iconPCR™:

Amplify. Quantify. Normalize. **All at Once.**

The world's first thermocycler with
individually **con**trolled wells and built-in AutoNorm™

The iconPCR Difference: AutoNorm & Workflow Revolution

AutoNorm: The Heart of iconPCR

- AutoNorm automates the most labor-intensive, error-prone part of NGS library prep.
- No more manual quantification, normalization, or guesswork.
- Every sample, no matter the input or quality, gets normalized automatically for consistent, high-quality sequencing.

Workflow Improvements:

- Cut the steps, keep the science
- The end of manual normalization
- Up to 50% less hands-on time
- 1 SPRI cleanup instead of 96 (for 96 samples)

Data Quality:

- Reject fewer samples
- Reliable results from a wider range of inputs
- Significantly reduced artifacts and amplification bias

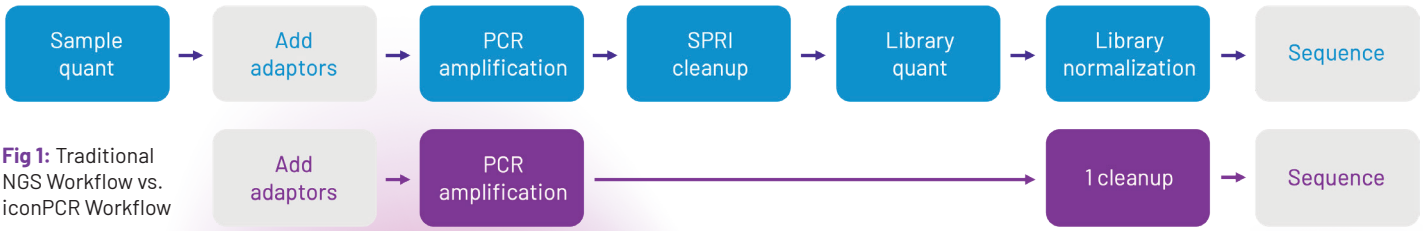

Fig 1: Traditional NGS Workflow vs. iconPCR Workflow

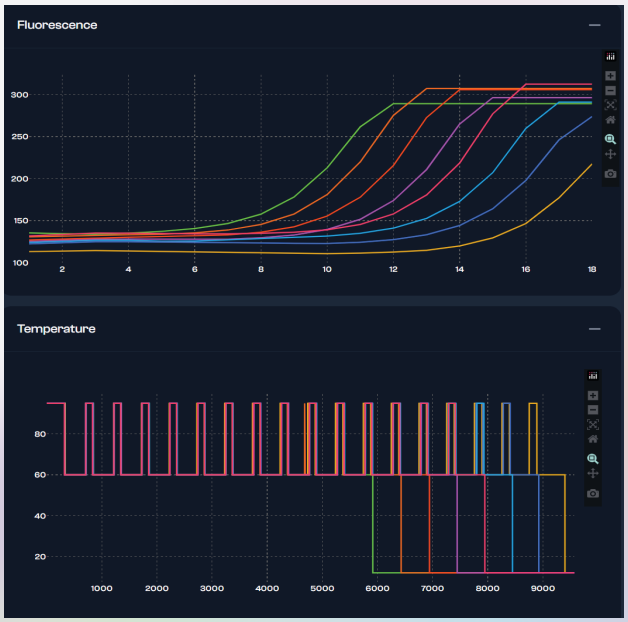

Fig 2: AutoNorm with iconPCR simplifies workflows and improves data quality. Users set a target amplification level, and each well stops cycling automatically once that level is reached. Shown is a dilution series of DNA libraries with fluorescence (top) and individual well temperatures (bottom) tracked in real time. High-concentration samples (green) reach the threshold first and enter a cold-hold phase, while lower-concentration wells continue cycling. Each sample stops precisely at the optimal point, with no manual intervention required.

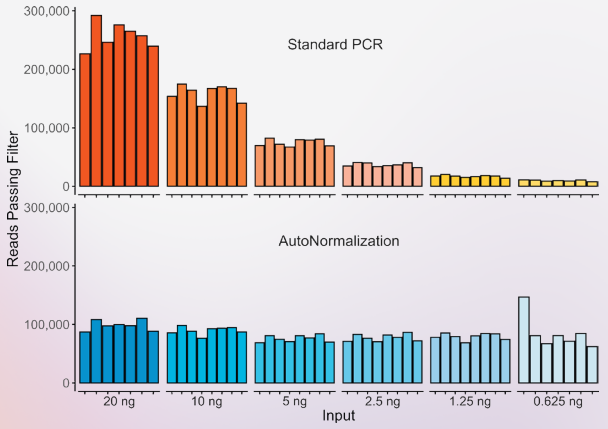

Fig 3: AutoNorm across different input DNA

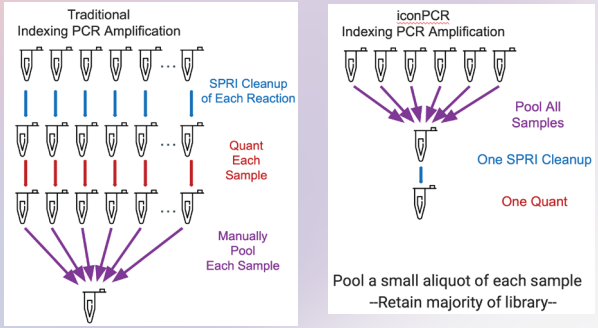

Fig 4: Traditional vs. iconPCR multiplex pooling

Real-World Impact: Application Spotlights

Metagenomics

Why iconPCR?

Manual normalization and pooling create errors, bias, and wasted time.

How it Works:

iconPCR auto-normalizes diverse samples, reduces chimeras, and streamlines pooling.

- 46% fewer chimeras in 16S libraries
- 2x increase in Shannon Diversity Index
- Over $15,000 saved in a 1,000-sample study

> **Support hundreds of diverse projects each month with 50% less hands-on time.**

Microbial Composition (Species)

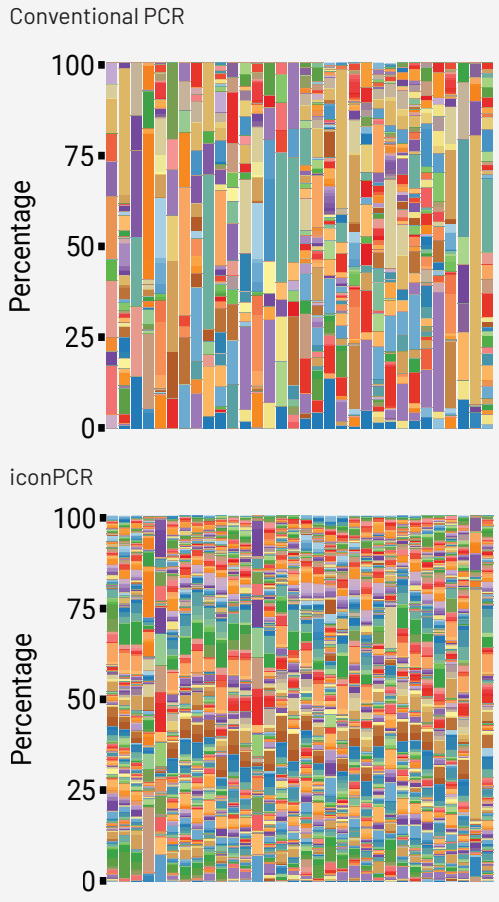

Fig. 5: Soil metagenomic samples using 1500 bp v9 16S amplicons sequenced using long read technology. Each color represents an independent species. iconPCR-generated libraries represent a much more accurate level of diversity by limiting the required amplification and prohibiting the over-amplification of high abundance species.

RNAseq with Degraded Samples (FFPE)

Why iconPCR?

Poor RNA quality and manual QC lead to high rejection rates and inconsistent data. Rescue low-quality samples without overamplifying others.

How it Works:

In-situ quantification and AutoNorm deliver high-quality libraries—even from 1 ng FFPE RNA.

- Reduced yield variability
- Consistent data quality metrics (no observed differences in QC metrics)
- 45-minute prep vs. 3+ hours

> **Streamline FFPE workflows, reduce failures and wasted sequencing, and rescue samples often lost with conventional PCR for more reliable results and consistent yields.**

Normalization of Degraded Samples

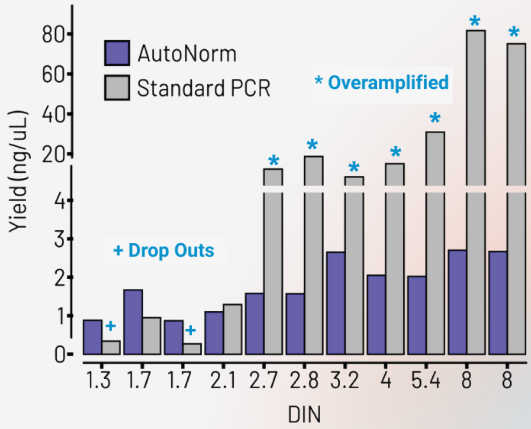

Fig 6: AutoNorm ensures consistent library yields from FFPE samples, regardless of DNA integrity. Samples spanning a wide range of DNA quality were processed using either a standard PCR workflow or iconPCR with AutoNorm. Standard PCR led to variable yields—high for intact DNA, low for degraded samples. In contrast, AutoNorm delivered uniform amplification across all samples. This eliminates the risk of over-amplifying high-quality DNA or under-amplifying poor-quality samples, enabling more reliable and streamlined NGS library prep from FFPE inputs.

Single-Cell RNA-Seq

Why iconPCR?

Bypass initial quantification and final normalization steps, producing high quality libraries with a much simpler workflow.

How it Works:

Precision normalization and closed-tube workflow ensure high cell capture and balanced libraries.

- Near perfect concordance with 10x Genomics controls
- 50% labor reduction

Simplified workflows, while maintaining the quality of the single-cell gene expression data.

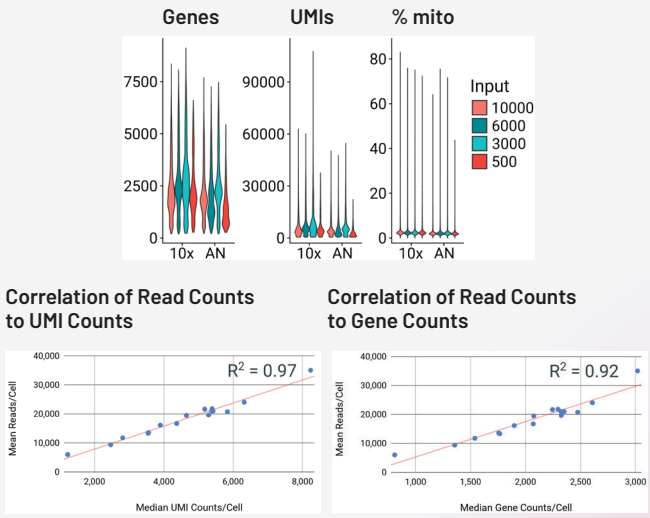

Fig. 7: AutoNormalized samples maintain the same quality as libraries prepared using the standard procedure. AutoNormalized libraries and libraries prepared using the standard protocol showed similar results in the number of genes and unique molecules (UMIs) detected, and did not change critical quality metrics such as the percent mitochondria (% mito). All samples showed a strong correlation between the mean reads per cell and both the median UMI counts per cell and median genes per cell, indicating that any difference in gene and UMI counts is due to differences in sequence depth between samples.

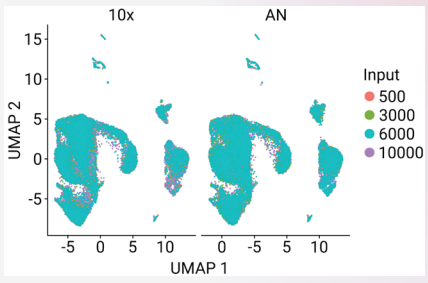

Fig. 8: Clustering of all samples reveals common gene signatures. Clustering of all 16 samples revealed no differences between the standard PCR method and AutoNorm, showcasing that the change in workflow does not negatively affect data quality.

Read Balancing

Why iconPCR?

Balancing sequencing pools is essential for efficient, cost-effective NGS. Traditional methods are error-prone and wasteful.

How it Works:

iconPCR's AutoNorm amplifies each sample to its ideal level in real time, enabling equal-volume pooling and consistent results.

- ±5% molarity accuracy (vs. ±25% manual)
- 98% first-pass success rate
- $1K+ cost savings per run

iconPCR ensures every sequencing pool is perfectly balanced—no more wasted reads, reruns, or surprises.

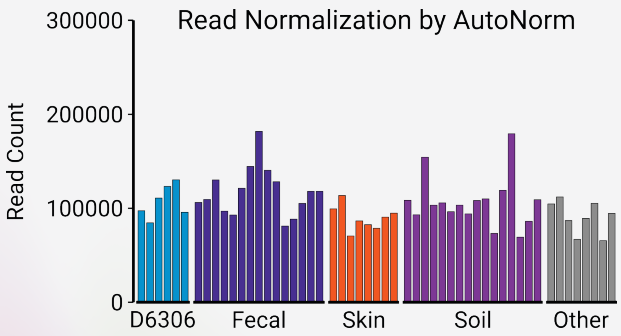

Fig. 9: Despite the differences in input amount and sample types, AutoNorm normalizes samples. A diverse range of samples, including controls (D6306), fecal, skin, and soil, were collected and used for 16S library preparation with AutoNorm. Following PCR, samples were pooled in an equal volume, cleaned, and sequenced. Shown are the numbers of reads passing filter for each sample. Despite the differences in input amount and sample types, AutoNorm was able to properly normalize the samples (CV = 23.4%).

Ready to Simplify Your Science? Contact Us:

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