TRANSCRIPTOMICS

Application	Sample Requirements	Read Length[$]	Average Output[&]	Platform	Sample Minimum*	Deliverables
mRNA-Seq	Integrity: RIN ≥ 8 Amount: ≥ 1 µg[#] Volume: ≥ 20 µl	1 x 75 bp	30M (gene expression)	NextSeq	10	Gene count matrix (TPM/COUNT), QC summary table, MultiQC report, FASTQ files
		2 x 50 bp	2 x 30M	NovaSeq	20	
Ultra-low input mRNA-Seq, RNA input	Integrity: RIN ≥ 8 Amount: ≥ 50 ng[#] Volume: ≥ 20 µl Other: No EDTA	1 x 75 bp	30M	NextSeq	10	
		2 x 50 bp	2 x 30M	NovaSeq	20	
Ultra-low input mRNA-Seq, whole cell input	Amount: 1 – 1000 cells Volume: up to 10.5 µl in lysis buffer (provided) Other: No EDTA	1 x 75 bp	30M	NextSeq	10	
		2 x 50 bp	2 x 30M	NovaSeq	20	
3' mRNA-Seq for degraded or FFPE RNA (UMI quantification)	Integrity: DV200 ≥ 30% Amount: ≥ 500 ng[#] Volume: ≥ 20 µl	1 x 75 bp	10M (gene expression only)	NextSeq Mid Output	8	
				NextSeq High Output	30	
				NovaSeq	60	
Total RNA-Seq	Integrity: RIN ≥ 8 Amount: ≥ 1 µg[#] Volume: ≥ 20 µl	1 x 75 bp	50M	NextSeq	6	
		2 x 50 bp	2 x 50M	NovaSeq	12	
miRNA-Seq (UMI quantification)	Integrity: RIN ≥ 8 Amount: ≥ 500 ng[#] Volume: ≥ 20 µl	1 x 75 bp	10M	NextSeq Mid Output	8	Raw/normalized expression analysis, Excel QC report, FASTQ files
				NextSeq High Output	30	
				NovaSeq	60	

* Turnaround time of 12-15 business days for library preparation and sequencing if sample minimum is met. If sample minimum is not met, please allow for extra lead time. Alternatively, samples may be processed sooner for an additional cost. Contact genomics@cshs.org for more information.

[#] As measured with a fluorescent dye, such as Qubit or QUANT-iT PicoGreen.

[$] For alternate read lengths or outputs, please contact genomics@cshs.org.

GENOMICS

Application	Sample Requirements	Read Length[&]	Average Output[&]	Platform	Sample Minimum*	Deliverables
Whole Genome Sequencing	Integrity: ≥ 12 kb Amount: ≥ 1 µg Volume: ≥ 20 µl	2 x 150 bp	30X coverage	NovaSeq	4	Raw SNP calling results (.vcf file), raw INDEL calling results (.vcf file), MultiQC report, FASTQ files
Whole Genome Sequencing for FFPE DNA	Integrity: ≥ 1500 bp Amount: ≥ 1 µg Volume: ≥ 20 µl	2 x 150 bp	30X coverage	NovaSeq	4	
Whole Exome Sequencing	Integrity: ≥ 12 kb Amount: ≥ 1 µg Volume: ≥ 20 µl	2 x 150 bp	120X coverage	NextSeq	8	
				NovaSeq	16	
Whole Exome Sequencing for FFPE DNA	Integrity: ≥ 1500 bp Amount: ≥ 1.5 µg Volume: ≥ 25 µl	2 x 150 bp	120X coverage	NextSeq	8	
				NovaSeq	16	

* Turnaround time of 12-15 business days for library preparation and sequencing if sample minimum is met. If sample minimum is not met, please allow for extra lead time. Alternatively, samples may be processed sooner for an additional cost. Contact genomics@cshs.org for more information.

[#] As measured with a fluorescent dye, such as Qubit or QUANT-iT PicoGreen.

[$] For alternate read lengths or outputs, please contact genomics@cshs.org.

EPIGENOMICS

Application	Sample Requirements	Read Length[&]	Average Output[&]	Platform	Sample Minimum*	Deliverables
ATAC-Seq	Cells: 5,000-50,000 from fresh or cyropreserved cells Viability: > 90% Other: 1.5 ml tube	Nucleosome positioning: 2 x 75 bp	2 x 40M reads	NextSeq	8	Excel peak calling table, QC report, FASTQ files
		TF profiling: 2 x 50 bp	2 x 120M reads	NovaSeq	6	
ChIP-Seq (H3K27ac)	Amount: $1x10^7$cells	1 x 75 bp	25M reads	NextSeq	12	
ChIP-Seq (library preparation only)	Amount: ≥ 50 ng Volume: ≥ 15 ml Other: ≥ 5-fold increase over negative control; input control	1 x 75 bp	TF profiling: 25M reads	NextSeq	12	
			Histone profiling: 50M reads	NextSeq	12	
Whole Genome Bisulfite Sequencing	Integrity: ≥ 12 kb Amount: ≥ 1 μg[#] Volume: ≥ 20 μl	2 x 150 bp	30X coverage	NovaSeq	4	Bedgraph with CpG sites, bedgraph with all C, summary QC table, MultiQC report, FASTQ files

* Turnaround time of 12-15 business days for library preparation and sequencing if sample minimum is met. If sample minimum is not met, please allow for extra lead time. Alternatively, samples may be processed sooner for an additional cost. Contact genomics@cshs.org for more information.

[#] As measured with a fluorescent dye, such as Qubit or QUANT-iT PicoGreen.

[$] For alternate read lengths or outputs, please contact genomics@cshs.org.

METAGENOMICS

Application	Region	Sample Requirements	Read Length[&]	Average Output[&]	Platform	Sample Minimum	Deliverables
Bacterial 16S rRNA amplicon sequencing	V1 – V2	Volume: ≥ 10 µl	2 x 300 bp	2 x 5k reads	MiSeq	50*	Biom format abundance OTU table, QC report, FASTQ files
	V1 – V3						
	V3 – V4						
Archaeal 16S rRNA amplicon sequencing	V3 – V4	Volume: ≥ 10 µl	2 x 300 bp	2 x 5k reads	MiSeq	50*	
Prokaryote 16S rRNA amplicon sequencing	V3 – V4	Volume: ≥ 10 µl	2 x 300 bp	2 x 5k reads	MiSeq	50*	
Fungal ITS amplicon sequencing	ITS1	Volume: ≥ 10 µl	2 x 300 bp	2 x 5k reads	MiSeq	50*	
	ITS2						
Shotgun Metagenomics	NA	Amount: ≥ 500 ng[#] Volume: ≥ 20 µl	2 x 150 bp	2 x 50M	NovaSeq	12[$]	FASTQ files only

* Sample minimum can consist of any combination of amplicon sequencing applications and regions for a total of 50 samples. Sequencing is performed when a total of ≥ 200 samples have been accumulated. Thus, turnaround time is variable. Contact genomics@cshs.org for the current turnaround time estimate.

[$] Turnaround time of 12-15 business days for library preparation and sequencing if sample minimum is met. If sample minimum is not met, please allow for extra lead time. Alternatively, samples may be processed sooner for an additional cost. Contact genomics@cshs.org for more information.

[#] As measured with a fluorescent dye, such as Qubit or QUANT-iT PicoGreen.

[$] For alternate read lengths or outputs, please contact genomics@cshs.org.

SEQUENCING ONLY

NovaSeq 6000 System						
Flow Cell Type	**SP**	**S1**	**S2**	**S4**	**Sample Requirements**	**Deliverables**
Output Per Flow Cell					• Pooled, multiplexed libraries • Sample names with letters, numbers, dashes, and underscores only • Library preparation kit name • Index kit name • Index names and sequences • Library concentration • Read length • SR or PE format • Sequencer loading concentration	FASTQ files
2 x 50 bp	65 – 80 Gb	134 – 167 Gb	333 – 417 Gb	NA		
2 x 100 bp	NA	266 – 333 Gb	667 – 833 Gb	1600 – 2000 Gb		
2 x 150 bp	200 – 250 Gb	400 – 500 Gb	1000 – 1250 Gb	2400 – 3000 Gb		
2 x 250 bp	325 – 400 Gb	NA	NA	NA		
Reads Passing Filter						
Single Reads*	650 – 800 million	1.3 – 1.6 billion	3.3 – 4.1 billion	8 - 10 billion		
Paired-end reads*	1.3 – 1.6 billion	2.6 – 3.2 billion	6.6 – 8.2 billion	16 – 20 billion		

* Reads specified is the maximum number of reads achievable and is NOT guaranteed-reads achieved is dependent on library quality, accurate quantification, and loading concentration.

SEQUENCING ONLY

NextSeq 500 System				
Flow Cell Type	**High**	**Mid**	**Sample Requirements**	**Deliverables**
Output Per Flow Cell			• Pooled, multiplexed libraries • Sample names with letters, numbers, dashes, and underscores only • Library preparation kit name • Index kit name • Index names and sequences • Library concentration • Read length • SR or PE format • Sequencer loading concentration	FASTQ files
1 x 75 bp	30 Gb	NA		
2 x 75 bp	60 Gb	19.5 Gb		
2 x 150 bp	120 Gb	39 Gb		
Reads Passing Filter				
Single Reads*	400 million	130 million		
Paired-end reads*	800 million	260 mllion		

* Reads specified is the maximum number of reads achievable and is NOT guaranteed-reads achieved is dependent on library quality, accurate quantification, and loading concentration.

SEQUENCING ONLY

MiSeq System, Reagent Kit V2				MiSeq System, Reagent Kit V3		Sample Requirements	Deliverables
Flow Cell Type	**Nano**	**Micro**				• Pooled, multiplexed libraries • Sample names with letters, numbers, dashes, and underscores only • Library preparation kit name • Index kit name • Index names and sequences • Library concentration • Read length • SR or PE • Sequencer loading concentration	FASTQ files
Output Per Flow Cell				**Output Per Flow Cell**			
2 x 25 bp	NA	NA	0.75 - 0.85 Gb	2 x 75 bp	3.3 - 3.8 Gb		
2 x 150 bp	0.3 Gb	1.2 Gb	4.5 - 5.1 Gb	2 x 250 bp	7.5 – 8.5 Gb		
2 x 250 bp	0.5 Gb	NA	8.5 Gb	2 x 300 bp	13.2 - 15 Gb		
Reads Passing Filter				**Reads Passing Filter**			
Single Reads*	1 million	4 million	12 - 15 million	Single Reads*	22 - 25 million		
Paired-end reads*	2 million	8 million	24 - 30 million	Paired-end reads*	44 - 50 million		

* Reads specified is the maximum number of reads achievable and is NOT guaranteed-reads achieved is dependent on library quality, accurate quantification, and loading concentration.

SEQUENCING ONLY

Single Cell Omics						
Application	**Platform**	**Read Length**	**Maximum Output**	**Sample Minimum***	**Sample Requirements**	**Deliverables**
10x Genomics 3’ scRNA-Seq libraries	NovaSeq	91 bp transcript read	400M	2	• Pooled, multiplexed libraries • Sample names with letters, numbers, dashes, and underscores only • Library preparation kit name • Index kit name • Index names and sequences	FASTQ files
10x Genomics scATAC-Seq libraries	NextSeq	2 x 70 bp	2 x 130M, 2 x 400M reads	1		
	NovaSeq	2 x 50 bp	2 x 400M	2		
10x Genomics scCNV libraries	NovaSeq	2 x 100 bp	2 x 1.6B	1		
	NovaSeq	2 x 150 bp	2 x 800M	1		
10x Genomics scV(D)J libraries	MiSeq	2 x 150 bp	2 x 15M	1		
	NovaSeq	2 x 150 bp	2 x 400M	2		
10x Genomics 5’ scRNA-Seq libraries	NovaSeq	91 bp transcript read	400M	2		

* Turnaround time of 3-5 business days if sample minimum is met. If sample minimum is not met, please allow for extra lead time. Alternatively, samples may be processed sooner for an additional cost. Contact genomics@cshs.org for more information.

SINGLE CELL OMICS

Capture and Library Preparation				
Application	**Platform**	**Capture Range**	**Optimal Cell Concentration**	**Deliverables**
3’ scRNA-Seq • Optional: With cell surface protein expression and/or sample multiplexing	10x Genomics Chromium	500 – 10,000 cells	700 – 1,200 cells/µl	Outputs from CellRanger, FASTQ files
3’ scRNA-Seq + CRISPR screening	10x Genomics Chromium	500 – 10,000 cells	700 – 1,200 cells/µl	
scATAC-Seq	10x Genomics Chromium	500 – 10,000 nuclei (nulcei isolation from 100,000 – 1,000,000)	NA	
scCNV	10x Genomics Chromium	250 – 5,000 cells or nuclei	200 – 4000 cells/µl, dependent on targeted cell recovery	
scV(D)J, B or T cell enrichment • Optional: With 5’ scRNA-Seq • Optional: With cell surface protein expression and/or sample multiplexing	10x Genomics Chromium	500 – 10,000 cells	700 – 1,200 cells/µl	
Cell lysis, RT, cDNA amplification, cDNA QC	Plate-based full transcript scRNA-Seq	Minimum 94 cells	NA	Gene count matrix (TPM/COUNT), QC summary table, MultiQC report, FASTQ files
Library preparation and QC				
Library preparation only for any 10x Genomics application				
Processing of cryopreserved cells				
Dead cell removal				

SINGLE CELL OMICS

Sequencing						
Application	**Platform**	**Read Length**	**Maximum Output**	**Sample Minimum***	**Sample Requirements**	**Deliverables**
10x Genomics 3’ scRNA-Seq libraries	NovaSeq	91 bp transcript read	400M	2	• Pooled, multiplexed libraries • Sample names with letters, numbers, dashes, and underscores only • Library preparation kit name • Index kit name • Index names and sequences	Outputs from CellRanger, FASTQ files
10x Genomics scATAC-Seq libraries	NextSeq	2 x 70 bp	2 x 130M, 2 x 400M reads	1		
	NovaSeq	2 x 50 bp	2 x 400M	2		
10x Genomics scCNV libraries	NovaSeq	2 x 100 bp	2 x 1.6B	1		
	NovaSeq	2 x 150 bp	2 x 800M	1		
10x Genomics scV(D)J libraries	MiSeq	2 x 150 bp	2 x 15M	1		
	NovaSeq	2 x 150 bp	2 x 400M	2		
10x Genomics 5’ scRNA-Seq libraries	NovaSeq	91 bp transcript read	400M	2		

* Turnaround time of 3-5 business days if sample minimum is met. If sample minimum is not met, please allow for extra lead time. Alternatively, samples may be processed sooner for an additional cost. Contact genomics@cshs.org for more information.

qPCR

Application	Sample Requirements	Platform	Reaction Size	Deliverables
Gene expression	• 2.5 pg – 250 ng cDNA • 10 µl cDNA/sample/replicate • Fluidigm DELTAgene™ Assay Plate - **OR** - 10 µL of 100 µM each mixed forward + reverse primers*	Fluidigm BioMark HD	48 (targets) x 48 (samples) 96 (targets) x 96 (samples)	• Ct values in table format • Heat map
* If not using DELTAgene™ Assays, contact genomimcs@cshs.org for information on primer design specific for the BioMark assay.				

QUALITY CONTROL – FRAGMENT ANALYSIS

Application	Platform	Assay	Sample Requirements*	Sample Minimum
RNA Integrity Analysis	Bioanalyzer	Pico	Concentration range: 50 pg/µl - 5 ng/µl	1
		Nano	Concentration range: 5 - 500 ng/µl	
		Small RNA	Concentration range: 1 – 100 ng/µl Size range: 6 - 150 bp	1
	Fragment Analyzer	High Sensitivity	Concentration range: 50 pg/µl - 5 ng/µl	24
	TapeStation	High Sensitivity	Concentration range: 1 - 25 ng/µl	1
dsDNA Integrity Analysis	Bioanalyzer	High Sensitivity	Concentration range: • PCR product: 0.1 - 10 ng/µl • Sheared DNA/NGS library: 0.1 - 10 ng/µl Sizing range: 50 - 7000 bp	1
		DNA 1000	Concentration range: 0.5 - 50 ng/µl Sizing range: 25 - 1000 bp	
	Fragment Analyzer	High Sensitivity	Concentration range: • PCR product: 5 - 500 pg/µl • Sheared DNA/NGS library: 50 pg/µl - 5 ng/µl Sizing range: 25 - 5000 bp	24
		Standard Sensitivity	Concentration range: • PCR product: 0.1 - 10 ng/µl • Sheared DNA/NGS library: 5 - 100 ng/µl Sizing range: 25 - 5000 bp	24
	TapeStation	High Sensitivity D1000	Concentration range: 10 pg/µl - 1 ng/µl Sizing range: 35 - 1000 bp	1
		D1000	Concentration range: 0.1 - 50 ng/µl Sizing range: 30 - 1000 bp	
Genomic DNA Integrity Analysis	Fragment Analyzer	High Sensitivity	Concentration range: 300 pg/µl - 12 ng/µl Sizing range: 75 – 60,000 bp	24
	TapeStation		Concentration range: 5 - 300 ng/µl Sizing range: 200 - >6000 bp	1

* Sample concentration must be within the range listed (higher end recommended). Dilutions necessary to be within the concentration range of the assay will incur an additional cost.

NUCLIEC ACID QUANTIFICATION

Application	Platform	Assay	Sample Requirements	Sample Minimum
Fluorescence-based RNA quantification	Qubit/QUANT-iT	High Sensitivity	Concentration range: 250 pg/µl – 100 ng/µl	1
		Broad Range	Concentration range: 1 ng/µl – 1 µg/µl	1
Fluorescence-based dsDNA quantification	Qubit/QUANT-iT	High Sensitivity	Concentration range: 10 pg/µl – 100 ng/µl	1
		Broad Range	Concentration range: 100 pg/µl – 1 µg/µl	1

NUCLIEC ACID ISOLATION

Application*	Sample Type	Sample Requirements	Sample Minimum
Total RNA#	Cells	1000 - $1x10^7$ cells	8
DNA	Cells	1000 - $1x10^7$ cells	8

* Includes isolation, fluorescence-based quantification, and integrity analysis.
# Includes genomic DNA removal.