Proteogenomics meta analysis for unraveling the sources of MHC class I neoantigens in cancer

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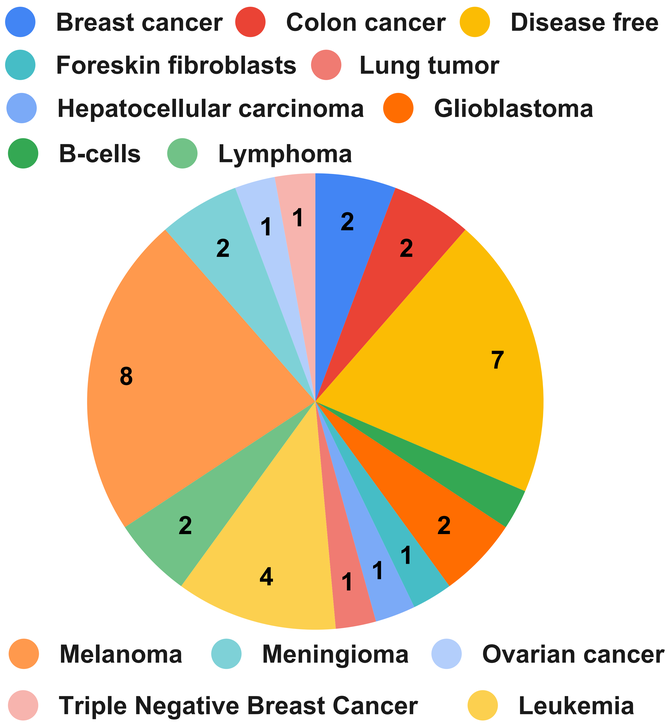
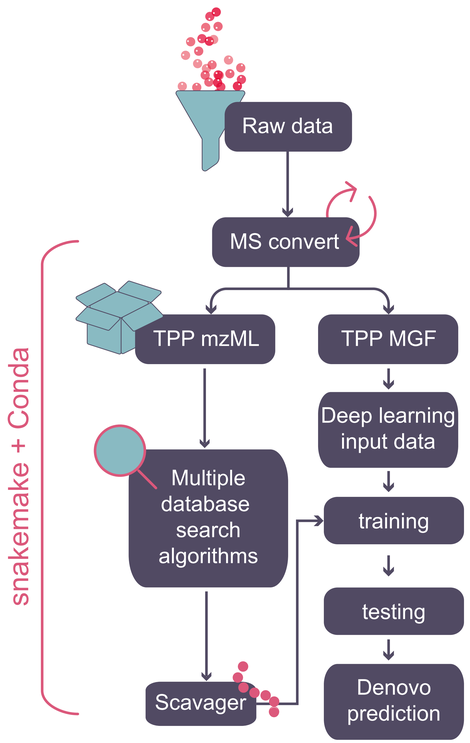
1. Introduction

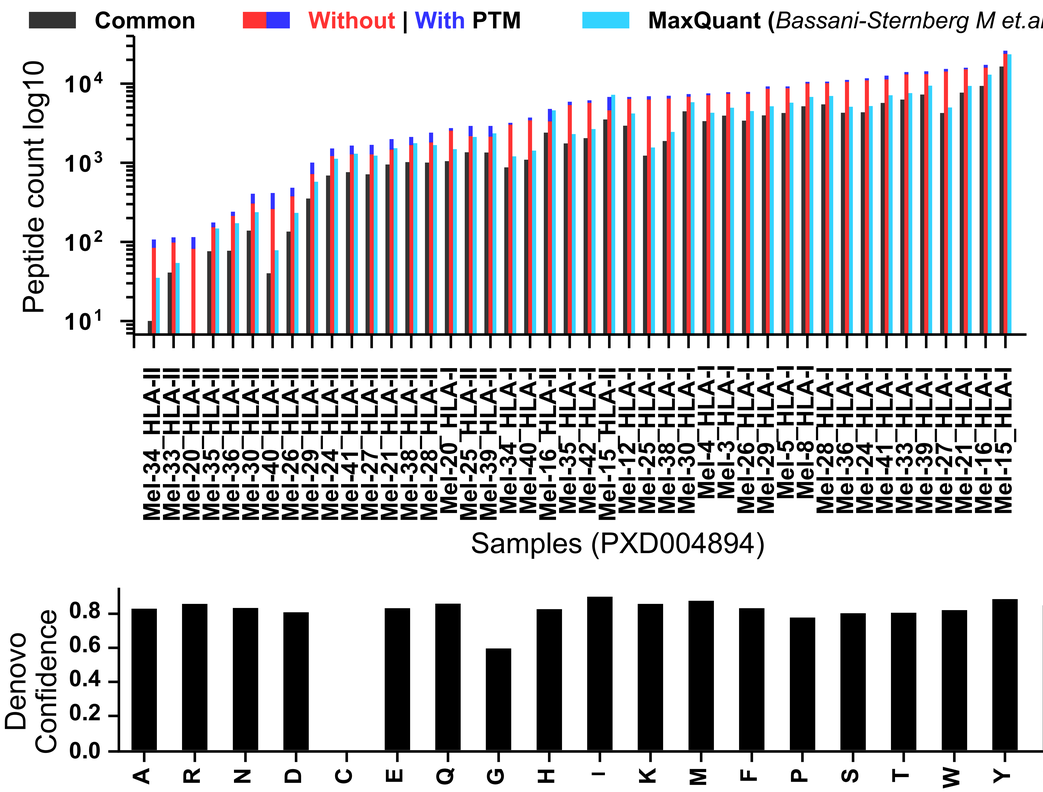
Immune system mobilization has become a promising approach in the fight against cancer. Tumour cells express aberrant gene products and it is expected that these should generate immunogenic neoantigens and stimulate immune-clearance. The canonical presentation mechanism has been challenged with new models suggesting the main source of these peptides being pioneer translation products deriving from aberrant mRNA with premature termination codon through the NMD pathway. We have leveraged the multitude of 27 publicly available immuno-peptidomics data to better understand and ask questions around the source of antigen peptide material for the MHC class I pathway, how this is regulated and how we can interfere with these processes to make cancer cells more immunogenic.



2. Methods



3. Results



5. Acknowledgements

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4. Discussion

We've checked the frequencies of amino acids occurrence which showed an under-representation of cysteine. This observation has been reported before (*Koumantou D 2019, Bassani-Sternberg M et. al 2017*) and treated as a technical bias in the database search parameters where the cysteine post translational modifications (PTMs) were not considered. However, our exhaustive set of cysteine PTMs revealed it's under-representation in generale on MHC class I peptides.

Considering the scale of our analysis, we're investigating the presented protein regions in pursuance of narrowing down the set of neo-antigen candidates for an effective vaccine design protocol.