AXELIOS

Roche

DEMONSTRATED DATA

AXELIOS 1 SBX-D Human Germline WGS

Consistent and reliable performance across operational parameters and sample replicates

For Research Use Only. Not for use in diagnostic procedures.

Overview

The AXELIOS 1 Platform delivers consistent and reliable performance across key operational parameters (hardware, operators, sensor modules, and experimental design). Data presented here were generated in-house with launch-configuration components across the complete SBX-D Human Germline WGS workflow—from sample prep to data analysis.

Data were generated across a total of 120 four-hour SBX-D human whole-genome sequencing runs, performed using different platforms, operators, and sensor modules (Figure 1).

- Library pools (16-plex) were prepared from human genomic DNA, including Genome in a Bottle (GIAB) samples HG001 – HG007[1] and converted to Xpandomer molecules (1 library pool per chip; 4 chips per 4 h synthesis run) as described in the AXELIOS 1 Germline WGS Workflow Guide.[2]
- Xpandomer molecules were sequenced in four-run queues (4 h of sequencing time per run, excluding pre-sequencing setup and post-run cleanup).
- Near real-time, integrated analysis (base calling, demultiplexing, intramolecular consensus, and reference-based alignment) was performed onboard the AXELIOS 1 Sequencing Instrument. Variant calling was subsequently performed off-instrument, using XOOS analysis tools 1.0.0 (github.com/Roche-AXELIOS/XOOS).

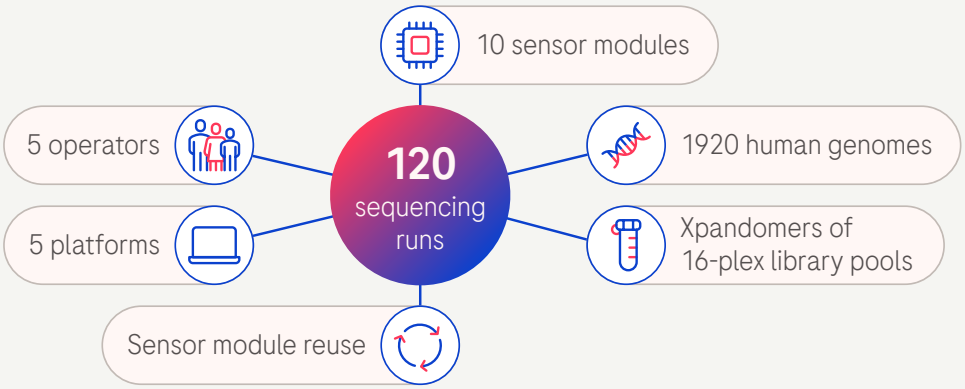
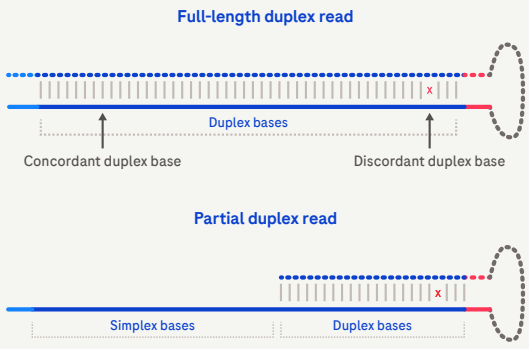


Figure 1. Experimental overview. Data were generated using a range of operational parameters and five AXELIOS 1 Platforms across 10 days.

A key feature of the SBX-D workflow is the high base accuracy for concordant duplex bases, which are the majority of bases obtained in a run (Figure 2). Performance metrics presented in Figures 3 and 4 (including accuracy and coverage), are primarily derived from concordant duplex bases.



Base category	Range (%)	Categorical quality scores	Used to calculate the following metrics
Concordant duplex bases	~68 – 74	Q39	Accuracy, coverage, coverage uniformity, throughput, insert length, F1 scores
Simplex bases	~24 – 30	Q22	Insert length, F1 scores
Discordant duplex bases	~1 – 2	Q5	Insert length

Figure 2. SBX-D read structure, base categories, and base composition metrics. The two read types obtained from SBX-D sequencing runs are illustrated on the left. The three SBX-D base categories are listed in the table on the right. Ranges represent the results from all 120 sequencing runs, across all operational and sample variables.

Consistent Performance Across Sequencing Runs and Run Queues

Run-level yield and accuracy metrics for four-hour SBX-D sequencing runs are shown in Figure 3. A typical run yields ≥1.8 Tb of concordant duplex bases, with ≥6.4 million active sequencing pores and a mean concordant duplex base accuracy of ~Q38.

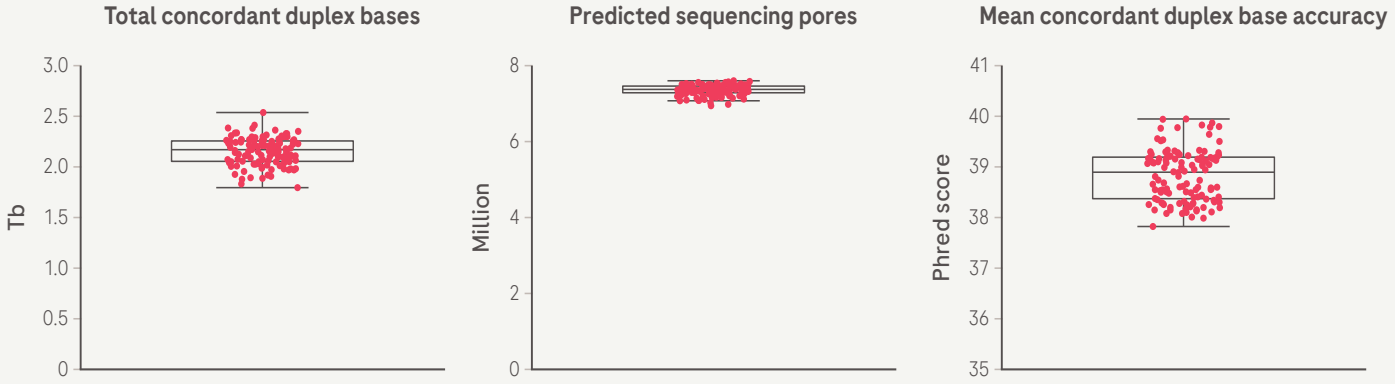


Figure 3. Data yield and accuracy for SBX-D sequencing runs on the AXELIOS 1 Platform. Data represents the results of all 120 four-hour sequencing runs (see Figure 1). Mean concordant duplex base accuracy was empirically determined by aligning consensus reads to the reference genome and quantifying errors within the GIAB 4.2.1 high-confidence regions.[3] This is not the same as the categorical base quality scores assigned during base calling.

In Figure 4, run-level performance metrics are parsed by run position in each of the 30 sequencing run queues performed in this study. These run queues consist of four sequencing runs, performed consecutively in an automated fashion on a single instrument. Exceptionally consistent results confirm that the automated reuse procedure is highly effective.

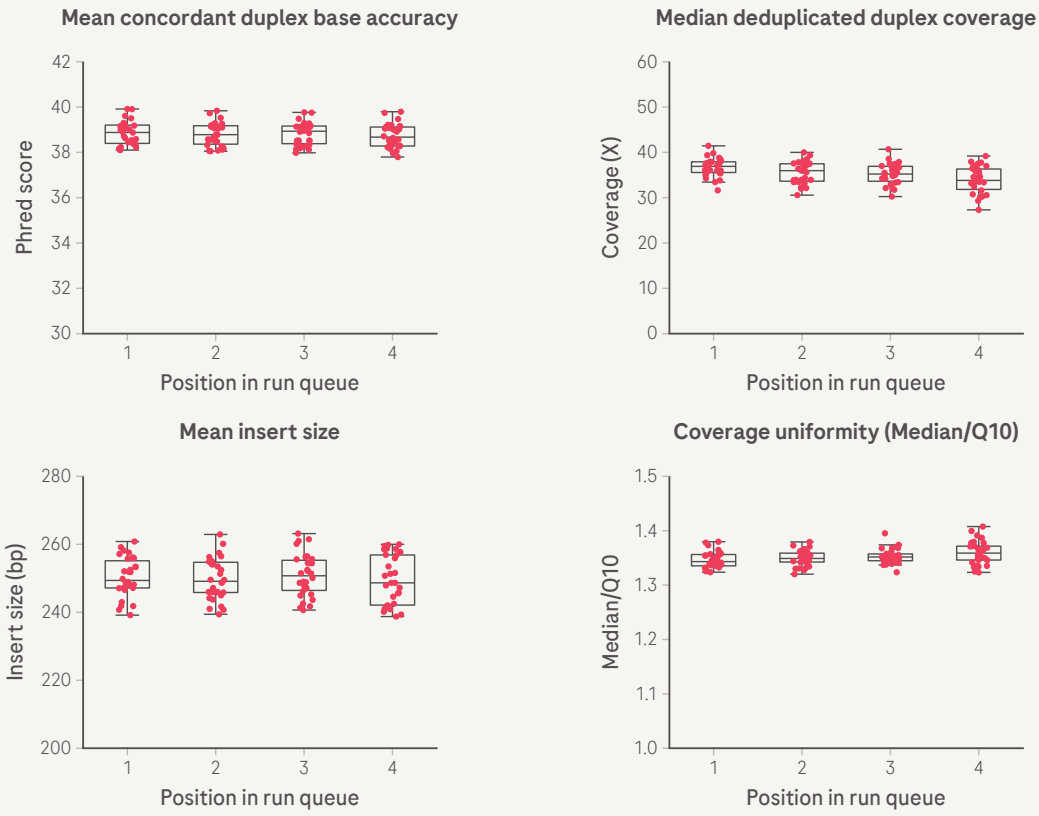


Figure 4. Highly consistent performance across sequencing run queues on the AXELIOS 1 Platform. Mean concordant duplex base accuracy (not the same as the categorical base quality scores assigned during base calling) was empirically determined by aligning consensus reads to the reference genome and quantifying errors within the GIAB 4.2.1 high-confidence regions.[3] Deduplicated duplex coverage and insert size were calculated for autosomes only. Coverage uniformity was calculated within the GIAB 4.2.1 high-confidence regions.

High-Confidence Germline Variant Calling

Accurate and reliable germline variant detection is a cornerstone of biomedical research. Results from variant calling for HG001 to HG007 samples included in this study, performed using the integrated pan-genome aligner and XOOS analysis tools 1.0.0, are given in Figure 5. SNV and indel F1 scores exceeded 99.6% and 99.2%, respectively. Variation in F1 scores between samples is expected.[1] Nevertheless, tight distributions indicate high consistency across synthesis and sequencing runs.

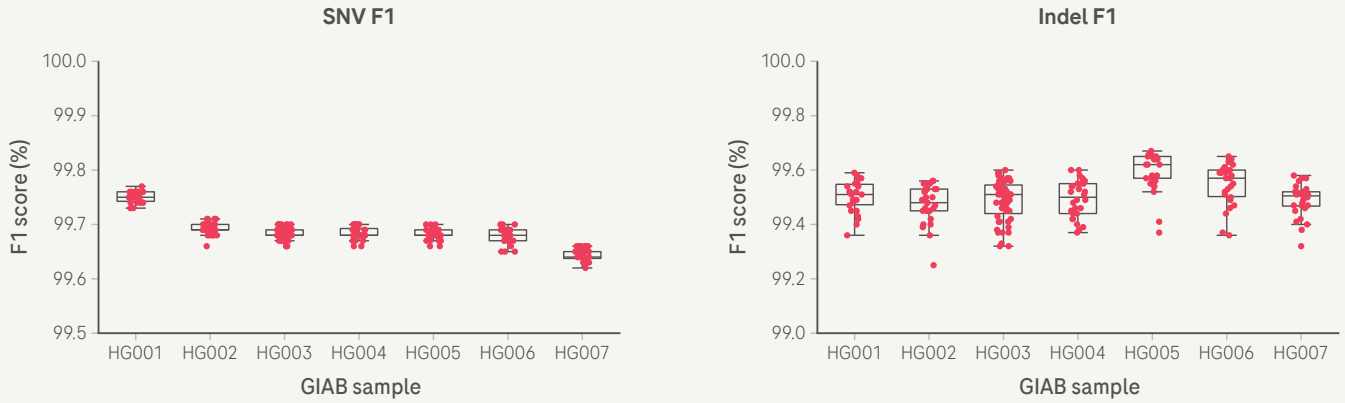


Figure 5. The AXELIOS 1 Platform and XOOS small variant caller deliver high-confidence variant calling. Samples from eight of the run queues in this study were randomly selected and downsampled to a median 30x deduplicated concordant duplex coverage within the GIAB 4.2.1 high-confidence regions.[3]



Reliable Sensor Module Performance

Longevity of the reusable AXELIOS 1 Sensor Module is a differentiating feature of the AXELIOS 1 Platform. Sensor module performance is maintained across multiple uses (up to 20 individual or queued runs within 90 days of first use). Representative data is given in Figure 6. No degradation of performance was observed across 20 sequencing runs.

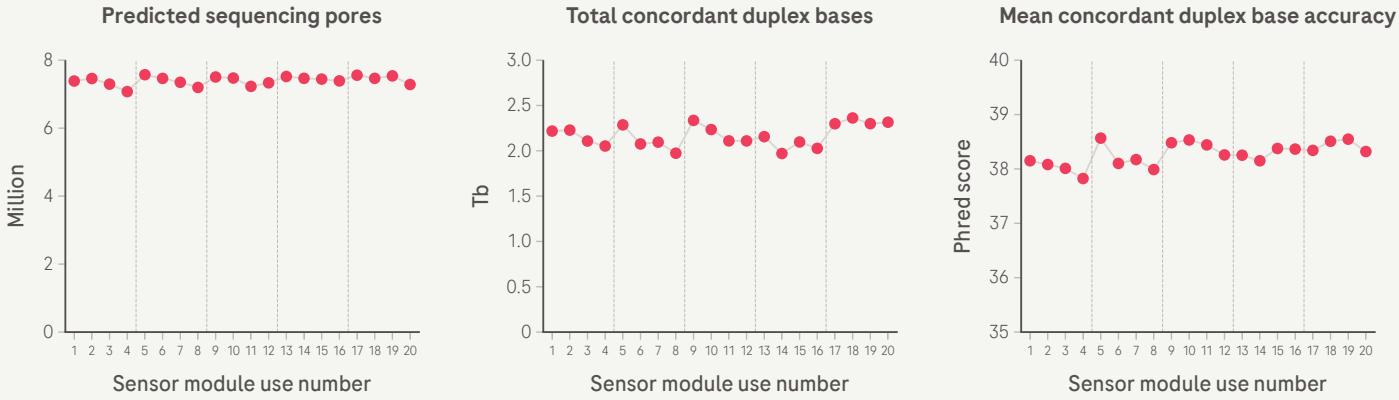


Figure 6. Representative performance of the AXELIOS 1 Sensor Module across 20 sequencing runs. Vertical lines indicate separate run queues. These data were collected over the course of 1 week, but sensor modules may be reused for up to 90 days (or 20 runs, whichever comes first). Mean concordant duplex base accuracy was empirically determined by aligning consensus reads to the reference genome and quantifying errors within the GIAB 4.2.1 high-confidence regions.[3] This is not the same as the categorical base quality scores assigned during concordant duplex base calling.

To assess potential read carry-over resulting from sensor module reuse, uniquely indexed HG001 libraries were prepared and converted to Xpandomer molecules. Libraries were sequenced in each position of an automated 4-run queue with a sensor module that had been used for nine previous runs (Figure 7). All reads were interrogated across all 96 available AXELIOS 1 sample indexes. No carry-over was observed in Run 1, whereas runs 2 to 4 showed less than 0.0015% carry-over. This negligible level of ready carry-over demonstrates the effectiveness of the standard, automated system cleaning protocols performed between runs and queues.

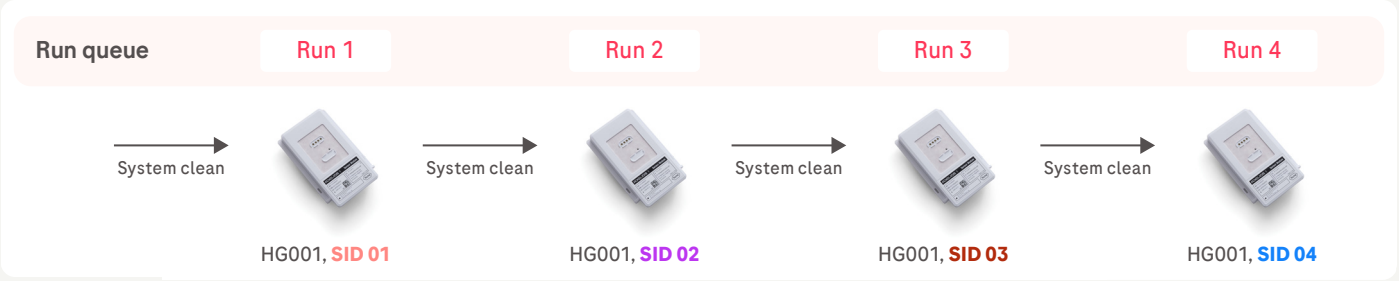


Figure 7. Assessment of read carry-over during sensor module reuse. Libraries were prepared as described above and sequenced on a previously used sensor module as described above (4-run sequencing queue; 4 hours sequencing time per run, excluding pre-sequencing setup and post-run cleanup).

Conclusion

The AXELIOS 1 Platform delivers consistent, highly reliable, and reproducible performance across the SBX-D workflow, from sample preparation through comprehensive data analysis for human germline WGS. Rigorous verification, involving 120 sequencing runs, was conducted to evaluate system robustness across an operational matrix that included 5 platforms, 5 unique operators, and 10 sensor modules. Utilizing 16-plex library pools prepared from human genomic DNA, including Genome in a Bottle (GIAB) benchmark materials (HG001 – HG007),[1] the platform successfully produced 1920 high-quality human genomes.

- The proportion of concordant duplex bases, which are used in the calculation of key performance metrics (e.g., accuracy, coverage, and sample throughput), ranged from ~68 – 74%.
- A per-run yield of ≥1.8 Tb of concordant duplex bases was achieved across all runs.
- Workflow consistency was demonstrated across sequential, automated runs. Key performance metrics such as accuracy, mean insert size, and coverage remained uniform for independent, uniquely composed library pools.
- Used in combination with XOOS analysis tools 1.0.0, the AXELIOS 1 Platform yielded consistent F1 scores for SNVs and indels.
- Longevity of the reusable AXELIOS 1 Sensor Module is a differentiating feature of the AXELIOS 1 Platform. Performance remains stable throughout the sensor module's 20-run lifespan.
- The standard, automated cleaning protocol performed between individual runs and within automated run-queues results in negligible (<0.0015%) read carry-over.

The AXELIOS 1 Platform establishes robust performance for human germline WGS, offering the reliability, high yield, and accuracy required for advanced and high-throughput germline research applications.



Performance metrics, such as output, mean read length, quality score, etc., can vary based on sample type and quality, library prep conditions, and loading concentration, along with other experimental conditions.

Be 1 step ahead with AXELIOS 1

References

1. Zook JM, et al. Extensive sequencing of seven human genomes to characterize benchmark reference materials. Sci Data. 2016 7(3):160025. doi: 10.1038/sdata.2016.25.
2. F. Hoffman-La Roche Ltd. AXELIOS 1 Germline WGS Workflow [Workflow guide; cited 2026 Aug 25]. Available here.
3. Wagner J, et al. Benchmarking challenging small variants with linked and long reads. Cell Genomics. 2022 2(5):100128. doi: 10.1016/j.xgen.2022.100128.

Published by

Roche Molecular Systems, Inc.
4300 Hacienda Drive
Pleasanton, CA USA 94588

diagnostics.roche.com

AXELIOS is a trademark of Roche.
All other trademarks and product names are the property of their respective owners.
All data on file unless otherwise indicated.
©2026 – All rights reserved.

MC--22723 v1.0.0926

For Research Use Only. Not for use in diagnostic procedures.