PD-L1 Multi-Omics Profiling User Manual

This program conducts a pan-cancer characterization of PD-L1 and its associated pathways, investigating their associations with any gene or pathway of interest. The analysis leverages proteomics, transcriptomics, and phosphoproteomics datasets.

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Thank you for using the PD-L1 Multi-Omics Profiling!

Any questions? Please email zhouhu@simm.ac.cn.

Introductions

This program profiles PD-L1 and its associated pathways, and examines their relationships with any query gene or pathway, integrating proteomics, transcriptomics, and phosphoproteomics data.

Cancer types included in the analysis are: Acute Myeloid Leukemia (AML), Clear Cell Renal Cell Carcinoma (ccRCC), Colon Adenocarcinoma (COAD), Glioblastoma (GBM), Hepatocellular Carcinoma (HCC), Head and Neck Squamous Cell Carcinoma (HNSCC), Lung Squamous Cell Carcinoma (LSCC), Lung Adenocarcinoma (LUAD), Ovarian high-grade serous cancer (OV), Pancreatic Ductal Adenocarcinoma (PDAC), Small cell lung cancer (SCLC), Endometrial carcinoma (UCEC). Please note that the samples included in this study are bulk tissues, which do not contain information regarding response to immunotherapy.

The patient counts for each cancer type are shown as follows:

Cancer	Transcriptomic data		Proteomic data		Reference
	NAT	T	NAT	T	
AML	-	44	3	44	[1]
ccRCC	75	110	84	110	[2]
COAD	-	106	100	97	[3]
GBM	-	99	10	99	[4]
HCC	-	-	159	159	[5]
HNSCC	53	109	63	108	[6]
LSCC	94	108	99	108	[7]
LUAD	101	110	101	110	[8]
OV	-	82	20	83	[9]
PDAC	21	140	67	140	[10]
SCLC	107	107	112	112	[11]
UCEC	14	95	49	95	[12]

Note: '-' represents that the dataset does not exist.

You can choose the cancer type and dataset (Proteomics or Transcriptomics) from the left panel. The analysis consists of six modules:

1) Expression: PD-L1 expression in tumors (T) and normal adjacent tissues (NAT).

2) DEGs: The significant differentially expressed genes (DEGs) in the PD-L1 high-expression group compared to the PD-L1 low-expression group.

3) Correlations: The Spearman correlations between PD-L1 expression and other genes.

4) Pathway Activity: The activity of the 'PD-L1 expression and PD-1 checkpoint pathway in cancer' (hereafter referred to as the PD-L1 pathway) in T and NATs.

5) Pathway crosstalk: The crosstalk between the PD-L1 pathway and other pathways annotated in the KEGG database.

6) Phosphorylation: The significantly differentially phosphorylated sites in the PD-L1 pathway-active group compared to the PD-L1 pathway-inactive group.

The detailed usage and interpretation of the results are shown in the next section.

Notice:

1. The program may run slowly, especially during the "Pathway Activity" section, which might take several minutes or even tens of minutes. Please be patient.

2. Try not to change the input too quickly to avoid lag. Once the input is modified, all results from the previous input will be cleared.

3. If the program is difficult to run, it may be because other users are using it at the same time. In that case, please try again later.

Instructions & Results Interpretation

1). Expression

This tab shows the normalized RNA expression or protein abundance of PD-L1 in the selected cancer type.

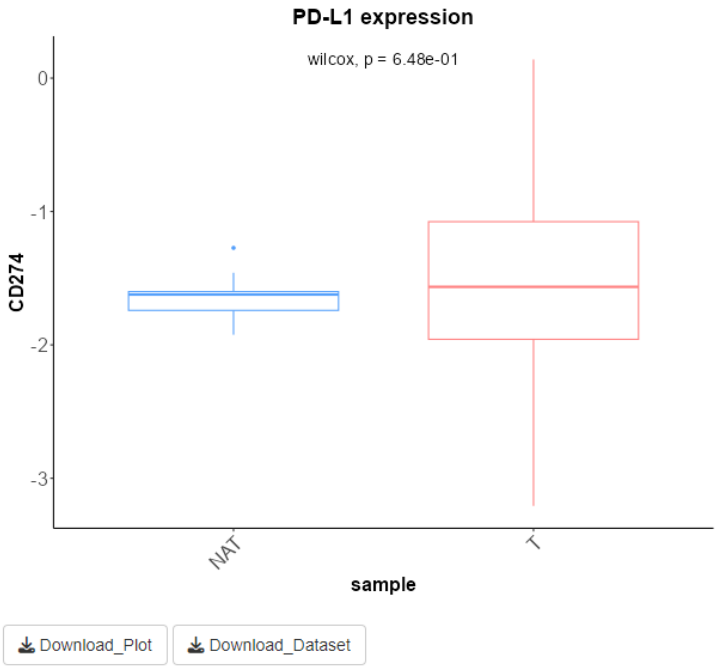

Fig 1 Expression

The normalized PD-L1 expression in NATs and T is provided, together with the p-value from the Wilcoxon rank-sum test. The plot and corresponding dataset can be downloaded.

However, in the proteomic data for some cancer types, PD-L1 could not be identified in more than 50% of patients. These data therefore do not provide results for PD-L1 expression, DEGs, and correlations.

2). DEGs

Tumor samples have been ranked by PD-L1 expression. The bottom 30% are defined as the ‘PD-L1 low-expression group’, and the top 30% as the ‘PD-L1 high-expression group’. Then the significant differentially expressed genes (DEGs) have been identified.

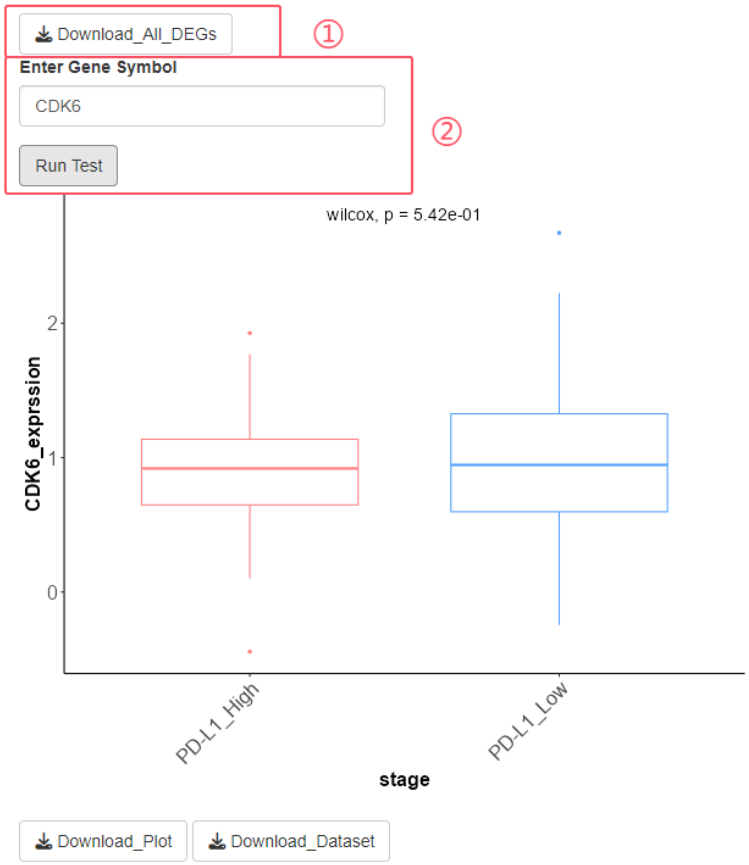

Fig 2. DEGs

① All identified DEGs are available for users to explore and download.

② Users can input a gene of interest and click ‘Run Test’. The normalized expression of the selected gene across different PD-L1 expression groups will then be visualized, accompanied by the p-value from the Wilcoxon rank-sum test. Both the plot and the corresponding dataset can be downloaded for further analysis.

3). Correlations

The Spearman correlations between PD-L1 expression and other genes have been analyzed in tumor samples.

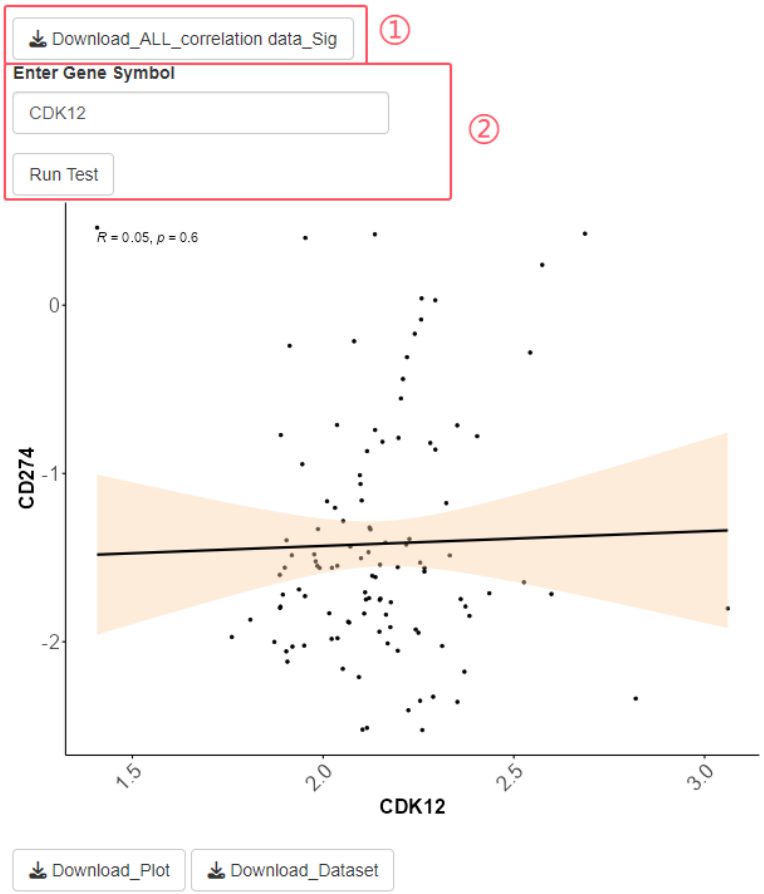

Fig 3. Correlations

① All genes significantly correlated with PD-L1 are available.

② Users can input a gene of interest and click 'Run Test' to visualize the Spearman correlation between the selected gene and PD-L1. Both the plot and the corresponding dataset can be downloaded for further analysis.

4). Pathway Activity

PD-L1 pathway activity have been evaluated based on ssGSEA scores. The plot and corresponding dataset can be downloaded.

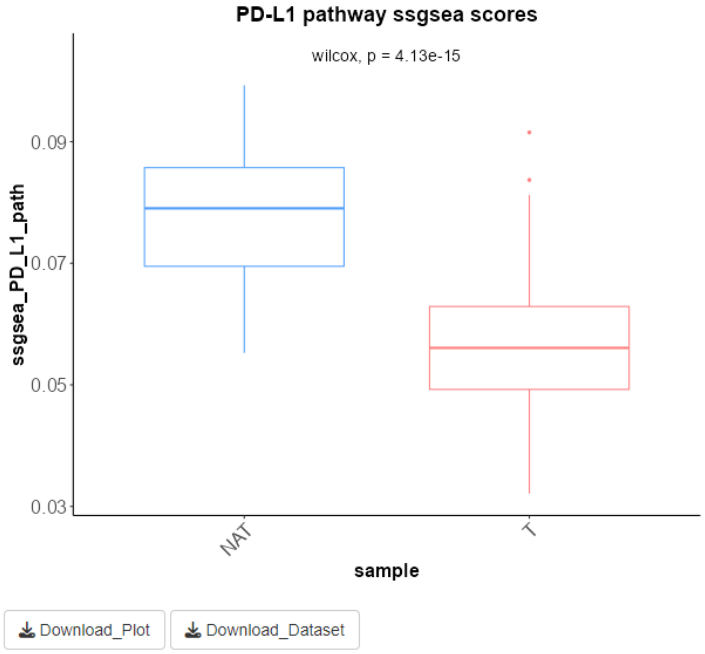

Fig 4. Pathway Activity

5). Pathway crosstalk

The pathway crosstalk is assessed by Spearman correlations between ssGSEA scores of the PD-L1 pathway and those of other pathways.

The analysis in this part depends on 'Pathway Activity' results. The system displays a warning when these results are unavailable.

Fig 5.1. Notice

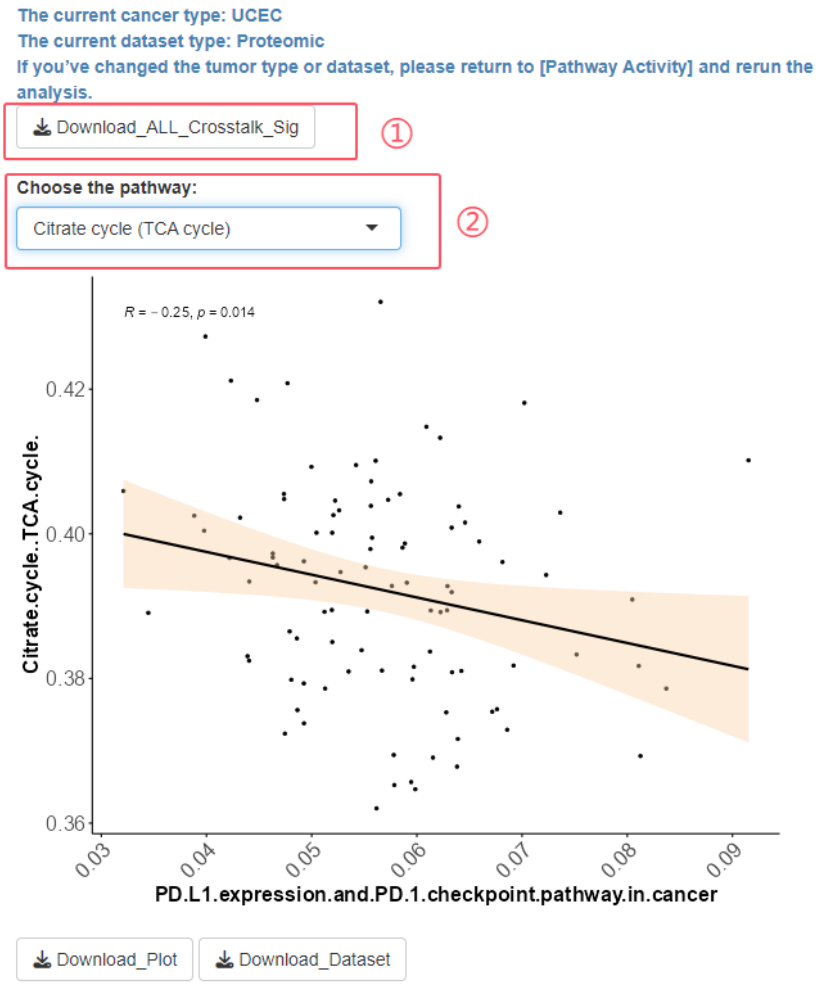

Fig 5.2. Pathway crosstalk

① All pathways significantly correlated with PD-L1 pathway are available for users to explore and download.

② Users can select a pathway of interest from the entries curated in the KEGG database. The correlation between the selected pathway and the PD-L1 pathway is then visualized. Both the plot and the corresponding dataset can be downloaded for further analysis.

6). Phosphorylation

We recommend using proteomic data to perform phosphoproteomic analysis.

This analysis requires 'Pathway Activity' results, and the system will display a warning if these results are unavailable.

Fig 6.1. Notice

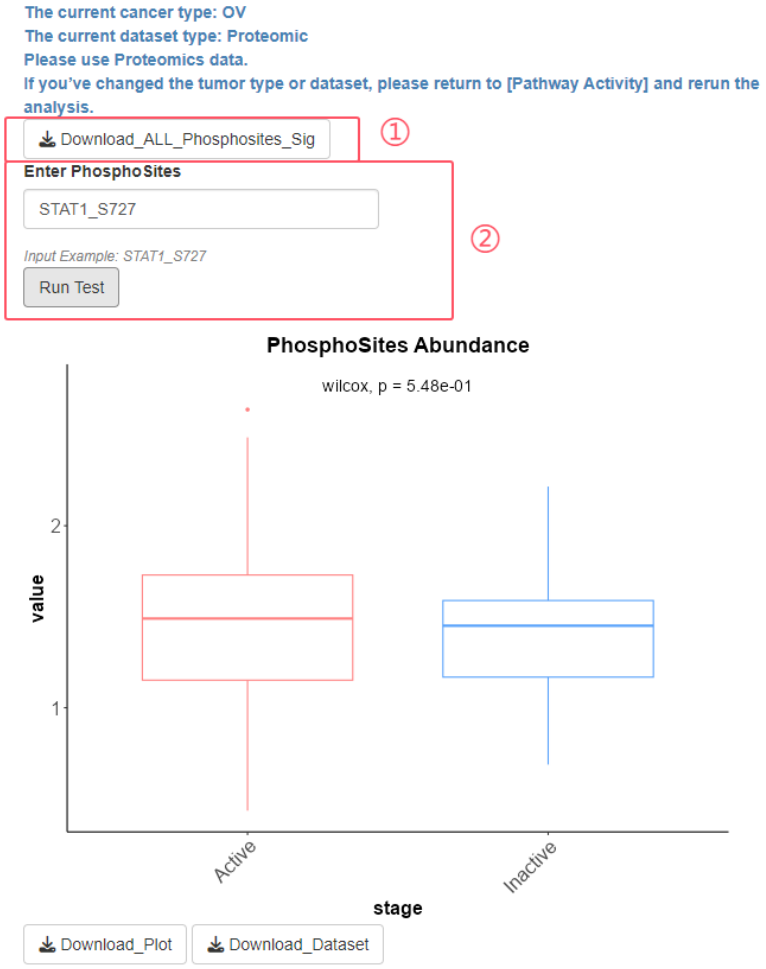

Fig 6.2. Pathway crosstalk

Tumor samples have been ranked by PD-L1 pathway ssGSEA score. The bottom 30% are defined as the ‘PD-L1 pathway-inactive group’, and the top 30% as the ‘PD-L1 pathway-active group’. Then the significant differentially expressed phosphorylated sites have been identified.

① All identified DEGs are available for users to explore and download.

② Users can input a phosphorylated site of interest and click ‘Run Test’. The normalized expression of the selected phosphorylated site across different groups will then be visualized, accompanied by the p-value from the Wilcoxon rank-sum test. Both the plot and the corresponding dataset can be downloaded for further analysis.

Reference

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