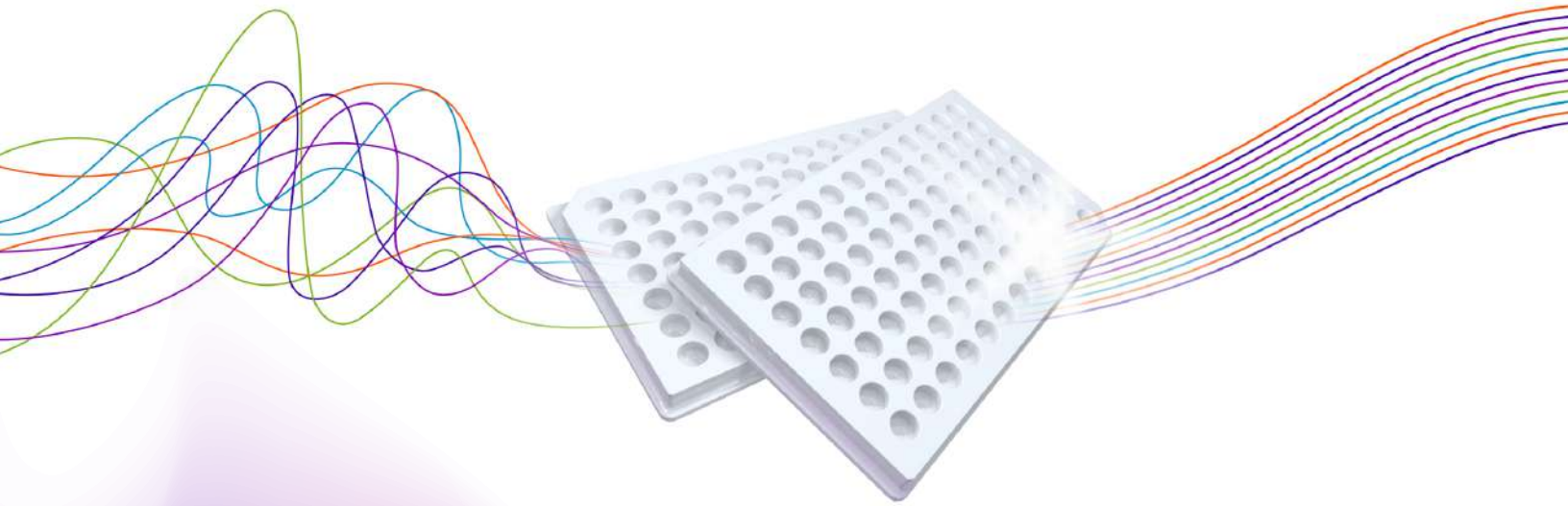


Bring amplification chaos into order.

The new standard for NGS library amplification.



icon96™



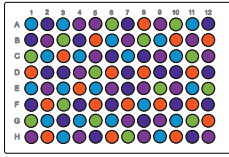
High throughput. High complexity.
No problem.

icon16™



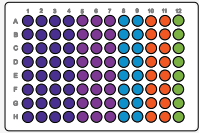
Small footprint. Small budget.
Big impact.

With **AutoNorm™** technology for adaptive amplification cycle control.



Samples vary by **concentration & quality**

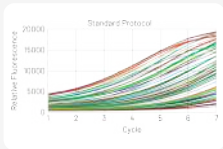
The **old** way



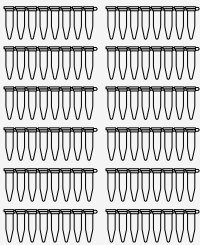
Quantify individually



Amplify using your best guess on cycles.



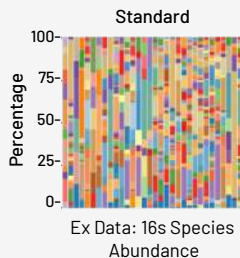
Under-cycled samples drop out. Over-cycled samples accumulate artifacts.



96 SPRI cleanups
96 quantifications
Pool & normalize

Outcome:

Unnecessarily deep sequencing, **lower** quality data (high **duplicates**)

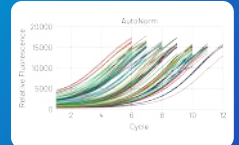


The **icon** way

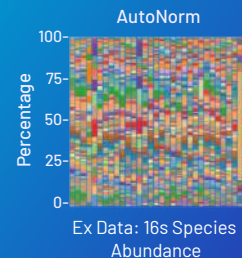
Choose your threshold. AutoNorm does the rest.



Each sample enters cold hold after ideal cycle number.



Pool
Single SPRI
Final Quant

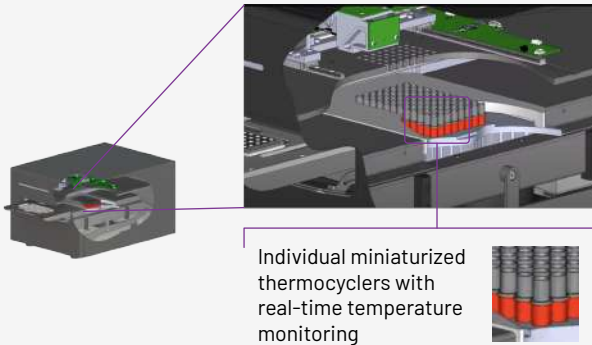


Outcome:

Efficient sequencing, **higher** quality data (more **diversity**)

From chaos to order

With the world's first real time thermocyclers with individually controlled wells



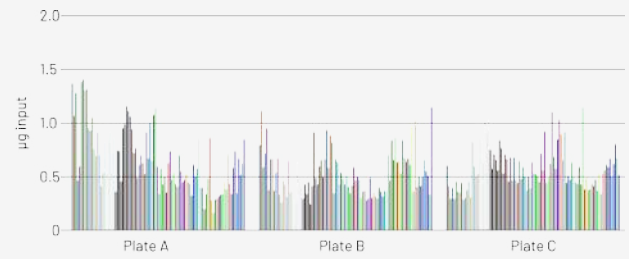
First, we built a better box, in 16 or 96-well format - Bringing the latest technology from semiconductor and telecom industry to genomics.

and adaptive amplification.

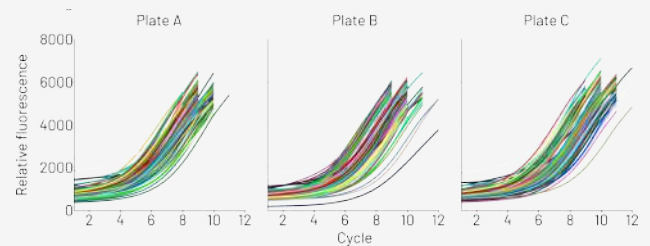


Then, we made it smart - AutoNorm technology monitors and stops cycling according to user-specified parameters.

RNA Input



Amplification Curves



Data generated by the HudsonAlpha Institute. Plant-derived RNA samples ranging from 0.5-1.5 micrograms were amplified with icon96. The stop cycle for each sample was dynamically selected using AutoNorm based on the slope of the amplification curve. This led to streamlined normalization, increased read alignment, and minimization of adapter dimer in the libraries, below 0.02%.

But wait...
there's **more...**

Universal Interoperability

Open chemistry, sequencing platform agnostic

Simplified Workflow

No individual normalization/quantification

Automation Ready

Full API package, standard plates/strips

Cost-saving

Save on labor and consumables

Cleaner, Better Data

Minimize dropout and artifacts

Certified Awesome

ISO 13485-compliant

icon technology is a must-have for virtually any sequencing application...

Single Cell

Whole Genomes

Spatial

RNAseq

Degraded/FFPE-extracted

Assay Development

16s Metagenomics

Genotyping

cfDNA/Liquid Biopsy

But don't just take our word for it



"This unique icon box allows us to differentially amplify these RNAs so that they're all identical. In other words, the input can be chaotic, but the output is perfect... The ultimate result to you is that we've achieved about a 30% reduction in the cost of generating this RNA-seq data for apple and pear biomarker projects."

Alex Harkess
Faculty Investigator at HudsonAlpha Institute for Biotechnology



"There are not many technologies that actually from the get-go can have a significant impact on established workflows. But with iconPCR technology we're able to really change the way you approach PCR or just in library prep in general."

James Docker
NGS Lead and Multi-Omics Sci., University of Oxford



"Redoing samples that drop out is costly...with iconPCR, you avoid that issue of sample dropout...If you're working with precious sample, knowing that you'll get enough library each time is also reassuring and a big benefit."

Eric Chow
Associate Professor at UCSF



"By incorporating iconPCR, we can remove several QC steps that are pretty expensive...Having the opportunity to do the normalization removes that cost as well."

Kerry Hair
Research Technologist at PennState Genomics Core Facility



"We are working with extremely low-input samples purified from ocean water. Our initial attempts to generate libraries using the manufacturer's standard protocols failed for roughly 95% of the samples; there was simply no library! After switching to the iconPCR instrument, the failure rate dropped to just 20%. iconPCR allowed us to run the optimal number of amplification cycles without any trial and error—something we could not have determined on our own, especially given the limited sample available for testing."

Kristen Jepsen
Director of IGM Genomics Center, UCSD



"We really do think this is an instrument that every Genomics Core should want to have...PCR is your enemy, and this is your best weapon against running too many PCR cycles, and I think we'll just see improved data quality coming out of reducing the number of PCR cycles before you go into sequencing."

Stefan Green
Associate Professor at Rush University



"iconPCR is key to improving our NGS workflows – eliminating QC and normalization while preventing over-amplification."

Anja Mezger
Head of Unit, National Genomics Infrastructure, SciLifeLab Sweden



Euroclone Spa
Via Figino 20/22 20016 Pero (MI), ITALY
Ph. +39 02.38195 - Fax +39 02.3391373
info@euroclone.it - www.euroclone.it

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