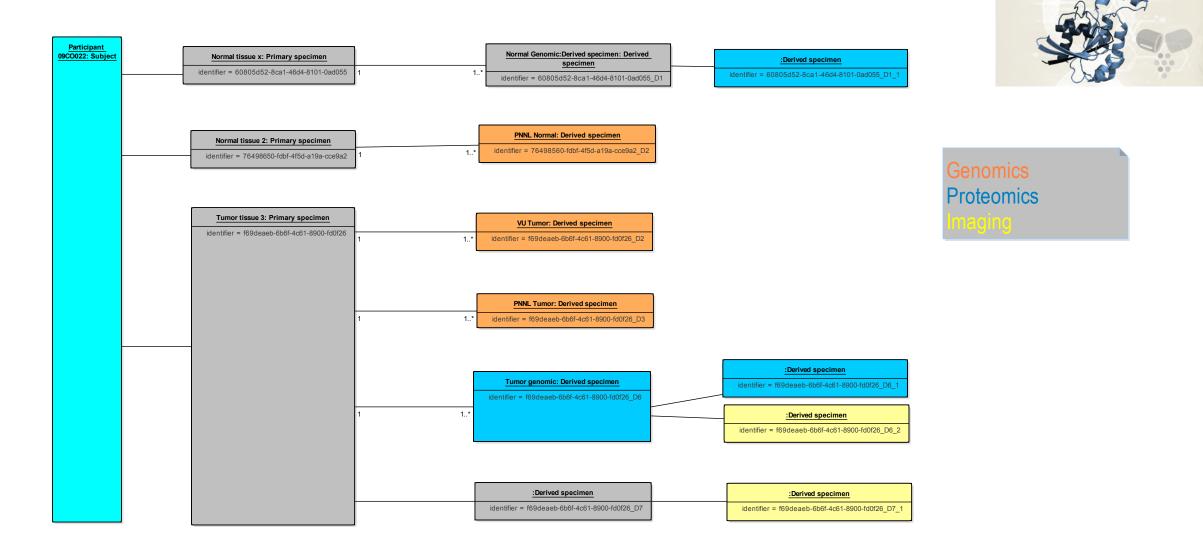
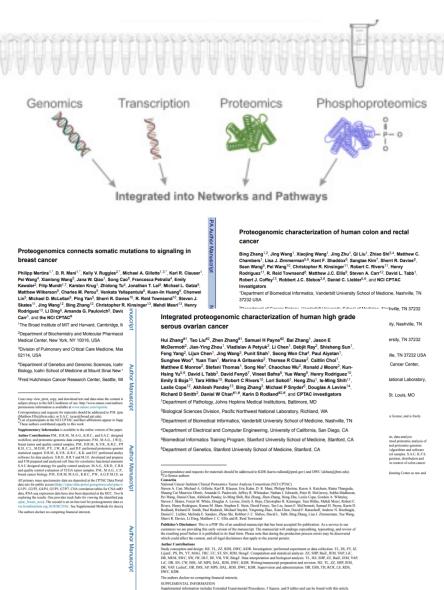
# <u>Slide 1</u> – Study design crosses nodes of the CRDC

CLINICAL PROTEOMIC TUMOR ANALYSIS CONSORTIUM



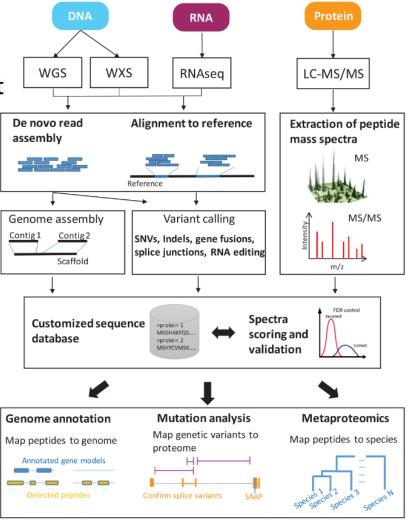
# <u>Slide 2</u> – Use Case : Proteogenomic Integration

- Identify variant protein sequences corresponding to somatic mutations and to evaluate the relationship between mutation frequency and variant protein expression.
- Determine how copy number variation translates into protein expression differences.
- Evaluate the impact of genomic features on the status of signaling networks through direct analysis of phosphoprotein intermediates
- Derive preliminary associations with clinical characteristics, such as platinum resistance in ovarian cancer.



# <u>Slide 3</u> – Use Case : Proteogenomic Integration

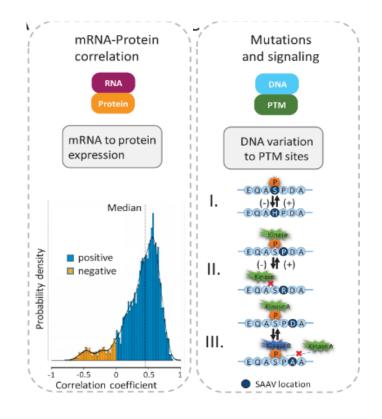
1) Sequence-centric Proteogenomics: describes aspects of sequence-centric proteogenomics and the combined use of genomic and proteomic data to augment gene or protein annotation



## <u>Slide 4</u> – Use Case : Proteogenomic Integration

1) Sequence-centric Proteogenomics: describes aspects of sequence-centric proteogenomics and the combined use of genomic and proteomic data to augment gene or protein annotation

2) Analysis of Proteogenomic Relationships: explores relationships between genomic and proteomic data using correlation, with application to deciphering the effect of mutations on signaling



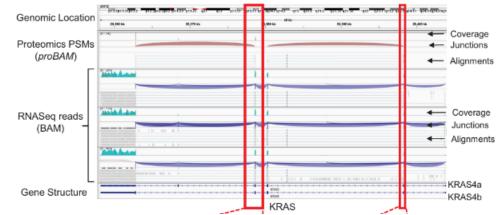
## <u>Slide 5</u> – Use Case : Proteogenomic Integration

1) Sequence-centric Proteogenomics: describes aspects of sequence-centric proteogenomics and the combined use of genomic and proteomic data to augment gene or protein annotation

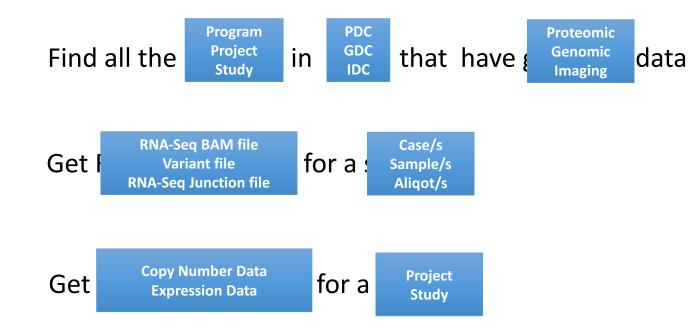
2) Analysis of Proteogenomic Relationships: explores relationships between genomic and proteomic data using correlation, with application to deciphering the effect of mutations on signaling

3) Data Visualization:

integrate mass spectrometry data with the genome.

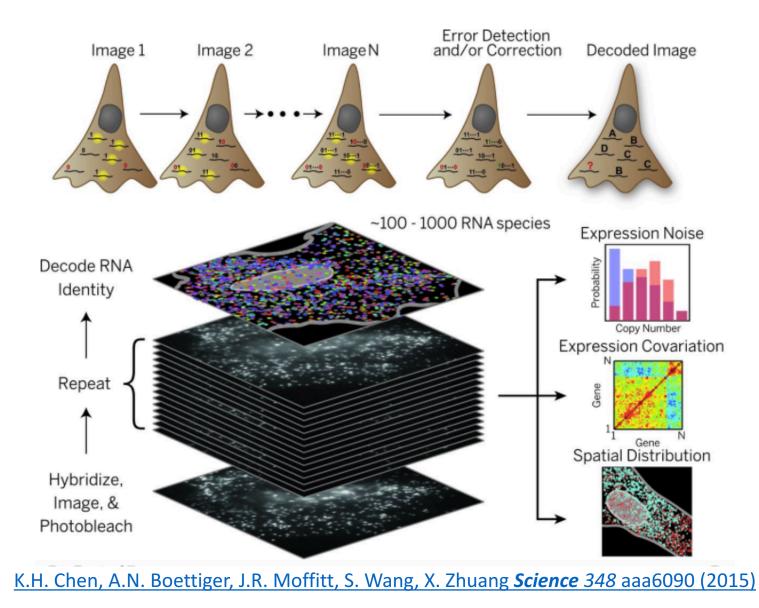


## <u>Slide 6</u> – Use Case : Proteogenomic Integration



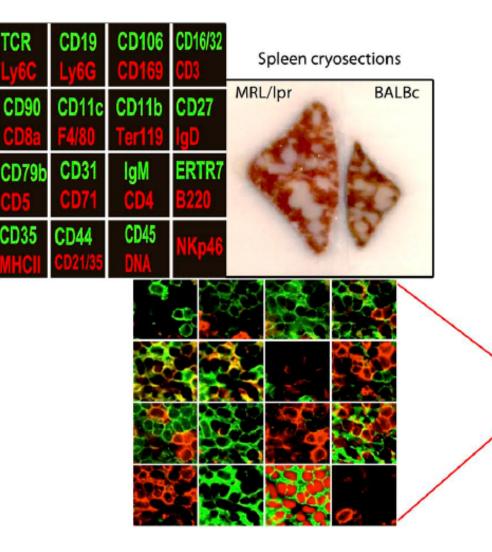
I know there is genomic information available for the PDC proteomic study I am interested in. How can I seamlessly integrate the somatic/germline variant, RNA-seq predicted junctions and fusion, etc to create a custom sample specific database to search against?

### <u>Slide 7</u> – Spatially resolved expression levels of 100s+ genes

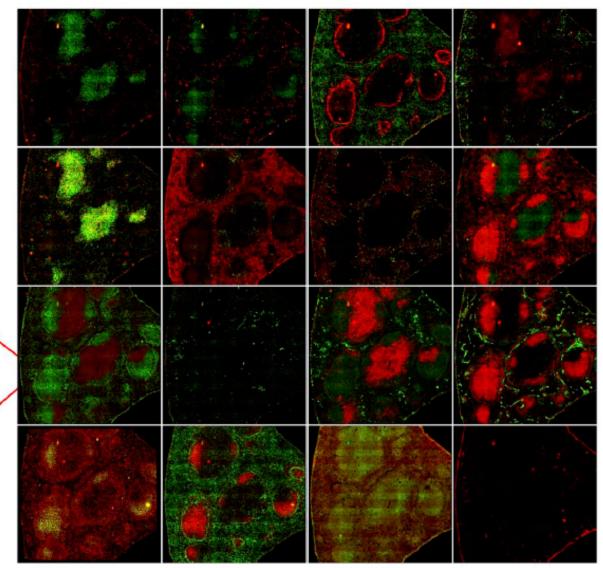


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## <u>Slide 8</u> – Immunofluorescence of up to 100 markers on the same tissue

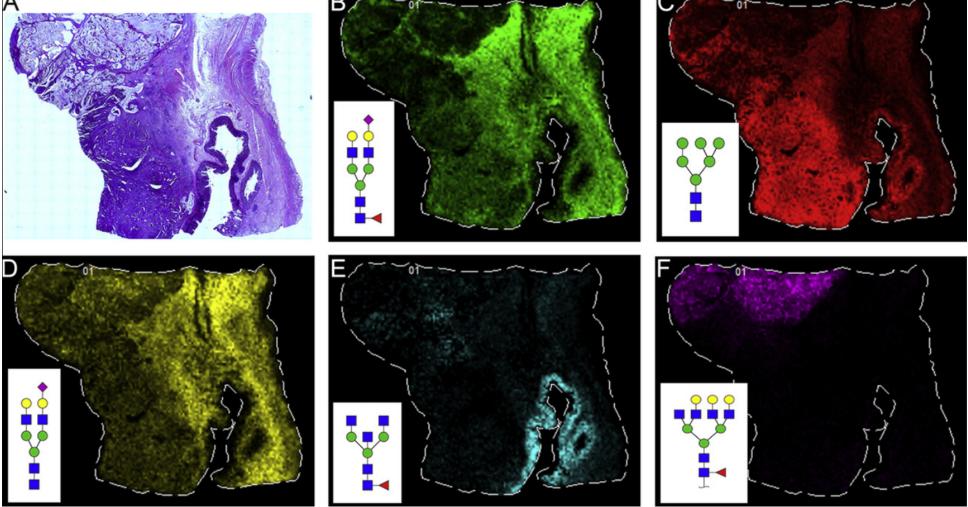


#### BALBC



Goltsev et al. <u>https://doi.org/10.1101/203166</u> Biorxiv

## <u>Slide 9</u> – Label free imaging using MALDI Mass Spectrometry



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## <u>Slide 10</u>– 3D Tissue Imaging

