

EasySeq™ ITS Microbiome Library Prep Kit

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

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 hands-on time by >50% and decreases 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 Microbiome Library Prep 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 Microbiome 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).

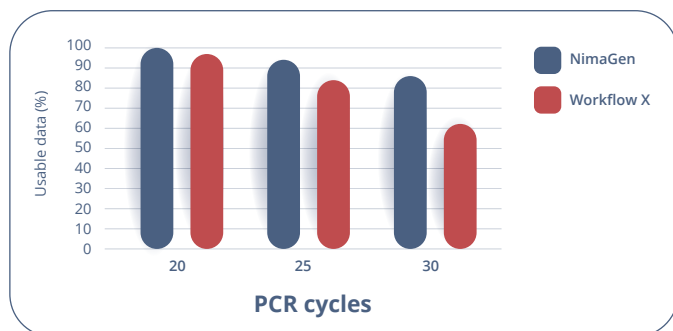


Figure 1A — Usable sequencing reads vs PCR cycles

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

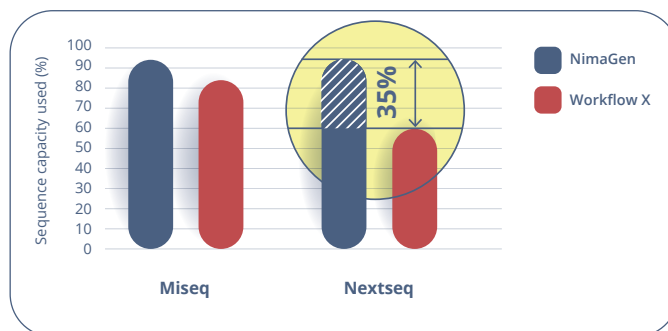


Figure 1B — Sequencing capacity utilization

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 Microbiome: 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 Microbiome labs

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 Microbiome kit.



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