Next-generation sequencing

Multicenter in-house evaluation of an amplicon-based NGS panel for comprehensive molecular profiling

Summary of original research article published in *Molecular Diagnosis & Therapy*, Jan 11, 2025 [1]

Study overview

- A multicenter evaluation of the Ion Torrent™ Oncomine™ Comprehensive Assay Plus for comprehensive genomic profiling (CGP) was performed using a cohort of pan-cancer research samples (>13 different tumor types, Figure 1).
- 193 pan-cancer research samples (125 DNA and 68 RNA samples) were analyzed to evaluate concordance of the Oncomine Comprehensive Assay Plus with orthogonal methods.
- The research samples were pre-characterized for single nucleotide variants (SNVs), insertions and deletions (indels), copy number variations (CNVs), fusions, homologous recombination deficiency (HRD), tumor mutational burden (TMB), and microsatellite instability (MSI).
- Reproducibility of results with replicate samples was also assessed across 5 academic and clinical research centers located in Europe.
- With an easy, highly automated workflow, the Oncomine Comprehensive Assay Plus allowed for CGP from >500 genes, including genomic signatures.

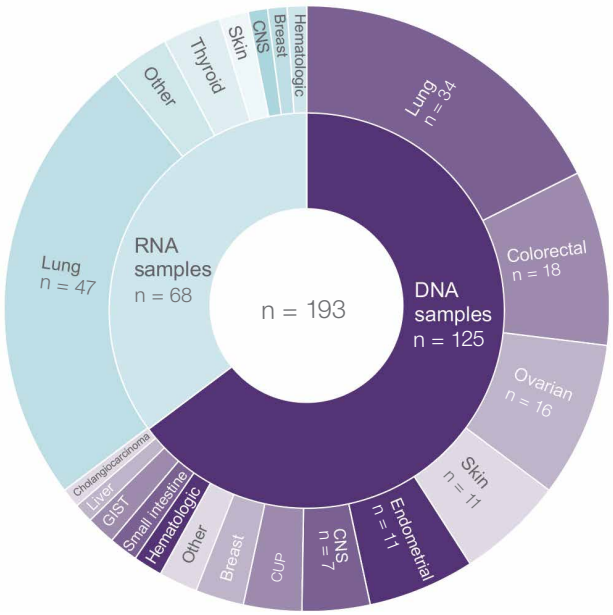

Figure 1. Distribution of tumor types for the analytical evaluation of the Oncomine Comprehensive Assay Plus. CNS: central nervous system. CUP: cancer of unknown primary. GIST: gastrointestinal stromal tumor. Other: includes tumor types represented by a single sample.

High sequencing success rate, even with challenging samples

The cohort of samples was composed of diverse tumor types with variable tumor cell content (Figure 2). Some samples contained only 10%–20% tumor cell content. Despite this heterogeneity, the Oncomine Comprehensive Assay Plus achieved a high overall (DNA and RNA) sequencing success rate of ~94% (Table 1).

Table 1. Sequencing success rate of the Oncomine Comprehensive Assay Plus.

	Samples (n)	Success rate
DNA	140	96.6%
RNA	61	89.7%
Overall (DNA and RNA)	**201**	**93.9%**

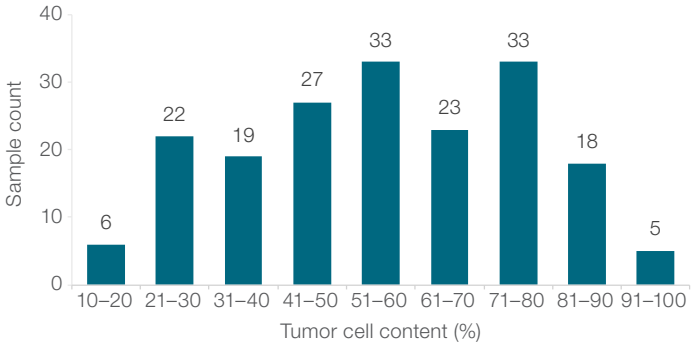

Figure 2. Variability of tumor cell content in pan-cancer samples evaluated.

Accurate detection of genomic alterations

The Oncomine Comprehensive Assay Plus demonstrated high concordance with orthogonal methods for the detection of SNVs, indels, CNVs, and fusions (Tables 2–4).

Table 2. Concordance of results for SNV and indel detection.

	Expected	Observed (≥5% AF*)	Observed (<5% AF)	Concordance**
SNVs	258	241	5	95.3%
Indels	32	28	1	90.6%
Total (SNVs and indels)	**290**	**269**	**6**	**94.8%**

* AF: allele fraction.
** Concordance was calculated irrespective of the 5% AF limit.

Table 3. Concordance of results for CNV detection.

	Expected	Observed	Concordance
Copy number gain (≥6 copy number)	44	44	100.0%
Copy number loss (≤0.5-fold difference)	13	11	84.6%
Total CNVs	**57**	**55**	**96.5%**

Table 4. Concordance of results for fusion detection.

		Orthogonal method	
		Positive	Negative
Oncomine Comprehensive Assay Plus	Positive	49	1
	Negative	2	0
	Concordance	**94.2%**	

Accurate detection of genomic signatures

The Oncomine Comprehensive Assay Plus demonstrated high concordance with orthogonal methods for the detection of HRD, TMB, and MSI (Table 5).

Table 5. Concordance of results for HRD, TMB, and MSI detection.

	Cancer types	Samples (n)	Concordance
HRD	Ovarian and breast cancer	18	100.0%
TMB (≥10 mutations/Mb)	Pan-cancer	32	81.3%
MSI	Pan-cancer	26	80.8%
MSI	Colorectal cancer	10	100.0%

High reproducibility demonstrated between laboratories

Across 5 laboratories, the Oncomine Comprehensive Assay Plus demonstrated a high level of reproducibility, with a median reproducibility for SNV and indel detection of 94.0% overall. Testing conducted on replicate samples across the laboratories also showed consistency for detecting HRD, TMB, and MSI.

Conclusions

- Based on this study, the Oncomine Comprehensive Assay Plus demonstrated excellent analytical performance as part of a sensitive and specific platform for CGP.
- The overall concordance between the Oncomine Comprehensive Assay Plus and orthogonal methods was 94.8% for SNVs and indels, 96.5% for CNVs, and 94.2% for fusions.
- The Oncomine Comprehensive Assay Plus also demonstrated high concordance with orthogonal methods for the detection of HRD, TMB, and MSI genomic signatures.
- The high concordance rates highlight the potential of the assay to advance research in the field of personalized medicine.*

* The Oncomine Comprehensive Assay Plus is for research use only, and this analysis was performed as part of a retrospective clinical research study; no patient management decisions were made based on these results.

Reference

1. Jantus-Lewintre E, Rappa A, Ruano D et al. (2025) Multicenter in-house evaluation of an amplicon-based next-generation sequencing panel for comprehensive molecular profiling. *Mol Diagn Ther* 29(2):249–261. **doi.org/10.1007/s40291-024-00766-2**

Learn more about the Oncomine Comprehensive Assay Plus and watch the webinar at **thermofisher.com/ocaplus**