

## Abbreviation

ACC:	Adrenocortical carcinoma
BLCA:	Bladder urothelial carcinoma
BRCA:	Breast invasive carcinoma
ccRCC	Clear Cell Renal Cell Carcinoma
CESC:	Cervical squamous cell carcinoma and endocervical adenocarcinoma
CHOL:	Cholangiocarcinoma
COAD:	Colon adenocarcinoma
DLBC:	Lymphoid neoplasm diffuse large B-cell lymphoma
ESCA:	Esophageal carcinoma
GBM:	Glioblastoma multiforme
HNSC:	Head and neck squamous cell carcinoma
KICH:	Kidney chromophobe
KIRC:	Kidney renal clear cell carcinoma
KIRP:	Kidney renal papillary cell carcinoma
LAML:	Acute myeloid leukemia
LGG:	Brain lower grade glioma
LIHC:	Liver hepatocellular carcinoma
LUAD:	Lung adenocarcinoma
LUSC:	Lung squamous cell carcinoma
MESO:	Mesothelioma
OV:	Ovarian serous cystadenocarcinoma
PAAD:	Pancreatic adenocarcinoma
PCPG:	Pheochromocytoma and paraganglioma
PRAD:	Prostate adenocarcinoma
READ:	Rectum adenocarcinoma
SARC:	Sarcoma
SKCM:	Skin cutaneous melanoma
STAD:	Stomach adenocarcinoma
TGCT:	Testicular germ cell tumors
THCA:	Thyroid carcinoma
THYM:	Thymoma
UCEC:	Uterine corpus endometrial carcinoma
UCS:	Uterine carcinosarcoma
UVM:	Uveal melanoma
OS:	Overall survival
DMFS:	Distant metastasis-free survival
RFS:	Relapse-free survival

PPS: Post-progression survival  
FP: First progression  
DFS: Disease-free survival  
DSS: Disease-specific survival  
PFS: Progression-free survival.

## Public Database Website

TIMER2.0	<a href="http://timer.cistrome.org">http://timer.cistrome.org</a>
GEPIA2	<a href="http://gepia2.cancer-pku.cn">http://gepia2.cancer-pku.cn</a>
CPTAC	<a href="http://www.cbioportal.org">http://www.cbioportal.org</a>
MEXPRESS	<a href="https://mexpress.be">https://mexpress.be</a>
MethSurv	<a href="https://biit.cs.ut.ee/methsurv/#tab-2291-1">https://biit.cs.ut.ee/methsurv/#tab-2291-1</a>
PhosphoNET	<a href="http://www.phosphonet.ca">http://www.phosphonet.ca</a>
STRING	<a href="https://cn.string-db.org">https://cn.string-db.org</a>
Venn Diagram tool	<a href="http://bioinformatics.psb.ugent.be/webtools/Venn">http://bioinformatics.psb.ugent.be/webtools/Venn</a>

## Code for KEGG analysis

```
rm(list=ls())
library(Cairo)
library(stringr)
library(ggplot2)

pathway=read.table("6-5kegg pathway.txt",header = T,sep="\t")
pathway$Term<-str_split_fixed(pathway@Term,":",2)[,2]
ggplot(pathway,aes(x=Fold.Enrichment,y=Term))+
  geom_point(aes(size=Count,color=-1*log10(PValue)))+
  scale_color_gradient(low="green",high="red")+
  labs(
    color=expression(-log[10](P.value)),
    size="Gene number",
    x="Fold enrichment"
  )+
  theme_bw()+
  theme(
    axis.text.y = element_text(size=rel(1.3)),
    axis.title.x = element_text(size=rel(1.3)),
    axis.title.y = element_blank()
  )
)
```

## **Code for snetplots and cnetplots of GO enrichment analysis**

```
rm(list=ls())
library(biomaRt)
library(clusterProfiler)
library(org.Hs.eg.db)
library(enrichplot)
library(data.table)

genelist_input <- fread(file="GENE.txt",header = T, sep = '\t', data.table = F)
genename <- as.character(genelist_input[,1])

GO_result_MF <- enrichGO(genename, 'org.Hs.eg.db', ont="MF", keyType = "SYMBOL")
dotplot(GO_result_MF,showCategory = 20)

cnetplot(GO_result_MF,colorEdge = TRUE,node_label = "all",circular = TRUE,showCategory =
5)
```