

Automated Genomic DNA Extraction from Whole Blood Using SwiftX™ Blood Genomic on the SwiftXtractor™ SL

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Summary

The SwiftX™ Blood Genomic kit (SXBG-100) enables extraction of human genomic DNA from anticoagulated whole blood. This application note describes the validation of an automated 200 µL whole-blood extraction protocol on the SwiftXtractor™ SL benchtop instrument, using program SXBG-SXT200 (Rev 2026-03). Three independent automated runs (n = 12 replicates total) were benchmarked against the manual reference protocol (n = 4). The automated workflow completed extraction in approximately 20 minutes per run, yielding a mean DNA concentration of 27.8 ± 2.8 ng/µL (~2.8 µg total yield per 200 µL input) with A260/A280 ratios of 1.51 ± 0.03 . Quantitative real-time PCR amplification of a multi-locus human DNA target demonstrated comparable amplifiability between automated and manually purified DNA (Δ Ct < 0.4 cycles). These results confirm that the SwiftXtractor SL delivers reproducible, automated genomic DNA extraction from whole blood with performance equivalent to the manual procedure.



SwiftXtractor™ SL
(Xpedite Diagnostics)

Introduction

Genomic DNA extraction from whole blood is a foundational step in molecular diagnostics and research workflows, including genotyping, pharmacogenomics, forensic analysis and infectious disease testing. Reliable extraction requires efficient lysis of white blood cells, effective removal of PCR inhibitors (hemoglobin, heparin, EDTA chelates), and consistent recovery of high-molecular-weight DNA suitable for downstream amplification.

The SwiftX™ Blood Genomic kit uses a magnetic bead-based capture chemistry optimized for whole-blood matrices. The manual protocol, described in the Instructions for Use (IFU), processes 200 µL anticoagulated blood through capturing & washing of white blood cells, and thermal cell lysis to yield purified genomic DNA in approximately 20 minutes.

Automation of nucleic acid extraction reduces hands-on time, minimizes operator variability, and improves reproducibility, critical considerations for laboratories seeking standardized workflows. The SwiftXtractor™ SL is a compact benchtop instrument designed to automate manual workflows of Xpedite's DNA/RNA extraction products.

For that, the instrument features passive liquid handling through magnetic rods. The instrument processes up to 4 samples per run through programmable mixing, magnetic separation, and thermal incubation steps.

This application note presents validation data for the SXBG-SXT200 automated program, comparing extraction performance against the established manual procedure using spectrophotometric and qPCR-based quantification.

Experimental Methods

Sample material. Citrate-anticoagulated whole blood was collected from a single donor and stored for a week at 2–8°C until processed. All automated and manual extractions used the same blood sample to enable direct comparison.

Reagents and consumables. Cell capturing and DNA purification were performed using the SwiftX Blood Genomic kit (Cat. No. SXBG-100, Xpedite Diagnostics GmbH). Consumables included injection-molded rod sleeves (SXT-RS-100), 5 mL tubes (SXT-5mL-500), and 2 mL tubes (SXT-2mL-250). For the automated process, molecular-grade water was used, which is not part of the SXBG-100 kit, but needs to be provided by the user.

Instrumentation. Automated extractions were performed on the SwiftXtractor™ SL (Xpedite Diagnostics GmbH). Manual extractions followed the SXBG IFU V1.0 protocol.

Automated protocol overview. The SXBG-SXT200 program executes a fully automated workflow that includes a molecular-grade water dip step does not present in the manual procedure, which improves DNA purity without compromising yield or processing time. Total run time is approximately 20 minutes. The complete workflow is illustrated in Figure 1.

Tube setup: Well 1 — 400 µL BGC + 10 µL Beads A + 200 µL blood; Well 2 — 400 µL BGW; Well 3 — 1000 µL H₂O; Well 6 — 100 µL BGL. Wells 4 and 5 remain empty.

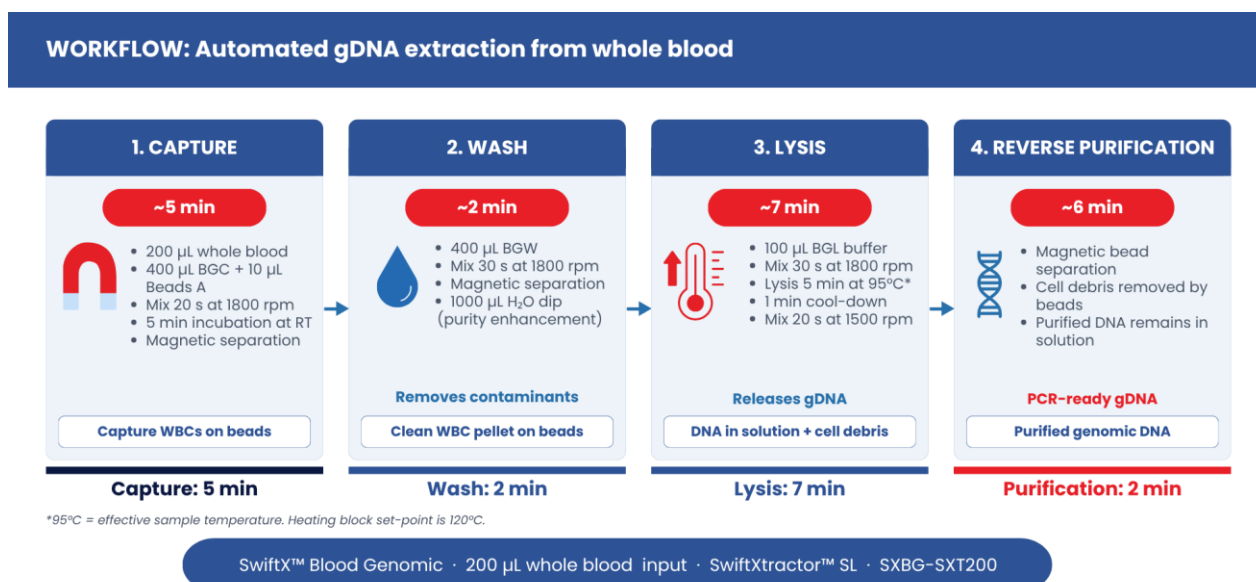


Figure 1 Automated workflow for genomic DNA extraction from 200 µL whole blood using the SwiftXtractor™ SL with program SXBG-SXT200. The 8-step protocol encompasses capture, wash (including an automated water dip for purity enhancement), thermal lysis, and final magnetic separation.

Experimental Design. Three independent automated runs were performed (4 replicates per run, n = 12 total). Four manual extractions served as the reference (n = 4). All extractions used 200 µL citrate whole blood as input.

Analysis. Extracted DNA was quantified by UV spectrophotometry (NanoPhotometer N60, Implen). DNA concentration was calculated from A260 values. Purity was assessed by A260/A280 and A260/A230 ratios. Amplifiability was confirmed by quantitative PCR with an in-house assay targeting a multi-locus target in human DNA. The assay was performed with SolisFAST Probe qPCR Mix (Solis Biodyne) using 5 μ L of purified DNA per reaction.

Results

The automated SwiftXtractor SL protocol yielded a mean DNA concentration of 27.8 ± 2.8 ng/ μ L in 100 μ L purified lysate across 12 replicates, corresponding to approximately 2.8 μ g total DNA per 200 μ L blood input. The manual reference protocol yielded 33.9 ± 2.2 ng/ μ L ($n = 4$). Both methods produced DNA with comparable A260/A280 ratios (automated: 1.51 ± 0.03 ; manual: 1.54 ± 0.03). A260/A230 ratios were equivalent between methods (0.50 ± 0.03 and 0.50 ± 0.01 , respectively).

Table 2 Summary of extraction performance: SwiftXtractor SL vs. manual reference. Values are mean \pm SD.

Sample Group	n	Conc. (ng/ μ L)	A260/A280	A260/A230	Ct (hnDNA qPCR)
SwiftXtractor SL	12	27.8 ± 2.8	1.51 ± 0.03	0.50 ± 0.03	20.60 ± 0.23
Manual reference	4	33.9 ± 2.2	1.54 ± 0.03	0.50 ± 0.01	20.24 ± 0.11

Run-to-run reproducibility was assessed across three independent automated runs. Concentration CV was 10.2% across all 12 automated replicates, with individual run average concentrations ranging from 24.8 to 29.6 ng/ μ L. Ct values showed excellent reproducibility (CV = 1.1%), with a total range of 20.33 to 20.96 across all automated samples.

Table 3 Per-run performance of the automated protocol. Values are mean \pm SD ($n = 4$ per run).

Run (n = 4 each)	Conc. (ng/ μ L)	A260/A280	Ct (hnDNA)	Total run time
Run 1	24.84 ± 2.35	1.476	20.53 ± 0.27	20 min 11 s
Run 2	28.95 ± 2.26	1.538	20.46 ± 0.11	20 min 12 s
Run 3	29.56 ± 1.12	1.502	20.81 ± 0.13	20 min 12 s

All automated extracts are amplified successfully in the qPCR assay. The mean Ct for automated samples was 20.60 ± 0.23 , compared to 20.24 ± 0.11 for manual extracts, a difference of 0.36 Ct cycles. This minor shift is consistent with the slightly lower DNA concentration in automated extracts and confirms that the automated workflow does not introduce PCR inhibitors or compromise DNA integrity.

Discussion

This validation demonstrates that the SwiftXtractor SL, running the SXBG-SXT200 program, delivers automated genomic DNA extraction from 200 μ L whole blood with performance comparable to the established manual protocol. The automated workflow achieves consistent yields (~ 28 ng/ μ L), acceptable purity ratios, and equivalent qPCR amplifiability, all within a 20-minute, walk-away run.

The slightly lower average concentration in automated extracts compared to the manual reference (27.8 vs. 33.9 ng/ μ L) likely reflects the addition of a water dip step (Step 4) in the automated protocol. This step, not present in the manual workflow, provides an additional purity-enhancing rinse of the captured white blood cell pellet prior to lysis, which may remove a small fraction of loosely bound material. The trade-off is favorable: the purity benefit of the water dip is reflected in equivalent or improved downstream amplification performance, with a Ct difference of only 0.36 cycles.

The qPCR Ct coefficient of variation of 1.1% across 12 automated replicates underscores the reproducibility of the extraction process. Run time consistency (± 1 second across three runs) confirms the deterministic nature of the automated protocol, eliminating operator-dependent timing variation inherent to manual workflows.

The SXBG-SXT200 protocol was validated on citrate-anticoagulated blood. The SwiftX Blood Genomic kit is designed for use with EDTA, citrate, and heparin-anticoagulated blood as well as untreated blood samples. Users working with alternative anticoagulants should expect comparable performance, though specific validation is recommended.

Conclusion

The SwiftXtractor™ SL with program SXBG-SXT200 provides a validated, fully automated workflow for genomic DNA extraction from 200 μ L whole blood using the SwiftX™ Blood Genomic kit. The 20-minute walk-away protocol delivers reproducible yields and PCR-ready DNA quality, making it suitable for routine laboratory use in molecular diagnostics and research settings.

Ordering Information

SwiftX™ Blood Genomic Kit — Cat. No. SXBG-100 (100 extractions)

SwiftXtractor™ SL Instrument — Cat. No. SXT-SL (Contact Xpedit Diagnostics for pricing)

Rod Sleeves — Cat. No. SXT-RS-100

5 mL Tubes — Cat. No. SXT-5mL-500

2 mL Tubes — Cat. No. SXT-2mL-250

Barcode Scanner — Cat. No. SXT-BCS

The SXBG-SXT200 program file and program sheet are available on request: contact our technical support via info@xpedit-dx.com.

SwiftX™ Blood Genomic and SwiftXtractor™ SL are for Research Use Only (RUO).
Not for use in diagnostic procedures.

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