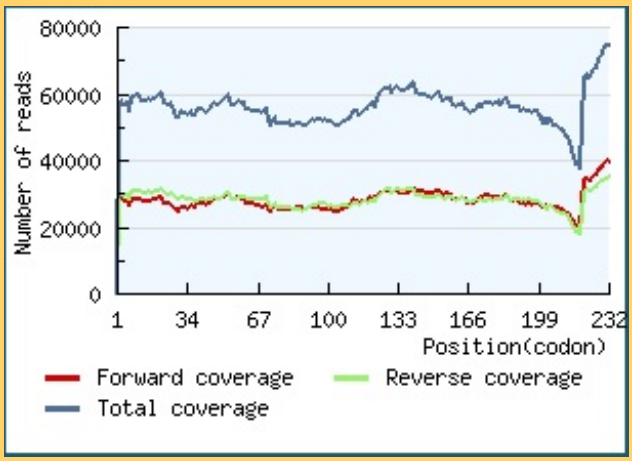
Matrix (P17)



Subtype B K03455 was used as the reference sequence for the alignment (using BWA v0.7.15 alignment tool).

Threshold	Minimum sequences for 99% confidence	Low covered position
Sanger	23	
NGS	92	
Threshold	153	

Capside (P24)



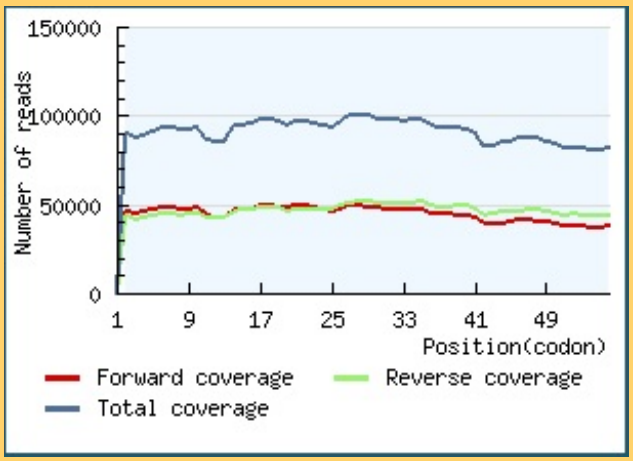
Subtype B K03455 was used as the reference sequence for the alignment (using BWA v0.7.15 alignment tool).

Threshold	Minimum sequences for 99% confidence	Low covered position
Sanger	23	
NGS	92	
Threshold	153	

DeepChek® Whole Genome HIV-1 Expert System

Coverage

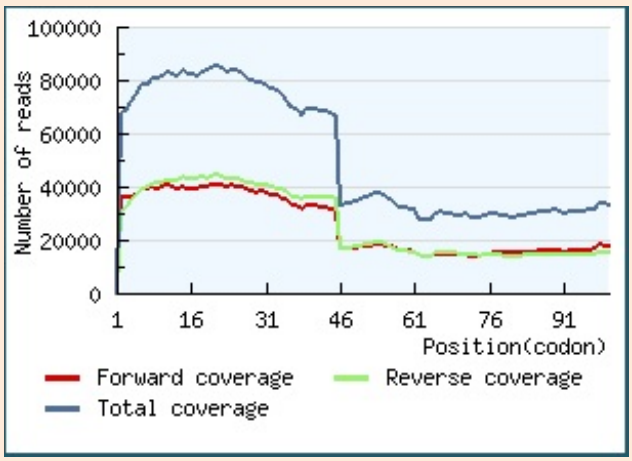
Nucleocapsid (P7)



Subtype B K03455 was used as the reference sequence for the alignment (using BWA v0.7.15 alignment tool).

Threshold	Minimum sequences for 99% confidence	Low covered position
Sanger	23	
NGS	92	
Threshold	153	

Protease (PROT)



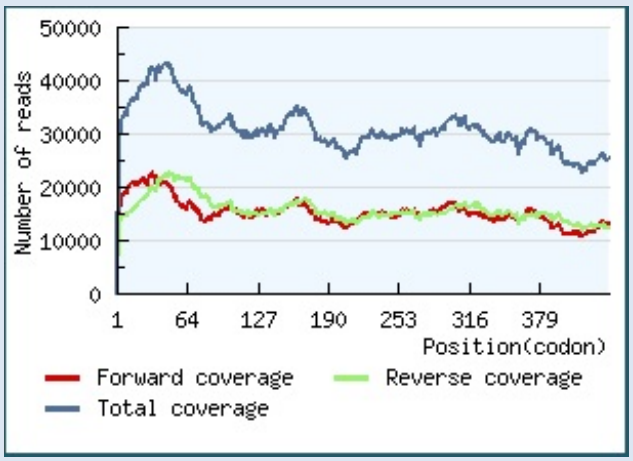
Subtype B K03455 was used as the reference sequence for the alignment (using BWA v0.7.15 alignment tool).

Threshold	Minimum sequences for 99% confidence	Low covered position
Sanger	23	
NGS	92	
Threshold	153	

DeepChek® Whole Genome HIV-1 Expert System

Coverage

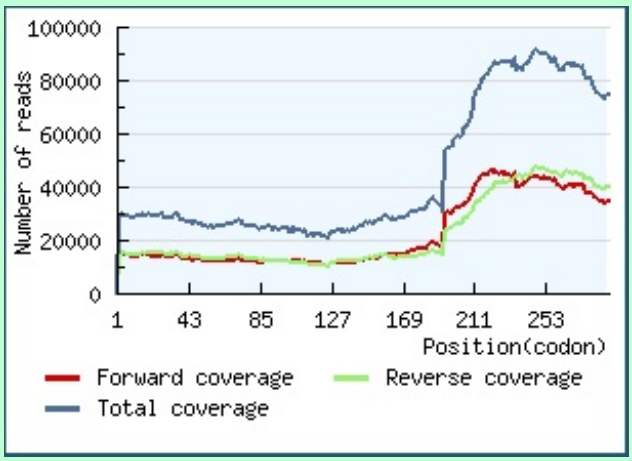
Reverse Transcriptase (RT)



Subtype B K03455 was used as the reference sequence for the alignment (using BWA v0.7.15 alignment tool).

Threshold	Minimum sequences for 99% confidence	Low covered position
Sanger	23	
NGS	92	
Threshold	153	

Integrase (INT)



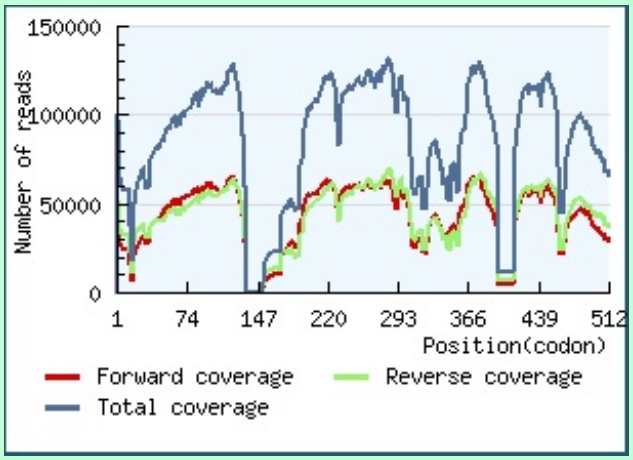
Subtype B K03455 was used as the reference sequence for the alignment (using BWA v0.7.15 alignment tool).

Threshold	Minimum sequences for 99% confidence	Low covered position
Sanger	23	
NGS	92	
Threshold	153	

DeepChek® Whole Genome HIV-1 Expert System

Coverage

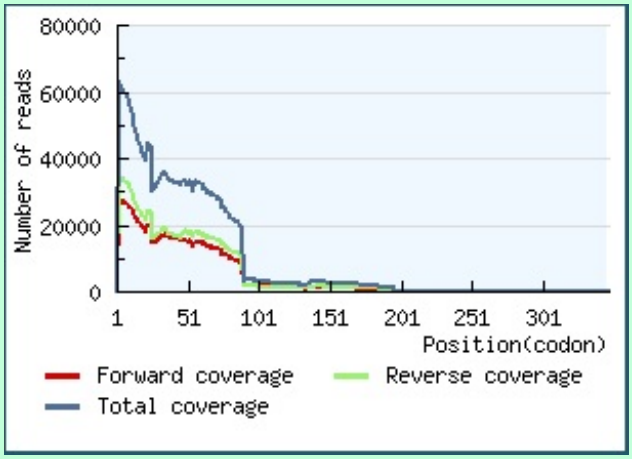
Glycoprotein 120 (or V3 loop) (GP120)



Subtype B K03455 was used as the reference sequence for the alignment (using BWA v0.7.15 alignment tool).

Threshold	Minimum sequences for 99% confidence	Low covered position
Sanger	23	140→152
NGS	92	136→152
Threshold	153	136→152

Glycoprotein 41 (GP41)



Subtype B K03455 was used as the reference sequence for the alignment (using BWA v0.7.15 alignment tool).

Threshold	Minimum sequences for 99% confidence	Low covered position
Sanger	23	
NGS	92	234→235,262→276,279→294
Threshold	153	195→346

DeepChek® Whole Genome HIV-1 Expert System

Discarded mutations

Matrix (P17)

Reasons excluded	Mutations
Noisy mutations filtering (Threshold : 3%)	2500 mutations (see details on Quality information report)
Coverage filtering	559 mutations (see details on Quality information report)
Forward/Reverse unbalanced frequency	41 mutations (see details on Quality information report)
Forward/Reverse unbalanced coverage	
Q-Score < 20	1460 mutations (see details on Quality information report)

Capside (P24)

Reasons excluded	Mutations
Noisy mutations filtering (Threshold : 3%)	4401 mutations (see details on Quality information report)
Coverage filtering	829 mutations (see details on Quality information report)
Forward/Reverse unbalanced frequency	92 mutations (see details on Quality information report)
Forward/Reverse unbalanced coverage	
Q-Score < 20	2866 mutations (see details on Quality information report)

Nucleocapsid (P7)

Reasons excluded	Mutations
Noisy mutations filtering (Threshold : 3%)	1122 mutations (see details on Quality information report)
Coverage filtering	178 mutations (see details on Quality information report)
Forward/Reverse unbalanced frequency	18 mutations (see details on Quality information report)
Forward/Reverse unbalanced coverage	
Q-Score < 20	743 mutations (see details on Quality information report)

Protease (PROT)

Reasons excluded	Mutations
Noisy mutations filtering (Threshold : 3%)	1811 mutations (see details on Quality information report)
Coverage filtering	388 mutations (see details on Quality information report)
Forward/Reverse unbalanced frequency	46 mutations (see details on Quality information report)
Forward/Reverse unbalanced coverage	
Q-Score < 20	1081 mutations (see details on Quality information report)

Reverse Transcriptase (RT)

Reasons excluded	Mutations
Noisy mutations filtering (Threshold : 3%)	7942 mutations (see details on Quality information report)
Coverage filtering	1711 mutations (see details on Quality information report)
Forward/Reverse unbalanced frequency	180 mutations (see details on Quality information report)
Forward/Reverse unbalanced coverage	
Q-Score < 20	4671 mutations (see details on Quality information report)

Integrase (INT)

Reasons excluded	Mutations
Noisy mutations filtering (Threshold : 3%)	5382 mutations (see details on Quality information report)
Coverage filtering	1100 mutations (see details on Quality information report)
Forward/Reverse unbalanced frequency	95 mutations (see details on Quality information report)
Forward/Reverse unbalanced coverage	
Q-Score < 20	3328 mutations (see details on Quality information report)

Glycoprotein 120 (or V3 loop) (GP120)

Reasons excluded	Mutations
Noisy mutations filtering (Threshold : 3%)	9000 mutations (see details on Quality information report)
Coverage filtering	2064 mutations (see details on Quality information report)
Forward/Reverse unbalanced frequency	199 mutations (see details on Quality information report)
Forward/Reverse unbalanced coverage	
Q-Score < 20	4549 mutations (see details on Quality information report)

Glycoprotein 41 (GP41)

Reasons excluded	Mutations
Noisy mutations filtering (Threshold : 3%)	3238 mutations (see details on Quality information report)
Coverage filtering	1417 mutations (see details on Quality information report)
Forward/Reverse unbalanced frequency	39 mutations (see details on Quality information report)
Forward/Reverse unbalanced coverage	
Q-Score < 20	1639 mutations (see details on Quality information report)

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DeepChek® Whole Genome HIV-1 Mutation Notes

Reverse Transcriptase

Algorithm	Related to	Comments
Stanford	106I	V106I occurs in 1% to 2% of viruses from untreated persons. It contributes to reduced NNRTI susceptibility only in combination with other NNRTI-resistance mutations. It is commonly selected in persons receiving DOR in combination with mutations at position 227.
Stanford	179D	V179D/E are somewhat polymorphic accessory NNRTI-selected mutation. In combination with other NNRTI DRMs, they appear to contribute low-levels of reduced susceptibility to each of the NNRTIs. In particular, the combinations of K103R/V179D and V106I/V179D act synergistically to reduce NVP and EFV susceptibility.

Protease

Algorithm	Related to	Comments
Stanford	71T	A71V/T are polymorphic, PI-selected accessory mutations that increase the replication of viruses with other PI-resistance mutations.

Integrase

Algorithm	Related to	Comments
Stanford	119R	S119R is a polymorphic mutation that is weakly selected by INSTIs usually in combination with several major INSTI-associated DRMs. Alone, it has little, if any effect, on INSTI susceptibility.
Stanford	147R	S147G is a nonpolymorphic mutation selected in patients receiving RAL, EVG, and DTG. Alone it reduces EVG susceptibility about 5-fold. 147R is an unusual mutation at this position.
Stanford	230R	S230R is a nonpolymorphic INSTI-selected mutation that primarily occurs in combination with other INSTI-resistance mutations. By itself, it appears to have minimal effect on susceptibility to available INSTIs.