

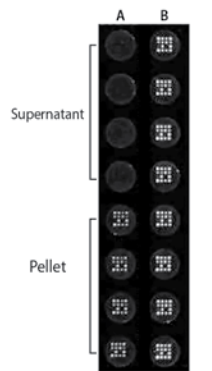
FFPE Tissue in the qNPA™ ArrayPlate System

FFPE TISSUE • GENE EXPRESSION

Gene expression analysis of FFPE tissue is this easy

With its simple sample preparation and novel approach for producing reliable, unbiased results from fragmented and cross-linked RNA, the **qNPA™ ArrayPlate System*** will unlock decades of gene expression data from archived tissue samples. No complicated purification schemes, no artifacts from amplification, just reliable gene expression data – **problem solved.**

- **Same-well, 47 gene multiplexing**—analyze gene profiles and save precious samples
- **20% data resolution**—detect small yet, biologically relevant changes
- **Scalable and flexible format**—test from a few dozen to thousands of samples per day
- **Save precious samples**—use a 1 cm square portion of a 5 µm thick tissue section



A. FFPE Tissue
B. Frozen Tissue Control

Matched samples of FFPE (A) and fresh frozen tissue controls (B) were run on the qNPA™ ArrayPlate. As with other techniques, the supernatant from FFPE samples contained little soluble RNA. Unlike other technologies, qNPA™ can analyze insoluble RNA cross-linked in the tissue pellet, saving time, money, and precious samples.



No More RNA Extraction.
No More cDNA Synthesis.
No More RNA Labeling.
No More RNA Amplification.
No More Wasted Samples.

An easy solution that works—

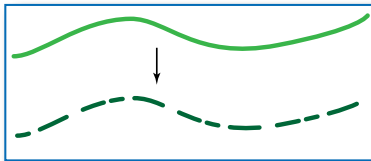
- 1. Scrape the fixed tissue off the slide.**
- 2. Place into a tube with Lysis Buffer.**
- 3. Incubate for 10 minutes.**

The qNPA™ Solution to Common FFPE Problems

FFPE TISSUE • GENE EXPRESSION

qNPA™ Technology is uniquely suited to produce robust gene expression results from formalin-fixed and paraffin embedded (FFPE) and other fixed tissues where RNA quality may be compromised. These samples typically yield poor gene expression results due to RNA cross-linking and fragmentation. Due to the inaccessibility of the RNA, significant time and resources were required to prepare the samples, but with qNPA it is no longer a problem.

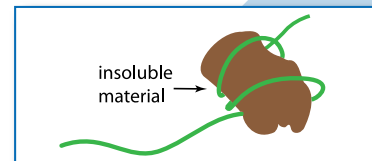
Damaged or fragmented RNA



Problem: Fragmented RNA causes small, incomplete cDNA transcripts to be formed. Most techniques will also suffer from a strong 3' bias in the data analysis results.

qNPA Solution: qNPA does not require cDNA synthesis, and the qNPA oligonucleotides can be arranged throughout the transcript. If the RNA fragments are over ~100 bases in length, qNPA is unaffected by RNA fragmentation.

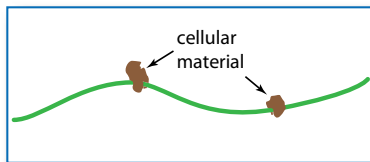
Soluble RNA with cellular material linked to it



Problem: Reverse transcriptase polymerases often cannot proceed due to physical blocking of the elongation process. This results in short, incomplete cDNAs.

qNPA Solution: As with degraded RNA, 'dirty' RNA with small amounts of cellular material attached to it can be measured thanks to multiple probe placements throughout the transcript.

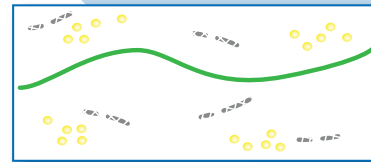
RNA bound to insoluble cellular material/ low amounts of soluble RNA available for extraction



Problem: Much of the RNA in fixed tissue samples is bound to large pieces of cellular debris preventing it from being soluble and available for purification. Large amounts of precious FFPE tissues are wasted.

qNPA Solution: qNPA does not use an RNA extraction prior to analysis. The qNPA oligos can enter cellular debris complexes, be protected by non-soluble, cross-linked RNA from S1 nuclease digestion, and collected for measurement on the ArrayPlate platform. Less sample is needed; none is wasted.

Contaminants and inhibitors in the 'purified' RNA



Problem: Common contaminants such as paraffin, melanin, and polysaccharides are often carried-over in RNA extraction techniques. These contaminants will inhibit polymerases and cause poor results.

qNPA Solution: The qNPA process effectively removes any paraffin in a sample with an oil-overlay step. The technology does not use polymerases or other enzymes which may be inhibited by polysaccharides or melanin.