Column1	Column2	Column3	Column4	Column5
Function	**Library**	**databaseUsed**	**Input (demonstrated examples)**	**Sample Configuration**
			Enrich functions	
enricher	**clusterProfiler**	**msigdbr/wiki-download/others**	**vectorOfGenes**	**enricher(gene, TERM2GENE = wpid2gene, TERM2NAME = wpid2name)**
enrichKEGG	**clusterProfiler**	**organism='hsa'**	**vectorOfGenes**	**enrichKEGG(gene=gene,organism='hsa',pvalueCutoff=0.05)**
enrichMKEGG	**clusterProfiler**	**organism='hsa'**	**vectorOfGenes**	**enrichMKEGG(gene = gene,organism = 'hsa')**
enrichGO	**clusterProfiler**	**OrgDb=org.Hs.eg.db**	**vectorOfGenes**	**enrichGO(gene=gene,universe=names(geneList),OrgDb=org.Hs.eg.db,ont="CC",pAdjustMethod="BH",pvalueCutoff=0.01,qvalueCutoff=0.05,readable=TRUE)**
enrichPathway	**ReactomePA**	**automatic**	**vectorOfGenes**	
enrichMeSH	**ReactomePA**	**MeSHDb="Mesh.Hsa.eg.db"**	**vectorOfGenes**	**enrichMeSH(de, MeSHDb = **"MeSH.Hsa.eg.db"**, database='gendoo', category = 'C')**
enrichDO	**DOSE**	**ont="DO'**	**vectorOfGenes**	**enrichDO(gene=gene,ont="DO",pvalueCutoff=0.05,pAdjustMethod="BH",universe=names(geneList),minGSSize=5,maxGSSize=500,qvalueCutoff=0.05,readable=FALSE)**
enrichNCG	**DOSE**	**automatic**	**vectorOfGenes**	
enrichDGN	**DOSE**	**automatic**	**vectorOfGenes**	**enrichDGN(gene)**
enrichDGNv	**DOSE**	**automatic**	**vectorOfGenes**	**enrichDGNv(snp)**
groupGO	**clusterProfiler**	**OrgDb=org.Hs.eg.db**	**vectorOfGenes**	**groupGO(gene= gene,OrgDb= org.Hs.eg.db,ont= "CC",level= 3,universe= names(geneList),readable = TRUE)**
			GSEA functions	
GSEA	**clusterProfiler**	**msigdbr/wiki-download/others**	**NamedVectorOfFoldchange**	**GSEA(geneList, TERM2GENE = wpid2gene, TERM2NAME = wpid2name, verbose=FALSE)**
gseKEGG	**clusterProfiler**	**organism='hsa'**	**NamedVectorOfFoldchange**	**gseKEGG(geneList=geneList,organism='mcc',nPerm=1000,minGSSize=120,pvalueCutoff=0.05,verbose=FALSE)**
gseMKEGG	**clusterProfiler**	**organism='hsa'**	**NamedVectorOfFoldchange**	
gseGO	**clusterProfiler**	**OrgDb=org.Hs.eg.db**	**NamedVectorOfFoldchange**	**gseGO(geneList=geneList,OrgDb=org.Hs.eg.db,ont="CC",nPerm=1000,minGSSize=100,maxGSSize=500,pvalueCutoff=0.05,verbose=FALSE)**
gsePathway	**ReactomePA**	**?**	**NamedVectorOfFoldchange**	
gseMeSH	**ReactomePA**	**MeSHDb="Mesh.Hsa.eg.db"**	**NamedVectorOfFoldchange**	**gseMeSH(geneList, MeSHDb = "MeSH.Hsa.eg.db", database = 'gene2pubmed', category = "G")**
gseDO	**DOSE**	**ont="DO'**	**NamedVectorOfFoldchange**	**gseDO(geneList,nPerm=100,minGSSize=120,pvalueCutoff=0.2,pAdjustMethod="BH",verbose=FALSE)**

gseNCG	**DOSE**	**automatic**	**NamedVectorOfFoldchange**	**gseNCG(geneList,nPerm=100,minGSSize=120,pvalueCutoff =0.2,pAdjustMethod="BH",verbose=FALSE)**
gseDGN	**DOSE**	**automatic**	**NamedVectorOfFoldchange**	**gseDGN(geneList,nPerm=100,minGSSize=120,pvalueCutoff =0.2,pAdjustMethod="BH",verbose=FALSE)**
Database & ID conversion				
get .gmt files	**msigdbr**	**no**	**species & category**	**msigdbr(species = "Homo sapiens", category = "C2") %>% dplyr::select(gs_name, gene_symbol) or read.gmt("./wikipathways-20200510-gmt-Homo_sapiens.gmt")**
bitr	**clusterProfiler**	**no**	**avector of gene ids**	**bitr(wpid2gene$gene,fromType="ENTREZID",toType=c("E NSEMBL","SYMBOL"),OrgDb=org.Hs.eg.db)**
Visulization				
barplot	**graphics**	**no**	**enrichResult**	**barplot(enricherRes, showCategory=20)**
dotplot	**enrichplot**	**no**	**enrichRseult, gseaResult & compareClusterResult**	**dotplot(edo2, showCategory=30) + ggtitle("dotplot for GSEA") && plot_grid(p1, p2, ncol=2)**
cnetplot	**enrichplot**	**no**	**enrichResult**	**options(repr.plot.width=16, repr.plot.height=24) && cnetplot(edox, foldChange=geneList, showCategory = 10,colorEdge=TRUE,circular=TRUE, node_label="all")**
upsetplot	**enrichplot**	**no**	**enrichRseult and gseaResult**	**upsetplot(kk2)**
ridgeplot	**enrichplot**	**no**	**gseaResult**	**ridgeplot(edo2)**
gseaplot	**enrichplot**	**no**	**gseaResult**	**gseaplot2(edo2, geneSetID = 2, title = edo2$Description[2]) # geneSetID are the row number in the edo2 object**
Multiple gene-lists				
compareCluster	**clusterProfiler**	**automatic**	**list of gene sets/ genes with different factor labels**	**formula_res <- compareCluster(Entrez~group+othergroup, data=mydf, fun="enrichKEGG"); ck <- compareCluster(geneCluster = gcSample, fun = "enrichKEGG")**
emapplot	**enrichplot**	**no**	**compareClusterResult**	**options(repr.plot.width=8, repr.plot.height=6) && emapplot(xx,pie="count", pie_scale=2, layout="kk",legend_n=4)ridgeplot(edo2) # show the fold change of core genes in the GSEA analysis.**