

Get more data from every sequencing run

Up to **45%** more usable reads compared to other workflows

NEW

ITS MICROBIOME KIT
Request a sample

Short-read fungal microbiome sequencing made easy

The **EasySeq™ ITS Microbiome Library Prep Kit** enables reliable profiling of fungal communities using short-read next-generation sequencing.

In a **Single reaction**, amplification, indexing and library preparation is done in one tube, simplifying the workflow while increasing sequencing efficiency and reducing costs.

Laboratories using EasySeq™ workflows report **improved accuracy, reproducibility and stable sequencing output**, even for challenging samples. The safe and easy workflows are enabled by the patented Reverse Complement PCR technology.



Key benefits

- ✓ **Single Reaction library prep**
Amplification, indexing and library preparation occur in a single reaction.
- ✓ **Lower cost per sample**
Improved sequencing efficiency reduces the cost per analyzed sample.
- ✓ **More samples per sequencing run**
Higher flow cell utilization allows more samples per run.
- ✓ **Reduced hands-on time**
Fewer pipetting steps reduce manual workload and contamination risk.

Fields of applications



Environmental
microbiome research



Soil and agricultural
microbiology



Food and
water testing

Improve your workflow with EasySeq™

Request a **sample** or receive updates about the EasySeq™ ITS kit



Increase flow cell efficiency in fungal microbiome sequencing

Single Reaction NGS library prep that increases usable reads and lowers cost per sample

Data explanation

The EasySeq™ ITS workflow improves amplicon quality and increases the proportion of **usable sequencing reads**, enabling laboratories to extract more value from every sequencing run (Figure 1A).

Traditional ITS workflows often require a significant fraction of up to 40% of **PhiX non-informative reads**, reducing sequencing output (Figure 1B).

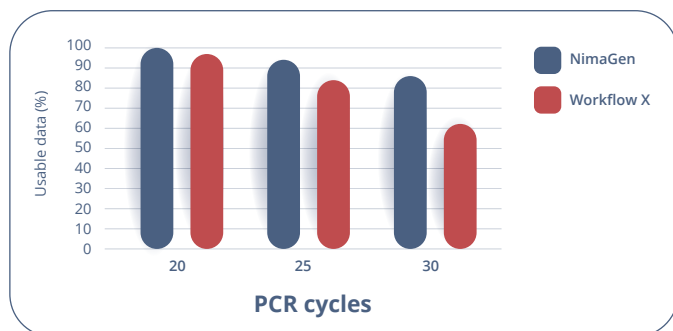


Figure 1A — Usable sequencing reads vs PCR cycles

Improved amplicon quality results in a higher percentage of usable sequencing reads compared to other workflows.

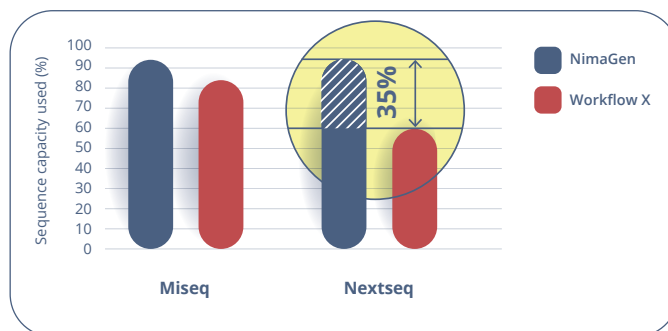


Figure 1B — Sequencing capacity utilization

Reduction in PhiX non-informative reads translates into improved flow cell utilization on sequencing platforms.

Efficiency gains per run

Typical microbiome sequencing workflow using a NextSeq 1000 P1 flow cell:

Metric	Standard workflow	EasySeq™ ITS
Samples per run*	~500	~900
Flowcell efficiency	baseline	+35%
Usable sequencing output	baseline	+10%

*100,000 usable reads per sample

Annual savings at scale

For a laboratory processing 20,000 samples per year:

- ✓ Standard workflow: 40 sequence runs
- ✓ EasySeq™ ITS: 23 sequence runs

Estimated saving on sequence reagents: **≈ €27,000 annually**

For large facilities processing 100,000 samples per year, savings can exceed: **≈ €140,000 annually**

(Indicative example based on typical reagent costs and sequencing throughput.)

Strategic benefit for core facilities

Higher sequencing efficiency means:

- ✓ Lower cost per sample
- ✓ Higher annual sequencing capacity
- ✓ More runs per instrument per year

See the difference in your own workflow

Scan the QR code to: Request a **sample** or receive updates about the EasySeq™ ITS kit.



NimaGen.

+31 (0)24 820 0241 info@nimagen.com www.nimagen.com

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