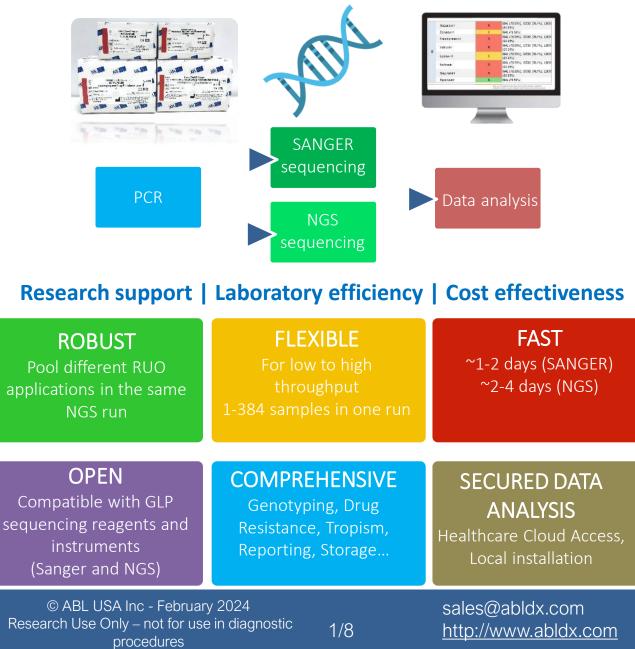
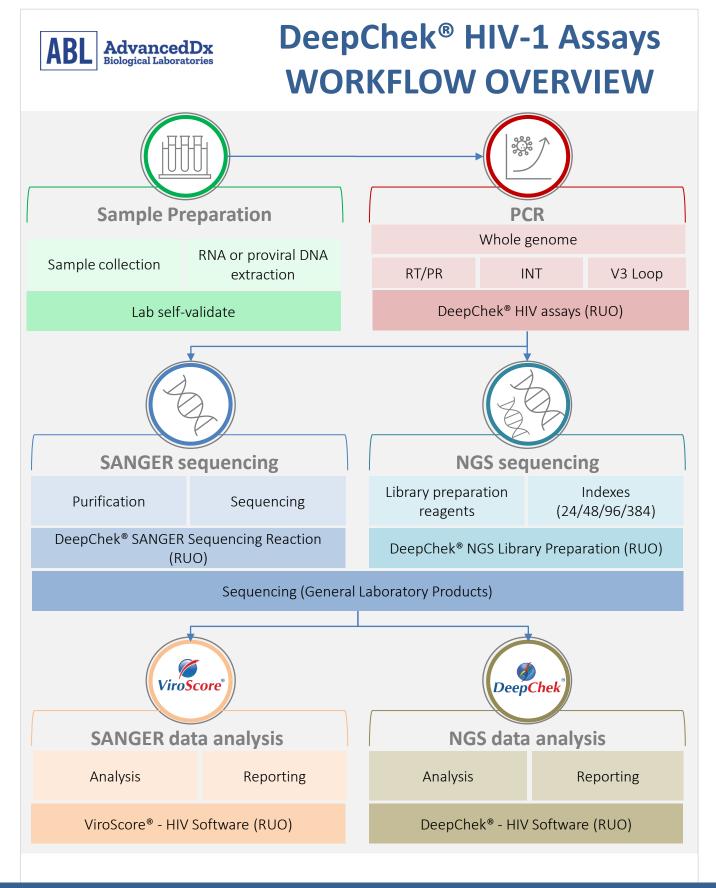


DeepChek[®] Assays for Carrying Out Research About HIV Drug Resistance

An array of Research Use Only (RUO) assays for use on sequencing platforms, next generation sequencing (NGS) and Sanger



Publication number: US-202402 1



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HIV GENOTYPING ANALYSIS REPORTS OVERVIEW

Q Y

179 V 180 181 Y 182 183 184 M 185 186 187 188 189

Integrase GP41

Tropism

Zido Dida Staw Lami Emtr I

SANGER



| A G | T | T | c | T T | G | T | c | Å | Å | T T | a A | c | a A | Ť | ₿ G | ₿ G | Å | T | Ğ | a A | Ť | 0 T | Ť | 6 G | T | Å | T T | G | T T | Å | G G | c | Å | 1 |
|--------------------------|-------------------|-------------|--------|--------|-------|-----|--------------|-------------|------|--------|--------|----------|--------|--------|--------|--------------|------|------|------|--------|-------|--------|-------------|--------|-----|-----|-------------|-----------|--------|---|-------------------------|------|------|---|
| \sim | W | \bigwedge | Δ | Δ | Δ | Λ | \mathbf{n} | ٨ | | Δ | Δ | \wedge | Δ | Δ | Λ | Λ | Δ | Δ | Δ | Δ | ٨ | Λ | ^ | Δ | Δ | Λ | Δ | Δ | Δ | Δ | Δ | Λ | Δ | |
| Subtype: | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
| Reverse transcriptase | B (10 similar | | F | Prote | ease | | | (91 mila | | | In | tegr | ase | | | (10 nila | | | GP | 41 | | | B (simi | | | | GP1 Loop | 120/ p | V3 | 4 | 3 (ch 16_B aimila | F) (| 45 9 | * |
| All Mutations I | Detected | (HXB: | 2 refe | eren | ice S | equ | ence | e) Ri | esis | tand | e m | utat | tions | s in t | old | bas | ed o | n St | anfo | ord v | 7.0.: | L (m | utati | on s | cor | e≠0 |) | | | | | | | _ |

D D L Y v G

 C
 A

 A G T T A T C T A T C A A T A C A T G G A T G A T T T G T A T G T A G C A

 A G T T A T C T G T C A A T A C A T G G A T G G A T G A T T T G T A T G T A G C A

 A G T T A T C T G T C A A T A C A T G G A T G G A T G A T T T G T A T G T A G C A

 A G T T A T C T G T C A A T A C A T G G A T G G A T T T G T A T G T A G C A

 A G T T A T C T G T C A A T A C A T G G A T G G A T T T G T A T G T A G C A

 A G T T A T C T G T C A A T A C A T G G A T G G A T T T G T A T G T A G C A

 A G T T A T C T G T C A A T A C A T G G A T G G A T G A T T T G T A T G T A G C A

 A G T T A T C T G T C A A T A C A T G C A T G G A T G G A T G A T A T G T A G C A

 A G T T A T C T G T C A A T A C A T G C A T G G A T G A T A C A T G G A T G A T G A T G G A T G A T G G A T G A T G G A T G A T G G A T

190

V3I, L10I, S37N, I54V, L63P, H69R, A71V, G73S, I84V, L90M

Val Luio, Salm, Dev Luisy, Hown, ArX, V 373, IDAV, LSOM Killin, Sillog, Tuzio, Kilzz, Gizsk, Alzz, Y. Szobol, Balance, K. Stark, K. Sta GP120/V3 Loop

| Drug | | ANRS 25 2015-09 | 7 | AN | | G2P (1) v3.4 2016 | |
|------------|---|--------------------|------------------|------------------------|---------------|----------------------|-----|
| | | | | | Z-Score | Interpretation | FPR |
| vudine | R | | R | L210W, T215Y | 5.137 | Resistant | |
| nosine | S | | <mark>.</mark> 1 | L210W, T215Y | 1.713 | Intermediate | |
| udine | R | | R | L210W, T215Y | 4.383 | Resistant | |
| ivudine | S | | S | L210W, T215Y | 1.467 | Sensible | (2) |
| ricitabine | S | | S | L210W, T215Y | 1.467 | Sensible | (2) |
| | | | - I. | L210W, T215Y | 3.849 | Resistant | |
| | | | <mark>- 1</mark> | L210W, T215Y | 3.658 | Resistant | |
| | | | R | K101E, Y181C, G190A | 5.915 | Resistant | |
| _ | | | R | K101E, Y181C, G190A | 4.136 | Resistant | |
| _ | | | R | K101E, Y181C, G190A | Not available | Resistant | (3) |
| | | | R | K101E, Y181C, G190A | Not available | Resistant | (3) |
| | | | Not available | | 1 | Not available | |
| | | le | R | 154V, G73S, 184V, L90M | 11.065 | Resistant | |
| | | | R | 154V, G73S, 184V, L90M | 14.423 | Resistant | |

| ROT | B (94.95%) | RT B (95.83 | 9%) PROT | 1-99 | RT | 1-327 |
|--------------------------|--|--|---|---------------|-------------------|-----------------------|
| INT | B (95.53%) | | INT | 32-289 | | |
| PROT, IN typing dates | 4T] : Subtype B K00455 was used as the reference mination performed through homology testing of a | e sequence for the alignment (using BW 20% consensus sequence generated fro | A v0.7.15 alignment tool). m all the reads mapped to | | | |
| s particular n | agion and compared to an updated set of reference | taparea. | | DEEPCHEK* HIV | (Stanford 8.8) | |
| | Generic name | Assessment | Resistance mutations > | 20.00% Resist | ince mutations be | tween >3% and <20.00% |
| | Atazanavir/r | R | I54L (78.56%), G73S (76. (90.98%) | 1%), L90M | | |
| | Darunavir/r | 1 | I54L (78.56%) | | | |
| | Fosamprenavir/r | R | I54L (78.56%), G73S (76. (90.98%) | 1%), L90M | | |
| <u>-</u> | Indinavir/r | R | I54L (78.56%), G73S (76. (90.98%) | 1%), L90M | | |
| - | Lopinavir/r | T. | I54L (78.56%), G73S (76. (90.98%) | | | |
| | Nelfinavir | R | I54L (78.56%), G73S (76. (90.98%) | | | |
| | Saquinavir/r | R | I54L (78.56%), G73S (76. (90.98%) | 1%), L90M | | |
| | Tipranavir/r | S | I54L (78.56%) | | | |
| | Abacavir | 1 | D67N (96.96%), M184V (99 | 9.35%) | | |
| | Didanosine | 1 | D67N (96.96%), M184V (99 | 9.35%) | | |
| - | Emtricitabine | R | M184V (99.35%) | | | |
| NRTI | Lamivudine | R | M184V (99.35%) | | | |
| 2 | Stavudine | S | D67N (96.96%), M184V (99 | 9.35%) | | |
| | Tenofovir | S | D67N (96.96%), M184V (99 | 9.35%) | | |
| | Zidovudine | S | D67N (96.96%), M184V (99 | 9.35%) | | |
| | Doravirine | S | | 1 | | |
| - | Efavirenz | S | | | | |
| NNRTI | Etravirine | s | | | | |
| ZZ | Nevirapine | 8 | | | | |
| | Rilpivirine | S | | | | |
| | Bictegravir | 1 | G140S (99.66%), Q148H (| 0 33%) | | |
| | Dolutegravir | | G140S (99.66%), Q148H (9 | | | |
| Z | Elvitegravir | R | G140S (99.66%), Q148H (| | | |
| | Raltegravir | R | G140S (99.66%), Q148H (9 | | | |
| S | Susceptible (S) Potential low-level resistance | | Low-level resistance (LLR Intermediate resistant (IR |) | High-lev | el resistance (HLR) |



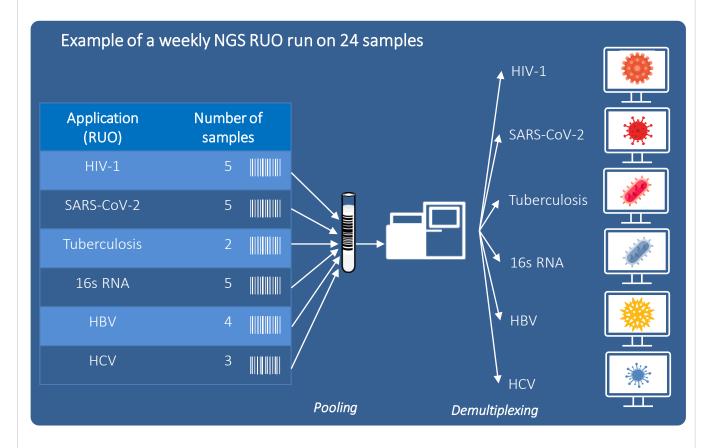
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REDUCE SIGNIFICANTLY NGS RELATED COSTS AND TURNAROUND TIME WHEN USING THE DEEPCHEK® TECHNOLOGY

- The DeepChek[®] assays & software can be used through NGS on a large variety of research applications simultaneously, providing high efficiency
 - Optimize NGS sequencing costs
 - Optimize turnaround time
 - Bring NGS capacity to any lab settings
- Adapt and customize your NGS panel/run to your research plans



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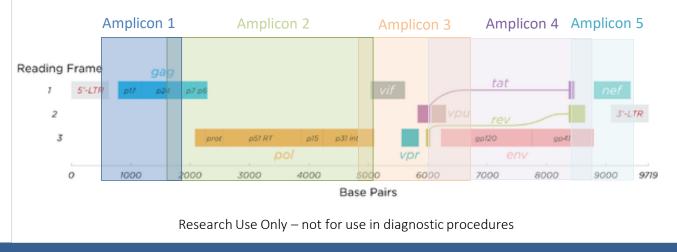


DeepChek[®] Assay Whole Genome HIV-1 Genotyping (RUO)

- Access to a comprehensive Next Generation Sequencing (NGS) kit for HIV Whole Genome genotyping.
- DeepChek® Assay Whole Genome HIV-1
 Genotyping has been developed for use with the leading next generation sequencing (NGS) platforms and includes optimized multiplex PCR master mixes with primers to amplify RNA and proviral DNA inputs with manual or automated
 library preparations.
- Ability to screen genomic variations in all HIV-1 genome genes targeted by current and under development HIV-1 inhibitors,
 including new entry & capside inhibitors.
- Number of amplicons: 5x ~700 to 3500 bp obtained from same thermal cycling program in five (5) distinct wells.
- Coverage : ~ 9600 bp.
- Inclusivity: excellent coverage of all representative HIV-1 subtypes from M group strains.
- Cross-reactivity: The assay reacted (i.e., good agarose gel band) for some of the

tested microorganisms commonly found in infectious diseases specimens. After NGS and data analysis, no reads mapped with HIV-1.

- Compatible with magnetic-beads RNA/DNA isolation instruments and reagents, and with any PCR thermal cycler with ramp rate of \geq 1°C/s, and leading NGS instruments and reagents equivalent to Illumina SBS chemistry.
- Shall be compatible with run of 48 / 96 and 384 samples to reach assay cut-off minimal median total coverage of 1000 reads for the amplicons and a Phred Quality Score Q30>80% (or equivalent)).
- The sequencing outputs can be analyzed with specific downstream sequencing analysis software (e.g. DeepChek[®] Software) to reduce laboratory staff burden and to alleviate the need for specialized bioinformatics expertise or on the contrary with using generic bioinformatics software and tools for more advanced research teams.



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HIV-1 genes associated with antiviral resistance when using the DeepChek[®] Assay Whole Genome HIV-1 Genotyping (RUO)

| Anti-HIV drug class | HIV-1 gene target | Related drugs | Assay fragment # |
|---|---------------------------------------|---|---------------------|
| Capsid inhibitors | gag | lenacapavir | 1 |
| Nucleoside reverse transcriptase inhibitors (NRTIs) | reverse transcriptase | zidovudine, lamivudine, emtricitabine,abacavir, tenofovir disoproxil fumarate, tenofovir alafenamide , islatravir, didanosine and stavudine | 2 |
| Non-nucleoside reverse transcriptase inhibitors (NNRTIs) | reverse transcriptase | efavirenz, nevirapine, etravirine, rilpivirine and doravirine | 2 |
| Protease inhibitors (PIs) | protease | lopinavir, atazanavir, darunavir, ritonavir, indinavir, saquinavir, nelfinavir, fosamprenavir and tipranavir | 2 |
| Integrase inhibitors (IIs) | integrase | raltegravir, elvitegravir, dolutegravir, cabotegravir, bictegravir | 2 |
| n.a | vif, vpr, vpu (accessory proteins) | enfuvirtide | 3 |
| Fusion inhibitors | gp41 | Fostemsavir | 4 |
| Post-attachment inhibitors | gp120 | n.a | 4 |
| n.a | nef (accessory protein) | n.a | 5 |
| R | Research Use Only – not fo | or use in diagnostic procedures | |

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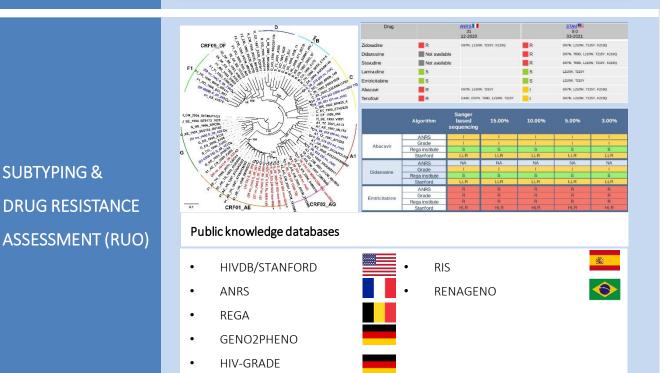
SUBTYPING &

Advanced IT research tools for new disease discovery

| A G G G G G A G A G G G A G A G G G A G A G | | A G A A A A | | | | | V T C T T T T T T | C C G G G | | G A G A G A G A | | | | | | V I T C T C T C | P C C T C C T C C T C C T | | /T utation(s) eference EQ5-1701 EQ5-1701 ontig | R E | | DDED |
|--|----------------|---------------------|---|-----|-----|------------------------------|-------------------------------|--------------|---------------------------------------|--------------------------|-----------|--------------|------------------------------|----------------|------------|-----------------------------|--|----------|---|--------|------|----------|
| A G A G G G G | A A | 41 42 A A A A | | A T | A C | 5 7 C | т т Л | 27 26 C G | τ τ τ τ τ τ τ τ τ τ τ τ τ τ τ τ τ τ τ | G A | A A | 10 20 C A | τ d d | c + τ Λ Λ Λ | ĂĈŦ | ÷ ċ | | -> | EEQ5-1701 | | GRAM | MATOGE |
| | <u>/vv</u> | | | | | <u>////</u> 5 † č \/// | <u>///</u> † † /// | : : ^ | <u>۷۷۷</u> ء ء ۸۸ | <u>۸۸</u> | /// :: | | <u>Ι ν</u> τ ε ε ο Λ / | | × * * | τι τι ΛΛ | <u>۱۷۷۸</u> د د ب ۸۸۸ | ~ | ▼ EEQ5-1701 | | D) | OR (RUO) |
| | Ň | Ŵ | W | Ŵ | Ň | 5 7 8 M | ;; \/\/ | :: M | : : \\\ | ۰۰ ۸۸ | ΛΛ | M | т ä d | a÷÷ ∕\\\ | * : † M | ÷ċ M | сст ЛМ | ~ | ' EEQ5-1701 | | D) |)R (RUO) |

INT

| | ation V3I L10I − | × | × | × | × | × | × | × | × | × | × |
|------------------|-------------------------------------|------------|------------|------------|------------|------------|------------|------------|------------|------------|------------|
| SINGLE or | K201 | ××× | XXX | XXXX | XXXXX | XXXX | ××××× | XXX | XXX | ××× | XXX |
| CUMULATIVE | .63P - 169K - 74S - /82A - | × | × | XXXX | XXXX | XXXX | XXXX | × | × | × | × |
| GENOTYPING (RUO) | 89M - 193L - | 19/08/1997 | 01.02/2000 | 09/11/2001 | 03/04/2003 | 08/07/2003 | 25/09/2003 | 29/10/2003 | 22/09/2006 | 12/01/2007 | 27/08/2007 |



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DeepChek[®] Assays (RUO)

PCR (RUO)

| WHOLE GENOME HIV-1 Genotyping (24 tests) | 170B24 |
|--|-----------|
| PROTEASE / REVERSE TRANSCRIPTASE Genotyping and Drug Resistance (24 or 96 tests) | 101B24 96 |
| INTEGRASE Genotyping and Drug Resistance (24 or 96 tests) | 102C24 96 |
| V3 LOOP / TROPISM (24 tests) | 103A24 |
| GP41/GP120 Genotyping and Drug Resistance (24 tests) | 194A24 |
| GAG Genotyping and Drug Resistance (24 tests) | 195A24 |
| REVERSE TRANSCRIPTASE SIMPLEX Genotyping and Drug Resistance (24 tests) | 197A24 |
| HIV-1 Full PR/RT/INT Drug Resistance (24 tests) | 198BA24 |
| | |

NGS SEQUENCING (RUO)

DeepChek[®] NGS Library Preparation

| 24 indexes | 116B24+124B24 |
|--|-----------------|
| 48 indexes | 116B48+124B48 |
| 96 indexes | 116B96+124B96 |
| 384 indexes | 116B384+124B384 |
| DeepChek [®] NGS Clean-up beads | N411-02 |
| | |

SANGER SEQUENCING (RUO)

| DeepChek [®] SANGER Sequencing Reaction (24 rx) | 123A24 |
|--|----------|
| DeepChek [®] SANGER Sequencing Reaction (48 rx) | 123A48 |
| DeepChek [®] 96x0.2 mL wells plate | B70501-1 |
| Opti-Seal Optical Sealing Sheet | 157300 |

DATA ANALYSIS (RUO)

DeepChek[®] - HIV Software (RUO) ViroScore[®] - HIV Software (RUO) DeepChek Whole Genome HIV-1 (RUO) S-12-023 (HL | HM) S-09-014 S-22-056 (WHL | WHM)

AdvancedDx Biological Laboratories



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