

# TRANSCRIPTOMICS

Application	Sample Requirements	Read Length <sup>§</sup>	Average Output <sup>&amp;</sup>	Platform	Sample Minimum*	Deliverables
mRNA-Seq	Integrity: RIN $\geq$ 8 Amount: $\geq$ 1 $\mu$ g <sup>#</sup> Volume: $\geq$ 20 $\mu$ l	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 $\geq$ 8 Amount: $\geq$ 50 ng <sup>#</sup> Volume: $\geq$ 20 $\mu$ l 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 $\mu$ l 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 $\geq$ 30% Amount: $\geq$ 500 ng <sup>#</sup> Volume: $\geq$ 20 $\mu$ l	1 x 75 bp	10M (gene expression only)	NextSeq Mid Output	8	
				NextSeq High Output	30	
				NovaSeq	60	
Total RNA-Seq	Integrity: RIN $\geq$ 8 Amount: $\geq$ 1 $\mu$ g <sup>#</sup> Volume: $\geq$ 20 $\mu$ l	1 x 75 bp	50M	NextSeq	6	
		2 x 50 bp	2 x 50M	NovaSeq	12	
miRNA-Seq (UMI quantification)	Integrity: RIN $\geq$ 8 Amount: $\geq$ 500 ng <sup>#</sup> Volume: $\geq$ 20 $\mu$ l	1 x 75 bp	10M	NextSeq Mid Output	8	
				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](mailto: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](mailto:genomics@cshs.org).