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, denturation, 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.

- Libraries must contain >20 ul of volume
- qPCR quantitation results >2 nM
- 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 200 ul.
- 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

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