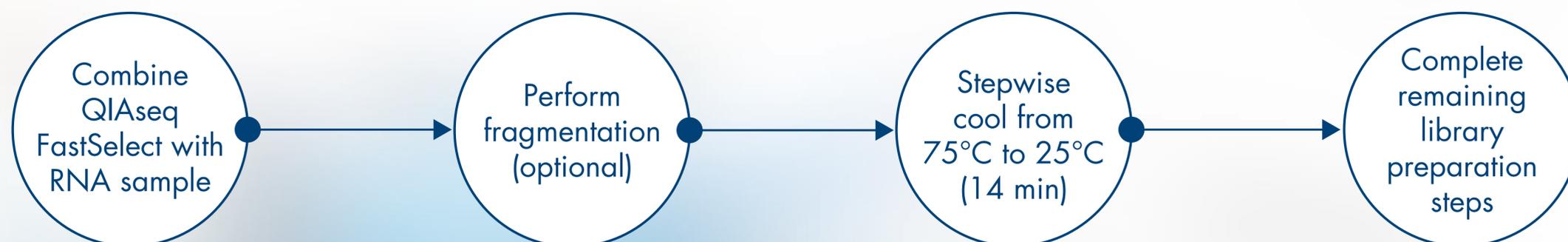# QIAseq FastSelect –rRNA HMR, –Globin and Epidemiology Kits

Fast, single-kit solutions for efficient removal of rRNA, globin mRNA and/or bacterial rRNA

- Streamline RNA removal using the fastest kit on the market
- No limits on RNA quantity or quality – compatible with intact and degraded RNA (e.g., FFPE RNA), with input from 1 ng – 1 µg
- Works with any RNA library prep kit
- Nearly complete removal of rRNA and/globin mRNA

One-step QIAseq FastSelect –rRNA HMR and –Globin protocols completed in just 14 minutes

```
Combine          Perform          Stepwise         Complete
QIAseq       →   fragmentation →  cool from     →  remaining
FastSelect with  (optional)       75°C to 25°C     library
RNA sample                        (14 min)         preparation
                                                   steps
```

- Single pipetting 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

- 14-minute incubation easily intergrates into existing workflow with no additional accessories or procedures

Single reagent for one-step rRNA and/or globin mRNA from human, mouse, rat and other mammalian species

A 14-min, one-step protocol means greater efficiency and speed

Ⓐ QIAseq FastSelect: one inline reaction step

# of workflow steps

40

30

20 **1 step**

10

0

Supplier I | Supplier N | Supplier T | QIAseq FastSelect human only | QIAseq FastSelect –rRNA HMR

Data provided by QIAGEN R&D
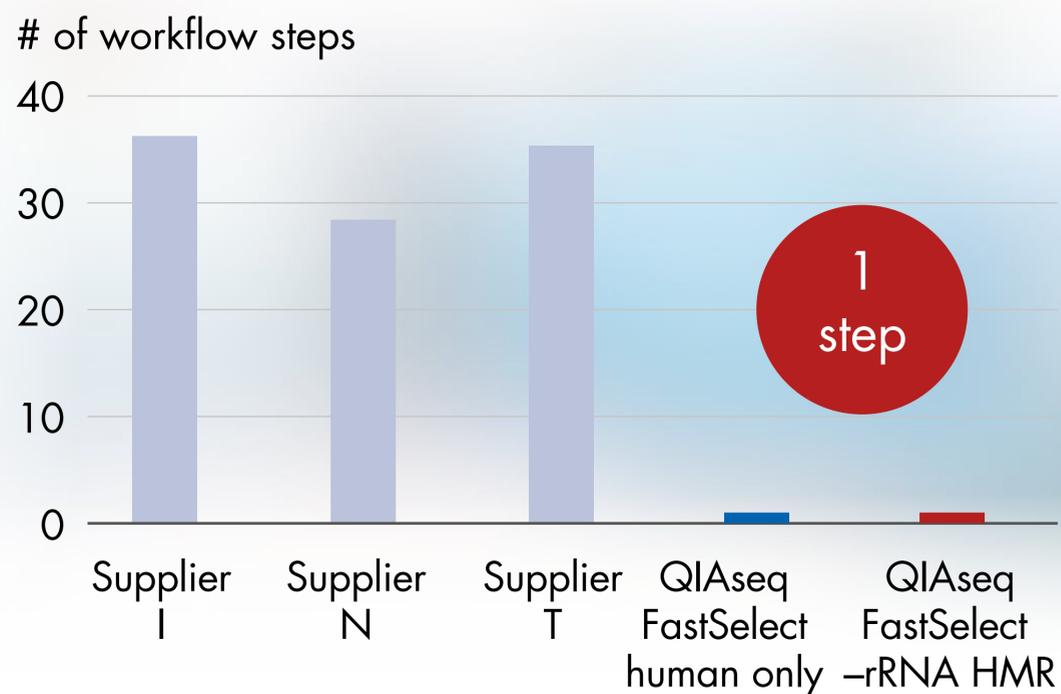
Ⓑ QIAseq FastSelect: 90% less time

Time (min)

120

80 **Save hours!**

40

0

Supplier I | Supplier N | Supplier T | QIAseq FastSelect human only | QIAseq FastSelect –rRNA HMR
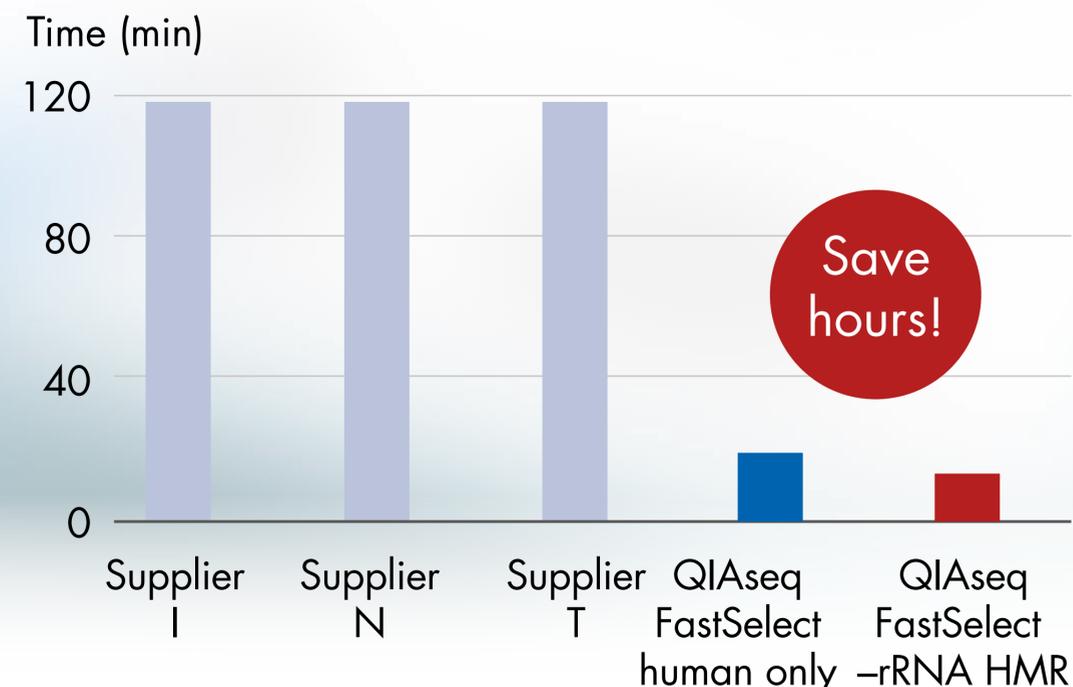
Save even more time and effort with a 30% faster protocol compared to previous kit version

A single-kit solution for various mammalian samples

QIAseq FastSelect −rRNA HMR Kit is a single solution that removes mitochondrial and cytoplasmic rRNA from human, mouse, rat and other mammalian samples

Species	Reads mapped to rRNA (%)		rRNA removed (%)
	No treatment	After QIAseq FastSelect −rRNA HMR	
Human	91.8	1.6	98.3
Mouse	92.9	2.2	97.6
Rat	93.0	2.6	97.2
Cow	70.0	1.2	98.3
Horse	74.1	1.8	97.6
Hamster	77.5	3.5	95.5
Sheep	87.3	4.0	95.4
Dog	87.8	9.1	89.6
Monkey	90.4	10.6	88.3
Chicken	88.3	16.3	81.5
Rabbit	88.8	16.5	81.4
Pig	87.6	17.3	80.3

Reduce the number of wasted reads from FFPE samples
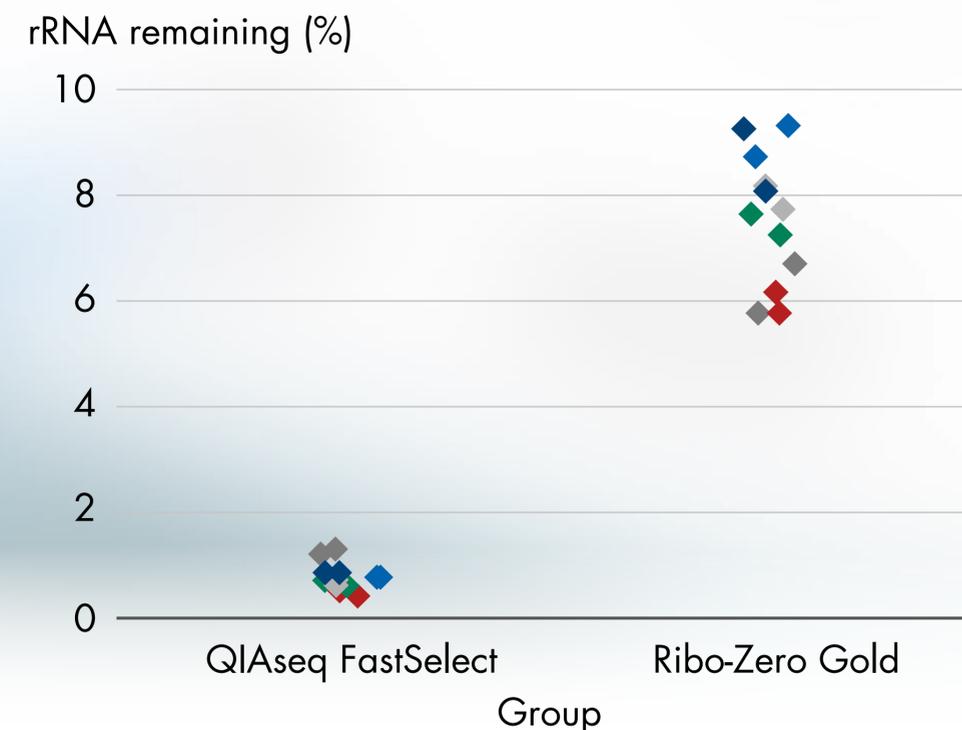
Superior rRNA removal compared to other suppliers

A

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

B

QIAseq FastSelect results in highly efficient removal of rRNA from fragmented samples. Total RNA was isolated from 5 µm normal and cancer lung FFPE sections using the miRNeasy FFPE Kit. The QIAseq Stranded Total RNA Lib Kit was used for RNA-seq library prep. 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 (Data provided by QIAGEN R&D).

Sequence what matters – efficient use of sequencing resources and capacity

Robust removal of rRNA and globin mRNA

Increased exon mapping
Exon/intron/intergenic reads

Human, no treatment

Human, QIAseq FastSelect
–rRNA HMR +/–Globin

Mapped reads (%)

■ Exon ■ Intron ■ Intergenic
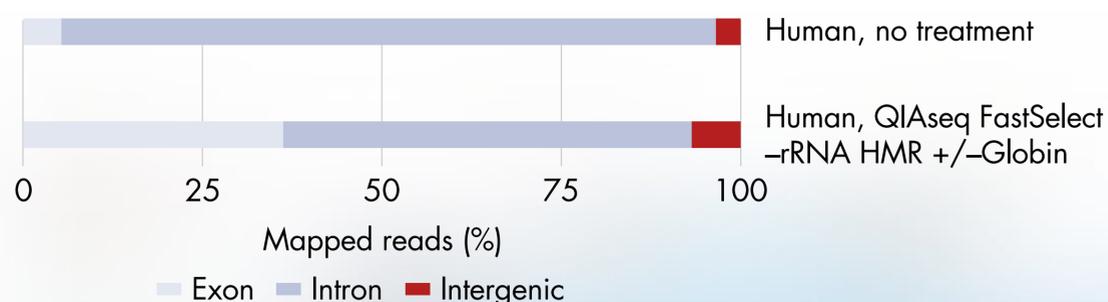
Strong correlation: Replicates
Gene expression analysis

QIAseq FastSelect
–rRNA HMR
+/–Globin, R2

R² = 0.9923

QIAseq FastSelect –rRNA HMR +/–Globin, R1
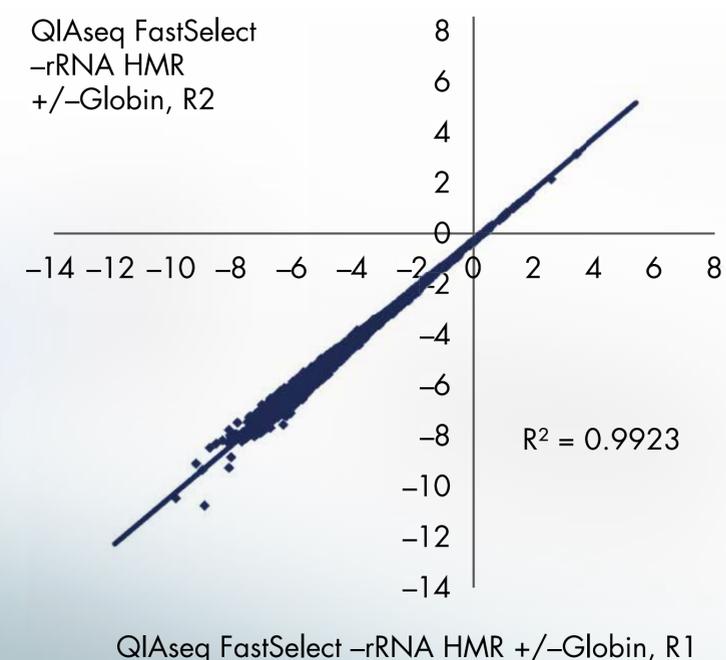
Substantial removal of rRNA and globin
Mapping metrics

Percentage of reads mapped to rRNA		Percentage of TPM mapped to Globin	
No treatment	QIAseq FastSelect –rRNA HMR +/–Globin	No treatment	QIAseq FastSelect –rRNA HMR +/–Globin
88.50	1.16	82.46	0.16

Experimental overview. As starting sample, 100 ng human whole blood total RNA was used. The QIAseq FastSelect –rRNA/Globin Kit was used for RNA removal. RNA-seq library prep was performed using the QIAseq Stranded Total RNA Lib Kit, with sequencing on the NextSeq 550 and read mapping using QIAGEN CLC Genomics Workbench.

Efficient rRNA and globin removal resulting in an increased percentage of reads mapped to exons, with gene expression values from FastSelect-treated samples highly correlative (Log2 RPKM >0.3)
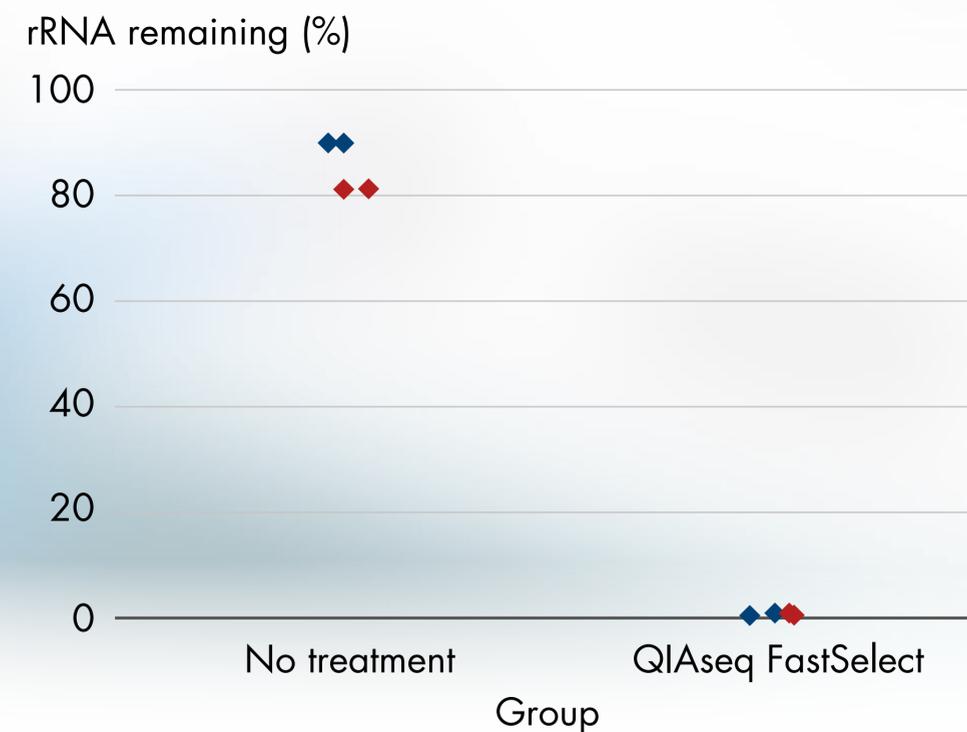
Sample to Insight

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

A

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

B

rRNA remaining (%)

QIAseq FastSelect integrated into Illumina TruSeq workflow (performance). A Average % rRNA remaining and % protein-coding reads shown. **B** rRNA remaining is shown when no rRNA removal is performed (no treatment) and when rRNA removal is performed using QIAseq FastSelect technology (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**.

Consistent performance and high downstream reproducibility

Separate reagents for bacteria and human/mouse/rat for flexibility in single or dual-seq applications

QIAseq FastSelect –rRNA HMR Kit + QIAseq FastSelect –5S/16S/23S Kit
= QIAseq FastSelect Epidemiology Kits

Combine QIAseq FastSelect with RNA sample → Perform fragmentation (optional) → Stepwise cool from 75°C to 25°C (14 min) → Bead cleanup → Complete remaining library prep

Use with mixed samples for co-expression studies to reduce costs, expand mRNA insights and uncover more biology

The QIAseq FastSelect Epidemiology Kit enables fast and effective removal of pan-bacterial 5S/16S/23S rRNA

	Reads mapped to total bacterial rRNA (%)		
Sample	No treatment	Treatment	rRNA removed (%)
Supplier T – method ME	95.0	89.9	89.9
Supplier T – method RM	95.0	87.6	87.6
QIAseq FastSelect –5S/16S/23S	93.3	8.5	8.5
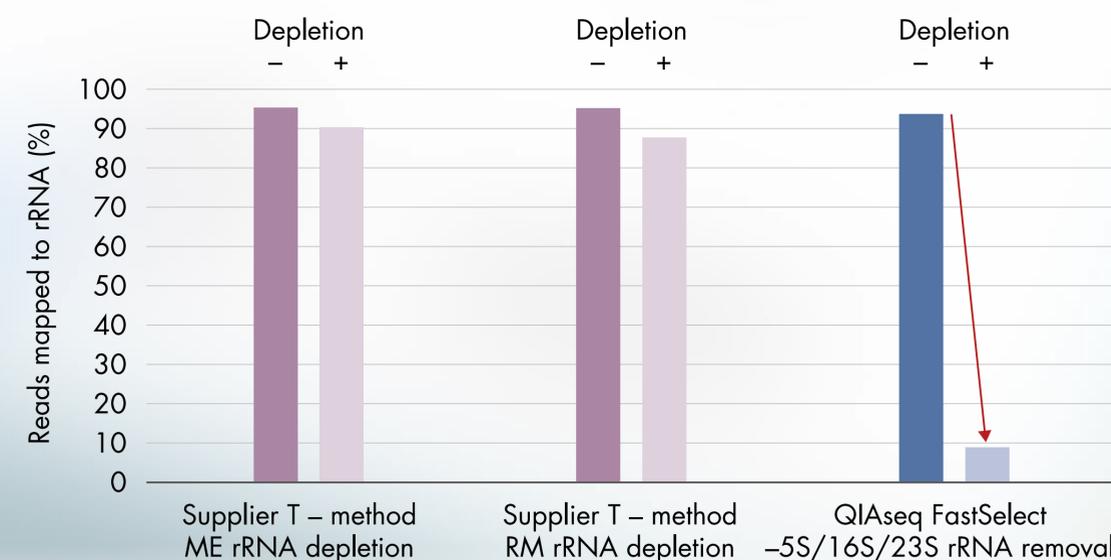
Total RNA was isolated from Gut Microbiome Whole cell Mix (ATCC) using the RNeasy PowerMicrobiome Kit (QIAGEN). Stranded transcriptome libraries were then prepared from 1 µg aliquots of the RNA using the QIAseq Stranded Total RNA Lib Kit. For rRNA removal, three methods were used: Supplier T – methods ME and RM, which used a hybrid capture workflow and QIAGEN's QIAseq FastSelect –5S/16S/23S Kit. Following a bead cleanup, the remaining library prep steps were completed (starting with 1st strand synthesis). Sequencing was performed on a NextSeq 550, and data analysis was performed using QIAGEN CLC Genomics Workbench. (Data provided by QIAGEN R&D).

Removal of over 90% of bacterial rRNA, unlike hybrid capture workflows, which remove less than 10% of the same rRNAs

Ordering Information

Product	Species available	Targets	Cat. no.
QIAseq FastSelect –rRNA HMR Kit (96)*	Human, mouse, rat and other mammalian species	rRNA	334387
QIAseq FastSelect –rRNA/Globin Kit (96)*	Human, mouse, rat and other mammalian species	rRNA and globin mRNA	335377
QIAseq FastSelect –Globin Kit (96)*	Human, mouse, rat and other mammalian species	Globin mRNA	334377
QIAseq FastSelect Epidemiology Kit (96)*	Human, mouse, rat and other mammalian species, and bacterial samples	rRNA	333275

* Other kit sizes and/or formats available; see **www.qiagen.com** for details.

Learn more and see key publications at **www.qiagen.com/QIAseqFastSelect/HMR** and **www.qiagen.com/QIAseqFastSelect/Epidemiology**

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** or can be requested from QIAGEN Technical Services or your local distributor.

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