

The QIAseq advantage

State-of-the-art technologies to fast-track and streamline NGS workflows



Overview

QIAseq
technologies

Streamlined
workflow

UMI-UDI
adapters

UMI

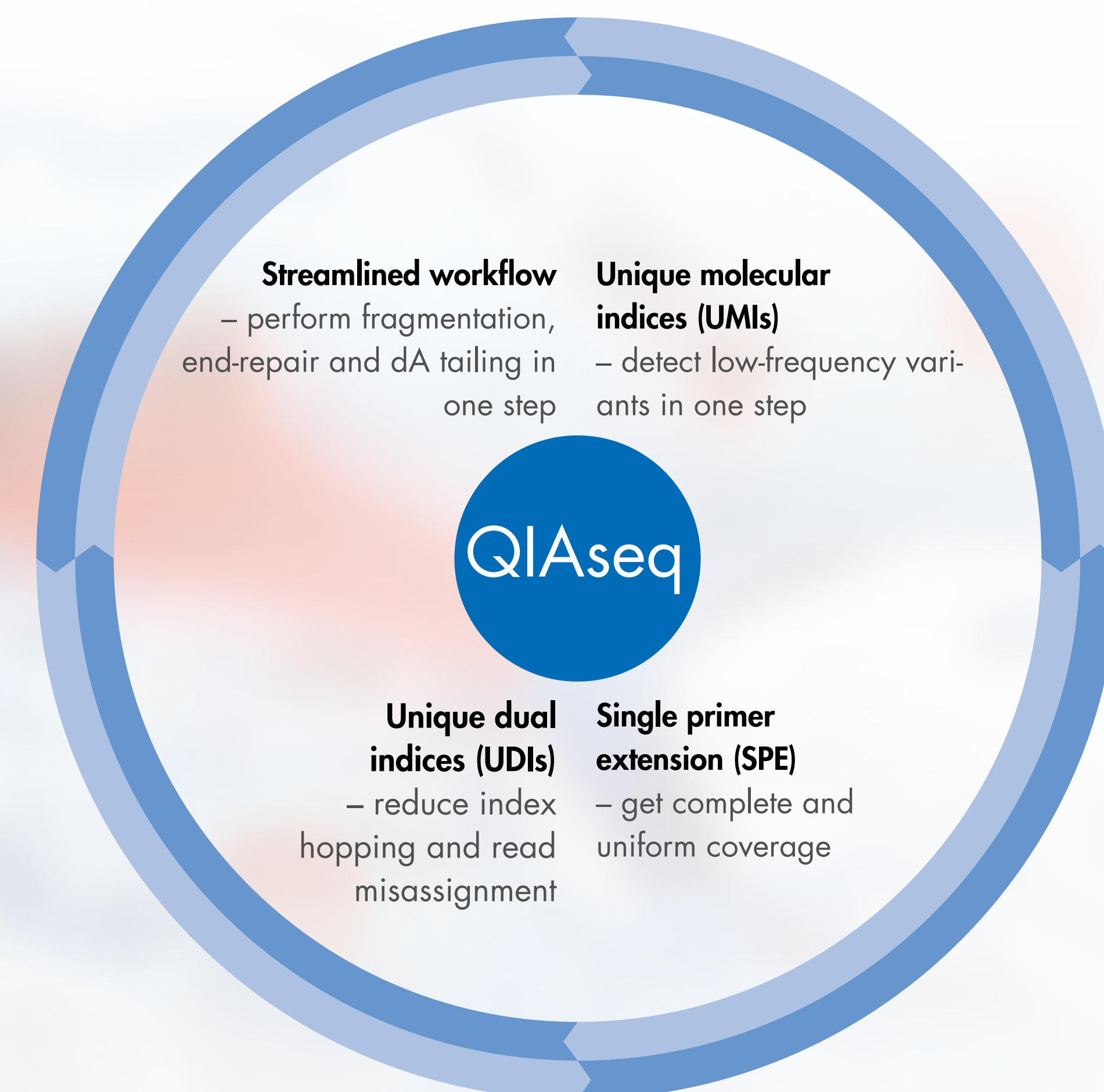
UDI

SPE

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NGS workflow challenges addressed by QIAseq technologies

Challenge	Consequence
Primer dimers	Lack of coverage
Non-specific enrichment and sequencing	Higher cost per sample
Non-uniform enrichment and sequencing	Higher cost per sample
PCR duplicates and errors	Inability to detect low-frequency variants



- Current approaches do not sufficiently address these challenges
- QIAseq technologies overcome these challenges enabling key applications

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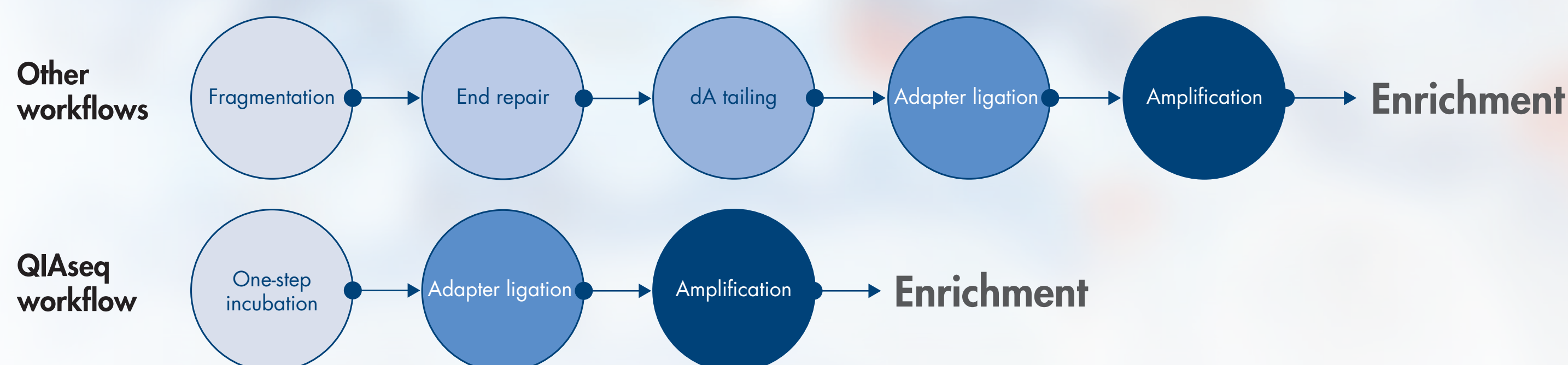
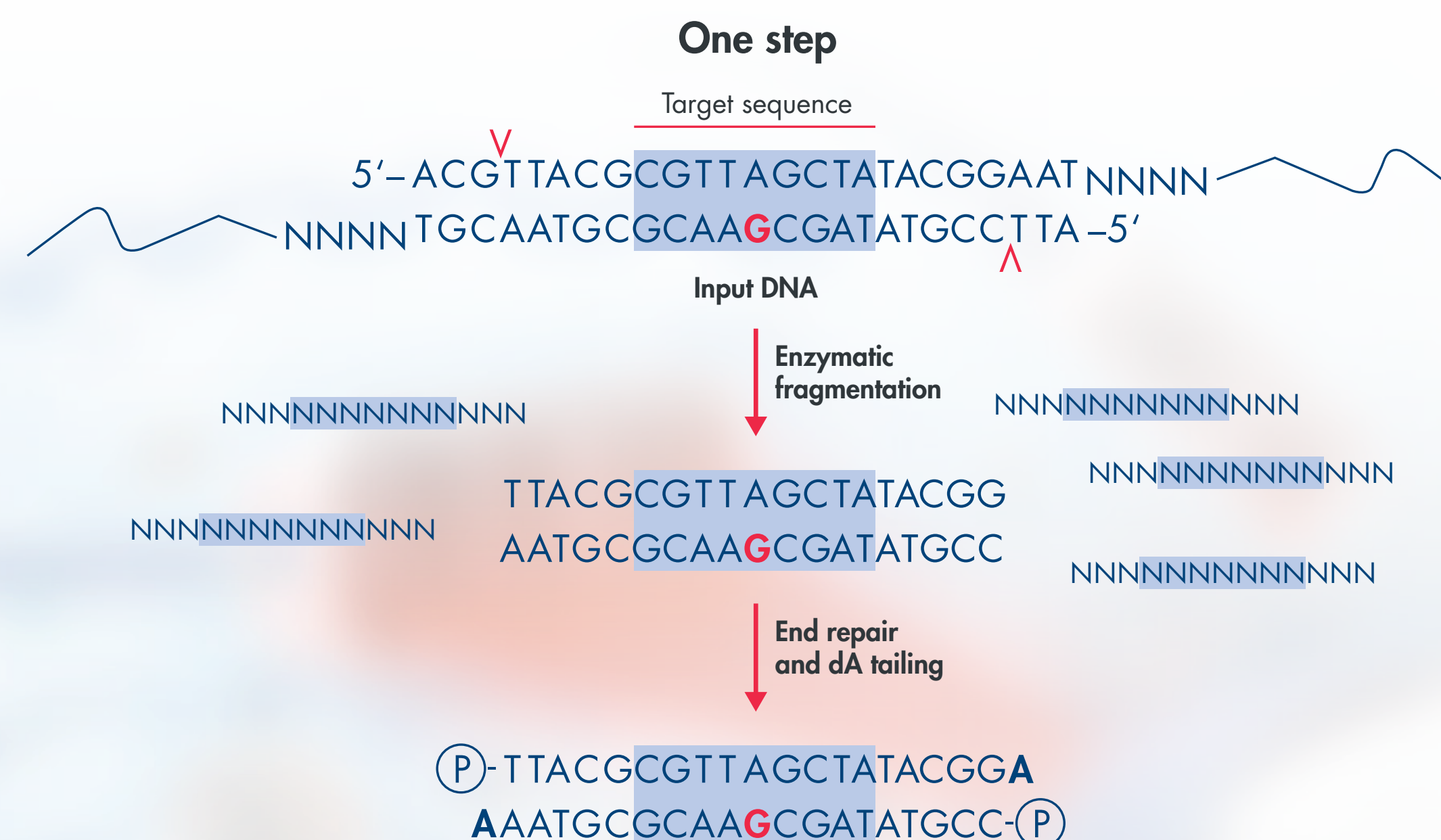
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The QIAseq advantage

Fragmentation, end-repair and dA tailing in a 45-minute one-step incubation

- Fragment sizes are optimized to complement recommended read lengths
- End-repair converts protruding ends into blunt ends
- dA tailing creates an overhang for adapter ligation



Combining 3 steps into a single 45-min incubation step
reduces hands-on time by up to 40%

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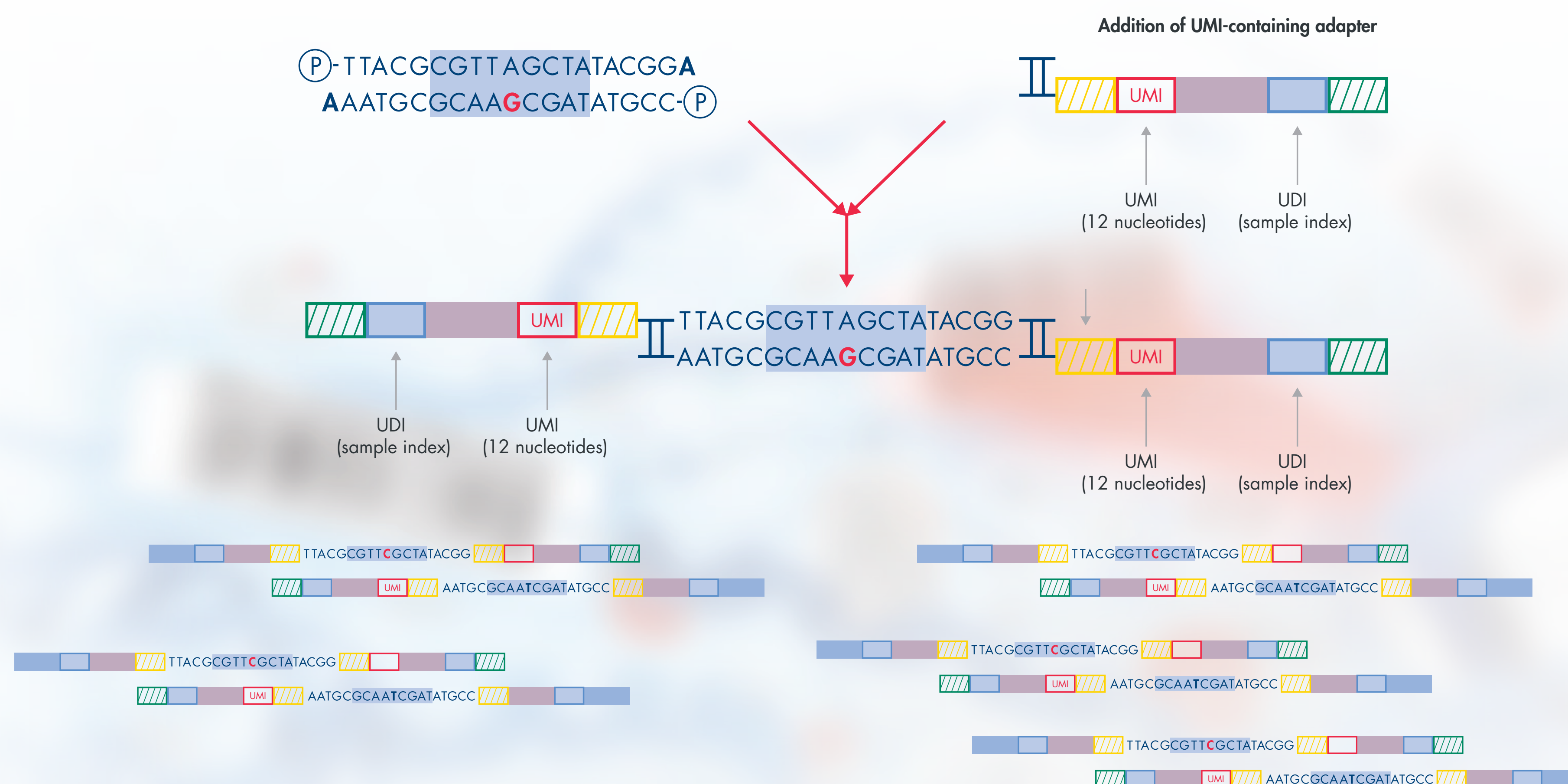
UMI

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UMI-UDI adapters for high confidence variant detection even at low allele frequencies



- UMIs tag each molecule within the sample prior to amplification
- UDIs, used as sample indices, track each individual sample, maximizing the number of samples multiplexed per run and lowering the per-sample sequencing cost

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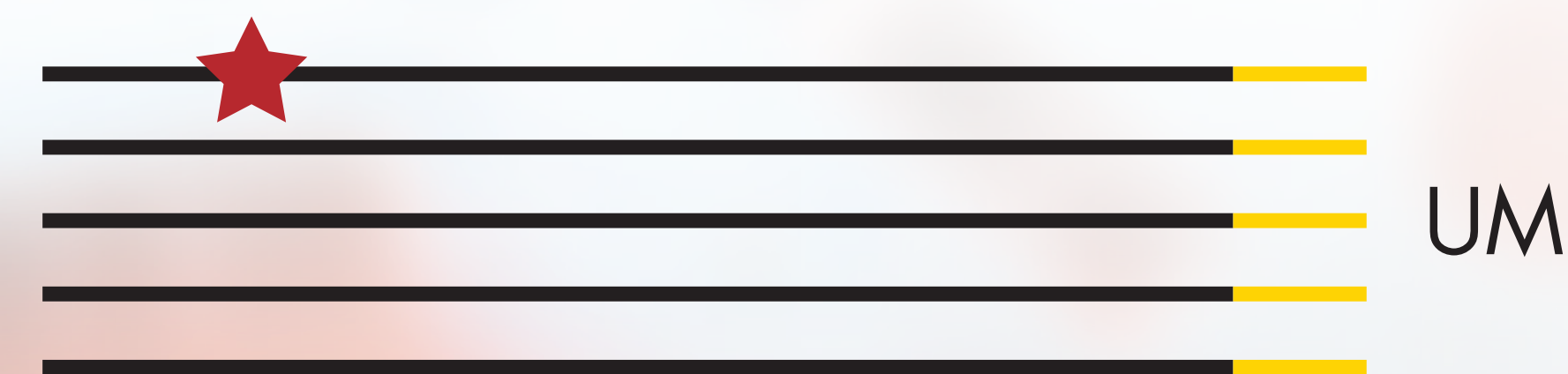
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UMIs for increased sensitivity and correction of PCR-induced errors

Distinguish true variants from artifacts with UMIs



True variant is present in all fragments carrying the same UMI



False variant is present in some fragments carrying the same UMI

- During ligation, each molecule from the starting sample population is labeled with a distinct UMI
- With 12 nucleotides in each UMI, over 16 million molecules can have a unique identifier
- UMIs help distinguish PCR-induced artifacts present at low copies from true variants, which may be present at low frequencies

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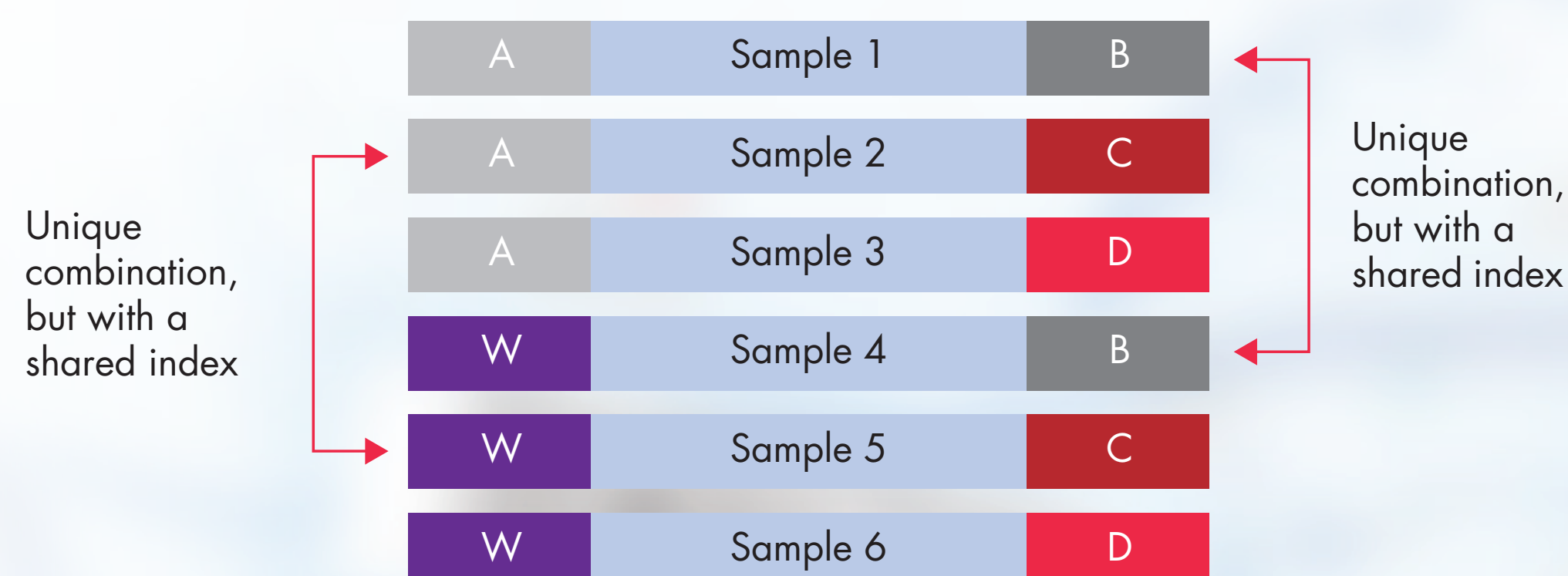
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UDIs for accurate read assignment and maximum flow cell utilization

Resolve your samples accurately with UDIs

Combinatorial dual indexing



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

Unique dual indexing



With 2 unique indices, each sample is resolved with confidence, regardless of batch size

- Efficient utilization of production-scale sequencers such as the NovaSeq requires maximizing the number of samples multiplexed in one sequencing run
- High-sensitivity applications, where sequences within the adapters are present at a much higher frequency than the unique insert sequences, require a way to confidently demultiplex samples

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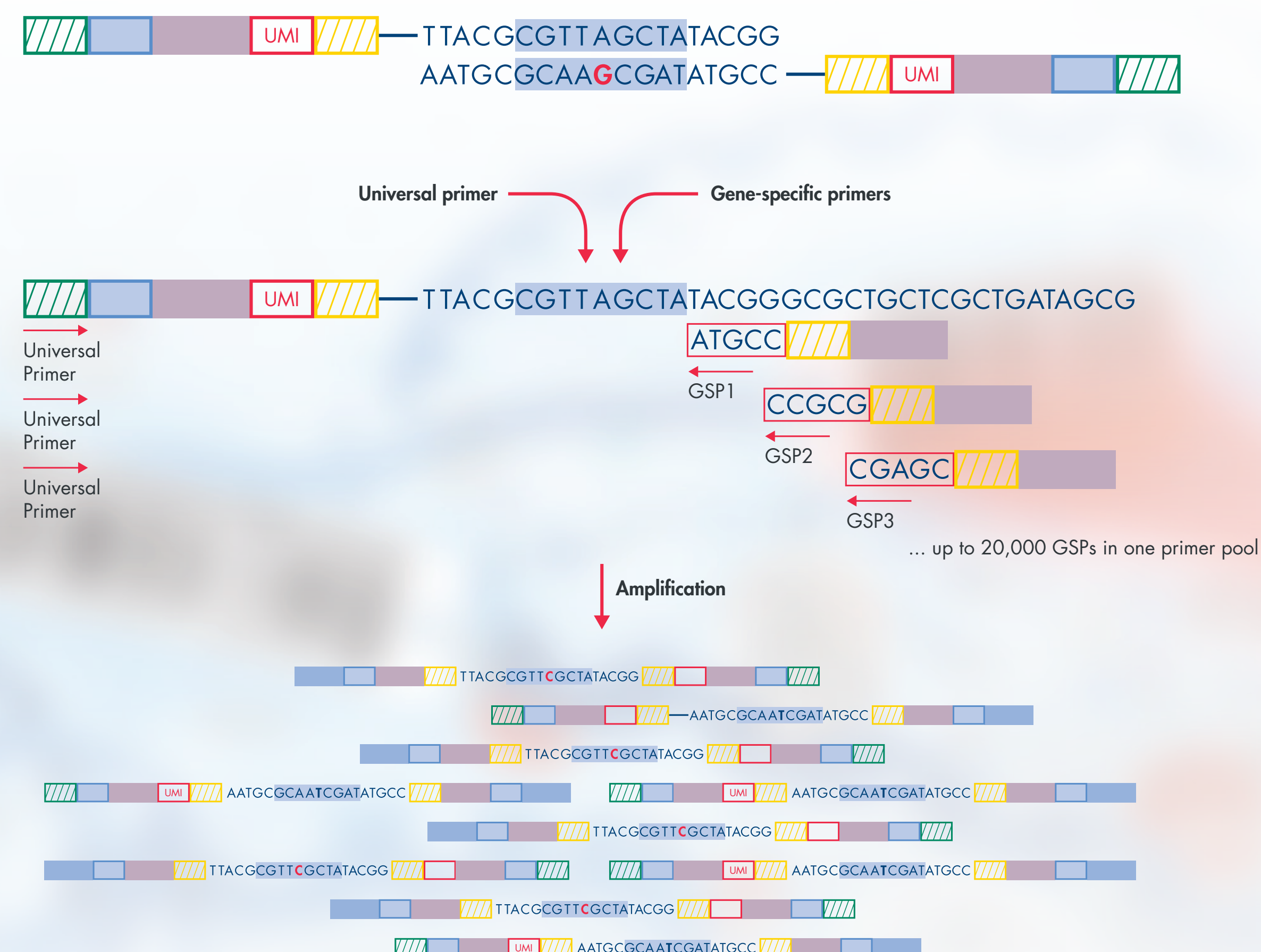
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SPE for complete and uniform target coverage

SPE overcomes the challenges of 2-primer amplicon technology



- SPE enables single-tube enrichment for up to 20,000 targets
- Staggered placement of primers across the target region ensures high uniformity and complete coverage

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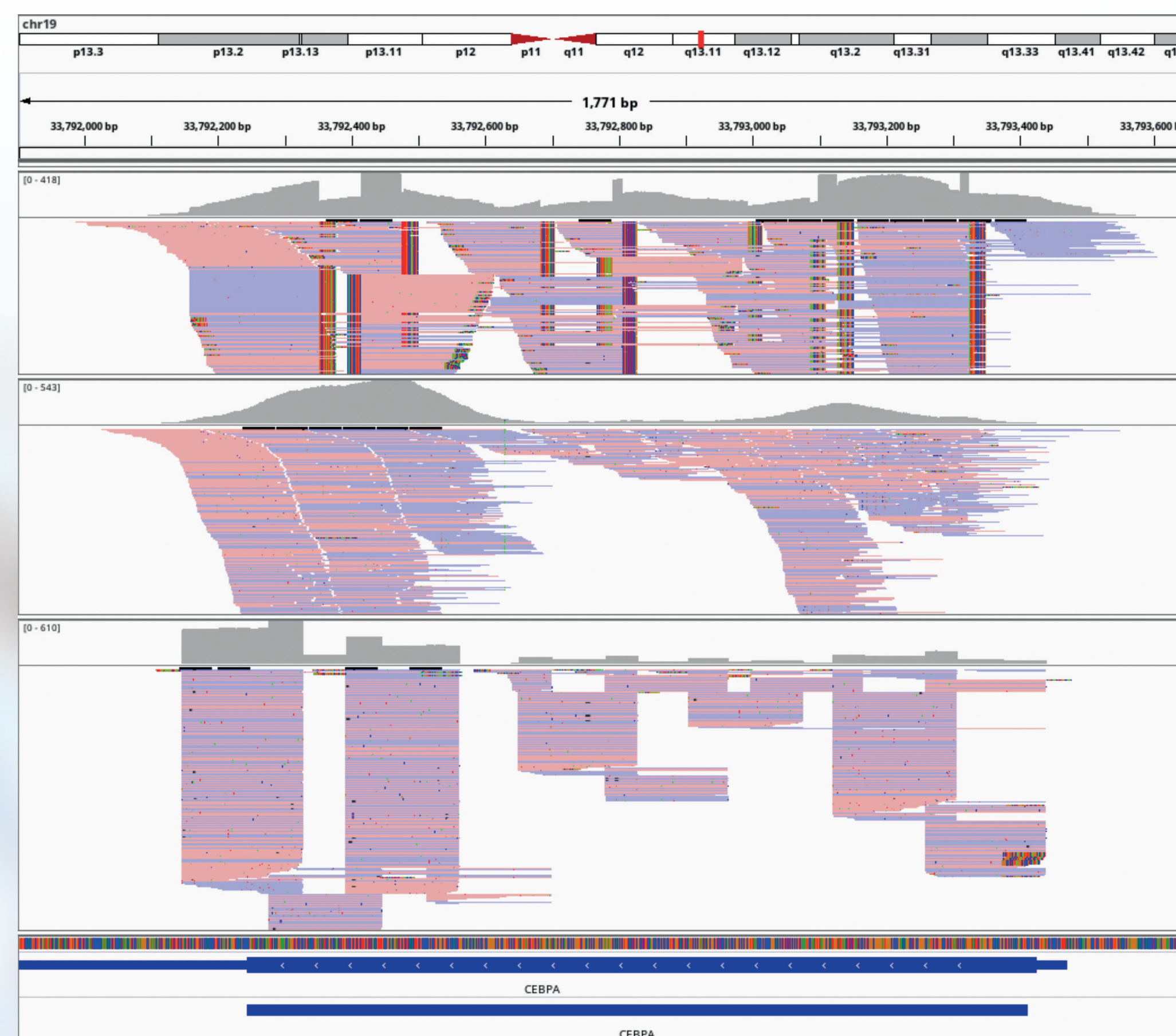
The QIAseq advantage: High-confidence variant detection for all NGS applications

QIAseq
Uniform coverage

Supplier A
Low uniformity

Supplier I
Large gaps

Target region



QIAseq panel: Myeloid Neoplasms
Sequencer: MiSeq, 2 x 150 bp

SPE and UMI technologies together ensure uniform coverage with minimal drop-outs



Source: Clark, B. Kings College Hospital, UK

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