# 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

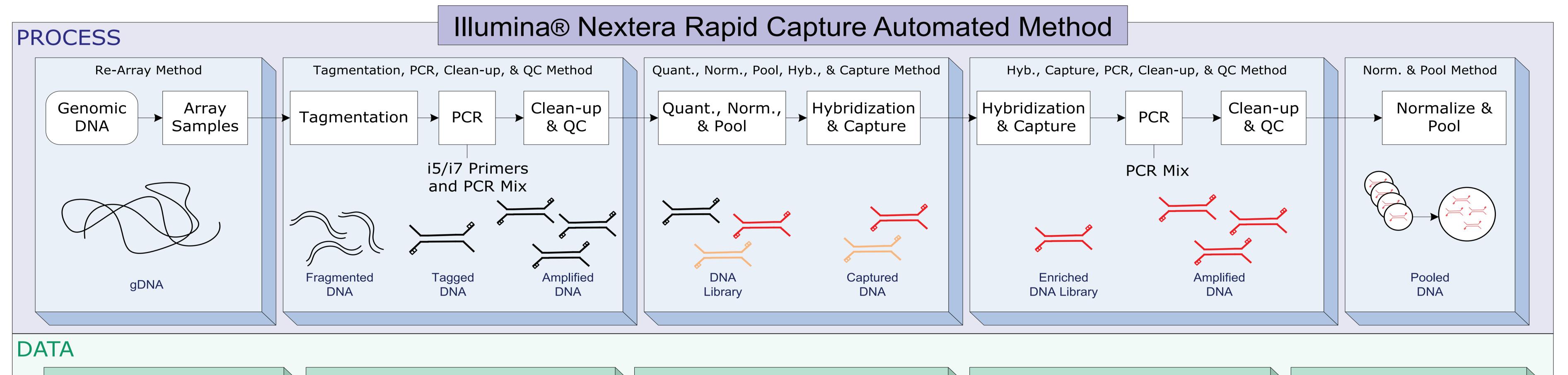
Biomek Datasets are a collection of tools native to the software that allow for the importation and manipulation of data from a variety of sources, including user supplied files and LIMS generated files. Such meta-data, including Agilent Bioanalyzer 2100 RIN scores and concentration data from fluorometric 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 datadriven 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.

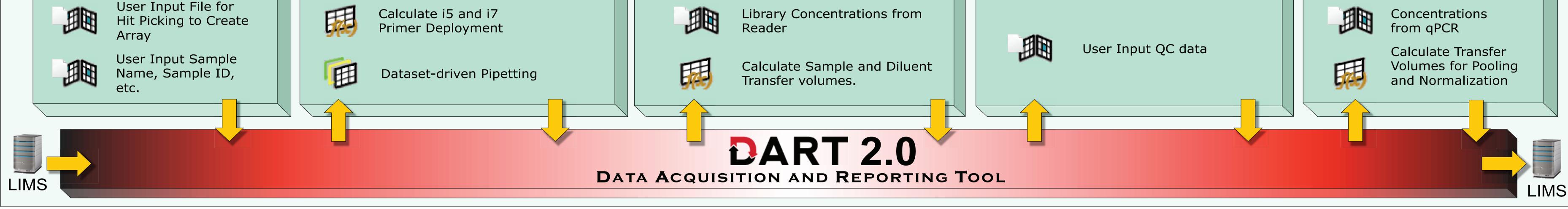
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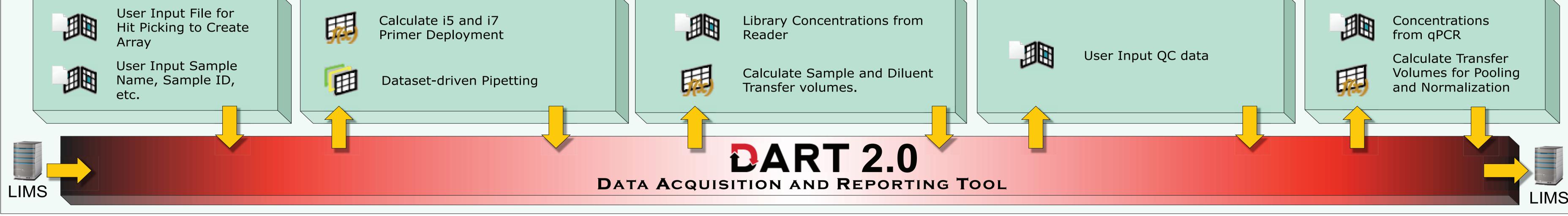
Life Sciences

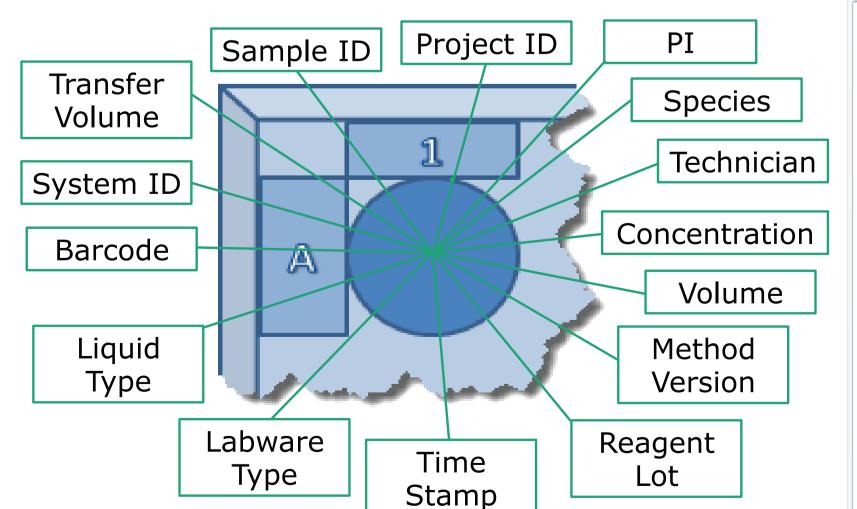
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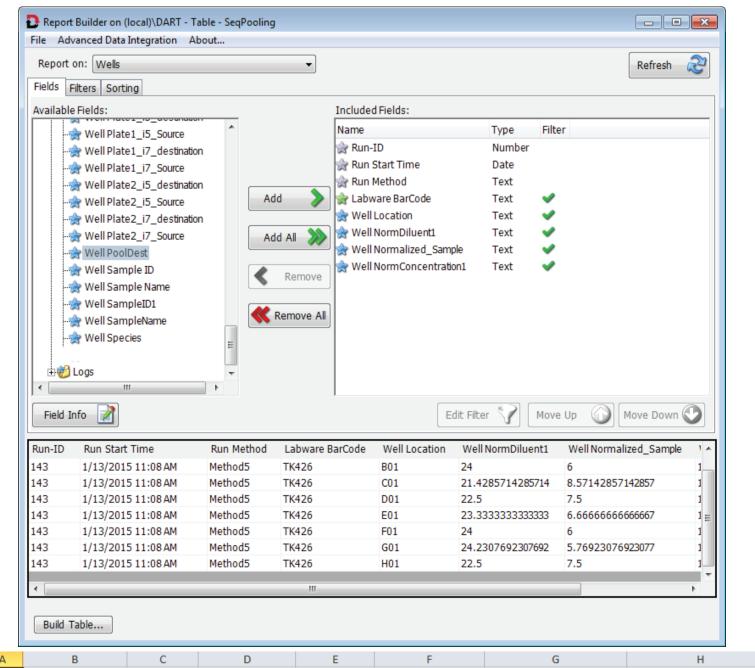


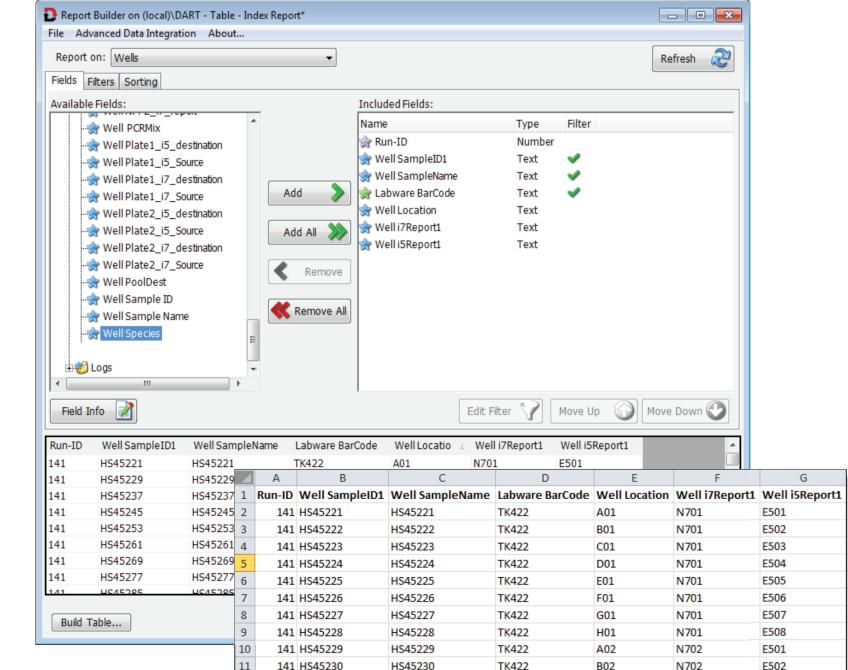




**Figure 1:** Examples of Sample and Run data

C E503 E504 E505 E506 E506 E506 E506 E506 E506 E506 E507 E507 E507 E507 E507 E507 E507 E507 E507 E508 <t< th=""><th>Rer</th><th></th><th></th><th></th><th></th><th></th><th></th><th>_</th><th></th><th></th><th></th><th></th><th></th></t<>	Rer							_					
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D   E504   E505   E506   E506   E506   E506   E506   E507   E508   E5	E	E502	E502	E502	E502	E502	E502	E502	E502	E502	E502	E502	В
E   ES05   ES06   ES06   ES06   ES06   ES07   ES08   ES08   ES08   ES08   ES08   ES	E	E503	E503	E503	E503	E503	E503	E503	E503	E503	E503	E503	С
F   E506   E507   E508   E5	E	E504	E504	E504	E504	E504	E504	E504	E504	E504	E504	E504	D
G E507 E508 <t< td=""><td>E</td><td>E505</td><td>E505</td><td>E505</td><td>E505</td><td>E505</td><td>E505</td><td>E505</td><td>E505</td><td>E505</td><td>E505</td><td>E505</td><td>E</td></t<>	E	E505	E505	E505	E505	E505	E505	E505	E505	E505	E505	E505	E
H   E508   E5	E	E506	E506	E506	E506	E506	E506	E506	E506	E506	E506	E506	F
Well property:   i7Report1   v   Go     1   2   3   4   5   6   7   8   9   10   11     A   N701   N702   N703   N704   N705   N706   N707   N708   N709   N710   N711     B   N701   N702   N703   N704   N705   N706   N707   N708   N709   N710   N711     C   N701   N702   N703   N704   N705   N706   N707   N708   N709   N710   N711	E	E507	E507	E507	E507	E507	E507	E507	E507	E507	E507	E507	G
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#### that can be managed and reported via DART 2.0

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G	N701	N702	N703	N704	N705	N706	N707	N708	N709	N710	N711	N712	
Н	N701	N702	N703	N704	N705	N706	N707	N708	N709	N710	N711	N712	
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**Figure 2:** i5 and i7 primer deployment by the Biomek method as shown in the DART 2.0 Web Browser

Run-ID	Run Start Time	<b>Run Method</b>	Labware BarCode	Well Location	Well NormDiluent1	Well Normalized_Sample	Well NormConcentration1
143	1/13/2015 11:08:10	Method5	TK426	A01	25	5	10
143	1/13/2015 11:08:10	Method5	TK426	B01	24	6	10
143	1/13/2015 11:08:10	Method5	TK426	C01	21.4285714285714	8.57142857142857	10
143	1/13/2015 11:08:10	Method5	TK426	D01	22.5	7.5	10
143	1/13/2015 11:08:10	Method5	TK426	E01	23.333333333333333	6.66666666666666	10
143	1/13/2015 11:08:10	Method5	TK426	F01	24	6	10
143	1/13/2015 11:08:10	Method5	TK426	G01	24.2307692307692	5.76923076923077	10
143	1/13/2015 11:08:10	Method5	TK426	H01	22.5	7.5	10

**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

		11010200	11010200	113122	202	11702	2002
12	141	HS45231	HS45231	TK422	C02	N702	E503
13	141	HS45232	HS45232	TK422	D02	N702	E504
14	141	HS45233	HS45233	TK422	E02	N702	E505
15	141	HS45234	HS45234	TK422	F02	N702	E506
16	141	HS45235	HS45235	TK422	G02	N702	E507
17	141	HS45236	HS45236	TK422	H02	N702	E508
18	141	HS45237	HS45237	TK422	A03	N703	E501
19	141	HS45238	HS45238	TK422	B03	N703	E502
20	141	HS45239	HS45239	TK422	C03	N703	E <u>503</u>

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