Tech Note
Measuring Immune Checkpoint Genes from FFPE Tissue

HTG

The immune system's response to a tumor is modulated by a series of receptor-ligand interactions commonly known as immune checkpoints. Encompassing an intricate balance of stimulatory and inhibitory signals, dysregulation of this system of checks and balances is believed to facilitate tumor immune escape. Due to their critical role in immune response, many of these checkpoints have be targeted for therapeutic intervention, however, due to the large number of potential checkpoints and varying contributions to specific regulatory processes, obtaining a full picture of expression is challenging with existing immunohistochemistry technologies. The HTG EdgeSeq Precision Immuno-Oncology Panel quantitatively measures all described checkpoint molecules from a single section of formalin-fixed, paraffin-embedded (FFPE) tissue, providing a fuller view of the immune response to the tumor.
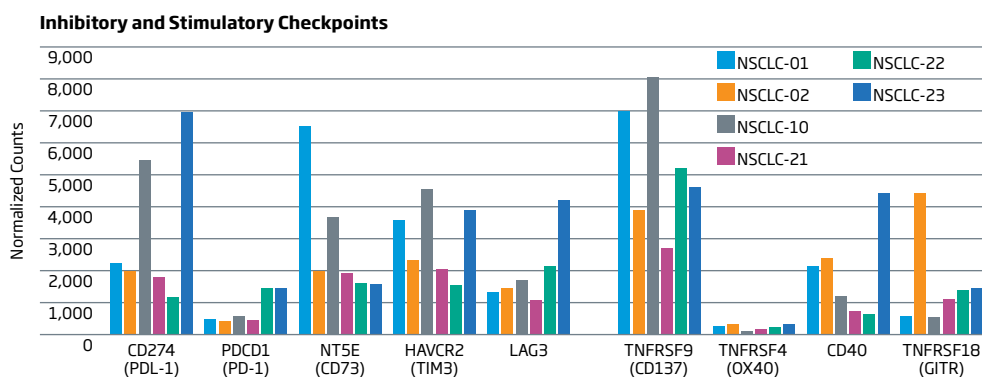
Other applications:

- Assessing tumor inflammation
- Cytokine profiling
- Immunophenotyping TILs
- Immunoresistance pathways
- Immunosuppression phenotyping
- DNA repair mechanisms
- TCGA tumor subtyping

Inhibitory and Stimulatory Checkpoints

Differing levels of stimulatory and inhibitory checkpoint genes can be measured across a set of non-small cell lung cancers indicating the presence of potentially different forms of immune dysfunction.

Inhibitory and Stimulatory Checkpoints

Stimulatory		Regulatory	
CD27	ICOS	ADORA2A	IDO2
CD28	ICOSL	ADORA2B	KIR-Family
CD40	IL2RB (CD122)	BTLA	LAG3
CD40L	TNFRSF4 (OX40)	CD274 (PDL-1)	PDCD1 (PD-1)
CD70	TNFRSF9 (CD137)	CD276 (B7H3)	PDCD1LG2 (PDL-2)
CD80	TNFRSF18 (GITR)	CTLA4	VSIR (VISTA)
CD86	TNFSF4 (OX40L)	IDO1	VTCN1

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.

HTGMolecular

Rev 2: 23-JAN-2019