

Enrichment tools to better understand the types of circulating nucleosomes and their genome patterns in the plasma of dogs with lymphoma



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Introduction

- ❖ Nucleosomes = most basic structural components of DNA
- ❖ Methods by which circulating nucleosomes are produced
 - ❖ Dying/activated WBCs
 - ❖ Apoptotic cells
 - ❖ Tumor cell secretion
- ❖ Elevated nucleosome levels in sepsis, severe burns, immune-mediated diseases, cancer
- ❖ H3.1 ELISA validated for measurement of nucleosome levels in canine lymphoma (LSA) patients
- ❖ H1 Nu.Q[®] Capture

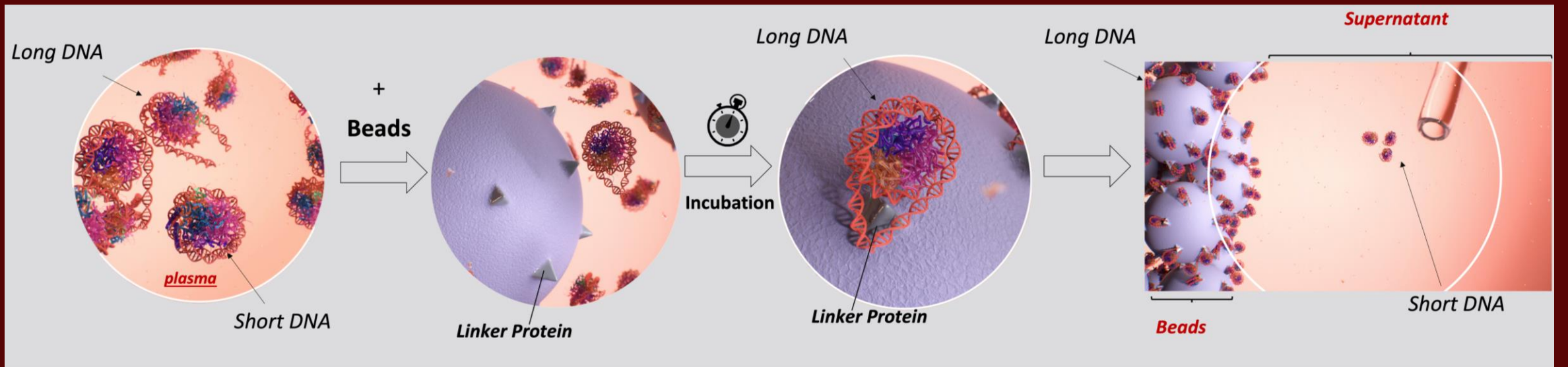
AIM: To isolate and sequence cancer-derived nucleosomes from dogs diagnosed with LSA

Methods

Sample Collection



Nu.Q[®] Capture



Methods (cont.)

Whole genome sequencing

- ❖ Illumina 2x150bp
- ❖ Average Depth 40x

Align to CanFam4

- ❖ Bwa-mem2

Variant calling

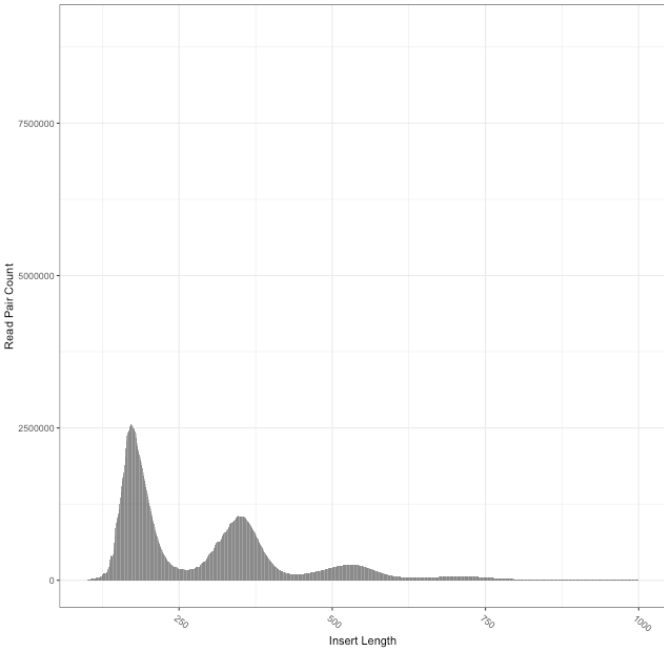
- ❖ GATK 4.1.10
- ❖ HaplotypeCaller
- ❖ Mutect2

Variant annotation

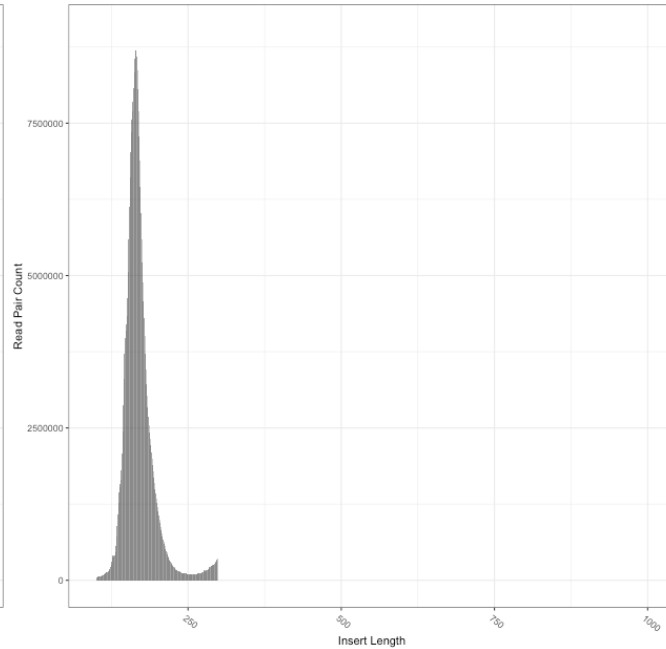
- ❖ SNPeff



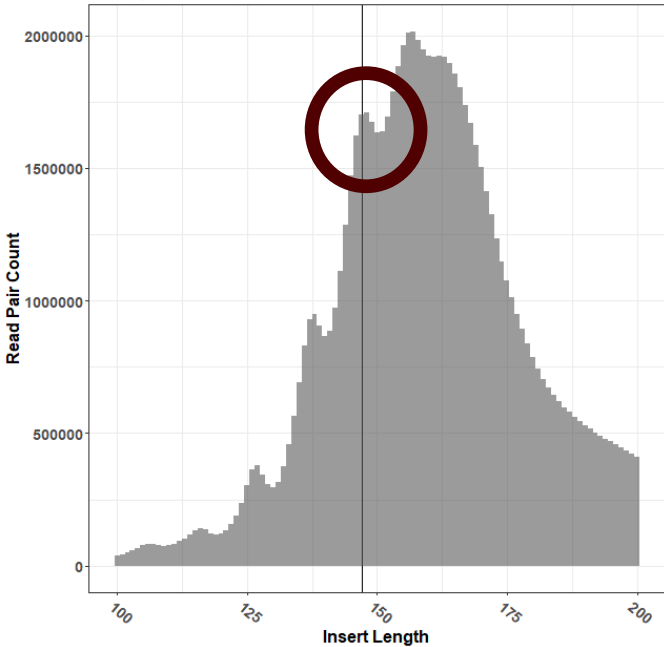
10016 (Lymphoma Case) Precipitate Fraction



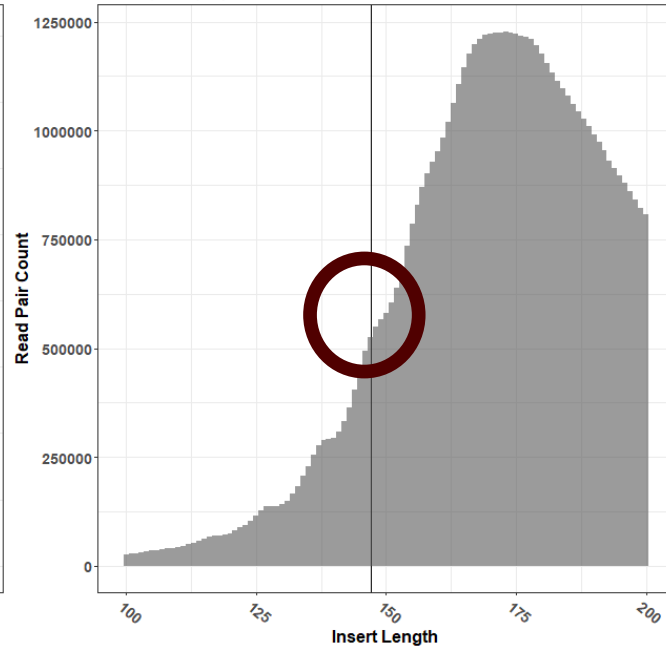
10016 (Lymphoma Case) Supernatant Fraction



60010 (Lymphoma Case) Supernatant Fraction



Chester (Control) Supernatant Fraction



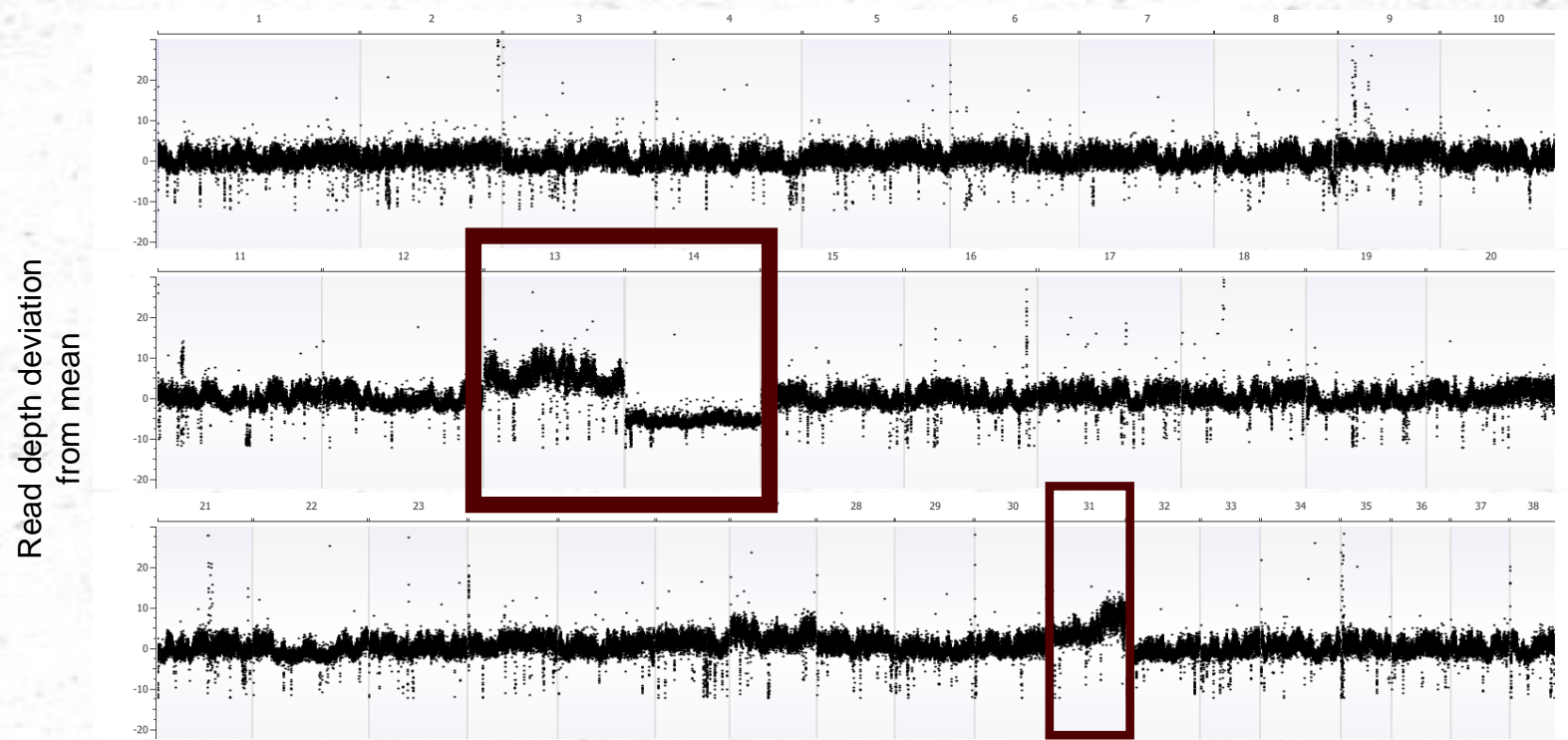
Results

Patient ID	Nucleosome Content (ng/mL)
Chester (c)	24.4
LSA (10016)	>2500
LSA (60010)	>2500

Figure 1: Plasma-derived nucleosome sequencing histograms. A: Sequencing histogram of lymphoma patient 10016 immunoprecipitated. B: Sequencing histogram of lymphoma-patient 10016 supernatant. C: Sequencing histogram of supernatant fraction highlighting enrichment of 147bp insert size. D: Sequencing histogram of control (healthy) patient supernatant fraction lacking the peak at 147bp.

Figure 2: Aneuploidy and copy number variation.

Depicting gain of chromosome 13, loss of chromosome 14, and potential gain of the q arm of chromosome 31 (highlighted panels). Other potential copy number variants exist across chromosomes.



Conclusions

- ❖ Canine lymphoma patients have circulating nucleosomes lacking linker DNA (i.e., shorter nucleosomes) that are not detected in plasma from healthy canines.
- ❖ The Nu.Q® Capture is capable of enriching canine cancer-associated nucleosomes in plasma of naïve multicentric lymphoma patients.
- ❖ These shorter, canine lymphoma-associated, nucleosomes demonstrate rare genetic variants, most notably gain of chromosome 13, loss of chromosome 14, and potential aberrations on chromosome 31.

References

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Future Directions

- ❖ Optimize Nu.Q® Capture assay for enhanced cancer-associated nucleosome enrichment.
- ❖ Deeper analysis of candidate genes and known drivers of canine lymphoma with the goal of identifying diagnostic and prognostic markers in a wider variety of lymphoma cases.
- ❖ Expansion of the Nu.Q® methodology and sequencing pipelines utilized in this study to additional canine cancers, including hemangiosarcoma and osteosarcoma.
- ❖ Combine H1 Nu.Q® Capture with additional assays to better understand cancer derived circulating nucleosomes

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