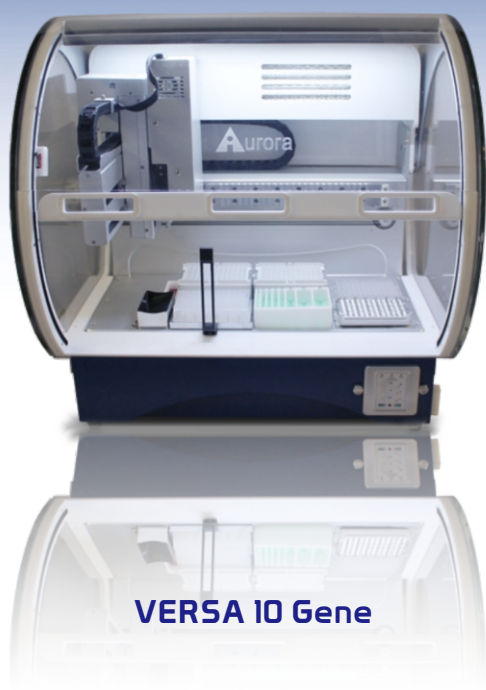
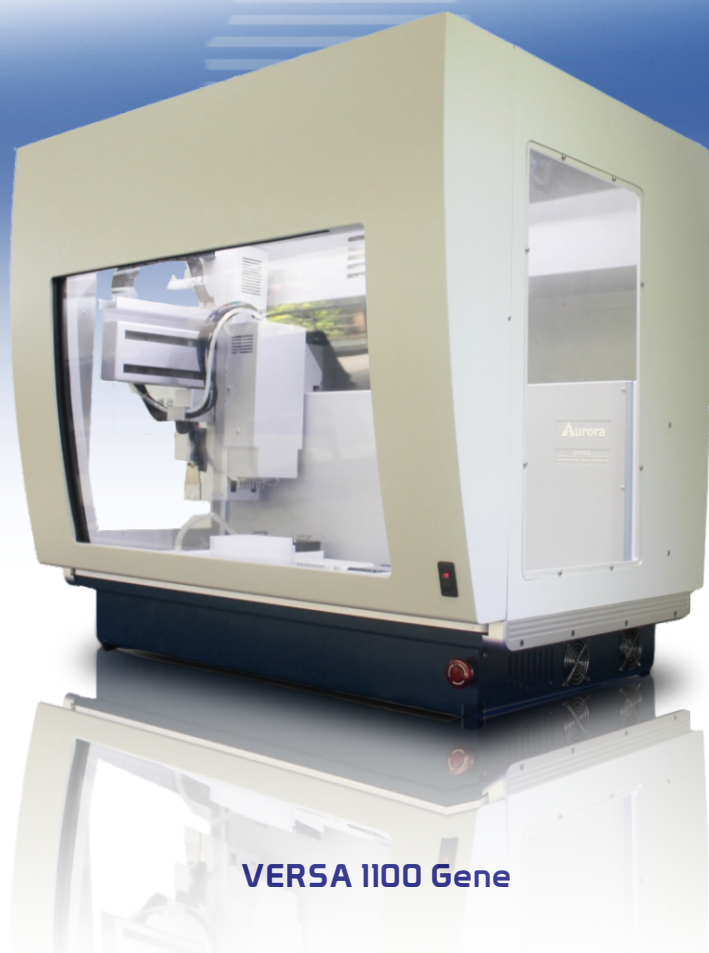




Is NGS Library Preparation Your Bottleneck?



VERSA 10 Gene



VERSA 1100 Gene

SOLUTIONS FOR LIFE SCIENCES & MOLECULAR DIAGNOSTICS

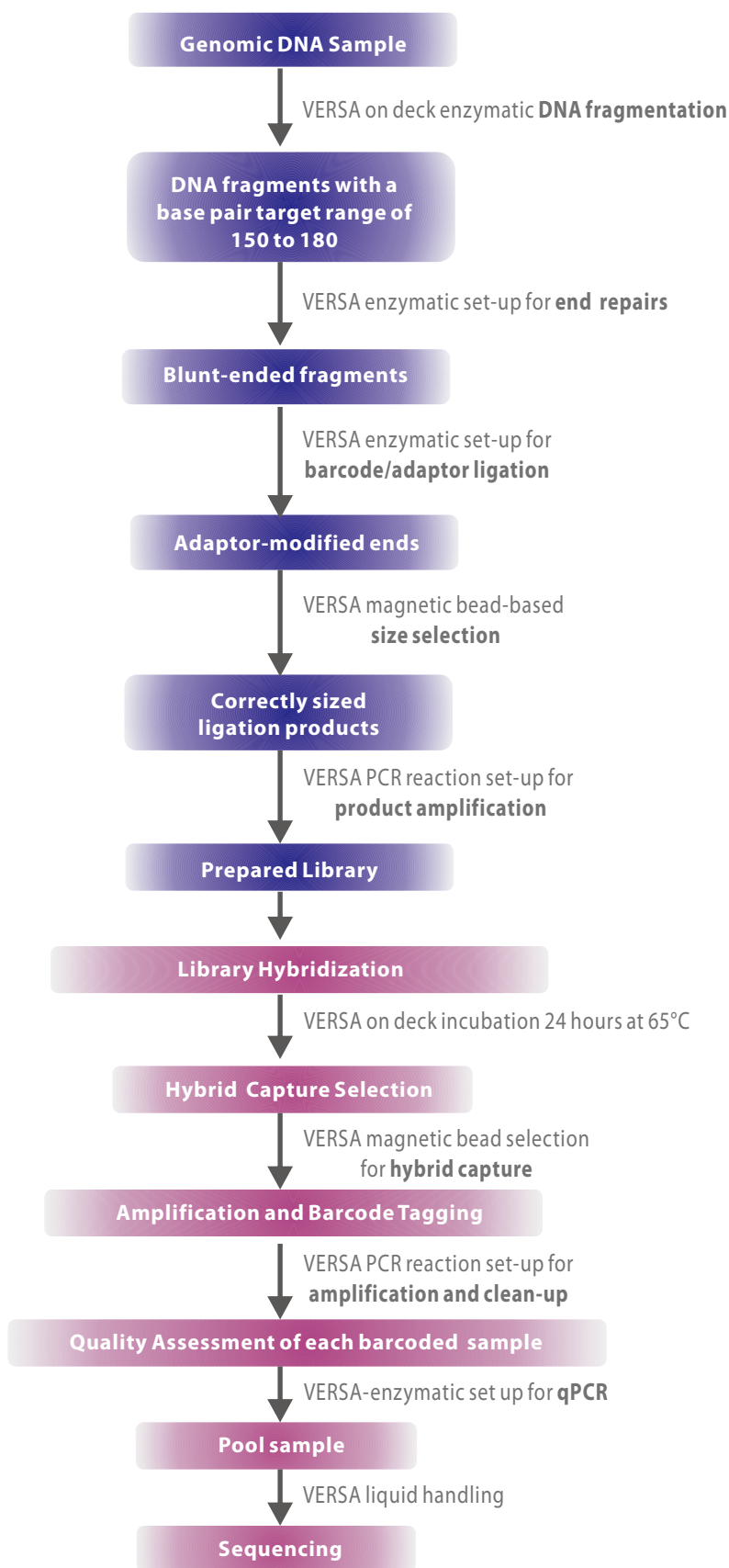
VERSA Gene Automated Liquid Handling Workstation is the Solution!

Aurora Biomed has combined proprietary deck and liquid handling modules to deliver a series of workstations that can optimize sample recovery, ensure data consistency and speed up tedious liquid handling steps associated with next generation sequencing library preparation workflows. The VERSA 10 Gene is a compact and cost-effective solution that can process 1 to 96 samples in parallel depending on throughput demands. The VERSA 1100 Gene offers a much larger footprint and deck capacity for a complete walk-away solution for all genomic protocols. The 8- or 96-channel pipetting head meets the high throughput demanded by NGS technologies.

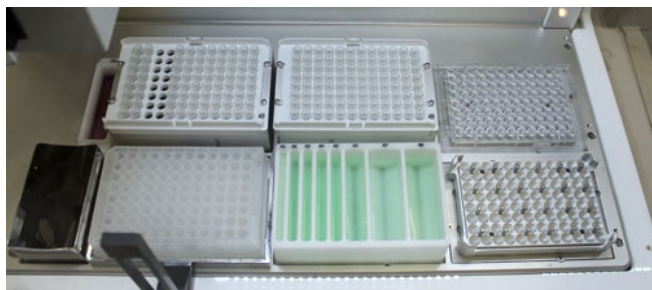
APPLICATIONS

- NGS library preparation
- DNA/RNA purification and cleanup
- DNA/RNA fragment size selection
- Enzymatic reaction setup
- Library normalization and pooling
- Single and multiplex real-time PCR setup
- Sequencing reaction setup
- Oligo-based gene synthesis plate setup
- Magnetic bead based applications

A Representative NGS Library Preparation Workflow on VERSA Gene



DECK LAYOUTS



VERSA 10 Gene



VERSA 1100 Gene

FEATURES & BENEFITS

- Magnetic bead vortex* ensures homogenous bead suspension
- 96-tip aspirator* increases efficiency, speed and reduces tip usage costs
- Shaker-heater-magnet elevator* reduces protocol time and increases available deck space
- ReagentDrop* module provides accurate dispensing of bulk reagents allowing conservation of reagents and tips
- HEPA-filtered UV/LED light enclosure with automatic door keeps samples contamination-free
- Open system - compatible with diverse kit chemistry and labware
- Scalable solution - processes 1 to 96 samples in parallel depending on throughput demands

* Only available on VERSA 1100 Gene

MODULES & ADAPTERS



Reagent Block



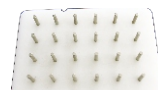
96-Channel Pipetting Head



Shaker



Gripper



Magnetic Block



Plate Cooler/Heater Block



8-Channel Pipetting Head



4-Channel Pipetting Head

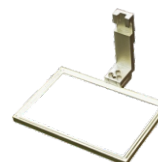


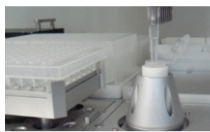
Plate Transporter



Shaker-Heater-Magnet Elevator



ReagentDrop & 8-Channel Pipetting Head



Magnetic Bead Vortex



96-Tip Aspirator

SPECIFICATIONS

	VERSA10 GENE	VERSA 1100 GENE	
		Basic Configuration	Recommended Configuration
Deck Capacity	6	15	15
Pipetting Head (with single channel function, disposable tip)	8-channel	8-channel	8 or 96-channel
ReagentDrop Channels (multiple reagents)	N/A	up to 8	8
96-Tip Aspirator	N/A	1	1
Temperature Regulation Block	1	2	4
Reagent Cooling Block	1	1	1
Plate Shaker	1	1	1**
Magnetic Block	1	1	1**
Plate Gripper/Transporter	Transporter	Gripper	Gripper
Liquid-Level Sensing	Optional	Optional	Optional
HEPA / UV / LED Light Enclosure	Optional	Optional	Included
Length x Depth x Height (cm)	65 x 43 x 52	98.5 x 75.2 x 89	98.5 x 75.2 x 108.2
Weight (kg)	27	165	200

**Optional Shaker-Heater-Magnet Elevator

Validation Data on VERSA Gene Workstation

Data on validation of magnetic bead vortex and its contribution to NGS library preparation alone with NGS data on Cancer Hotspot Panel is presented below:

Validating Magnetic Bead Vortex

In every NGS library preparation protocol, magnetic beads play an essential role and thus have a direct impact on the yield, concentration, consistency and quality of NGS library. Therefore, uniform bead distribution and accurate dispensing is critical.

Advantages

- **More efficient bead mixing** limits bead clumping and wastage as a result of beads attaching to the pipette tip and reservoir.
- **Bead distribution is no longer time-sensitive** because the beads are kept in constant suspension versus the risk of bead settling in a reservoir.
- **Minimizes dead volume** as magnetic beads are dispensed from the source tube and not a reservoir.

Library preparation on the VERSA Gene¹

- Purified amplified NGS library concentrations for positive and negative controls for both manual and automated procedures within the acceptable quality control limits as outlined by the end-user (Table 1).
- Correlation (r^2) of sequencing data obtained by manual and automated NGS library preparation procedures suggesting that automated procedures produce high quality sequencing data (Table 2). Sequencing quality and reproducibility can be attributed to the uniform suspension and accurate dispensing on magnetic beads by the VERSA Gene magnetic bead vortex and automated liquid handling modules.

Table 1 - Purified amplified NGS library concentrations for positive and negative controls for both manual and automated preparations.

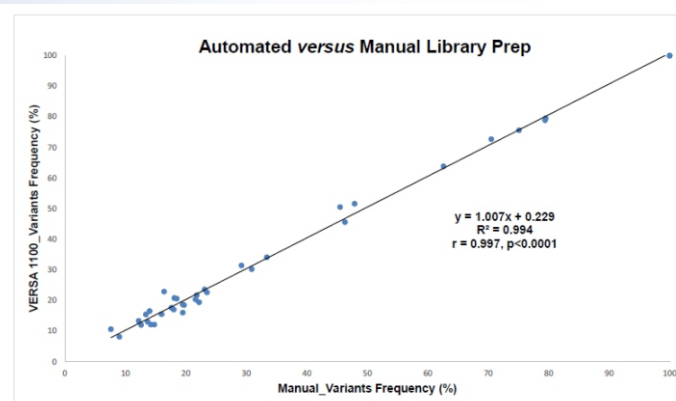
Tube No.	Sample ID	Qubit Reading (ng/mL)	Library Conc. (ng/mL)	QC
1A	POS Ctrl_2 (Manual Library)	78.1	1562	PASSES QC
2A	POS Ctrl_2a	71.9	1438	PASSES QC
3A	NEG Ctrl1a	81.8	1636	PASSES QC
4A	POS Ctrl_2b	71.5	1430	PASSES QC
5A	NEG Ctrl1b	86.2	1724	PASSES QC
6A	POS Ctrl_2c	60.6	1212	PASSES QC
7A	NEG Ctrl1c	101.0	2020	PASSES QC
8A	NEG Ctrl (Manual Library)	93.9	1878	PASSES QC

Table 2 - Correlation of sequencing data obtained by manual and automated NGS library preparations.

Automated library versus positive control manual library (r^2)	Automated library versus negative control manual library (r^2)
0.997	0.998
0.995	0.998
0.995	0.999
0.993	0.982
0.994	
0.995	

NGS data from Ion AmpliSeqTM Cancer Hotspot Panel²

- The checker board experiments concluded that VERSA automated liquid handling system showed no evidence of cross-contamination, by either no library in the NTC wells, or no variants called on negative samples after sequencing the CHP2 assay.
- High reproducibility observed in both library yields and variants called across all technical replicates of the quality control materials.
- All patient DNA samples yielded good quality libraries, including those difficult samples that had previously failed in the manual library preparation method.
- The variants called with highly correlated (Pearson's $r^2 > 0.990$) frequencies to those obtained with the manual method as shown on the right by representative curve on the 36 variants frequency identified in the positive control sample by both library preparation methods.



References

1. Gill *et al.* (2015). Validation of a Magnetic Bead Mixer on an Automated Next-Generation Sequencing Library Preparation System. *American Laboratory*.
2. Dumur *et al.* (2015, November). Validation of an Automated Method for Library Preparation for a Next Generation Sequencing-Based Assay for Oncology. Poster presented at American Molecular Pathology, Austin, TX.

NOTE: Instrument specifications may change without notice as an ongoing effort of product improvement.

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