Optimizing Clinical NGS: Comparative Evaluation of Illumina iSeq100 and Complete Genomics G10-FR* Using DeepChek® Workflows

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The G10-FR is marketed as E25 Flash in some territories

ID046

Background

Next-generation sequencing (NGS) is transforming infectious disease diagnostics by enabling comprehensive genotyping, resistance detection, and microbial identification[1,2]. However, accessibility is often limited by cost, workflow complexity, and platform availability. While Illumina platforms are widely adopted[3], newer systems like the Complete Genomics G10-FR* offer rapid sequencing with simplified workflows. In this study, we compared the performance of the Illumina iSeq100 and the Complete Genomics G10-FR (marketed as DNBSEQ-E25 Flash in some territories) using validated DeepChek® (ABL) kits and MicrobioChek® software, with a focus on pooling multiple applications in a single run to reduce per-sample costs.

Materials & Methods

DeepChek® HIV kits were used to amplify protease, reverse transcriptase, integrase regions (121A, 122A) and full HIV genome (170B) from Quality Control for Molecular Diagnostics. In parallel, bacterial and fungal targets were amplified using DeepChek® 16S and ITS kits for identification. Library preparation was performed using platform-specific DeepChek® NGS kits. Sequencing was conducted on the Illumina iSeq100 (PE150, 19hr) and Complete Genomics G10-FR* (SE100, 3.2 hr). The libraries were circularized and DNBs generated using a single-step protocol. Amplicons from different assays (HIV, 16S, ITS) were pooled into a single sequencing run to maximize efficiency. Data were analyzed with MicrobioChek®, which includes the Stanford HIVdb and a taxonomic classification engine.

Complete Genomics DNA Nanoball Sequencing:
- ☑ No clonal error
- ☑ No index hopping
- ☑ Low duplication rates

DeepChek® (ABL, Luxembourg) is a CE marked:
The pipelines consist of 10 major steps which are :
1) Data cleaning, 2) Subtyping, 3) Tropism analysis, 4) Alignment, 5) Post-alignment cleaning, 6) Consensus creation, 7) Variant calling, 8) Expert system filtering, 9) Drug resistance calculation, 10) Reporting

- ☑ DeepChek® HIV version 2.0 / expert system 2.3 /algorithms 13.1
- ☑ ANRS 33 10-2022 / Grade 2021 9-2021 / HIVdb 9.4 12-2022
- ☑ Classification of mutations of interest ANRS 33
- ☑ Microbiochek identification

Figure 1. End-to end Solution for HIV-1 Genotyping and Drug Resistance for Routine Diagnostic Sequencing.

Results

Both platforms generated high-quality sequencing data with high Q-scores and full genome coverage across applications. The Complete Genomics G10-FR* produced a significantly higher number of reads per run (~25M) compared to the Illumina iSeq100 (~4M), enabling greater depth and broader detection capacity, particularly in pooled workflows.

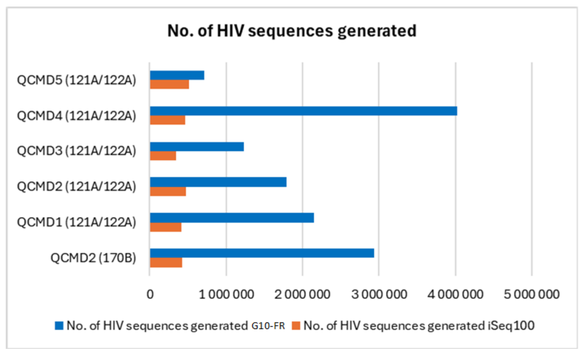

Figure 2. Comparison of the number of HIV sequences generated by the sequencing platforms Complete Genomics G10-FR* versus iSeq100 (Illumina). 121A/122A : target specific kit. 170B: whole genome kit.

Phylogenetic analyses demonstrated strong concordance between sequences obtained on both platforms.

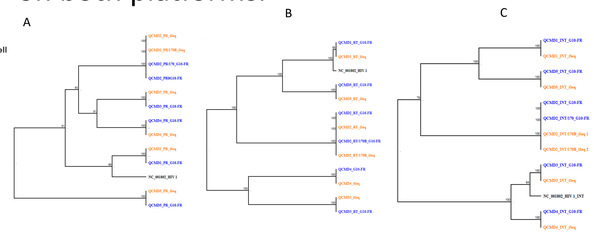

Figure 3. Phylogenetic trees constructed using consensus sequences of protease (a), reverse transcriptase (b), and integrase (c) targets obtained from sequencing on the NGS platforms Complete Genomics G10-FR* versus Illumina iSeq100.

HIV genotyping showed >99% agreement, with only two low-frequency mutations (<5%) showing discordance between platforms: M46V (3.32%) detected only by G10-FR* in the protease region, and D67N (3.25%) detected only by iSeq100 in the reverse transcriptase region. Importantly, these minor discrepancies (<5%) did not affect drug resistance interpretation thresholds. The complete workflow from DNA to data analysis takes approximately 24 hours on the Illumina iSeq100, including library preparation and sequencing. In comparison, Complete Genomics G10-FR* can deliver results in just 5-9 hours, offering a 50-70% faster turnaround.

Table 1. Bioinformatics analysis using MicrobioChek (ABL) to identify HIV-1 drug resistances obtained from Complete Genomics G10-FR* versus iSeq100 (Illumina) platforms.

N°	Sequencer	Subtype						Mutation					
		PR	%	RT	%	INT	%	PR	%	RT	%	INT	%
QCMD2	MGIE25	95_02B	96.63	02_AG	95.15	B	96.66	NA	NA	NA	NA	NA	NA
	Iseq 100	95_02B	96.63	02_AG	95.15	B	96.66	NA	NA	NA	NA	NA	NA
QCMD1	G10-FR	48_01B	93.27	B	99.58	08_BC	97.09	43 K→T 46 M→I 54 I→V 82 V→A 90 L→M	12.56 95.95 98.41 95.76 95.92	NA	NA	NA	NA
	Iseq 100	48_01B	93,27	B	99,58	08_BC	97,09	43 K→T 46 M→I ***46 M→V*** 54 I→V 82 V→A 90 L→M	12,07 96,3 ***3,32*** 99,63 91,35 96,33	NA	NA	NA	NA
QCMD2	G10-FR	95_02B	96.63	02_AG	94.86	B	99.45	NA	NA	190 G→E	4.35	NA	NA
	Iseq 100	95_02B	96.63	02_AG	94,86	B	99,45	NA	NA	190 G→E	4,59	NA	NA
QCMD3	G10-FR	C	97.31	C	94.4	B	99.45	88 N→S	10.65	41 M→L 67 D→N 69 T→D 98 A→G 184 M→I 188 Y→L 190 G→A 210 L→W 215 T→Y	99.35 98.56 99.31 99.17 98.6 98.05 99.44 99.05 98.29	NA	NA
	Iseq 100	C	97,31	C	94.4	B	99,45	88 N→S	12,1	41 M→L 67 D→N 69 T→D 98 A→G 184 M→I 188 Y→L 190 G→A 210 L→W 215 T→Y	99,63 99,01 98,08 99,18 99,13 99,37 99,48 98,85 99,17	NA	NA
QCMD4	G10-FR	146_BC	93.92	57_BC	94.93	B	99.58	46 M→I 54 I→V 82 V→A	95.52 94.93 91.8	***67 D→N*** 185 M→V	***3.25*** 98.08	143 Y→H NA	4.98 NA
	Iseq 100	146_BC	93,92	57_BC	94.93	B	99.58	46 M→I 54 I→V 82 V→A	96,01 96,06 90,55	184 M→V	99,54	143 Y→H NA	4,68 NA
QCMD5	G10-FR	B	99.66	B	96.14	121_0107	96.77	NA	NA	40 E→F 41 M→L 184 M→V 210 L→W 215 T→Y	96.43 100 96.88 97.56 100	NA	NA
	Iseq 100	B	99.66	154_0755	98,21	121_0107	96.77	NA	NA	40 E→F 41 M→L 184 M→V 210 L→W 215 T→Y	100 100 100 100 100	NA	NA

Microbial identification via 16S/ITS was consistent across platforms at species/strain level.

Table 2. Bioinformatics analysis using MicrobioChek (ABL) to identify bactreria and fungi obtained from Complete Genomics G10-FR* platform.

N°ABL	PCR	Expected result	Result Complete Genomics G10-FR_MicobioChek	Accession
60	16Sv3	*Bordetella pertussis A639*	Bordetella pertussis strain NCTC13251 chromosome 1	NZ_LR590467.1
62	16Sv3	*Haemophilus influenzae tybe b (Eagan)*	Haemophilus influenzae isolate KR271 chromosome 1, complete sequence	NZ_OV040584.1
64	16Sv3	*Streptococcus pyogenes (2018)*	Streptococcus pyogenes strain NCTC8318 chromosome 1	NZ_LR590483.1
67	16Sv3	*Pseudomonas aeruginosa clinical isolate*	Pseudomonas aeruginosa isolate MINF_3A-sc-2280432 chromosome 1, complete sequence	NZ_LR886887.1
69	16Sv3	*Streptococcus salivarius (Z127)*	Streptococcus salivarius strain NCTC8618 chromosome 1, complete sequence	NZ_LR134274.1
5A	16Sv3	Staphylococcus aureus	Staphylococcus aureus strain ST20190863 isolate ST20190863 chromosome 1, complete sequence	NZ_OX344719.1
65	ITS_Primers 2	Pneumocystis jirovecii-S cerevisiae recombinant	Saccharomyces cerevisiae S288C chromosome XII, complete sequence	NC_001144.5
66	ITS_Primers 2	*Candida albicans Z006*	Candida albicans SC5314 chromosome R, complete sequence	NC_032096.1
65	ITS_Primers 3	Pneumocystis jirovecii-S cerevisiae recombinant	Saccharomyces cerevisiae S288C chromosome XII, complete sequence	NC_001144.5
66	ITS_Primers 3	*Candida albicans Z006*	Candida albicans SC5314 chromosome R, complete sequence	NC_032096.1
63	16Sv3 (100ng)	*Streptococcus pneumoniae (19F ; 2022)*	Streptococcus pneumoniae strain RMV7 isolate RMV7dom chromosome 1, complete sequence	NZ_OV904788.1

Conclusion

DeepChek® NGS workflows are polyvalent, platform-independent, and compatible with a multiplexed, pooled sequencing approach, which significantly enhances cost-efficiency without sacrificing analytical performance. The Complete Genomics G10-FR* emerges as a robust alternative to traditional systems like Illumina iSeq100, making routine clinical NGS faster, more accessible and scalable for laboratories handling diverse diagnostic applications.

References

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