The genomic application that characterizes the complex mutational landscape of the major solid tumors by combining DNA target capture and RNA target amplicon with the analytical capabilities and advanced features of the SOPHiA DDM™ Platform.

Main Features

SOPHiA DDM™ Solid Tumor Plus Solution (STS+) targets DNA variants and RNA transcripts of fusion genes associated with solid tumors, including lung, colorectal, skin, and brain cancers. The DNA panel covers 42 genes including 6 unique loci to detect MSI status associated with colorectal cancer, and the RNA panel targets 137 clinically relevant gene fusions. Probe design is optimized to guarantee high on-target rate and coverage uniformity throughout the entire target regions.

Gene Panel

<table>
<thead>
<tr>
<th>Gene</th>
<th>Variants Called</th>
<th>Recommendations</th>
<th>Wet Lab</th>
</tr>
</thead>
<tbody>
<tr>
<td>AKT1 (3), ALK (21-25), BRCA2 (11,13), CDX2 (4, 2), CDKN2A (1,2,3), CTHRB1 (1,3), DCCD (2), DICER1 (24,25), EGFR (18-21), ESRB2 (8,17,20), ERBB4 (10,12), FBXW7 (7-11), FGFR1 (3,12), FGFR2 (7,12,14), FGFR3 (7,9,14,16), FOXJ2 (1,2), GNA11 (4,5), GNAQ (4,5), GNAT2 (6), GATA3 (7), GNAS (1,3,8,13,17,18), KRAS (2-4), MAP2K1 (2,3), MET (2,14-20), MYOD1 (1), NRGAS (2-4), PDGFRα (12,14,18), PHKB (2,3,4,6,9,10,21), PTPN11 (3,4,5,7,9), RAF1 (3,4,5,7,9,11,12,13,14,15), RET (11,13,15,16), ROS1 (38,41), SF3B1 (15-17), SMAD4 (4,8,12), TERT (promoter*,1,4,9,13), TPS3 (2-11)</td>
<td>• SNVs and Indels • TERT promoter mutations C228T and C250T • MSI status in BAT-25, BAT-26, CAT-25, NR-21, NR-22 and NR-27 • 137 gene fusions in addition to MET exon 14 skipping and EGFR variant III • Gene amplification in 24 genes including EGFR, ERBB2, FGF2 and MET</td>
<td>Day 1: DNA and RNA Library Preparation Sample type: FFPE, fresh-frozen tissue Samples per run / Sequencer: 24 DNA + 24 RNA on Illumina MiSeq® v3 (2x300bp) 48 DNA + 48 RNA on Illumina NextSeq® v2 500/550 Mid-Output (2x150bp) Total library preparation time: 1.5 days for DNA, 6 hours for RNA</td>
<td>DNA RNA</td>
</tr>
<tr>
<td></td>
<td></td>
<td></td>
<td>Observed (%)</td>
</tr>
<tr>
<td></td>
<td></td>
<td></td>
<td>Sensitivity</td>
</tr>
<tr>
<td></td>
<td></td>
<td></td>
<td>98.77</td>
</tr>
</tbody>
</table>

*5% quantile

Analysis time from FASTQ: from 4 hours

Analytical Performance

The SOPHiA DDM™ Platform analyzes complex NGS data by detecting, annotating and pre-classifying genomic alterations and RNA fusions in the genes of this panel.

One Simple Intuitive Platform: Beyond Analytics

Accelerated assessment and reporting of genomic variants

The platform helps users to immediately focus on relevant genomic alterations. Several features facilitate their interpretation process:

- Hotspot screening
- Algorithm-supported variant pre-classification
- Fully customizable filters
- Comprehensive report

Product code: BS0151LSRSMY10

Confident decision-making

The OncoPortal™ Plus add-on module for SOPHiA DDM™ Platform matches tumor molecular profiles with clinical associations and available clinical trials, leveraging expertly curated evidence powered by JAX-CKB. After interpretation, the flexible reporting tools enable users to prepare push-button, comprehensive reports that are customizable to their needs.

Global support at every step

We offer local support anywhere in the world.

Access to the SOPHiA GENETICS Community

Through the SOPHiA DDM™ Platform genomics experts from hundreds of healthcare institutions interpret their findings and flag the pathogenicity level of variants. This highly valuable information enriches the variant knowledge base and is safely shared among the members of the community, supporting their decision-making process for research purposes.

For Research Use Only. Not for Use in Diagnostic Procedures.

OncoPortal™ Plus is for Clinical Decision Support Use Only. Not intended as a primary diagnostic tool.

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CI: confidence interval, FFPE, formalin-fixed paraffin-embedded, Indels, insertions/deletions, MSI, microsatellite instability, NGS, next-generation sequencing, SNP, single nucleotide variant.
RNA Gene Fusion Panel

ATF7IP(13)-JAK2(9,11,13,15,17,18,19), BCR(1,4,6,7,12,13,14,19)-ABL1(2,3,4), BCR(1,4,6,7,12,13,14,19)-PDGFRA(12), BMP2K(14,15)-ZNF384(2,3,4,7), CBFA2T3(10,11)-GLIS2(4,5), CBFB(4,5)-MYH11(29,30,31,32,33,34,35), CCDC6(1,7)-PDGFRA(9,11), CHIC2(3)-ETV6(2,3), CNTRL(38)-FGFR1(11), CREBBP(4,5,6)-ZNF384(2,3,4,7), CUX1(11)-FGFR1(11), DEK(9)-NUP214(17,18), EBF1(10,13,14,15)-JAK2(9,11,13,15,17,18,19), EBF1(10,13,14,15)-PDGFRA(9,11), EML1(18)-ABL1(2,3,4), EP300(6)-ZNF384(2,3,4,7), ET6V(4,5,6,7)-ABL1(2,3,4), ET6V(4,5,6,7)-JAK2(9,11,13,15,17,18,19), ET6V(4,5,6,7)-NTRK3(15), ET6V(4,5,6,7)-PDGFRA(9,11), ET6V(4,5,6,7)-RUNX1(1), ET6V(4,5,6,7)-RUNX1(3), FGFR1OP(5,6,7)-FGFR1(11), FIP1L1(12)-PDGFRA(12), FOXP1(19)-ABL1(2,3,4), INPP5D(8)-ABL1(2,3,4), KAT6A(16)-CREBBP(2,3), KMT2A(8,9,10,11), KMT2A(8,9,10,11)