

## Service Profile

# Digital PCR Services

## Mutation Detection & Copy Number Variation

Helping you simplify going digital with an all-in-one solution

Digital PCR (dPCR) is revolutionizing the way rare target detection and copy number variation analyses are performed, such as in the context of liquid biopsy. Where researchers used to find themselves struggling to identify faint genetic signals, dPCR now provides unparalleled sensitivity, precision and reproducibility for detecting low-abundance targets, targets in complex mixtures, allelic variants and small fold-change differences. However, onboarding dPCR in your lab can seem daunting given the investments in training, standardization and resources required.

QIAGEN Genomic Services overcomes these hurdles by providing a convenient, all-in-one dPCR mutation and copy number variation detection service. Extend your in-house resources with the expertise and custom services that you expect from QIAGEN®. Using our proven sample preparation technologies and powerful QIAcuity™ Digital PCR System, we deliver end-to-end service to help accelerate your research. Our dPCR mutation detection and copy number variation solutions offer the following benefits:

- **End-to-end service:** we take care of every step, from sample preparation to data analysis
- **Guidance and flexibility:** we aid in designing your project and help you make the right decisions
- **Expertise in nanoplate-based dPCR technology:** we provide years of experience in nanoplate-based dPCR using our sensitive QIAcuity Digital PCR System
- **Ready-to-publish data:** we deliver comprehensive reports and data packages, and provide guidance on the next steps

Partner with us for expert guidance and dedicated service – from Sample to Insight – to detect the single positive today.

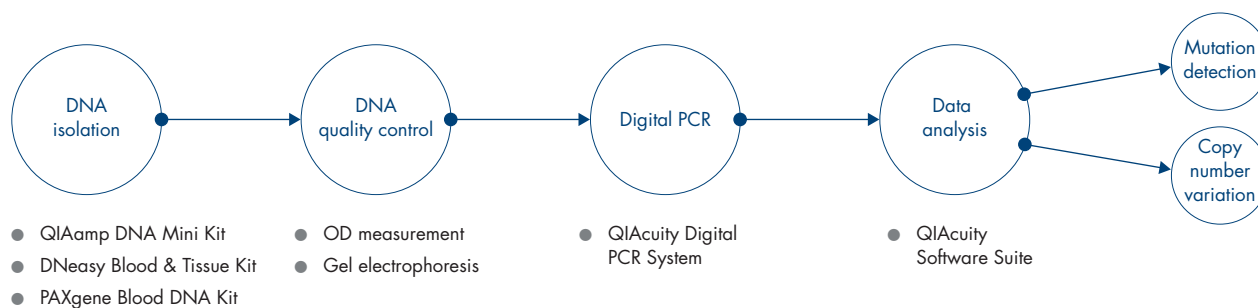


Figure 1. Digital PCR Mutation Detection and Copy Number Variation workflow.

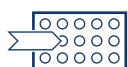
## Transforming the PCR experience with digital PCR

dPCR is a highly precise approach to sensitive and reproducible nucleic acid detection and quantification. Measurements are performed by dividing the sample into partitions, with zero or one target molecule present in any individual reaction. Each partition is analyzed after end-point PCR cycling for the presence or absence of a fluorescent signal, and the absolute number of molecules present in the sample is calculated. Compared to other techniques, dPCR provides:



### Absolute target quantification

No need for references or standard curves



### High tolerance to inhibitors

Due to partitioning and end-point measurement



### Superior precision

Detect very small fold change differences



### Increased sensitivity

Detect rare mutations and low-abundance targets



### High reproducibility

Eliminate amplification efficiency bias

Figure 2. The top 5 benefits of dPCR.







## Comprehensive data analysis

QIAGEN Genomic Services performs your data analysis using the QIAcuity Software Suite. Your final data package will contain absolute quantifications of your samples, with the concentration in copies per microliter of your target sequence. Further, a complete overview of the mutation detection results presented as a mutation fraction table or the copy number variation results are delivered with detailed explanations.

Table 1. An example extract mutation fraction table that is included in the mutation detection package

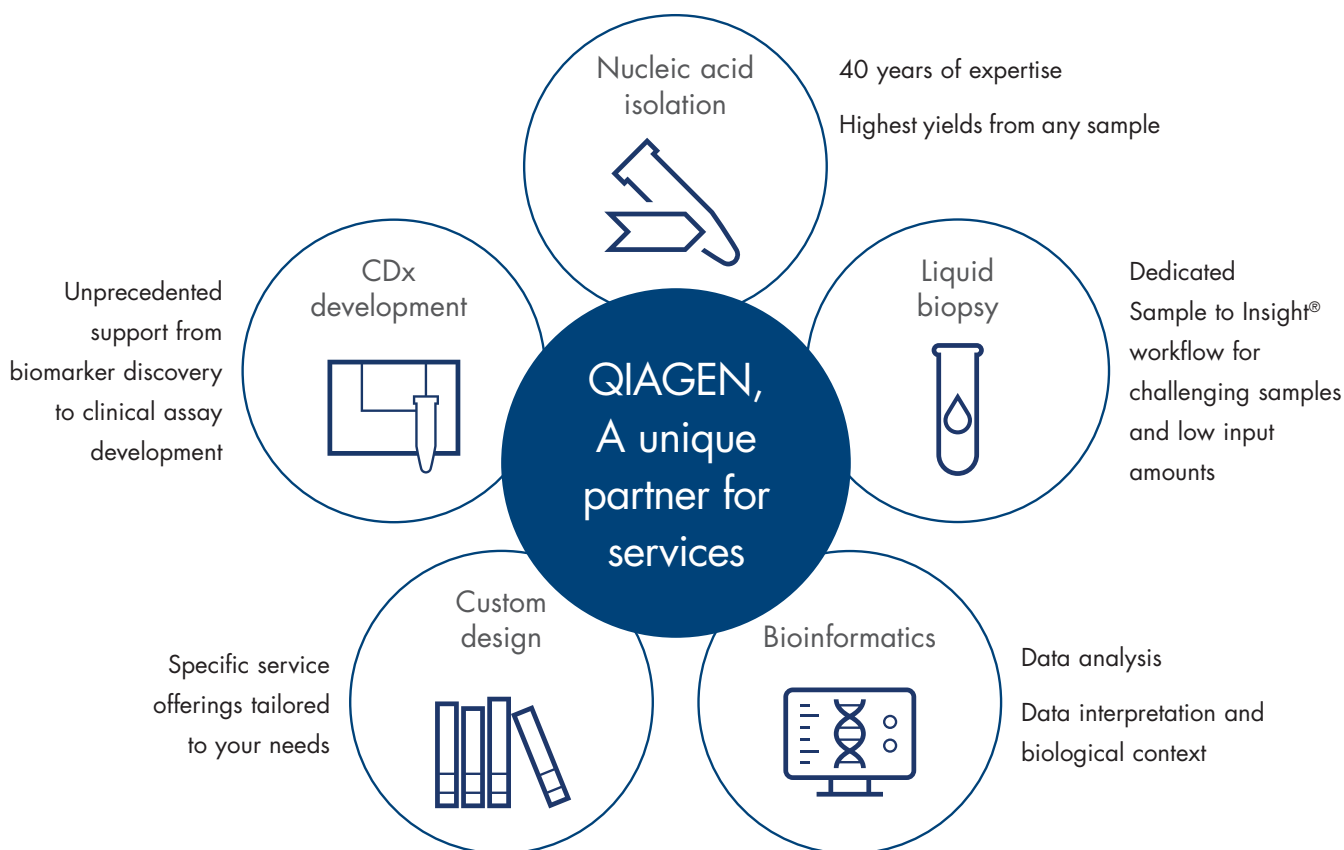
	Sample/ NTC/ control	Type	Reaction mix	Target	IC	Concentration (copies/ $\mu$ L)	CI (95%)	Mutation fraction	CI (95%)
<b>A1</b>	Sample 1	Mutation	BRAF V600M	MT	-	1979.3	2.60%	100%	4%
<b>A1</b>	Sample 1	Wildtype	BRAF V600M	WT	-	0	-	-	-
<b>A2</b>	Sample 2	Mutation	BRAF V600M	MT	-	927.1	3.9%	47.23%	11%
<b>A2</b>	Sample 2	Wildtype	BRAF V600M	MT	-	1035.7	3.7%	-	-
<b>B5</b>	NTC	Mutation	BRAF V600M	WT	-	0	-	n.a.	n.a.
<b>B5</b>	NTC	Wildtype	BRAF V600M	MT	-	0	-	-	-

## Service specifications

 <p><b>Consultation</b></p>	<p>Free consultation with an expert to design an experimental setup that best meets your needs and budget.</p>														
 <p><b>Sample requirements</b></p>	<p><b>Input sample</b></p>	<p><b>Isolation kit</b></p>	<p><b>Input requirements</b></p>												
	<p>Customer-isolated human DNA</p>	<p>Not applicable</p>	<p>500 ng (&gt;10 ng/μl)</p>												
	<p>Cell-free circulating DNA (ccfDNA) from human plasma or serum</p>	<p>QIAamp® ccfDNA/RNA Kit QIAamp MinElute® ccfDNA Kit</p>	<p>Minimum: 1 ml Maximum: 4 ml</p>												
	<p>Cells (human)</p>	<p>QIAamp DNA Mini Kit</p>	<p>Minimum: 1 x 10<sup>6</sup> cells pelleted and frozen</p>												
	<p>Fresh-frozen tissue (human)</p>	<p>DNeasy® Blood &amp; Tissue Kit</p>	<p>Minimum: 4–5 mg Maximum: 50 mg</p>												
	<p>FFPE samples (human)</p>	<p>QIAamp DNA FFPE Tissue Kit GeneRead® DNA FFPE Kit</p>	<p>Minimum: 2 x 10 μm sections of 250 mm<sup>2</sup> Maximum: 4 x 10 μm sections of 250 mm<sup>2</sup></p>												
	<p>Blood (PAXgene®, human)</p>	<p>PAXgene Blood DNA Kit</p>	<p>Recommended: 1 tube</p>												
	<p>Other</p>	<p>Please inquire</p>													
 <p><b>DNA quality control</b></p>	<p>OD measurement, including A260/A280 ratio (Capillary) gel electrophoresis (e.g., DIN value) (optional) This is a <b>STOP/GO</b> point where it is possible to omit samples, replace samples before proceeding or terminate the project.</p>														
 <p><b>Digital PCR</b></p>	<p>Mutation detection is performed using the QIAcuity Probe PCR Kit and the dPCR LNA Mutation Assay on our QIAcuity Digital PCR System. A QIAcuity Nanoplate 26k is used for highly sensitive and accurate detection of mutations with a high reaction volume</p> <p>CNV analysis is performed using the QIAcuity EG PCR Kit and the dPCR Copy Number Assay on our QIAcuity Digital PCR System. A QIAcuity Nanoplate 26k is used for sensitive detection of rare CNV events with a high reaction volume A QIAcuity Nanoplate 8.5k is used for high-throughput routine CNV screening with a low reaction volume</p> <p>For CNV analysis, 2 reference samples and 2 reference assays need to be provided for normalization.</p>														
 <p><b>Complete data analysis</b></p>	<p>Results can only be provided per plate</p> <table border="1" data-bbox="383 1255 1428 1627"> <tr> <td data-bbox="383 1255 694 1289"> <p>Raw data</p> </td> <td data-bbox="697 1255 1428 1289"> <p>Number of partitions valid / positive / negative</p> </td> </tr> <tr> <td data-bbox="383 1293 694 1349"> <p>Raw data QC</p> </td> <td data-bbox="697 1293 1428 1349"> <p>Image quality controls and image corrective measures included in QIAcuity Software Suite</p> </td> </tr> <tr> <td data-bbox="383 1353 694 1387"> <p>Normalization approach</p> </td> <td data-bbox="697 1353 1428 1387"> <p>For CNV normalization to reference assays/samples</p> </td> </tr> <tr> <td data-bbox="383 1391 694 1447"> <p>Absolute quantification</p> </td> <td data-bbox="697 1391 1428 1447"> <p>Absolute quantification data (concentration in copies/μl and confidence interval at a 95% confidence level)</p> </td> </tr> <tr> <td data-bbox="383 1451 694 1536"> <p>Mutation detection</p> </td> <td data-bbox="697 1451 1428 1536"> <p>Mutation detection statistics (Mutation fraction in percent and confidence interval at a 95% confidence level) For simplex tests, individual replicate results are not available.</p> </td> </tr> <tr> <td data-bbox="383 1540 694 1627"> <p>Copy number variation analysis</p> </td> <td data-bbox="697 1540 1428 1627"> <p>Copy number variation statistics (number of copies per genome and confidence interval at a 95% confidence level) For simplex tests, individual replicate results are not available.</p> </td> </tr> </table>			<p>Raw data</p>	<p>Number of partitions valid / positive / negative</p>	<p>Raw data QC</p>	<p>Image quality controls and image corrective measures included in QIAcuity Software Suite</p>	<p>Normalization approach</p>	<p>For CNV normalization to reference assays/samples</p>	<p>Absolute quantification</p>	<p>Absolute quantification data (concentration in copies/μl and confidence interval at a 95% confidence level)</p>	<p>Mutation detection</p>	<p>Mutation detection statistics (Mutation fraction in percent and confidence interval at a 95% confidence level) For simplex tests, individual replicate results are not available.</p>	<p>Copy number variation analysis</p>	<p>Copy number variation statistics (number of copies per genome and confidence interval at a 95% confidence level) For simplex tests, individual replicate results are not available.</p>
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 <p><b>Final report and consultation</b></p>	<p>The final data analysis package contains an overview of data analysis and algorithms used, the files and tables listed above and publication-ready figures (PDFs provided as standard, please inquire for SVG or other formats). A teleconference is scheduled with QIAGEN scientists to discuss analysis and validation of results. Consultation and support will be provided for 90 days following delivery of data (for data delivery only projects), or delivery of data analysis (for data analysis inclusive projects). For extended support beyond 90 days, please inquire.</p>														

# How can we accelerate your research?

Our expert team is looking forward to learning about your research project and designing your customized service with QIAGEN.



[Tell us about your project](#)

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