BROAD INSTITUTE

GENOMIC SERVICES

Human Whole Genome Sequencing

Product Data Sheet

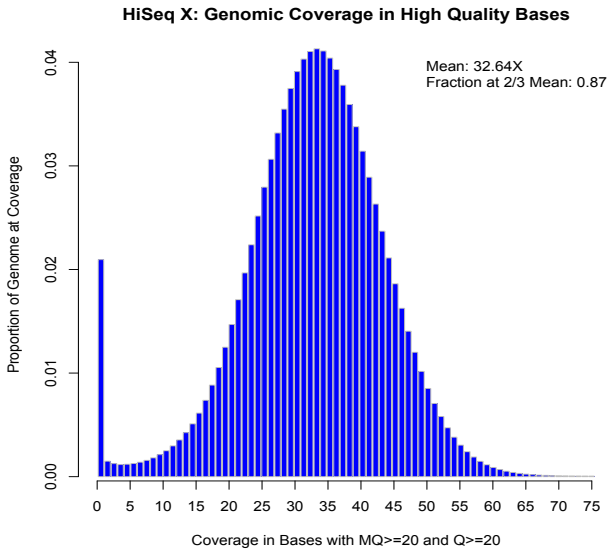
Highlights

- Catalogue Total Genetic Variation
- Discover Rare Variants
- Scale to Medical and Population Genetics

Leveraging over twenty years of experience in human whole genome sequencing, the Broad Institute offers whole genome sequencing utilizing the Illumina HiSeq X™ platform. This latest advancement in sequencing technology combines significant advantages in cost and turn-around-time with best-in-class sample qualification and bioinformatics, allowing the Broad Institute to provide global researchers the tools to recognize the promise of human whole genome sequencing.

Thorough analysis of data produced using well-characterized samples was measured for sensitivity to detect variants, and compared with reference data to ensure concordance. These analyses have driven the definition of whole genome sequencing products to satisfy requirements of analysis tools in order to seamlessly test fundamental hypotheses related to human health.

What's Included: Whole Genome Sequencing includes plating, library preparation, size selection, sequencing (150bp paired reads), sample identification QC and contamination fingerprinting via genotyping. The product provides a size selected library with a median insert size of 350bp +/- 20% and sequence coverage to specified mean target coverage. Data delivery will include a de-multiplexed, aggregated Picard BAM file, which will be accessed *via* secure online digital transfer. Please note that these products are solely applicable to human samples.



Genome-wide Coverage Distribution of representative sample sequenced to mean coverage of ~30X

Input Requirements:

- 100ng/350ng of purified genomic DNA
- Fresh frozen or FFPE tissue, blood, saliva, slides, cell pellets, or buffy coats that preferably yield >250ng of DNA (note extra cost will be applied for extractions.)
- Samples not meeting these specifications can be designated by the collaborator to be processed "on risk" and will be subject to billing regardless of data quality
- Minimum Sample data including - Collaborator Participant ID, Collaborator Sample ID, Gender
- Tumor/Normal or Case/Control pairs must be received together if indel co-cleaning is required

For more information please visit
web: genomics.broadinstitute.org
email: genomics@broadinstitute.org

Product Details

Product Name	Mean Coverage	Sample Preparation Method	Input DNA Amount	Compatible Extraction Products
Standard Coverage Human WGS	30X	PCR library amplification	100ng	FFPE*, fresh frozen tissue, blood, saliva*, cell pellets, or buffy coats
Deep Coverage Human WGS	60X	PCR library amplification	100ng	FFPE*, fresh frozen tissue, blood, saliva*, cell pellets, or buffy coats
Standard Coverage PCR-Free WGS	30X	PCR-Free	350ng	Fresh frozen tissue, blood, saliva*, cell pellets, or buffy coats
Deep Coverage PCR-Free WGS	60X	PCR-Free	350ng	Fresh frozen tissue, blood, saliva*, cell pellets, or buffy coats

* refer to our application notes for special considerations when working with these material types, www.genomics.broadinstitute.org/products/nucleic-acid-extractions