BROAD CLINICAL LABS

PRODUCT DATASHEET

Whole Exome Sequencing

Product Overview

Leveraging vast experience in the production and analysis of human whole exome sequence data, Broad Clinical Labs' (BCL) CLIA-certified, CAP accredited facility offers both clinical and research-grade whole exome sequencing offerings. With experience processing >775,000 samples in support of a variety of large scale resource building efforts in medical genetics and cancer, our whole exome sequencing offerings represent the cumulative output of the Broad Institute's knowledge, maximizing utility for variant discovery in specific disease areas. Careful analysis workflows, library construction methods, and coverage deliverables result in a flexible set of offerings that provide optimal data to drive scientific discovery.

Using a commercially available probe design co-developed with the Broad scientific community and TWIST Bioscience (34.9Mb target), samples will achieve coverage across >98% of RefSeq and GENCODE v12 territory. Coverage deliverables are based on minimum depth of coverage in targeted bases to ensure samples are appropriately balanced across exome targets.

BCL's whole exome service offerings are:

- Research Germline Human Exome
- Research Somatic Human Exome
- Clinical Somatic Human Exome; can be combined with companion Transcriptome Capture RNA sequencing

What's Included

- Sample receipt and Incoming QC, including sample fidelity/identity QC
- Library construction, hybrid capture, and QC
- Sequencing, data analysis, and delivery (data accessed online via secure digital transfer)
- Clinical Somatic Human Exome service also includes a clinical technical report and ≤28 day TaT.

Minimum Input Requirements

Table 1. Minimum Input Requirements

Exome Version	DNA Quantity	DNA Concentration
Research Germline Human Exome	≥250 ng	≥3ng/µL
Research Somatic Human Exome	≥250 ng	≥5ng/µL
Clinical Somatic Human Exome	≥500 ng	≥10ng/µL
Input types: DNA meeting the requirements above; or FFPE tissue, fresh frozen tissue, plasma, whole blood, buffy coat, saliva, buccal swab		

Data Deliverables

Table 2. Data Deliverables by Whole Exome Sequencing Product

Exome Version	Deliverable
Research Germline Human Exome	De-multiplexed, aligned CRAM file and summary metrics
Research Somatic Human Exome	De-multiplexed, aggregated BAM file and summary metrics
Clinical Somatic Human Exome	Technical report, de-multiplexed aggregated BAM files (Tumor & Normal), summary metrics, germline and somatic SNV and indel variant call files (MAF, VCF), Copy number variants (Seg)

Table 3. Performance Specification of Clinical Somatic Human Exome

Coverage Deliverable	≥150X MTC	
Sample Format	Tumor/Normal Pairs	
Analytical Sensitivity+	**Specification (Recall)**	**Observed (Recall)**
SNV	95%	96.5%
Indel	80%	93.4%
Analytical Specificity (FBR/Mb)	**Specification (FP/Mb)**	**Observed (FP/Mb)**
SNV	<1	.05
Indel	<1	.008
+ Sensitivity for SNV > 10% VAF, Indel > 20% VAF		

Table 3 BCL's Clinical Somatic Whole Human Exome Sequencing test (performance specifications above) utilizes the Illumina DRAGEN™ analytic pipeline and provides the depth of coverage necessary for delivery of high quality somatic variant calling across tumor/normal pairs including SNV, indel and CNV calls.