

IOSig: immuno-oncology signatures explorer in immunotherapy treated pan-cancer cohorts

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Introduction

- Immune Signature Explorer (IOSig) is a web interface that allows the user to query and explore immune checkpoint blockage treated cohorts with gene expression signatures for the purpose of predicting response to treatment.
- Users can upload their own signature, expression and clinical dataset, or simply query the built-in signatures and data.
- Note: Only datasets with included survival information will appear in the survival cohort drop down

Outline

- This guide will walk through the 3 analysis methods within IOSig
1. Dataset Analysis
 - User uploads RNA-seq expression data with respective clinical data.
 2. User Signature Analysis
 - User uploads a list of genes to query the built-in datasets.
 3. Published Signature Analysis
 - User queries the built-in gene signatures and datasets.

About Page

Page Selection Tabs



The About page for IOSig

provides a written in-depth

description of the analysis

methods. These methods

include Area Under Receiver

Operating Characteristic Curve

(AUROC), Survival analysis,

Mann-Whitney U-test, and Gene

Set Enrichment Analysis (GSEA).

Immuno-Oncology Signature Explorer (IOSig) is an interactive Shiny application meant to facilitate the investigation of immune checkpoint inhibitor (ICI) treated datasets with gene expression biomarker signatures for prediction of responder / non-responder. Previously published gene expression signatures have been collected in addition to publicly available ICI treated RNA-seq cohorts to allow for query their own datasets or signatures against. In addition, it also possible to explore the data within the application without providing your own.

IOSig Methods

Dataset Analysis

The Dataset Analysis tab is meant for users to upload their own RNA-seq expression datasets coupled with the necessary clinical data. The RNA-seq data is expected to be in a comma or tab separated format with the columns containing the sample ids and rows containing genes. The genes should be in HUGO format. Additionally the samples cannot start with a number. If your samples start with a numerical value, add a character, like 'X' at the start.

It is also necessary for the uploaded clinical data to have specific column names. These column names are: 'Sample_ID' (sample name), 'response' (ICI response), 'os' (overall survival time), and 'os_event' (overall survival event). 'reponse' and 'os_event' should be binary columns where 1 represents responder to ICI treatment and censoring in os_event.

Genes	Sample_1	Sample_2	Sample_3	Sample_4	Sample_5	Sample_6
HHAT	0.13835056	1.53806270	0.13290465	0.51870962	0.3466875	0.10772357
TSPAN2	0.58200595	0.42199425	1.06235372	0.98291794	2.19382289	0.31626312
	0.05076419	0.00889259	0.20097367	0.1219807	0.60675926	0.02002472
MIR533	0	30.153936	8.02314899	0	21.0635426	3.99707263
TAF12	3.1017381	5.31114301	5.58928237	3.79294216	4.10813913	4.19424231
SRGAP2B	0.06112194	0.24251952	0.21939487	0.20104764	0.15246727	0.11315856
MIR3671	0	7.74066557	18.5364208	6.25030364	8.11067445	3.07820536
CFHR1	0	0	2.46464012	0.34992047	0	0.15079047
TMEN23A	0	0	0	0	0	0

Sample_ID	OS	OS_event	response
Sample_1	1300	0	1
Sample_2	977	0	1
Sample_3	977	0	1
Sample_4	163	1	0
Sample_5	163	1	0
Sample_6	163	1	0

Example RNA-seq and Clinical files can be downloaded from the left side panel on the Dataset Analysis page. Additionally, the datasets used for comparison in the AUROC portion can be filtered and selected in the left side panel.

User Signature Analysis

The User Signature Analysis tab allows a user to upload a list of genes in HUGO format to query against the datasets within IOSig. The genes should be separated by a new line and pasted into the left side panel. A unique name for the uploaded gene signature is also required. An example gene signature file can be downloaded from the left side panel as well.

Published Signature Analysis

The 'Published Signature Analysis' tab is similar to the 'User Signature Analysis' tab except that you can select from a variety of previously published gene signatures to query the IOSig datasets.

AUROC Analysis

Area under the receiver operating characteristic curve (AUROC) is a performance measurement metric for a binary classifier. In IOSig, AUROC is utilized to assess the ability of gene signature to distinguish responder and non-responder based on the gene expression values for a sample. The curve is plotted with the true positive rate on the y-axis and false positive rate on the x-axis. A higher area under the

Dataset Overview

- The “Expression Data Overview” tab in the “Dataset Overview” contains a table which details the datasets within IOSig

Page Selection []

IOSig: Immuno-Oncology Signature Explorer

About **Dataset Overview** Dataset Analysis User Signature Analysis Published Signature Analysis

Expression Data Overview Signature Overview

Expression data included in this application:

Data Set ID	N	Cancer Type	Drug	Pre On Post	Biosources	Clinical Trials ID	Platform	PMID
1 GSE67501	11	Kidney	Nivolumab	Pre	Tissue	NCT00441337, NCT00730639, NCT01354431, NCT01358721	Microarray	27491898
2 GSE99070	10	Malignant Pleural Mesothelioma	anti-PD1	Pre	Tissue		Microarray	29618661
3 GSE111414	20	NSCLC	Nivolumab	Pre/On	PBMC		RNA-seq	30765392
4 GSE154538	26	GI cancer	Nivolumab	Pre/Post	Tissue		RNA-seq	34014607
5 GSE158403	81	Melanoma	Durvalumab	Pre/On	Tissue	NCT02027961	RNA-seq	33288749
6 GSE165252	71	Esophageal Cancer	Atezolizumab	Pre/On/Post	Tissue	NCT03087864	RNA-seq	33504550
7 GSE165278	22	Melanoma	Ipilimumab	Pre/Post	Tissue	NCT00796991, NCT00495066, NCT00920907, NCT00324155, NCT00162123, NCT0140045 and NCT00289640, NCT00495066, NCT00636168, NCT01515189, NCT00086489, NCT00471887	RNA-seq	33588426
8 GSE173839	71	Breast	Durvalumab	Pre	Tissue	NCT01042379	Microarray	34143979
9 GSE176307	87	Bladder	anti-PD1 or anti-PDL1	Pre	Tissue		RNA-seq	34294892
10 GSE179351	52	GI cancer (CRC & PDAC)	Ipi + Nivo	Pre/Post	Tissue	NCT03104439	RNA-seq	35122060

Showing 1 to 10 of 36 entries

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Signature Overview

The “Signature Overview” page details the previously published gene expression signatures included in IOSig. Various information including the PubMed ID, a brief description of the signature, and the number of genes within a signature are found in the table. Additionally, the genes within a signature can be viewed in the left panel.

Page Selection

About **Dataset Overview** Dataset Analysis User Signature Analysis Published Signature Analysis

Expression Data Overview **Signature Overview**

View Genes Within Signature

angio genesis

Show entries Search:

	Name	Description	Number of Genes	PMID
1	Angiogenesis	This signature is constructed from genes which are highly coexpressed in the angiogenesis pathway.	16	34965943
2	Auslander - Impres	IMPRES score based on logical comparison of quantile-normalized expression of pre-defined checkpoint gene pairs.	15	30127394
3	Chaurio	A set of genes that reflect T and B cell responses in human cancer. CXCL13 is the crucial marker	7	35021053
4	Chemokine	Chemokine gene set	12	21703392; 23097687
5	Davoli Cytotoxic Immune Signature	A signature based on scoring the immune infiltration based on gene expression profile.	7	28104840

Showing 1 to 5 of 16 entries Previous **1** 2 3 4 Next

View genes within a signature

Signature data included in this application:

Show 5 entries Search:

Gene Signature Name	Description	Number of Genes	PMID
Angiogenesis	This signature is constructed from genes which are highly coexpressed in the angiogenesis pathway.	16	34965943
Auslander - Impres	IMPRES score based on logical comparison of quantile-normalized expression of pre-defined checkpoint gene pairs.	15	30127394
Chaurio	A set of genes that reflect T and B cell responses in human cancer. CXCL13 is the crucial marker	7	35021053
Chemokine	Chemokine gene set	12	21703392; 23097687
Davoli Cytotoxic Immune Signature	A signature based on scoring the immune infiltration based on gene expression profile.	7	28104840

Showing 1 to 5 of 30 entries Previous 1 2 3 4 5 6 Next

Dataset Analysis

- The dataset analysis method in IOSig allows the user to import a tab or comma separated RNA-sequencing file and clinical data file.

RNA-Seq File

- Prior cleaning and normalization recommended
- HUGO format for genes
- Column 1 must contain the genes
- Sample IDs cannot begin with a number

Clinical File

- 4 columns required: 'Sample_ID', 'response', 'os', 'os_event'
- Sample IDs cannot begin with a number
- Response must be 1 (responder) or 0 (non-responder)
- 'os' must be in numerical format
- os_event must be 1 (event occurred) or 0 (no event occurred)

Genes	Sample_1	Sample_2	Sample_3	Sample_4	Sample_5	Sample_6
HHAT	0.13825056	1.53826279	0.15290465	0.51870962	0.3466875	0.10772357
TSPAN2	0.58290595	0.42199425	1.06235372	0.98291794	2.19382289	0.31626312
TNN	0.05076419	0.00839259	0.20097367	0.1219807	0.60676926	0.02002472
MIR553	0	30.153936	8.02314899	0	21.0635426	3.99707263
TAF12	3.1017382	5.31114303	5.58928237	3.79294216	4.10813913	4.19424231
SRGAP2B	0.06112194	0.24251952	0.21939487	0.20104764	0.15246727	0.11315856
MIR3671	0	7.74066557	18.5362408	6.25030364	8.11067445	3.07820536
CFHR1	0	0	2.46464012	0.34992047	0	0.15079047
TMEM234	0	0	0	0	0	0

Sample_ID	os	os_event	response
Sample_1	1300	0	1
Sample_2	977	0	1
Sample_3	977	0	1
Sample_4	163	1	0
Sample_5	163	1	0
Sample_6	163	1	0

Dataset Analysis - Import

Link to download example RNA-seq file

Button to upload RNA-seq file

Link to download example clinical file

Button to upload clinical file

Button to confirm file upload and cohort selection

Optional cancer type cohort filter

Individual cohort filter

IOSig: Immuno-Oncology Signature Explorer

Dataset Analysis

[Click for example sequence file](#)
Please upload an expression dataset
[Browse...](#) example_seq_f
Upload complete

[Click for example clinical data](#)
Please upload relevant clinical data
[Browse...](#) example_clin_f
Upload complete

Run analysis on dataset

Filter datasets by cancer type
Melanoma

Select datasets to use for AUROC Comparison and Correlation
 GSE158403_Pre
 GSE158403_On
 GSE165278_Pre
 GSE165278_On
 GSE186143
 Hintzsche
 Du_on
 Du_pre
 Gis_Jon_01_PD1_CTL_A4

Import AUROC Overview AUROC Comparison AUROC Correlation Mann Whitney Survival GSEA

Show 10 entries Search:

Invalid_Genes
141 WDR60
142 C7orf26
143 C7orf77
144 TWISTNB
145 FAM71F1
146 KIAA0895
147 C7orf69
148 MPP6
149 FAM71F2
150 ZBED6CL

Showing 141 to 150 of [Previous](#) [1](#) ... [14](#) [15](#) [16](#) ... [19](#) [Next](#) entries

Uploaded Expression Data

RNA-seq and Clinical data, uploaded by user, is displayed below after upload confirmation

Genes	Sample_1	Sample_2	Sample_3	Sample_4	Sample_5	Sample_6
1 HHAT	0.138250563	1.53826279	0.152904653	0.518709618	0.346687499	0.107723567
2 TSPAN2	0.582905954	0.421994253	1.062353719	0.982917943	2.193822889	0.316263122
3 TNN	0.050764194	0.008392586	0.200973673	0.121980702	0.606769257	0.020024715
4 MIR553	0	30.15393604	8.023148985	0	21.06354259	3.997072629

Dataset Analysis – AUROC Overview

IOSig: Immuno-Oncology Signature Explorer

The screenshot shows the 'AUROC Overview' section of the IOSig interface. Key features highlighted include:

- Dataset Analysis tab:** Selected by a red box.
- AUROC Overview tab:** Selected by a red box.
- Average AUC is: 0.4926:** Displayed in a red box.
- Table:** Shows the Average AUC value for various signatures against uploaded data. The table includes columns for AUC, Cohort, and Signature. The first row is highlighted in red.

	AUC	Cohort	Signature
1	0.67	example_seq_file	gMDSC
2	0.67	example_seq_file	ifn γ 18
3	0.67	example_seq_file	impres
4	0.67	example_seq_file	ipi_neo
5	0.67	example_seq_file	mMDSC
6	0.67	example_seq_file	Ock
7	0.67	example_seq_file	tip_hot
8	0.56	example_seq_file	chemokines
9	0.56	example_seq_file	glycolysis
10	0.56	example_seq_file	pan
- Select signature to view AUROC plot:** A dropdown menu shows 'ipi_neo' selected. A red arrow points from the text to the dropdown.
- Download AUROC Plot button:** A blue button with a download icon labeled 'Download AUROC Plot'. A red arrow points from the text to the button.
- AUROC Plot:** A graph showing the relationship between the false positive fraction and the true positive fraction. The x-axis is 'false_positive_fraction' (0.00 to 1.00) and the y-axis is 'true_positive_fraction' (0.00 to 1.00). The plot title is 'ipi_neo' and the AUC value is 0.66667. The Z Score method is indicated at the bottom right.
- Table displaying the AUC value of uploaded data against all signatures in IOSig:** A red bracket highlights the entire table area.

Dataset Analysis – AUROC Comparison

IOSig: Immuno-Oncology Signature Explorer

The screenshot shows the 'Dataset Analysis' section of the IOSig platform. The 'Dataset Analysis' tab is selected, highlighted with a red box. Below it, the 'AUROC Comparison' tab is also highlighted with a red box. A red arrow points from the text 'Download the AUROC Comparison plot' to the 'Download Plot' button.

Dataset Analysis

Click for example sequence file

Please upload an expression dataset

Browse... example_seq_f
Upload complete

Click for example clinical data

Please upload relevant clinical data

Browse... example_clin_f
Upload complete

Run analysis on dataset

Filter datasets by cancer type

Melanoma

Select datasets to use for AUROC Comparison and Correlation

GSE158403_Pre
 GSE158403_On
 GSE165278_Pre
 GSE165278_On
 GSE186143
 Hintzsche
 Du_on
 Du_pre
 Gile_On_PD1_CTLA4

AUROC Comparison

Download Plot

Cohorts are columns, signatures are rows

Gene Signature AUROC Performance

Cohorts

	Average	Du_on	Du_pre	example_seq_file	Gile_On_PD1	Gile_On_PD1_CTLA4	Gile_Pre_PD1	Gile_Pre_PD1_CTLA4	GSE158403_On	GSE158403_Pre	GSE165278_On	GSE165278_Pre	GSE186143	Hintzsche	Hugolo_IPRES_2016	Lauss	Lee_on	Lee_pre	Liu_naive	Liu_prog	Riaz_on	Riaz_pre	VanAllen_antitCTLA4_2015
ifng18-	0.68	0.77	0.63	0.67	0.9	0.95	0.83	0.77	0.48	0.47	0.87	0.9	0.6	0.48	0.52	0.72	0.83	0.55	0.46	0.66	0.66	0.66	0.5
effector_t-	0.67	0.67	0.56	0.44	0.95	0.95	0.84	0.78	0.53	0.48	0.81	1	0.61	0.6	0.48	0.7	0.79	0.61	0.44	0.64	0.67	0.64	0.53
ifng-effector-	0.67	0.68	0.56	0.44	0.95	0.95	0.86	0.81	0.43	0.48	0.85	1	0.62	0.5	0.5	0.69	0.8	0.62	0.47	0.64	0.63	0.65	0.5
ipi_neo-	0.66	0.66	0.6	0.67	0.9	0.95	0.83	0.75	0.47	0.5	0.83	0.8	0.6	0.5	0.49	0.74	0.82	0.52	0.47	0.7	0.7	0.66	0.45
Davoli-	0.66	0.73	0.55	0.44	0.95	0.95	0.81	0.74	0.5	0.49	0.85	0.8	0.6	0.5	0.47	0.71	0.84	0.56	0.47	0.66	0.71	0.67	0.52
tip_hot-	0.66	0.61	0.53	0.67	0.9	0.95	0.83	0.78	0.44	0.49	0.83	1	0.58	0.5	0.47	0.7	0.82	0.56	0.47	0.63	0.66	0.66	0.43
chaurio-	0.66	0.76	0.55	0.44	0.85	0.9	0.85	0.72	0.51	0.48	0.85	0.9	0.53	0.56	0.5	0.7	0.79	0.58	0.46	0.7	0.72	0.68	0.47
Rooney-	0.66	0.65	0.49	0.33	0.9	0.95	0.81	0.76	0.58	0.52	0.81	1	0.63	0.6	0.41	0.69	0.76	0.56	0.47	0.65	0.72	0.65	0.52
Roh-	0.66	0.62	0.62	0.56	0.85	0.95	0.83	0.78	0.52	0.48	0.81	0.9	0.57	0.5	0.52	0.73	0.8	0.53	0.49	0.64	0.65	0.63	0.47
mhc_2-	0.65	0.62	0.65	0.44	0.95	0.95	0.74	0.76	0.49	0.52	0.81	0.6	0.57	0.62	0.61	0.77	0.75	0.48	0.53	0.68	0.69	0.61	0.48
chemokines-	0.65	0.6	0.58	0.56	0.9	0.85	0.82	0.77	0.47	0.51	0.83	1	0.49	0.5	0.39	0.73	0.83	0.57	0.48	0.7	0.61	0.66	0.49
mMDSC-	0.64	0.68	0.59	0.67	0.85	0.9	0.7	0.75	0.54	0.52	0.8	0.8	0.45	0.46	0.42	0.71	0.86	0.48	0.49	0.69	0.67	0.64	0.47

Dataset Analysis – AUROC Correlation

Select a correlation method →

Please upload an expression dataset →

Download AUROC Correlation plot ←

The screenshot shows the 'AUROC Correlation' section of the application. On the left, there's a sidebar with options for 'Dataset Analysis' (including upload fields for expression and clinical data), a dropdown for selecting a correlation method (set to 'pearson'), and a list of datasets for comparison. The main area displays a 'Pearson Correlation heatmap' where red indicates positive correlation and blue indicates negative correlation. The axes are labeled 'Signatures' and feature a mix of biological terms like 'chemokines', 'Roh', 'NRS', 'Rooney', etc., and clinical/molecular terms like 'TLS', 'mhc_1', 'hypoxia', 'Ras', 'Mitoscore', 'Buffa', 'proliferation', 'stroma', 'angiogenesis', 'WNT', 'pan', and 'Myc'. A color scale bar on the right ranges from -1 (blue) to 1 (red), with 0 being white.

Dataset Analysis – Mann Whitney

Select a signature to view the Mann Whitney U-test boxplot

IOSig: Immuno-Oncology Signature Explorer

Dataset Analysis **Mann Whitney**

Mann Whitney U Test

Select a Mann Whitney plot to view
ipi_neo

Download Plot

Average Z Score

Responder Status

Method: Z Score

Response Type

Non-Responder Responder

p value: 0.7

Download Mann Whitney plot

Show 10 entries

Signature	P_Value	n	Responders	Non_Responders
1 Mitoscore	0.4	6	3	3
2 angiogenesis	0.7	6	3	3
3 gMDSC	0.7	6	3	3
4 hypoxia	0.7	6	3	3
5 ifng18	0.7	6	3	3
6 ifng6	0.7	6	3	3
7 impres	0.7	6	3	3
8 ipi_neo	0.7	6	3	3
9 mMDSC	0.7	6	3	3
10 Ock	0.7	6	3	3

Showing 1 to 10 of 30 entries

Previous **1** 2 3 Next

A data table showing the p-values for each signature tested against the user uploaded dataset

Dataset Analysis – Survival

IOSig: Immuno-Oncology Signature Explorer

Select a signature to view the survival plot for

Please upload an expression dataset

Please upload relevant clinical data

Filter datasets by cancer type

Select datasets to use for AUROC Comparison and Correlation

GSE158403_Pre
 GSE158403_On
 GSE165278_Pre
 GSE165278_On
 GSE186143
 Hintzsche
 Du_on
 Du_pre
 GSE158403_DD1_CTLMM

Dataset Analysis **Dataset Analysis** (highlighted)
User Signature Analysis Published Signature Analysis

Import AUROC Overview AUROC Comparison AUROC Correlation Mann Whitney **Survival** (highlighted) GSEA

Survival Download the survival plot

Select a survival plot to view chaurio

chaurio Method: Z Score

High Low

Survival probability

Time

p = 0.46

Show 10 entries Search:

Signature	P_Value	n	High.Category	Low.Category
1 stroma	0.1138	6	2	4
2 TLS	0.3173	6	1	5
3 chaurio	0.4561	6	3	3
4 Davoli	0.4561	6	3	3
5 ifng18	0.4561	6	3	3
6 ifng6	0.4561	6	3	3
7 impres	0.4561	6	3	3
8 mMDSC	0.4561	6	3	3
9 Ock	0.4561	6	3	3
10 pan	0.4561	6	3	3

Showing 1 to 10 of 30 entries Previous 1 2 3 Next

A table that displays the p-value for the signatures queried against the upload data

Dataset Analysis - GSEA

Dataset Analysis - GSEA

Dataset Analysis User Signature Analysis Published Signature Analysis

Import AUROC Overview AUROC Comparison AUROC Correlation Mann Whitney Survival **GSEA**

GSEA GSEA Comparison

Dataset Analysis

Click for example sequence file
Please upload an expression dataset

Browse... example_seq_f
Upload complete

Click for example clinical data
Please upload relevant clinical data

Browse... example_clin_f
Upload complete

Run analysis on dataset

Filter datasets by cancer type

Melanoma

Select datasets to use for AUROC Comparison and Correlation

GSE158403_Pre
 GSE158403_On
 GSE165278_Pre
 GSE165278_On
 GSE186143
 Hintzsche
 Du_on
 Du_pre
 Gide_On_PD1_CTL44
 Gide_On_PD1
 Gide_Pre_PD1_CTL44

GSEA

Select a gene set to use for GSEA

Hallmark

Download GSEA plot

Download Plot

example_seq_file

Cohort

example_seq_file

IL6_JAK_STAT3_SIGNALING
ALLOSTERIC_SIGNALING
PANCREAS_BETA CELLS
SPERMATOGENESIS
INTERFERON_ALPHA_RESPONSE_APICAL_SURFACE
APICAL_SURFACE
IL2_STAT5_SIGNALING
APICAL_SURFACE
INTERFERON_GAMMA_SPECIES_PATHWAY
REACTIVE_OXYGEN_SPECIES_PATHWAY
HEME_METABOLISM
MITO_CHECKPOINT
G2M_CHECKPOINT
E2F_TARGETS
TGF_BETA_SIGNALING
ESTROGEN_RESPONSE_LATE
PIK3CA_MELOD_SIGNALING
ESTROGEN_RESPONSE
INFLAMMATORY_RESPONSE
MYC_TARGETS_Y2
TNFA_SIGNALING_VIA_NFKB
COAGULATION
DNA_REPAIR
XENOBIOTIC_METABOLISM
PROTEIN_SECRETION
WNT_BETA_CATENIN_SIGNALING
UNFOLDED_PROTEIN_RESPONSE
HEDGEHOG_SIGNALING
ANDROGEN_RESPONSE
KRAS_SIGNALING
APOTOPSIS
BILE_ACID_METABOLISM
MTOR_SIGNALING
NOTCH_SIGNALING
HYPOXIA
UV_RESPONSE
ANGIOGENESIS
MYD44_SIGNALING
FATTY_ACID_METABOLISM
CHOLESTEROL_HOMEOSTASIS
ADIPOGENESIS
OXIDATIVE_PHOSPHORYLATION
EPITHELIAL_MESENCHYMAL_TRANSITION

NES

pathway pval padj ES NES nMoreExtreme size le

pathway	pval	padj	ES	NES	nMoreExtreme	size	le
1 HALLMARK_IL6_JAK_STAT3_SIGNALING	0.0321	0.0891	0.34	1.45	15	85	T
2 HALLMARK_KRAS_SIGNALING_DN	0.0142	0.0592	0.29	1.42	6	190	IN
3 HALLMARK_ALLOGRAFT_REJECTION	0.0209	0.0679	0.29	1.39	9	193	IL
4 HALLMARK_PANCREAS_BETA_CELLS	0.0817	0.1945	0.38	1.37	40	38	S
5 HALLMARK_SPERMATOGENESIS	0.048	0.1263	0.29	1.32	23	125	D
6 HALLMARK_INTERFERON_ALPHA_RESPONSE	0.1568	0.3135	0.27	1.18	78	95	IL
7 HALLMARK_APICAL_SURFACE	0.3333	0.5556	0.29	1.08	165	43	M
8 HALLMARK_COMPLEMENT	0.4242	0.6629	0.21	1.01	209	198	K
9 HALLMARK_IL2_STAT5_SIGNALING	0.5592	0.7812	0.2	0.95	268	196	T
10 HALLMARK_APICAL_JUNCTION	0.6577	0.8888	0.19	0.92	316	192	F

Show 10 entries Search: _____

Showing 1 to 10 of 50 entries

Previous 1 2 3 4 5 Next

The result table for the gene set enrichment analysis

Dataset Analysis– GSEA Enrichment

Scroll down on the page to view the specific enrichment plot output

Select an enrichment pathway to view 

Dataset Analysis  

Import AUROC Overview AUROC Comparison AUROC Correlation Mann Whitney Survival 

GSEA  GSEA Comparison

Enrichment Plots
Select a pathway to view  

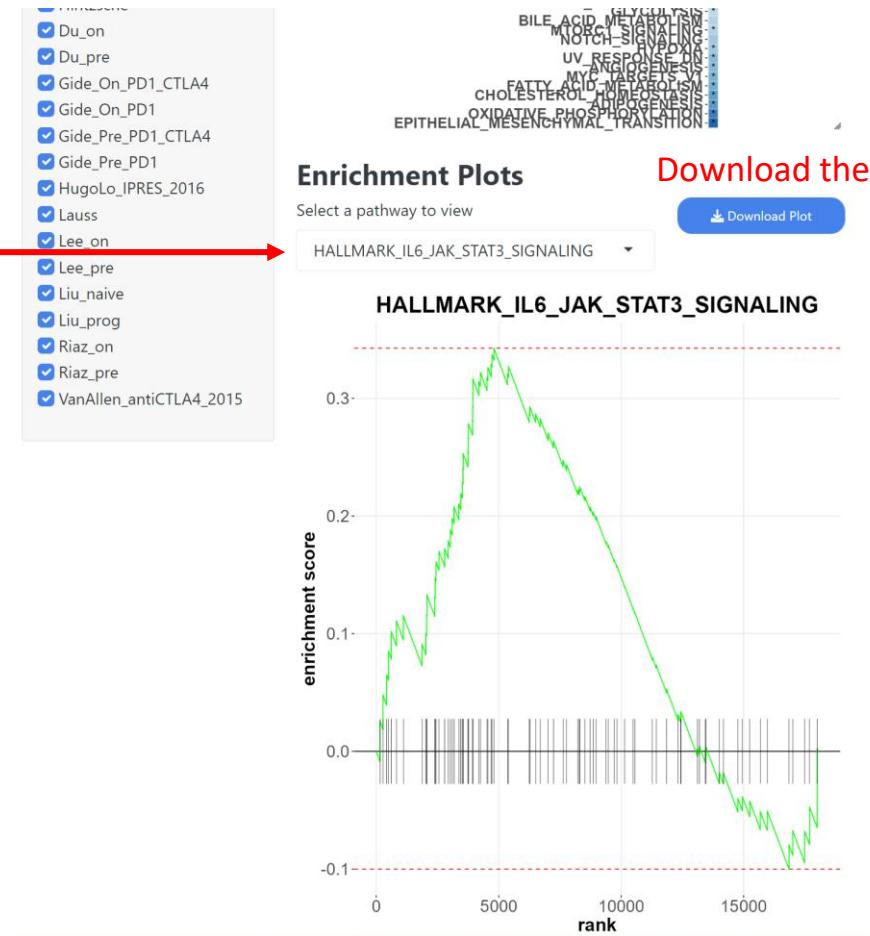
HALLMARK_IL6_JAK_STAT3_SIGNALING

enrichment score

rank

BILE_ACID_METABOLISM
MORPHOGENESIS
NITRIC_SIGNS
UV_RESPONSE
MYC_TARGETS_V2
FATTY_ACID_METABOLISM
CHOLESTEROL_HOMEOGENESIS
OXIDATIVE_PHOSPHORYLATION
EPITHELIAL_MESENCHYMAL_TRANSITION

Download the enrichment pathway plot 



Dataset Analysis – GSEA Comparison

The screenshot shows a web-based dataset analysis tool interface for GSEA Comparison. The top navigation bar includes links for About, Dataset Overview, Dataset Analysis (highlighted with a red box), User Signature Analysis, Published Signature Analysis, Import, AUROC Overview, AUROC Comparison, AUROC Correlation, Mann Whitney, Survival, and GSEA (also highlighted with a red box). Below the navigation, there are two main sections: **User Data** and **Comparison Data**.

User Data: This section allows users to upload expression datasets and clinical data. It includes fields for "example_seq_f" (Browse... and Upload complete), "example_clin_f" (Browse... and Upload complete), and a "Run analysis on dataset" button. A dropdown menu for "Gene Set" is set to "Hallmark". A red arrow points to this dropdown with the text "Select a gene set for the comparison". A blue "Download Plot" button is available below the dropdown.

Comparison Data: This section allows users to select cohorts for comparison. It includes a dropdown menu for "Cohort" set to "Braun". A red arrow points to this dropdown with the text "Select a cohort for the comparison". A blue "Download Plot" button is available below the dropdown.

Central Plot Area: The plot displays the results of the GSEA comparison between the Hallmark gene set and the Braun cohort. The y-axis lists various biological pathways, and the x-axis represents the Normalized Enrichment Score (NES). A color scale at the bottom indicates NES values from -2 (blue) to 1 (red). The plot title is "Hallmark: Braun Cohort".

Left Sidebar: This sidebar contains a "Dataset Analysis" section with a link to "Click for example sequence file" and "Click for example clinical data". It also includes a "Filter datasets by cancer type" dropdown set to "Melanoma" and a list of selected datasets for AUROC Comparison and Correlation, all marked with checked checkboxes.

User Signature Analysis

The User Signature Analysis method in IOSig allows the user to upload a **newline separated list of HUGO formatted genes** and query their ability to predict responder / non-responder in the datasets included in IOSig.

Users must provide a name for their signature that does match with one of the signatures already included in IOSig.

Signature Analysis

Enter a unique signature name

New_Signature

Enter new line separated HGNC symbols. [Example Signature File](#)

CD3E
CD8A
IFNG

User Signature Analysis - Summary

IOSig: Immuno-Oncology Signature Explorer

The screenshot shows the 'User Signature Analysis' section of the IOSig interface. On the left, a sidebar allows users to enter a signature name ('Custom_Signature'), upload a file ('Example Signature File'), paste HUGO genes ('Fake-Gene IDO1'), and confirm the upload ('Confirm signature and datasets'). It also includes filters for cancer type ('Breast Cancer NSCLC') and individual cohorts ('GSE111414_Pre', 'GSE111414_On', 'GSE173839', 'GSE190265', 'GSE194040'). The main area displays a 'Signature Summary' table comparing the user's signature ('ifng6') with 30 other signatures from the database. The table includes columns for Signature, Gene_Signature_Length, Gene_Count_Overlap, and Signature_Overlap_Percentage. A red box highlights the 'Summary' tab in the navigation bar. Red arrows point to various UI elements: the signature name input, the uploaded genes list, the confirmation button, the cancer type filter, the cohort selection checkboxes, the 'Genes' dropdown, and the 'Genes' table. Red text annotations provide instructions for each step: 'Signature Name', 'Download example signature file', 'Paste newline separated HUGO genes', 'Confirm gene signature upload and cohort selection', 'Optionally filter datasets by cancer type', 'Select individual cohorts to include / remove', 'Genes not detected as valid HUGO symbols', 'Select a signature to view gene overlap with user uploaded signature', 'View overlapping genes between user uploaded signature and signatures included in IOSig', and 'Gene overlap statistics between user uploaded signature and signatures included in IOSig'.

Signature Analysis

Enter a unique signature name

Signature Name → Custom_Signature

Download example signature file → Example Signature File

Paste newline separated HUGO genes → Fake-Gene
IDO1

Confirm gene signature upload and cohort selection → Confirm signature and datasets

Optionally filter datasets by cancer type → Breast Cancer NSCLC

Select individual cohorts to include / remove → GSE111414_Pre
GSE111414_On
GSE173839
GSE190265
GSE194040

User Signature Analysis

Summary → AUROC Overview
AUROC Comparison
AUROC Correlation
Survival
Mann Whitney
GSEA

Signature Summary

Show 10 entries Search:

Invalid Genes

1	Fake-Gene
1	Fake-Gene

Showing 1 to 1 of 1 entries Previous 1 Next

Signature	Gene_Signature_Length	Gene_Count_Overlap	Signature_Overlap_Percentage
ifng6	6	4	66.667
ifng-effector	8	3	37.5
chemokines	12	2	16.667
effector_t	6	1	16.667
mhc_1	6	1	16.667
tip_hot	12	2	16.667
chauro	7	1	14.286
ifng18	18	2	11.111
Roh	41	4	9.756
ipi_neo	32	3	9.375

Showing 1 to 10 of 30 entries Previous 1 2 3 Next

Genes

1	IDO1
1	IDO1
2	CXCL10
3	CXCL9
4	IFNG

Genes not detected as valid HUGO symbols

Select a signature to view gene overlap with user uploaded signature

ifng6

ifng6

View overlapping genes between user uploaded signature and signatures included in IOSig

Gene overlap statistics between user uploaded signature and signatures included in IOSig

User Signature Analysis – AUROC Overview

IOSig: Immuno-Oncology Signature Explorer

The screenshot illustrates the User Signature Analysis interface on the IOSig platform, specifically focusing on the AUROC Overview section.

Signature Analysis: A sidebar on the left allows users to enter a signature name (e.g., Custom_Signature), add HGNC symbols from a file, and select cancer types (e.g., Breast Cancer, NSCLC). It also lists datasets selected for querying.

AUROC Overview: This section displays the average AUC value (0.602) across all selected cohorts. It includes a table showing AUC values for each cohort and a plot of the ROC curve.

Data Table: The table shows the following data:

Cohort	AUC	Signature
1 GSE190265	0.77	Custom_Signature
2 GSE194040	0.76	Custom_Signature
3 GSE173839	0.72	Custom_Signature
4 GSE111414_Pre	0.48	Custom_Signature
5 GSE111414_On	0.28	Custom_Signature

Plot: An ROC curve plot titled "GSE111414_Pre" shows the relationship between the true positive fraction and the false positive fraction. The AUC is indicated as 0.48. A red arrow points to the "Download Plot" button, and another red arrow points to the "Select a cohort plot to view" dropdown menu.

Annotations:

- A red box highlights the "User Signature Analysis" tab in the navigation bar.
- A red box highlights the "AUROC Overview" tab in the sub-navigation bar.
- A red box highlights the "AUROC Overview" section title.
- A red box highlights the "Average AUC is: 0.602" text.
- A red box highlights the "Select an AUROC plot to view" dropdown menu.
- A red box highlights the "Download Plot" button.
- A red box highlights the "Select a cohort plot to view" dropdown menu.
- A red box highlights the "true_positive_fraction" axis label.
- A red box highlights the "false_positive_fraction" axis label.
- A red box highlights the "Z Score method" label.
- A red bracket groups the "AUROC Overview" table and the "AUROC Plot".
- A red bracket groups the "AUROC Plot" and the "Select a cohort plot to view" dropdown.
- A red bracket groups the "AUROC Plot" and the "Download Plot" button.
- A red bracket groups the "AUROC Plot" and the "Select an AUROC plot to view" dropdown.
- A red bracket groups the "AUROC Plot" and the "true_positive_fraction" axis label.
- A red bracket groups the "AUROC Plot" and the "false_positive_fraction" axis label.
- A red bracket groups the "AUROC Plot" and the "Z Score method" label.

User Signature Analysis – AUROC Comparison

The screenshot shows a web application interface for "User Signature Analysis – AUROC Comparison". The top navigation bar includes links for "About", "Dataset Overview", "Dataset Analysis", "User Signature Analysis" (which is highlighted with a red box), and "Published Signature Analysis". Below this, a secondary navigation bar includes "Summary", "AUROC Overview", "AUROC Comparison" (also highlighted with a red box), "AUROC Correlation", "Survival", "Mann Whitney", and "GSEA".

The main content area is titled "AUROC Comparison". It features a blue button labeled "Download Plot" and a red arrow pointing to it with the text "Download AUROC Plot". A red box highlights the "AUROC Comparison" link in the top navigation.

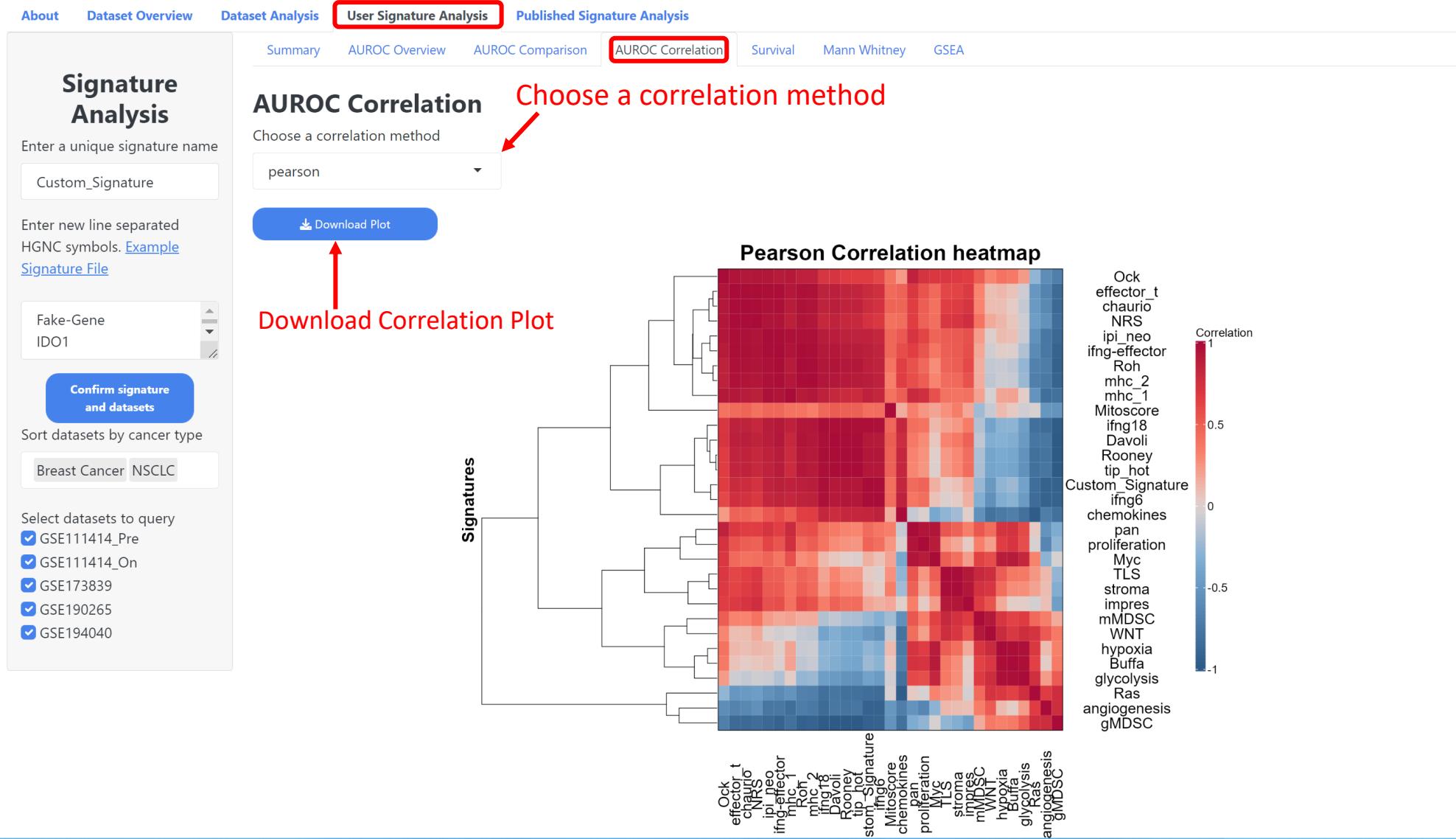
A central text box contains the instruction: "Gene signatures are in rows cohorts are columns".

To the right is a heatmap titled "Gene Signature AUROC Performance". The rows represent gene signatures (e.g., gMDSC-, chemokines, glycolysis, Roh-, tip_hot, mMDS-, Buffa, Ras, NRS, impress, ifng6-, hypoxia, ifng-effector, ifng18-, ipi_neo-) and the columns represent cohorts (Average, GSE111414_On, GSE111414_Pre, GSE173839, GSE190265, GSE194040). The heatmap uses a color scale from light orange (low AUROC) to dark red (high AUROC). A legend at the bottom right indicates the scale: "AUROC" with values 0.9 (light orange) and 1.0 (dark red).

The left sidebar contains several input fields and lists:

- "Signature Analysis" section:
 - Text input: "Enter a unique signature name" with value "Custom_Signature".
 - Text input: "Enter new line separated HGNC symbols. [Example](#) [Signature File](#)".
 - Autocomplete dropdown: "Fake-Gene IDO1".
 - Blue button: "Confirm signature and datasets".
- "Sort datasets by cancer type" section:
 - Buttons: "Breast Cancer" and "NSCLC".
- "Select datasets to query" section:
 - Checkboxes:
 - GSE111414_Pre
 - GSE111414_On
 - GSE173839
 - GSE190265
 - GSE194040

User Signature Analysis – AUROC Correlation



User Signature Analysis - Survival

IOSig: Immuno-Oncology Signature Explorer

Select a survival plot to view →

Custom_Signature

Enter new line separated HGNC symbols. [Example](#) [Signature File](#)

Fake-Gene
IDO1

Confirm signature and datasets

Sort datasets by cancer type

Breast Cancer NSCLC

Select datasets to query

GSE111414_Pre
 GSE111414_On
 GSE173839
 GSE190265
 GSE194040

Signature Analysis

Enter a unique signature name

Survival

Select a survival plot to view

GSE190265

Download survival plot

Download Plot

Survival

Survival probability

Time

High Low

p = 0.21

Survival

Mann Whitney

GSEA

Show 10 entries

Cohort P_Value n High.Category Low.Category

1 GSE190265 0.2072 43 22 21

Showing 1 to 1 of 1 entries

Previous 1 Next

A table that shows the p-value and other stats for the cohort survival analysis with the user signature

User Signature Analysis – Mann Whitney

IOSig: Immuno-Oncology Signature Explorer

About Dataset Overview Dataset Analysis **User Signature Analysis** Published Signature Analysis

Summary AUROC Overview AUROC Comparison AUROC Correlation Survival **Mann Whitney** GSEA

Mann Whitney U Test
Select a Mann Whitney plot to view
GSE194040 Download Boxplot Download Plot

Signature Analysis

Select Boxplot to view

Enter a unique signature name
Custom_Signature

Enter new line separated HGNC symbols. [Example Signature File](#)

Fake-Gene
IDO1

Confirm signature and datasets

Sort datasets by cancer type
Breast Cancer NSCLC

Select datasets to query
 GSE111414_Pre
 GSE111414_On
 GSE173839
 GSE190265
 GSE194040

GSE194040
p value: 2e-04

Average Z Score

Response Type
Non-Responder Responder

Non-Responder Responder

Responder Status

Method: Z Score

Show 10 entries Search: _____

Cohort	P_Value	n	Responders	Non_Responders
1 GSE194040	0.0002	69	31	38
2 GSE173839	0.0011	71	29	42
3 GSE190265	0.0078	43	11	32
4 GSE111414_On	0.3095	10	5	5
5 GSE111414_Pre	1	10	5	5

Showing 1 to 5 of 5 entries Previous 1 Next

View p-value and other statistics

User Signature Analysis - GSEA

Signature Analysis

Select a gene set to use

Custom_Signature

Enter new line separated HGNC symbols. [Example Signature File](#)

Fake-Gene
IDO1

Confirm signature and datasets

Sort datasets by cancer type

Breast Cancer NSCLC

Select datasets to query

GSE111414_Pre
 GSE111414_On
 GSE173839
 GSE190265
 GSE194040

GSEA

Select a cohort to view

GSEA Comparison

Select a set to use

Hallmark

GSE111414_Pre

Download Plot

Hallmark: GSE111414_Pre Cohort

ANGIOGENESIS-UV_RESPONSE_DN-MYC_TARGETS_V2-IL2_STAT5_SIGNALING-GLYCOLYSIS-ANDROGEN_RESPONSE-PROTEIN_SECRETION-WNT_BETA_CATENIN_SIGNALING-XENOBIOTIC_METABOLISM-ADIPOGENESIS-ESTROGEN_RESPONSE_LATE-COMPLEMENT-DNA_REPAIR-OXIDATIVE_PHOSPHORYLATION-MITOTIC_SPINDLE-BILE_ACID_METABOLISM-INFLAMMATORY_RESPONSE-IL6_JAK_STAT3_SIGNALING-P53_PATHWAY-MYC_TARGETS_V1-ALLOGRAFT_REJECTION-MTORC1_SIGNALING-COAGULATION-KRAS_SIGNALING_DN-HEDGEHOG_SIGNALING

NES

Summary AUROC Overview AUROC Comparison AUROC Correlation Survival Mann Whitney GSEA

Select a cohort to view

Download Plot

Show 10 entries

Search:

pathway	pval	padj	ES	NES	nMoreExtreme	size	I
1 HALLMARK_ANGIOGENESIS	0.1311	0.7738	0.76	1.52	63	25	↑
2 HALLMARK_UV_RESPONSE_DN	0.1226	0.7738	0.7	1.5	57	117	↑
3 HALLMARK_MYC_TARGETS_V2	0.1295	0.7738	0.7	1.45	64	58	↑
4 HALLMARK_IL2_STAT5_SIGNALING	0.1797	0.7738	0.61	1.31	84	188	↓
5 HALLMARK_GLYCOLYSIS	0.1928	0.7738	0.59	1.29	90	177	↑
6 HALLMARK_ANDROGEN_RESPONSE	0.2591	0.7738	0.56	1.17	127	89	↓
7 HALLMARK_PROTEIN_SECRETION	0.2846	0.7738	0.54	1.15	141	90	↓
8 HALLMARK_WNT_BETA_CATENIN_SIGNALING	0.325	0.7738	0.56	1.14	155	39	↑
9 HALLMARK_XENOBIOTIC_METABOLISM	0.3184	0.7738	0.51	1.1	148	154	↑
10 HALLMARK_ADIPGENESIS	0.2972	0.7738	0.51	1.1	139	176	↓

Showing 1 to 10 of 50 entries

Previous 1 2 3 4 5 Next

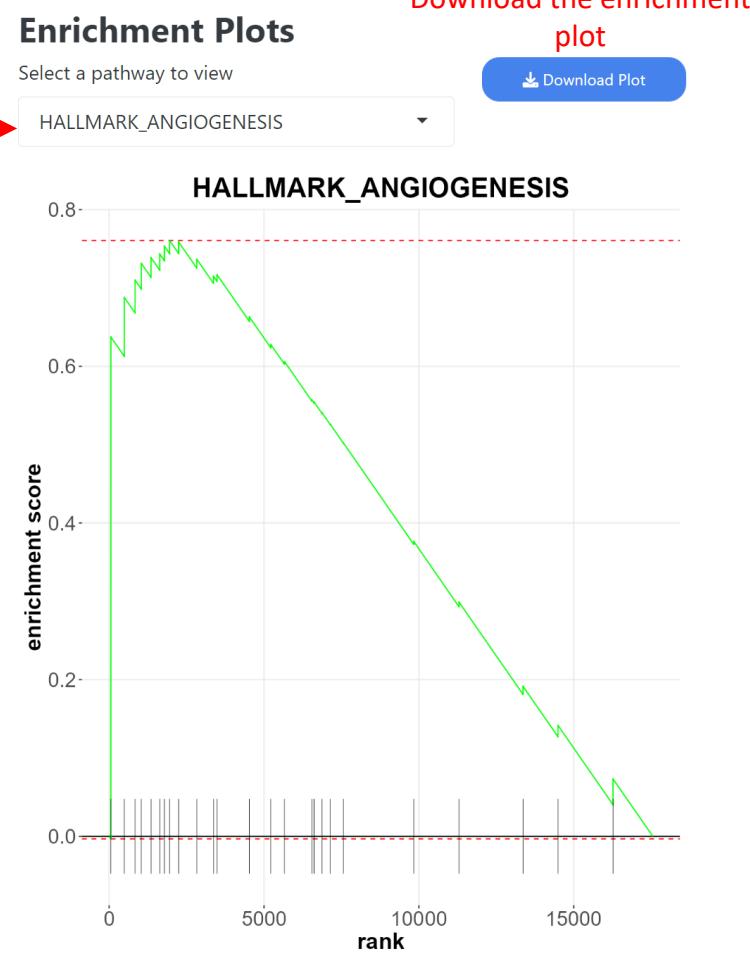
Resulting gene set enrichment data table

User Signature Analysis – GSEA Enrichment

Screenshot of the User Signature Analysis – GSEA Enrichment interface. The top navigation bar includes links for About, Dataset Overview, Dataset Analysis (selected), User Signature Analysis (highlighted with a red box), Published Signature Analysis, Summary, AUROC Overview, AUROC Comparison, AUROC Correlation, Survival, Mann Whitney, and GSEA (highlighted with a red box). A sidebar on the left shows 'Signature Analysis'. Below the navigation is a search bar with 'Show 10 entries' and 'Search:'.

Scroll down on the User Signature GSEA page

Select an enrichment pathway to view →



User Signature Analysis – GSEA Comparison

The screenshot shows the User Signature Analysis interface with several UI elements highlighted by red boxes and arrows:

- Header:** A navigation bar with tabs: About, Dataset Overview, Dataset Analysis, User Signature Analysis (highlighted), Published Signature Analysis.
- User Signature Analysis Tab:** A sub-navigation bar with tabs: Summary, AUROC Overview, AUROC Comparison, AUROC Correlation, Survival, Mann Whitney, GSEA (highlighted).
- GSEA Tab:** A sub-navigation bar with tabs: GSEA (highlighted), GSEA Comparison (highlighted).
- User Data Section:** "Select a gene set for the comparison" dropdown menu showing "Hallmark". An arrow points to this dropdown with the text "Select a gene set for User Data the comparison".
- Comparison Data Section:** "Select a gene signature for the comparison" dropdown menu showing "angiogenesis". An arrow points to this dropdown with the text "Select a signature to compare user signature against".
- Cohort Selection:** "Select a cohort to view" dropdown menu showing "GSE111414_Pre". An arrow points to this dropdown with the text "Select a cohort to use for the comparison".
- Download Plots:** Two blue download buttons labeled "Download Plot" are located below the comparison data sections.
- Signature File:** A section for entering a unique signature name ("Custom_Signature") and a file input field for "Signature File" containing "Fake-Gene" and "IDO1". A "Confirm signature and datasets" button is present.
- Dataset Filtering:** A section for "Sort datasets by cancer type" with options "Breast Cancer" and "NSCLC".
- Dataset Selection:** A section for "Select datasets to query" with checked checkboxes for "GSE111414_Pre", "GSE111414_On", "GSE173839", "GSE190265", and "GSE194040".
- Heatmaps:** Two heatmaps titled "Hallmark" show gene expression profiles across various biological pathways. The left heatmap is for "User Data" and the right is for "Comparison Data". Both heatmaps have a color scale from -1 (blue) to 1 (red) labeled "NES".

Annotations with red text and arrows:

- Select a gene set for User Data the comparison
- Select a signature to compare user signature against
- Select a cohort to use for the comparison

Previously Published Signature Analysis

The previously published signature analysis method is for users who want to query the data built into IOSig. IOSig contains RNA-seq, with accompanying clinical data, with previously published gene expression signatures.

This method allows users to explore the data without needing to provide any of their own.

Published Signature Analysis

Select a previously published signature.

ifng18 ▾

Confirm selections

Optionally sort by cancer type

GI Cancer
Esophageal Cancer

Select datasets to query.

GSE154538_Post
 GSE154538_Pre
 GSE165252_On
 GSE165252_Pre
 GSE165252_Post
 GSE183924

Previously Published Signature - Summary

IOSig: Immuno-Oncology Signature Explorer

The screenshot shows the 'Published Signature Analysis' section of the IOSig interface. On the left, a sidebar allows selecting a published signature (set to 'ifng6'), filtering by cancer type (Kidney), and choosing datasets to query (GSE67501, Braun, Motzer, Choueiri, IMmotion150, Miao). The main area displays a 'Signature Overview' table and a 'Gene Overview' table. The 'Signature Overview' table shows one entry: IFNg-6, a 6 gene IFNg associated gene set, referenced by Ayers et al (2017) with DOI doi:10.1172/JCI91190. The 'Gene Overview' table lists six genes: IDO1, CXCL10, CXCL9, HLA-DRA, IFNG, and STAT1. Red annotations provide instructions for interacting with the interface and describe the data presented.

Select a signature to view

Confirm signature and dataset selections

Optional filter datasets by cancer type

Select individual datasets to use for the analysis

Summary

AUROC Overview

AUROC Comparison

AUROC Correlation

Survival

Mann Whitney

GSEA

Published Signature Analysis

Signature Overview

Gene Overview

Show 10 entries

Search:

Gene Signature Name

Description

Number of Genes

Reference

DOI

1 IFNg-6 6 gene IFNg associated gene set 6 Ayers et al (2017) doi:10.1172/JCI91190

Showing 1 to 1 of 1 entries

Previous 1 Next

Genes

1 IDO1

2 CXCL10

3 CXCL9

4 HLA-DRA

5 IFNG

6 STAT1

Showing 1 to 6 of 6 entries

Previous 1 Next

A table that displays various data points about the selected signature

A table of the genes within the selected signature

Gene Signature Name	Description	Number of Genes	Reference	DOI
1 IFNg-6	6 gene IFNg associated gene set	6	Ayers et al (2017)	doi:10.1172/JCI91190

Genes
1 IDO1
2 CXCL10
3 CXCL9
4 HLA-DRA
5 IFNG
6 STAT1

Previously Published Signature – AUROC Overview

IOSig: Immuno-Oncology Signature Explorer

The navigation bar includes: About, Dataset Overview, Dataset Analysis, User Signature Analysis, **Published Signature Analysis**, Summary, AUROC Overview, AUROC Comparison, AUROC Correlation, Survival, Mann Whitney, GSEA.

AUROC Overview

The average AUC value is: 0.66

Show 10 entries Search:

Cohort	AUC
1 GSE158403_Pre	0.5
2 GSE158403_On	0.47
3 GSE165278_Pre	0.8
4 GSE165278_On	0.83
5 GSE186143	0.6
6 Hintzsche	0.5
7 Du_on	0.66
8 Du_pre	0.6
9 Gide_On_PD1_CTL4	0.95
10 Gide_On_PD1	0.9

Showing 1 to 10 of 21 entries Previous 1 2 3 Next

Select and AUROC to view

Select a cohort to view: GSE158403_Pre

Download the AUROC plot

GSE158403_Pre: ipi_neo

AUC: 0.49825

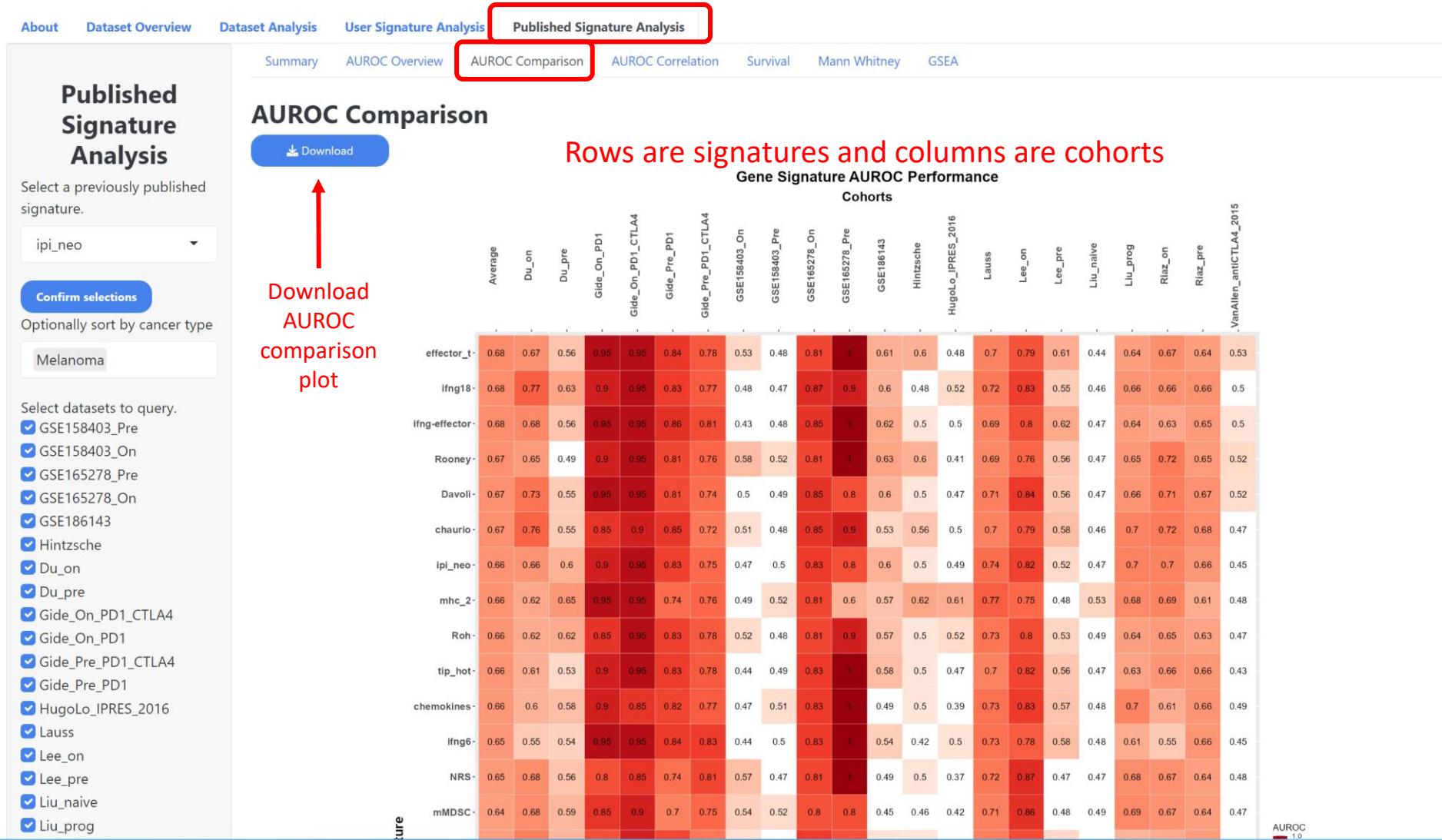
true_positive_fraction

false_positive_fraction

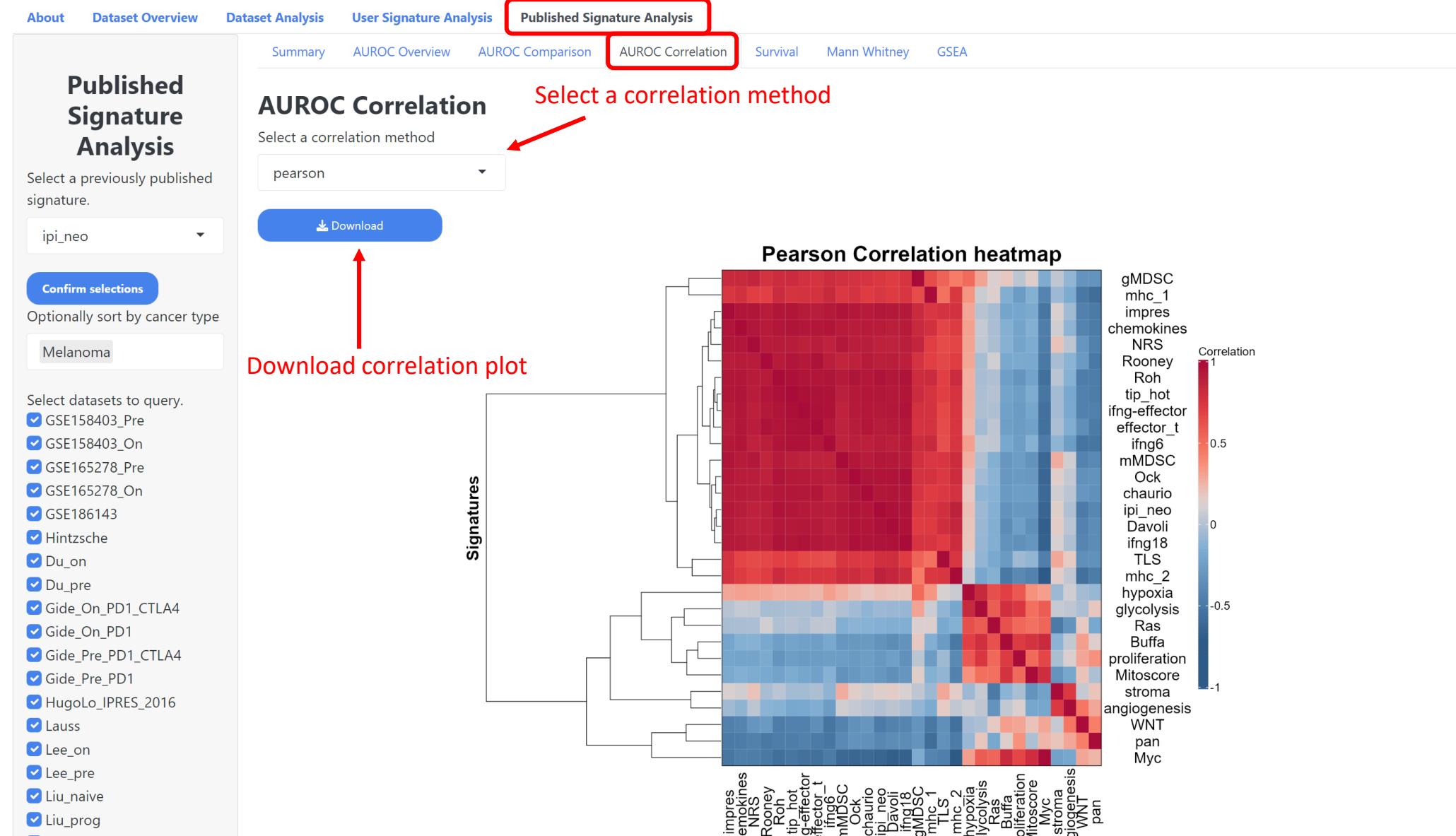
Z Score method

Table displaying the AUC values in each cohort

Previously Published Signature – AUROC Comparison



Previously Published Signatures – AUROC Correlation



Previously Published Signature - Survival

Published Signature Analysis Survival

Select a cohort to view

Select a cohort

GSE165278_On

Download Survival Plot

Download

GSE165278_On
Method: Z Score

High Low

Survival probability

Time

p = 0.0011

Survival

Mann Whitney GSEA

Show 10 entries

Search:

Cohort	P_Value	n	High.Category	Low.Category
1 GSE165278_On	0.0011	15	6	9
2 Gide_Pre_PD1	0.0278	41	21	20
3 VanAllen_antiCTLA4_2015	0.0442	41	22	19
4 Riaz_on	0.0604	49	25	24
5 Liu_prog	0.0617	48	25	23
6 Du_pre	0.0638	19	7	12
7 Gide_On_PD1	0.0653	9	5	4
8 Lee_pre	0.1055	43	15	28
9 Du_on	0.1905	31	17	14
10 Gide_Pre_PD1_CTL4	0.2026	32	16	16

Showing 1 to 10 of 19 entries

Table showing p-value and other survival analysis stats

Previously Published Signature – Mann Whitney

Published Signature Analysis

Select a previously published signature.

ipi_neo

Confirm selections

Optionally sort by cancer type

Melanoma

Select datasets to query.

- GSE158403_Pre
- GSE158403_On
- GSE165278_Pre
- GSE165278_On
- GSE186143
- Hintzsche
- Du_on
- Du_pre
- Gide_On_PD1_CTL4
- Gide_On_PD1
- Gide_Pre_PD1_CTL4
- Gide_Pre_PD1
- HugoLo_IPRES_2016
- Lauss
- Lee_on
- Lee_pre
- Liu_naive
- Liu_prog

Mann Whitney U Test

Select a cohort

Gide_Pre_PD1

Download

Gide_Pre_PD1

p value: 0.00022

Average Z Score

Non-Responder Responder Status

Method: Z Score

Response Type

Non-Responder Responder

Select a cohort to view

Download Plot

Mann Whitney

Survival GSEA

Show 10 entries

Cohort	P_Value	n	Responders	Non_Responders
Gide_Pre_PD1	0.0002	41	19	22
Lee_on	0.0122	35	6	29
Liu_prog	0.0212	48	17	31
Gide_Pre_PD1_CTL4	0.022	32	21	11
Gide_On_PD1_CTL4	0.0317	9	5	4
GSE165278_On	0.036	15	6	9
Lauss	0.0475	25	10	15
Riaz_on	0.0536	49	10	39
Gide_On_PD1	0.0635	9	4	5
Riaz_pre	0.135	49	10	39

Showing 1 to 10 of 21 entries

Previous 1 2 3 Next

Data table containing Mann Whitney p-value and other statistics

Previously Published Signature - GSEA

Published Signature Analysis

Select a previously published signature.

ipi_neo

Confirm selections

Optionally sort by cancer type

Melanoma

Select datasets to query.

- GSE158403_Pre
- GSE158403_On
- GSE165278_Pre
- GSE165278_On
- GSE186143
- Hintzsche
- Du_on
- Du_pre
- Gide_On_PD1_CTL4
- Gide_On_PD1
- Gide_Pre_PD1_CTL4
- Gide_Pre_PD1
- HugoLo_IPRES_2016
- Lauss
- Lee_on
- Lee_pre
- Liu_naive
- Liu_prog

Select a gene set

Hallmark

Select a cohort

GSE158403_Pre

Download

ipi_neo: GSE158403_Pre Cohort

ALLOGRAFT_REJECTION GLYCOLYSIS BILE_ACID_METABOLISM KRAS_SIGNALING_DN EPITHELIAL_MESENCHYMAL_TRANSITION MITOTIC_SPINDLE SPERMATOGENESIS APICAL_SURFACE HYPOXIA IL6_JAK_STAT3_SIGNALING CÖMPLEMENT ESTROGEN_RESPONSE_LATE UV_RESPONSE_UP MYOGENESIS PANCREAS_BETA_CELLS ANDROGEN_RESPONSE NOTCH_SIGNALING TGF_BETA_SIGNALING MTORC1_SIGNALING UV_RESPONSE_DN PI3K_AKT_MTOR_SIGNALING HEME_METABOLISM APOPTOSIS G2M_CHECKPOINT UNFOLDED_PROTEIN_RESPONSE PROTEIN_SECRETION DNA_REPAIR

NES

allmark

Published Signature Analysis

Summary AUROC Overview AUROC Comparison AUROC Correlation Survival Mann Whitney GSEA

Show 10 entries Search:

pathway	pval ↑↑	padj ↑↑	ES ↑↑	NES ↑↑	nMoreExtreme ↑↑	si ↑↑
1 HALLMARK_ALLOGRAFT_REJECTION	0.0363	0.7426	0.9	1.88	13	
2 HALLMARK_GLYCOLYSIS	0.1362	0.7426	0.71	1.47	52	
3 HALLMARK_BILE_ACID_METABOLISM	0.1418	0.7426	0.7	1.45	55	
4 HALLMARK_KRAS_SIGNALING_DN	0.2031	0.7426	0.62	1.31	77	
5 HALLMARK_EPITHELIAL_MESENCHYMAL_TRANSITION	0.259	0.7426	0.57	1.19	100	
6 HALLMARK_MITOTIC_SPINDLE	0.2674	0.7426	0.56	1.17	103	
7 HALLMARK_SPERMATOGENESIS	0.3282	0.7923	0.53	1.1	126	
8 HALLMARK_APICAL_SURFACE	0.4247	0.7951	0.48	0.99	157	
9 HALLMARK_HYPOXIA	0.4611	0.7951	0.45	0.94	177	
10 HALLMARK_IL6_JAK_STAT3_SIGNALING	0.5183	0.8318	0.43	0.89	197	

Showing 1 to 10 of 50 entries

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A data table showing the results of the GSEA analysis