

MERIDIAN GENOMICS CORE

High-Throughput DNA/RNA Sample Processing Manifest
Advanced Genomics Facility · Building B, Suite 400 · Apex Research Park

Project ID: PRJ-2026-NEX-0842
Intake Date: 2026-07-24
Batch Status: QC PASSED – IN PREP
Seq Platform: NovaSeq X Plus

Principal Investigator: Dr. Eleanor Vance (Apex Bio)
Primary Workflow: Whole Genome Sequencing (WGS)
Lab Technician: Marcus Thorne, CLS
Sample Count: 24 Samples (1 Plate, Wells A01–C08)

Submitting Org: Synapse Therapeutics Inc.
Target Reads/Cell: 30x Human WGS / 50k scRNA
Scheduled Run: 2026-07-26 (Lane 3 & 4)
QC Protocol: ISO/IEC 17025 Standard

1 Section 1: Sample Intake Checklist & Threshold Criteria

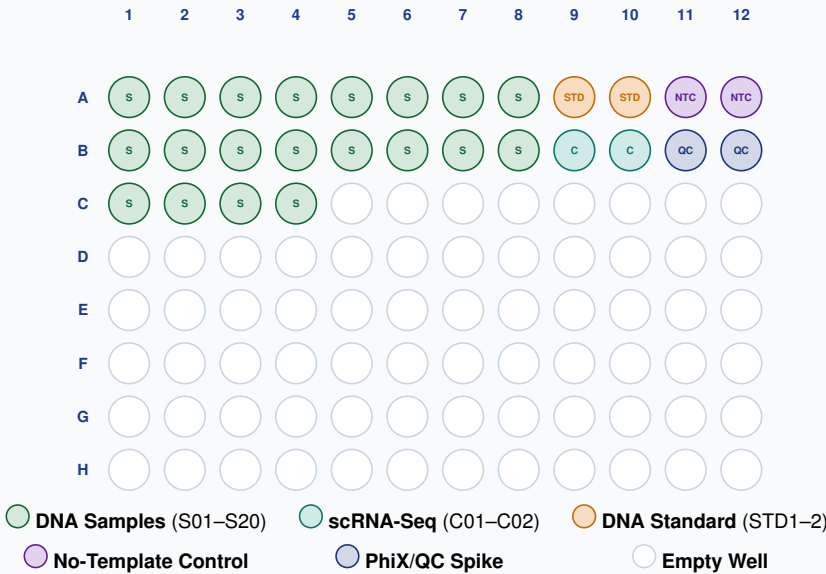
Technical Acceptance Criteria

Parameter	WGS Standard	scRNA-Seq
Min Concentration	≥ 10.0 ng/μL	≥ 500 cells/μL
Total Input Mass	≥ 100 ng	≥ 50,000 cells
Min Volume	≥ 20 μL	≥ 15 μL
A260/A280 Ratio	1.80 – 2.00	N/A
A260/A230 Ratio	2.00 – 2.20	N/A
RIN / DIN Score	DIN ≥ 7.5	RIN ≥ 8.0
Buffer Media	10mM Tris-HCl	1x PBS + 0.04% BSA

Intake Quality Assurance Log

- ✓ Sample tubes inspected for seal integrity and leakage.
- ✓ Barcodes scanned and matched against submission manifest.
- ✓ Fluorometric quantification (Qubit 4.0 BR DNA Assay).
- ✓ Microfluidic electrophoresis (Agilent TapeStation 4200).
- ✓ Cell viability assessed via automated trypan blue counting (> 92%).
- ✓ Samples aliquoted into 96-well reaction plate (Lot #20260710).

2 Section 2: 96-Well Plate Batch Map (Plate Barcode: PLT-96-NEX-4412)



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Section 3: High-Throughput Sample Extraction & QC Manifest

Well	Sample ID	Client Label	Tissue / Specimen	Conc (ng/ μ L)	Vol (μ L)	Yield (μ g)	260/280	260/230	RIN/DIN	Status
A01	NEX-0842-01	PBMC-Norm-101	Human Blood PBMC	42.5	35.0	1.49	1.88	2.12	DIN 8.9	PASS
A02	NEX-0842-02	PBMC-Norm-102	Human Blood PBMC	38.2	35.0	1.34	1.86	2.08	DIN 8.7	PASS
A03	NEX-0842-03	T-Tumor-FFPE-A	FFPE Liver Carcinoma	18.4	25.0	0.46	1.79	1.94	DIN 6.8	WARN
A04	NEX-0842-04	T-Tumor-FFPE-B	FFPE Liver Carcinoma	22.1	25.0	0.55	1.82	2.01	DIN 7.1	PASS
A05	NEX-0842-05	Organoid-C3-d14	Cerebral Organoid	54.0	40.0	2.16	1.91	2.15	RIN 9.2	PASS
A06	NEX-0842-06	Organoid-C3-d28	Cerebral Organoid	49.8	40.0	1.99	1.90	2.14	RIN 9.0	PASS
A07	NEX-0842-07	CSF-CellFree-01	Cell-Free Plasma DNA	4.2	50.0	0.21	1.75	1.82	DIN 5.4	LOW-IN
A08	NEX-0842-08	CSF-CellFree-02	Cell-Free Plasma DNA	5.1	50.0	0.26	1.78	1.88	DIN 5.9	LOW-IN
A09	STD-NEX-01	Control-gDNA-100	Human Reference gDNA	100.0	50.0	5.00	1.89	2.18	DIN 9.8	PASS
A10	STD-NEX-02	Control-gDNA-50	Human Reference gDNA	50.0	50.0	2.50	1.88	2.17	DIN 9.7	PASS
A11	NTC-BLANK-1	Buffer-Control-1	Nuclease-Free H2O	0.02	50.0	0.00	–	–	–	PASS
A12	NTC-BLANK-2	Buffer-Control-2	Nuclease-Free H2O	0.01	50.0	0.00	–	–	–	PASS
B01	NEX-0842-09	Mouse-Brain-CTX	C57BL/6 Cortex Tissue	68.4	30.0	2.05	1.92	2.19	RIN 8.8	PASS
B02	NEX-0842-10	Mouse-Brain-HIP	C57BL/6 Hippocampus	61.2	30.0	1.84	1.91	2.16	RIN 8.6	PASS
B03	NEX-0842-11	CellLine-HEK293T	Cultured Cell Lysate	112.5	40.0	4.50	1.94	2.21	RIN 9.6	PASS
B04	NEX-0842-12	CellLine-K562	Cultured Cell Lysate	108.0	40.0	4.32	1.93	2.20	RIN 9.5	PASS
B05	NEX-0842-13	Plant-Arabidopsis	Leaf Tissue Extract	31.7	35.0	1.11	1.81	1.92	DIN 7.4	PASS
B06	NEX-0842-14	Plant-ZeaMays	Root Tip Tissue	28.4	35.0	0.99	1.78	1.89	DIN 7.2	PASS
B07	NEX-0842-15	Skin-Biopsy-01	Dermal Punch Biopsy	15.2	20.0	0.30	1.84	1.98	DIN 7.6	PASS
B08	NEX-0842-16	Skin-Biopsy-02	Dermal Punch Biopsy	14.8	20.0	0.30	1.83	1.95	DIN 7.6	PASS
B09	SINGLE-CELL-01	scRNA-PBMC-Fresh	Single-Cell Suspension	–	20.0	–	–	–	Viab 94%	PASS
B10	SINGLE-CELL-02	scRNA-Tumor-Single	Single-Cell Suspension	–	20.0	–	–	–	Viab 91%	PASS
B11	QC-SPIKE-01	ERCC-Control-Mix	Synthetic RNA Spikes	10.0	15.0	0.15	1.95	2.20	Standard	PASS
B12	QC-SPIKE-02	PhiX-Library-v3	Control Library Spike	10.0	15.0	0.15	–	–	–	PASS
C01	NEX-0842-17	Saliva-Swab-A1	Buccal Epithelial Swab	26.5	40.0	1.06	1.82	2.04	DIN 8.1	PASS
C02	NEX-0842-18	Saliva-Swab-A2	Buccal Epithelial Swab	29.1	40.0	1.16	1.85	2.07	DIN 8.3	PASS
C03	NEX-0842-19	Stool-Metagenome	Gut Microbiome Extract	44.0	30.0	1.32	1.76	1.68	DIN 6.5	LOW-230
C04	NEX-0842-20	Soil-Metagenome	Environmental Soil	12.0	30.0	0.36	1.68	1.45	DIN 5.8	FAIL-RE-EXT

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Section 4: Library Preparation Protocol & Dual-Index Barcode Scheme

Kit Name: NEBNext Ultra II FS DNA	Kit Lot #: LOT-2026-0618-A	Index Set: Unique Dual Index (UDI) 96	Index Lot #: UDI-SET-96-04
Enzymatic Frag: 12.5 min @ 37°C	Adapter Ligation: 15 min @ 20°C	PCR Amplification: 6 Cycles	Bead Clean (SPRI): 0.8x Size Select

Well	Sample ID	i7 Index ID	i7 Sequence (P7)	i5 Index ID	i5 Sequence (P5)	Target Reads
A01	NEX-0842-01	UDI001_i7	GATCGATC	UDI001_i5	ATCGATCG	40 M Paired-End
A02	NEX-0842-02	UDI002_i7	AGCTAGCT	UDI002_i5	CGATCGAT	40 M Paired-End
A03	NEX-0842-03	UDI003_i7	TCGATCGA	UDI003_i5	GATCGATC	40 M Paired-End
A04	NEX-0842-04	UDI004_i7	CTAGCTAG	UDI004_i5	AGCTAGCT	40 M Paired-End
A05	NEX-0842-05	UDI005_i7	GCTAGCTA	UDI005_i5	TCGATCGA	50 M Paired-End
A06	NEX-0842-06	UDI006_i7	TAGCTAGC	UDI006_i5	CTAGCTAG	50 M Paired-End
B01	NEX-0842-09	UDI009_i7	CGATCGAT	UDI009_i5	GCTAGCTA	40 M Paired-End
B02	NEX-0842-10	UDI010_i7	ATCGATCG	UDI010_i5	TAGCTAGC	40 M Paired-End
B09	SINGLE-CELL-01	10x-SI-TT-A1	GTAACATGCG	10x-SI-NT-A1	AGGTCATCGT	100 M scRNA
B10	SINGLE-CELL-02	10x-SI-TT-A2	GTCCATGCAT	10x-SI-NT-A2	GACTAGCTAG	100 M scRNA

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Section 5: Pre-Sequencing QC & Pool Normalization

Fragment Size Distribution (TapeStation 4200)

Library Pool ID	Peak Size (bp)	Molarity (nM)
POOL-NEX-0842-WGS	450 bp	14.8 nM
POOL-NEX-0842-scRNA	520 bp	22.1 nM
POOL-NEX-STD-CTRL	440 bp	15.2 nM
Final Sequenced Pool	465 bp	18.4 nM

Pass Criteria: Average library peak size between 400–550 bp. Adapter dimer (< 120 bp) must be < 1.0%.

Final Pooling & PhiX Control Setup

- Total Pool Volume:** 100 µL @ 10.0 nM target.
- PhiX Control Spike-In:** 1.5% (v/v) Illumina PhiX Control v3.
- Denaturation Protocol:** 5 µL 0.2N NaOH for 5 min at room temp.
- Neutralization:** 5 µL 200mM Tris-HCl pH 8.0.
- Final Loading Conc:** 2.2 pM onto NovaSeq X Plus Reagent Cartridge.

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Section 6: Flow Cell Loading & Sequencing Run Configuration

Sequencer Instrument:	NovaSeq X Plus (SN: NSX-2024-884)	Flow Cell Serial:	LH-10k-202607-0091
Flow Cell Type:	10B 300-Cycle Flow Cell	Lane Assignment:	Lane 3 & Lane 4
Read Configuration:	Read 1: 151bp · Read 2: 151bp	Index Cycle Setup:	Index 1 (i7): 10bp · Index 2 (i5): 10bp
Primary Analysis:	DRAGEN v4.2 On-Instrument Pipeline	Output Path:	s3://meridian-genomics-raw/20260724_NEX0842/

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Section 7: Chain of Custody & Authorization Sign-Off

Sample Received By:	Library Prep Technician:	QA/QC Manager Approval:
Signature: _____	Signature: _____	Signature: _____
Name: Marcus Thorne, CLS	Name: Dr. Elena Rostova	Name: Dr. Arthur Pendelton
Date: 2026-07-24	Date: 2026-07-25	Date: 2026-07-25

Storage & Archive Disposition:

- Remaining stock DNA/RNA stored at **-80°C Freezer #4, Rack B, Box 12**.
- Constructed libraries archived at **-20°C Post-PCR Library Vault 2**.
- Sample retention policy: Standard 6-month hold post-delivery unless extended by PI agreement.