iconPCR for challenging sample types

Goals

- Unravel cancer evolution
- Detect early-stage cancer
- Find drug targets
- Predict treatment response
- Monitor MRD
- Characterize tumor microenvironment
- Improve early detection/risk stratification
- Accelerate biomarker discovery
- Understand cancer heterogeneity
- Elucidate therapy resistance mechanisms

Starting with

ctDNA/cfDNA

Single cells (CTCs, scRNA-seq)

Whole genomes

Tumor tissue (FFPE)/patient models

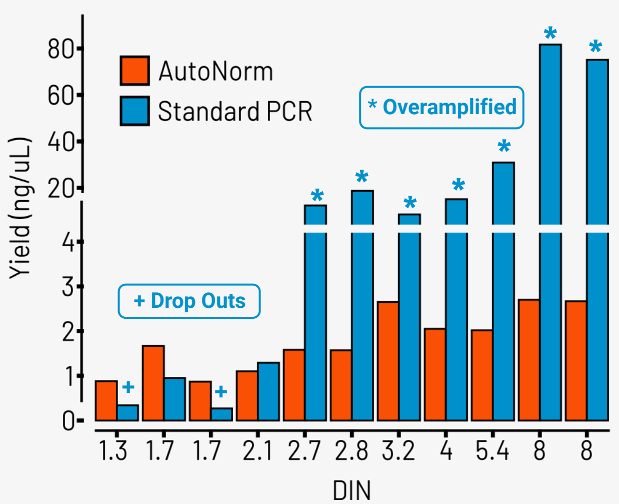
Tumor biopsies

Pain Points

- Low input or degraded samples
- Lab-to-lab or tech-to-tech variability
- Bias or missed variants do to over- or under-amplification
- PCR or sequencing errors introduce false positives/negatives
- Contamination risks
- High data noise complicates variant interpretation
- Workflow bottlenecks slow turnaround and increase costs

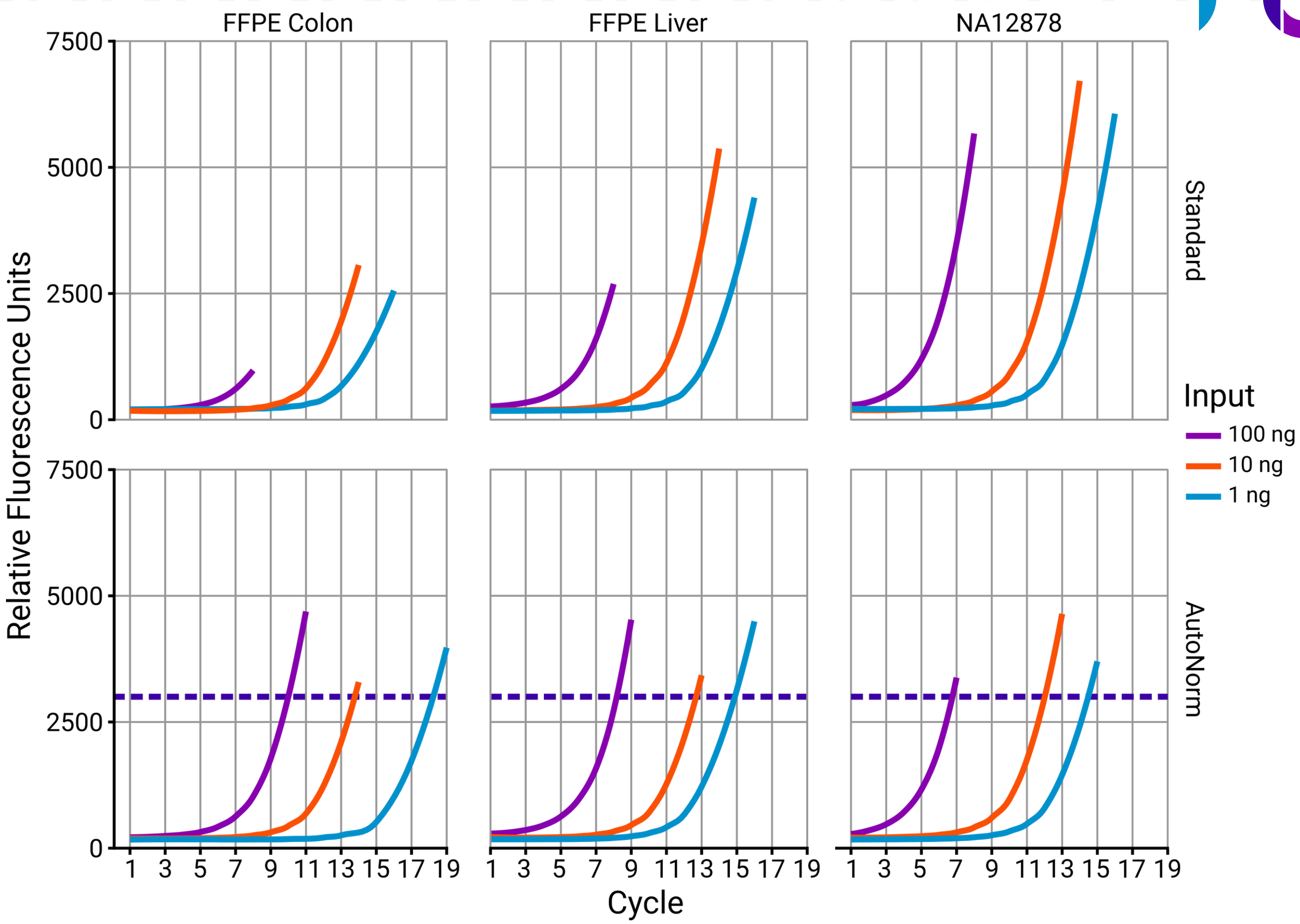
iCON PCR

Normalization of Degraded Samples

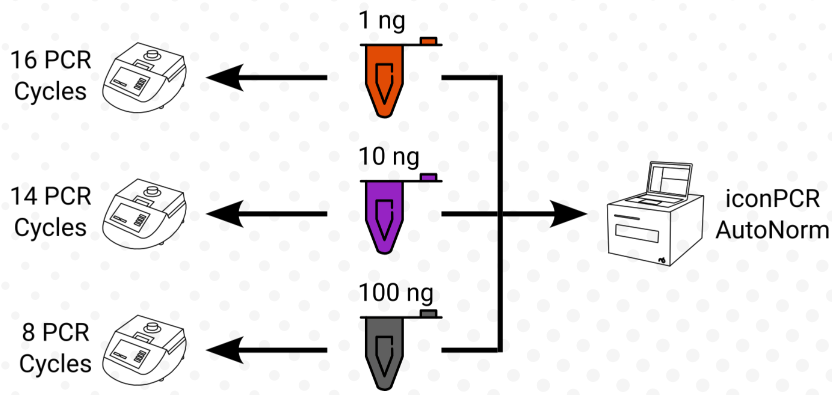


n6 and iconPCR provide solutions for processing and amplifying nucleic acids from degraded or low-quality samples

iconPCR for challenging sample types



Maximize your RNA-Seq and WGS data quality—even from degraded or low-input samples.



Streamlined workflows and reduced hands-on time free researchers to focus on discovery.

Turn challenging samples into actionable cancer research data.

EuroClone®
serving science through innovation
Euroclone SpA
Via Figino, 20/22 - 20016 Pero (MI) Italy
Ph. +39 02 38195.1 - Fax +39 023391373
info@euroclone.it - www.euroclone.it

Download the FFPE App Notes here

n6tec.com