



## Enabling molecular laboratories to maximize the utility of Illumina's TST170 panel

SOPHiA DDM™ for TST170 is a fully integrated bioinformatic workflow (FASTQ to Report) for Illumina TruSight™ Tumor 170 panel. The SOPHiA DDM™ platform combines analytical performance\* with streamlined interpretation of complex genomic variants in the context of comprehensive genomic profiling. Its intuitive interface and capabilities have been developed based on the feedback from our 1000+ customers. It offers several features to facilitate variant assessment and maximize the utility of genomic detection.

### Analytical performance\*

#### Detection of:

- SNVs & Indels in 153 genes
- Partner-agnostic detection of 55 fusion genes with full coverage of NTRK 1,2,3 fusions and splice variants
- CNVs in 152 genes (versus 59 genes with standard analysis solutions)<sup>1</sup>

#### Full access to analytical output:

- Ability to access source files and quality reports for analysis

The pipeline is compatible with Illumina NextSeq® sequencers.

Analysis time from FASTQ files: 8 hours<sup>7</sup>

|  | Performance metrics <sup>2,3</sup> | Observed | Lower CI (95%) |
|--|------------------------------------|----------|----------------|
| <b>DNA Variants</b>                    |                                    |          |                |
| SNV & Indels                           | Sensitivity <sup>4</sup>           | 100%     | 95.71%         |
|  | Precision                          | 98.58%   | 97.81%         |
| CNV/Amplifications <sup>5</sup>        | Sensitivity <sup>5</sup>           | 100%     | -              |
| <b>RNA Variants</b>                    |                                    |          |                |
| Fusions & Splice Variants <sup>6</sup> | Sensitivity                        | 96.38%   | -              |
|  | True Positive                      | 133/138  | -              |
|  | False Negative                     | 5/138    | -              |

### One Simple Intuitive Platform: Beyond Analytics

#### Accelerated assessment and reporting of genomic variants

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

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

#### Confident decision-making

The SOPHiA DDM™ platform integrates the OncoPortal™. This feature provides the latest scientific evidence on the actionability and significance of each genomic alterations to support informed decision for research purpose.

#### Global support at every step

We offer local support available globally. Our Set Up Program provides assistance with assay setup for fast and worry-free transition to routine testing. All along the usage, our robust support including re-analysis and dedicated bioinformaticians help save time and resources, ensuring fast resolution of workflow disruptions.

#### Secure and unlimited data storage

The SOPHiA DDM™ platform provides unlimited and unrestricted storage, while keeping data safe by applying the highest industrial standards of encryption in compliance with your local data security policies.

#### Access to SOPHiA community

Through the SOPHiA DDM™ platform genomics experts from >1000 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.

#### Match genomic profiles with clinical trials opportunities

SOPHiA DDM™ can support the identification of subjects who could benefit from investigational therapies. If the institution chooses to activate the feature, when a genomic profile matches a research opportunity, SOPHiA DDM™ notifies relevant healthcare professionals. As a result, identified subjects are offered to participate in corresponding clinical trials, contingent on eligibility assessment and consent.

1. Based on benchmarking studies comparing SOPHiA GENETICS with a standard analysis  
 2. Performance metrics calculated in samples processed on Illumina NextSeq® 500/550  
 3. Based on analysis of 71 confirmed variants from 43 FFPE tumor samples from multiple tissues types  
 4. Based on analysis of 504 confirmed variants from AcroMetrix® Oncology Hotspot Control  
 5. Based on analysis of 15 samples with confirmed gene amplifications  
 6. Based on analysis of 65 confirmed fusions from 105 clinical and reference samples  
 7. Analysis time may vary depending on the number of genes, samples analyzed and server load

Somatic gene variant annotations and related content have been powered by, without limitation, The Jackson Laboratory Clinical Knowledgebase (JAX-CKB™).

#### \*For Research Use Only. Not for Use in diagnostic procedures.

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