

DeepChek® Assays Fully Validated on the Illumina iSeq 100 Sequencing System

ANNOUNCEMENT



ABL is pleased to announce the validation of its **DeepChek® Line of Assays** on the Illumina iSeq 100 Sequencing System



DEEPCHEK® ASSAYS*

Sequencing-based genotyping assays for microbiology and virology applications



HIV

HBV

HCV

CMV

TB

NEW HSV



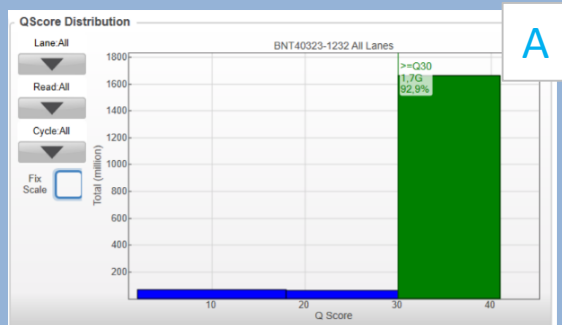
* Also validated on other Sanger or NGS platforms (protocols available for MiSeq, MiniSeq, S5, PGM, ABI, SeqStudio...)

PERFORMANCES & EXAMPLES OF RESULTS

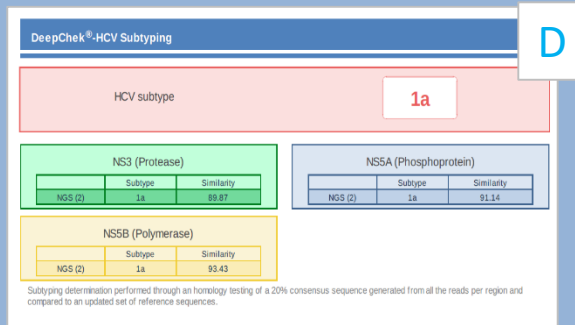


PERFORMANCES

- Fully validated on the DeepChek Library Preparation assays
- Q30 = 93% (A)
- >5.6 millions reads passing QC
- Variants $\geq 3\%$ similar to other NGS platforms (MiSeq, S5...) (B, E)
- Variants $\geq 20\%$ similar to Sanger sequencing platforms
- 100% agreement on clinical interpretations (C) and subtyping (D)
- More than 96 samples per run to reach a 1% interpretation with good coverage (F)!



A



D

DeepChek®-HIV Mutation Analysis

HIV Reverse Transcriptase mutations

Position	Mutation	3.00%	Prevalence %
17	D=N	✓	10.75
28	E=K	✓	89.02
43	K=Q	✓	99.4
49	K=H	✓	99.48
67	D=N	✓	95.95
83	R=K	✓	96.4
122	E=K	✓	99.4
123	D=E	✓	99.56
159	E=D	✓	99.45
184	M=V	✓	99.35
207	Q=S	✓	99.19
211	R=K	✓	99.14
214	L=F	✓	99.07
245	V=M	✓	24.03
272	P=A	✓	99.77
276	V=L	✓	11.95
277	R=K	✓	99.23

Fragment between amino acid 328 and 348 could not be amplified

Subtype B_030455 was used as the reference sequence for the alignment (using BWA v0.7.15 alignment tool).
Mutations of interest based on Stanford v8.6.1 (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.

B

DeepChek®-HBV/HDV Mutation Analysis

HBV reverse transcriptase domain mutations

Position	Mutation	3.00%	Prevalence %
187	I=V	✓	99.19
207	M=V	✓	99.53
227	F=I	✓	5.78
259	V=H	✓	99.41
266	V=T	✓	50.73
267	V=I	✓	14.87
267	Q=H	✓	14.04
271	M=L	✓	94.28
272	W=C	✓	99.32
322	T=S	✓	3.14
332	T=N	✓	3.09
333	K=N	✓	96.19
343	R=E	✓	3.61

Fragment between amino acid 80 and 167 could not be amplified

Subtype B_000300 was used as the reference sequence for the alignment (using BWA v0.7.15 alignment tool).
Mutations of interest based on SeqRepB 6 (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.

E

DeepChek®-HIV Drug Resistance Determination

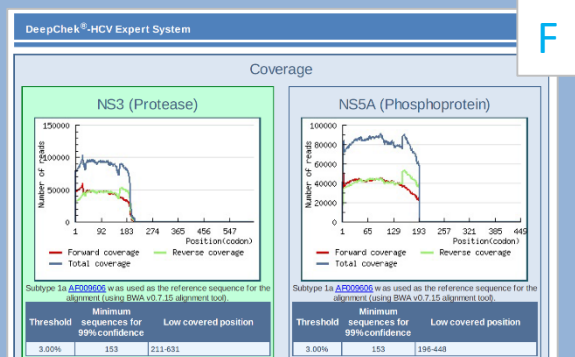
HIV Nucleoside Reverse Transcriptase Inhibitors

Algorithm	3.00%
Abacavir	ANRS
Didanosine	ANRS
Emtricitabine	ANRS
Lamivudine	ANRS
Stavudine	ANRS
Tenofovir	ANRS
Zidovudine	ANRS

Algorithm	Stanford
S	Susceptible
I	Possible resistance
R	Resistance

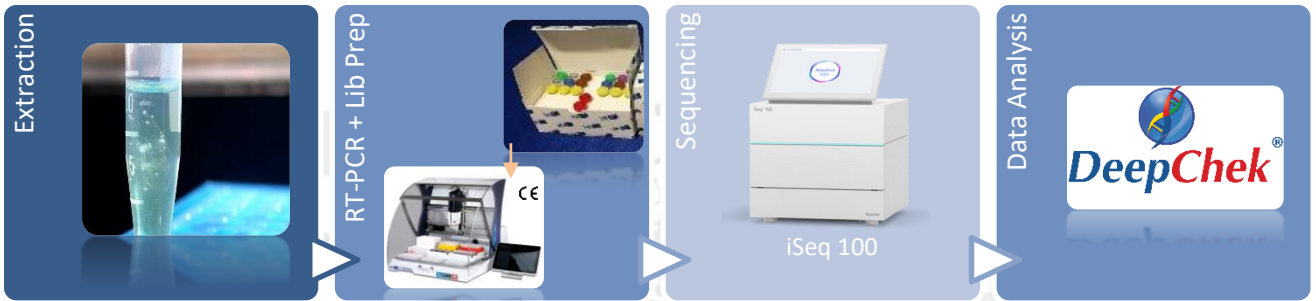
Stanford	Potential low-level resistance (PLLIR)
S	Susceptible (S)
I	Low-level resistance (LLR)
R	Intermediate resistant (IR)
R	High-level resistance (HLR)

C



F

THE WORKFLOW



TAT ~27h30*
HOT ~1h00*

HOT: Hands-on time
TAT: Turnaround time
* For 24 samples

Terms and Conditions:

Advanced Biological Laboratories terms and conditions apply. **For Research Use Only. Not for use in diagnostic procedures.**

