

HARNESS THE POWER OF THE IMMUNE SYSTEM TO FIGHT CANCER

OncoPept identifies and delivers
prioritized T-cell neo-epitopes from
the patient's tumor mutanome

What is OncoPept?

OncoPept is an integrated platform that uses exome sequencing, RNA sequencing and computational methods to:

- Characterize tumor neo-antigens
- Analyze T-cell neo-epitopes
- Reveal gene expression signatures

Why is it important?

CHARACTERIZE TUMOR NEO- ANTIGENS

Measures the mutational load and therefore the probability the tumor will respond to immune therapy

Defines the immune response before, during and after therapy

PRIORITIZE T-CELL NEO-EPITOPES

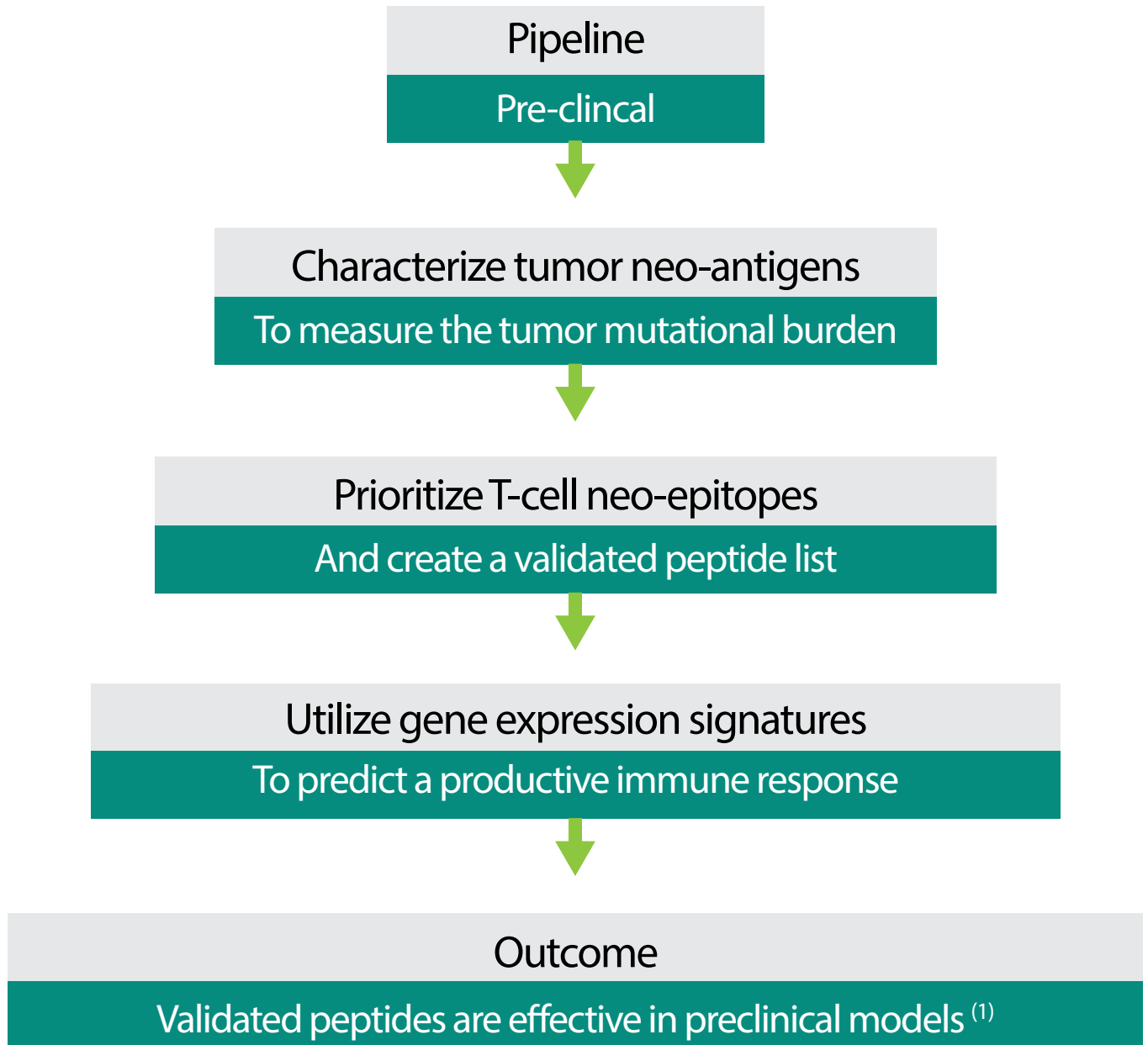
UTILIZE GENE EXPRESSION SIGNATURES

Analyzes the quality of the immune response environment

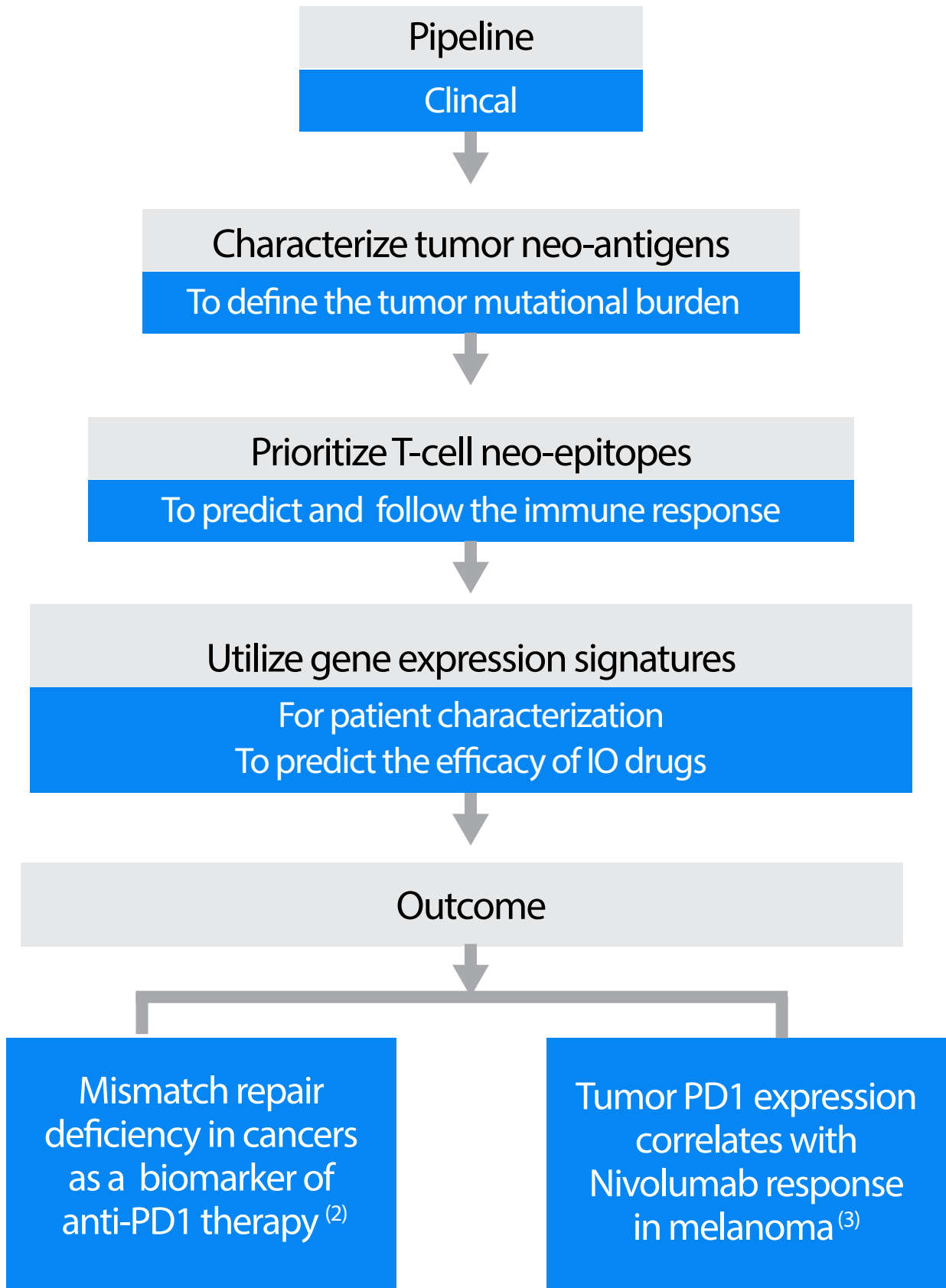
The flowchart illustrates the process of developing a personalized cancer vaccine, starting with sample collection and ending with efficacy evaluation. The process is divided into five main stages, each represented by a colored box on the left, with corresponding data and visualizations on the right.

- Samples:** The process begins with "Samples" (blue box). To the right, icons of a person and a mouse are shown above the text "Tumor Tissues".
- DNA and RNA Sequencing:** The next stage is "DNA and RNA Sequencing" (red box). To the right is an illustration of a DNA sequencer.
- Mutation Identification:** The third stage is "Mutation Identification" (green box). To the right is a bar chart titled "EGFR" showing the "Substitution Mutation Count" (y-axis, 0 to 2693) across the "EGFR" gene. The chart shows a high peak at position 2693. Below the chart is a diagram of the EGFR protein structure with various domains and mutations indicated by colored triangles.
- Mutation Prioritization:** The fourth stage is "Mutation Prioritization" (orange box). To the right is a funnel diagram showing the selection process:
 - 1632 Protein altering variants from exome sequencing
 - 552 Expressed variants from RNA sequencing
 - 65 HLA binding peptides from multiple HLA-binding algorithms
 - 23 Peptides defined by optimal HLA-binding motif
 - 10 Peptides defined by optimum processing sites
- Efficacy:** The final stage is "Efficacy" (dark blue box). To the right is a Kaplan-Meier survival plot showing "Percent survival" (y-axis, 0 to 100) versus "Days after tumor inoculation" (x-axis, 0 to 55). The plot compares two groups: "+ Peptide" (blue line) and "- Peptide" (red line). The "+ Peptide" group shows significantly higher survival, remaining near 100% throughout the 55-day period, while the "- Peptide" group shows a sharp decline in survival, reaching approximately 20% by day 35.

Preclinical Applications



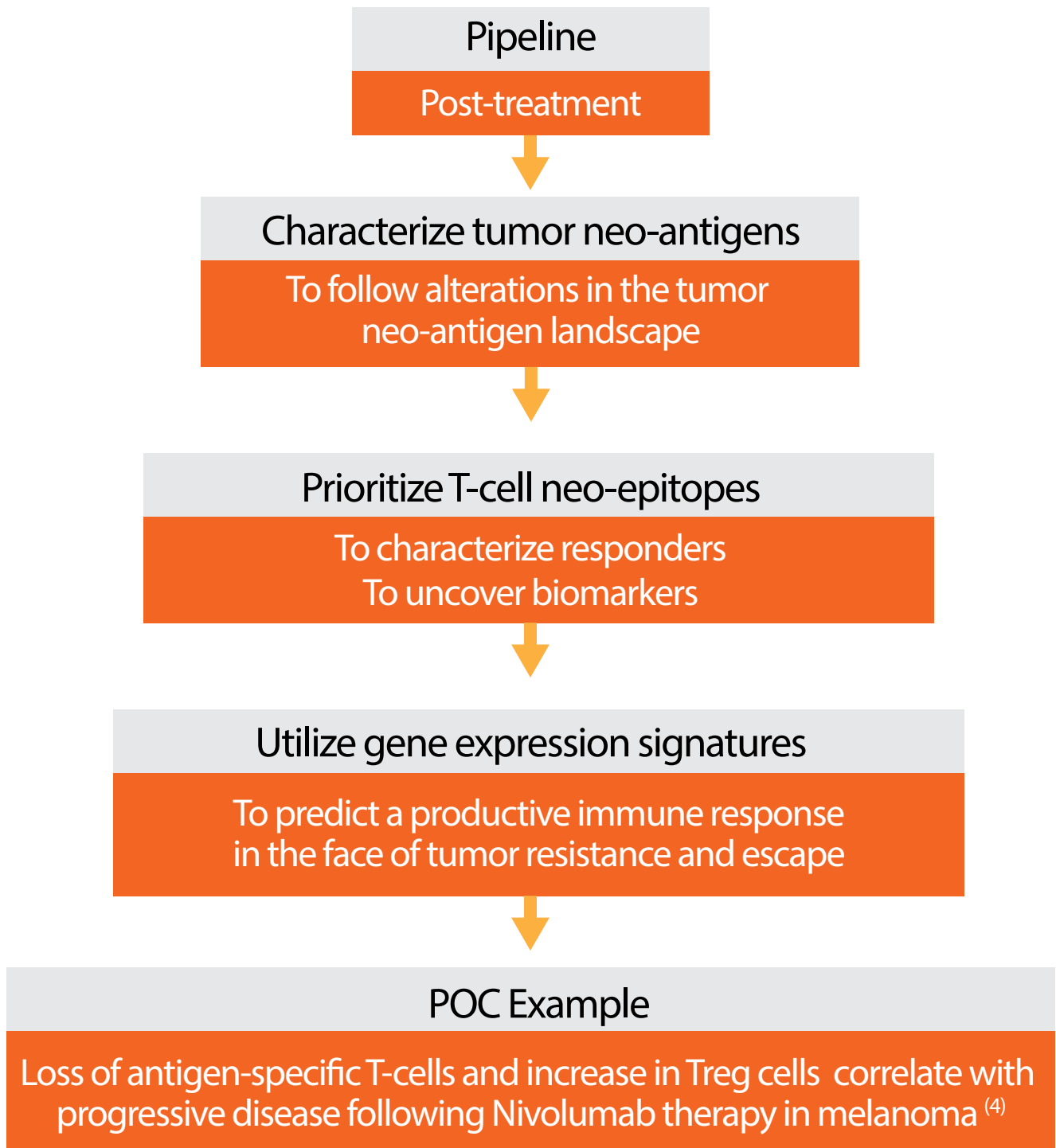
Clinical Research Applications



2. Le et al. 2015. NEJM 372: 2509-2520

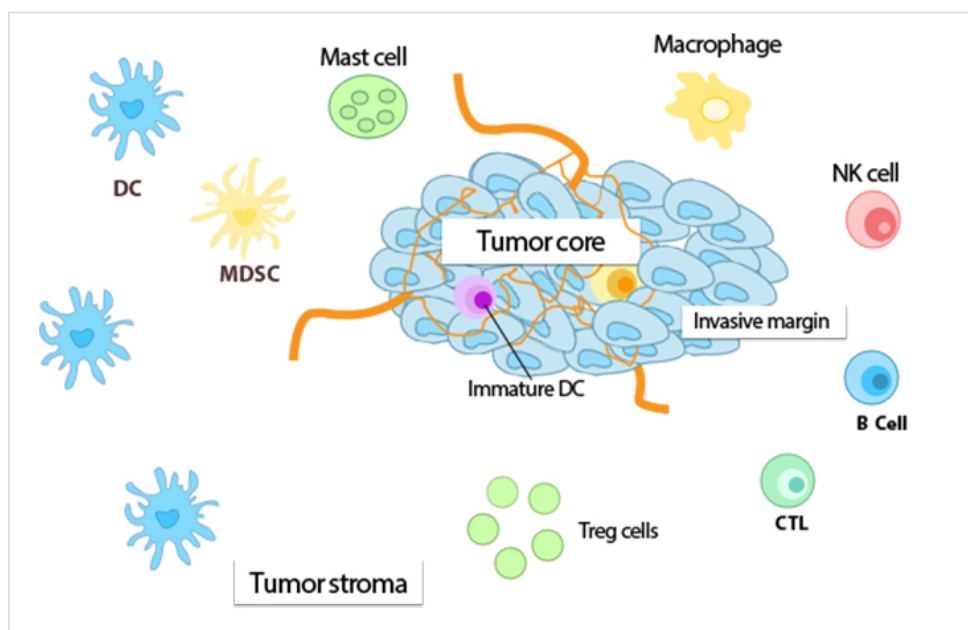
3. Tumei et al. 2015. Nature 515: 568-572

Clinical Therapeutic Applications



Querying the Immune Microenvironment

- Hypothesized signatures of response and progression are being proposed across indications: we are poised to address such hypotheses as they are validated
- Addressing tumor immune microenvironment will provide insight that will inform treatment decisions for patients: this is the concept of "immune conjecture" ⁽⁵⁾



Examples

- ✓ immunosuppression (IDO, FOXP3)
- ✓ cell surface markers (PD-L1, ICOS)
- ✓ transcription factors (EOMES, Batf)
- ✓ cytokines (IFN γ)
- ✓ chemokines (CXCR4)
- ✓ growth factors (VEGF, TGF β)
- ✓ innate immunity (HMGB3, TLRs)
- ✓ metabolism (Adenosine, lactate)
- ✓ proteases (MMP13, ADAM8)

Examples of our work

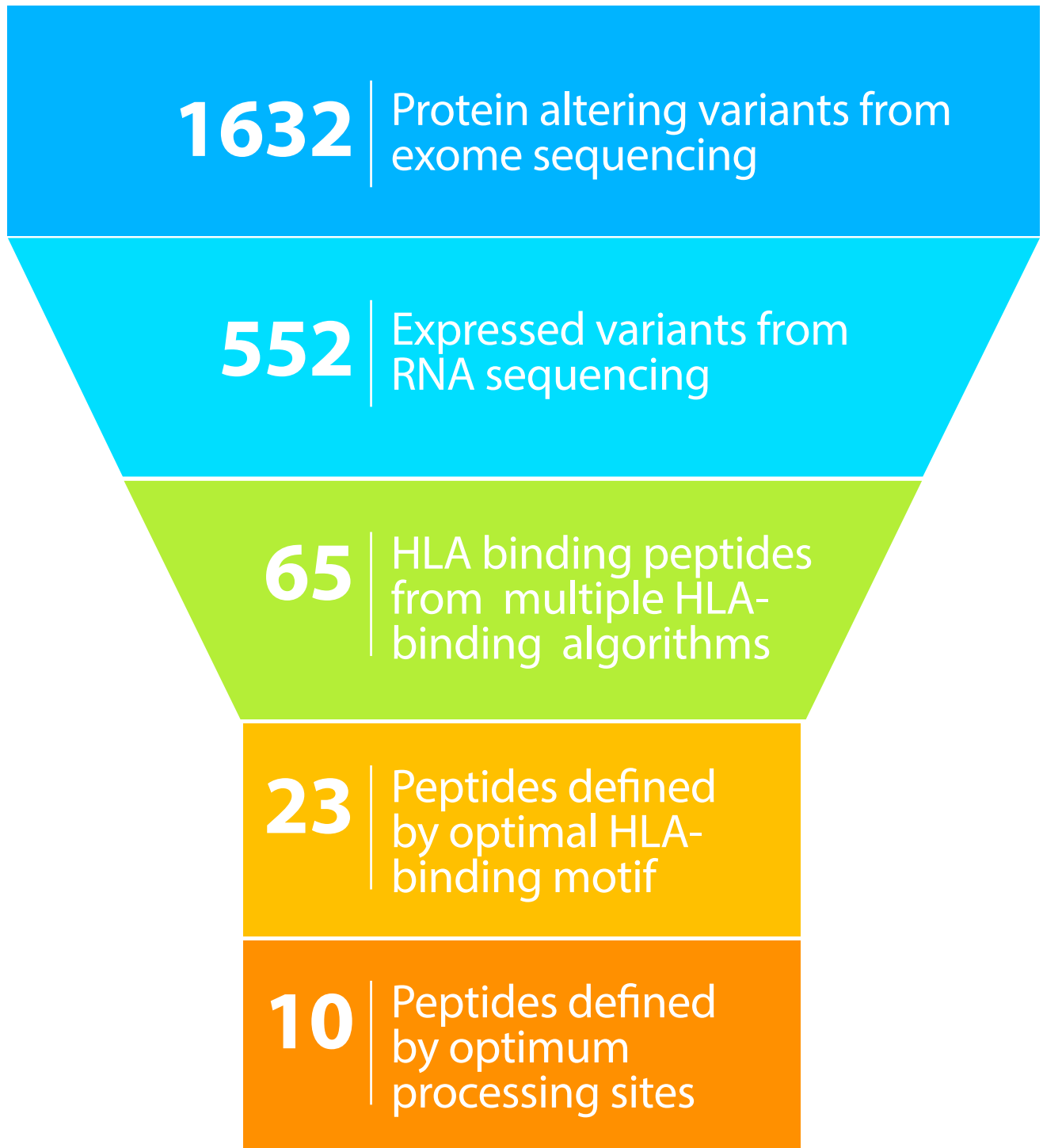
Case Study 1

- ✚ *A vaccine company prioritized 8-10 neo-epitopes from 400 neo-antigens from human glioblastoma samples for validation*

Case Study 2

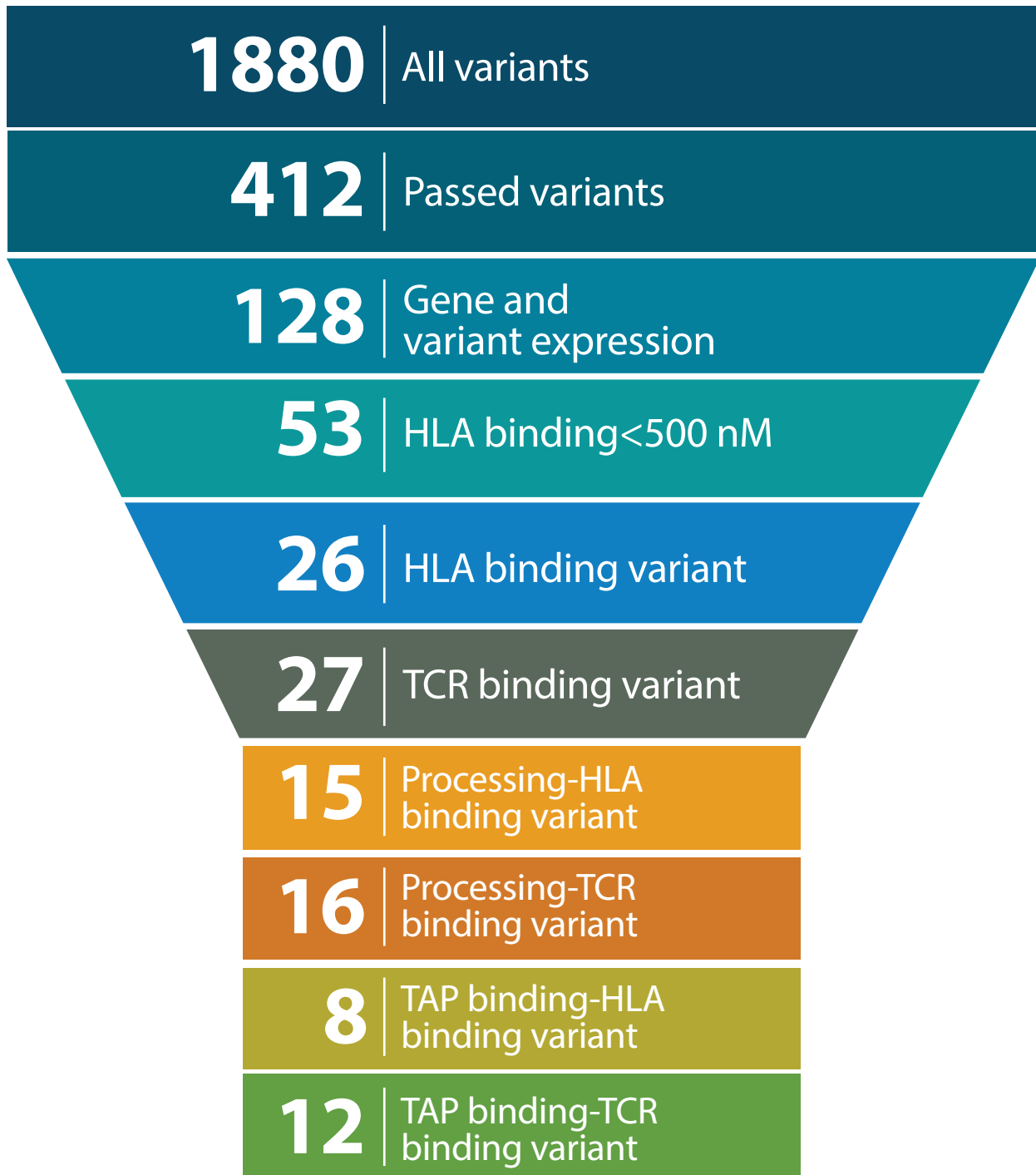
- ✚ *A pharma company identified neo-epitopes in multiple mouse cancer cell lines and tumors that drove preclinical efficacy studies*

Neo-antigens to Neo-epitopes in a mouse cell line



OncoPept work flow achieved >2 -log enrichment of neo-epitopes from the mutational load of a mouse tumor cell line

T-cell neo-epitopes from a Head & Neck cancer sample



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