

GO富集分析

GO富集

GO (Gene ontology) 按照生物过程(Biology Process) , 分子功能 (Molecular Function) 和细胞组成 (cellular component) 对基因进行注释和分类。

通过对差异表达基因进行GO terms富集度统计学的分析 , 计算出差异基因GO term的p-value和p-value的FDR值 (q-value) , 定位差异基因最可能相关的GO term。

| | 差异基因 | 总基因 |
|------|------|-------|
| 基因数目 | 100 | 20000 |
| 某个GO | 20 | 200 |

主要内容

- UniProt (<http://www.uniprot.org/>)
- DAVID (<http://david.abcc.ncifcrf.gov/>)
- 可视化
- GOplot R package

GO - Molecular functionⁱ

- androgen receptor binding Source: UniProtKB ▼
- damaged DNA binding Source: Ensembl
- DNA binding Source: ProtInc ▼
- enzyme binding Source: UniProtKB ▼
- RNA binding Source: MGI ▼
- transcription coactivator activity Source: UniProtKB ▼
- transcription regulatory region DNA binding Source: BHF-UCL ▼
- tubulin binding Source: UniProtKB ▼
- ubiquitin protein ligase binding Source: UniProtKB ▼
- ubiquitin-protein transferase activity Source: UniProtKB ▼
- zinc ion binding Source: ProtInc ▼

视频资料网址 : www.xixibio.com

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

Complete GO annotation...

GO - Biological processⁱ

- androgen receptor signaling pathway Source: UniProtKB ▼
- apoptotic process Source: UniProtKB ▼
- cellular response to DNA damage stimulus Source: ProtInc ▼
- cellular response to indole-3-methanol Source: UniProtKB ▼

DAVID

Shortcut to DAVID Tools

► Functional Annotation

Gene-annotation enrichment analysis, functional annotation clustering , BioCarta & KEGG pathway mapping, gene-disease association, homologue match, ID translation, literature match and more

► Gene Functional Classification

Provide a rapid means to reduce large lists of genes into functionally related groups of genes to help unravel the biological content captured by high throughput technologies. [More](#)

► Gene ID Conversion

Convert list of gene ID/accessions to others of your choice with the most comprehensive gene ID mapping repository. The ambiguous accessions in the list can also be determined semi-automatically. [More](#)

Recommending: A [paper](#) published in *Nature Protocols* de

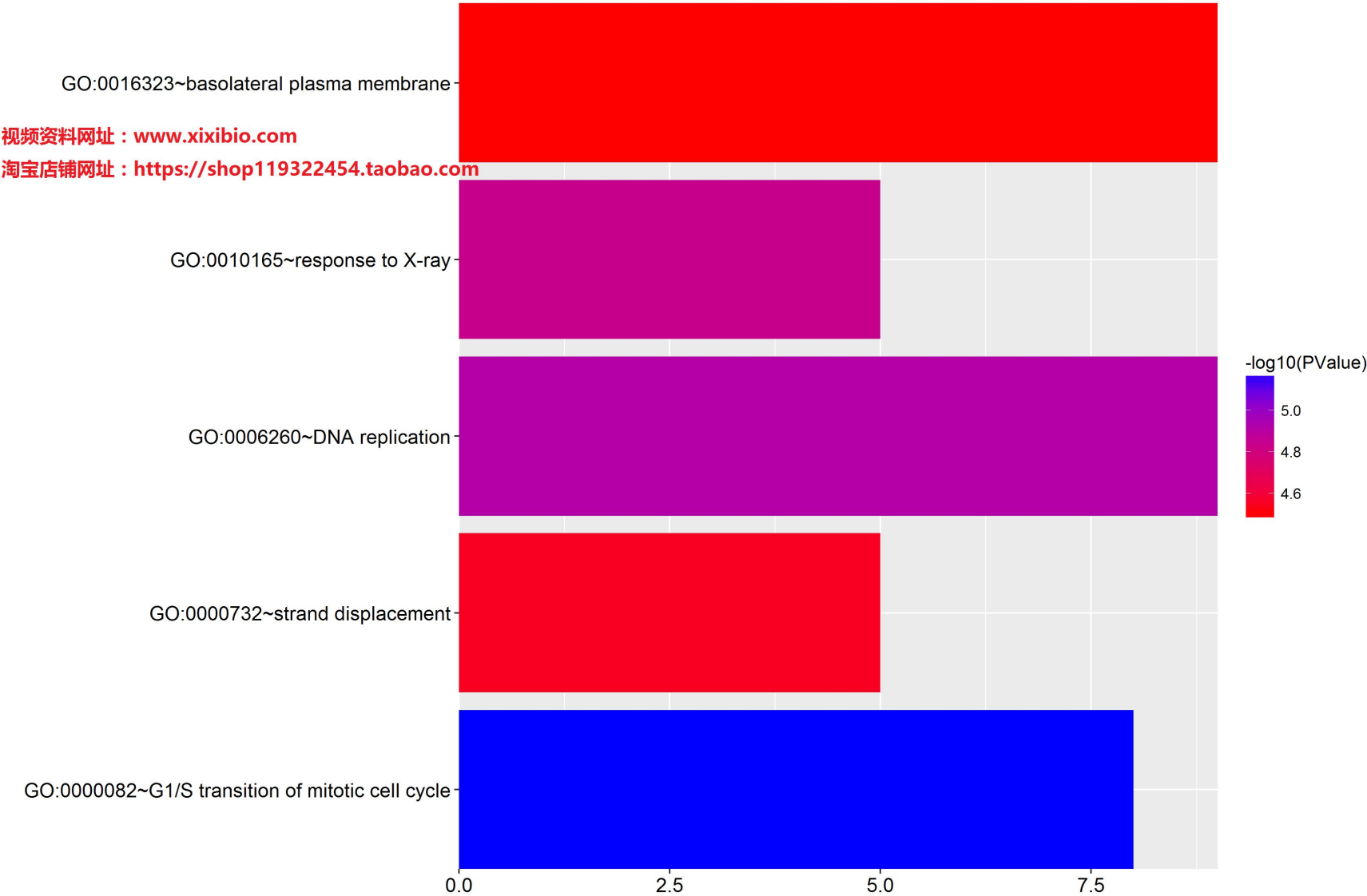
Welcome to DAVID 6.8

2003 - 2017

The **D**atabase for **A**nnotation, **V**isualization and **I**ntegrated **D**iscovery (**DAVID**) v6.8 comprises a full Knowledgebase update to the sixth version of our original web-accessible programs. DAVID now provides a comprehensive set of functional annotation tools for investigators to understand biological meaning behind large list of genes. For any given gene list, DAVID tools are able to:



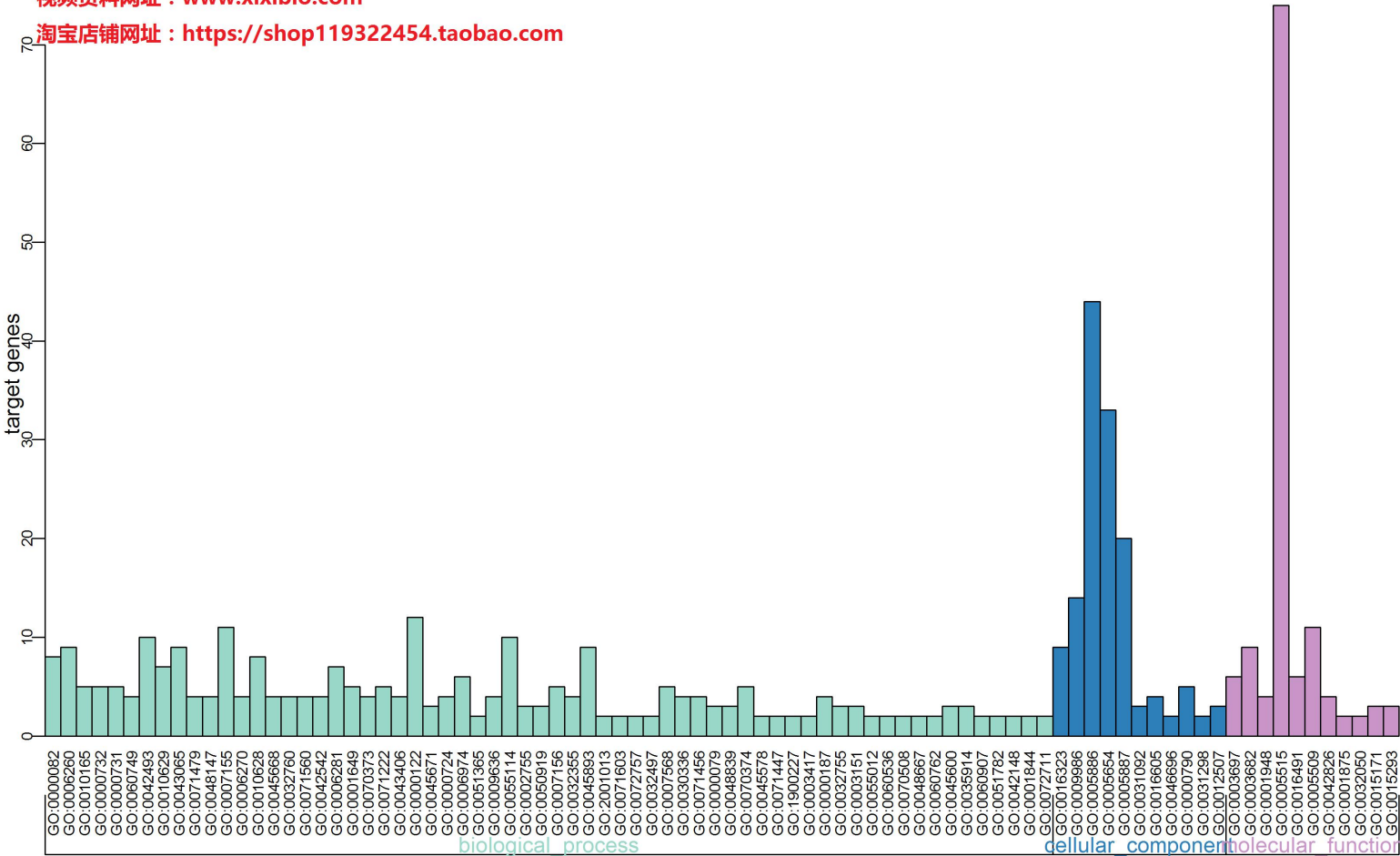
可视化



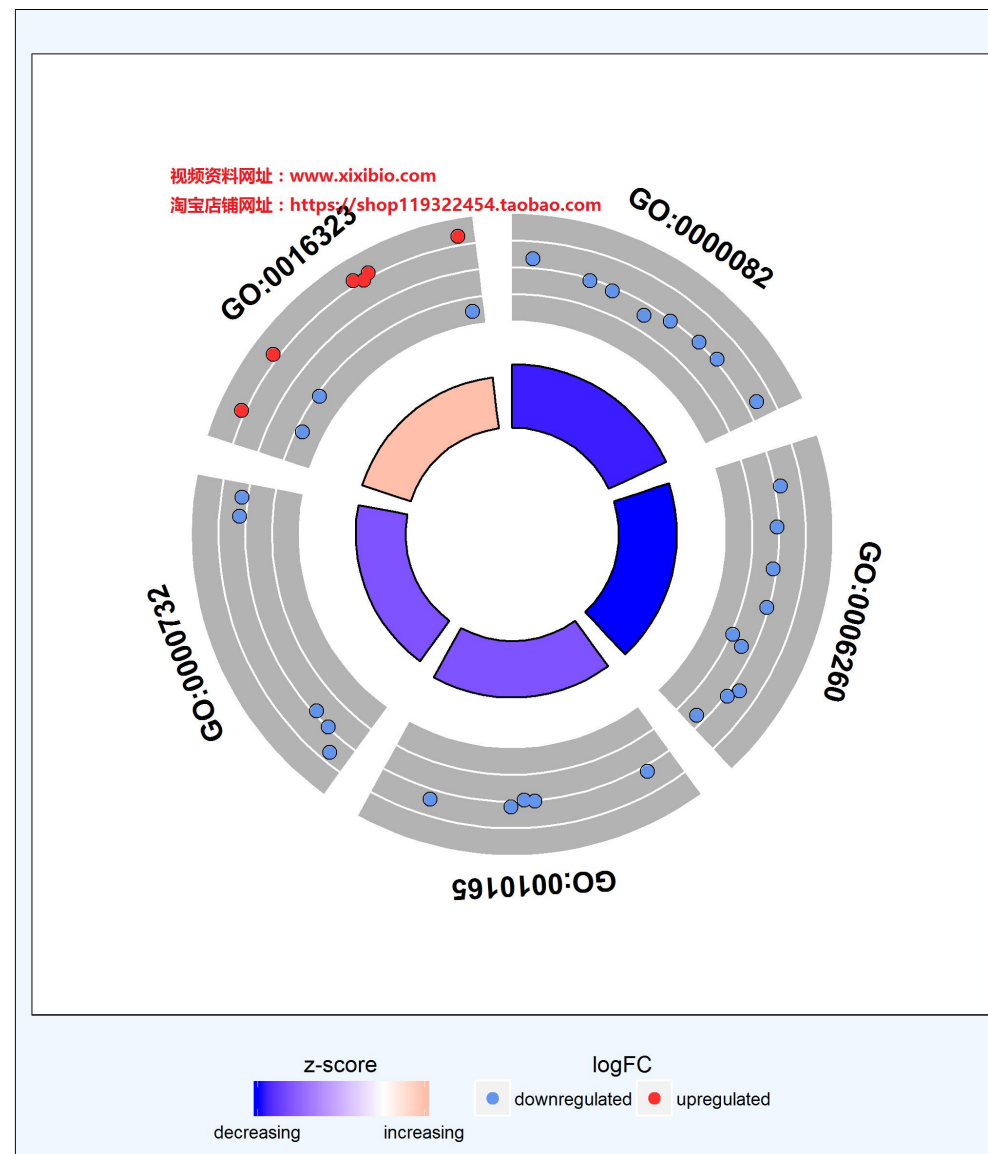


可视化

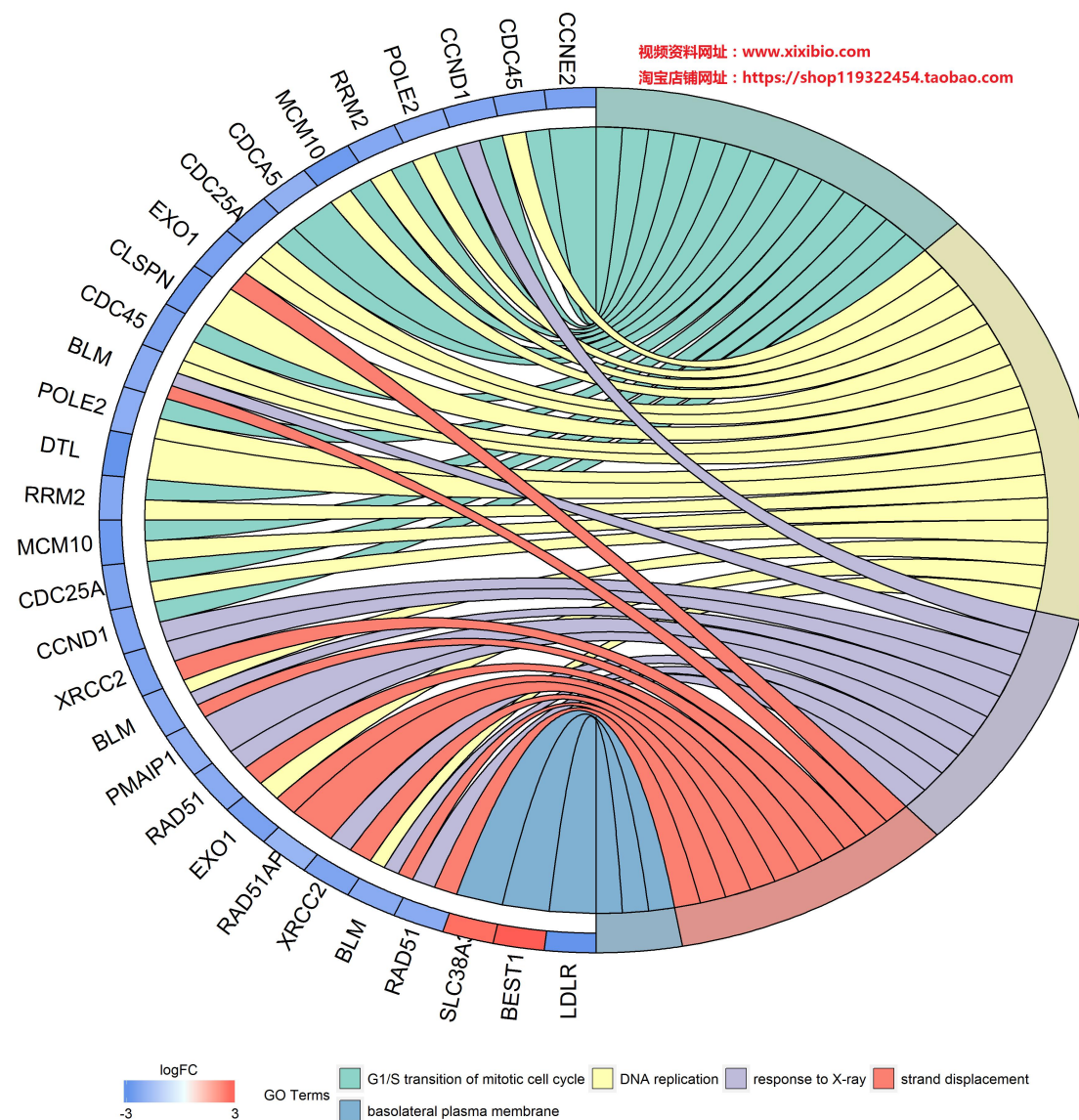
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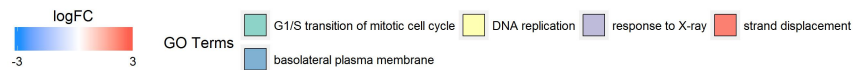
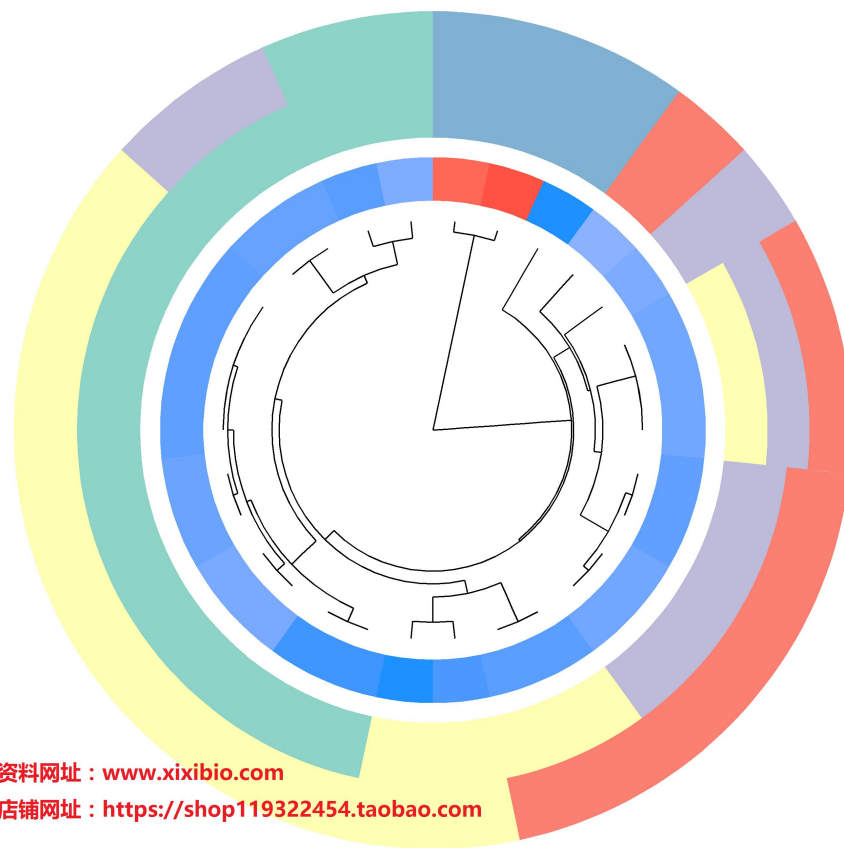
GOplot可视化



GOplot可视化



GOplot可视化





Thanks!!!