Integrative-omics of UPS and strategies for neoantigen discovery for personalized immunotherapeutics.

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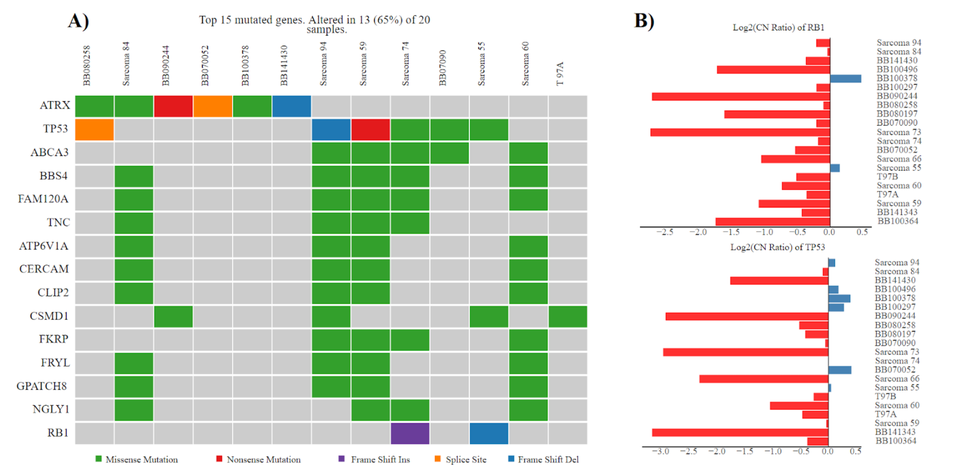
Main research focus

- UPS integrative -omics
- Neoantigen characterization
- Immunopeptidomics
- Computational mass-spectrometry.

Computational resources provided by:

Introduction / Aims

Undifferentiated pleiomorphic sarcomas (UPS) are the most common form of adult sarcoma. As with most rare cancers, there are limited systemic treatment options. To seek novel therapeutic approaches we characterized the proteogenomic landscape of UPS. Next generation sequencing (NGS) of 20 UPS exomes and their matched normal tissue defined the somatic mutational landscape of single nucleotide variants (SNVs) and copy number variants (CNVs). CNV analysis identified co-mutation or deletion in RB1 and p53 loci. At the transcript and protein level, one sample observed a truncated isoform of p53 (TP53-207), which might contribute to this disease. Understanding how the aberration landscape in UPS can be leveraged for the generation of personalized immuno-therapeutics is of vital interest.



Identifying cancer vaccine targets

At the International Centre for Cancer Vaccine Science (ICCVS), the informatics group has been focused on multi-omic strategies for the recomendation of cancer vaccines. Our pipelines leverage genomics, transcriptomics, proteomics or immunopeptidomics datasets to develop cancer vaccines. Here, we are focusing on immuno-peptidomics as the least-explored layer in our understanding of antigen-processing and presentation. We demonstrate the integration of 27 publicly available datasets to produce insights regarding mutations and other aberrations detected using mass-spectrometry alone.

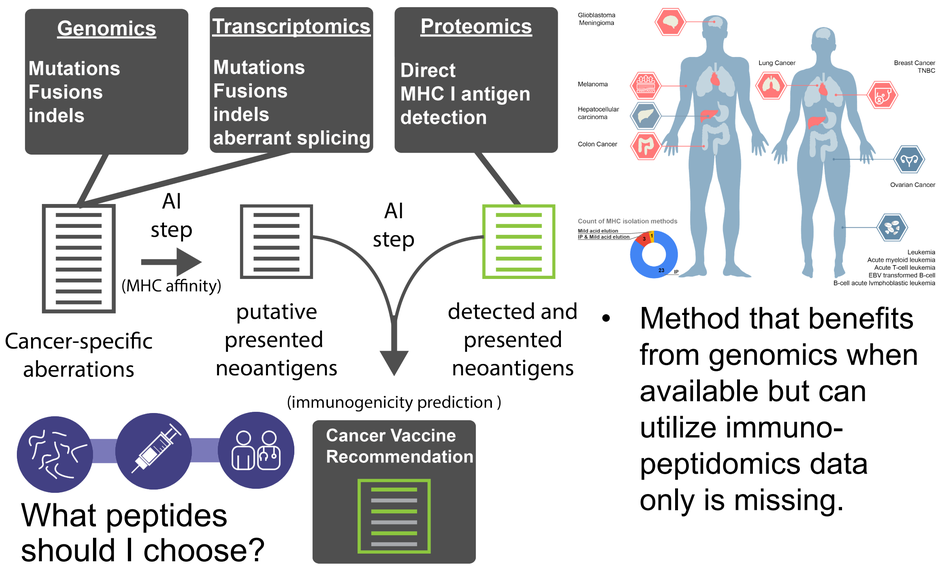
Summary / Outlook

These pipelines, in conjuction to matched genomics and transcriptomics will lead to new new targets for personalized immunotherapies in UPS.

What could help me
Access to samples with good clinical followup. Genomics/transcriptomics would be an asset.

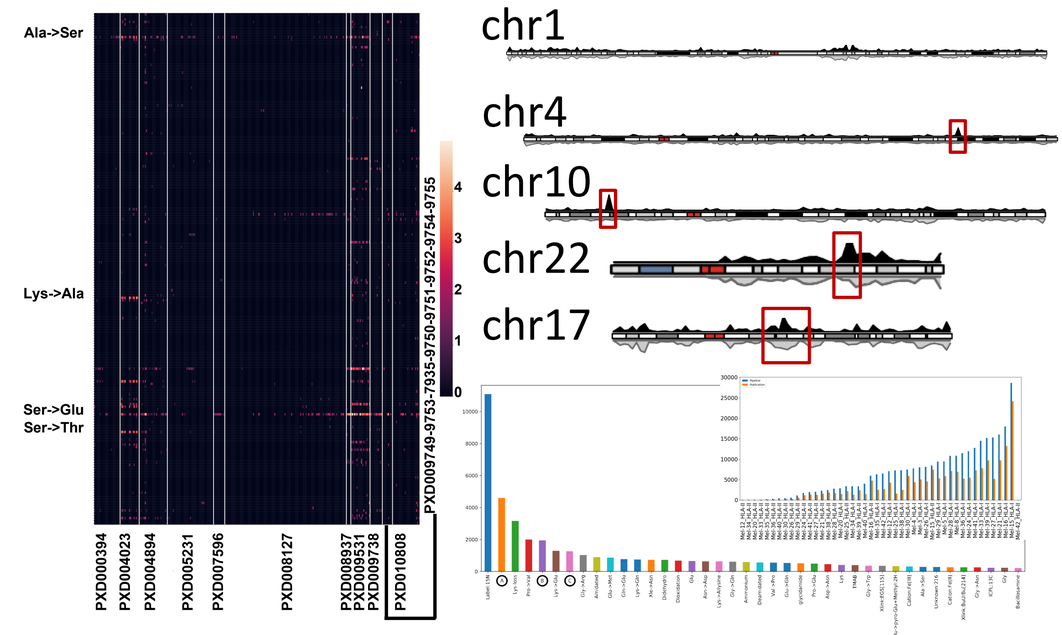
What technology ocan I put into collaborations
Multi-omic neoantigen characterization. Analysis from genomics through proteomics + sample-processing

Aberrations in UPS could make for interesting cancer vaccine targets, but which targets to carry forward?



- Method that benefits from genomics when available but can utilize immuno-peptidomics data only is missing.

We have developed a cancer vaccine recommendation Platform using all three layers of the central dogma



Immunopeptidomics datasets are understudied, and we are performing a harmonized re-analysis