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 has resulted in a set of offerings to provide optimal data to drive scientific discovery.

The Broad Institute’s research Whole Exome Sequencing products leverage our experience in producing >200,000 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, QC & Plating & Sample Preparation
- Illumina HiSeq 2500 or 4000 Sequencing
- Sample Fidelity QC (96 SNP fingerprinting)

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

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

### Highlights
- Industry leader in Whole Exome Sequencing produced >200,000 Exomes to Date
- Optimized products drive variant discovery in focused disease areas

### Product Details

<table>
<thead>
<tr>
<th>Product Name</th>
<th>Utility</th>
<th>Input DNA Amount</th>
<th>Compatiable Extraction Products</th>
<th>Library Construction Method</th>
<th>Read Length</th>
<th>Coverage Deliverable</th>
<th>Equivalent MTC</th>
</tr>
</thead>
<tbody>
<tr>
<td>Standard Coverage Germline Exome</td>
<td>non-cancer, including population genomics, rare and common disease cohort studies</td>
<td>100ng</td>
<td>Blood, stool, *saliva, slides, cell pellets or buffy-coat</td>
<td>Transposase Base</td>
<td>2 x 150 bp</td>
<td>85% targeted bases at &gt;20X</td>
<td>~60-80X</td>
</tr>
<tr>
<td>Standard Coverage Human WES *Available in Express (28 Day TAT)</td>
<td>control for case-control tumor/normal &amp; trio/somatic analysis</td>
<td>100ng</td>
<td>Fresh frozen tissue, blood, stool, *saliva, cell pellets, or buffy coat</td>
<td>Ligation Based</td>
<td>2 x 76bp</td>
<td>80% targeted bases at &gt;20X</td>
<td>~50-80X</td>
</tr>
<tr>
<td>Deep Coverage Human WES *Available in Express (28 Day TAT)</td>
<td>case/proband for case-control tumor/normal &amp; trio/somatic analysis</td>
<td>100ng</td>
<td>Fresh frozen tissue, blood, stool, *saliva, cell pellets, or buffy coat</td>
<td>Ligation Based</td>
<td>2 x 76bp</td>
<td>85% targeted bases &gt;50X</td>
<td>~120-150X</td>
</tr>
<tr>
<td>FFPE Deep Coverage Somatic Exome *Available in Express (28 Day TAT)</td>
<td>optimized processing for material derived from FFPE</td>
<td>100ng</td>
<td>FFPE</td>
<td>Ligation Based</td>
<td>2 x 76bp</td>
<td>85% targeted bases &gt;50X</td>
<td>~120-150X</td>
</tr>
</tbody>
</table>

For more information please visit genomics.broadinstitute.org