## **For Any Technical Questions, Please Contact at** <u>info@nodesus.com</u> Product Name: VERSA 1100 Next Generation Sequencing Work Station

Part Number:

### Product Description:

#### VERSA 1100 Next Generation Sequencing Work Station

Next generation sequencing (NGS) has revolutionized the ability to perform genomic analyses by providing the power to sequence an entire genome economically in a single day.

Automation to support NGS technologies needs to meet the throughput required by NGS workflows and offer robustness and Flexibility to fully realize the power of NGS. The VERSA Gene 1100 workstation was developed as a complete walk- away solution for all genomic workflows.

Aurora's VERSA1100 Next Generation Sequencing Sample Preparation workstation features an 8-channel pipetting head to enable the high throughput demanded by NGS technologies but offers the flexibility to handle other tasks such as library normalization and sample pooling via the single channel function of the head. Aurora has worked to streamline the library preparation process by offering unique features such as the magnetic bead vortex, the magnet/shaker elevator, and the 96-tip aspirator. These modules were designed with the goal of reducing library preparation time while improving sample recovery and consistency.

VERSA's innovative modules are designed to tackle the challenging steps of Automated NGS Library Preparation (also known as NGS automation). The Magnetic Bead Vortex ensures homogeneous bead suspension and distribution. The combination of ReagentDrop bulk reagent dispensing module and 96-Tip Aspirator offers fast and efficient bead washing steps while saving tip costs. The VERSA automated Next Generation Sequencing (NGS) library preparation and sample preparation workstations are compatible with various commercial available kits, reagents, and labware. VERSA automated NGS library and sample preparation workstations are highly scalable for different throughputs and budget.

#### **Application:**

- $\checkmark$  Genomics:
- --NGS library preparation
- --DNA/RNA Extraction and Purification
- --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
- $\checkmark$  General liquid handling:
- --Cherry picking / reagent and sample pooling
- --Plate transfer, replication and reformatting
- --Serial and parallel dilution
- --Master mix preparation and distribution

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#### User cases

Health

CUMASSEY

Here, we present the validation and implementation of an open liquid handling platform, the VERSA<sup>™</sup> 1100 GENE (Aurora Biomed, Vancouver, BC) for medium to high-throughput library preparation for routine utilization with the Ion AmpliSeq<sup>™</sup> Cancer Hotspot Panel v2 (CHP2) assay on FFPE clinical specimens, including FFPE Quality Control (QC) materials (1).

Catherine I. Dumur, Paula Anderson, M. Fernanda Sábato, Celeste N. Powers, Andrea Ferreira-Gonzalez

Validation of an Automated Method for Library Preparation for a Next-



Virginia Commonwealth University 弗吉尼亚联邦大学

CANCER CENTER Department of Pathology, Virginia Commonwealth University, Richmond, VA checker-board cross-contamination experiment

Generation Sequencing-Based Assay for Oncology





Gene ID	CDS_mut_syntax	AA_mut_syntax	Chrom	hg19 Position	Ref	Variant	Frequency	Quality	Coverage	Allele Cov	Strand Bias
APC	Not a HotSpot	Not a HotSpot	chr5	112175770	G	A	74.7	19084.4	1997	1491	0.50
FGFR3	Not a HotSpot	Not a HotSpot	chr4	1807894	G	A	100.0	11210.6	699	699	0.50
FLT3	Not a HotSpot	Not a HotSpot	chr13	28610183	A	G	64.0	14997.7	2000	1281	0.52
HRAS	c.81T>C	p.His27His	chr11	534242	A	G	53.1	5543.6	993	527	0.51
KDR	Not a HotSpot	Not a HotSpot	chr4	55980239	С	Т	100.0	7165.1	455	455	0.50
KRAS	c.34G>T	p.Gly12Cys	chr12	25398285	С	A	100.0	31607.9	1986	1986	0.50
MET	Not a HotSpot	Not a HotSpot	chr7	116339672	С	T	68.3	16596.2	1999	1366	0.51
NOTCHI	Not a HotSpot	Not a HotSpot	chr9	139390822	G	C	100.0	21173.3	1325	1325	0.50
PDGFRA	Not a HotSpot	Not a HotSpot	chr4	55141055	A	G	100.0	14758.1	924	924	0.50
RET	Not a HotSpot	Not a HotSpot	chr10	43613843	G	Т	67.6	15035.5	1846	1247	0.50
RET	Not a HotSpot	Not a HotSpot	chr10	43615633	C	G	65.9	12191.1	1564	1030	0.52
STK11	Not a HotSpot	Not a HotSpot	chr19	1220321	T	C	67.2	8842.7	1094	735	0.51
			chr17	7577520	G	A	100.0	31556 4	1983	1983	0.50
TP53	c.742C>T	p.Argz461rp	CIETY	1011038						10,000	
TP53	c.742C>T	p.Argzeotrp	CIETY	1011038						0.000	
TP53	c.742C>T	p.Argzeerrp	Chrom	Neg	ative (	Control	Engineer	Quality	Coverage	Allele Cer	Strand Dia
Gene ID	c.742C>T	AA_mut_syntax	Chrom	hg19 Position	pative (	Control	Frequency	Quality 9248.7	Coverage 1890	Allele Cov	Strand Bia
Gene ID APC ATM	c.742C>T CDS_mut_syntax Not a HotSpot	AA_mut_syntax Not a HotSpot	Chrom chr5 chr11	Neg hg19 Position 112175770 108138003	Ref G T	Control Variant A	Frequency 48.8 51.4	Quality 9248.7 10550.2	Coverage 1890	Allele Cov 923 1025	Strand Bia 0.51 0.50
Gene ID APC ATM FGFR3	c.742C>T CDS_mut_syntax Not a HotSpot c.2672T>C Not a HotSpot	AA_mut_syntax Not a HotSpot p.Phe858Leu Not a HotSpot	Chrom chr5 chr11 chr4	Neg hg19 Position 112175770 108138003 1807894	ative ( Ref G T G	Control Variant A C A	Frequency 48.8 51.4 100.0	Quality 9248.7 10550.2 16809.8	Coverage 1890 1995 1048	Allele Cov 923 1025 1048	Strand Bia 0.51 0.50 0.50
Gene ID APC ATM FGFR3 FLT3	c.742C>T CDS_mut_syntax Not a HotSpot c.2672T>C Not a HotSpot Not a HotSpot	AA_mut_syntax Not a HotSpot p.Phe858Leu Not a HotSpot Not a HotSpot	Chrom chr5 chr11 chr4 chr13	Neg hg19 Position 112175770 108138003 1807894 28602992	ative ( Ref G T G T	Control Variant A C A C	Frequency 48.8 51.4 100.0 47.6	Quality 9248.7 10550.2 16809.8 9375.2	Coverage 1890 1996 1048 1996	Allele Cov 923 1025 1048 950	Strand Bia 0.51 0.50 0.50 0.52
Gene ID APC ATM FGFR3 FLT3 FLT3	c.742C>T CDS_mut_syntax Not a HotSpot c.2872T>C Not a HotSpot Not a HotSpot	AA_mut_syntax Not a HotSpot p.Phe858Leu Not a HotSpot Not a HotSpot Not a HotSpot	Chrom chr5 chr11 chr4 chr13 chr13	Neg hg19 Position 112175770 108138003 1807894 28602292 28610183	ative ( Ref G T G T A	Control Variant A C A C G	Frequency 48.8 51.4 100.0 47.6 100.0	Quality 9248.7 10550.2 16809.8 9375.2 32079.3	Coverage 1890 1996 1048 1996 2000	Allele Cov 923 1025 1048 950 2000	Strand Bia 0.51 0.50 0.50 0.52 0.50
Gene ID APC ATM FGFR3 FLT3 FLT3 HRAS	c.742C>T CDS_mut_syntax Not a HotSpot c.2872T>C Not a HotSpot Not a HotSpot Not a HotSpot c.81T>C	AA_mut_syntax Not a HotSpot p.Phe588Leu Not a HotSpot Not a HotSpot Not a HotSpot p.His27His	Chrom chr5 chr11 chr4 chr13 chr13 chr11	Neg hg19 Position 112175770 108138003 1807894 28002292 29610183 534242	G Ref G T G T A A	Control Variant A C A C G G	Frequency 48.8 51.4 100.0 47.6 100.0 47.9	Quality 9248.7 10550.2 16809.8 9375.2 32079.3 5761.1	Coverage 1890 1996 1048 1996 2000 1220	Allele Cov 923 1025 1048 950 2000 584	Strand Bia 0.51 0.50 0.50 0.52 0.50 0.50
Gene ID APC ATM FGFR3 FLT3 FLT3 HRAS KDR	c.742C>T CDS_mut_syntax Not a HotSpot Not a HotSpot Not a HotSpot Not a HotSpot Not a HotSpot Not a HotSpot	AA_mut_syntax Not a HotSpot p.Phe58Leu Not a HotSpot Not a HotSpot Not a HotSpot Not a HotSpot Not a HotSpot	Chrom chr5 chr11 chr4 chr13 chr13 chr11 chr4	Net hg19 Position 112175770 108138003 1807894 28002292 28610183 534242 55872874	ative ( Ref G T G T A A T	Control Variant A C A C G G A	Frequency 48.8 51.4 100.0 47.6 100.0 47.9 50.3	Quality 9248.7 10550.2 16809.8 9375.2 32079.3 5761.1 7480.7	Coverage 1890 1996 1048 1996 2000 1220 1465	Allele Cov 923 1025 1048 950 2000 584 737	Strand Bia 0.51 0.50 0.50 0.52 0.50 0.50 0.50 0.51
Gene ID APC ATM FGFR3 FLT3 FLT3 FLT3 HRAS KDR KDR	c.742C>T CDS_mut_syntax Not a HotSpot c.2572T>C Not a HotSpot Not a HotSpot Not a HotSpot Not a HotSpot Not a HotSpot	AA_mut_syntax Not a HotSpot p.Phe858Leu Not a HotSpot Not a HotSpot p.His27His Not a HotSpot Not a HotSpot Not a HotSpot	Chrom chr5 chr11 chr4 chr13 chr13 chr11 chr4 chr4	Ner hg19 Position 112175770 108139003 1807394 29602292 29610183 534242 55972974 55980239	ative ( Ref G T G T A A T C	Control Variant A C A C G G G A T	Frequency 48.8 51.4 100.0 47.6 100.0 47.9 50.3 100.0	Quality 9248.7 10550.2 16809.8 9375.2 32079.3 5761.1 7480.7 9211.1	Coverage 1890 1996 1048 1996 2000 1220 1465 580	Allele Cov 923 1025 1048 950 2000 584 737 580	Strand Bia 0.51 0.50 0.50 0.52 0.50 0.50 0.50 0.51 0.50
Gene ID APC ATM FGFR3 FLT3 FLT3 HRAS KDR PDGFRA	c.742C>T CDS_mut_symtax Not a HotSpot c.28727>C Not a HotSpot Not a HotSpot Not a HotSpot Not a HotSpot Not a HotSpot Not a HotSpot Not a HotSpot	AA_mut_syntax Not a HotSpot p.Phe558Leu Not a HotSpot Not a HotSpot	Chrom chr5 chr11 chr4 chr13 chr13 chr13 chr11 chr4 chr4	Neg hg19 Position 112175770 108138003 1807894 28602292 28610183 534242 55972974 55962239 55141055	ative ( Ref G T G T A A T C A	Control Variant A C A C G G G A T G	Frequency 48.8 51.4 100.0 47.6 100.0 47.9 50.3 100.0 100.0	Quality 9248.7 10550.2 16809.8 9375.2 32079.3 5761.1 7480.7 9211.1 19542.4	Coverage 1890 1996 1048 1996 2000 1220 1465 580 1226	Allele Cov 923 1025 1048 950 2000 584 737 580 1226	Strand Bia 0.51 0.50 0.52 0.50 0.50 0.51 0.50 0.51 0.50 0.50
Gene ID APC ATM FGFR3 FLT3 FLT3 HRAS KDR PDGFRA RET	c.742C>T CDS_mut_syntax Not a HotSpot c.8272T>C Not a HotSpot Not a HotSpot Not a HotSpot Not a HotSpot Not a HotSpot Not a HotSpot Not a HotSpot	AA_mut_syntax Not a HotSpot p.Phe58Leu Not a HotSpot Not a HotSpot	Chrom chr5 chr11 chr4 chr13 chr13 chr11 chr4 chr4 chr4 chr4 chr4 chr4	Neg hg19 Position 112175770 108138003 1807894 28602292 28610183 534242 5592974 55980239 55141055 43613843	pative ( Ref G T G T A A T C A G	Control Variant A C A C G G G A T G T	Frequency 48.8 51.4 100.0 47.6 100.0 47.9 50.3 100.0 100.0	Quality 9248.7 10550.2 16809.8 9375.2 32079.3 5761.1 7480.7 9211.1 19542.4 30332.6	Coverage 1890 1996 1048 1996 2000 1220 1465 580 1226 1892	Allele Cov 923 1025 1048 950 2000 584 737 580 1226 1892	Strand Bia 0.51 0.50 0.52 0.50 0.50 0.50 0.51 0.50 0.50 0.50 0.50
Gene ID APC ATM FGFR3 FLT3 HRAS KDR KDR KDR RDGFRA RET STK11	c.742C>T CDS_mut_syntax Not a HolSpot vot a HolSpot Not a HolSpot	AA_mut_syntax Not a HotSpot p.Phe888Leu Not a HotSpot Not a HotSpot	Chrom chr5 chr11 chr4 chr13 chr13 chr13 chr11 chr4 chr4 chr4 chr4 chr4 chr4 chr10 chr10 chr10	Net hg19 Position 112175700 108178700 20800229 20801028 534242 5597297 45690029 5514105 4301343 1220321	ative ( Ref G T G T A A T C A G T	Control Variant A C A C G G G T C	Frequency 48.8 51.4 100.0 47.6 100.0 47.9 50.3 100.0 100.0 100.0 51.0	Quality 9248.7 10550.2 16809.8 9375.2 32079.3 5761.1 7480.7 9211.1 19542.4 30332.6 4307.5	Coverage 1890 1996 2000 1220 1465 580 1226 1892 828	Allele Cov 923 1025 1048 950 2000 584 737 580 1226 1892 422	Strand Bia 0.51 0.50 0.52 0.50 0.50 0.51 0.50 0.50 0.50 0.50 0.50
Gene ID APC ATM FGFR3 FLT3 HRAS KDR KDR PDGFRA RET STK11 STK11	c.742C>T CDS_mut_syntax Not a HotSpot Not a HotSpot	AA_mut_syntax Not a HotSpot Dot a HotSpot Not a HotSpot	Chrom cht5 chr11 chr4 chr13 chr13 chr13 chr11 chr4 chr4 chr4 chr4 chr4 chr10 chr19 chr19	Net hg19 Pocition 112175770 108138003 1807894 269002292 265012974 5544205 55441005 5441005 5443013843 1220321	ative ( Ref G T G T A A T C A G T C	Control Variant A C A C G G A T G G T C G G	Frequency 48.8 51.4 100.0 47.6 100.0 47.9 50.3 100.0 100.0 100.0 100.0 51.0 49.5	Quality 9248.7 10550.2 16809.8 9375.2 32079.3 5761.1 19542.4 30332.6 4307.5 8451.3	Coverage 1890 1996 2000 1220 1465 580 1226 1892 828 1704	Allele Cov 923 1025 1048 950 2000 584 737 550 1226 1892 422 843	Strand Bia 0.51 0.50 0.52 0.50 0.51 0.51 0.50 0.50 0.50 0.50 0.50
Gene ID APC ATM FGFR3 FLT3 FLT3 HRAS KDR PDGFRA RET STK11 STK11 TP53	c.742C>T Not a HotSpot c.2572*C Not a HotSpot c.2572*C Not a HotSpot Not a HotSpot	AA_mut_syntax Not a HotSpot Not a HotSpot	Chrom chr5 chr11 chr4 chr13 chr13 chr13 chr11 chr4 chr4 chr4 chr4 chr4 chr4 chr4 chr19 chr19 chr19 chr19 chr19	Ner hg19 Position 112175770 108138033 1807894 28050183 554242 55697291 55141055 43013843 1220321 1223125 7578210	pative ( Ref G T G T A A T C A G T C T	Control Variant A C A C G G G T C C G C C	Frequency 48.8 51.4 100.0 47.6 100.0 47.9 50.3 100.0 100.0 100.0 51.0 49.5 51.3	Quality 9248.7 10550.2 18609.8 9375.2 32079.3 6761.1 7480.7 9211.1 19542.4 30332.6 4307.5 8451.3 10551.7	Coverage 1890 1996 1048 1996 2000 1220 1465 580 1226 1892 828 1704 1999	Allele Cov 923 1025 1048 950 2000 584 737 580 1226 1892 422 843 1026	Strand Bia: 0.51 0.50 0.52 0.50 0.51 0.50 0.51 0.50 0.53 0.51 0.51

#### NGS Data from Ion AmpliSeq Cancer Hotspot Panel v2



Dr. Catherine Dumur from Virginia Commonwealth University validated VERSA1100 GENE performance by
using FFPE clinical samples and Ion AmpliSeqTM
KIT. From the checkerboard experiments, it was
concluded that this automated liquid handling system
library on the no template control (NTC) wells or no
variants called on negative samples after sequencing
using the CHP2 assay. The results show that the
performance of the VÉRSA™ 1100 Gene automated
liquid handling workstation is very robust and helps
eliminate human-introduced errors, when compared to
the manual library preparation method for the CHP2
assay.
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#### **Features:**

√ The complete NGS sample preparation process can automatically complete the construction of enzymatic reaction systems such as nucleic acid extraction, nucleic acid purification, PCR, and liquid handling processes such as concentration normalization and merger sequencing. It also covers DNA-Seq, RNA-Seq, Exome-Seq, Chip-Seq, microRNA-Seq and other applications.

√ Open system - compatible with diverse kit chemistry and labware such as illumina, Life Technology, Pacific Biosystems and a variety of third-party Brand Library Building reagents, including but not limited to Roche KAPA, Agilent, etc.

 $\checkmark$  96-tip aspirator reduces protocol time and tip usage

- $\checkmark$  Magnetic bead vortex ensures homogenous bead suspension
- √ ReagentDrop module provides accurate dispensing of bulk reagents allowing conservation of reagents and tips

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 $\checkmark$  Cooling plate - suitable for various consumables on the market, such as centrifugal tubes, PCR plates, etc., preserves precious dNTPs, buffers and enzymes at 4 degrees

 $\checkmark$  Gripper - moves sample plates between magnetic bead separator and shaker for on-deck mixing and washing

 $\checkmark$  Magnetic Bead Separator- pulls down magnetic beads for sample purification and facilitates homogenous suspension of the sample

- $\checkmark$  HEPA Filtered UV/Fluorescent light enclosure with automatic door keeps samples contaminant free
- $\checkmark$  Software interface is friendly, concise, easy to learn and powerful
- $\checkmark$  Personalized customization can be accepted according to user's scheme

#### **Deck Layout**



Sample VERSA 1100 Gene Deck Layout

#### **Product Specification:**

# Engineering Your Needs

Syringe Pipettor (Disposable Tips)	8-channel	8 or 96-channel
Reagent Drop Channgels (Multiple Reagents)	5	8
Liquid-Level Sensing	Optional	Optional
Plate Shaker	1	1
96-tip Aspirator	1	1
Temperature Regulation Block	2	2
Reagent Cooling Block	1	1
Magnetic Block	Included	Included
Plate Gripper	Included	Included
HEPA / UV/ Fluorescent Light Enclosure	Optional	Included
Length	98.5 cm / 38.8 in	98.5 cm / 38.8 in
Depth	75.2 cm / 29.6 in	75.2 cm / 29.6 in
Height	89 cm / 35 in	108.2 cm / 46.2 in
Weight	162 kg / 357 lbs	225 kg / 496 lbs
Deck Capacity	15	15

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Configuration