Salus

Innovation in biomed

Saluseq Nimbo
Strike Fast & Hit the Target

Saluseq Nimbo Low Throughput NGS Platfrom

Salus BioMed is dedicated to delivering a superior next-generation sequencing (NGS) platform to empower users in life science industry. By leveraging the sequencing-by-synthesis (SBS) principles, Saluseq Nimbo integrates multiple technical advancements such as larger optical, rapid chemistry systems and highdensity chip design, enabling the fastest sequencing time of 3.4 hours. Featuring fast, accurate, comprehensive and intelligent, the innovative platform is engineered to excel across multiple clinical and scientific research scenarios, including personalized diagnosis, NIPT, forensics, eDNA, targeted NGS, infectious detection, etc.

CE CERTIFIED CE-IVDR

Key Features

Fast	Accurate	Compre-hensive	Intelligent
Run Time	Index Hopping	Multiple read lengths supporting diverse applications	Accelerated bioinformatics analysis and visualization
3.4 hr ~ 12 hr	**≤ 0.0004%**	**SE 50 ~ PE 300**	**Easy to Understand**

Specifications

Sequencing Reagent Set	Read Length	Data Output	Time	Q30
20 M	SE 400	8.0 Gb	20 hr	≥ 80%
	PE 300	12.0 Gb	28 hr	≥ 80%
25 M	SE 50	1.2 Gb	3.4 hr	≥ 90%
	SE 75	1.8 Gb	4.1 hr	≥ 90%
	SE 100	2.5 Gb	4.7 hr	≥ 85%
	PE 150	7.5 Gb	10.9 hr	≥ 85%
60 M	SE 50	3.0 Gb	3.8 hr	≥ 90%
	SE 75	4.5 Gb	4.6 hr	≥ 90%
	SE 100	6.0 Gb	5.4 hr	≥ 85%
	PE 150	18.0 Gb	12 hr	≥ 85%

*The sequencing time is for dual index (8+8);
*The time mentioned above is the theoretical sequencing time;
*Sequencing time and data quality may fluctuate due to the different libraries used.

Methods	Applications	Data Volume / Sample	Read Length	20M Samples / Run	25M Samples / Run	60M Samples / Run
Low-pass Whole Genome Sequencing	NIPT	~5 M reads	SE 50	/	5	12
Targeted Sequencing (Capture / Multiplex Amplification)	Targeted Pathogen Sequencing (tNGS)	0.5 M ~ 1 M reads	SE 50	/	25 ~ 50	60 ~ 120
	Small Panel for Tumor Companion Diagnostics	~1 Gb	PE 150	/	7	18
	Small Panel for Genetic Diseases (Deafness, Metabolism)	3 ~ 5 Gb	PE 150	/	1 ~ 2	3 ~ 6
	16S Sequencing	~0.5 M reads	PE 300	40	/	/
	Forensic DNA Identification	~0.5 M reads	SE 400	40	/	/
Small Genomes Sequencing (Tuberculosis, Tnfluenza, etc.)	Bacterial / Virus	~1 Gb	PE 150	/	7	18
Methylation Sequencing	Pan-cancer Early Screening	~1 Gb	PE 150	/	2	4

*The number of samples is estimated after careful consideration of library pooling bias and is for reference only.

Data Demostrations

## Reference Standard - Zymo sample metagenomic sequencing

Sample: Metagenomic Standards (Zymo Research)

Sample	mNGS-01	mNGS-02	mNGS-03	mNGS-04	mNGS-05	mNGS-06	mNGS-07	mNGS-08	mNGS-09	mNGS-10	mNGS-11	mNGS-12
TotalReads(M)	20.21	20.70	17.35	16.13	18.97	19.43	18.37	17.71	19.44	18.63	17.35	19.51
Q20(%)	99.50	99.47	99.48	99.29	99.43	99.46	99.43	99.37	99.39	99.43	99.32	99.44
Q30(%)	94.85	94.68	94.76	93.92	94.47	94.58	94.43	94.19	94.16	94.52	94.03	94.44
Host_Proportion(%)	0	0	0	90	90	90	99	99	99	99.9	99.9	99.9
Zymo_Proportion(%)	100	100	100	10	10	10	1	1	1	0.1	0.1	0.1

Q30 between each run are larger than 94%
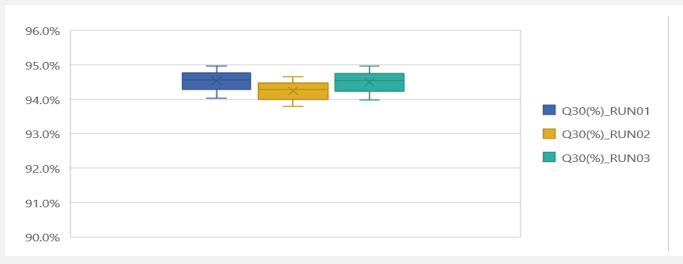
The data output between runs is greater than 70M; data splitting rate > 98%
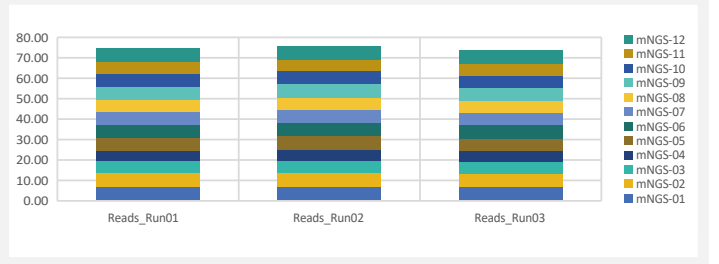
*The Q30 of the three runs was greater than 94%, and the data homogeneity between different runs was good.
*All the targets in different proportion samples were detected, and the abundance was consistent with the standard.

Index Hopping < 0.000344%

Sample_id	Total_reads	DU-6	DU-10	DU-64	DU-12	DU-20	DU-22	DU-32	DU-56	DU-2	DU-28	DU-29	DU-35	DU-43	DU-7
Raw_total_reads (M)	68.87	1.66	2.08	4.57	2.56	1.28	7.05	3.30	4.02	5.24	6.07	4.91	12.67	7.35	6.10
Raw_Q30 (%)	93.83	93.12	95.08	93.64	94.42	95.24	93.50	92.00	93.18	94.49	93.61	94.51	93.34	93.98	93.49
Clean_total_reads(M)	63.38	1.53	2.00	4.18	2.44	1.21	6.64	2.96	3.20	5.01	5.65	4.45	11.79	6.58	5.75
Clean_total_reads_rate(%)	92.04	91.80	95.85	91.46	95.38	94.56	94.13	89.67	79.72	95.64	93.09	90.46	93.07	89.45	94.27
Clean_Q30 (%)	96.01	96.06	96.47	95.61	96.14	96.71	95.78	95.66	96.07	96.16	95.65	96.29	95.62	96.05	95.91

Sample_id	Total_reads	DU-6	DU-10	DU-64	DU-12	DU-20	DU-22	DU-32	DU-56	DU-2	DU-28	DU-29	DU-35	DU-43	DU-7	Hop_reads	Hop_rate (ppm)
All_reads (rm Host reads)	4216904	98880	309881	235272	174180	29882	713633	391077	2201174	8420	7506	10629	14508	15537	6325	–	–
Mapped_reads (MapQ=60; rmdup)	2324250	78025	249	60969	95781	18155	411174	266409	1393480	3	1	0	1	2	1	8	3.44
Klebsiella pneumoniae	85156	77979	241	69	0	0	28	2737	4102	0	0	0	0	0	0	0	0.00
Corynebacterium resistens	63386	0	0	59865	15	0	174	3332	0	0	0	0	0	0	0	0	0.00
Pneumocystis jirovecii	95775	0	0	1	95751	0	5	3	15	0	0	0	0	0	0	0	0.00
Staphylococcus aureus	18731	0	2	424	10	18155	76	12	52	0	0	0	0	0	0	0	0.00
Pseudomonas aeruginosa	397530	0	5	0	4	0	396142	0	1372	2	1	0	1	2	1	7	17.61
Corynebacterium striatum	275499	0	0	570	1	0	14615	260313	0	0	0	0	0	0	0	0	0.00
Enterobacter hormaechei	1388173	46	1	40	0	0	134	12	1387939	1	0	0	0	0	0	1	0.72

Reference Standard - UHRR sample transcriptome sequencing

Test sample: RNA library constructed based on Universal Human Reference RNA (UHRR) standard v1ad

Platform	Saluseq Nimbo			N Platform		
Sample	mRNA1_1	mRNA1_2	mRNA1_3	mRNA1_1	mRNA1_2	mRNA1_3
Raw_total_Reads(M)	70	70	70	70	70	70
Clean_Q30(%)	94.29	93.79	94.15	93.38	93.10	93.63
GC_content(%)	49.97	49.97	50.08	49.84	49.84	50.28
rRNA_Rate(%)	0.68	0.68	0.68	3.05	3.02	3.04
Mapping_Rate_Genome(%)	98.86	98.91	98.97	97.25	97.13	97.62
Mapping_Rate_mRNA(%)	92.78	92.81	92.90	85.27	84.44	84.76
Transcript_Number(K)	49.02	48.81	48.76	48.29	48.37	48.21
Total_Gene_Number(K)	16.23	16.21	16.20	16.28	16.25	16.25
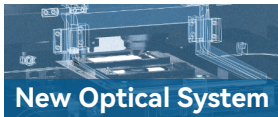
Comparison of Annotation Results

Comparison of correlation between samples
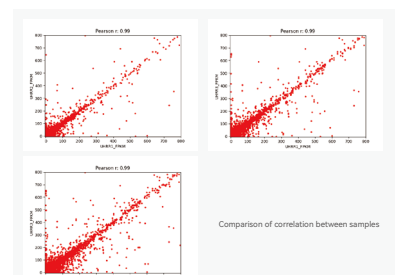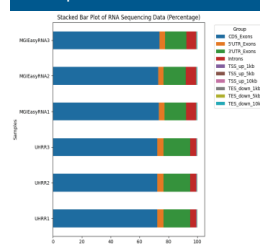
*FPKM correlation>99%
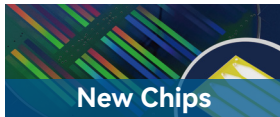
Tech Innovations

R&D capabilities
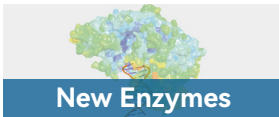
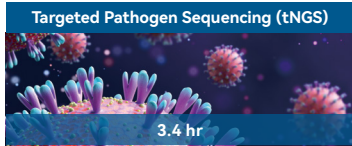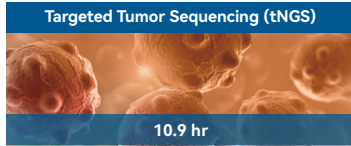|				
New Optical System	**New Chips**	**New Enzymes**	**New Fluorescent Dye**	**New Chemistry**
100% larger field of view and 50% less imaging time	Robustness and better reaction efficiency	Read length up to SE 400 with better quality	Proprietary dyes systems to optimized for better imaging performance	In fast sequencing mode, the SE 50 + 8 + 8 test can be completed in as fast as 3.4 hours

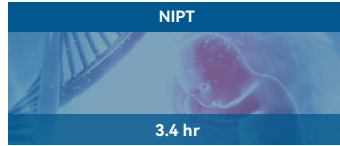# Multiple Applications

Targeted Pathogen Sequencing (tNGS)	Targeted Tumor Sequencing (tNGS)	NIPT	Environmental DNA (eDNA)
3.4 hr	10.9 hr	3.4 hr	4.7 hr

Saluseq Nimbo Instrument Specifications

Parameter	Specifications	
Dimensions	619 mm(W) x 682 mm(D) x 738 mm(H)	
Weigh	115 Kg	
Power Requirements	Input voltage	100 V - 240 V~
	Frequency	50 / 60 Hz
	Power	1000 VA
	Fuse	T10AH250V
Instrument Configuration	Display	13.3 inch
	Resolution	1920 x 1080
Operating Environment	Temperature	15℃ ~ 30℃
	Humidity	20%RH ~ 80%RH (No condensation)
	Altitude	≤ 3000m
Instrument Control Compute	CPU	12th Gen Intel(R) Core(TM) i9-12900
	Storage	64GB DDR5
	Memory	2TB SSD
OS	Windows 11 X64	

After-sale Service
400-80-SALUS(72587)

Salus BioMed or its authorized partners offer comprehensive after-sales services, including installation, commissioning, repairs, maintenance, technical support, and any other necessary assistance.

Free installation, commissioning, reagents and consumables for performance validation are available. The company reserved all the rights for final explanation.

Sequencer Safety

The products comply with IEC6010-2010, IEC6010-2010 / AMD /:2016, IEC61010-2010: 2019, and IEC61010-2-081-2019. Featuring a rounded shape design, Saluseq Nimbo is user-friendly for researchers and operators, significantly reducing the risk of scratching.

Crafted from flame-retardant and environmentally friendly materials, our instruments are designed for easy cleaning and sterilzation with alcohol.

Salus BioMed

Empower and Cooperate

Founded in Shenzhen, Salus BioMed specializes in developing high-throughput genetic sequencing platforms and is a world leader in high resolution spatial omics research platforms, serving both research and clinical applications. The company is dedicated to providing a wide range of cutting-edge instruments and solutions to the sequenceing and life sciences industry.

Sequencing Lab

Assembly Line

Enzyme Development

Office Area

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