

METAGENOMICS

Application	Region	Sample Requirements	Read Length ^{&}	Average Output ^{&}	Platform	Sample Minimum	Deliverables
Bacterial 16S rRNA amplicon sequencing	V1 – V2	Volume: $\geq 10 \mu\text{l}$	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: $\geq 10 \mu\text{l}$	2 x 300 bp	2 x 5k reads	MiSeq	50*	
Prokaryote 16S rRNA amplicon sequencing	V3 – V4	Volume: $\geq 10 \mu\text{l}$	2 x 300 bp	2 x 5k reads	MiSeq	50*	
Fungal ITS amplicon sequencing	ITS1	Volume: $\geq 10 \mu\text{l}$	2 x 300 bp	2 x 5k reads	MiSeq	50*	
	ITS2						
Shotgun Metagenomics	NA	Amount: $\geq 500 \text{ ng}^{\#}$ Volume: $\geq 20 \mu\text{l}$	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.