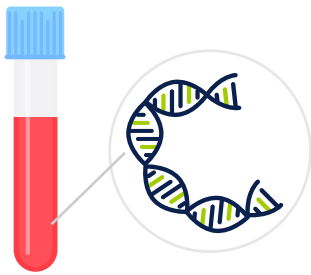


NiX tipsTM

Product Guide

DPX offers innovative technology for fast and effective genomic sample preparation.



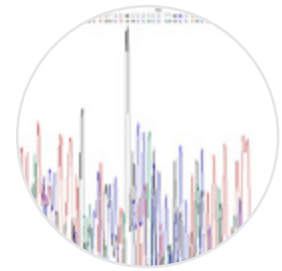
Nucleic Acid Extraction

MPX technology provides automated extraction for genomic DNA from whole blood. Download the MPX product guide to learn more.



Library Preparation

NiX technology provides automated size selection, PCR cleanup, and ligation reaction cleanup.

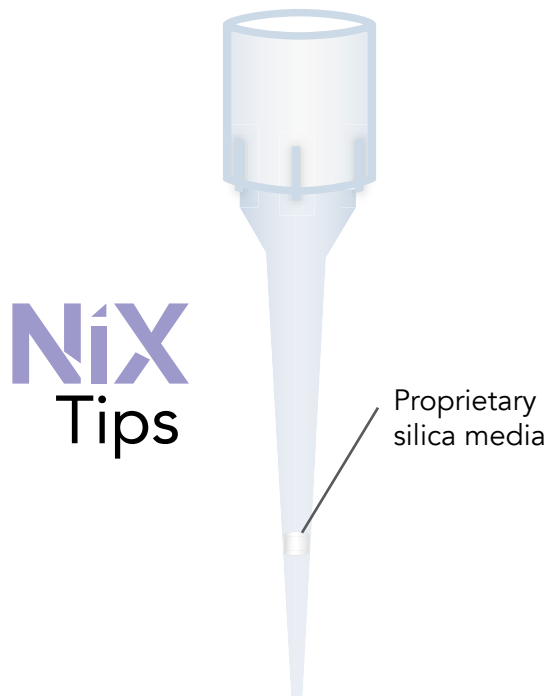


Sequencing & Analysis

MPX and NiX technology provide high yield solutions for next generation sequencing and other downstream DNA enzymatic reactions.

Solid Phase Reversible Immobilization powered by NiX tips

Anatomy:



Solid Phase Reversible Immobilization (SPRI) is commonly used for purifying and size selecting nucleic acids in Next Generation Sequencing (NGS) library preparation methods and a variety of applications for genomics research. Our innovative NiX tips utilize a proprietary microporous media and buffer system to allow for fast and effective removal of primers, primer-dimers, dNTPs, unincorporated labeled nucleotides, enzymes, and salts from PCR and other reaction mixtures.

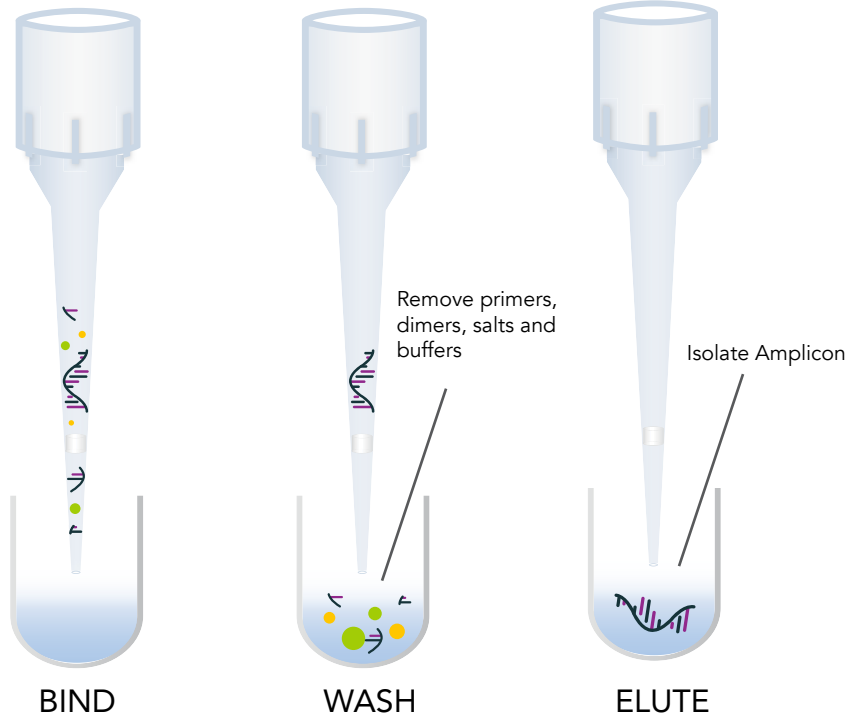
Technology Advantages:

- Eliminate need for ancillary equipment like centrifuges, vortex mixers, vacuum manifolds or magnet setups
- Reduce risk of nucleic acid shearing
- Pure sample ready for NGS and other downstream applications

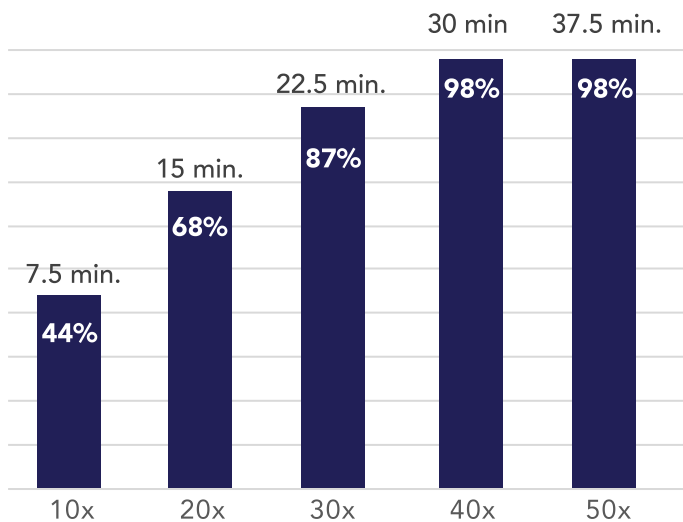
Robust and reliable methods for processing up to 384 samples in less than 30 minutes!

NiX Methods

Boost efficiency and reproducibility with fully automated methods using NiX tips. NiX tips can power INTip SPRI methods to replace traditional spin column or magnetic bead methods while reducing the opportunity for sample contamination and experimental errors.

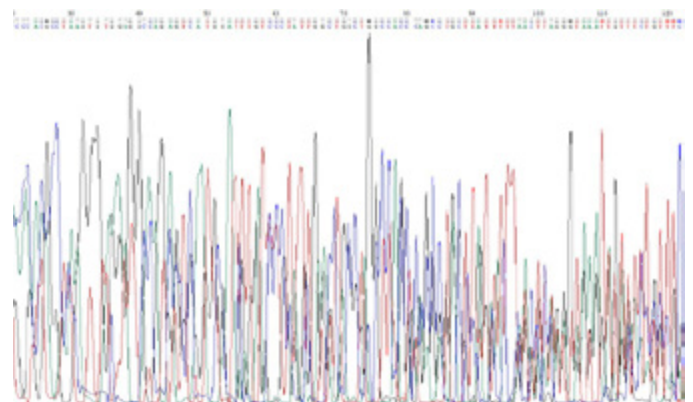


Average Yield Based on Number of Binding Cycles



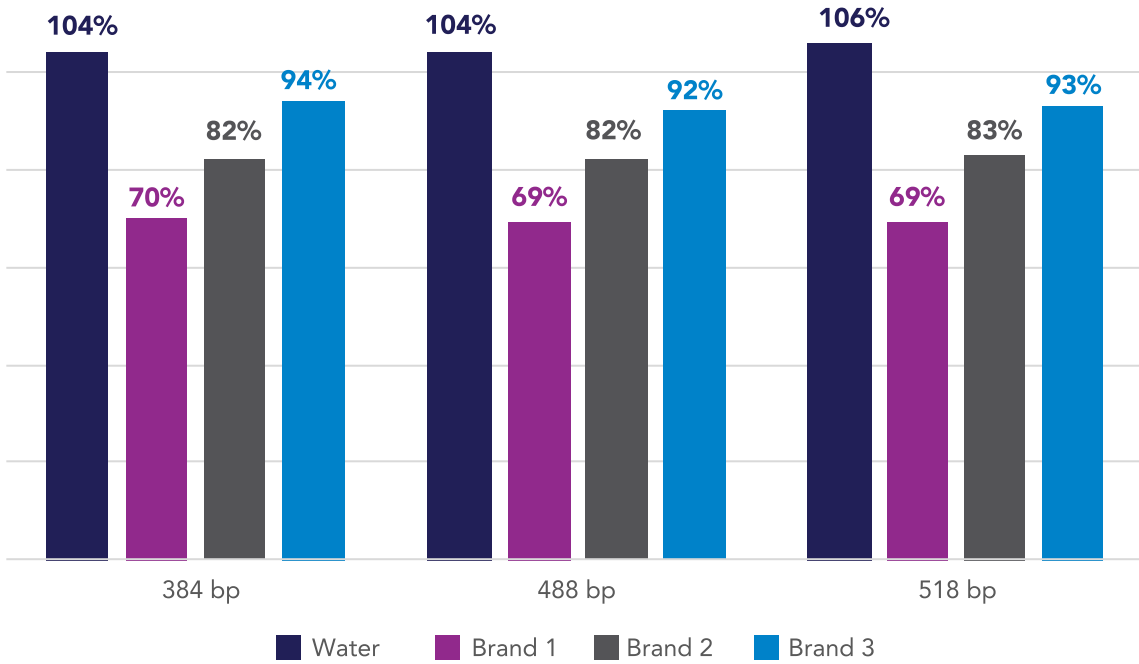
The chart above shows close to 100% yield with 40 or more binding cycles based on the response of 4 fragments ranging from 325-510 bp. Applications requiring less yield can reduce binding cycles for even faster workflows.

Quality Assurance



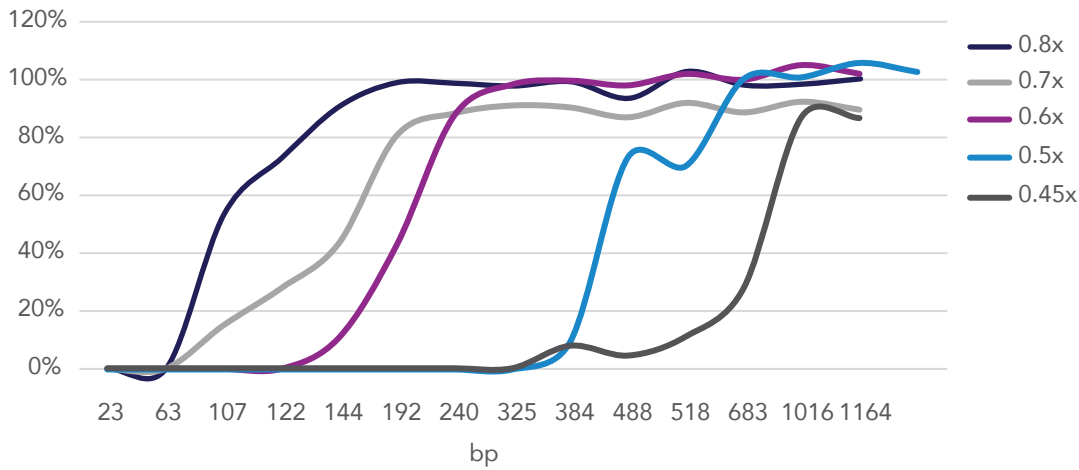
Sanger sequencing of replicates of an amplicon from the human GAPDH gene serves as a validation, affirming the efficacy and quality of NiX tips for PCR cleanup.

DNA Yield



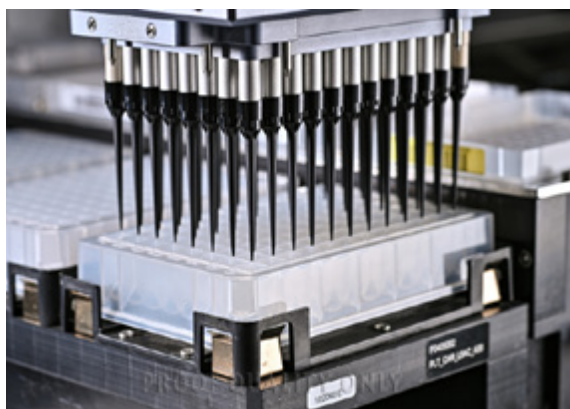
Comparison of DNA yield using different PCR master mixtures.

Left Side Size Selection



The ratio of binding buffer to sample solution can provide optimization of specific removal of desired range of bp. In the chart on the left, a 25 μ L sample was utilized with a DNA MWM ranging from 19 bp-1164 bp. The amount of binding buffer was decreased by the fraction shown to reduce recovery of the smaller DNA fragments.

Specifications



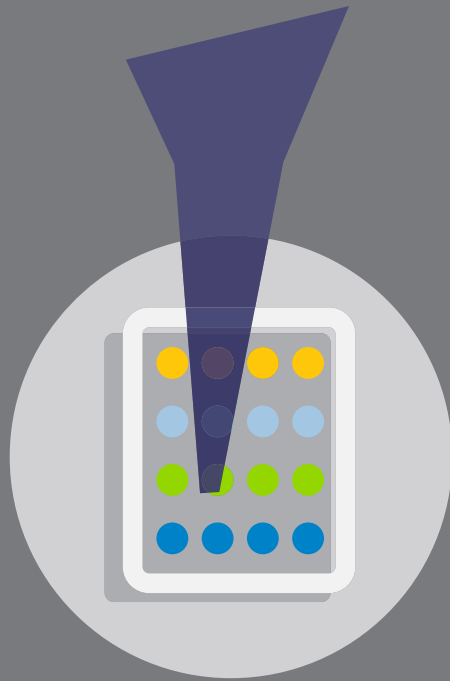
NiX tips on a Hamilton STAR system shown above.

NiX methods currently compatible with Hamilton Robotics systems and Agilent Bravo. Kits contents include tips and binding buffer

NiX Tip Formats:

- 50 μ L Hamilton, 96 tips/ rack
- 70 μ L Bravo, 384 tips/ rack

| | |
|-------------------------|---|
| Downstream Applications | PCR reactions and other DNA enzymatic reactions |
| Starting Material | dsDNA, DNA fragments, PCR products |
| Starting Amount | 20-25 μ L |
| Elution Volume | 25-50 μ L |
| Separation Range | > 100 bp |
| DNA Recovered | up to 100% depending on fragment size and buffer composition |
| Binding Capacity | 40 μ g |
| Processing Mode | Manual, automated |
| Throughput | 1- 384 depending on tip format |
| DNA Binding Technology | Proprietary silica media |
| Processing Time | 25 min. |
| Special Notes | Different PCR master mixtures affect binding and yield of DNA fragments |



dpxtechnologies.com