PRODUCT DATA SHEET

Whole Exome Sequencing

PRODUCT OVERVIEW

Leveraging vast experience in the production and analysis of human whole exome sequence data, our research offerings represent the cumulative output of the Broad Institute's knowledge, maximizing specific utility for variant discovery in specific disease areas. Careful analysis of sample inputs, library construction methods, and coverage deliverables results in a set of offerings that provide optimal data to drive scientific discovery.

The Broad Institute Genomic Service's research Whole Exome Sequencing products leverage our experience in producing ~300,000 human exomes to date. Using a content bait set containing 38Mb target territory, this content includes all of our previous exome content plus additional coding content that brings the total coverage of the RefSeq and GENCODE v12 databases to >98%. Our coverage deliverables look closer than mean target coverage, providing valuable insight into the actual percentage of targets achieving a minimum guaranteed coverage.

WHAT'S INCLUDED

- Sample Receipt and QC
- Sample Fidelity QC (96 SNP fingerprinting)
- · Library Construction, Hybridization and QC
- Sequencing and Data Delivery

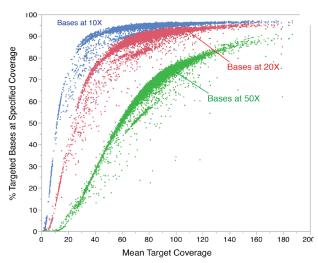
Industry leader in Whole Exome Sequencing ~300,000 Exomes to date

Optimized products drive variant discovery in focused disease areas

DATA DELIVERABLE

- Data accessed via secure online digital transfer
- De-Multiplexed, aggregated Picard BAM file and summary metrics
- Germline Variant Call Format (VCF) and Somatic
 Mutation Variant Format (MAF) files are also available

COVERAGE ACROSS THE EXOME



Distribution of coverage levels for targeted bases for representative samples sequenced to \sim 10X, \sim 20X, and \sim 50X mean target coverage

EXOME OFFERINGS

| | | DNA | | Library | Read | Coverage | Equivalent |
|---|---|-----------------|---|---------------------|-----------|-------------------------------|------------|
| Product | Utility | input | Compatible Extractions | Construction | Length | Deliverable | MTC |
| Germline Exome | Non-cancer, including population genomics, rare and common disease cohort studies | 100ng | Blood, saliva*, cell pellets or buffy coat | Transposase Base | 2 x 150bp | 85% targeted bases at >20X | ~60-80X |
| Somatic Exome Standard Coverage -Available with Express 28 day TAT | Control for case-control tumor/ normal & trio/somatic analysis | 100ng | Fresh frozen tissue, blood, saliva*, cell pellets, or buffy coat | Ligation Based | 2 x 76bp | 80% targeted bases at >20X | ~50-80X |
| Somatic Exome Deep Coverage -Available with Express 28 day TAT | Case/proband for case-control tumor/normal & trio/somatic analysis | 100ng | Fresh frozen tissue, blood, FFPE*, saliva*, cell pellets, or buffy coat | Ligation Based | 2 x 76bp | 85% targeted bases >50X | ~120-150X |
| Liquid Biopsy Germline and Somatic Exome | Compatible with liquid biopsy sample prep | 2-20ng cfDNA | Blood, Plasma | Ligation Based | 2 x 76bp | Germline 60X Somatic 150X | |

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



FOR MORE INFORMATION

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