

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, 500bp, or 600bp	≥5 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, 100bp, 152bp, or 202bp	≥800 million reads
NovaSeq 6000 SP	100bp, 300bp, or 500bp	≥500 million reads
NovaSeq 6000 S1	100bp, 200bp, or 300bp	≥1 billion reads
NovaSeq 6000 S2	100bp, 200bp, or 300bp	≥3 billion reads
NovaSeq 6000 S4	300bp	≥6 billion reads

FOR MORE INFORMATION

Web: genomics.broadinstitute.org
Email: genomics@broadinstitute.org
or walkupseq@broadinstitute.org



GENOMIC SERVICES

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.