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Physical isolation of tumor associated ctDNA fragments for novel prostate cancer liquid biopsy

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First report of ChIP of transcription factor associated ctDNA from plasma

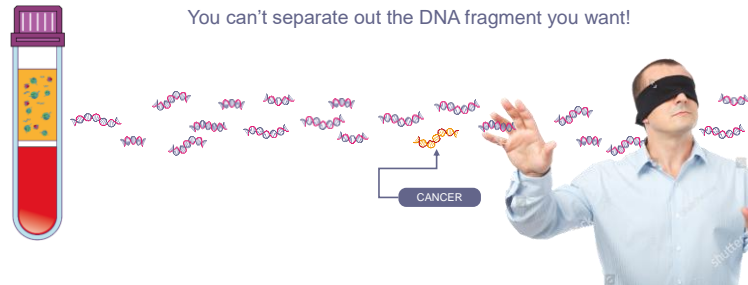
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Why?

- NGS ctDNA methods identify whether any cfDNA in a plasma sample is of tumor origin
- If separate out pure, tumor derived DNA – no need to sequence!
- Isolate pure tumor origin ctDNA from all background DNA in the plasma of same sequences
- Rapid, low cost liquid biopsy (no library prep, no NGS, no bioinformatics)

How?

- CTCF has some 70,000 specific binding sites in human genome
- Around half occupied in any cell type. Other sites are nucleosome covered
- Cancer associated CTCF gain (and loss) of occupancy is a hallmark of cancer
- CTCF ChIP/PCR of gain of occupancy sites identifies cancer in a plasma sample – **THIS WORKS**



Results in prostate cancer

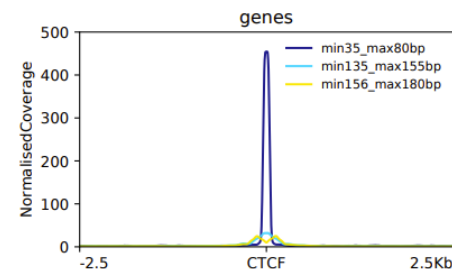
AML Cancer Model

- POC using PCR targets derived from AML cancer model
 - 61% of AML cases positive at 98% specificity
 - 50% of PCa cases positive at 98% specificity
 - 70% of PCa cases positive at 90% specificity

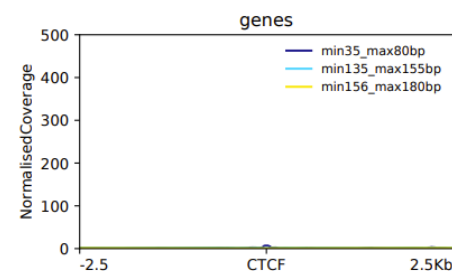
PCa Cancer Model

- All nucleosomes removed
- 30-80bp ctDNA fragments
- Binding site in center of all fragments
- 300 CTCF binding site sequences present in plasma of PCa patients but absent control plasma
- 300 candidate PCR targets for PCa
- Expect improved accuracy for PCa over POC results using AML derived target sequences
- Expect some disease specific PCa target sequences

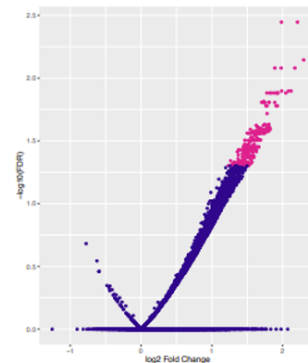
Anti-CTCF



Mouse IgG



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300 CTCF sites selected occupied in PCa
False Discovery Rate < 0.05, a p-value < 0.05