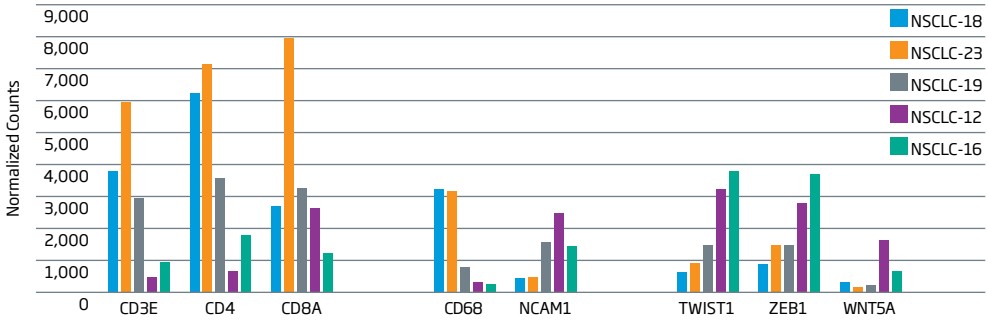
Tech Note
Epithelial Mesenchymal Transition in Immuno-Oncology

Tumors undergoing the epidermal to mesenchymal transition (EMT) have been described as having lower levels of T cells than more differentiated tumors. The term "immune desert" has been coined to describe this phenomenon. The HTG EdgeSeq Precision Immuno-Oncology Panel measures genes associated with both the presence of T cells and a variety of genes indicative of the EMT pathway, allowing multiple assessments of the tumor and host response to be measured in the same assay.

Expression of EMT Pathway Genes



A range of infiltrating T cell levels can be detected using the canonical T cell markers CD3E, CD4, and CD8A, as can the presence of macrophages via CD68. Measurement of EMT-associated transcription factors TWIST1 and ZEB1, as well as WNT ligands such as WNT5A, shows the expected inverse relationship between T cells and EMT-associated gene expression. Additionally, NK cells are present in higher number (as measured by NCAM1/CD56) in tumors undergoing EMT, consistent with multiple reports.*

Other applications:

- Cytokine profiling
- Immunophenotyping TILs
- Immunoresistance pathways
- Immunosuppression phenotyping
- DNA repair mechanisms
- Drug target assessment
- TCGA tumor subtyping

Selected Immune Response Profiling Genes

General T Cell Markers		Macrophage Markers	NK Cell Markers	EMT-Associated Genes
CD14	CD8A	ATG7	CD160	EPCAM
CD2	CD8B	CCL7	DUSP4	FAP
CD247	CD96	CD163	FOXJ1	FN1
CD28	IL2RB	CD68	FUT5	SNAI1
CD3D	LAMP1	CD84	GTF3C1	SNAI2
CD3E	LCK	CHIT1	IL21R	TWIST1
CD3G	SH2D1A	CLEC5A	KIR2DL1/3/4	TWIST2
CD4	TNFRSF25	CXCL5	KIR3DL1/2/3	WNT5A
CD5	TRAT1	EMP1	KIR3DS1	WNT7B
CD6	ZAP70	MARCO	MPPED1	ZEB1
		MS4A4A	NCAM1	

About the HTG EdgeSeq Precision Immuno-Oncology Panel

The next-generation sequencing (NGS)-based HTG EdgeSeq Precision Immuno-Oncology Panel is designed to measure the immune response both inside the tumor and the surrounding microenvironment. HTG's quantitative nuclease protection assay does not require nucleic acid extraction and is automated using the HTG EdgeSeq processor. By leveraging the high sensitivity and dynamic range of NGS instrumentation, this powerful tool interrogates 1,392 genes from a single section of formalin-fixed, paraffin-embedded (FFPE) tissue, RNA samples that have previously been extracted, or PAXgene samples.

* Cantoni, C., et al. NK Cells, Tumor Cell Transition, and Tumor Progression in Solid Malignancies: New Hints for NK-Based Immunotherapy? 2016;2016:4684268. doi: 10.1155/2016/4684268. Epub 2016 May 12

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