Salus
innovation in life science

Saluseq Nimbo Genetic Sequencer

Strike Fast **Hit the Target**



Saluseq Nimbo Low Throughput NGS Platfrom

Salus BioMed is dedicated to delivering superior next-generation sequencing (NGS) platforms 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 2.2 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 IVDR

V3.0

Key Features

Fast

Run Time

2.2 hr - 25 hr

Accurate

Index Hopping

≤ 0.0004%

Compre-hensive

Multiple read lengths supporting diverse applications

50 - 600 Cycles

Intelligent

Accelerated bioinformatics analysis and visualization

Easy to Understand

Specifications

Flow cell type	Read Length	Data Output	Time	Q30
25 M	SE50	1.25 Gb	2.2 hr	≥ 90%
	SE75	1.875 Gb	2.7 hr	≥ 90%
	SE100	2.5 Gb	3.1 hr	≥ 90%
	PE100	5.0 Gb	5.5 hr	≥ 90%
	PE150	7.5 Gb	7.2 hr	≥ 90%
	SE400	10.0 Gb	18.0 hr	≥ 80%
	PE300	15.0 Gb	25.0 hr	≥ 80%
60 M	SE50	3.0 Gb	2.4 hr	≥ 90%
	SE75	4.5 Gb	2.9 hr	≥ 90%
	SE100	6.0 Gb	3.5 hr	≥ 90%
	PE100	12.0 Gb	6.0 hr	≥ 90%
	PE150	18.0 Gb	8.2 hr	≥ 90%
100 M	SE50	5.0 Gb	2.8 hr	≥ 90%
	SE75	7.5 Gb	3.5 hr	≥ 90%
	SE100	10.0 Gb	4.2 hr	≥ 90%
	PE100	20.0 Gb	7.1 hr	≥ 90%
	PE150	30.0 Gb	10.0 hr	≥ 90%
	SE400	40.0 Gb	20.5 hr	≥ 80%

*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	25M Samples / Run	60M Samples / Run	100M Samples / Run
Low-pass Whole Genome Sequencing	NIPT	~5 M reads	SE 50	5	12	20
Targeted Sequencing (Capture / Multiplex Amplification)	Targeted Pathogen Sequencing (tNGS)	0.5 M - 1 M reads	SE 50	25 ~ 50	60 ~ 120	100 ~ 200
	Small Panel for Tumor Companion Diagnostics	~1 Gb	PE 150	7	18	30
	Small Panel for Genetic Diseases (Deafness, Metabolism)	3 - 5 Gb	PE 150	1 - 2	3 - 6	6 - 10
	16S Sequencing	~0.5 M reads	PE 300	50	/	/
	Forensic DNA Identification	~0.5 M reads	SE 400	50	/	200
Small Genomes Sequencing (Tuberculosis, Tnfluenza, etc.)	Bacterial / Virus	~1 Gb	PE 150	7	18	30
Methylation Sequencing	Pan-cancer Early Screening	~4 Gb	PE 150	2	4	7

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

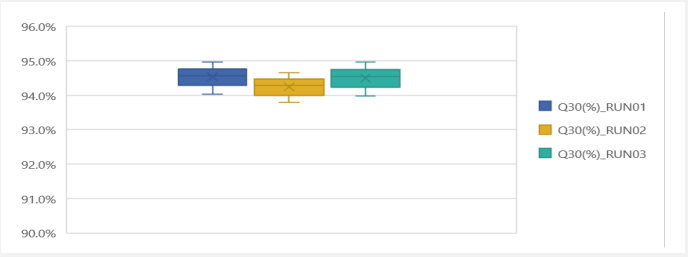
Data Demostrations

Reference Standard – Zymo sample metagenomic sequencing

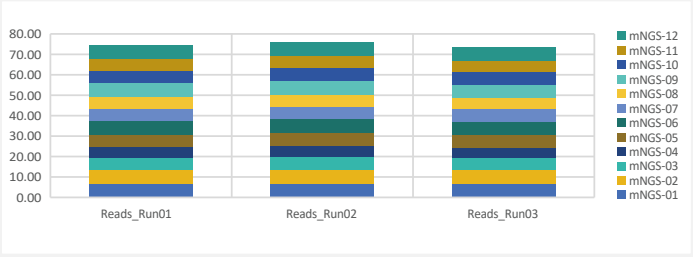
Sample: Metagenomic Standards (Zymo Research)

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

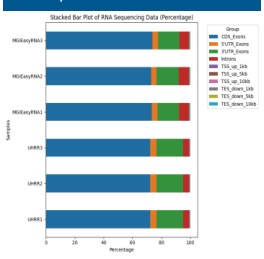
Sample_id	Total_reads	DU-6	DU-10	DU-64	DU-12	DU-20	DU-22	DU-32	DU-56	DU-2	DU-28	DU-29	DU-35	DU-43	DU-7	Hop_reads	Hop_rate (ppm)
All_reads (rm Host reads)	4216904	98880	309881	235272	174180	29882	713633	391077	2201174	8420	7506	10629	14508	15537	6325	-	-
Mapped_reads (MapQ=60; rmdup)	2324250	78025	249	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

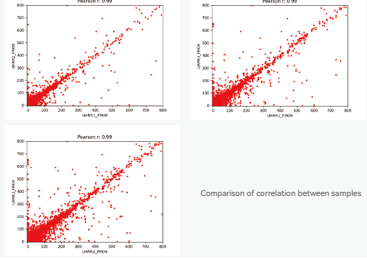
Reference Standard – UHRR sample transcriptome sequencing

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



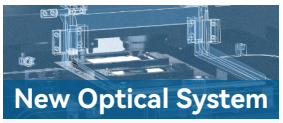


Comparison of correlation between samples

*FPKM correlation>99%

Tech Innovations

R&D capabilities



New Optical System

100% larger field of view and 50% less imaging time



New Chips

Robustness and better reaction efficiency



New Enzymes

Read length up to SE 400 with better quality



New Fluorescent Dye

Proprietary dyes systems to optimized for better imaging performance



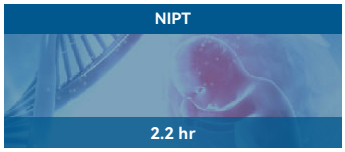
New Chemistry

In fast sequencing mode, the SE 50 + 8 + 8 test can be completed in as fast as 2.2 hours

Multiple Applications









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	128GB
	Memory	2TB SSD
OS	Windows 11 X64	

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.

FOR ORDERING AND GUIDANCE
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