

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

IOSig: Immuno-Oncology Signature Explorer

About IOSig

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.

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).

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
TNN	0.05076419	0.00889259	0.20097367	0.1219807	0.60675926	0.02002472
MIR553	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	18.53634086	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:

Expression data included in this application:									
Show 10 entries									
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

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- [Dataset Overview](#)
- [Dataset Analysis](#)
- [User Signature Analysis](#)
- [Published Signature Analysis](#)

- [Expression Data Overview](#)
- [Signature Overview](#)

IOSig: Immuno-Oncology Signature Explorer

View genes within a signature

View Genes Within Signature

Show entries Search:

Gene Signature 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

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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

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_PD1_CTL_A4

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 'Dataset Analysis' section of the IOSig platform. The 'AUROC Overview' tab is selected. A red box highlights the 'AUROC Overview' button in the top navigation bar. Another red box highlights the 'Average AUC is: 0.4926' text. A third red box highlights the table below, which displays the AUC values for various signatures. A fourth red box highlights the 'Download AUROC Plot' button. Red arrows point from the annotations to their respective elements.

Annotations:

- Plot download button:** Points to the blue 'Download AUROC Plot' button.
- Select signature to view AUROC plot:** Points to the dropdown menu labeled 'ipi_neo'.
- Average AUC value of all signatures in IOSig on uploaded data:** Points to the text 'Average AUC is: 0.4926'.
- Table displaying the AUC value of uploaded data against all signatures in IOSig:** Points to the table below.

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
 GSE186143_GSM341514

AUROC Overview

Average AUC is: 0.4926

AUC	Cohort	Signature
0.67	example_seq_file	gMDSC
0.67	example_seq_file	ifn γ 18
0.67	example_seq_file	impres
0.67	example_seq_file	ipi_neo
0.67	example_seq_file	mMDSC
0.67	example_seq_file	Ock
0.67	example_seq_file	tip_hot
0.56	example_seq_file	chemokines
0.56	example_seq_file	glycolysis
0.56	example_seq_file	pan

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

AUROC Overview

Average AUC value of all signatures in IOSig on uploaded data

Select a signature to view ipi_neo

Download AUROC Plot

AUROC Plot for ipi_neo

AUC: 0.66667

true_positive_fraction

false_positive_fraction

Z Score method

IOSig

Dataset Analysis – AUROC Comparison

IOSig: Immuno-Oncology Signature Explorer

Dataset Analysis – AUROC Comparison

Dataset Analysis User Signature Analysis Published Signature Analysis

Import AUROC Overview AUROC Comparison AUROC Correlation Mann Whitney Survival GSEA

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

AUROC Comparison

Download the AUROC Comparison 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	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
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_CTL4A
 Gide_On_PD1
 Gide_Pre_PD1_CTL4A

Dataset Analysis Dataset Overview Dataset Analysis User Signature Analysis Published Signature Analysis

Import AUROC Overview AUROC Comparison AUROC Correlation Mann Whitney Survival GSEA

AUROC Correlation

Choose a correlation method
pearson ▾
pearson
spearman
kendall

Download Plot ← Download AUROC Correlation plot

Pearson Correlation heatmap

Signatures

Chemokines, impres, Roh, tip_hot, NRS, Rooney, ifng-effector, effector_t, ifng6, chaurio, Davoli, Ock, mMDSC, ipi_neo, ifng18, mhc_1, TLS, mhc_2, hypoxia, glycolysis, Ras, Mitoscore, Buffa, proliferation, stroma, angiogenesis, WNT, pan, Myc

Correlation

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 Mann Whitney plot

Download Plot

Average Z Score

Responder Status

Method: Z Score

Response Type

Non-Responder Responder

Signature **P_Value** **n** **Responders** **Non_Responders**

Signature	P_Value	n	Responders	Non_Responders
Mitoscore	0.4	6	3	3
angiogenesis	0.7	6	3	3
gMDSC	0.7	6	3	3
hypoxia	0.7	6	3	3
ifng18	0.7	6	3	3
ifng6	0.7	6	3	3
impres	0.7	6	3	3
ipi_neo	0.7	6	3	3
mMDSC	0.7	6	3	3
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

Survival

Download the survival plot

chaurio

Method: Z Score

High Low

Survival probability

Time

p = 0.46

Survival

Dataset Analysis User Signature Analysis Published Signature Analysis Import AUROC Overview AUROC Comparison AUROC Correlation Mann Whitney Survival GSEA

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

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

Dataset Analysis - GSEA

Select a gene set to use

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_CTL4
- Gide_On_PD1
- Gide_Pre_PD1_CTL4

GSEA

Select a gene set to use for GSEA

Hallmark

[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
MTORC1_SIGNALING
NOTCH_SIGNALING
HYPOXIA
UV_RESPONSE
ANGIOGENESIS
MYD44_SIGNALING
CHOLESTEROL_HOMEOSTASIS
ADIPOGENESIS
OXIDATIVE_PHOSPHORYLATION
EPITHELIAL_MESENCHYMAL_TRANSITION

NES

Dataset Analysis

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[GSEA](#) [GSEA Comparison](#)

Show 10 entries

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

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

Dataset Analysis → GSEA

Import AUROC Overview AUROC Comparison AUROC Correlation Mann Whitney Survival GSEA

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

Select an enrichment pathway to view

- 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
- Riaz_on
- Riaz_pre
- VanAllen_antiCTLA4_2015

BILE_ACID_METABOLISM
GLYCOLYSIS
MORPHOGENESIS
NODAL_SIGNALING
NUCLEAR_HYPOXIA
UV_RESPONSE_SNP
MYC_TARGETS_SFV
FATTY_ACID_METABOLISM
CHOLESTEROL_HOMEOGENESIS
OXIDATIVE_PHOSPHORYLATION
EPITHELIAL_MESENCHYMAL_TRANSITION

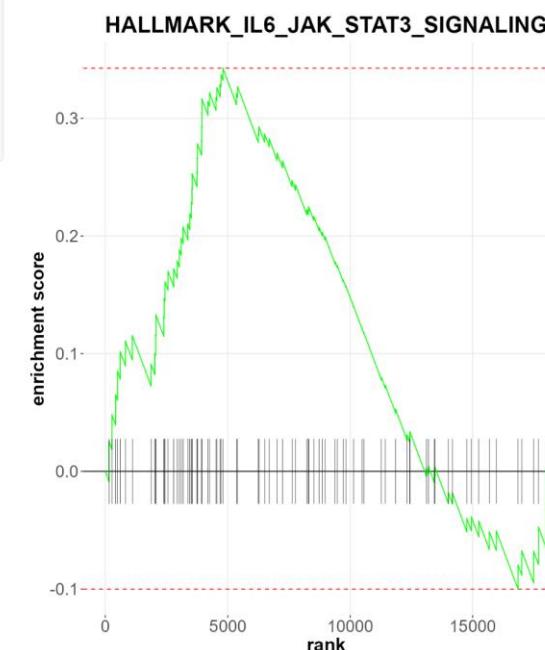
Enrichment Plots

Select a pathway to view

HALLMARK_IL6_JAK_STAT3_SIGNALING

Download the enrichment pathway plot

Download Plot



Dataset Analysis – 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

Dataset Analysis

[Dataset Overview](#) **Dataset Analysis** [User Signature Analysis](#) [Published Signature Analysis](#)

[Import](#) [AUROC Overview](#) [AUROC Comparison](#) [AUROC Correlation](#) [Mann Whitney](#) [Survival](#) **GSEA**

[GSEA](#) **GSEA Comparison**

User Data

Select a gene set for the comparison

Gene Set: Hallmark

[Download Plot](#)

Comparison Data

Select a cohort for the comparison

Cohort: Braun

[Download Plot](#)

example_seq_file Cohort

example_seq_file

Hallmark Gene Sets

IL6_JAK_STAT3_SIGNALING, KRAS_SIGNALING_DN, ALLOGRAFT_REJECTION, PANCREAS_BETA_CELLS, SPERMATOGENESIS, INTERFERON_ALPHA_RESPONSE_APICAL_SURFACE, COMPLEMENT, IL2_STATS_SIGNALING_APICAL_JUNCTION, INTERFERON_GAMMA_RESPONSE, REACTIVE_OXYGEN_SPECIES_PATHWAY, HEME_METABOLISM, MITOTIC_SPINDLE, G2M_CHECKPOINT, E2F_TARGETS, P53_PATHWAY, TGF_BETA_SIGNALING, ESTROGEN_RESPONSE_LATE, PI3K_AKT_MTOR_SIGNALING, ESTROGEN_RESPONSE_EARLY, INFLAMMATORY_RESPONSE, MYOGENESIS, MYC_TARGETS_V2, UV_RESPONSE_UP, TNFA_SIGNALING_VIA_NFKB, COAGULATION, DNA_REPAIR, XENOBIOTIC_METABOLISM, PROTEIN_SECRETION, WNT_BETA_CATENIN_SIGNALING, UNFOLDED_PROTEIN_RESPONSE, HEDGEHOG_SIGNALING, PEROXISOME, ANDROGEN_RESPONSE

NES

Hallmark: Braun Cohort

Braun

UNFOLDED_PROTEIN_RESPONSE, ESTROGEN_RESPONSE_LATE, NOTCH_SIGNALING, SPERMATOGENESIS, UV_RESPONSE_DN, ESTROGEN_RESPONSE_EARLY, INTERFERON_ALPHA_RESPONSE, COMPLEMENT, PANCREAS_BETA_CELLS, E2F_TARGETS, KRAS_SIGNALING_DN, COAGULATION, INTERFERON_GAMMA_RESPONSE, EPITHELIAL_MESENCHYMAL_TRANSITION, FATTY_ACID_METABOLISM, HEME_METABOLISM, MYOGENESIS, ANGIOGENESIS, TGF_BETA_SIGNALING, G2M_CHECKPOINT, APICAL_SURFACE, PEROXISOME, CHOLESTEROL_HOMEOSTASIS, HEDGEHOG_SIGNALING, ALLOGRAFT_REJECTION, UV_RESPONSE_UP, OXIDATIVE_PHOSPHORYLATION, PROTEIN_SECRETION, INFLAMMATORY_RESPONSE, TNFA_SIGNALING_VIA_NFKB, HYPOXIA, IL6_JAK_STAT3_SIGNALING, DNA_REPAIR, MYC_TARGETS_V2, MITOTIC_SPINDLE, MTORC1_SIGNALING

NES

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 platform. 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, titled 'Signature Summary', displays gene overlap statistics between the user's signature and existing ones. A table lists 'Signature', 'Gene_Signature_Length', 'Gene_Count_Overlap', and 'Signature_Overlap_Percentage'. The table shows results for 'ifng6', 'ifng-effector', 'chemokines', 'effector_t', 'mhc_1', 'tip_hot', 'chauro', 'ifng18', 'Roh', and 'ipi_neo'. A red box highlights the 'Summary' tab in the navigation bar.

Annotations provide instructions for using the tool:

- Signature Name:** Points to the 'Custom_Signature' input field.
- Download example signature file:** Points to the 'Example Signature File' link.
- Paste newline separated HUGO genes:** Points to the 'Fake-Gene IDO1' input field.
- Confirm gene signature upload and cohort selection:** Points to the 'Confirm signature and datasets' button.
- Optionally filter datasets by cancer type:** Points to the 'Breast Cancer NSCLC' filter buttons.
- Select individual cohorts to include / remove:** Points to the list of checked cohorts.
- Genes not detected as valid HUGO symbols:** Points to the 'Invalid_Genes' section listing 'Fake-Gene'.
- Select a signature to view gene overlap with user uploaded signature:** Points to the dropdown menu set to 'ifng6'.
- View overlapping genes between user uploaded signature and signatures included in IOSig:** Points to the 'Genes' section listing 'IDO1', 'CXCL10', 'CXCL9', and 'IFNG'.
- Gene overlap statistics between user uploaded signature and signatures included in IOSig:** Points to the bottom of the table.

User Signature Analysis – AUROC Overview

IOSig: Immuno-Oncology Signature Explorer

The average AUC value of the signature across all selected cohorts

Average AUC is: 0.602

Select a cohort plot to view

Select an AUROC plot to view

Download AUROC plot

Signature Analysis

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

AUROC Overview

Show 10 entries

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

Showing 1 to 5 of 5 entries

Previous 1 Next

AUROC: 0.48

true_positive_fraction

false_positive_fraction

Z Score method

GSE111414_Pre

Detailed description of the AUROC plot: The plot shows the relationship between the false positive fraction (x-axis) and the true positive fraction (y-axis). The x-axis ranges from 0.00 to 1.00 with major ticks at 0.25, 0.50, 0.75, and 1.00. The y-axis ranges from 0.00 to 1.00 with major ticks at 0.25, 0.50, 0.75, and 1.00. A black step-like curve starts at (0.0, 0.0), remains flat until x ≈ 0.25, then jumps to y ≈ 0.35, remains flat until x ≈ 0.50, then jumps to y ≈ 0.75, remains flat until x ≈ 0.75, then jumps to y ≈ 0.95, and finally reaches (1.0, 1.0). The area under this curve is labeled 'AUROC: 0.48'.

User Signature Analysis – AUROC Comparison

User Signature Analysis

AUROC Comparison

Download AUROC Plot

**Gene signatures are in rows
cohorts are columns**

Gene Signature AUROC Performance

Signature	Cohorts					
	Average	GSE111414_On	GSE111414_Pre	GSE173839	GSE190265	GSE194040
gMDSC-	0.72	0.92	0.8	0.69	0.53	0.66
chemokines	0.72	0.52	0.76	0.72	0.79	0.8
glycolysis-	0.67	1	0.4	0.8	0.51	0.66
Roh-	0.67	0.56	0.56	0.67	0.8	0.75
tip_hot-	0.66	0.48	0.6	0.68	0.83	0.72
mMDSC-	0.64	0.76	0.52	0.58	0.66	0.68
Buffa-	0.63	0.8	0.44	0.74	0.55	0.64
Ras-	0.63	0.84	0.6	0.65	0.57	0.51
NRS-	0.62	0.56	0.48	0.61	0.77	0.69
impres-	0.62	0.64	0.56	0.56	0.71	0.63
ifng6-	0.62	0.28	0.52	0.74	0.78	0.76
hypoxia-	0.61	0.88	0.32	0.74	0.54	0.6
ifng-effector-	0.61	0.44	0.4	0.66	0.83	0.73
ifng18-	0.6	0.32	0.48	0.67	0.82	0.73
ipi_neo-	0.6	0.44	0.36	0.67	0.81	0.73
					AUROC	
					1.0	0.9

User Signature Analysis – AUROC Correlation

Signature Analysis

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

AUROC Correlation

Choose a correlation method

pearson

Download Plot

Choose a correlation method

Pearson Correlation heatmap

Download Correlation Plot

Ock_effector_t
chauroi
NRS
ipi_neo
ifng-effector
Roh
mhc_2
mhc_1
Mitoscoring
ifng18
Davoli
Rooney
tip_hot
Custom_Signature
ifng6
chemokines
pan
proliferation
Myc
TLS
stroma
impres
mMDSC
WNT
hypoxia
Buffa
glycolysis
Ras
angiogenesis
gMDSC

Correlation

User Signature Analysis - Survival

IOSig: Immuno-Oncology Signature Explorer

Select a survival plot to view →

Signature Analysis

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

Survival

Select a survival plot to view
GSE190265

Download survival plot →

Survival probability vs Time

GSE190265 Method: Z Score

High Low

Survival probability

Time

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

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

Select Boxplot to view

User Signature Analysis

Mann Whitney

Download Boxplot

Download Plot

Signature Analysis

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
GSE194040	0.0002	69	31	38
GSE173839	0.0011	71	29	42
GSE190265	0.0078	43	11	32
GSE111414_On	0.3095	10	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

Select a gene set to use

Custom_Signature →

GSEA →

Select a cohort to view →

Download Plot →

Resulting gene set enrichment data table

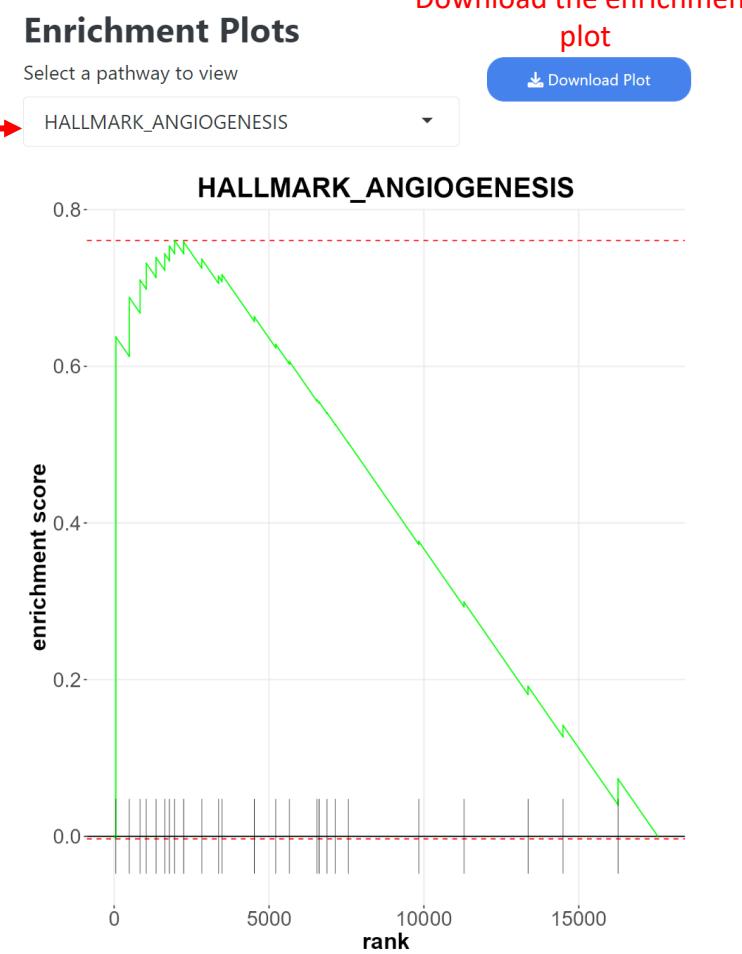
pathway	pval	padj	ES	NES	nMoreExtreme	size
HALLMARK_ANGIOGENESIS	0.1311	0.7738	0.76	1.52	63	25 ↑
HALLMARK_UV_RESPONSE_DN	0.1226	0.7738	0.7	1.5	57	117 ↓
HALLMARK_MYC_TARGETS_V2	0.1295	0.7738	0.7	1.45	64	58 ↑
HALLMARK_IL2_STAT5_SIGNALING	0.1797	0.7738	0.61	1.31	84	188 ↓
HALLMARK_GLYCOLYSIS	0.1928	0.7738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

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, User Signature Analysis (highlighted with a red box), and Published Signature Analysis. Below the navigation is a sidebar titled "Signature Analysis". The main content area shows tabs for Summary, AUROC Overview, AUROC Comparison, AUROC Correlation, Survival, Mann Whitney, and GSEA (highlighted with a red box). A "GSEA Comparison" link is also present. On the right, there are buttons for "Show 10 entries" and "Search:", and a "Download the enrichment plot" button.

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 Panel:**
 - Signature Analysis:** A section where users can enter a unique signature name (e.g., Custom_Signature) and a file containing HGNC symbols (e.g., Signature File). It also lists genes like Fake-Gene and IDO1, with a "Confirm signature and datasets" button.
 - Sort datasets by cancer type:** Buttons for Breast Cancer and NSCLC.
 - Select datasets to query:** A list of checked datasets: GSE111414_Pre, GSE111414_On, GSE173839, GSE190265, GSE194040.
- Dataset Analysis Panel:**
 - GSEA Tab:** Sub-tabs include Summary, AUROC Overview, AUROC Comparison, AUROC Correlation, Survival, Mann Whitney, and GSEA (highlighted).
 - GSEA Comparison Tab:** Sub-tabs include GSEA and GSEA Comparison (highlighted).
 - User Data:** A dropdown menu set to Hallmark.
 - Comparison Data:** A dropdown menu set to GSE111414_Pre.
 - Download Plot:** Buttons for both User Data and Comparison Data.
- Comparison Data Plots:**
 - User Data Plot:** Shows a GSEA plot for the Hallmark dataset. The y-axis is labeled "GSE111414_Pre" and the x-axis is labeled "NES". The plot shows a significant enrichment for pathways like UV_RESPONSE_DN_ANIOGENESIS, MYC TARGETS_V2, IL2_STAT5_SIGNALING, GLYCOLYSIS, ANDROGEN_RESPONSE, PROTEIN_SECRETION, WNT_BETA_CATEININ_SIGNALING, ADIPOGENESIS, XENOBIOTIC_METABOLISM, ESTROGEN_RESPONSE, LATE_COMPLEMENT, DNA_REPAIR, OXIDATIVE_PHOSPHORYLATION, MITOTIC_SPINDLE, P53_PATHWAY, INFLAMMATORY_RESPONSE, MYC TARGETS_V1, BILE_ACID_METABOLISM, IL6_JAK_STAT3_SIGNALING, ALLOGRAFT_REJECTION, MTORC1_SIGNALING, COAGULATION, KRAS_SIGNALING_DN, HEDGEHOG_SIGNALING, PANCREAS_BETA CELLS, UNFOLDED_PROTEIN_RESPONSE, MYOGENESIS, PI3K_AKT_MTOR_SIGNALING, HEME_METABOLISM, REACTIVE_OXYGEN_SPECIES_PATHWAY, APOPTOSIS, INTERFERON_ALPHA_RESPONSE, KRAS_SIGNALING_UP, APICAL_JUNCTION, ESTROGEN_RESPONSE_EARLY, TGF_BETA_SIGNALING.
 - Comparison Data Plot:** Shows a GSEA plot for the GSE111414_Pre cohort. The y-axis is labeled "GSE111414_Pre" and the x-axis is labeled "NES". The plot shows significant pathways like UNFOLDED_PROTEIN_RESPONSE, TGF_BETA_SIGNALING, NOTCH_SIGNALING, ADIPOGENESIS, CHOLESTEROL_HOMEOSTASIS, HYPOXIA, EPITHELIAL_MESENCHYMAL_TRANSITION, PANCREAS_BETA CELLS, INFLAMMATORY_RESPONSE, TNFA_SIGNALING_VIA_NFKB, COAGULATION, G2M_CHECKPOINT, ANDROGEN_RESPONSE, GLYCOLYSIS, APOPTOSIS, ESTROGEN_RESPONSE_LATE, ESTROGEN_RESPONSE_EARLY, IL2_STAT5_SIGNALING, KRAS_SIGNALING_UP, REACTIVE_OXYGEN_SPECIES_PATHWAY, OXIDATIVE_PHOSPHORYLATION, P53_PATHWAY, PROTEIN_SECRETION, MYOGENESIS, UV_RESPONSE_UP, HEME_METABOLISM, MITOTIC_SPINDLE, ALLOGRAFT_REJECTION, ANIOGENESIS, APICAL_SURFACE, KRAS_SIGNALING_DN, HEDGEHOG_SIGNALING, COMPLEMENT, WNT_BETA_CATEININ_SIGNALING, PEROXISOME, UV_RESPONSE_DN, INTERFERON_GAMMA_RESPONSE.

Annotations with red arrows and text:

- An arrow points to the "Hallmark" dropdown in the User Data section with the text: "Select a gene set for User Data the comparison".
- An arrow points to the "angio genesis" dropdown in the Comparison Data section with the text: "Select a signature to compare user signature against".
- An arrow points to the "GSE111414_Pre" dropdown in the Comparison Data section with the text: "Select a cohort to view" and "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.

The screenshot shows a user interface for 'Published Signature Analysis'. At the top, the title 'Published Signature Analysis' is displayed in bold black font. Below it, a subtitle reads 'Select a previously published signature.' A dropdown menu is open, showing the selection 'ifng18'. A blue button labeled 'Confirm selections' is visible. To the right of the dropdown, there is a note: ' Optionally sort by cancer type' with two options: 'GI Cancer' and 'Esophageal Cancer'. At the bottom, another section titled 'Select datasets to query.' lists six datasets, each preceded by a checked checkbox: GSE154538_Post, GSE154538_Pre, GSE165252_On, GSE165252_Pre, GSE165252_Post, and GSE183924.

IOSig

Previously Published Signature - Summary

IOSig: Immuno-Oncology Signature Explorer

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

Select a previously published signature.

ifng6

Confirm selections

Optional sort by cancer type

Kidney

Select datasets to query.

GSE67501
 Braun
 Motzer
 Choueiri
 IMmotion150
 Miao

Signature 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

Gene Overview

Show 10 entries Search:

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

Showing 1 to 6 of 6 entries

A table that displays various data points about the selected signature

A table of the genes within the selected signature

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 [**Download**](#)

GSE158403_Pre: ipi_neo

AUC: 0.49825

true_positive_fraction

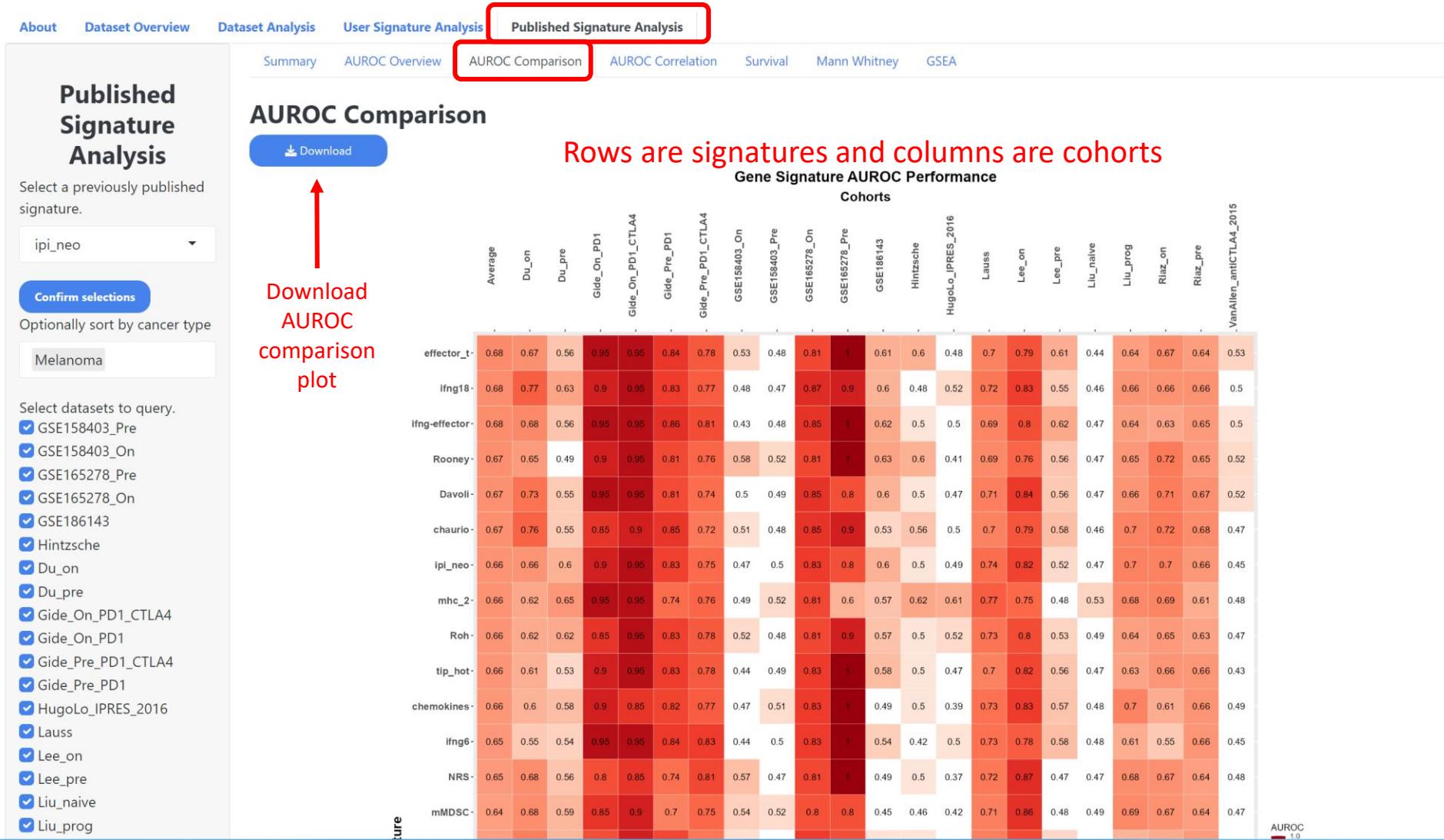
false_positive_fraction

Z Score method

Table displaying the AUC values in each cohort

Download the AUROC plot

Previously Published Signature – AUROC Comparison



Previously Published Signatures – AUROC Correlation

Published Signature Analysis Published Signature Analysis

Select a correlation method

AUROC Correlation Select a correlation method

Download

Download correlation plot

Pearson Correlation heatmap

Correlation

Signatures

imprimes
NRS
Rooney
Roh
tip_hot
ifng-effector
effector_t
ifng6
mMDSC
Ock
chaudio
ipi_neo
Davoli
ifng18
TLS
mhc_2
hypoxia
glycolysis
Ras
Buffa
proliferation
Mitoscore
stroma
angiogenesis
WNT
pan
Myc

About Dataset Overview Dataset Analysis User Signature Analysis Published Signature Analysis

Summary AUROC Overview AUROC Comparison AUROC Correlation Survival Mann Whitney GSEA

Selected signature: ipi_neo

Optional 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_CTLA4
- Gide_On_PD1
- Gide_Pre_PD1_CTLA4
- Gide_Pre_PD1
- HugoLo_IPRES_2016
- Lauss
- Lee_on
- Lee_pre
- Liu_naive
- Liu_prog

Previously Published Signature - Survival

Published Signature Analysis Survival

Select a cohort to view

GSE165278_On

Method: Z Score

High Low

Download

Survival

Select a cohort

GSE165278_On

Show 10 entries

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

Plot

Gide_Pre_PD1

p value: 0.00022

Average Z Score

Non-Responder Responder

Responder Status

Method: Z Score

Response Type

- Non-Responder
- Responder

Published Signature Analysis

Summary AUROC Overview AUROC Comparison AUROC Correlation Survival Mann Whitney GSEA

Show 10 entries

Cohort	P_Value	n	Responders	Non_Responders
1 Gide_Pre_PD1	0.0002	41	19	22
2 Lee_on	0.0122	35	6	29
3 Liu_prog	0.0212	48	17	31
4 Gide_Pre_PD1_CTL4	0.022	32	21	11
5 Gide_On_PD1_CTL4	0.0317	9	5	4
6 GSE165278_On	0.036	15	6	9
7 Lauss	0.0475	25	10	15
8 Riaz_on	0.0536	49	10	39
9 Gide_On_PD1	0.0635	9	4	5
10 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 gene set: Hallmark

Select a cohort: GSE158403_Pre

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ipi_neo: GSE158403_Pre Cohort

allmark

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

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

Previous 1 2 3 4 5 Next

Select a gene set

Select a cohort

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A data table showing the results of the GSEA analysis