Overview

One-step protocol

Fast, 20-min protocol

Robust performance with FFPE samples

Reproducibility

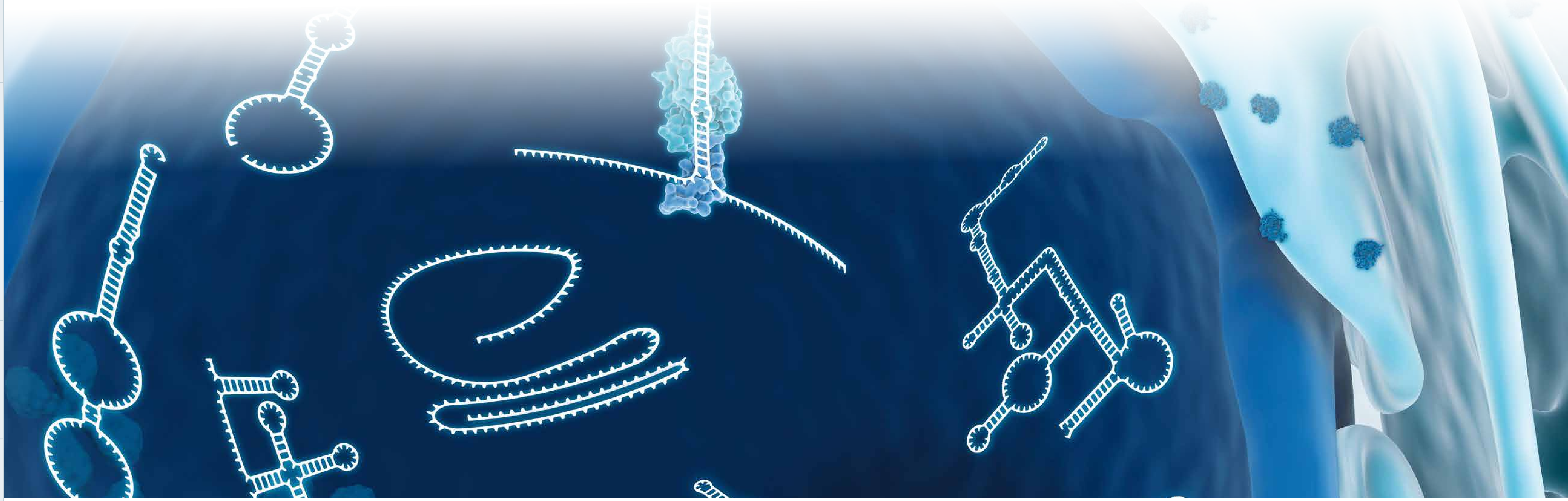
Works with any RNA-seq protocol

QIAseq RNA-seq

Ordering Information

QIAseq FastSelect RNA Removal Kits

Efficient removal of unwanted RNA in a single pipetting step



- Convenient, single, integrated step during RNA fragmentation and cDNA synthesis
- Compatible with QIAGEN, Illumina®, NEB® and KAPA® RNA stranded library kits
- Flexible – use 1 ng to 1 µg fresh, high-quality RNA, FFPE RNA or degraded RNA
- Efficient – high-performance rRNA and/or globin removal in just 20 minutes
- Versatile – customizable by RNA transcript

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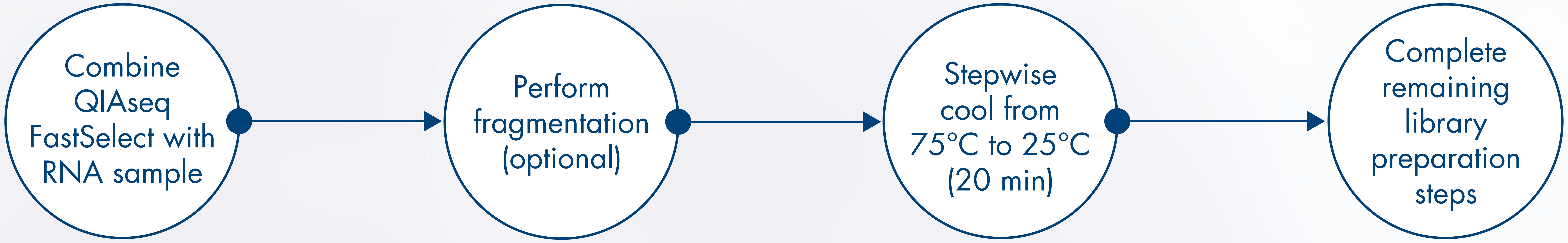
One-step protocol completed in just 20 minutes



Combine QIAseq FastSelect with RNA sample

Perform fragmentation (optional)

Stepwise cool from 75°C to 25°C (20 min)

Complete remaining library preparation steps

- Single pipet step – simply add QIAseq FastSelect reagent to RNA sample

- QIAseq FastSelect works with or without fragmentation, which depends on library prep kit and sample type

- 20 min incubation easily intergrates into existing workflow with no additional accessories or procedures

A simple, one-step rRNA and/or globin mRNA depletion procedure that's completed in just 20 min

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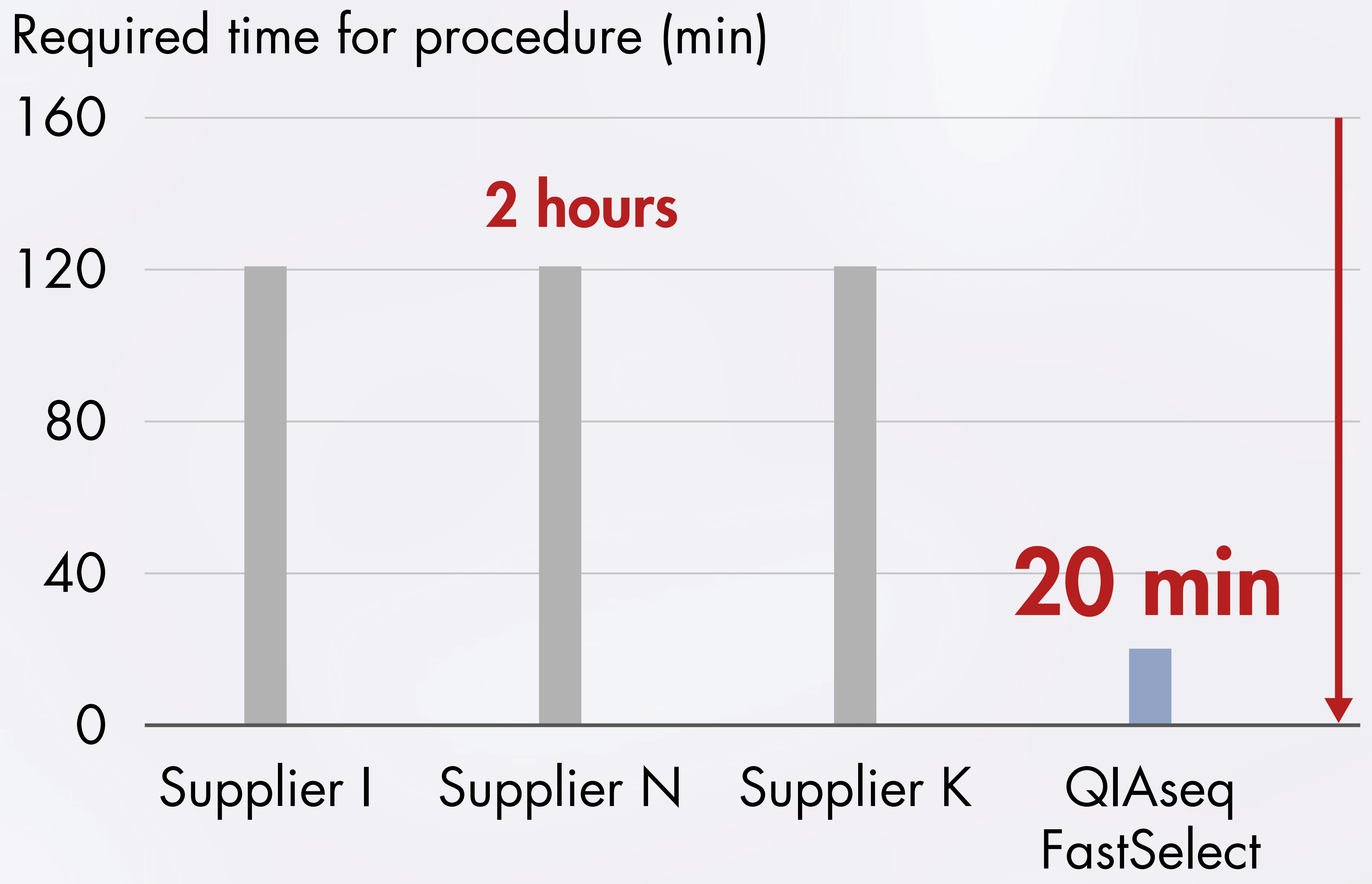
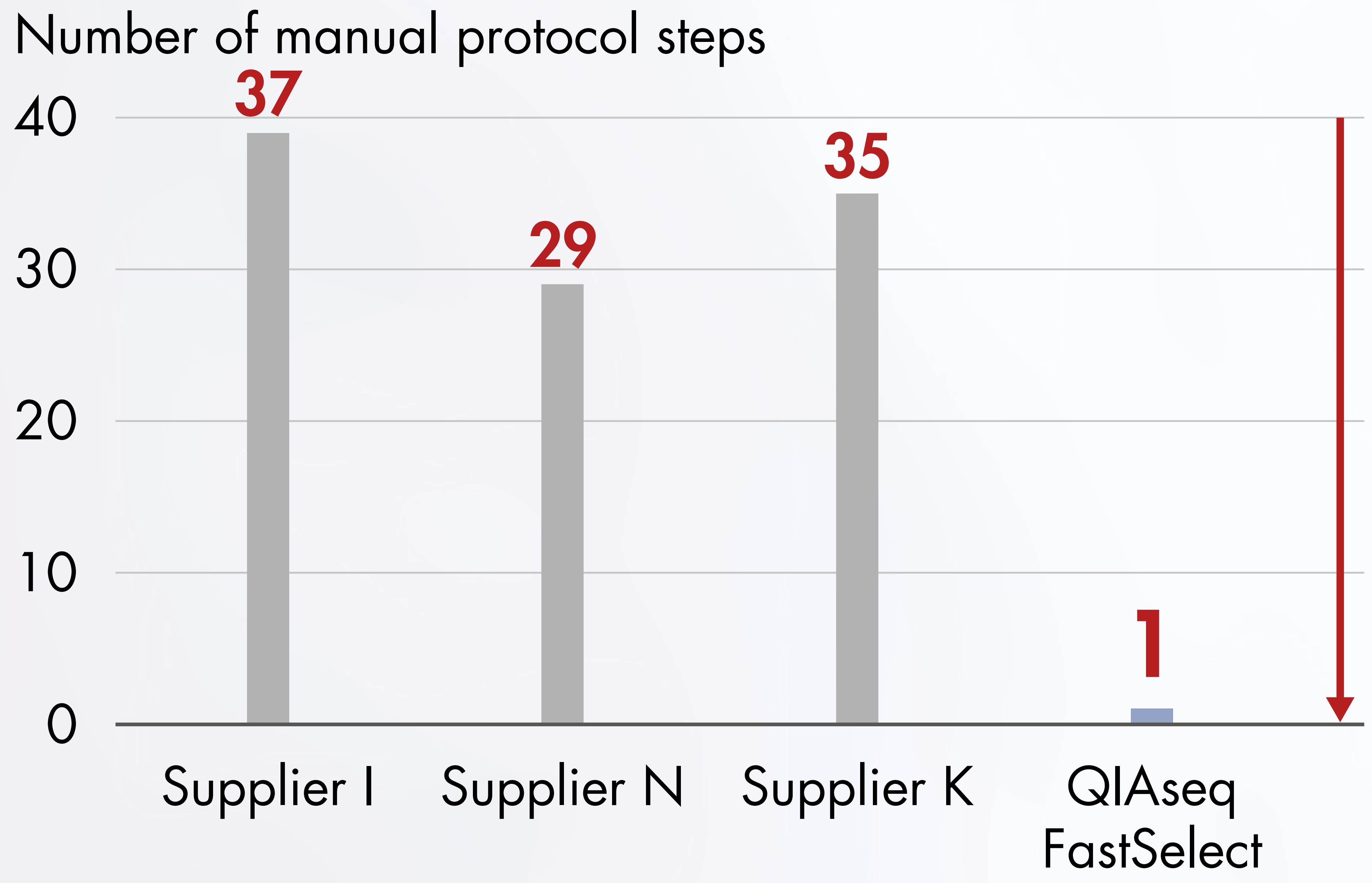
A 20-min, one-step protocol means greater efficiency and speed

Complete in 20 min vs. hours



1 pipette step vs. >29 steps



Fewer protocol steps means reduced effort and greater time savings

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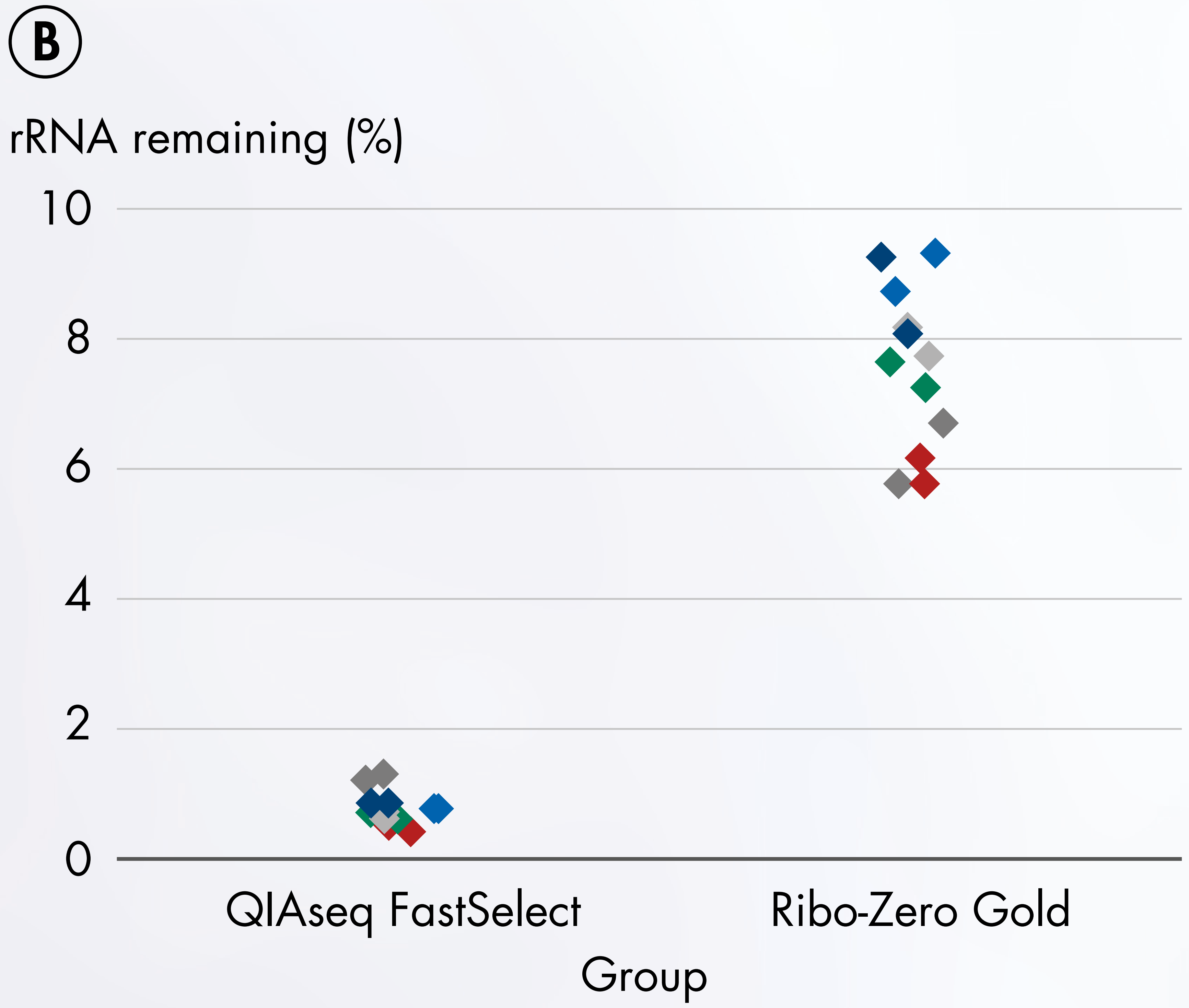
Reduce the number of wasted reads from FFPE samples

Great removal of rRNA than competitors

Ⓐ

Sample	QIAseq FastSelect % rRNA remaining	Ribo-Zero Gold % rRNA remaining
S34022 N	0.69	7.46
S34022 C	0.72	7.94
S34019 N	0.89	8.65
S34019 C	0.84	9.05
S33119 N	1.30	6.23
S33119 C	0.50	5.97

Superior rRNA removal than competitors



Total RNA was isolated from 5 µm normal and cancer lung FFPE sections using the miRNeasy FFPE Kit. QIAseq FastSelect results in highly efficient removal of rRNA from fragmented samples. Average % rRNA remaining is provided in **A** and plotted in **B**. Ribo-Zero Gold required substantially more amplification cycles than the QIAseq FastSelect libraries, suggesting some sample may be lost with Ribo-Zero Gold.

Sequence what matters – efficient use of sequencing resources and capacity

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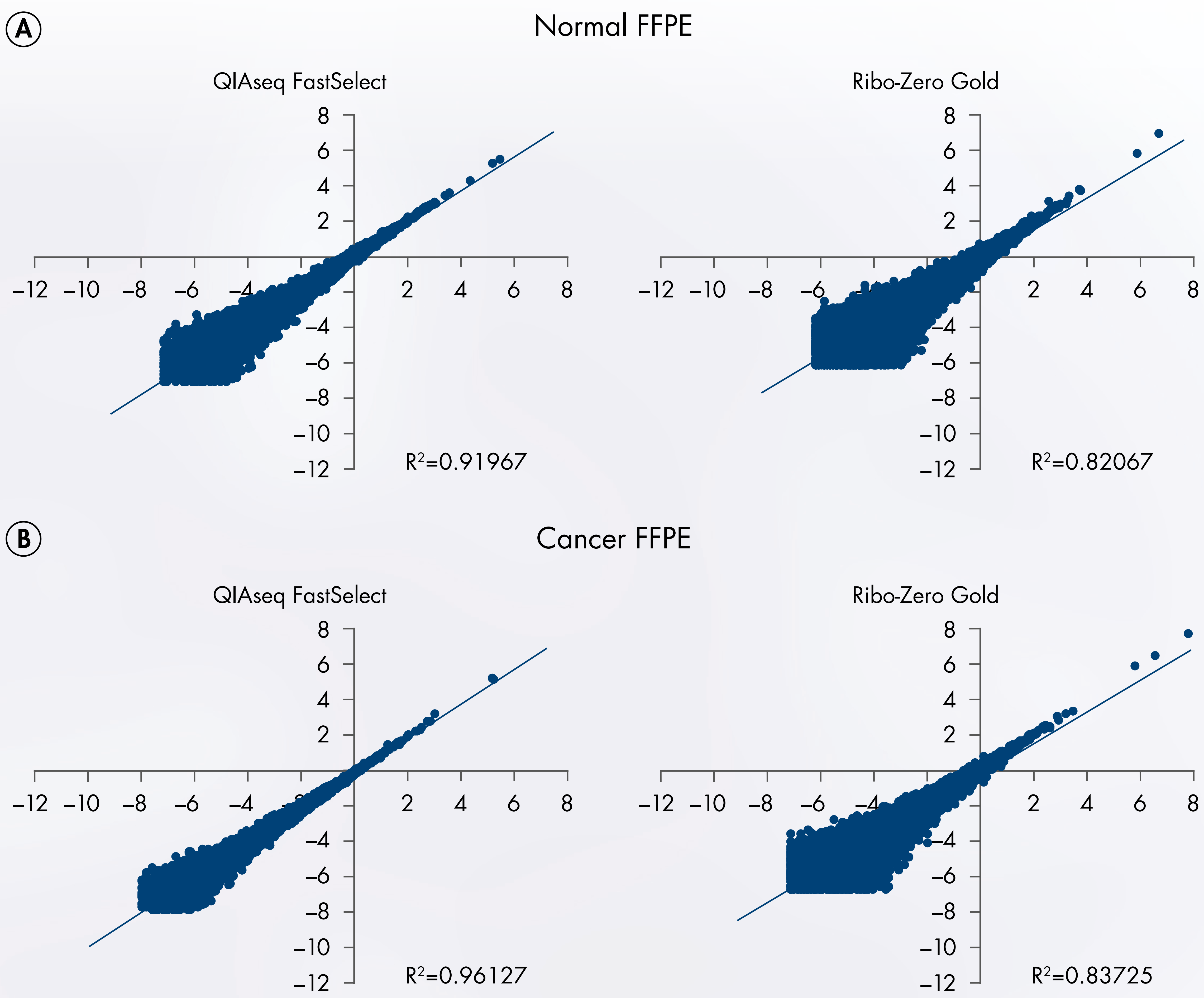
Highly reproducible results from fresh or FFPE samples



Highly reproducible gene expression data following rRNA depletion for RNA from FFPE samples. For rRNA depletion, QIAseq FastSelect or Ribo-Zero Gold was used. Performing rRNA depletion using QIAseq FastSelect achieved highly reproducible gene expression results ($\log_2$ normalized gene expression) for **A** normal FFPE RNA and **B** cancer FFPE RNA. Two replicates were performed for each sample type.

Consistent performance and high downstream reproducibility

Compatible with QIAGEN, Illumina, KAPA and NEB RNA-seq library prep workflows

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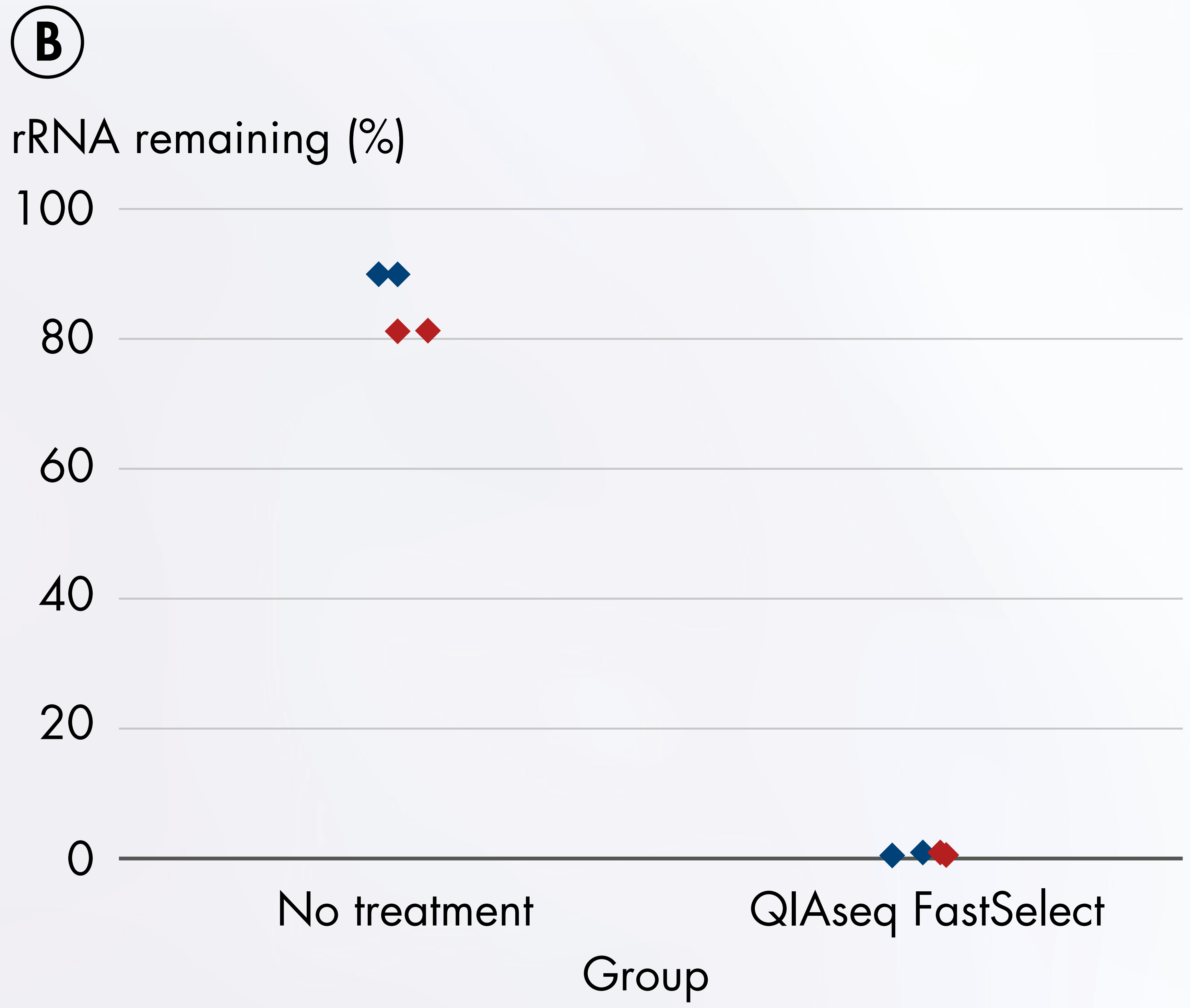
Sample	rRNA remaining (%)	Protein coding (%)
100 ng UHRR	1.01	89.4
1 µg UHRR	1.09	89.7

Download Handbook



QIAseq FastSelect integrated into Illumina TruSeq® workflow (performance). A Average % rRNA remaining and % protein coding reads shown. **B** rRNA remaining is shown when no depletion is performed (no treatment) and when depletion is performed using QIAseq FastSelect (blue = 100 ng and red = 1 µg). QIAseq FastSelect results in highly efficient removal of rRNA. Average % rRNA remaining is provided in **A** and plotted in **B**.

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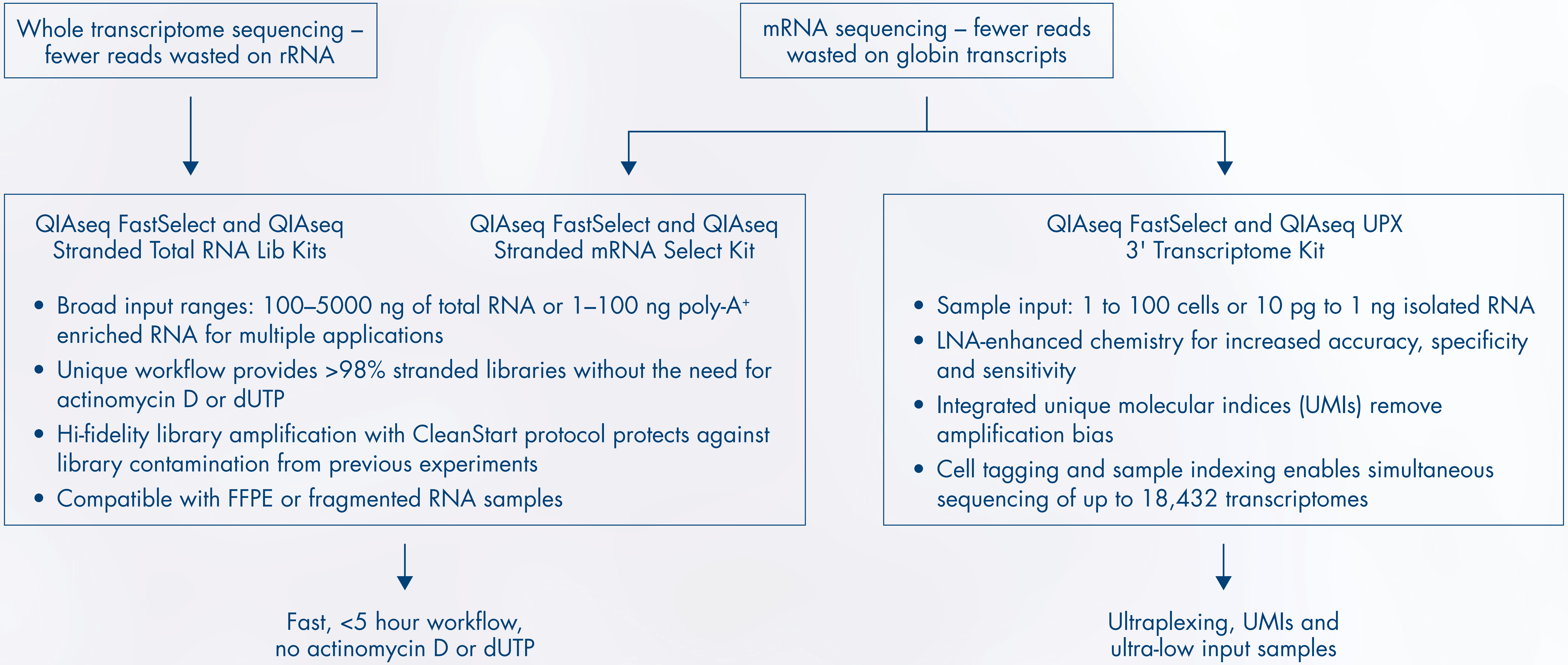
QIAseq RNA-seq – sequence what matters



Whole transcriptome sequencing – fewer reads wasted on rRNA

mRNA sequencing – fewer reads wasted on globin transcripts

QIAseq FastSelect and QIAseq Stranded Total RNA Lib Kits

QIAseq FastSelect and QIAseq Stranded mRNA Select Kit

- Broad input ranges: 100–5000 ng of total RNA or 1–100 ng poly-A^{+} enriched RNA for multiple applications
- Unique workflow provides >98% stranded libraries without the need for actinomycin D or dUTP
- Hi-fidelity library amplification with CleanStart protocol protects against library contamination from previous experiments
- Compatible with FFPE or fragmented RNA samples

Fast, <5 hour workflow, no actinomycin D or dUTP

QIAseq FastSelect and QIAseq UPX 3' Transcriptome Kit

- Sample input: 1 to 100 cells or 10 pg to 1 ng isolated RNA
- LNA-enhanced chemistry for increased accuracy, specificity and sensitivity
- Integrated unique molecular indices (UMIs) remove amplification bias
- Cell tagging and sample indexing enables simultaneous sequencing of up to 18,432 transcriptomes

Ultraplexing, UMIs and ultra-low input samples

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Product	Species available	Targets	No. of samples	Cat. no.
QIAseq FastSelect RNA Removal Kit	Human, Mouse, Rat	rRNA or globin	24, 96, 384	333180
QIAseq FastSelect Multi-RNA Removal Kit	Human, Mouse, Rat	rRNA and globin	24, 96, 384	333280
QIAseq FastSelect Custom RNA Removal Kit	Your choice	Any	1156	Inquire
QIAseq Stranded Total RNA Lib Kits	Any	Transcriptome	24, 96	180743 180745
QIAseq Stranded mRNA Select Kits	Any	Poly(A) transcripts	24, 96	180773 180775
QIAseq UPX 3' Transcriptome Kits	Human, Mouse	Poly(A) transcripts	96, 384	333088 333090

Find out more about at **www.qiagen.com/QIAseqFastSelect**.

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