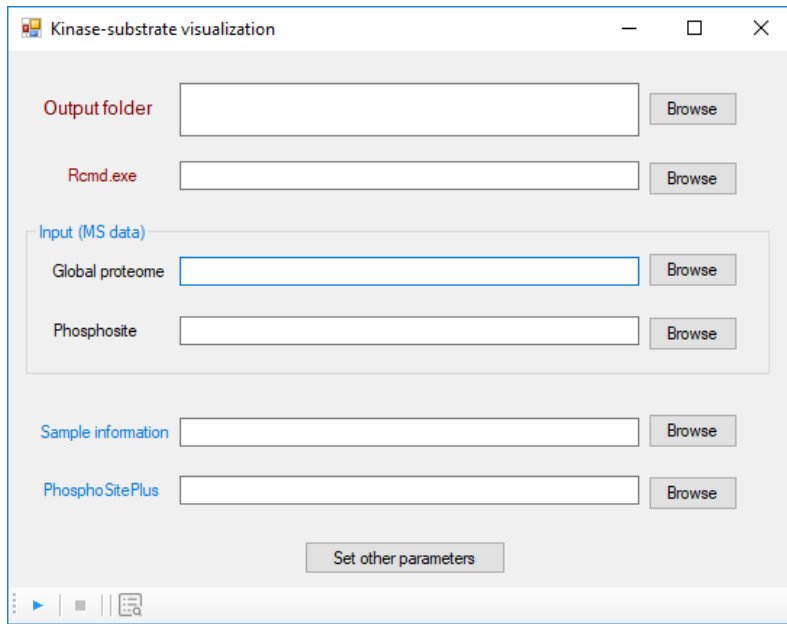


Omic-Sig

User Guide

Input parameters



Outputfolder

Specify an output directory for exporting results.

Rcmd.exe

Specify the location of Rcmd.exe file since the data visualization is done in R. Rcmd.exe file is usually located in “..\bin\i386” of R.

Example: C:\Program Files\R\R-3.5.3\bin\i386

Global proteome

Expression matrix of global proteins (normalized and log-transformed).

Phosphosite




Expression matrix of phosphosites (normalized and log-transformed).

Sample information

- (1) Sample.ID: sample IDs that are corresponding to the sample IDs in uploaded expression matrices.
- (2) Pair.Tag: a paired sample (e.g., tumor and its normal adjacent tissue) must be given the same identification tag.
- (3) Tissue: type of sample (e.g., Tumor or NAT).

PhosphoSitePlus

Kinase_Substrate_Dataset file download from PhosphoSitePlus.

-  Start the process
-  Cancel the process
-  Show results

Parameter setting

Additional input

RNA-seq Browse

Phosphoprotein Browse

Target kinase and substrate pair(s) Browse

% of quantified samples % Fold change Top %

RNA-Seq (optional)

Expression matrix of mRNA (normalized and log-transformed).

Phosphoprotein (optional)

Expression matrix of phosphoproteins (normalized and log-transformed).

Target kinase and substrate pair(s)

If you would like to use your own list of kinases and substrates instead of the ones from PhosphoSitePlus.

% of samples quantified

Only consider substrates and kinases quantified in 75% (by default) of samples.

Fold change

Either 1.5 fold or 2 fold changes currently.

Top k %

Only phospho-substrates (based on phosphosite data) have more than k % ($k=60$ by default) of tumors with > 1.5 fold changes (by default) are considered for analysis.



OK (i.e., save changes made)



Cancel

Input file format

Basic format for phospho, global, and mRNA expression matrices

Index	Sample 1	Sample 2	...	Sample n-1	Sample n

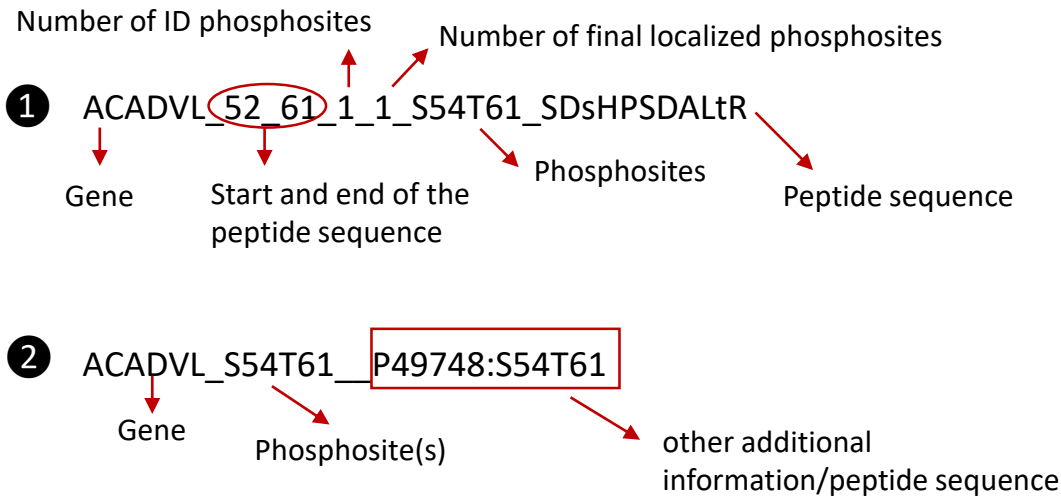
Row = phosphosites/proteins/genes
Columns = samples

• Global/RNA/Phosphoprotein

The index should be the official gene symbols/gene names, such as SYNM, CD44, and COL6A1.

• Phosphosites

Format of the index can be one of the following:



- **Sample information**

- (1) Sample.ID: sample IDs that are corresponding to the sample IDs in uploaded expression matrices.
- (2) Pair.Tag: a paired sample (e.g., tumor and its normal adjacent tissue) must be given the same identification tag.
- (3) Tissue: type of sample (e.g., Tumor or NAT).

Example:

Sample.ID	Pair.Tag	Tissue
Sample 1	1	NAT
Sample 2	1	Tumor
Sample 3	S3	NAT
Sample 4	S3	Tumor

This is a pair

This is another pair

- **Target kinase and substrate pairs**

Kinase	Substrate	Substrate.Site
PRKCD	GSK3A	S21
EIF2AK1	EIF2S1	S52

One line per kinase-substrate pair

Output

Kinase-substrate table

Results						
Plot						
Kinases and substrates						
Differential expression of phospho						
Differential expression of kinases						
Select	Kinase	Substrate Protein	Substrate Seq	Substrate Sites	# of Rank 1	
<input checked="" type="checkbox"/>	PRKCD	FCER1G	SDGVYTGaTR	S69	59	1
<input type="checkbox"/>	PRKCD	CYBA	ERPGIGGK	T147	15	1
<input type="checkbox"/>	PRKCD	SHC1	HGdFVKKPTR	S29	4	0
<input checked="" type="checkbox"/>	PRKCD	LCP1	GeVSDDEEMELR	S5	10	0
<input type="checkbox"/>	PRKCD	PRKCD	LLAEALNGVITQ	S299	0	-4
<input type="checkbox"/>	PRKCD	PRKCD	ARLaYSDK	S645	0	-4
<input type="checkbox"/>	PRKCD	PRKD1	RvVSTPAYLAP	S742	0	-4
<input type="checkbox"/>	CSNK2A1	CAV2	FADuGDDPDRHR	S36	64	1
<input type="checkbox"/>	CSNK2A1	NOL3	ASDPDEAGGRE	T149	2	0
<input type="checkbox"/>	CSNK2A1	MCM2	RGLLYDnDEED	S139	1	0

By selecting the kinases and substrates (highlighted rows) in the kinase-substrate table, the same group of substrates and kinases in the phospho-substrate and kinase tables will also be automatically selected.

Phospho-substrate table

Results						
Plot						
Kinases and substrates						
Differential expression of phospho						
Differential expression of kinases						
Select (phospho)	Protein	Phospeptide	Phosphosite	Sample 1	Sample 2	
<input checked="" type="checkbox"/>	LCP1	NEALLIALLREGE...	S257	0.624	0.011	1.
<input type="checkbox"/>	LCP1	IGNFzTDIK	S290	0.982	0.791	1.
<input checked="" type="checkbox"/>	LCP1	GeVSDDEEMELR	S5	0.553	-0.267	1.
<input type="checkbox"/>	LCP1	GSVdDEEMELR	S7	0.839	0.325	0.
<input type="checkbox"/>	PRKCD	VLMsVQYFLED...	S130	-1.129	-1.293	-0.
Select (RNA)	Gene	Sample 1	Sample 2	Sample 3	Sample 4	
<input checked="" type="checkbox"/>	LCP1	2.364	2.543	1.906	2.186	1
<input type="checkbox"/>	PRKCD	-0.437	-0.677	-1.607	-0.494	0
<input type="checkbox"/>	PRKD1	-0.766	-0.995	-1.848	-0.305	-4
<input type="checkbox"/>	PRKCD	-0.437	-0.677	-1.607	-0.494	0
<input type="checkbox"/>	CYBA	0.824	0.274	1.679	1.526	0
<input type="checkbox"/>	SHC1	1.176	0.873	1.766	1.266	0
<input checked="" type="checkbox"/>	FCER1G	2.396	3.232	2.899	2.422	2
<input type="checkbox"/>	MME	-0.431	-0.984	-0.588	-1.382	-4
<input type="checkbox"/>	CAV2	2.907	2.391	2.542	2.418	2
<input type="checkbox"/>	CTNNA1	0.412	0.451	-0.423	-0.237	0
Select (phospho)	Protein	Sample 1	Sample 2	Sample 3	Sample 4	
<input checked="" type="checkbox"/>	PRKCD	-0.776	-0.522	-0.418	-0.17	
<input type="checkbox"/>	GTF2F1	-0.311	-0.501	-0.019	-0.388	
<input type="checkbox"/>	CDK7	0.02	1.084	0.654	0.577	
<input type="checkbox"/>	PRKAA1	0.213	0.269	-0.246	-0.004	

Kinase table

Results						
Plot						
Kinases and substrates						
Differential expression of phospho						
Differential expression of kinases						
Select (phospho)	Protein	Phospeptide	Phosphosite	Sample 1	Sample 2	Sam
<input checked="" type="checkbox"/>	LCP1	NEALLIALLREGE...	S257	0.624	0.011	1.193
<input type="checkbox"/>	LCP1	IGNFzTDIK	S290	0.982	0.791	1.004
<input checked="" type="checkbox"/>	LCP1	GeVSDDEEMELR	S5	0.553	-0.267	1.513
<input type="checkbox"/>	LCP1	GSVdDEEMELR	S7	0.839	0.325	0.845
<input type="checkbox"/>	PRKCD	VLMsVQYFLED...	S130	-1.129	-1.293	-0.89
<input type="checkbox"/>	PRKCD	VLMsVQYFLED...	S130	-1.039	-1.188	-0.79
<input type="checkbox"/>	PRKCD	LLAEALNGVITQ...	S299	-0.03	-0.011	-0.68
<input type="checkbox"/>	PRKCD	ASfCGTPDYIA...	T507	-0.31	-0.582	-0.79
<input type="checkbox"/>	PRKCD	ARLaYSDK	S645	-0.16	-1.349	-0.73
<input type="checkbox"/>	PRKD1	TSaELSTSAPD...	S219	-1.164	-1.594	-1.01
Select (RNA)	Gene	Sample 1	Sample 2	Sample 3	Sample 4	Sam
<input checked="" type="checkbox"/>	LCP1	2.364	2.543	1.906	2.186	1.962
<input type="checkbox"/>	PRKCD	-0.437	-0.677	-1.607	-0.494	0.395
<input type="checkbox"/>	PRKD1	-0.766	-0.995	-1.848	-0.305	-0.69
<input type="checkbox"/>	PRKCD	-0.437	-0.677	-1.607	-0.494	0.395
<input type="checkbox"/>	CYBA	0.824	0.274	1.679	1.526	0.033
Select (Global)	Protein	Sample 1	Sample 2	Sample 3	Sample 4	Sam
<input checked="" type="checkbox"/>	LCP1	1.642	1.317	1.133	0.994	0.24
<input type="checkbox"/>	PRKCD	0.069	-0.544	-0.219	-0.323	0.293
<input type="checkbox"/>	PRKD1	-0.281	-0.576	-0.457	-0.24	-0.28