ACT Onco®+

Find the right treatment for your cancer patient

Planning treatment strategies through comprehensive genomic profiling for 440 cancer-related genes

www.actgenomics.com
ACTOnco®+ is a next-generation sequencing based assay, sequencing more than 440 cancer-related genes simultaneously from cancer specimens in our ISO17025 and CAP accredited lab. This assay is specially designed for patients with all types of solid tumors, providing comprehensive genomic profile and recommendations of targeted drugs well-selected from FDA-approved lists and clinical trials.

**ANALYZING CANCER SIGNALING PATHWAY TO IDENTIFY ALL MATCHING DRUGS**

Comprehensively identifies genetic alterations of each signaling pathway to evaluate drug options based on upstream and downstream interactions and increase treatment efficacy.

**Copy Number Variation Analysis**

**Identify more genetic alterations with CNV analysis**

**Cancer Signaling Pathway Analysis**

Identify more treatment options with pathway integration

In addition to EGFR, its downstream genes and other signaling pathways involve other cancer-related genes. Related target drugs can therefore be selected to treat patients with these mutations, avoiding drug resistance and providing more therapeutic options.

### Example

<table>
<thead>
<tr>
<th>Upstream Gene</th>
<th>Downstream Genes in Signaling Pathways</th>
</tr>
</thead>
<tbody>
<tr>
<td>VEGFR</td>
<td>PIP2, PLK, PTEN, AKT, TSC1, TSC2, RHEB, mTOR</td>
</tr>
<tr>
<td>EGFR</td>
<td>RAS, RAF, MEK1/2, ERK1/2, PIP3, STK11</td>
</tr>
</tbody>
</table>

**Table**

<table>
<thead>
<tr>
<th>Aberrant Genes</th>
<th>Drug Suggestion</th>
</tr>
</thead>
<tbody>
<tr>
<td>EGFR</td>
<td>EGFR inhibitors</td>
</tr>
<tr>
<td>BRAF (V600E)</td>
<td>BRAF inhibitors</td>
</tr>
<tr>
<td>RAF/RAS</td>
<td>MEK inhibitors</td>
</tr>
<tr>
<td>VEGFR</td>
<td>VEGFR inhibitors</td>
</tr>
<tr>
<td>PI3K, PTEN, TSC1/2</td>
<td>mTOR inhibitors</td>
</tr>
</tbody>
</table>
Prediction of Immunotherapy Response

Sequencing of 440 cancer-related genes covering most key cancer signaling pathways for targeted therapy

Analyzing single nucleotide variations (SNV), small insertions / deletions (InDel) and copy number variations (CNV) to provide more drug options based on pathway analysis

Providing professional solutions within 14 calendar days

Using next-generation sequencing (NGS) for microscale specimens

Integrating cancer biology, medical biology, molecular biology, cell biology, immunology, bioinformatics, data science, and pharmaceutical biology to provide insightful interpretation

Incorporating mutation burden, immune-related gene information and MSI status for a more accurate immunotherapy recommendation

Responses to treatment may be affected by inherited genetic variations

Pharmacogenetics information can be used to match patients with the treatment that is most effective, while causing less side-effects.

Comprehensive Exon Sequencing

440 Cancer-related genes

NGS Sequencing Mean Depth

>800x

Hotspots

>6800

Sample Types

• FFPE
• Core needle biopsy
• Frozen tissue
• Pleural effusion
• Ascites samples
• Purified DNA

Prediction of Immunotherapy Response

Microsatellite instability (MSI) testing

Additional Assay for Lung Cancer

ALK, RET, ROS1 and NTRK1 fusion gene detection (including 72 fusion transcripts)