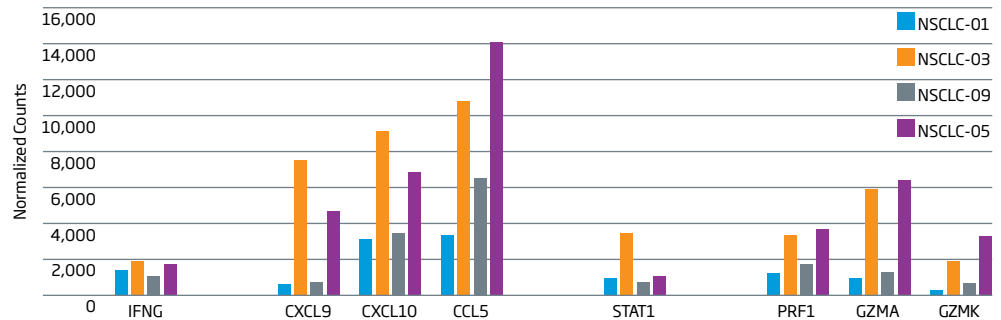


Tumor inflammation associated with cytotoxic T cell responses has been identified as being important in understanding response to checkpoint inhibitors. The recruitment of new T cells and clonal expansion of those which successfully recognize a tumor antigen has been shown to elicit potent anti-tumor activity. The HTG EdgeSeq Precision Immuno-Oncology Panel measures the genes associated with anti-tumor immune responses, including the interferon- γ mediated response illustrated below.

Other Applications

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

Expression of Inflammation Genes



Elevated levels of interferon gamma is observed in cases NSCLC-03 and NSCLC-05 consistent with a proinflammatory tumor microenvironment. Expression of chemokines known to play a role in T cell and NK cell recruitment, CXCL9, CXCL10, and CCL5 are upregulated, and signaling through the STAT signal transduction pathway (represented by induction of STAT1) are observed. The expression of cytolytic molecules perforin and granzymes GZMA and GZMK indicate an effector-driven immune response.

Selected Immune Response Profiling Genes

Responses						Macrophages			
Th1	Th2	Th17	MDSC	M1	M2	M2			
BST2	IFNG	ADCY1	IL26	CCR4	IL21	ANPEP	CD80	ARG1	TLR8
CCL4	IL12A	BIRC5	IL4	CCR6	IL22	ARG1	CD86	CCL2	VEGFA
CCR5	IL12B	CDC25C	IL5	IL17A	IL24	CD33	IL1R1	CD14	VEGFC
CD38	IL12RB2	CDC7	LAI2	IL17B	IL26	CD34	IL1R2	CD163	
CD70	IL2	CENPF	LIMA1	IL17C	RORC	FUT4	NOS2	FCGR1A_FCGR1B	
CSF2	IL22	CXCR6	MAF	IL17F	STAT3	IL10	NOS3	FCGR3A_3B	
CTLA4	LTA	GATA3	NEIL3	IL17RA	TGFB	ITGAM	SOCS3	IL10	
CXCL10	STAT1	HELLS	PMCH	IL1B		TGFB1	TLR2	PCNA	
CXCL9	STAT4	IL10	SMAD2				TLR4	PECAM1	
CXCR3	TBX21	IL13	STAT6					TFRC	
DPP4	TNF	IL25	WDHD1					TLR1	

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, extracted RNA, or PAXgene samples.