

Clinical Verification of an FDA-Approved NGS Solid Tumor IVD Assay



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INTRODUCTION

- In light of the recent FDA final ruling regarding increased oversight of laboratory developed tests (LDTs), implementation of FDA-approved assays may provide an avenue for affordable compliance in clinical reference and hospital laboratories.
- The Pillar Biosciences' oncoRevealTM CDx Pan Cancer Solid Tumor IVD assay is a 22 gene amplicon-based target enrichment NGS assay with FDA approval at all steps from library preparation, sequencing, bioinformatic analysis, and qualitative reporting, including a companion diagnostic (CDx) of clinically significant single nucleotide variants (SNVs) and small insertions and deletions.
- This assay is marketed with a detection rate as low as 1.5% variant allele frequency (VAF) in SNVs, 2.2% for insertions, and 1.6% for deletions.

NCCN Guidelines Version 5.2024 Colon Cancer (CRC)

- All patients with metastatic CRC should have tumor genotyped for RAS (KRAS and NRAS) and BRAF mutations individually or as part of a next-generation sequencing (NGS) panel (preferred).
- Patients with any known KRAS mutation (exons 2, 3, and 4) or NRAS mutation (exons 2, 3, and 4) should not be treated with either cetuximab or panitumumab, unless given as part of a regimen targeting a KRAS G12C mutation.
- BRAF V600E mutation makes response to panitumumab or cetuximab highly unlikely unless given with a BRAF inhibitor.

Genes and Codons Tested in oncoReveal™CDx Pan Cancer Solid Tumor IVD Assay

Gene	Exon	Codons Covered	Gene	Exon	Codons Covered	Gene	Exon	Codons Covered
AKT	3	17-42	FBXW7	9	445-472		19	890-909
ALK	22	1151-1171		10	479-508	РІКЗСА	21	1016-1050
	23	1174-1206		11	560-592		21	1066-1069
	25	1256-1278	FGFR1	4	121-147		1	1-26
BRAF	11	439-472		7	250-285		3	56-69
	15	582-609		7	251-279		5	98-140
CTNNB1	3	2-46		7 297-313		5	153-164	
DDR2	5	99-139	FGFR2	9	369-404	PTEN	6	165-178
	8	229-261		12	532-557		7	213-215
	12	453-488	FGFR3	7	248-274		7	230-267
	13	512-547		9	368-401		8	276-301
	14	587-619		14	633-653		8	312-342
	15	624-660		16	678-716		3	100-132
	17	762-784		18	784-807		4	143-151
	3	95-128	KRAS	2	4-37		5	164-198
	7	275-296		3	39-73		6	242-262
	12	457-492		4	113-147	SMAD4	8	309-318
	15	588-621	MAP2K1	2	32-68		9	330-362
EGFR	18	696-726	MET	2	153-185		10	383-413
	19	729-761		2	354-385		11	443-473
	20	762-800		11	826-866		12	499-540
	21	846-875		14	986-1019		1	23-62
ERBB2	19	754-769		16	1108-1131		4	193-199
	20	770-805		19	1243-1277	STK11	6	247-281
	21	840-878		26	1569-1602		8	323-361
	3	109-140	NOTCH1	27	1674-1679		2	1-24
	4	166-185	NRAS	2	1-35		4	82-114
	6	223-247		3	42-69		5	118-223
	7	260-288		4	117-150		5	126-138
ERBB4	8	296-323		2	82-117	TP53	6	150-186
	9	334-359	РІКЗСА	5	315-352		7	225-256
	15	591-622		7	389-417		8	263-306
	23	918-948		8	418-422		10	332-366
FBXW7	5	250-287		10	538-554			
	8	382-406		14	692-723			

METHODOLOGY

- A clinical verification of the assay was performed using 20 DNA samples extracted from formalin-fixed, paraffin-embedded tissue from colon, lung, and skin.
- The MiSeqTM Dx instrument (Illumina) and oncoRevealTM CDx PiVAT® software were used for sequencing and data analysis, respectively.
- Accuracy was assessed based on concordance with results generated using a clinically-validated solid tumor NGS LDT.
- Reproducibility, sensitivity, and specificity were verified across different tumor types, assay runs, and operators, generating a total of 40 libraries.



RESULTS

- Mutational status was concordant in all samples compared to the reference results, resulting in an overall accuracy of 100%.
- Inter- and intra-assay and inter-operator reproducibility all yielded results of 100%.
- The data showed no evidence of false positives or negatives, performing at 100% for analytical sensitivity and specificity.

	Pilla	nel Cancer Solid Tumo	mor		
		Positive	Negative (WT)	Total	
TST15 Assay	Positive	A (26)	B (0)	A+B (26)	
	Negative (WT)	C (0)	D (134)	C+D (134)	
	Total	A+C (26)	B+D (134)	A+B+C+D (160)	

Parameter	Result
Sample Concordance	100%
Variant Call Agreement	100%
Intra-assay Reproducibility	100%
Inter-assay Reproducibility	100%
Inter-operator Reproducibility	100%
Analytical Sensitivity	100%
Analytical Specificity	100%

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CONCLUSIONS

significant findings

BENEFITS

- Robust assay requiring $\geq 30\%$ tumor burden and $> 4.5 \text{ ng/}\mu\text{L}$ of DNA.
- Streamlined wet lab process.
- Scalable library prep (6-46 samples + controls) that can be completed in one day.
- Accessible sequencing process that utilizes a MiSeqDx.
- Easy-to-interpret reports generated within a few hours on CDx server.
- FDA-approved assay with companion diagnostic component.
- Reimbursable as a small NGS panel.

LIMITATIONS

- Difficulty achieving passing criteria with limited tumor specimens.
- CDx indications limited to EGFR and KRAS.
- VAFs are not currently included in the clinical report.

ACKNOWLEDGMENTS



