



CASE STUDY: Revitalizing Archived IHC Slides to Unlock New Quantitative Insight

Executive Summary

HistoSpring worked with a research team to re-analyze archived p53 immunohistochemistry (IHC) slides originally generated in 2007. Using high-resolution whole-slide scanning and HALO® AI-driven image analysis, semi-quantitative visual scoring was transformed into objective, quantitative data—revealing stronger biological trends that expanded the study's value without repeating the original experiments.

The Client

A research group interested in studying p53 expression in human breast tissue and how reproductive history influences responses to oxidative stress and ionizing radiation.

The Challenge

The original study relied on blinded reviewers using semi-quantitative scoring methods based on staining intensity and percent positivity. While this method captured overall trends, it offered limited dynamic range, introduced reviewer-to-reviewer variability, and made it difficult to detect subtle but biologically meaningful differences. Nearly a decade after the slides were generated, the research team revisited the archived samples to determine whether the observed differences in p53 expression reflected true biological variation—or were simply a limitation of the scoring method—despite the dataset not being easily re-evaluated using traditional approaches.

The Solution

To address this challenge, HistoSpring digitized the archived slides and applied HALO® AI-based image analysis to re-evaluate the dataset using a standardized, quantitative approach. Staining was quantified using H-scores, which integrate staining intensity and percent positivity, enabling a more sensitive and reproducible assessment of protein expression. By applying consistent parameters across all samples, this approach eliminated subjective scoring variability and allowed the dataset to be re-examined despite the limitations of traditional methods.

The Results

Digital re-analysis revealed clearer, more reliable biological trends. The expanded dynamic range of H-scores (2.9–194.5 vs. 3–5 with visual scoring) enabled detection of differences that were previously difficult to resolve. p53 expression increased following explant culture across all donors, with further induction after ionizing radiation in most cases. This quantitative approach provided consistent, objective data, confirming that the observed differences reflected true biological variation—unlocking new insights to archived slides.