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QIAseq Multimodal: The power of one

Simultaneous profiling of DNA variants, RNA fusions and gene expression

Sample input

Profile both genomic and transcript-level variants from as low as 10 ng

1

Workday

Go from sample to sequencing in 9 hours

Combined workflow

For simultaneous DNA and RNA extraction, enrichment and sequencing
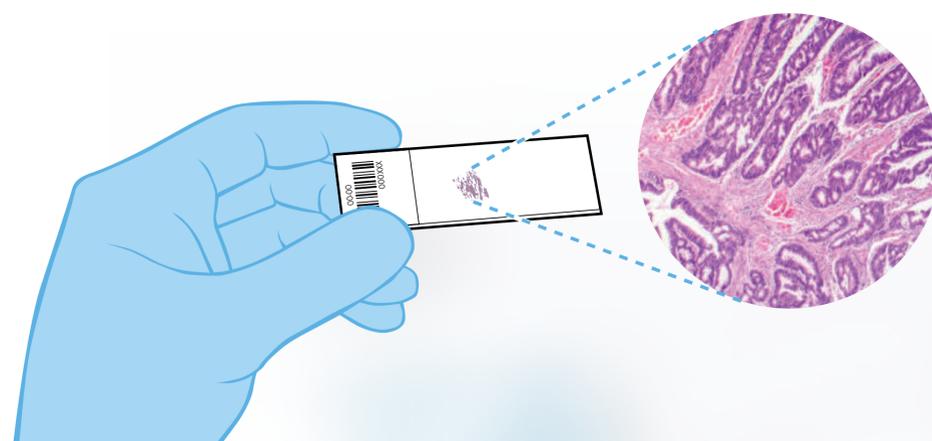
Compatible with Illumina sequencing chemistry

1 The power of one

Profile both genomic and transcript-level variants from ONE sample, as little as 10 ng

Sample types	• Blood
	• FFPE
	• Cells
	• Tissues
DNA biomarkers	• SNVs such as in CEBPA and FLT3
	• InDels such as in CALR
	• CNVs
RNA biomarkers	• RNA fusions such as in NTRK, ETV6, ALK, RET and ROS
	• Gene expression changes
	• Exon-skipping events

- Extract more information from one total nucleic acid input

- Minimize sampling bias by deriving DNA and RNA signatures from the same population of molecules

- Compatible with samples of limited availability and ensures sample availability for archiving and further analysis

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Two in ONE workflow with reduced cost and hands-on time

Separate DNA and RNA workflows

Sample

DNA isolation   RNA isolation

Fragmentation   Fragmentation

Library prep   Library prep

Enrichment   Enrichment

Amplification   Amplification
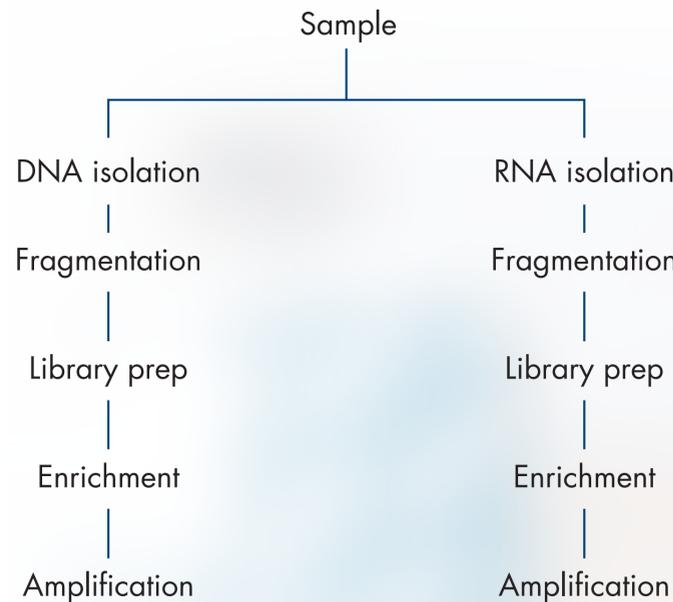
QIAseq Multimodal combined workflow

Sample

Total nucleic acid isolation

Nucleic acid fragmentation

Simultaneous DNA and RNA library prep

Simultaneous DNA and RNA targeted enrichment and sample index assignment

Library amplification and sample index assignment
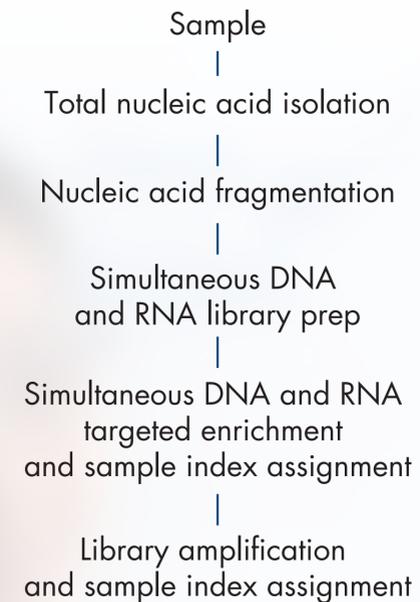
QIAseq Multimodal enables 50% less

- Sample input – as low as 10 ng
- Hands-on time – as low as 3.5 h
- Reagents and consumables

1 The power of one

ONE day workflow reduces turnaround time by up to 66%

Workday 1 Workday 2 Workday 3

Current approaches | Sample extraction → DNA library prep and enrichment → RNA library prep and enrichment

QIAseq Multimodal | Sample extraction → Simultaneous DNA and RNA library prep and enrichment

Reduce turnaround time from 3 days to a single day

Overview

One sample input

One combined workflow
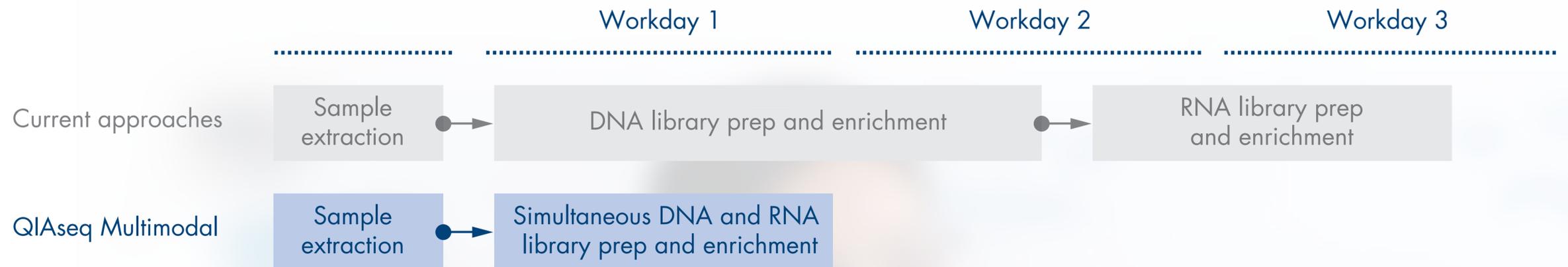
One workday

Powered by SPE

Error correction with UMI

Sample resolution with UDI

Integrated insights

SPE — Complete and uniform target coverage

Single primer extension (SPE) overcomes the challenges of 2-primer amplicon technology

TTACGCGTTAGCTATACGGGCGCTGCTCGCTGATAGCG

Universal Primer

ATGCC
GSP1

Universal Primer

CCGCG
GSP1

Universal Primer

CGAGC
GSP1

Primer read depth (UMIs)

2800
2400
2000
1600
1200
800
400
0

0.2x mean

0   1000 2000 3000 4000 5000 6000 7000 8000 9000 10,000 11,000 12,000

Comprehensive Cancer Panel
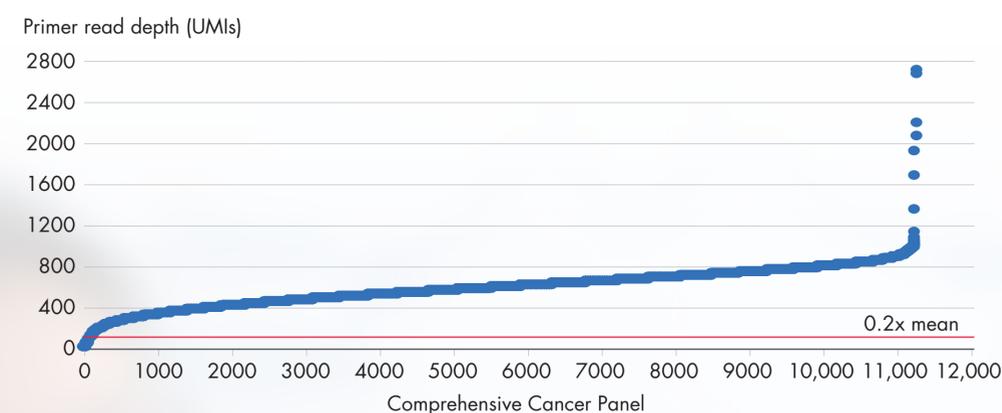
One universal primer that pairs with up to thousands of gene-specific primers (GSPs) enables targeting of tens of thousands of regions. Staggered design enables redundancy, reducing drop outs.

The panel achieved a uniformity of 99.2% at 0.2x mean coverage, and 94.2% at 0.5x of mean coverage. 311 SNPs were enriched from 20 ng of NA12878 DNA. Library was sequenced on a NextSeq, with 10 million reads generated.

- Simultaneously detect genomic alterations and transcript-level changes

- Minimize drop outs and maximize sequencing bandwidth

- Up to 20,000 target DNA and 8000 RNA amplicons per single-tube enrichment

UMI Increase sensitivity, reduce false positives

Tag >16 million unique molecules using unique molecular index (UMI) technology

- With each DNA and RNA molecule labeled with a distinct UMI, each read can be traced back to the original molecule
- Without UMIs, PCR artifacts, present at low copies, cannot be distinguished from the true variant at low frequency

UMI

UMI

True variant is present in all fragments carrying the same UMI

False variant is present in some fragments carrying the same UMI

- Confidently call variants at <1% VAF, as low as 0.5%
- Recognize true variants, eliminate artifacts

UDI Accurate read assignment for high-plex workflows

Maximize sequencing bandwidth with unique dual indices (UDIs)

Unique combination, but with a shared index

Unique combination, but with a shared index

A shared index increases the likelihood of reads being mis-assigned during demultiplexing

Unique combination without any shared indices

Unique combination without any shared indices
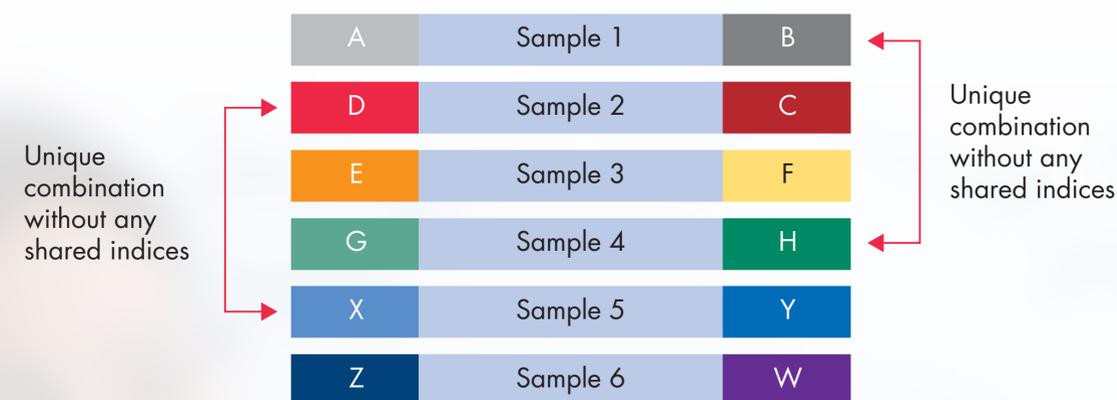
With 2 unique indices, each sample is resolved with confidence, regardless of batch size

- Overcome index hopping issues, especially for high-sensitivity applications
- Compatible with Illumina benchtop and production-scale sequencers

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Integrated workflow, integrated insights

From gold-standard nucleic acid extraction to production-grade informatics

Sample collection and stabilization → Nucleic acid isolation → NGS library prep → Sequencing → Data analysis and interpretation

FFPE
Blood
AllPrep
QIAamp

QIAseq Multimodal Panels
Leukemia, Lung, Sarcoma,
Custom Panels

Illumina sequencers
(MiniSeq, MiSeq,
NextSeq, HiSeq,
NovaSeq)

CLC Genomics Workbench

QIAGEN Clinical Insight Interpret for QIAseq

- Custom panel design enabled by GeneGlobe and Enterprise Genomic Services

- Variant interpretation powered by QIAGEN Knowledge Base with >15 million biological and clinical findings

Visit Webpage

Sample to Insight