Neoantigens Discovery and In Vitro Immunology Validation

Tumor neoantigens are derived from mutated genes specifically expressed in tumor cells, resulting from nonsynonymous SNV mutations, insertions/deletions(indels), gene fusions, etc. A subset of tumor specific somatic mutations can be translated into immunogenic and MHC-bound epitopes and presented on the cell surface called neoantigens, which can induce the activation of helper and cytotoxic T lymphocytes.

Solution for Neoantigens

The peptides containing mutation sites, which are presented by MHC molecules on the cell surface (neoantigens), are obtained through different splicing pathways of proteasomes. Genome sequencing or transcriptome sequencing cannot directly determine the sequence of antigenic peptides presented on the cell surface and their post-translational modifications. Therefore, mass spectrometry analysis techniques with high sensitivity, efficiency, and accuracy can be utilized to achieve sequence identification of immunopeptidomics, obtaining more accurate and reliable results.

- Identification of immunopeptidomics
- Discovery and Screening of Neoantigens
- Immunogenicity Validation of Neoantigens

Our Advantages

- **Highly Accurate neural network algorithm for Screening of Neoantigens**
- **Authentic and reliable data**
  - Using IP-MS for the identification of immunopeptides and the discovery of post-translational modifications.
  - Validation of neoantigen immunogenicity via ELISPOT assay
- **Offering an end-to-end solution for the discovery of neoantigens and the assessment of their immunogenicity.**

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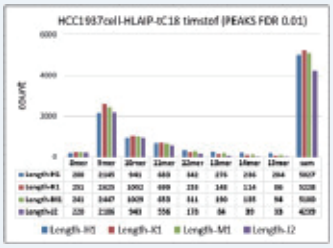
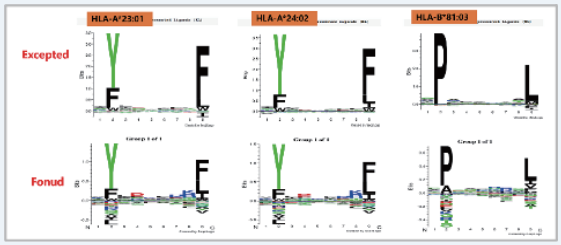
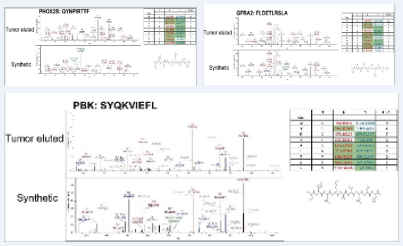
Technical Workflow

Sample Collection → (Genomic or Transcriptomic Sequencing / Immunopeptide Mass Spectrometry Analysis) → Algorithmic Prediction → Obtaining Candidate Neoantigen Peptides → Synthesis and Immunogenicity Validation


Immunopeptide Length Distribution



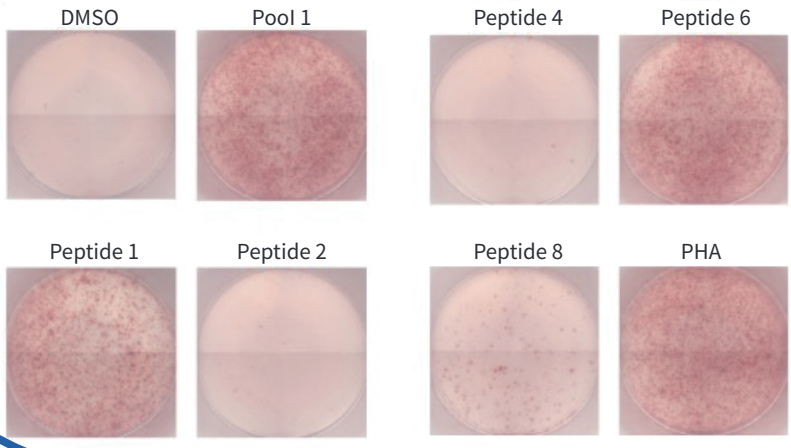
MOTIF analysis



Immunopeptide Secondary Spectrum Diagram [1]

- Identify mutation sites based on sequencing results and further validate using immunopeptidomic data.
- Determine HLA typing based on genomic sequencing data, then perform MOTIF analysis on immunopeptidomic results.
- Analyze the affinity between HLA typing and candidate peptides.
- Provide a report on the identification and prediction of neoantigen.

Validation of neoantigen immunogenicity



References:

[1] Yarmarkovich M, et al. Cross-HLA targeting of intracellular oncoproteins with peptide-centric CARs. Nature. 2021 Nov;599(7885):477-484.

[2] Bulik-Sullivan, B, et al. Deep learning using tumor HLA peptide mass spectrometry datasets improves neoantigen identification. Nat Biotechnol 37, 55–63 (2019).

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