Automated Genomic DNA Isolation from Cell Lines Using NiXTips™

HIGHLIGHTS: Efficient, Reproducible, Scalable, Reduced Consumable Waste

NIX

INTRODUCTION

Extraction and purification of genomic DNA (gDNA) is a critical step in molecular biology and genomics workflows. The quality, purity, and yield of isolated gDNA directly affect downstream applications such as sequencing, mutation screening, and genetic engineering. While manual nucleic acid extraction methods remain common due to their accessibility and low cost, they are often labor intensive, time consuming, and prone to contamination or variability. Increasing demands for throughput, consistency, and automation have driven the development of more efficient solutions.

DPX Technologies has developed NiXTips (patent-pending) to address these needs. Designed for use on automated liquid handlers, NiXTips enable fully automated isolation of high-quality gDNA from diverse sample types, including adherent and suspension cell lines. The technology uses a proprietary microporous media that integrates lysis, binding, washing, and elution within a single pipette tip. This enclosed format minimizes contamination risk, simplifies workflow design, and streamlines high-throughput processing.

In this study, we demonstrated the performance of 300 µL Hamilton NiXTips for automated gDNA extraction. Results highlight the ability of the system to deliver reproducible yields of pure gDNA with minimal user intervention. Collectively, these features position NiXTips as an efficient, scalable alternative to manual extraction methods, enabling high-quality gDNA isolation for demanding genomic applications.

MATERIALS AND METHODS

Genomic DNA was extracted from human whole blood–derived induced pluripotent stem cells (iPSCs) using DPX Technologies' NiXTips along with DPX's proprietary buffer system. (Lysis, Wash and Elution Buffer) (*Cat#: NIX-HM300-96*). Extractions were performed with 300 µL NiXTips on a Hamilton STARlet Liquid Handler. iPSC suspensions (50 µL in PBS) were combined with 10 µL Proteinase K and 50 µL Lysis Buffer, then incubated at 56 °C for 10 minutes. Following lysis, 75 µL isopropyl alcohol was added and mixed by pipetting with blank tips. The NiXTips were then used to capture the gDNA via repeated aspirate/dispense cycles. Samples were washed three times with Wash Buffers, dried by air expulsion, and eluted in 50 µL Elution Buffer at 56 °C. Automated extractions were performed using a DPX-designed, commercially available, Hamilton script **Figure 1**.

DNA yield and integrity were assessed with an Agilent 5200 Fragment Analyzer using the Genomic DNA 50 kb Kit. Quantification and quality control were performed with a QuantStudio 3 Real-Time PCR System using the TaqMan™ Copy Number Reference Assay (RNase P) with TaqMan Genotyping Master Mix and by 1.5% agarose gel electrophoresis with GelRed (Biotium Inc., 10,000X in water) staining.

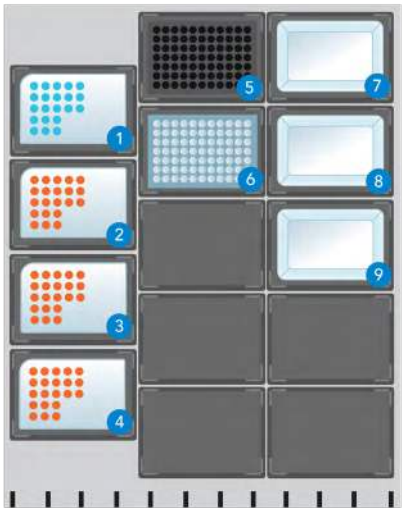

Figure 1. *Deck layout of Hamilton STARlet used for NiXTip workflow. Customizable to customer's needs.*

RESULTS

The 300 µL NiXTips were evaluated using 1:2 serially diluted iPSCs (N=5, starting at 88,500 cells per 50 µL sample in growth media). gDNA was isolated with high purity, as evidenced by A260/280 ratios >1.8 and A260/230 ratios >2.0, indicating minimal protein or salt contamination. qPCR confirmed consistent gDNA yields across dilutions, as shown in **Figure 2**, suitable for sensitive downstream applications. NiXTips resulted in 113% of the concentration of DNA compared to beads when averaged across the concentration range. NiXTips also produced improved Ct values with superior reproducibility as shown in **Figure 3**.

Gel electrophoresis compared gDNA from NiXTips to a bead-based method. Each lane was loaded with 10 µL of isolated gDNA, with Lane 1 containing 1 µL of 1 kb Plus DNA Ladder (Invitrogen) for size reference. NiXTips produced sharper, higher-molecular-weight bands, indicating superior gDNA integrity, as shown in **Figure 4**.

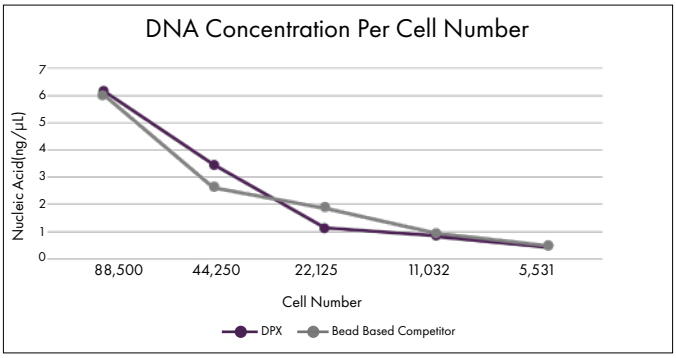

Figure 2. *Comparison of gDNA yields (ng/µL or total ng) from 300 µL NiXTips vs. bead-based method across the 5 dilutions, based on qPCR data from QuantStudio 3.*

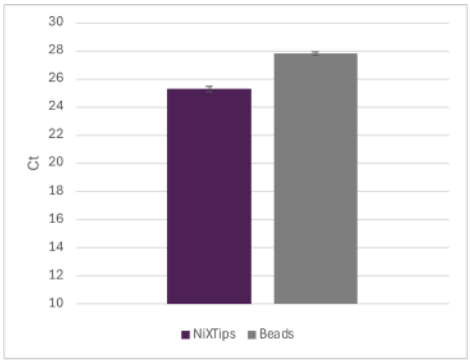

Figure 3. *PCR results if eight replicates of 88,500 iPSC input were processed with NiXTips using a 50 µL elutions. Average yield was 15.16 ng/µL.*

Sizing analysis on the Agilent 5200 Fragment Analyzer with the Genomic DNA 50 kb Kit, shown in **Figure 5**, revealed high-molecular-weight gDNA from NiXTips with minimal shearing compared to the bead-based method, supporting its suitability for NGS, including both short- and long-read sequencing.

The NiXTips consistently produced high yield, purity, and fragment integrity, demonstrating robustness across a range of cell concentrations. The method was optimized for 50 µL samples in growth media or PBS, but can process samples containing anywhere from 2,500 to 100,000 cells, with a maximum input volume of 100 µL. If higher capacity and/ or sample volume are required, 1 mL NiXTips are recommended.

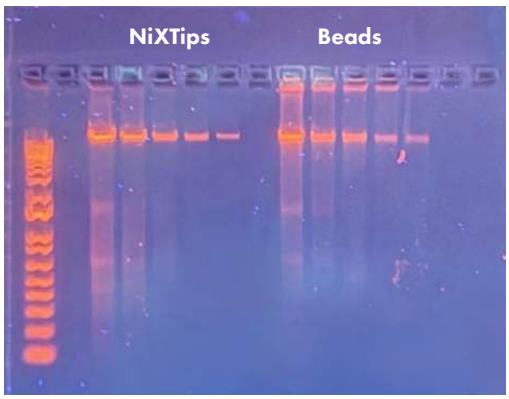

Figure 4. *1.5% agarose gel image stained with GelRed Nucleic Acid Stain, showing 5 lanes of 1:2 serially diluted iPSC samples (10 µL gDNA/ lane) isolated via 300 µL NiXTips vs. a bead-based method. Lane 1: 1 kb Plus DNA Ladder (1 µL, Invitrogen).*

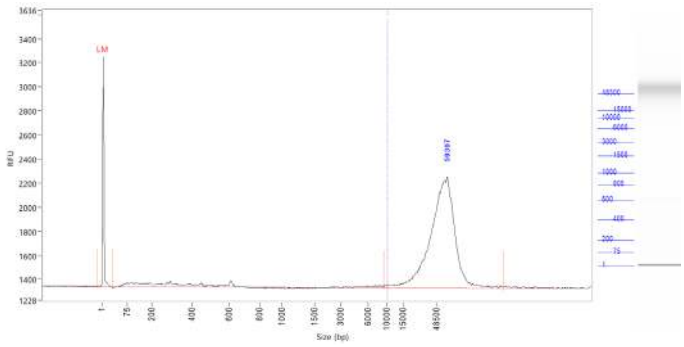

Figure 5. *Agilent 5200 Fragment Analyzer trace using the Genomic DNA 50 kb Kit, showing high-molecular-weight gDNA from 300 µL NiXTips with minimal shearing.*

DISCUSSION

This study demonstrates that NiXTips facilitate automated, high-quality genomic DNA isolation on the Hamilton STARlet platform. Using iPSCs as a representative sample, the workflow consistently produced high-yield gDNA with excellent purity and fragment integrity; as confirmed by spectrophotometry, qPCR quantification, agarose gel electrophoresis, and Fragment Analyzer traces. Yields were high, and the resulting DNA was of high molecular weight with minimal shearing, comparable to traditional bead-based methods. These results highlight the system's ability to reliably isolate gDNA from sensitive cell types while minimizing manual handling and user error. The NiXTip method integrates lysis, binding, washing, and elution within a single tip, streamlining the workflow and reducing both contamination risk and consumable waste. This efficient, automation-friendly approach accelerates processing times and is adaptable to a wide range of sample types, including cultured cell lines, whole blood, and other biologically relevant materials. The high-quality gDNA recovered using this method is suitable for numerous downstream applications, including mutation screening, transfection and CRISPR-based editing, next-generation sequencing (NGS) library preparation, genotyping, and clonal stability analysis, supporting robust and reproducible results while conserving resources.

Available NiXTips Formats:

Automations	Volume			Amount	
Hamilton	50 µL	300 µL		96 tips/rack	
Integra	125 μL_1	300 µL*	1250 µL*	384 $tips/box_1$	96 tips/rack*
Agilent	70 µL			384 tips/box	
Tecan	200 µL*			96 tips/rack*	

*Coming Soon

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