Supplemental Online Content

Supplemental Table 1. Genes used in Inflammatory, EMT, and IPRES signatures

Inflammatory Genes		EMT Genes		IPRES Genes
CCL5		**Epithelial**		ANGPT2
CCR5		CDH1		AXL
CD274 (PDL1)		CDH3		CCL13
CD3D		CLDN4		CCL2
CD3E		EPCAM		CCL7
CD8A		ST14		CDH1
CIITA		MAL2		FAP
CTLA4				FLT1
CXCL10		**Mesenchymal**		1L10
CXCL11		VIM		LOXL2
CXCL13		SNAI2		RORS
CXCL9		ZEB2		TAGLN
GZMA		FN1		TWIST2
GZMB		MMP2		VEGFA
HLA-DRA		AGER		VEGFC
HKA.DRB1				WNT5A
HLA-E				
IDO1				
IL2RG				
ITGAL				
LAG3				
NKG7				
PDCD1				
PRF1				
PTPRC				
STAT1				
TAGAP				

Supplemental Table 2. EMT Gene Lists from the Literature

Genes	Ref 1 (lung)	Ref 2 (lung)	Ref 3 (lung)	Ref 4 (lung)	Ref 5 (lung)	Ref 6 (pan tumor)	Ref 7 EMT database	Ref 8 (breast)	Avg gene reads	Notes
Epithelial										
CDH1	X	X	X	X	X	x	X	X	45	
CDH3		X	X	X		x			136	
CLDN4				X			X	X	127	
EPCAM		X	X	X		x	X		158	
ST14		X	X	X		x			202	
MAL2			X			x			155	
Mesencyhmal										
VIM	X	X	X	X		x	X	X	326	
SNAI2	X	X		X	X		X	X	39	
ZEB2		X		X	X		X	X	34	
FN1	X		X						71	
MMP2	X		X				X		265	
AGER				X			X		33	
SNAI1	X				X		X	X	9	1
TWIST1	X	X		X	X			X	9	1
ZEB1		X	X	X	X	x	X	X	8	1
FOXC1							X	X	5	1
TWIST2		X			X			X	2	1
CDH2	X			X	X			X	2	1

Notes.

1. Classic EMT gene, but expression level too low so not used

References:

Reference 1. Chae YK, Chang S, Ko T, et al: Epithelial-mesenchymal transition (EMT) signature is inversely associated with T-cell infiltration in non-small cell lung cancer (NSCLC). Sci Rep 8:2918, 2018

Reference 2. Schliekelman MJ, Tagiuchi A, Zhu J, et al. Molecular portraits of epithelial, mesenchymal and hybrid states in lung adenocarcinoma and their relevance to survival. Cancer Res. 75: 1789–1800, 2015.

Reference 3. Byers LA, Diao LX, Wang J, et al: An Epithelial-Mesenchymal Transition Gene Signature Predicts Resistance to EGFR and PI3K Inhibitors and Identifies Axl as a Therapeutic Target for Overcoming EGFR Inhibitor Resistance. Clinical Cancer Research 19:279-290, 2013

Reference 4. Tan ZT, Miow QH, Miki Y, et al. Epithelial-mesenchymal transition spectrum quantification and its efficacy in deciphering survival and drug responses of cancer patients. EMBO Mol Med 6: 1279–1293, 2014

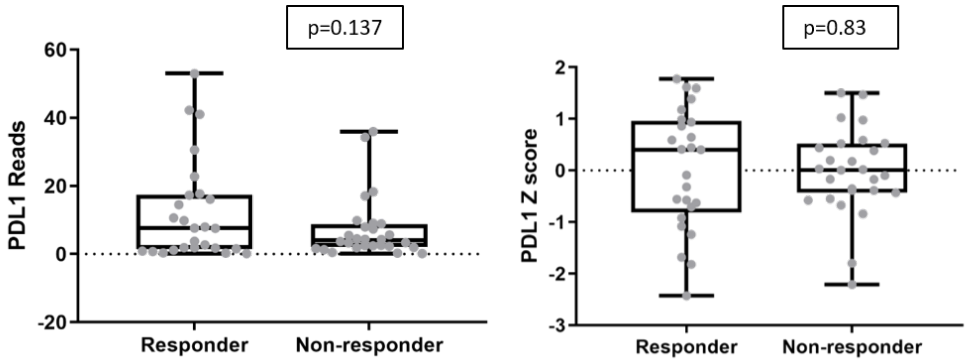
Reference 5. Kuner R, Muley T, Meister M, et al: Global gene expression analysis reveals specific patterns of cell junctions in non-small cell lung cancer subtypes. Lung Cancer 63:32-38, 2009

Reference 6. Huang RY-J, Wong MK, Tan TZ, et al. An EMT spectrum defines an anoikis-resistant and spheroidogenic intermediate mesenchymal state that is sensitive to e-cadherin restoration by a src-kinase inhibitor, saracatinib (AZD0530)/ Cell Death and Disease (2013) 4, e915; 2013

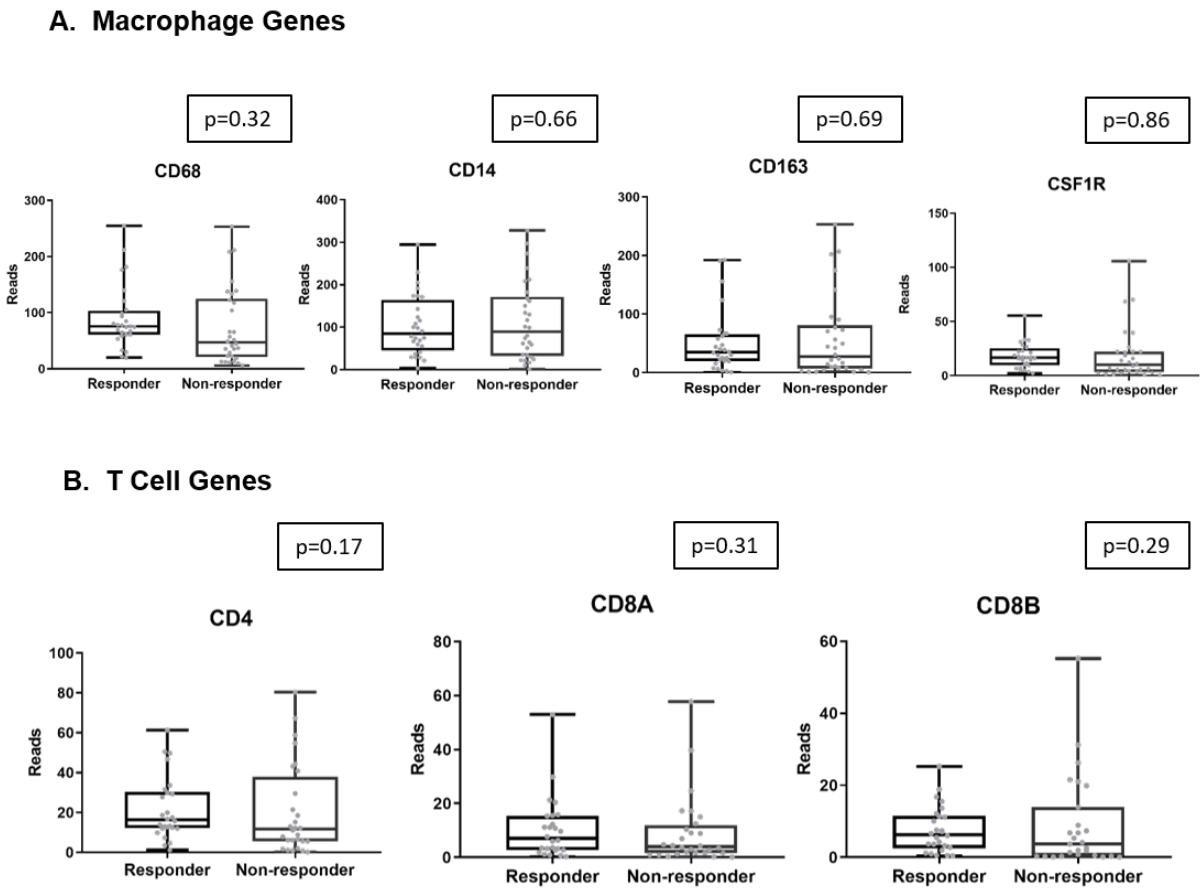
Reference 7. Zhao M., Kong L, Liu Y. Qu, H. dbEMT: a literature-based resource for Epithelial-Mesenchymal Transition genes. Sci Rep. 11459. 2015: http://dbemt.bioinfo-minzhao.org/index.html

Reference 8. Taube JH, Herschkowitz JI, Komurov K, et al. Core epithelial-to-mesenchymal transition interactome gene-expression signature is associated with claudin-low and metaplastic breast cancer subtypes. Proc. Nat. Acad. Sci. 107:15449-15454, 2010.

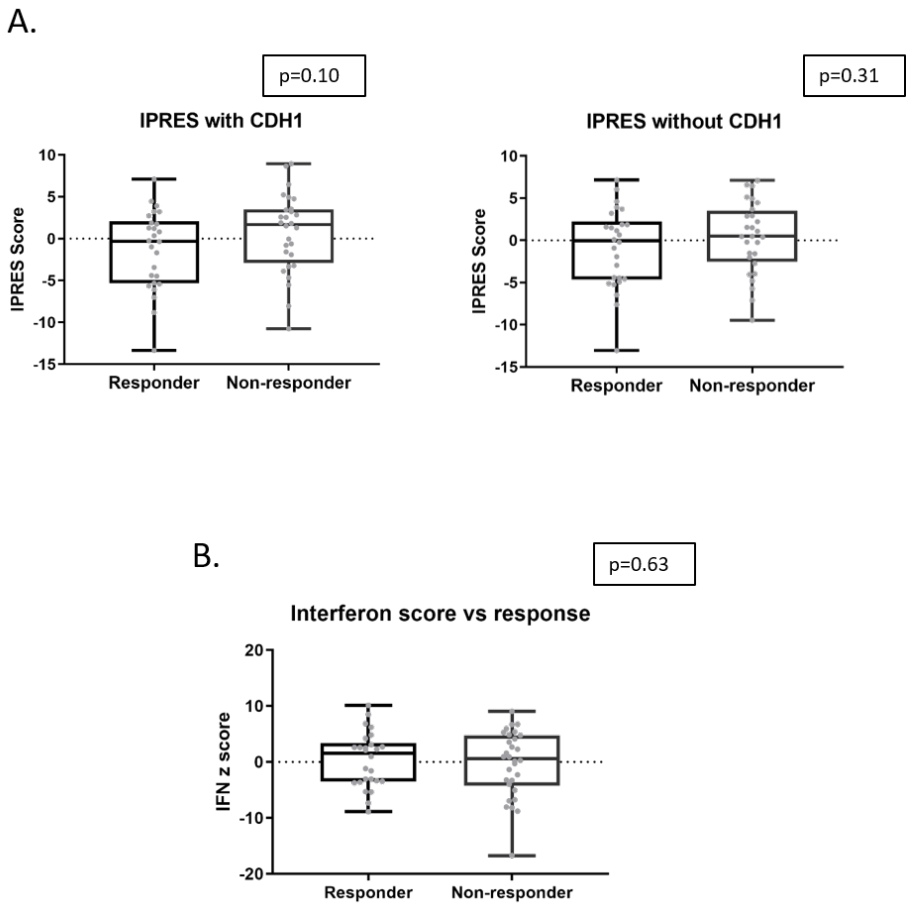
Supplemental Figure 1: PD-L1 gene expression and response. (A) Number of counts of PD-L1 gene expression levels in responders and PD patients. (B) log2 z-scores of PD-L1 gene expression levels in responders and PD patients.



Supplemental Figure 2: Comparison of markers of T cells and Macrophages with response. (A) Expression levels (number of reads) of established macrophage associated genes (CD68, CD14, CD163, CSF1R) in responders and PD patients. (B) Expression levels of established T cell associated genes (CD4, CD8A, CD8B) in responders and PD patients.



Supplemental Figure 3: Innate PD-1 resistance score (IPRES) and chronic IFN activation score and response. (A) Comparison of the log2 z-scores of the IPRES signature in responders and non-responders. The IPRES score was calculated with and without expression levels of CH1 (E-cadherin). (B) Comparison of a chronic interferon activation score in responders and non-responders. This score included 9 established genes involved in chronic interferon activation (STAT1, IFI44, IFIT1, IFIT3, OAS1, OAS2, MX1, IRF7, and ISG15).



Supplemental Figure 4. Markers of TGFβ signaling and response. Expression levels (reads) of 5 established genes involved in TGFβ signaling (TGFB1, TGFBR2, ACTA2, COL4A2, and TAGLN) in responders and non-responders.