

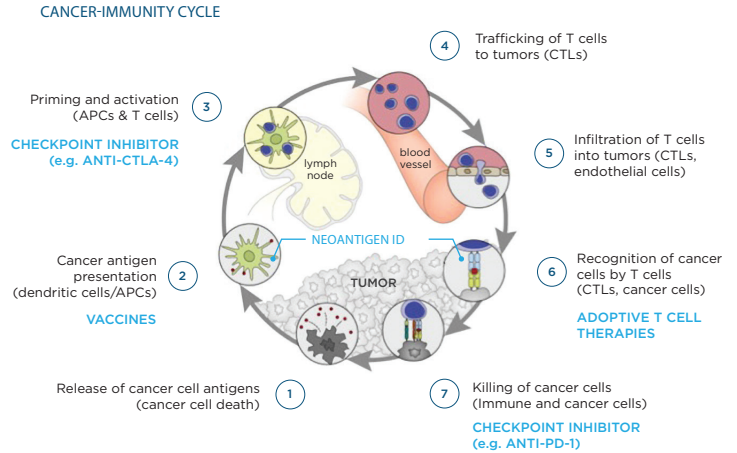
IDENTIFY AND PRIORITIZE CANDIDATE NEOANTIGENS FROM CANCER EXOME SEQUENCING RESULTS WITH UNMATCHED ACCURACY

WHAT IS IMMUNOSELECT™?

Neoantigens are a class of immunogens based on the personal, exquisitely tumor-specific mutations found uniquely in each patient's tumor. Combining PGDx's highly accurate cancer exome analyses (CancerXome™) with *in silico* neoantigen prediction, ImmunoSELECT identifies and prioritizes the most relevant mutation-derived neoantigens to enable adoptive T-cell transfer, cancer vaccine development, and prediction of clinical utility of checkpoint inhibitors.

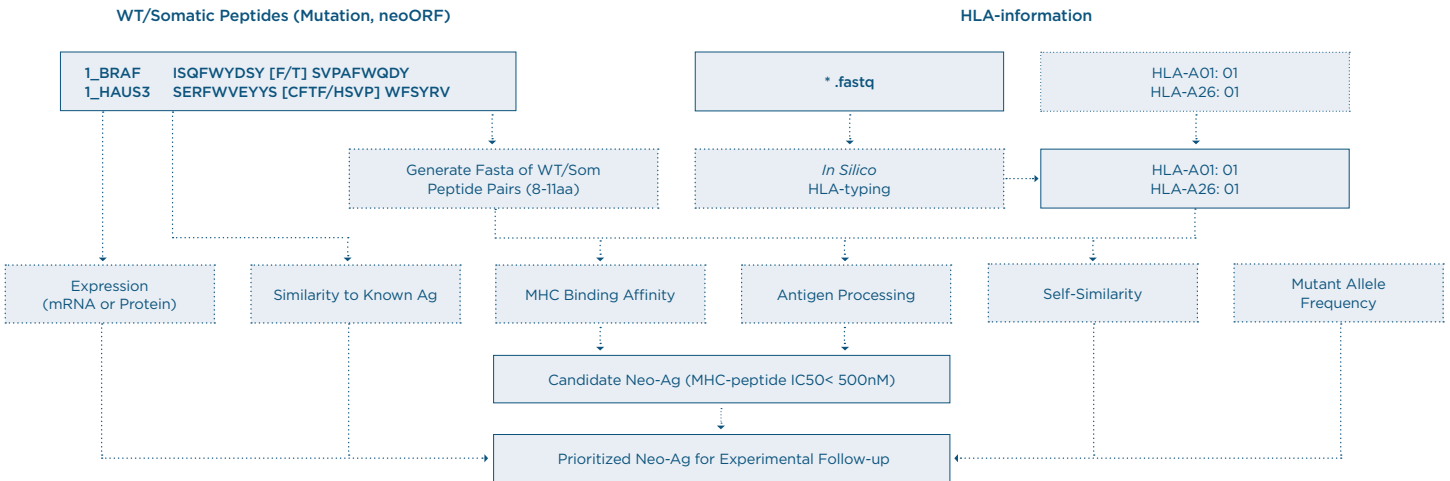
IMMUNOSELECT DELIVERABLES

- Unparalleled cancer exome sequencing accuracy to ensure identification of true somatic mutations with >95% sensitivity and 97% PPV (10% mutant allele frequency) at 150x coverage
- Accurate HLA typing using whole exome sequencing
- Prediction and prioritization of the most relevant neoantigens from exome-based mutations and novel open-reading-frames



SOURCE: "Oncology meets immunology: the cancer-immunity cycle", *Immunity*, 25 July 2013

IMMUNOSELECT PIPELINE



EXAMPLE REPORT OUTPUT

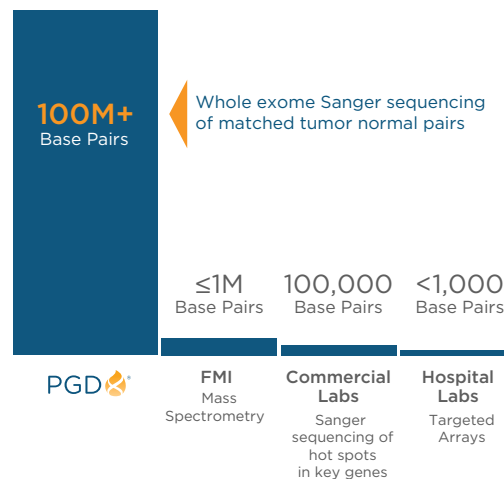
Patient ID	HLA Type	Gene Name	Peptide ID	MUT Peptide	MUT MHC Affinity	MUT CTL Class	Mean Exp in Tumors	Priority
Patient 1	HLA-A*02:01	GAS7	1_p09490_10	SLADEAEVYL	14.4	E	236	High
Patient 1	HLA-B*44:03	CSNK1A1	59_p06000_8	GLFGDIYL	5.72	E	4633	High
Patient 1	HLA-A*24:02	KIAA031	124_p11981_11	KLLQQLNGWYM	25.3	E	2063	High
Patient 1	HLA-A*02:01	RRP1B	197_p19240_11	FLPKPLFFRA	16.63	E	1111	High

ONLY CANCERXOME™ DELIVERS THE SENSITIVITY AND SPECIFICITY REQUIRED TO PREVENT FALSE POSITIVE MUTATIONS FROM CONFOUNDING NEOANTIGEN IDENTIFICATION

NUMBER OF DNA BASE PAIRS VALIDATED WITH AN INDEPENDENT METHOD USED FOR PIPELINE OPTIMIZATION

Using 100 to 1,000 times more independently validated data points to optimize the bioinformatics pipeline ensures unmatched accuracy of PGDx exome sequencing.

Mutation-Calling Pipeline Optimization



IMMUNOSELECT™ VALIDATION

- Identified 18 out of 19 experimentally validated neoantigens as being strong neoantigen candidates, suggesting an assay sensitivity of greater than 90%

SOURCE OF DATA: Retrieved from <http://cancerimmunity.org/peptide/mutations/>

- Reproduced the tetra-peptide signature predictive of clinical benefit of CTLA-4 blockade in melanoma

SOURCE OF DATA: "Genetic Basis for Clinical Response to CTLA-4 Blockade in Melanoma." *New England Journal of Medicine*. 04 December 2014.

IMMUNOSELECT CONSISTENTLY RANKED EXPERIMENTALLY VALIDATED NEOANTIGENS WITHIN TOP 20% OF ALL NEOANTIGEN CANDIDATES DERIVED FROM WHOLE EXOME SEQUENCING

Sample	#Mutations	#Neo-Ag (IC50<500nM)	#Neo-Ag Post Prioritization	Rank of Validated Neo-Ag
Patient 1	504	128	55	1,14,15,16
Patient 2	257	277	30	1,2,3,4,15,16
Patient 3	58	97	30	9,10,14,15,16

SOURCE OF DATA: "Mining exomic sequencing data to identify mutated antigens recognized by adoptively transferred tumor-reactive T cells." *Nature Medicine*. 05 May 2013.

IMMUNOSELECT KEY PERFORMANCE ATTRIBUTES

- Unparalleled cancer exome sequencing accuracy to ensure research is focused on true somatic mutations for neoantigen prediction**
 - 95% sensitivity and 97% positive predictive value (10% mutant allele frequency) at 150x coverage
- Works on FFPE or frozen tissue**
- Matched patient normal (germline DNA) is required for optimal results**
- Accurate inference of HLA typing from whole-exome sequencing**
- Neoantigen analysis can be offered alone or in combination with CancerXome™**
- Effective in silico pipeline to discover and prioritize candidate neoantigens by incorporating the following:**
 - Comprehensive Identification of tumor-specific mutated peptides and neo-ORF
 - State-of-the-art prediction of HLA-types, antigen processing and MHC-peptide binding
 - Proprietary strategy to select most-relevant candidate neoantigens for experimental validation

IMMUNOSELECT IS FOR RESEARCH USE ONLY, NOT FOR DIAGNOSTIC PURPOSES.