

Overcome Data Analysis Challenges with the QuantideX® NGS Reporter

Quality Results, Every Time

Our *Sample-Aware™* bioinformatics solution combines machine-learning algorithms with integrated QC capabilities to ensure constant result quality monitoring and reduce false positive results while highlighting false negative risk.

Simple to Run, Easy to Install

The QuantideX NGS Reporter provides push-button analytics and can be installed locally on a Windows® desktop computer. No prior bioinformatics experience or large server environments required.

Automated Reporting of Results

Full bioinformatics and reporting of variants (SNVs, indels), and standard QC metrics are automatically calculated.

Robust sample QC assessment

Each row expands to provide more information on variants



Run summary displays results for each sample



QuantideX®
NGS DNA Hotspot 21 Kit (CE-IVD)

Ordering

Product Name	Number of Samples	Catalog Number
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QuantideX NGS DNA Hotspot 21 Kit*

48

76044

*CE-IVD. For US export only.



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For more information on the QuantideX products, please visit asuragen.com/portfolio/oncology

QuantideX[®]

NGS DNA Hotspot 21 Kit (CE-IVD)



The QuantideX[®] NGS DNA Hotspot 21 Kit (CE-IVD) is an *in vitro* diagnostic test that screens for over 1,500 variants, including single nucleotide variants (SNVs), insertions/deletions (indels), and structural rearrangements, many of which are treatable with approved therapies, inform on patient management, or are the subject

of further clinical evaluation. Leveraging our proprietary NGS-in-a-Box[™] workflow and *Sample-Aware*[™] bioinformatics quality control system, the assay detects the most common genomic variants in a variety of tumor types with sensitivity and accuracy you and your clinicians can trust.

QuantideX[®] NGS DNA Hotspot 21 Kit Mutation Coverage

Quickly identify therapeutic targets and other variants being evaluated in clinical trials.

GENE	CODON RANGE	GENE	CODON RANGE	GENE	CODON RANGE	GENE	CODON RANGE	GENE	CODON RANGE	
ABL1	249-258	EGFR	486-493	FGFR3	248-260	JAK2	607-620	NRAS	9-20	
	304-318		709-721		362-374		55-67			
ALK1	1174-1196		737-761	FLT3	829-840	KIT	557-579		PDGFRA	560-572
	1274-1278		767-798		638-653		815-826			840-852
AKT1	17-27	ERBB2	755-769	HRAS	9-20	KRAS	4-15	PIK3CA	540-551	
AKT2	17-26		774-788		59-76		55-65		104-118	1038-1049
			839-847	113-121	137-148		RET		916-926	
BRAF	465-474	877-883	IDH1	122-134	MET	1245-1256		RET	916-926	
	591-612	FGFR1		123-136		138-145	163-174			
			250-262	IDH2						



21 GENES



46 HOTSPOTS



C_ACTG >1500 VARIANTS

REDUCED COMPLEXITY

- Detects >1,500 variants from commonly mutated genomic regions across multiple tumor types
- End-to-end kitted solution
- Fully integrated data analysis pipeline

OPTIMIZED WORKFLOW

- Reduced labor vs. current commercially available kits (>50% improvement)
- Improved turnaround time enables higher throughput
- Common workflow across NGS portfolio streamlines training, testing, and implementation

QUALITY PERFORMANCE

- Highly sensitive detection of DNA-based variants
- Low input (~20 ng) of DNA from FFPEs
- *Sample-Aware*[™] bioinformatics analysis and sample quality control

Sample-to-Result in as Little as One Day



ASURAGEN
 ~5 hr Asuragen Hands-on Time
 5 1/2 hr QuantideX Workflow
TOTAL = 10 1/2 HOURS

Accurate and Sensitive Detection of Variants at Low Percent Mutation

Accuracy in DNA Isolated from FFPE Samples

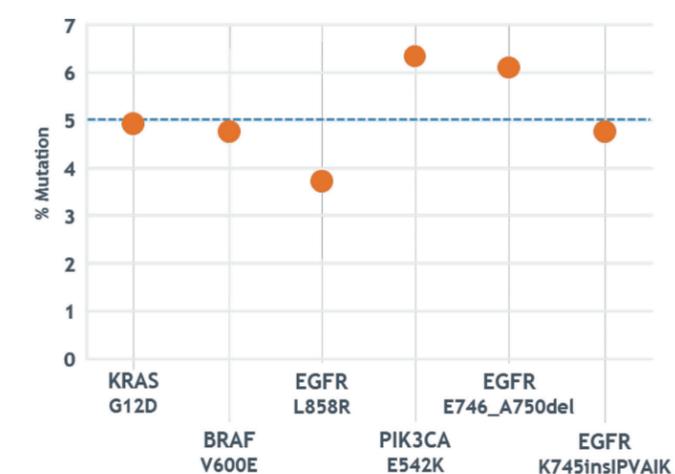
Comparator: OncoPrint[™] Focus Assay, Thermo Fisher Scientific

Variant Group	Agreement Type	Number of Calls	Accuracy
SNV	PPA ¹	77/81	95.06%
	NPA ²	1/45133	99.99%
Indel	PPA ¹	4/4	100.00%
	NPA ²	2/19236	99.99%
All	PPA ¹	81/85	95.29%
	NPA ²	3/64369	99.99%

¹ PPA = [(# Hotspot 21 true positive calls) + (# Comparator Method positive calls)] * 100
² NPA = [(# Hotspot 21 true negative calls) + (# Comparator Method negative calls)] * 100

Near perfect concordance with reference method for detection of variant from clinical FFPE specimens.

Limit of Detection (95% Call Rate)



Low-level detection of SNVs and indels.