# **Nucleosome changes associated with Cancer and NETosis related** diseases



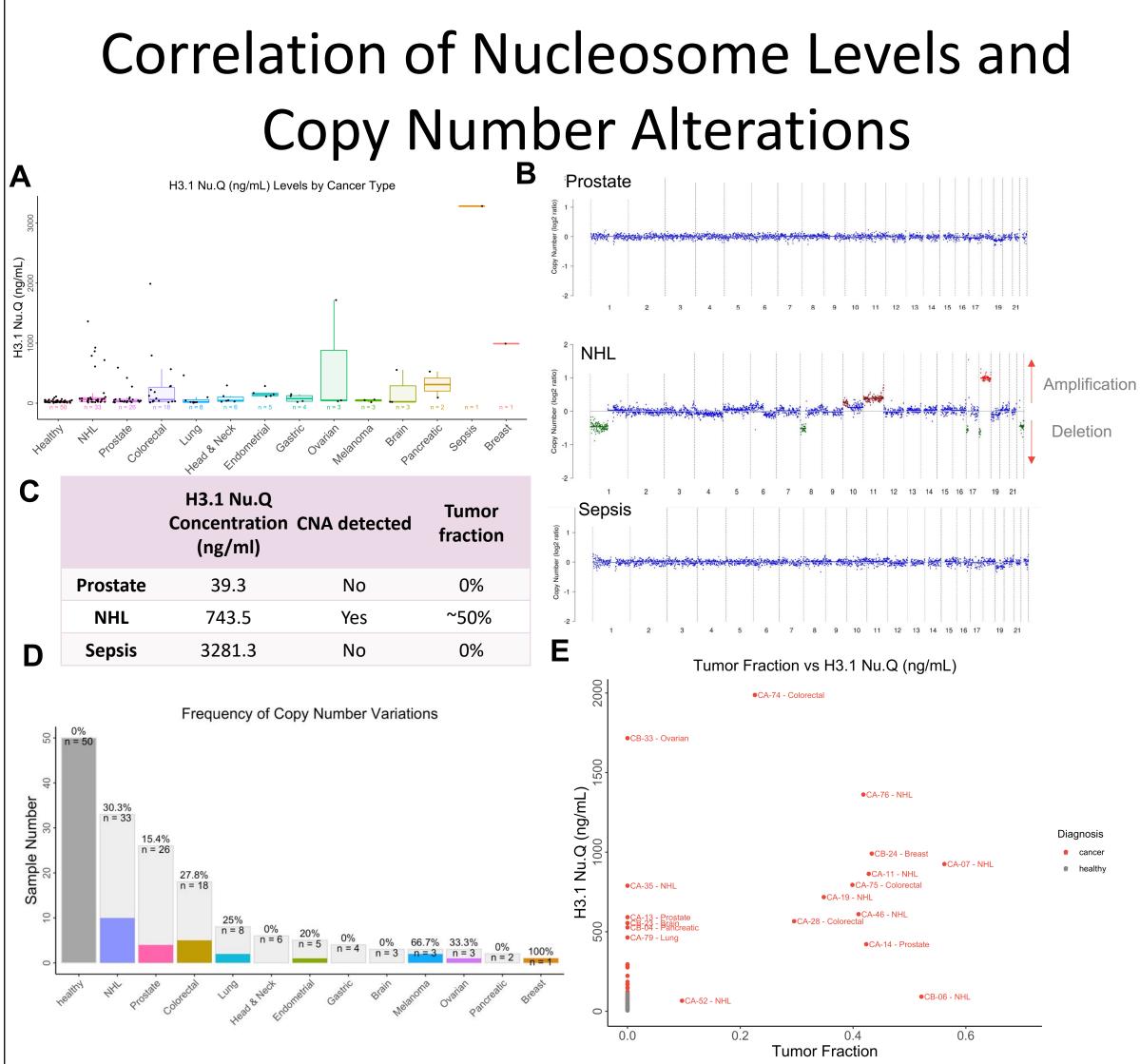
Volition

Theresa K Kelly<sup>1</sup>, Sarah Erdman<sup>1</sup>, Kieran Zukas<sup>1</sup>, Justin Cayford<sup>1</sup>, Mark Eccleston<sup>1</sup> <sup>1</sup>Volition America, 6086 Corte Del Cedro Carlsbad, CA 92011

### Introduction

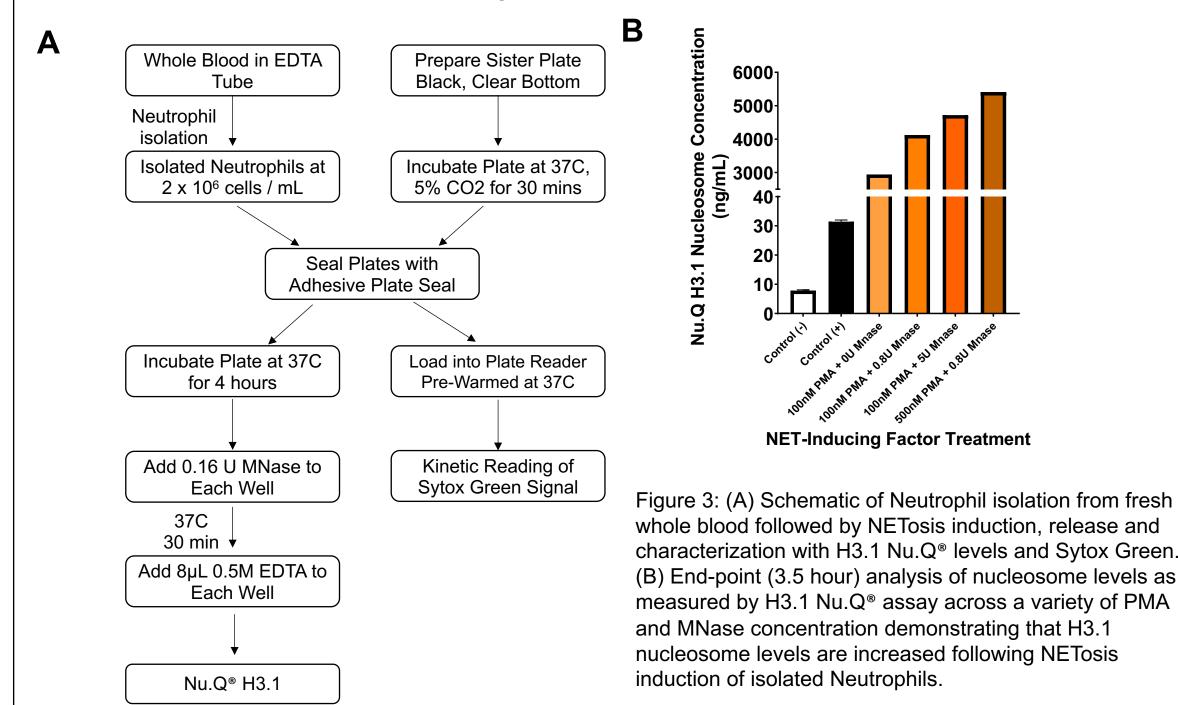
- Nucleosomes are the repeating unit of chromatin
- Chromatin becomes decondensed in Cancer and NETosis related diseases resulting in nucleosomes being released into circulation as cell free (cfDNA)
- Nucleosome levels are elevated in patients with a variety of Cancers as well as COVID and Sepsis

#### Results



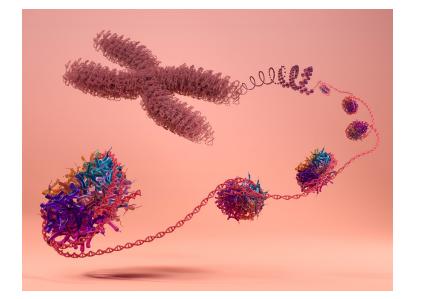
#### Results

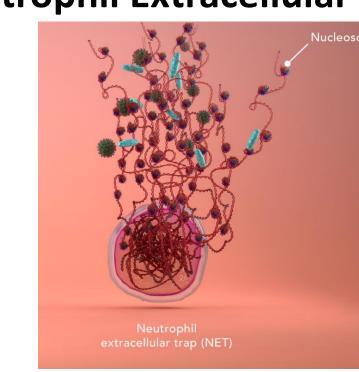
**Isolated Neutrophil NETosis Induction** 



- Nucleosomes contain important information about the cells from which they were derived
- Nucleosome modifications associated with Cancer have been studied for decades, but there is relatively less known about the nucleosome changes associated with NETosis and Sepsis

**NETosis** Cancer Neutrophil Extracellular Traps **Chromatin Decondensation** 

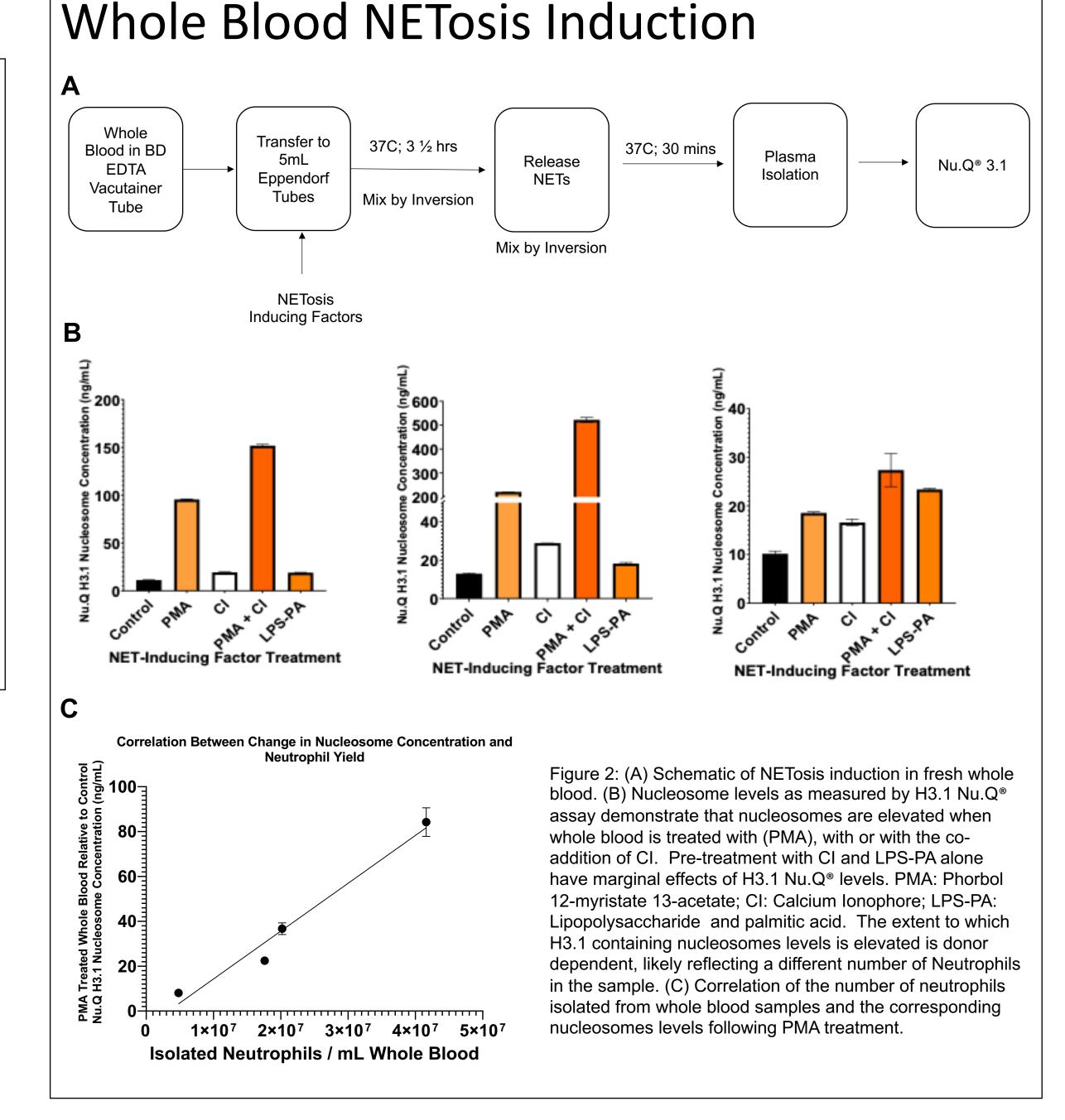


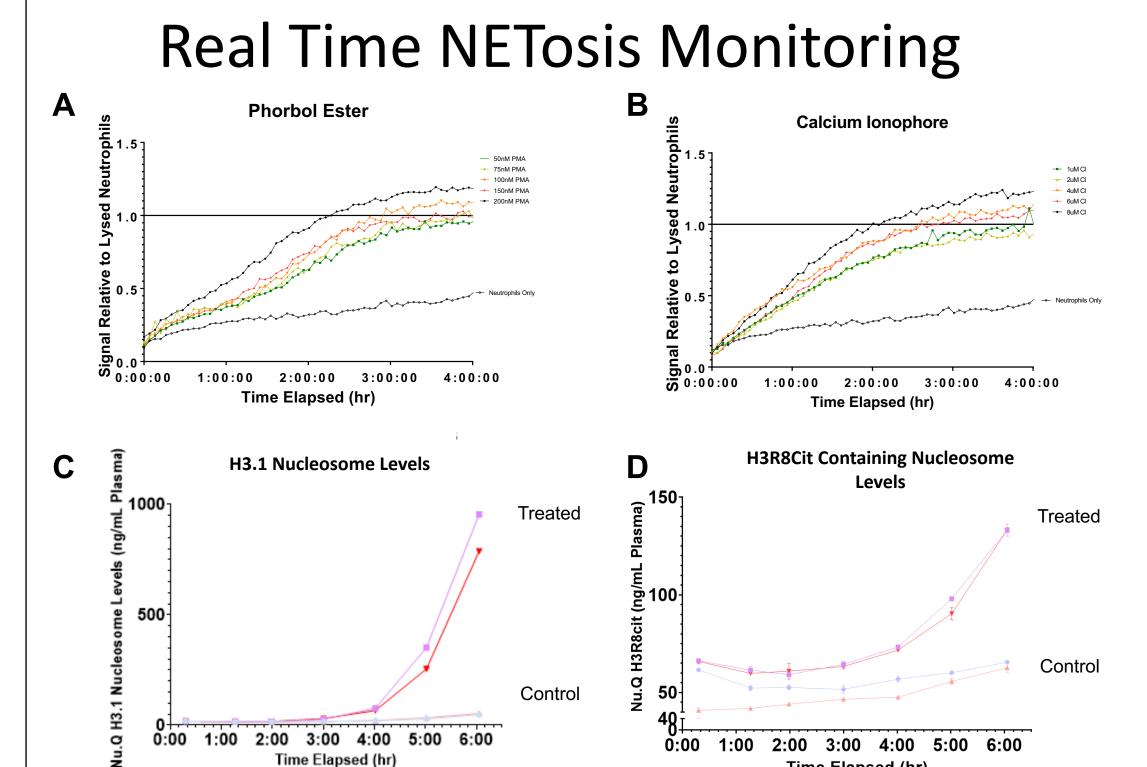


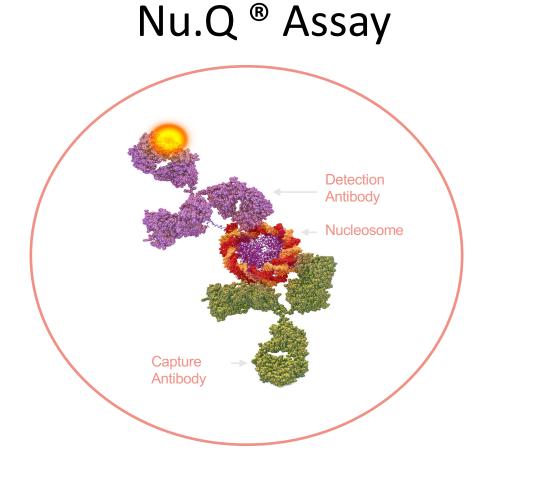
### Methods

- Nucleosomes were measured using Volition's H3.1 Nu.Q<sup>®</sup> Assay
- Neutrophils were isolated using MACSxpress<sup>®</sup> Whole Blood Neutrophil Isolation Kit • 100 bp paired end sequencing was performed (Illumina) • Copy Number Analysis (CNA) was done using iChor CNA and default settings (https://github.com/broadinstitute/ichorCNA) • Real-time Netosis was measured buy inclusion of Sytox green and continual fluorescent measurements using a SpectraMax plate reader

Figure 1: (A) H3.1 containing nucleosomes are elevated in some but not all cancer samples as well as in sepsis. (B) iChor CNA shows genomic amplifications and deletions across the genome in plasma from a non-Hodgkin's lymphoma patient, but not a prostate cancer or sepsis sample. (C) Representative samples and the corresponding nucleosome level and CNA and tumor fraction characterization. Nucleosome levels are correlated with copy number alterations in cancer but not sepsis. (D) Number of samples characterized and percentage that contained copy numbers alterations using default iChor CNA settings. (E) Correlation of Nucleosome level, measured using H3.1 Nu.Q<sup>®</sup> assay, and tumor fraction, as assessed by iChorCNA across a variety of healthy and cancer samples.







Next Generation Sequencing

Figure 4: Time course of NET release in response to Phorbol Ester (A) and Calcium Ionophore (B) as measured by fluorescence from Sytox green intercalation normalized to total DNA content. Time course of H3.1 (C) and H3R8 Citrulline (D) nucleosome levels during NET release.

## **Summary & Conclusions**

- H3.1 containing nucleosome levels and the presence of copy number alterations vary across cancer types and samples
- Elevated Nu.Q<sup>®</sup> levels correlate with copy number alterations for cancer but not sepsis samples
- NETosis can be chemically induced in whole blood and isolated neutrophils
- Nucleosome and H3R8 Citrullination levels increase during NETosis
- These models can be used to understand the underlying signaling cascades and chromatin mechanisms underlying NETs release







