

KEGG富集分析

KEGG通路

在生物体内，不同基因相互协调行使其生物学功能，基于Pathway的分析有助于更进一步了解基因的生物学功能。通路数据库(PATHWAY database) 储存了基因功能的相关信息，包括代谢，膜运输，信号传导和细胞的生长周期等。

Pathway显著性富集分析以KEGG Pathway为单位，应用超几何检验，找出与整个基因组背景相比，在差异表达基因中显著性富集的Pathway。

	差异基因	总基因
基因数目	100	20000
某个KEGG通路	20	200



主要内容

- KEGG数据库
- id转换
- KOBAS
- clusterProfiler R package
- Cytoscape可视化

KEGG Database



KEGG PATHWAY Database

Wiring diagrams of molecular interactions, reactions, and relations

[Menu](#) [PATHWAY](#) [BRITE](#) [MODULE](#) [KO](#) [GENOME](#) [GENES](#) [LIGAND](#) [DISEASE](#) [DRUG](#) [DBGET](#)

Select prefix

Enter keywords

[Help](#)

[\[New pathway maps | Update history \]](#)

Pathway Maps

KEGG PATHWAY is a collection of manually drawn [pathway maps](#) representing our knowledge on the molecular interaction and reaction networks for:

1. Metabolism

[Global/overview](#) [Carbohydrate](#) [Energy](#) [Lipid](#) [Nucleotide](#) [Amino acid](#) [Other amino](#) [Glycan](#)
[Cofactor/vitamin](#) [Terpenoid/PK](#) [Other secondary metabolite](#) [Xenobiotics](#) [Chemical structure](#)

2. Genetic Information Processing

3. Environmental Information Processing

4. Cellular Processes

5. Organismal Systems

6. Human Diseases

and also on the structure relationships (KEGG drug structure maps) in:

7. Drug Development

Pathway Mapping

视频资料网址：www.xixibio.com

淘宝店铺网址：<https://shop119322454.taobao.com>

id转换

gene	logFC
CCL23	-4.066608903
COLEC10	-4.122671832
FAM189B	1.747953745
CDC45	4.38682126
RCAN1	-2.257915165
N4BP2L1	-1.847750259
FCN3	-4.120767162
UHRF1	4.353192433
HMMR	4.008655285
NEK2	4.36024922
TTK	4.987051203
AZI1	2.038631835
HIGD1B	3.484327107
BMPER	-4.377918473



gene	logFC	entrezID
CCL23	-4.066608903	6368
COLEC10	-4.122671832	10584
FAM189B	1.747953745	10712
CDC45	4.38682126	8318
RCAN1	-2.257915165	1827
N4BP2L1	-1.847750259	90634
FCN3	-4.120767162	8547
UHRF1	4.353192433	29128
HMMR	4.008655285	3161
NEK2	4.36024922	4751
TTK	4.987051203	7272
AZI1	2.038631835	NA
HIGD1B	3.484327107	51751
BMPER	-4.377918473	168667

视频资料网址: www.xixibio.com

淘宝店铺网址: <https://shop119322454.taobao.com>

Input

Type: ?

☒ Fasta Protein Sequence ☐ Fasta Nucleotide Sequence ☐ Tabular BLAST Output

☐ Entrez Gene ID ☐ UniProtKB AC ☐ Refseq Protein ID ☐ Ensembl Gene ID

Species: ?

Input key words here, and choose the species below.(Default:human)

Homo sapiens (human) Mus musculus (mouse) Drosophila melanogaster (fruit fly) Arabidopsis thaliana (thale cress)
Saccharomyces cerevisiae (budding yeast) Escherichia coli K-12 MG1655 Caenorhabditis elegans (nematode)

Input **protein**
sequences in
FASTA format:

#example

Or upload a file:

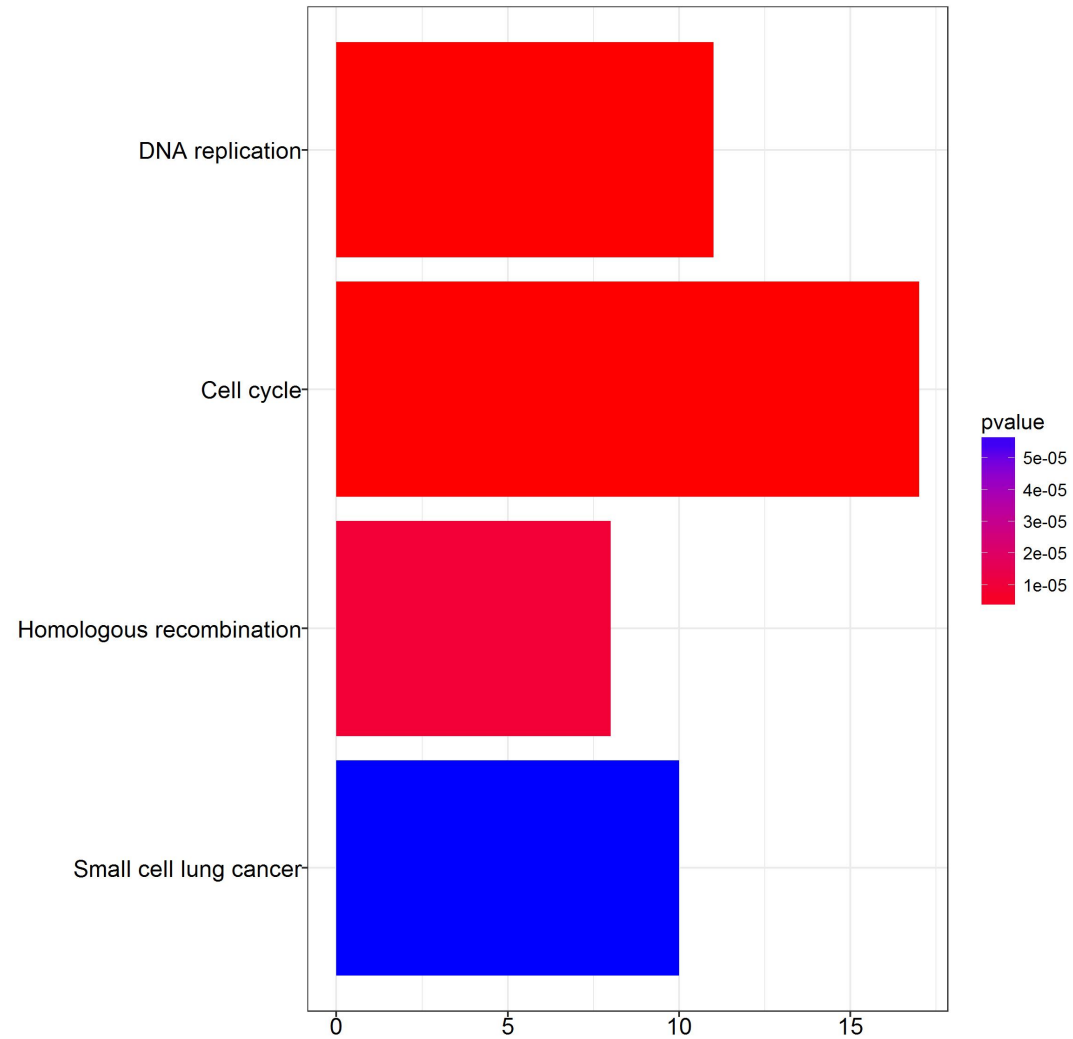
浏览... 未选择文件。

☐ Use KO to do orthologous analysis between different species? (This may take a long time.)

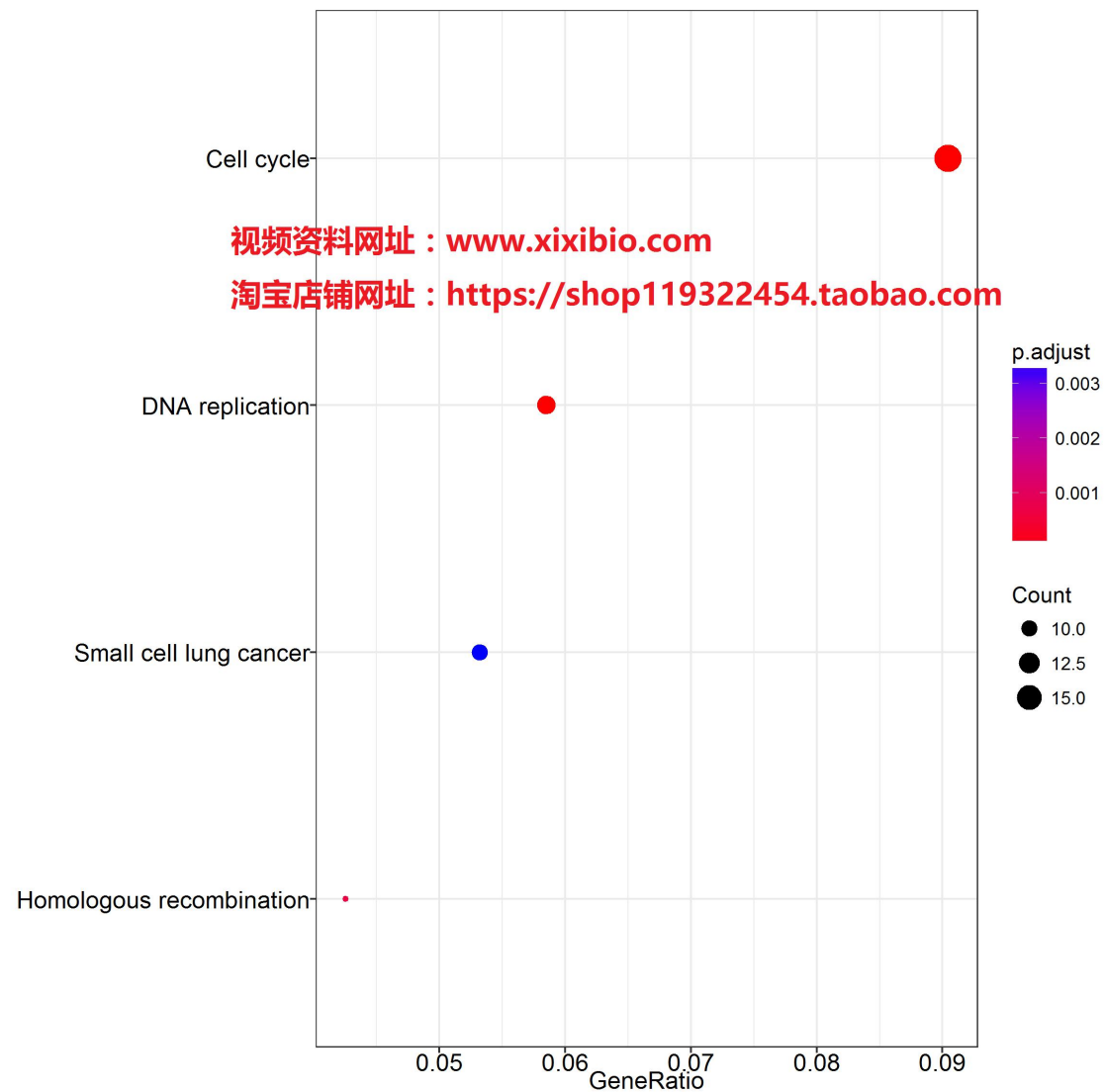
clusterProfiler R package

ID	Description	pvalue	qvalue	geneID
hsa03030	DNA replication	9.22E-10	2.03E-07	FEN1/MCM2/MCM6/RNASEH2A/RFC4/MCM3/PRIM2/POLD1/POLA2/MCM7/MCM5
hsa04110	Cell cycle	1.64E-08	1.80E-06	CDC45/TTK/CCNA2/E2F2/BUB1B/MAD2L1/MCM2/MCM6/CCNE1/CDKN2C/MCM3/GADD45B/CDC7/MCM7/MCM5/CCNE2/CDC25A
hsa03440	Homologous recombination	8.16E-06	0.000598762	EME1/RAD54L/RAD51/XRCC3/POLD1/BLM/XRCC2/RAD54B
hsa05222	Small cell lung cancer	5.71E-05	0.003142919	E2F2/CCNE1/LAMA4/COL4A1/ITGA6/COL4A2/CCNE2/PTGS2/LAMC1/CKS1B

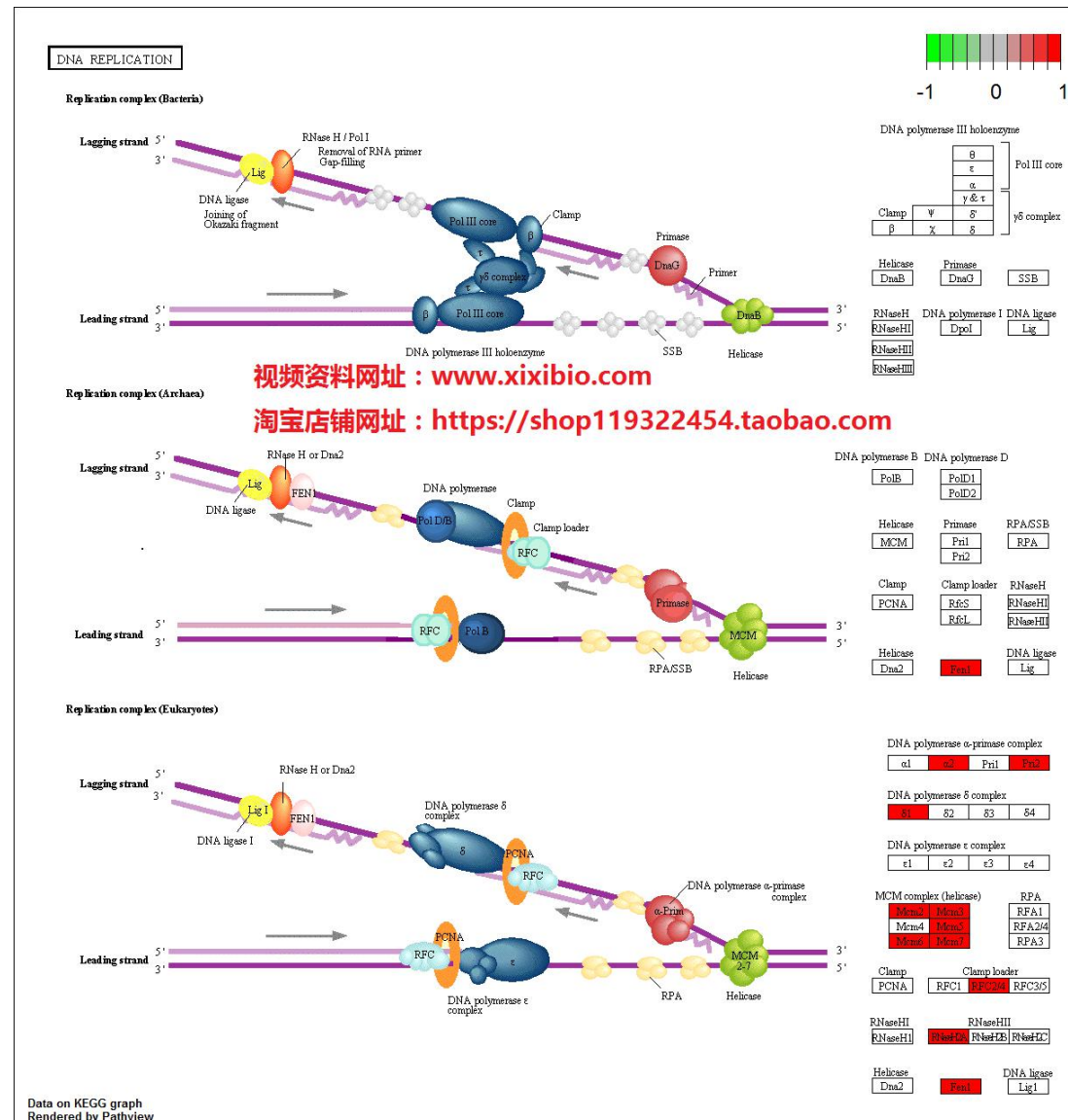
clusterProfiler R package



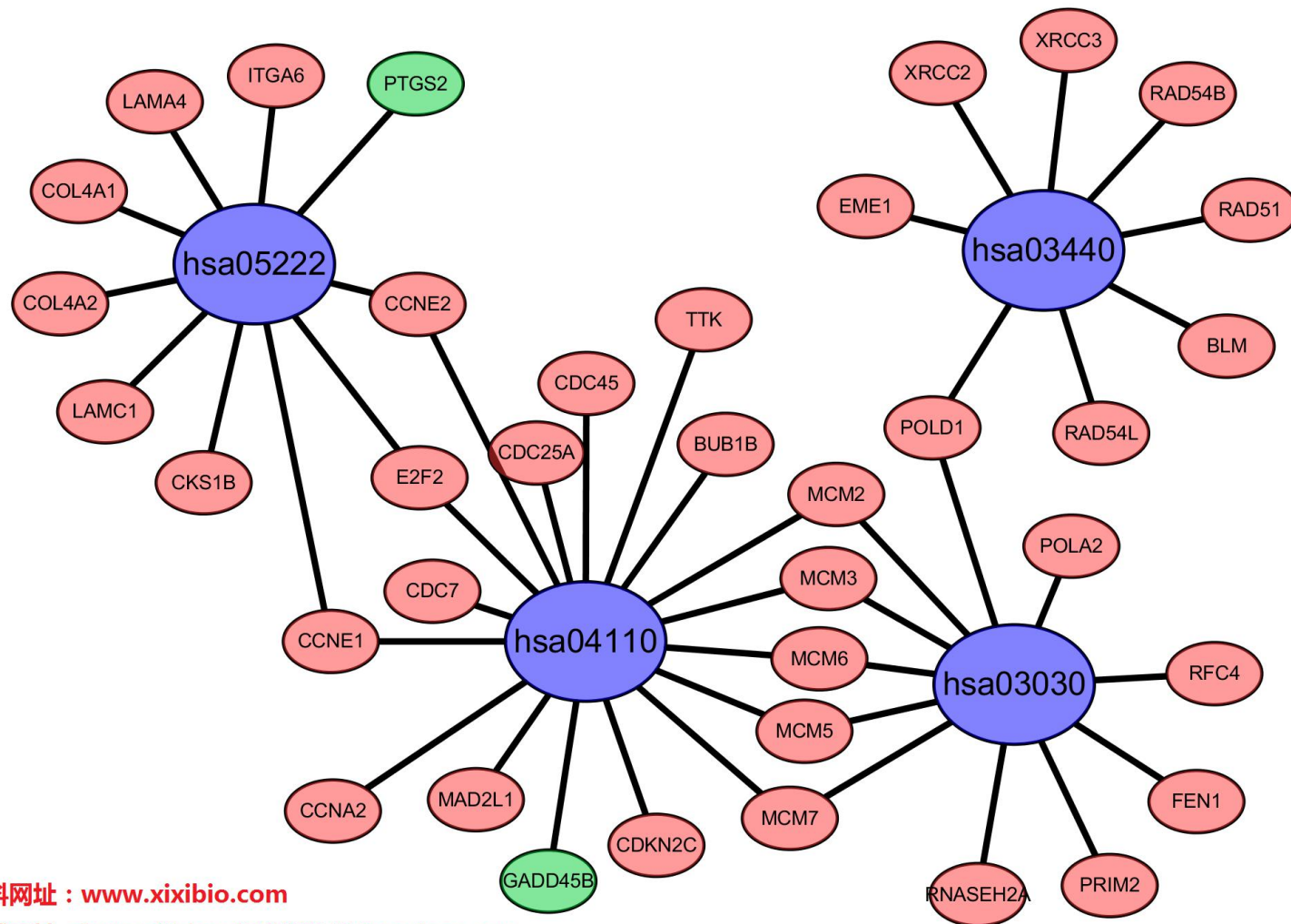
clusterProfiler R package



clusterProfiler R package



Cytoscape可视化



视频资料网址：www.xixibio.com

淘宝店铺网址：<https://shop119322454.taobao.com>



Thanks!!!