

SEQUENCING ONLY

NovaSeq 6000 System						
Flow Cell Type	SP	S1	S2	S4	Sample Requirements	Deliverables
Output Per Flow Cell					<ul style="list-style-type: none"> • 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.						

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NextSeq 500 System				
Flow Cell Type	High	Mid	Sample Requirements	Deliverables
Output Per Flow Cell			<ul style="list-style-type: none"> • 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 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.				

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MiSeq System, Reagent Kit V2				MiSeq System, Reagent Kit V3		Sample Requirements	Deliverables
Flow Cell Type	Nano	Micro				<ul style="list-style-type: none"> • 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.							

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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	<ul style="list-style-type: none"> • 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.