

## PRODUCT DATA SHEET

# Walk-Up Sequencing

### OVERVIEW

Walk-Up Sequencing is an efficient sequencing service for pre-constructed DNA libraries providing sequence data delivery. With funding in place, IRB consent, and concentrations within the specified submission range, a sample submitted to Walk-Up Sequencing will be on a sequencer within two business days of receipt, allowing for quick data delivery.

Sample submission consists of using a web-based interface and providing a constructed library along with the relevant adapter and index information. Walk-Up Sequencing services include library quantification, denaturation, sequence data generation and delivery. The service allows you to perform your specific library sequencing while providing convenient, rapid-turnaround times for a wide variety of sample preparation approaches.

MiSeq	50bp, 300bp, or 500bp	≥50 million reads
NextSeq 500	75bp, 150bp, or 300bp	≥320 million reads
HiSeq2500 Rapid	50bp, 200bp, 250bp, 300bp, or 500bp	≥200 million reads
HiSeq2500 High Yield	50bp, 152bp, or 202bp	≥800 million reads
NovaSeq 6000 S2	100bp, 200bp, or 300bp	≥2 billion reads
NovaSeq 6000 S4	300bp	≥4 billion reads

Sequencing of samples starts within 48 hours of receipt

Flexibility to handle non-standard library types

### CONSIDERATIONS FOR SUBMISSION

- Libraries must contain >20ul of volume\*
- qPCR quantitation results >2nM\*
- Any library pooling must be completed prior to submission
- Funded quote and IRB/ORSP must be in place
- Projects on the NovaSeq S2 & S4 require a minimum input of 200ul.
- Samples not meeting these requirements can be accepted but will be processed "on-risk" without guaranteed data output.

### DATA DELIVERABLES

Users can choose from three options for the data format provided:

- .fastq (no demultiplexing)
- .fastq and de-multiplexed .fastq
- .fastq, de-multiplexed .fastq, and Picard generated .bam file

Data is delivered via access to a restricted, temporary FTP site. All generated data may be downloaded for up to 30 days. Long-term storage, data submission (e.g. NCBI) and data aggregation are not included.

### FOR MORE INFORMATION

Web: [genomics.broadinstitute.org](http://genomics.broadinstitute.org)

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