The QIAseq advantage

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

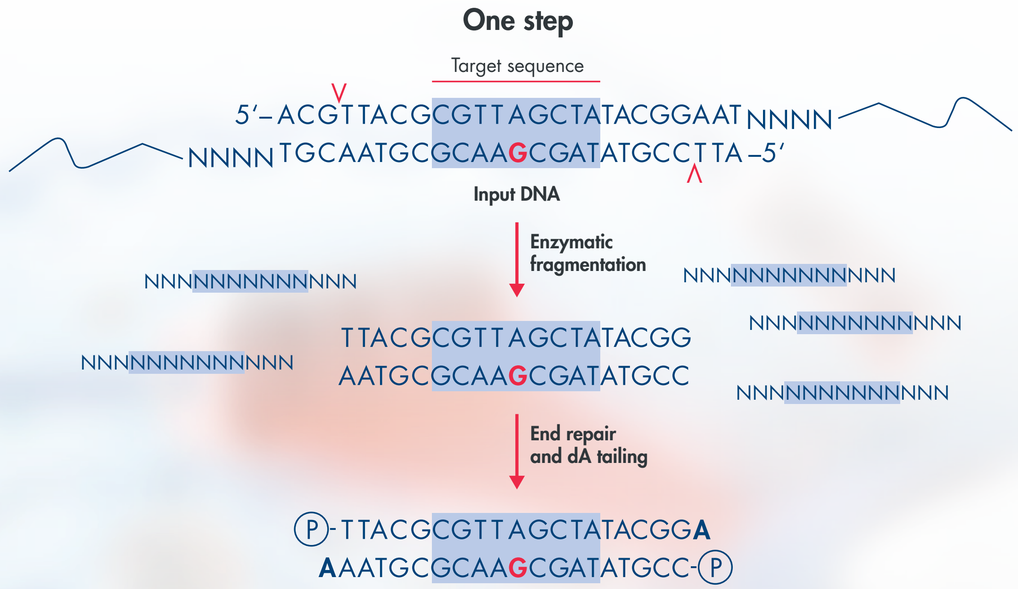
NGS workflow challenges addressed by QIAseq technologies

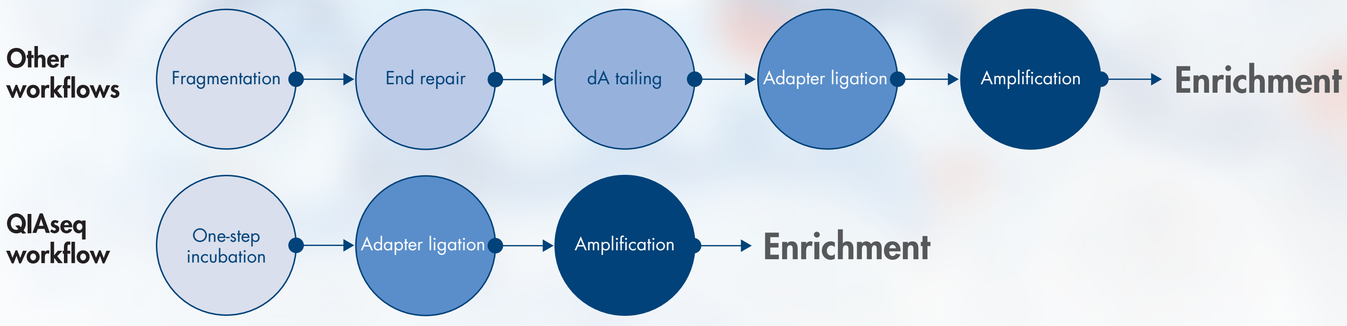
Challenge	Consequence
Primer dimers	Lack of coverage
Non-specific enrichment and sequencing	Higher cost per sample
Non-uniform enrichment and sequencing	Higher cost per sample
PCR duplicates and errors	Inability to detect low-frequency variants

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

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

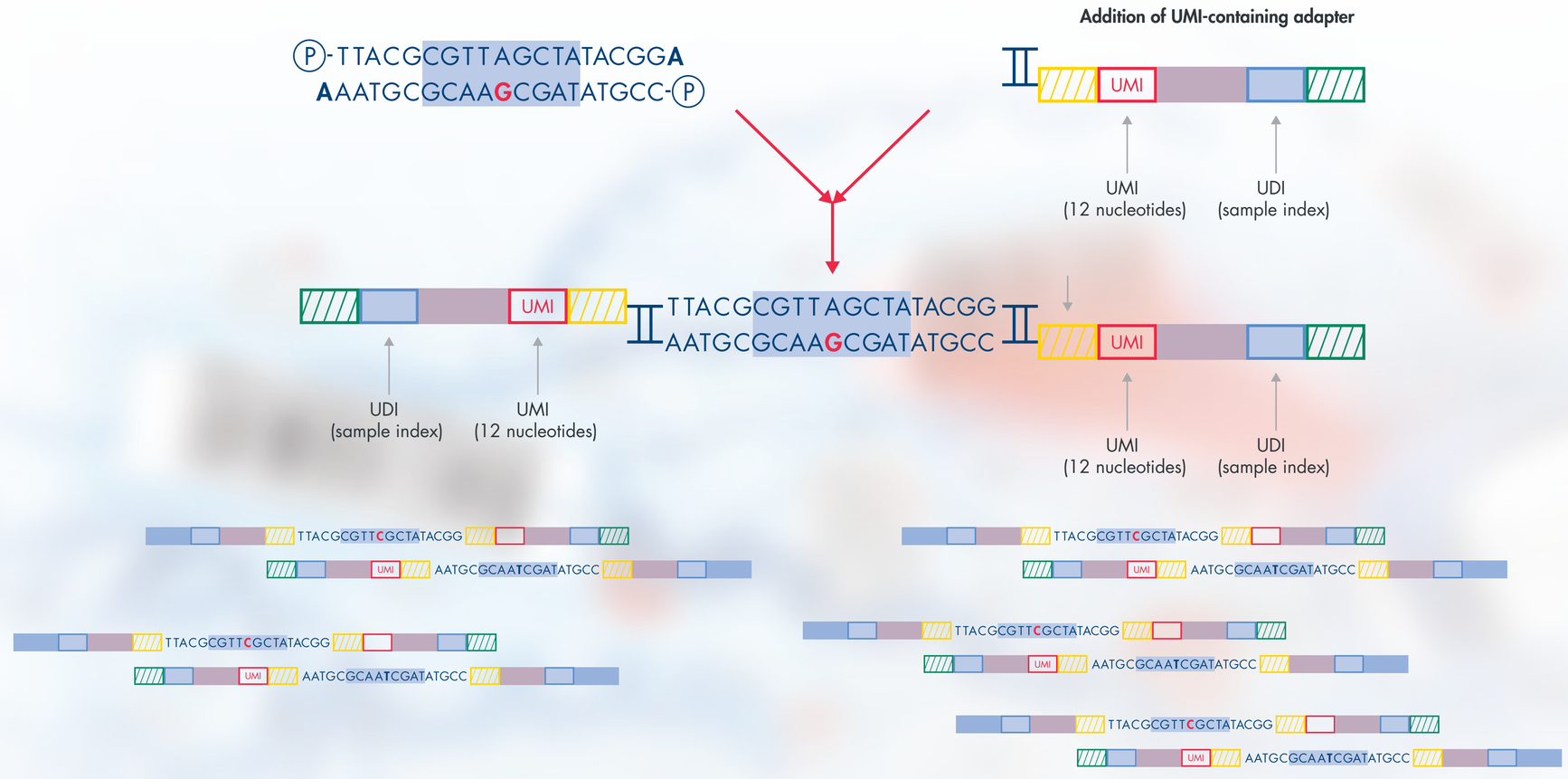
- Fragment sizes are optimized to complement recommended read lengths
- End-repair converts protruding ends into blunt ends
- dA tailing creates an overhang for adapter ligation





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

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

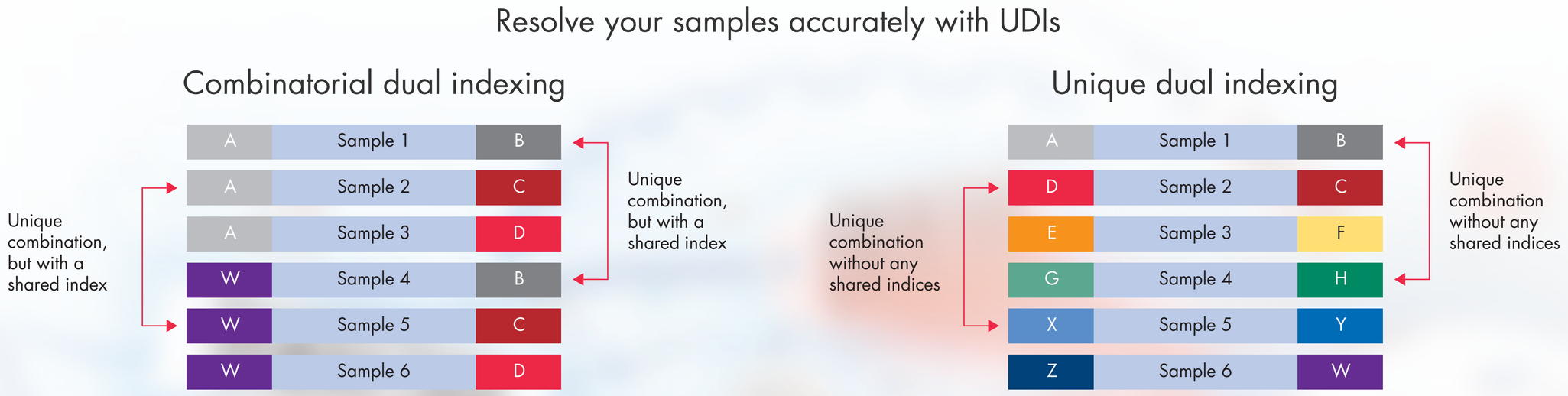


- UMIs tag each molecule within the sample prior to amplification
- UDIs, used as sample indices, track each individual sample, maximizing the number of samples multiplexed per run and lowering the per-sample sequencing cost

UMIs for increased sensitivity and correction of PCR-induced errors

- 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

UDIs for accurate read assignment and maximum flow cell utilization



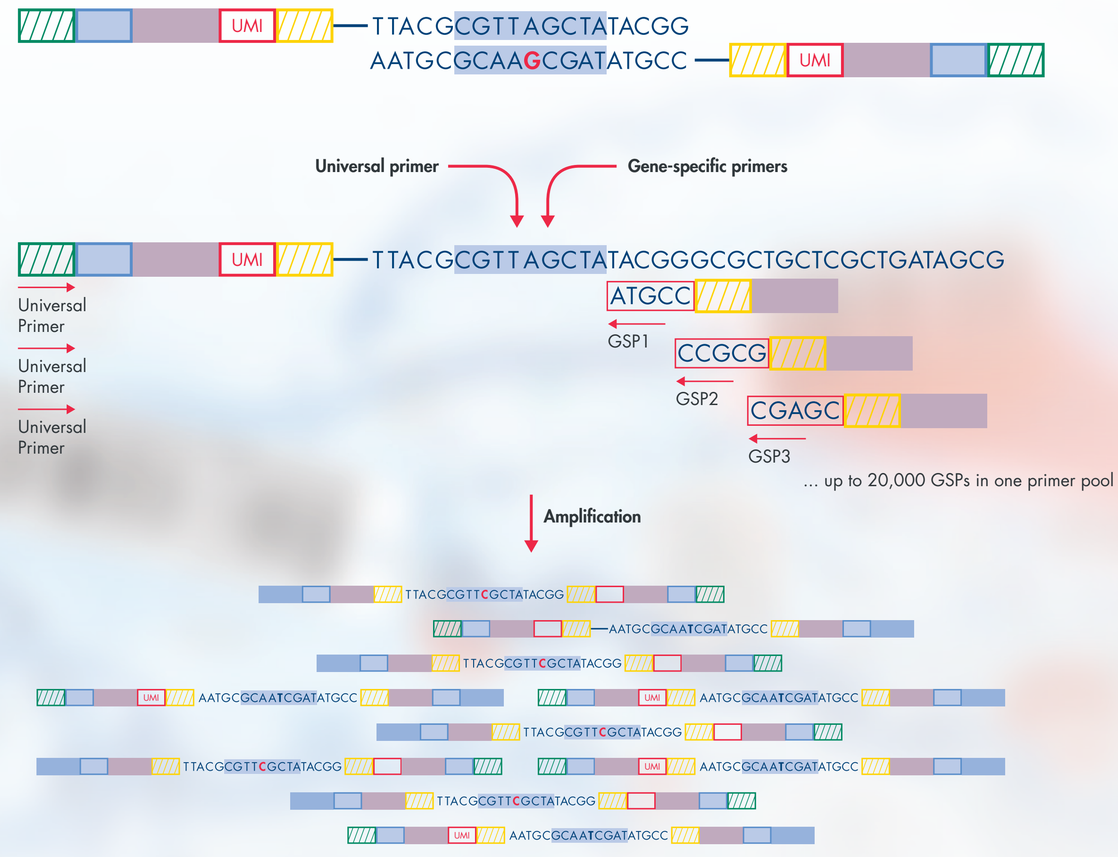
A shared index increases the likelihood of reads being mis-assigned during demultiplexing

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

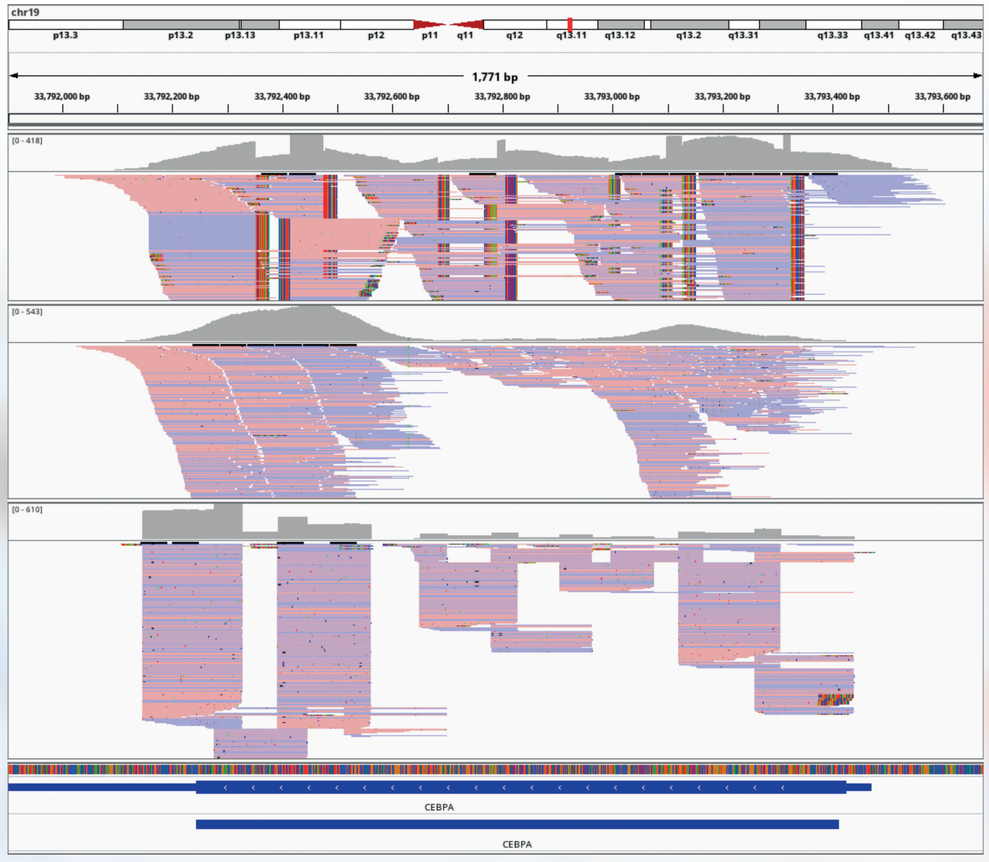
SPE for complete and uniform target coverage

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

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