T cells targeting tumor-exclusive neoepitopes (neoE) have been postulated to represent the primary mediators of clinical benefit for patients with solid tumors treated with immunotherapies. Identifying and tracking these T cells in patients can help to understand the mechanism for immune checkpoint inhibitor therapies, as well as provide new therapeutic candidates for personalized adoptive cell therapies. However, this has been hampered by the low frequency of neoE-specific T cells in peripheral blood. To this end, we demonstrate the use of the imPACT Isolation Technology, an ultra-sensitive high-throughput technology, to capture neoE-specific CD8+ T (neoE-T) cells from peripheral blood. In addition, this technology can be utilized to quantify and monitor neoE-T cells longitudinally during therapy. We show here preliminary data applying the imPACT technology to clinical trial samples for the characterization of mutation-targeted T cell responses from patients associated with clinical benefit.

Peripheral blood mononuclear cells (PBMC) from patients with ovarian cancer treated with single agent or combinations containing an anti-PD-1 antibody (AB122) were analyzed. Briefly, tumor-exclusive neoE-HLA target candidates were predicted and barcoded snare libraries comprising personalized neoE-HLA reagents were produced for capture of neoE-specific CD8+ T cells from PBMCs. Longitudinal analysis of neoE-T cell responses throughout the duration of treatment was performed to obtain valuable information on neoTCR sequences and T-cell quantification & phenotype.

**Abstract**

Peripheral blood mononuclear cells (PBMC) from patients with ovarian cancer treated with single agent or combinations containing an anti-PD-1 antibody (AB122) were analyzed. Briefly, tumor-exclusive neoE-HLA target candidates were predicted and barcoded snare libraries comprising personalized neoE-HLA reagents were produced for capture of neoE-specific CD8+ T cells from PBMCs. Longitudinal analysis of neoE-T cell responses throughout the duration of treatment was performed to obtain valuable information on neoTCR sequences and T-cell quantification & phenotype.