

Overview

Methylation as a cancer biomarker

Designed for liquid biopsy

Low input, high correlation

Generate high-quality libraries

Single-day workflow

Fast, easy data analysis

Ordering

# QIAseq<sup>®</sup> Targeted Methyl Panels – unlock your precious samples

Methylation analysis of your priceless liquid biopsy and FFPE samples, from as little as 10 ng DNA

Customizable methylation analysis!

- As little as 10 ng input DNA needed from liquid biopsy and FFPE samples, and only 1 ng input for gDNA
- Single-day sample-to-sequencer workflow
- Fast, easy data analysis with separately available pre-built pipelines

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# Why use QIAseq Targeted Methyl Panels to analyze your precious samples for methylation status?

To explore whether methylation patterns can be potential biomarkers for use in:

## Disease detection



- Research the frequency of epigenetic changes in cancer
- Possibly identify robust and stable biomarkers, even in ccfDNA samples, such as liquid biopsies

## Studying response to therapy



- Explore treatment responses
- Research aspects of treatment resistance
- Identify cancer stage

## Cancer screening research



- Help determine the specificity of methylation patterns for different tissue types, differentiation statuses and disease states



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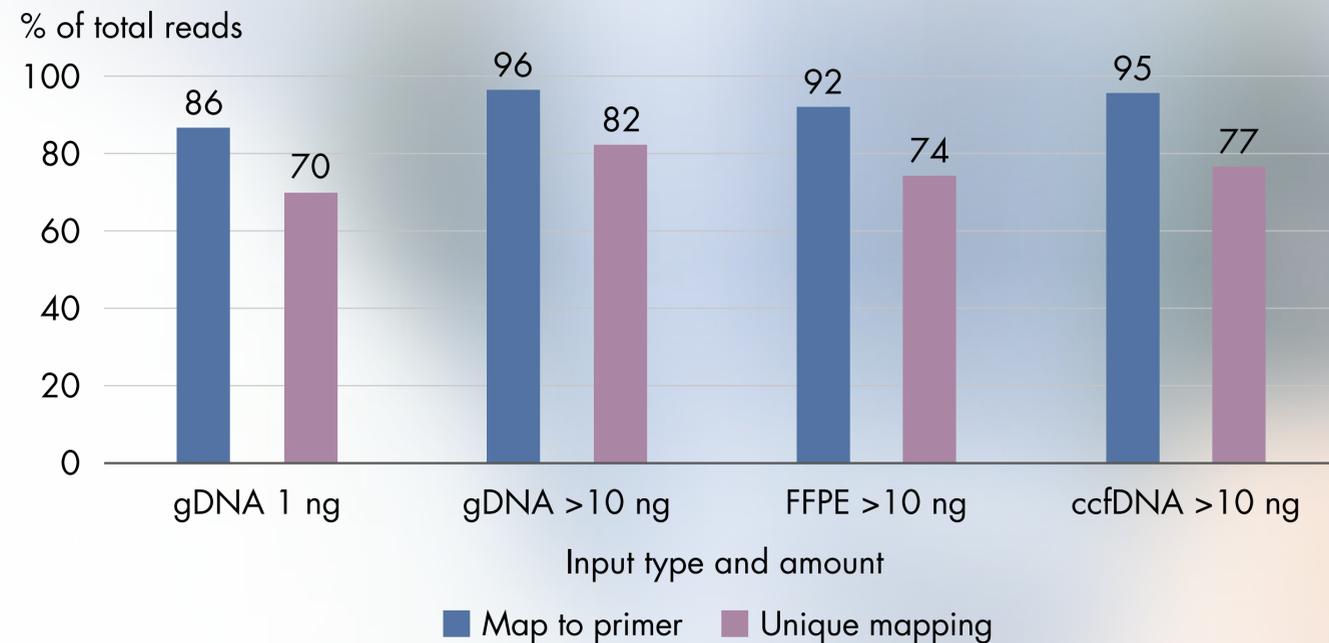
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# High performance with only 1/5<sup>th</sup> the amount of input DNA

Non-NGS methylation analysis approaches require at least 50 ng input DNA



Comparable methylation analysis methods, such as hybrid capture, require 5x more input DNA than QIAseq Targeted Methyl Panels

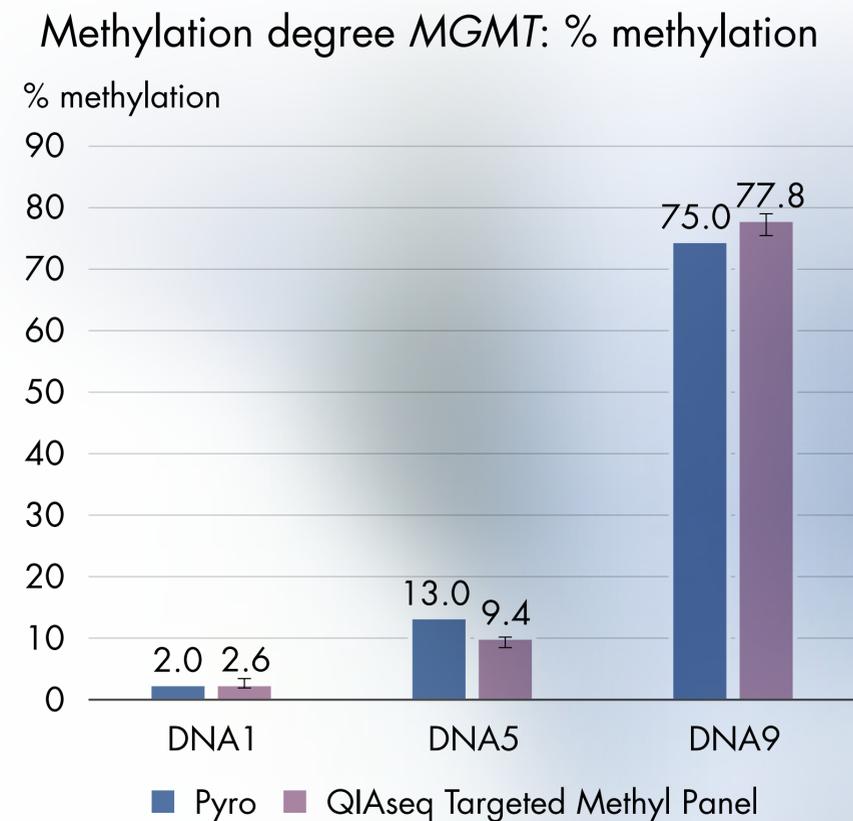


QIAseq Targeted Methyl Panels yield high on-primer and unique-read mapping scores:

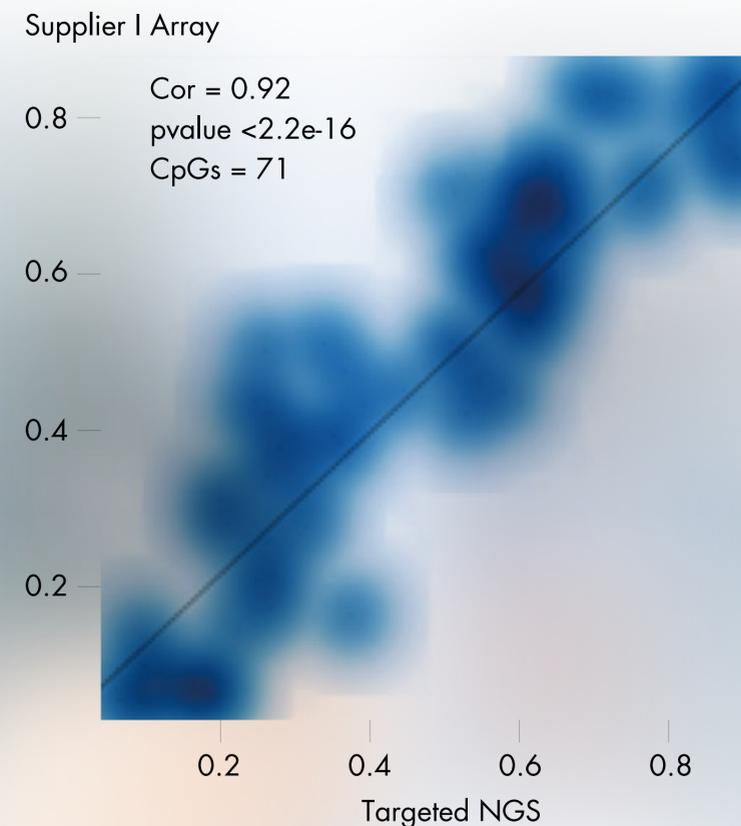
- From 10 ng FFPE and ccfDNA
- From 1 ng genomic DNA

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# Much lower input amounts, high correlation with established methods



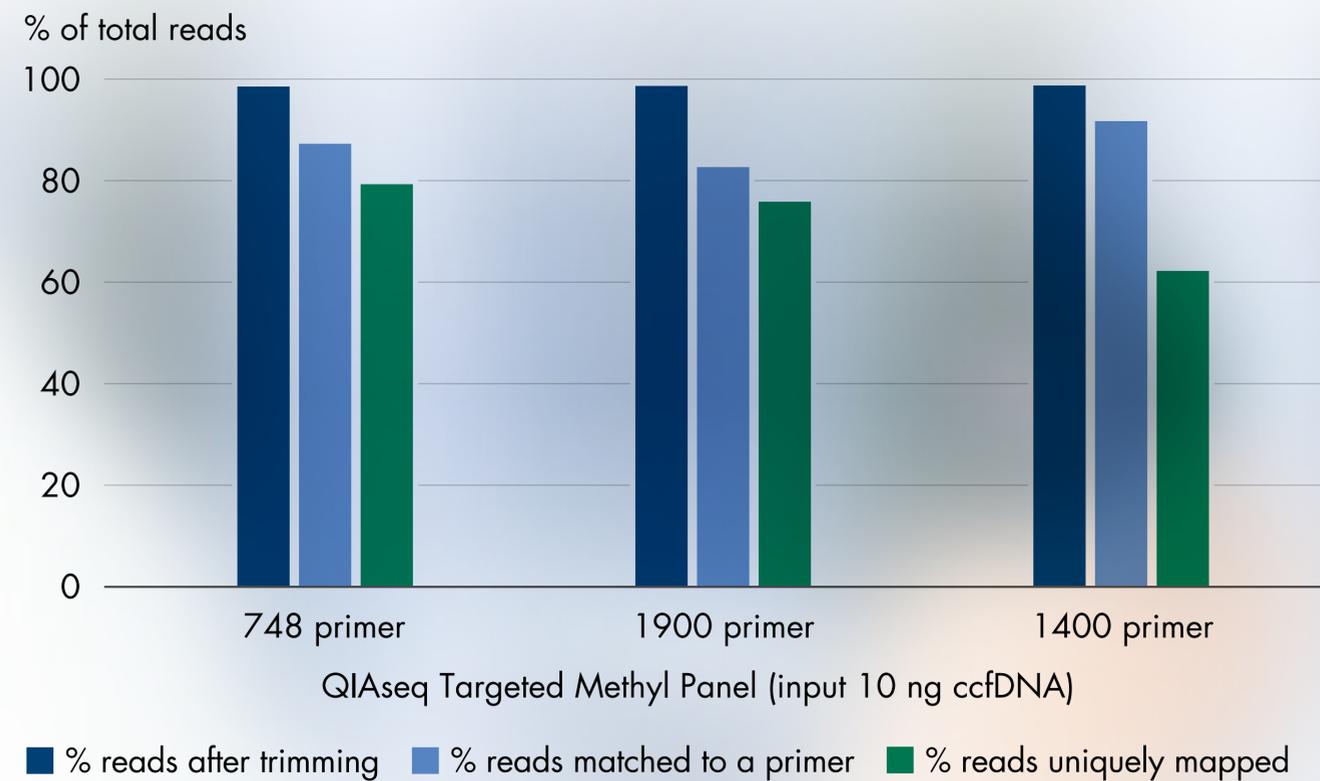
High correlation with PyroMark<sup>®</sup> assays



92% correlation with Supplier I array with only 1/5<sup>th</sup> the input

# Generate high-quality libraries from ccfDNA with different panel sizes

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High-quality libraries that result in high percentages of unique reads

## Single-day sample-to-sequencer workflow

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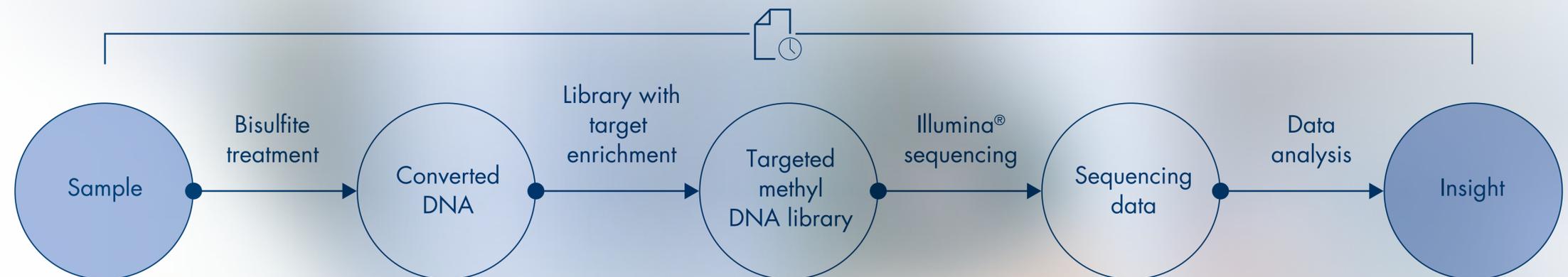
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### Sample types and input amounts

- Circulating cell-free DNA (ccfDNA): 10–200 ng
- FFPE DNA: 10–200 ng
- gDNA: 1–100 ng

Total workflow time: 7.5–9 h  
Total hands-on time: 2.5–4.5 h



### EpiTect® Fast Bisulfite Conversion Kits

- EpiTect Fast Bisulfite Kit
- EpiTect Fast DNA Bisulfite Kit
- EpiTect Fast FFPE Bisulfite Kit
- EpiTect Fast LyseAll Bisulfite Kit

### QIAseq Targeted Methyl Panels

- Pre-designed panels
- Custom panels

### Data analysis options

- GeneGlobe® Data Analysis Center
- QIAGEN CLC Genomics Workbench



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# Fast, easy data analysis

With QIAGEN CLC Genomics Workbench software

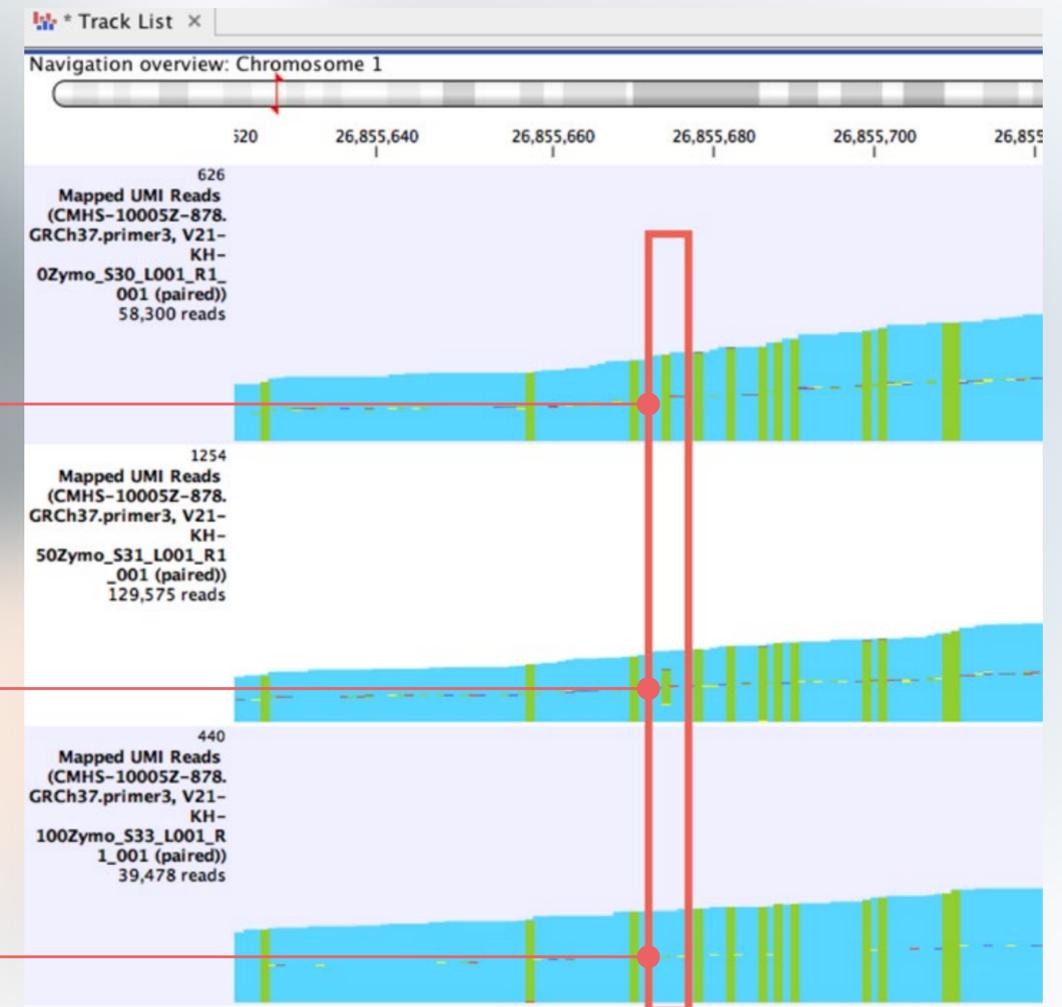
Quickly and easily analyze methylation patterns in your samples:

- Pre-built, push-button workflows – for all QIAseq Targeted Methyl Panels
- Comprehensive methylation analysis toolbox – including for custom panels
- Interactive visualization of methylation patterns – integrated in the powerful genome browser

Unmethylated CpG

50% methylated CpG

Fully methylated CpG



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## Ordering Information

Product	Description	Cat. no.
QIAseq Targeted Methyl Panel (8)	Fixed panel for a total of 3 reactions, each using 8 samples (3 x 8 samples)	335501
QIAseq Targeted Methyl Panel (96)	Fixed panel for a total of 96 samples	335511
QIAseq Targeted Methyl Custom Panel (96)	Custom panel for a total of 96 samples	335602
QIAseq Targeted Methyl Custom Panel (384)	Custom panel for a total of 384 samples	333603
QIAseq Methyl DNA 8-Index I	Indices to process a total of 24 samples, for indexing up to a total of 8 samples	335580
QIAseq Targeted Methyl 96 Index Set A	Set A indices, enough to process a total of 96 samples; one of four sets required for multiplexing 384 samples	335591
QIAseq Targeted Methyl 96 Index Set B	Set B indices, enough to process a total of 96 samples; one of four sets required for multiplexing 384 samples	335592
QIAseq Targeted Methyl 96 Index Set C	Set C indices, enough to process a total of 96 samples; one of four sets required for multiplexing 384 samples	335593
QIAseq Targeted Methyl 96 Index Set D	Set D indices, enough to process a total of 96 samples; one of four sets required for multiplexing 384 samples	335594

QIAseq Targeted Methyl Panels are intended for molecular biology applications. These products are not intended for the diagnosis, prevention, or treatment of a disease.

For up-to-date licensing information and product-specific disclaimers, see the respective QIAGEN kit handbook or user manual. QIAGEN kit handbooks and user manuals are available at [www.qiagen.com](http://www.qiagen.com) or can be requested from QIAGEN Technical Services or your local distributor.

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