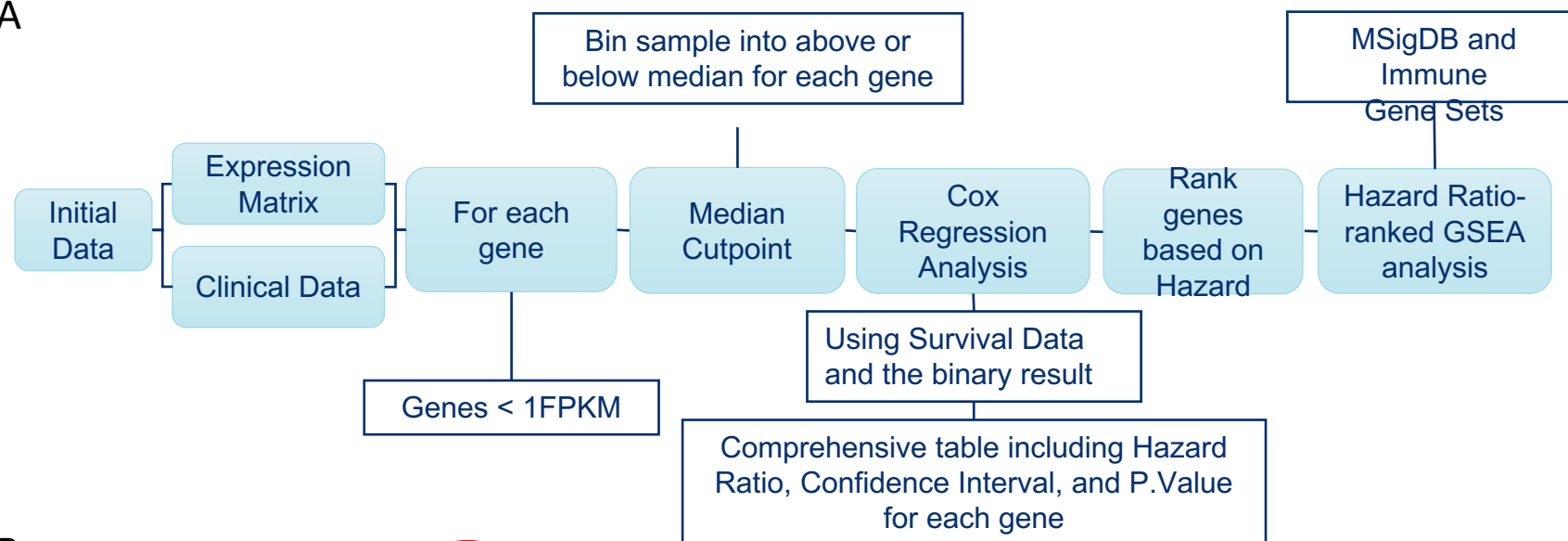


# Supplementary Figure S2.

A



B

{ Hazard Ratio Ranked GSEA } Enrichment Table **Enrichment Plot** 5

Please note this may take excess time depending on the number of gene sets being analyzed.

Upload Ranked Gene List 1  
 Browse... ICI\_Atlas\_Skin\_Pre\_OS\_G...  
 Upload complete  
 GSEA Adj Pvalue Cutoff: 1  
 Set Seed: 101 3  
 Choose Specimen Type:  Human  Mouse 2  
 Choose Gene Set: MSigDB - Hallmark  
 Upload Gene Set  
 Preview Selected Gene Set

Show 25 entries 4

ID	Description	setSize	enrichmentScore	NES	pvalue	p.adjust	qvalues	rank	lead
HALLMARK.INTERFERON.GAMMA.RESPONSE		194.0000	0.5413	4.5399	0.0000	0.0000	0.0000	4,974.0000	
HALLMARK.ALLOGRAFT.REJECTION		189.0000	0.5008	4.1804	0.0000	0.0000	0.0000	3,493.0000	
HALLMARK.INTERFERON.ALPHA.RESPONSE		96.0000	0.5347	3.8982	0.0000	0.0000	0.0000	6,067.0000	
HALLMARK.MYC.TARGETS.V1		200.0000	-0.2831	-5.4371	0.0000	0.0000	0.0000	10,041.0000	
HALLMARK.INFLAMMATORY.RESPONSE		200.0000	0.3552	2.9944	0.0000	0.0000	0.0000	5,555.0000	
HALLMARK.COMPLEMENT		200.0000	0.3427	2.8886	0.0000	0.0000	0.0000	5,445.0000	
HALLMARK.IL6.JAK.STAT3.SIGNALING		87.0000	0.4513	3.2072	0.0000	0.0000	0.0000	2,992.0000	
HALLMARK.IL2.STAT5.SIGNALING		199.0000	0.2954	2.4878	0.0000	0.0000	0.0000	5,601.0000	
HALLMARK.TNFA.SIGNALING.VIA.NFKB		200.0000	0.2873	2.4215	0.0000	0.0000	0.0000	5,642.0000	
HALLMARK.KRAS.SIGNALING.UP		200.0000	0.2674	2.2542	0.0000	0.0000	0.0000	3,869.0000	
HALLMARK.E2F.TARGETS		200.0000	-0.1252	-2.4051	0.0001	0.0003	0.0002	14,644.0000	

C

{ Hazard Ratio Ranked GSEA } Enrichment Table **Enrichment Plot**

Select Gene Set:  
 Show 20 entries  
 Search:

ID	NES	pvalue
HALLMARK.INTERFERON.GAMMA.RESPONSE	4.5399	0.0000
HALLMARK.ALLOGRAFT.REJECTION	4.1804	0.0000
HALLMARK.INTERFERON.ALPHA.RESPONSE	3.8982	0.0000
HALLMARK.MYC.TARGETS.V1	-5.4371	0.0000
HALLMARK.INFLAMMATORY.RESPONSE	2.9944	0.0000
HALLMARK.COMPLEMENT	2.8886	0.0000
HALLMARK.IL6.JAK.STAT3.SIGNALING	3.2072	0.0000
HALLMARK.IL2.STAT5.SIGNALING	2.4878	0.0000
HALLMARK.TNFA.SIGNALING.VIA.NFKB	2.4215	0.0000
HALLMARK.KRAS.SIGNALING.UP	2.2542	0.0000
HALLMARK.E2F.TARGETS	-2.4051	0.0001
HALLMARK.DNA.REPAIR	-2.1093	0.0011
HALLMARK.APOPTOSIS	1.8783	0.0013
HALLMARK.APICAL.JUNCTION	1.8916	0.0038
HALLMARK.EPITHELIAL.MESENCHYMAL.TRANSITION	1.7579	0.0037
HALLMARK.KRAS.SIGNALING.DN	1.6751	0.0046
HALLMARK.XENOBIOTIC.METABOLISM	1.7073	0.0059
HALLMARK.UV.RESPONSE.DN	1.6848	0.0087
HALLMARK.COAGULATION	1.6737	0.0093
HALLMARK.G2M.CHECKPOINT	-1.5258	0.0141

GSEA Enrichment Plot  
 NES: 4.53985746689279  
 Pvalue: 2.50651317803591e-40

2 HALLMARK.INTERFERON.GAMMA.RESPONSE

Running Enrichment Score

Ranked List Metric

Rank in Ordered Dataset

Download as SVG Download as PDF

Leading Edge Genes  
 Download Leading Edge Gene Table

Search:

Leading_Edge_Rank	Gene_Symbol	Hazard_Ratio
137	ADAR	1.14
28	APOL6	1.56
39	B2M	1.52

3

**Supplementary Figure S2.** A) Schematic workflow of gene-level survival analysis followed by hazard ratio gene set enrichment analysis. With the input data of an expression matrix, clinical data. Patients were binned into categories of above and below the median for each gene expression level. A cox regression analysis was performed on each gene expression to generate a comprehensive table of gene sets to filter according to significant, high-risk patients (hazard ratio > 1, p.value < 0.05). GSEA was then performed in MsigDB and Immune Gene Sets. B) Hazard Ratio Ranked GSEA User Interface: 1) The user must upload the output derived from pipeline mode of the Cox regression analysis pipeline. 2) Next select the gene set pathway database to use for performing the GSEA on their data. 3) A seed can be set to ensure reproducibility. 4) The page will load and then present the enriched signatures table. 5) The enriched pathways can be visualized in the “Enrichment Plot” tab. C) Hazard Ratio Ranked GSEA User Interface: 1) The user can select pathways from the enrichment table that was derived. 2) These pathways as well as their normalized enrichment score and Pvalue can be visualized and downloaded. 3) The user can view the leading-edge genes ranked from the pathway they are visualizing.