

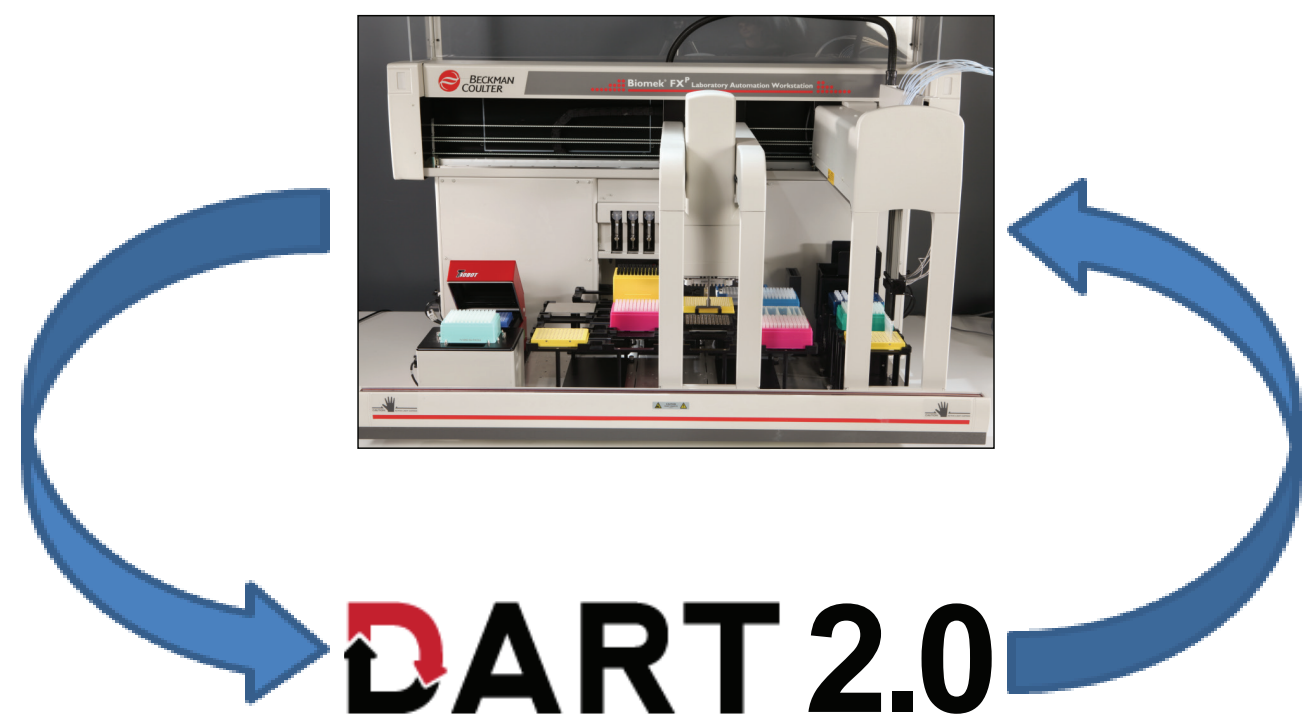
Automated NGS Sample Prep with Integrated Data Management and Reporting Tools



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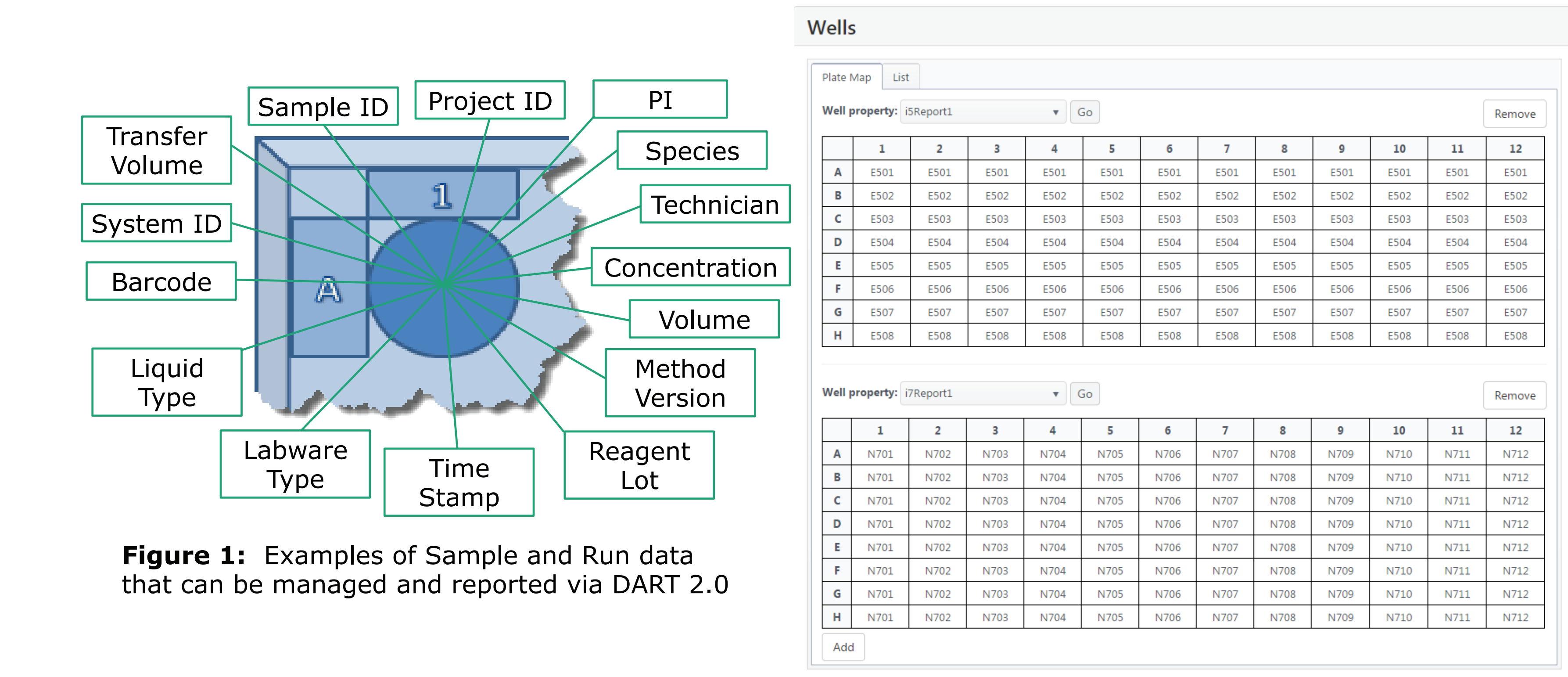
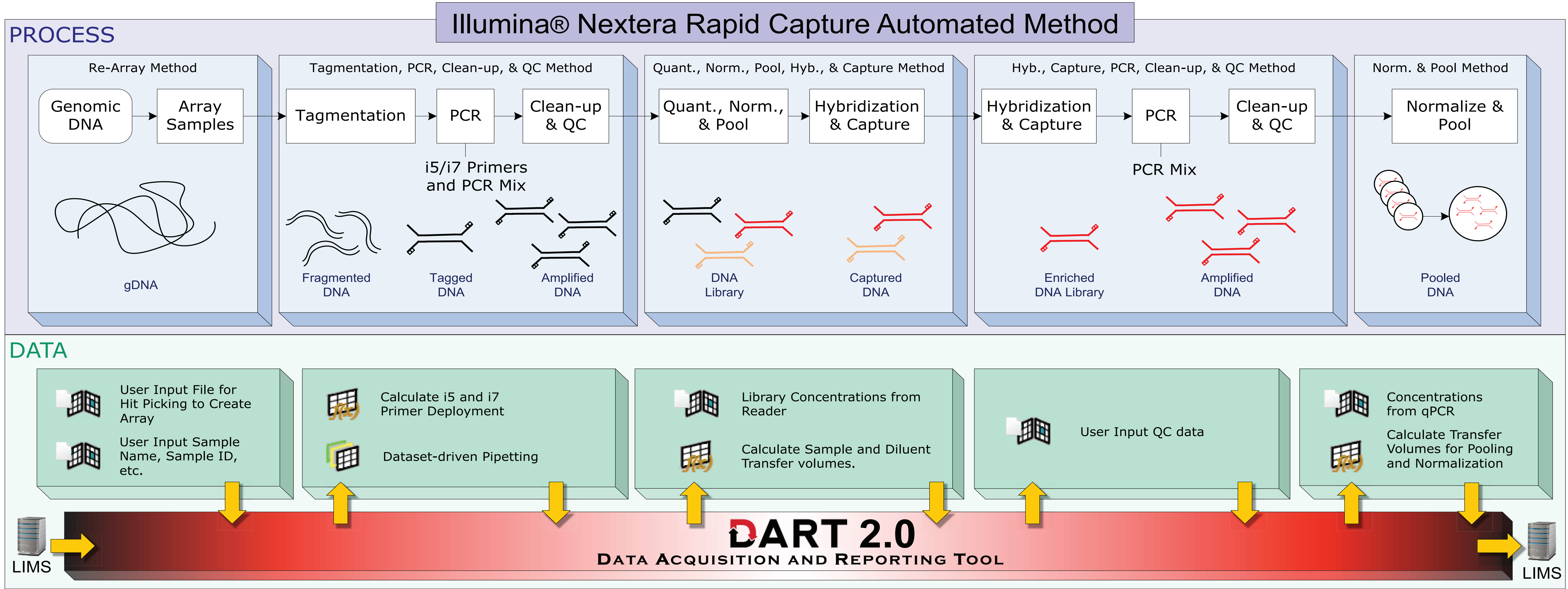
Introduction

Given the high capacity of modern next generation sequencing platforms, high throughput library construction of multiplexed next generation sequencing libraries has become standard practice in many facilities. Many Sequencing Core and Services labs have implemented liquid handling automation to streamline their process, lower costs, and reduce the labor burden. However, there's still the challenge of managing the massive amount of data that flows through the library construction process. Tracking and managing sample IDs and their associated meta-data is vital to ensuring that samples are processed correctly. An effective liquid handling data management system enables data tracking, importing, data driven actions, reporting and interaction with a laboratory information management system (LIMS). This poster demonstrates these capabilities through the use of Beckman's Biomek datasets and the Data Acquisition and Reporting Tool.



Data Tools

Biomek Datasets are a collection of tools native to the software that allow for the importation and manipulation of data from a variety of sources, including user supplied files and LIMS generated files. Such meta-data, including Agilent Bioanalyzer 2100 RIN scores and concentration data from fluorometric plate readers, can be employed in data-driven transfer tasks like normalization and size selection. DART 2.0 (Data Acquisition and Reporting Tool) is a software package that gathers meta-data and synthesizes runtime information from Biomek log files to capture every manipulation of the sample during the course of the method. DART 2.0 also introduces new steps that can be integrated into Biomek methods which allows for the creation of new datasets for pipetting and reporting functions, the addition of user or LIMS supplied information for data-driven pipetting, and the creation of customizable reports during the course of a Biomek method. These steps also simplify the method writing process by reducing the need for custom scripts. Finally, the addition of DART 2.0 allows the efficient porting of data between Biomek method and between individual liquid handlers, which allows for more complex workflows to be envisioned.



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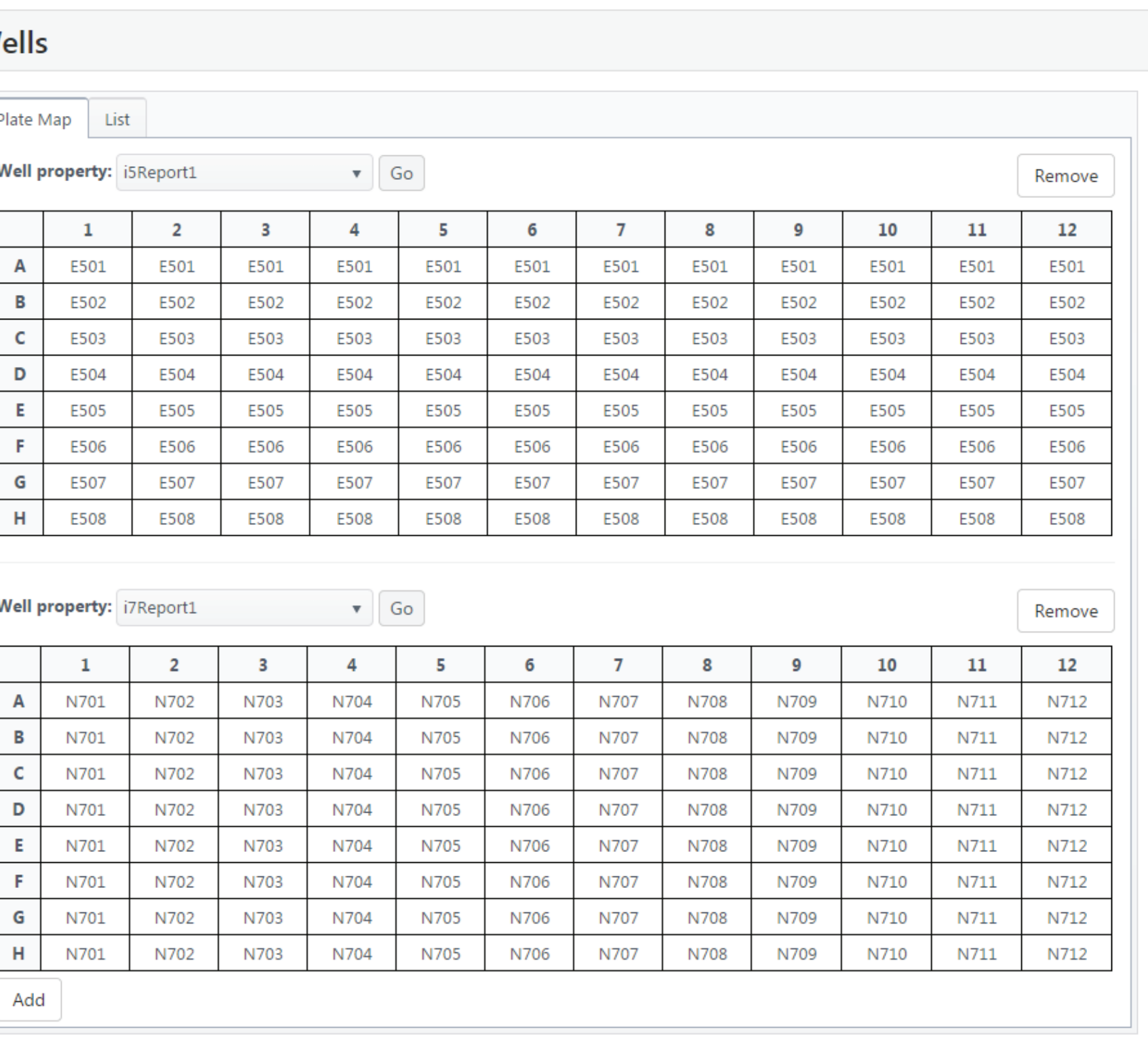


Figure 2: i5 and i7 primer deployment by the Biomek method as shown in the DART 2.0 Web Browser

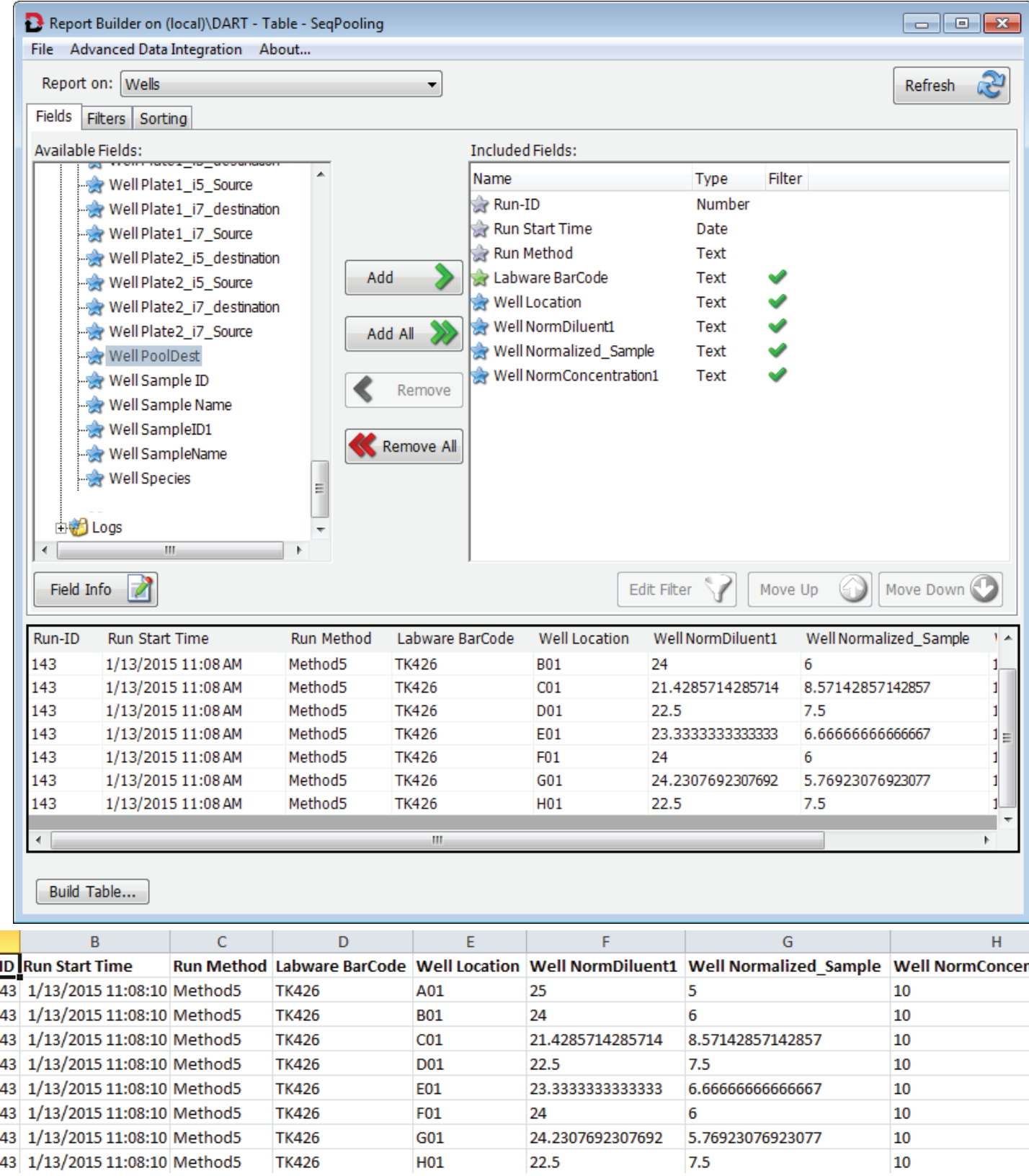


Figure 3: Target Pool Concentration (nM) and the volumes of sample and diluent required for pool normalization prior to sequencing. Report generated from DART 2.0 Report Builder

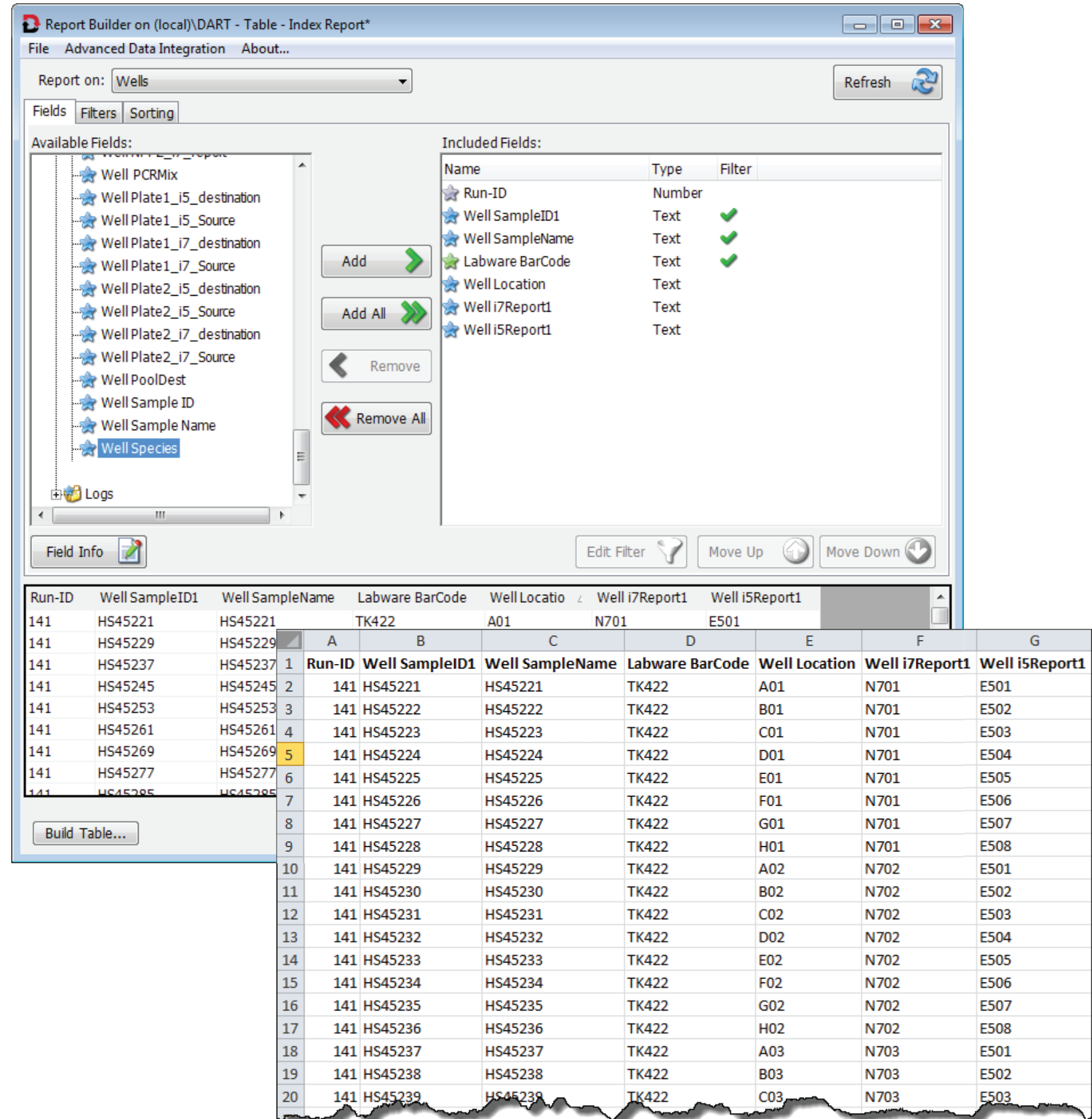


Figure 4: DART 2.0 report containing Sample Name, Sample ID, i5 primers, and i7 primers for entry into Illumina® Experiment Manager software. Report generated using DART 2.0 Report Builder