

NUCLEOSOMICS®- TRANSLATING EPIGENETIC BIOMARKERS INTO CLINICAL DIAGNOSTICS

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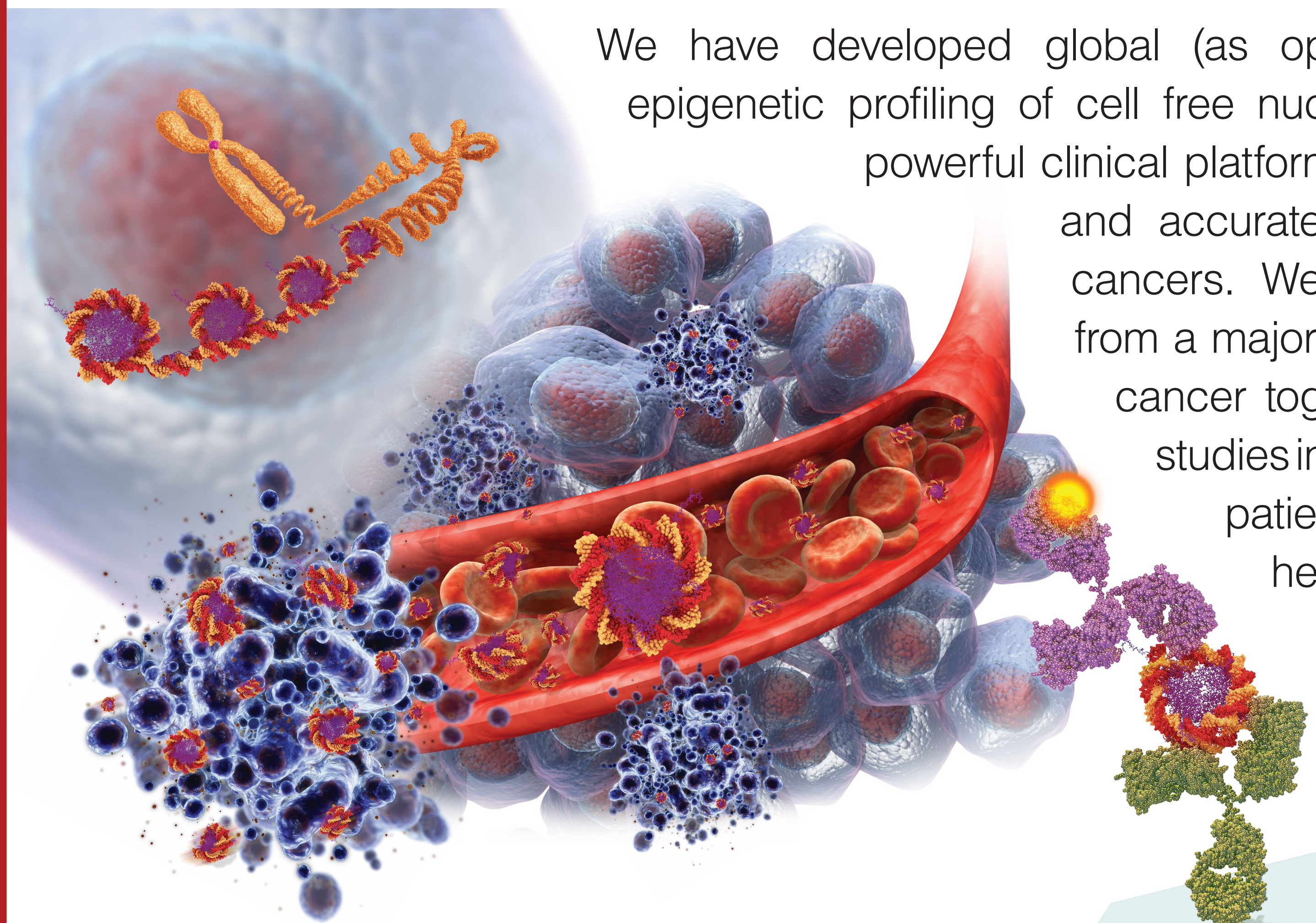
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METHODOLOGY

Nucleosomics® combines cutting edge epigenetic profiling with a simple, low cost immunoassay technology to improve clinical diagnosis of cancer.

Immunohistochemistry studies show genome-wide epigenetic changes in cancer tissue and have identified histo-oncoproteins - histone modifications linked to cancer. In addition, nucleosomes (147 base pair DNA sequences wrapped around four pairs of histone proteins) are released as chromatin fragments on cell death. Total levels of cell free nucleosomes can be elevated by inflammation, infectious disease and cancer, limiting diagnostic utility. However, circulating cell-free, nucleosome bound DNA fragments contain mutations found in cancer tissue from the same patients suggesting a tumor chromatin origin for, at least some, circulating nucleosomes. Profiling of global levels of epigenetic modifications in nucleosomes can provide disease specific diagnostic information.

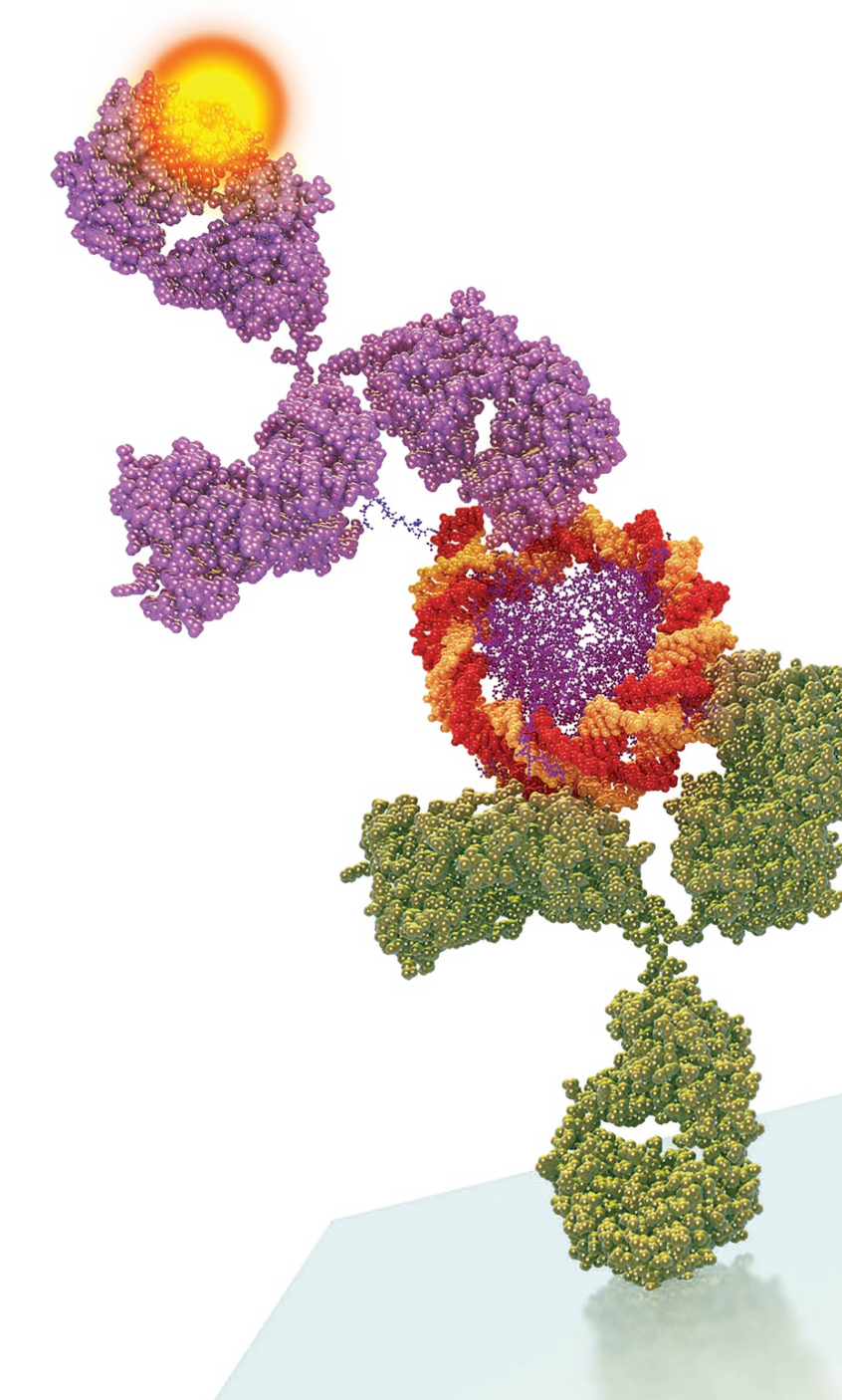


We have developed global (as opposed to gene specific) epigenetic profiling of cell free nucleosomes as a potentially powerful clinical platform for accessible, affordable and accurate diagnosis of a range of cancers. We present preliminary data from a major validation trial in colorectal cancer together with a series of pilot studies in pancreatic and lung cancer patients vs. benign disease and healthy controls.

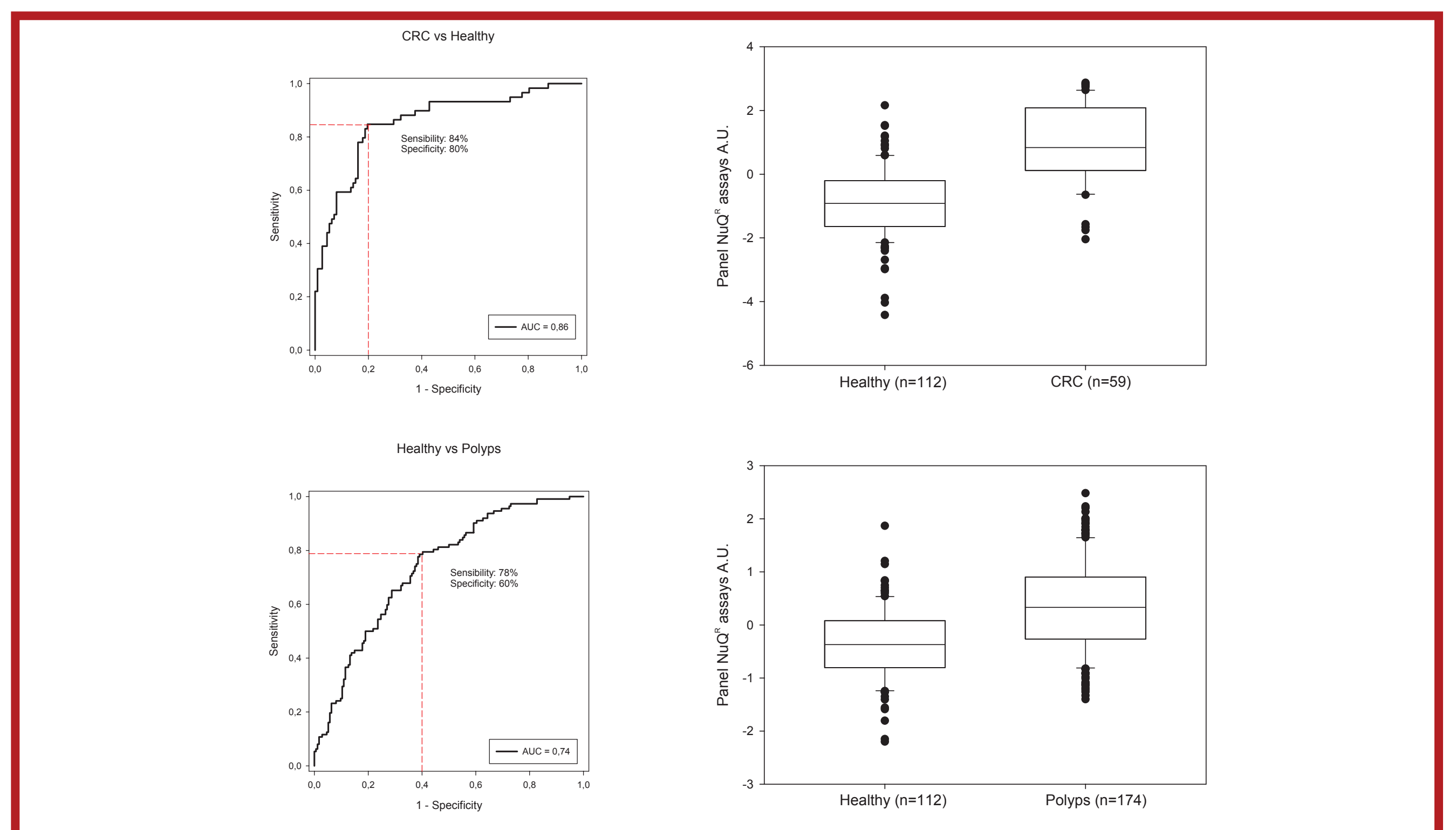
FIVE ASSAY FAMILIES

Five assay families, with multiple assays: hundreds of possible panel combinations

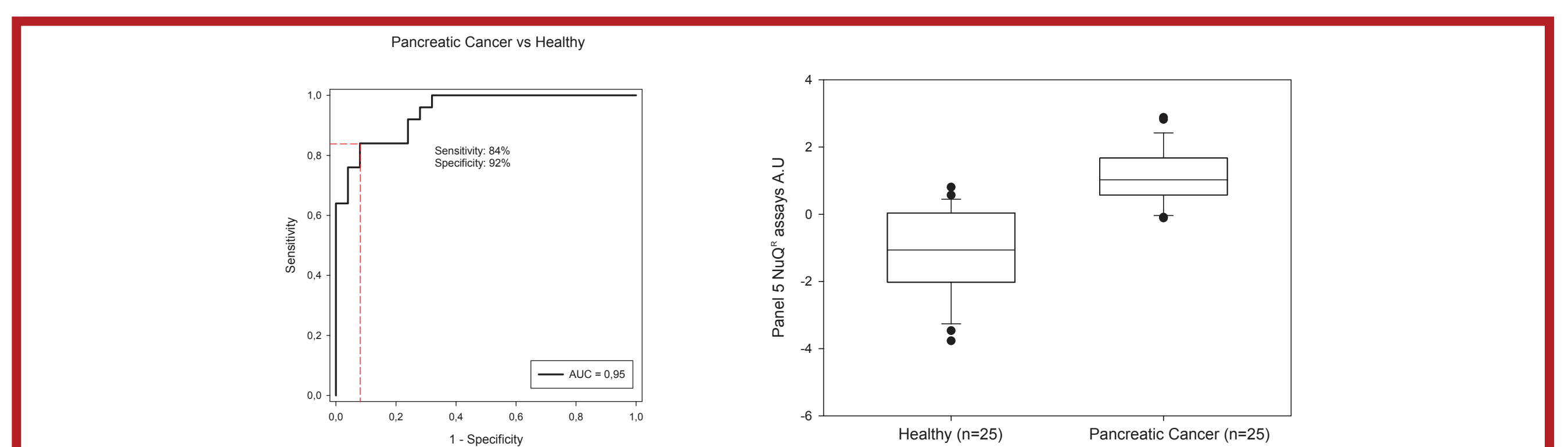
- NuQ®-X specific DNA modifications
- NuQ®-V histone variants
- NuQ®-M histone modifications
- NuQ®-A nucleosome-protein adducts
- NuQ®-T total nucleosomes



COLORECTAL CANCER



PANCREATIC CANCER



LUNG CANCER

