

# Fast, Automated Method for Improved Genomic DNA Isolation from Human Whole Blood Using NiXTips®

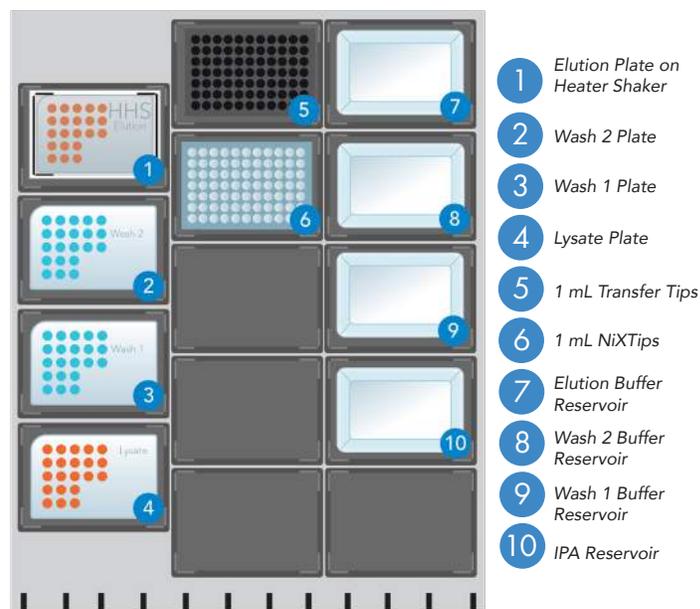
SLAS 2026 Poster Summary: Leighton Buckner, Paul Meeh, William Brewer, PhD, Kaylee Mastrianni, PhD

**HIGHLIGHTS:** Fully automated, reproducible, high-quality gDNA



## INTRODUCTION

High-quality genomic DNA (gDNA) is critical for downstream molecular biology and genomic applications. While magnetic bead technology has been widely adopted for gDNA extractions, bead capture time, bead carryover, bead resuspension and requirements for magnets complicate the process. Increasing demands for consistency and automation have driven the development of more streamlined extraction solutions. DPX Technologies' patent-pending NiXTips® address these challenges. Designed for automated liquid handlers, NiXTips enable fully automated isolation of high-quality gDNA from whole blood. The proprietary microporous media integrates bind, wash, and elute steps within a single pipette tip, reducing consumable use, minimizing contamination risk, and supporting high-throughput processing. In this study, 1 mL Hamilton style NiXTips were evaluated for automated gDNA isolation from single-donor human whole blood. Results demonstrate reproducible recovery of pure, high-molecular-weight gDNA across variable blood inputs with minimal user intervention, highlighting NiXTips as a scalable alternative to bead-based methods.

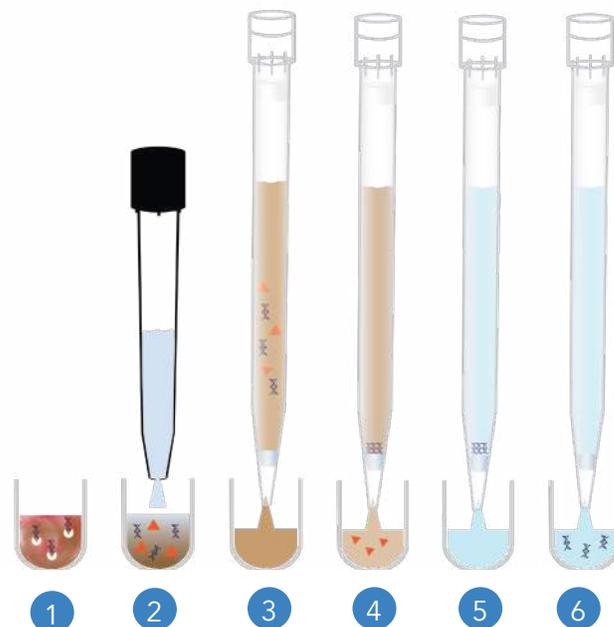


**Figure 1.** Deck layout of Hamilton STARlet used for NiXTips workflow. Customizable to customer's needs.

## MATERIALS AND METHODS

Genomic DNA was extracted from single-donor human whole blood collected in K<sub>2</sub>EDTA tubes (Innovative Research) using 1 mL Hamilton style NiXTips (DPX Technologies, Cat # NIX-HM1000-96) and the accompanying room temperature stable buffer system that includes lysis buffer, proteinase K, wash 1 buffer, wash 2 buffer, and elution buffer. Isopropanol (IPA) was also utilized but is not included in the NiXTips kit.

The NiXTip extraction method was performed on a Hamilton STARlet automated liquid handler (ALH) using a DPX-designed, commercially available automation script (**Figure 1**). For the NiX protocol, 250 µL of whole blood was lysed and then loaded onto the ALH. Well plates were loaded with wash 1, wash 2, and elution buffers. IPA was added to a reservoir. Lysis and accessioning can be performed on the larger Hamilton robots as well. Blank 1 mL transfer tips and the NiXTips were also loaded on the deck. The steps for extraction are shown in **Figure 2/**Table 1. For comparison, a leading bead-based gDNA extraction kit was utilized following the manufacturer's recommended protocol for a 250 µL human whole blood sample.



**Figure 2.** Schematic of the 1 mL NiXTips workflow outlined in Table 1.

**Table 1.** Method for DNA extraction from 250  $\mu\text{L}$  of single donor human whole blood using 1 mL NixTips.

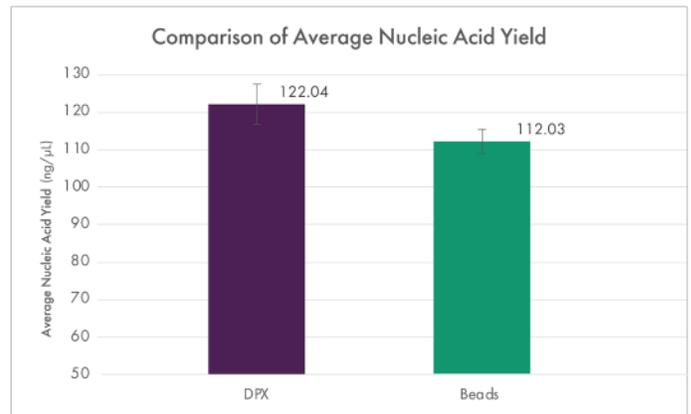
<b>1 Lyse</b>	Combine 250 $\mu\text{L}$ blood + 250 $\mu\text{L}$ lysis buffer + 25 $\mu\text{L}$ pro K. Incubate at 56°C for 10 min.
<b>2 Precipitate</b>	Add 350 $\mu\text{L}$ of IPA to lysate with transfer tips. Aspirate and dispense 25x.
<b>3 Bind</b>	Aspirate and dispense lysate 15x with 1 mL NiXTips.
<b>4 Wash 1</b>	Aspirate and dispense 900 $\mu\text{L}$ of wash 1 buffer 2x.
<b>5 Wash 2</b>	Aspirate 900 $\mu\text{L}$ wash 2 buffer, dispense to waste. Aspirate and dispense second aliquot of 900 $\mu\text{L}$ wash 2 buffer. Dry by aspirating and dispensing 1 mL of air 4x.
<b>6 Elute</b>	Aspirate and dispense 100 $\mu\text{L}$ of elution buffer at 56°C 5x.

A linearity study was conducted using NiXTips with blood inputs ranging from 100-400  $\mu\text{L}$  and proportional amounts of lysis buffer, proteinase K, wash 1 buffer, and wash 2 buffer. Elution buffer volume remained constant at 100  $\mu\text{L}$  and was heated to 56°C for all input volumes. To ensure reproducibility across days and manufacturing batches, the linearity study was repeated on two days with a different product batch each day.

DNA yield and purity were measured using a Thermo Fisher NanoDrop One Microvolume UV-Vis Spectrophotometer. DNA integrity was assessed using an Agilent 5200 Fragment Analyzer with the Genomic DNA 50 kb Kit. DNA quality was confirmed by performing real-time PCR on a QuantStudio™ 3 with the TaqMan™ Copy Number Reference Assay (RNase P) and TaqMan Genotyping Master Mix (Thermo Fisher). gDNA isolated using both NiXTips and beads was sent out for Oxford Nanopore sequencing at the USC Genomics Core Facility.

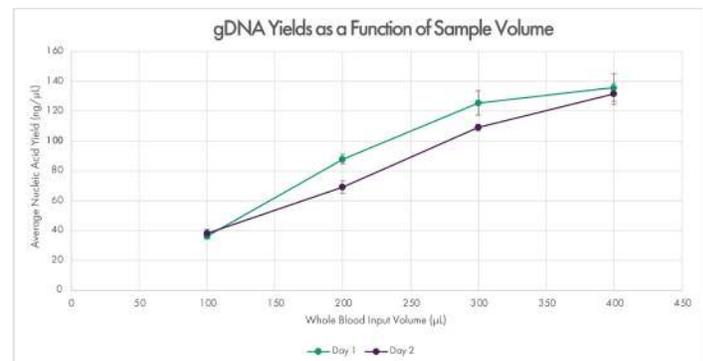
## RESULTS

NiXTips consistently isolated high-quality gDNA from human whole blood. Spectrophotometry confirmed high purity with an average A260/280 of 1.88 and an average A260/230 of 2.29, indicating minimal protein and salt contamination. Average DNA yield obtained with NiXTips (122.04 ng/ $\mu\text{L}$ ) exceeded a leading bead-based kit (112.03 ng/ $\mu\text{L}$ ) (**Figure 3**).



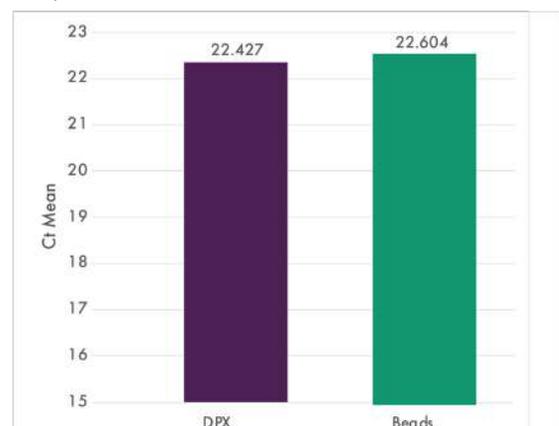
**Figure 3.** Direct comparison of average DNA yields from 250  $\mu\text{L}$  of human whole blood with DPX NiXTips (n=4) versus a leading bead-based competitor (n=4).

The results of the linearity and reproducibility study shown in **Figure 4** illustrate that the performance of NiXTips is consistent across days and batch numbers.



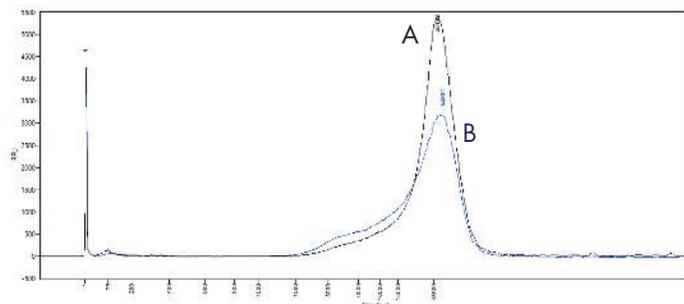
**Figure 4.** Comparison of gDNA yields (ng/ $\mu\text{L}$ ) using 1 mL NiXTips as a function of sample volume (100, 200, 300, 400  $\mu\text{L}$  whole blood) measured over a two-day study. Separate lines represent data collected on Day 1 and Day 2, with a different batch of NiXTips used on each day. For each volume, four replicates were tested (n=4 per volume; 16 samples per day).

Real-time PCR resulted in comparable mean cycle threshold (Ct) values for gDNA isolated using NiXTips versus the bead-based competitor (**Figure 5**). Lower Ct values indicate earlier target detection, allowing direct comparison of performance between the two products.



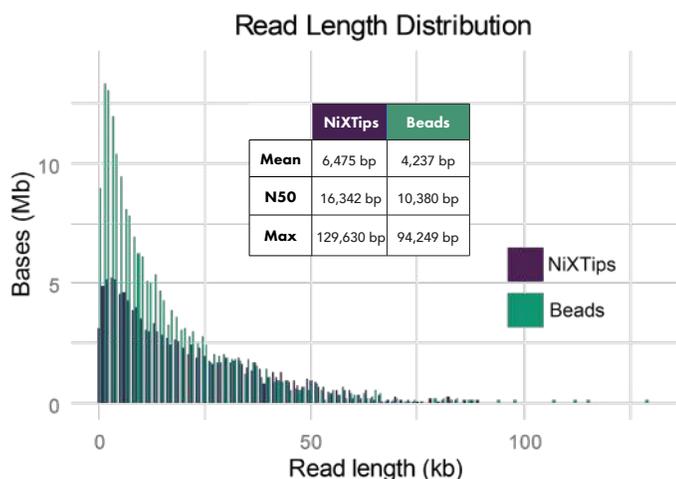
**Figure 5.** PCR was performed on replicates of gDNA isolated from 250  $\mu\text{L}$  of whole blood using 1 mL NiXTips (n=8) and a leading bead-based competitor (n=4).

DNA fragment analysis confirmed recovery of high-molecular-weight gDNA using both NiXTips and beads (**Figure 6**). However, DNA concentration was greater in the NiXTips sample as demonstrated by the higher RFU peak. Additionally, the shape of the peak indicates the NiXTips sample resulted in less shearing than the magnetic bead method. Comparison of the average fragment sizes supports this observation (NiXTips: 44,185 bp, beads: 37,422 bp).



**Figure 6.** Agilent 5200 Fragment Analyzer traces of genomic DNA (gDNA) isolated using DPX NiXTips compared to bead-based extraction. Analysis was performed with the Genomic DNA 50 kb Kit. (A) gDNA isolated using DPX NiXTips. (B) gDNA isolated using a bead-based method.

**Figure 7** demonstrates the compatibility of gDNA isolated using NiXTips with Oxford Nanopore Sequencing. gDNA isolated from single-donor human whole blood using NiXTips exhibited superior read lengths compared to a bead-based competitor, enabling better resolution of complex genomic regions. Although the beads yielded a higher number of total bases (197.6 Mb vs. 129.2 Mb), both samples showed excellent mapping rates to the human reference (>99.6%), with DPX achieving the highest (99.74%).



**Figure 7.** Read length distribution comparing gDNA isolated using DPX NiXTips (purple) and a bead-based competitor (green). The DPX sample shows a right-shifted distribution with an enrichment of ultra-long fragments (>50 kb), reflecting superior preservation of high-molecular-weight DNA and enhanced long-read sequencing performance.

## CONCLUSIONS

This study demonstrates that 1 mL NiXTips enable efficient, fully automated isolation of high-quality genomic DNA from human whole blood on the Hamilton STARlet platform. The workflow consistently produced gDNA with strong yields, excellent purity, and preserved molecular integrity across a range of blood input volumes, confirming the suitability of NiXTips for processing a complex and variable sample matrix.

Compared to a leading bead-based extraction method, NiXTips delivered higher average gDNA yields while maintaining comparable or improved purity and reproducibility. The consistency observed across replicate extractions, multiple tip batches, and different processing days highlights the robustness of the NiXTips format and its reliability in routine automated workflows.

Integration of binding, washing, and elution within a single enclosed tip simplifies the extraction process, reduces workflow complexity, and minimizes opportunities for contamination. Elimination of magnetic separation steps further enhances automation efficiency and scalability, making NiXTips well suited for high-throughput laboratories.

The high quality of the recovered DNA, supported by qPCR performance, fragment analysis, and successful long-read sequencing, demonstrates compatibility with a broad range of downstream genomic applications, including genotyping, next-generation sequencing, and short-read sequencing. Collectively, these results position NiXTips as a robust and scalable alternative to bead-based technologies for automated genomic DNA isolation from whole blood.