

Supplementary Materials

Figure S1

A

Run on terminal

```
Functional Enrichment Analysis
-----
1 Gene Ontology Enrichment
2 KEGG Pathways Enrichment
3 KEGG Pathways Enrichment using blastp
-----
Select an analysis (e.g., 1 / 2 / 3)
=====> : |
```

B

Hypergeometric Distribution

$$p\text{-value} = \frac{\left(\frac{m}{X}\right)\left(\frac{n}{k-X}\right)}{\left(\frac{N}{k}\right)}$$

Table S1. Comparison of GOMics features with other functional enrichment tools

Enrichment tool	Organism	GO Ontology	KEGG Pathways	Statistical method	Correction	Graphical Visualization	Time	Ref
g:Profiler*	213 (species)	A	L	H	FDR	Network	1 min	[1]
GORILLA*	8	A	Na	H	FDR	DAG	30 sec	[2]
DAVID*	Unknown	A	A	F	FDR Bonferroni	NA	2 min	[3]
GOEAST*	60 (species)	A	Na	F, H, Chi-square	FDR Bonferroni	DAG	20 min	[4]
WebGIVI*	Unknown	A	Na	F	Unknown	Network and Graphics	3 min	[5]
WebGestalt*	12	A	A	H	FDR	DAG Network	3 min	[6]
BiNGO	Unknown	A	Na	H	FDR Bonferroni	Network	Unknown	[7]
Funrich	Annotated species	A	Na	Unknown	Unknown	Network and Graphics	Unknown	[8]
GOMics	Annotated species	A	A	H	FDR Bonferroni	Network and Graphics	2-5 min	

A: Applicable

Na: Not Applicable

L: Limited, not applicable to all organisms

H: Hypergeometric distribution

F: Fisher's exact test

FDR: False discovery Rate

DAG: Directed Acyclic Graph

* : Web tools

References

- [1] J. Reimand *et al.*, “g:Profiler-a web server for functional interpretation of gene lists (2016 update).,” *Nucleic Acids Res.*, vol. 44, no. W1, pp. W83-9, 2016.
- [2] E. Eden, R. Navon, I. Steinfeld, D. Lipson, and Z. Yakhini, “GOrilla: a tool for discovery and visualization of enriched GO terms in ranked gene lists.,” *BMC Bioinformatics*, vol. 10, p. 48, Feb. 2009.
- [3] D. W. Huang *et al.*, “The DAVID Gene Functional Classification Tool: a novel biological module-centric algorithm to functionally analyze large gene lists.,” *Genome Biol.*, vol. 8, no. 9, p. R183, 2007.
- [4] Q. Zheng and X.-J. Wang, “GOEAST: a web-based software toolkit for Gene Ontology enrichment analysis.,” *Nucleic Acids Res.*, vol. 36, no. Web Server issue, pp. W358-63, Jul. 2008.
- [5] L. Sun *et al.*, “WebGIVI: a web-based gene enrichment analysis and visualization tool,” *BMC Bioinformatics*, vol. 18, no. 1, p. 237, Dec. 2017.
- [6] B. Zhang, S. Kirov, and J. Snoddy, “WebGestalt: an integrated system for exploring gene sets in various biological contexts.,” *Nucleic Acids Res.*, vol. 33, no. Web Server issue, pp. W741-8, Jul. 2005.
- [7] S. Maere, K. Heymans, and M. Kuiper, “BiNGO: a Cytoscape plugin to assess overrepresentation of Gene Ontology categories in Biological Networks,” *Bioinforma. Appl. NOTE*, vol. 21, no. 16, pp. 3448–3449, 2005.
- [8] M. Pathan *et al.*, “A novel community driven software for functional enrichment analysis of extracellular vesicles data,” *J. Extracell. Vesicles*, vol. 6, no. 1, p. 1321455, Dec. 2017.

Figure set created automatically by Gomics

Case study 1: Enrichment analysis in early-stage lung or head of pancreas cancer

Figure S1. Circular network

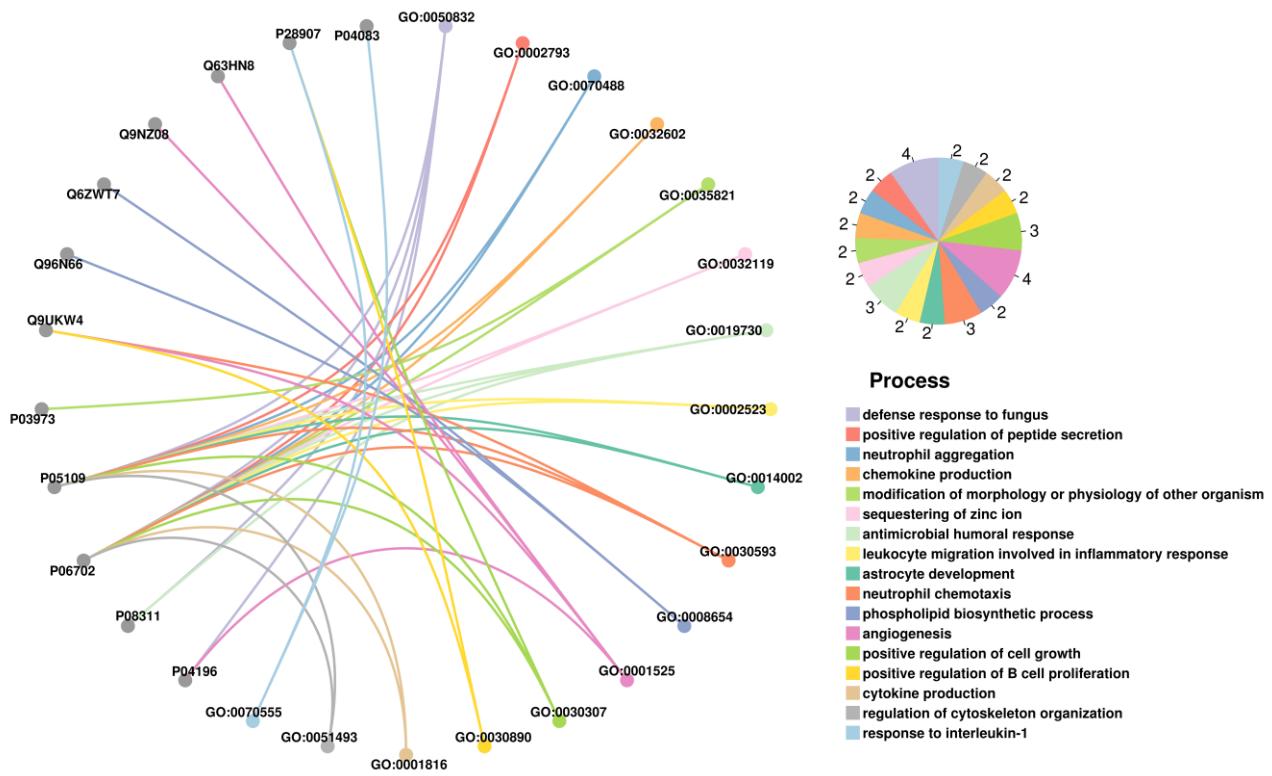


Figure S2 Random network

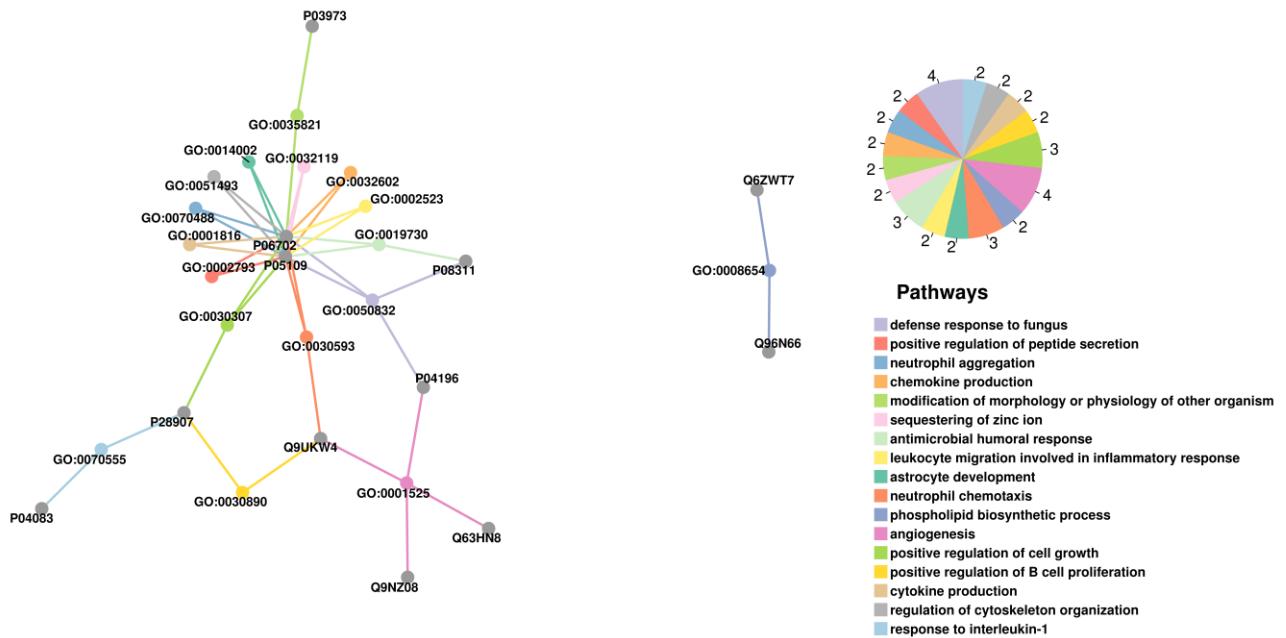


Figure S3 Chord plot

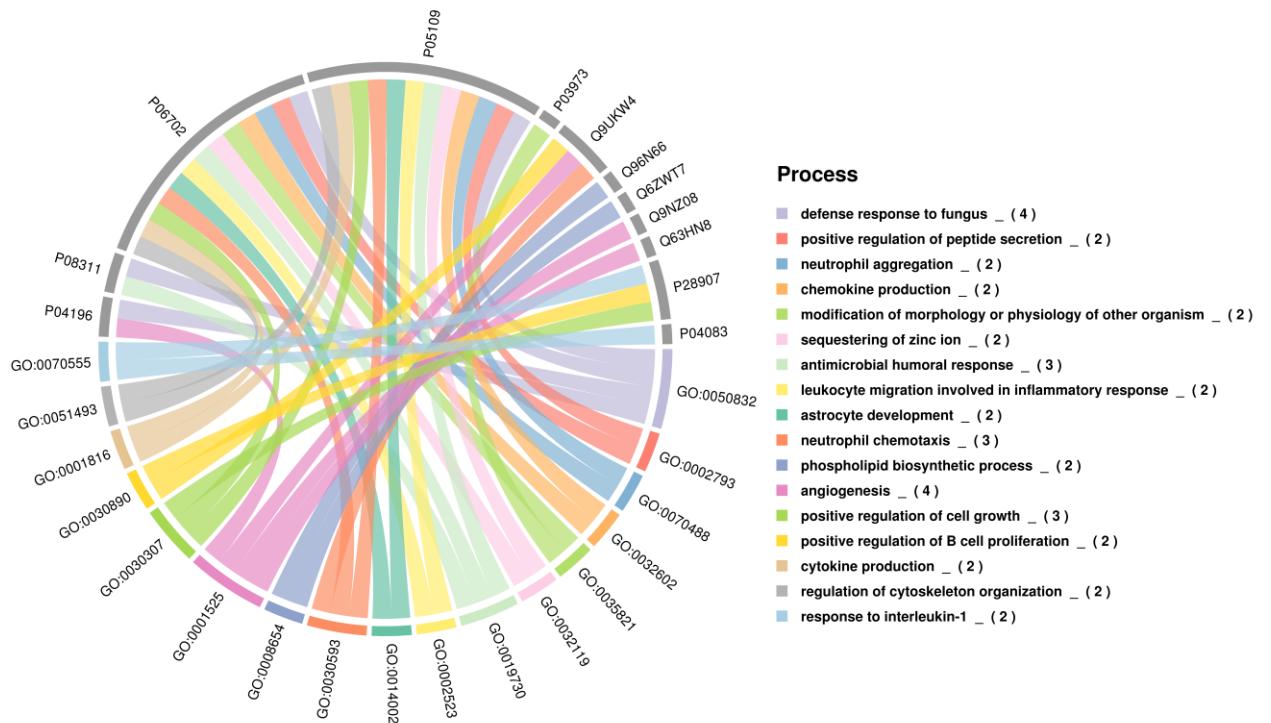


Figure S4 Circular network

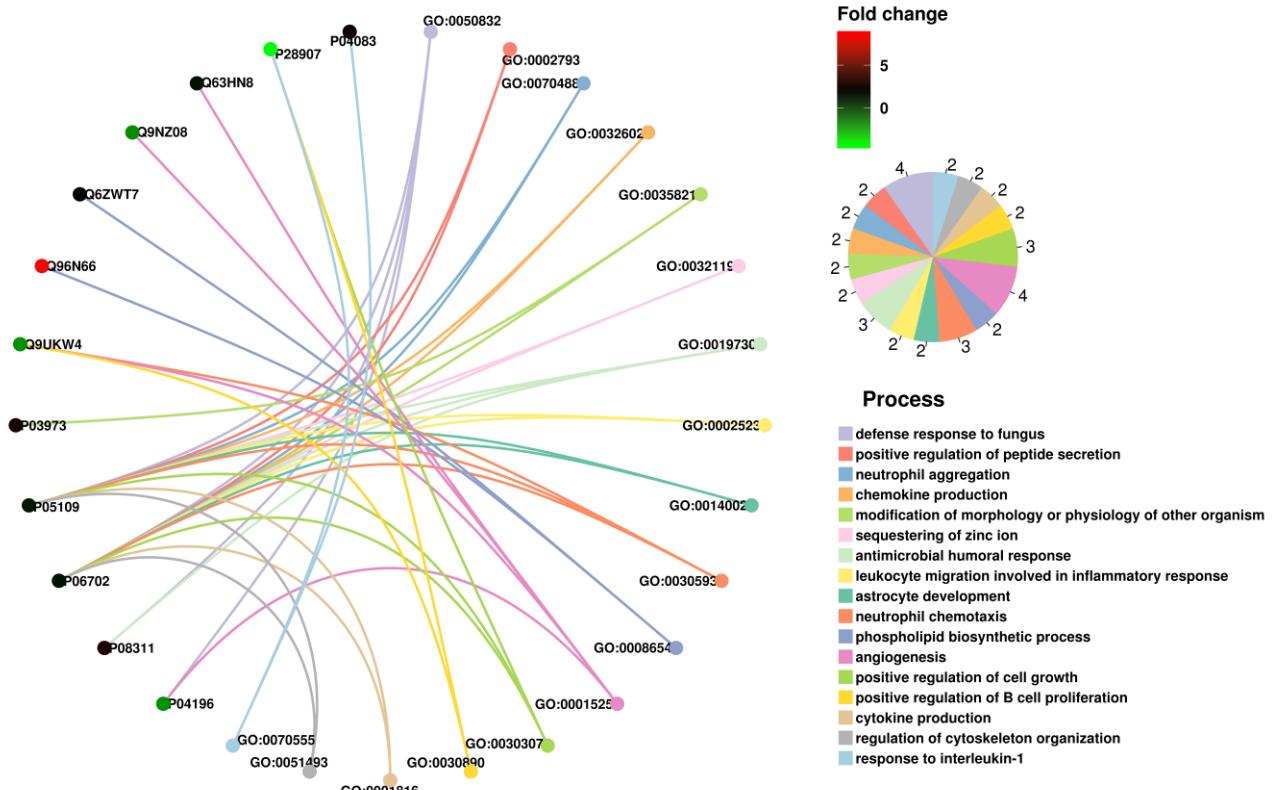


Figure S5 Random network

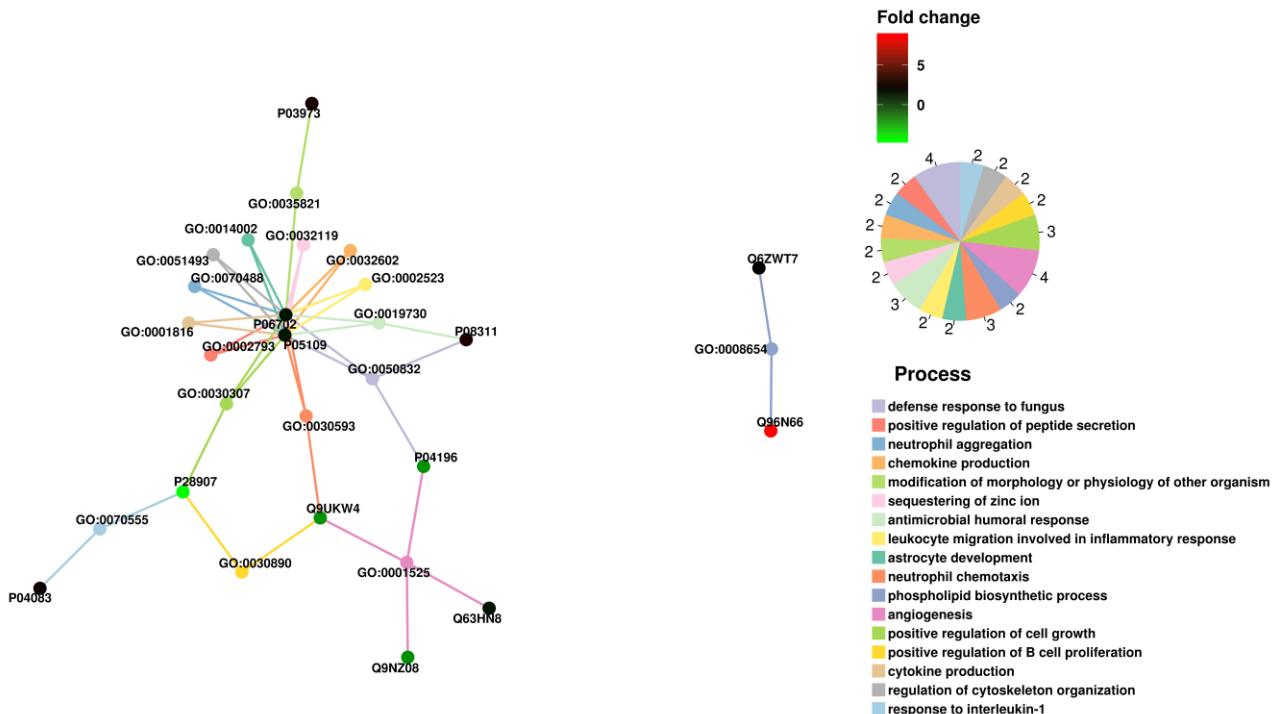
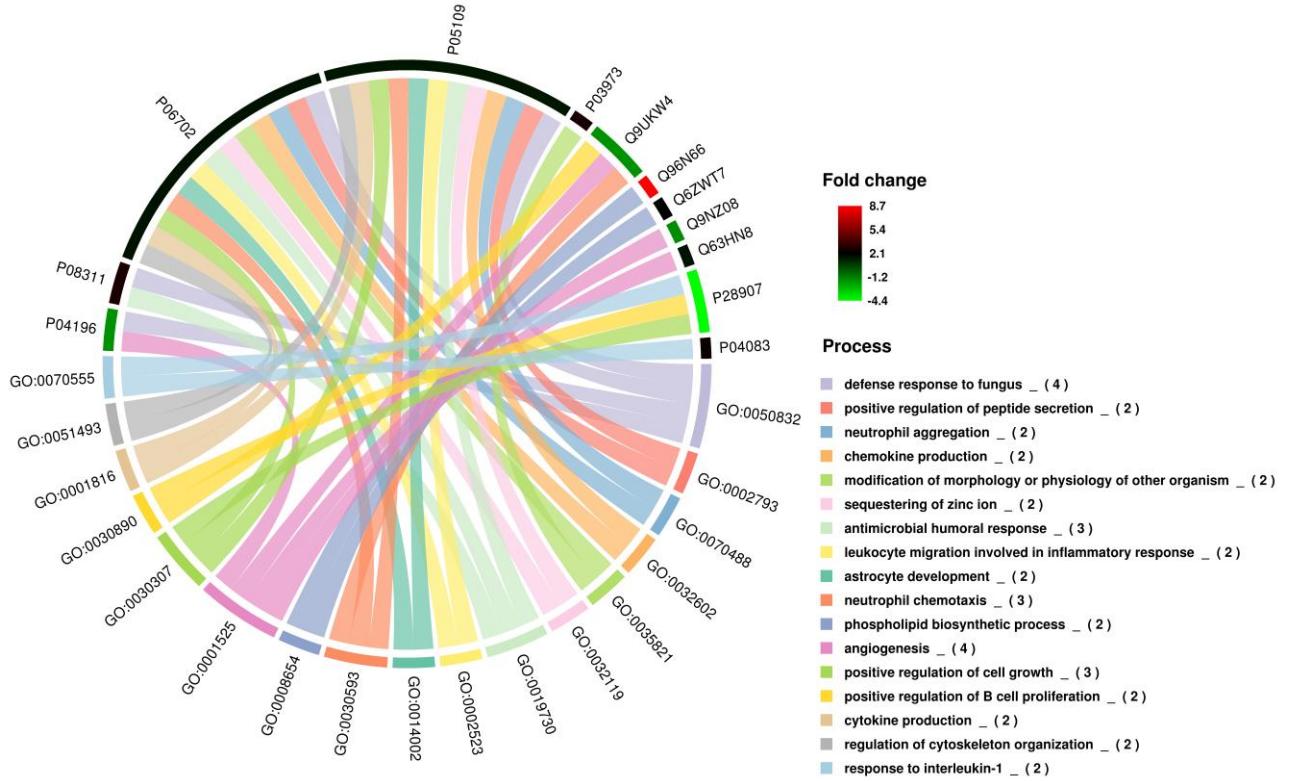


Figure S6 Chord plot



Case study 2: Function Enrichment from Proteome and Phosphoproteome dataset in *Beauveria bassiana*

Proteome under NaCl (1 M) stress

Figure S7 Circular network

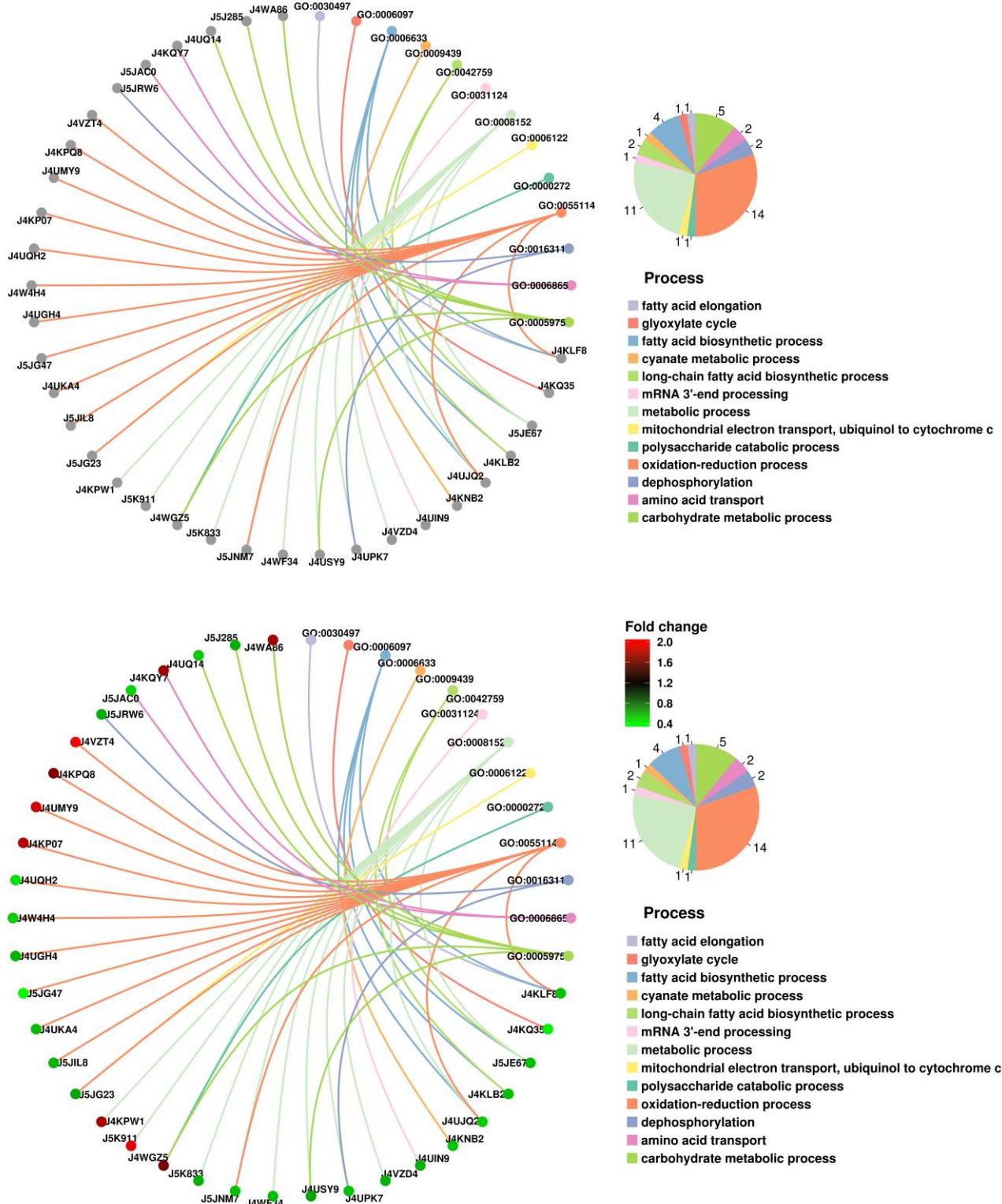


Figure S8 Random network

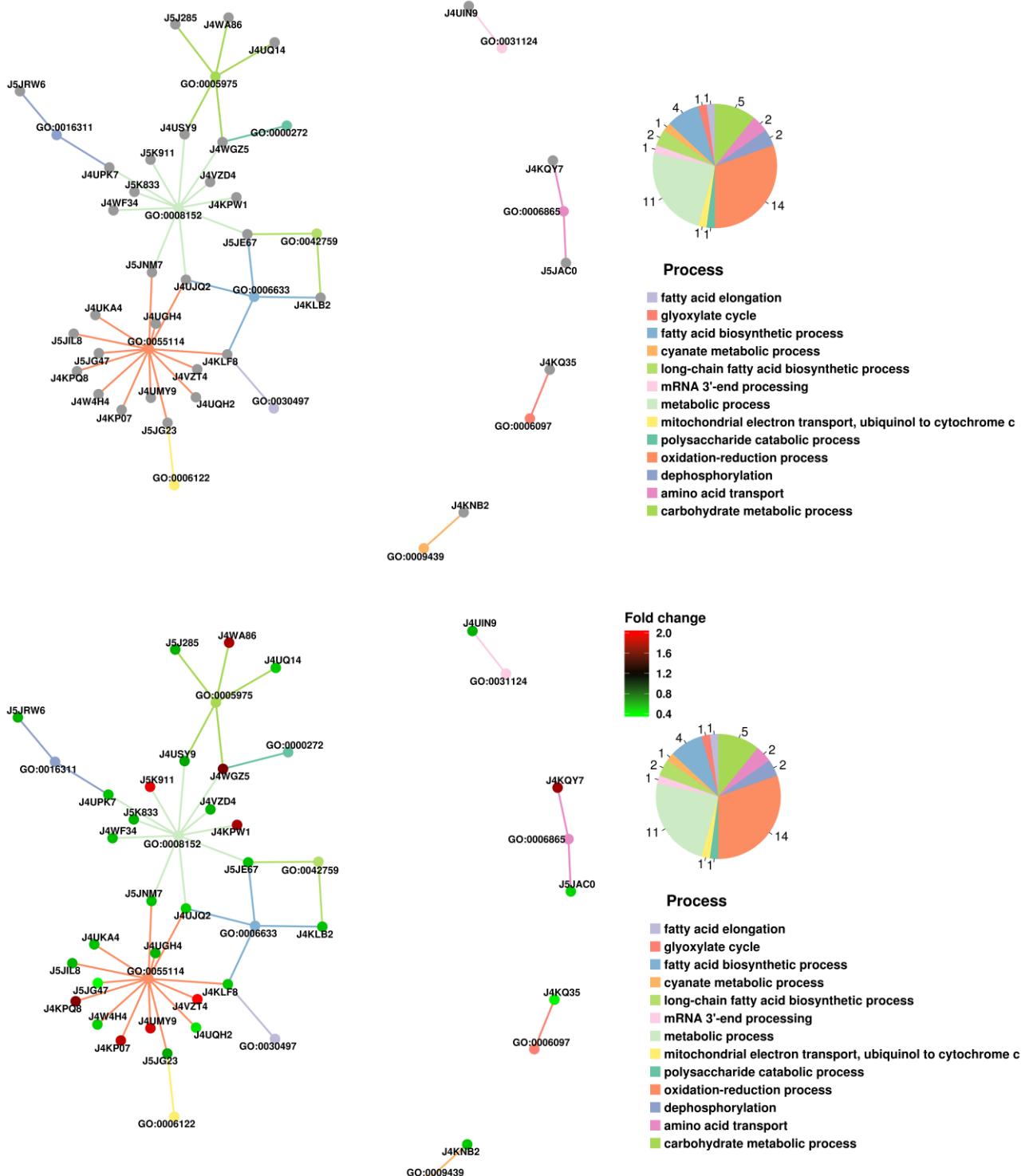


Figure S9 Chord plot

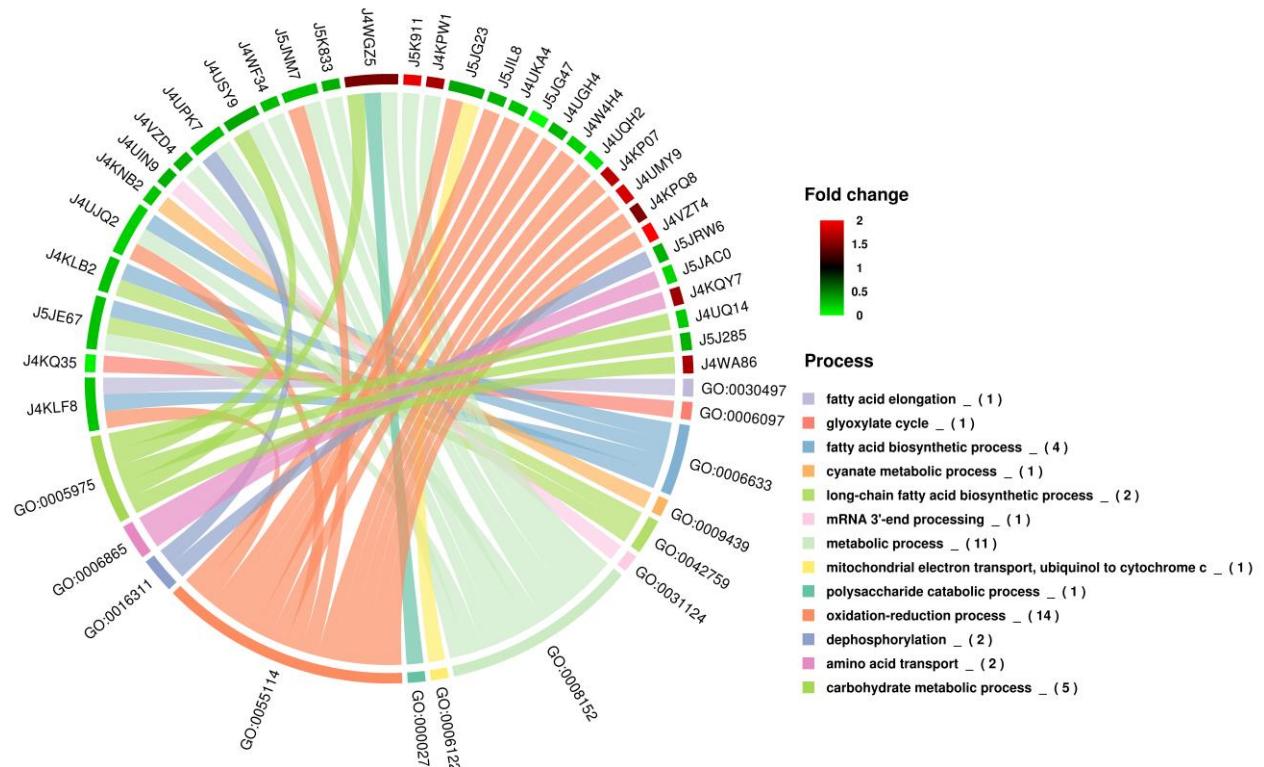
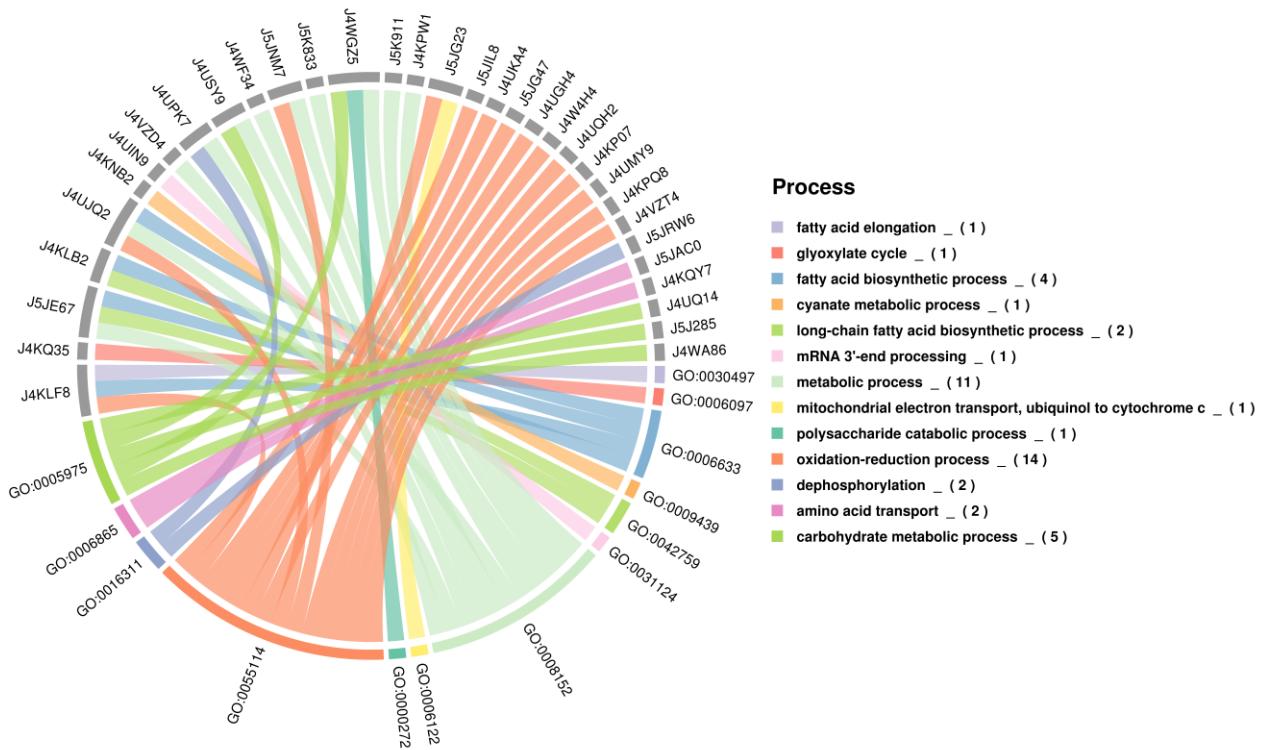
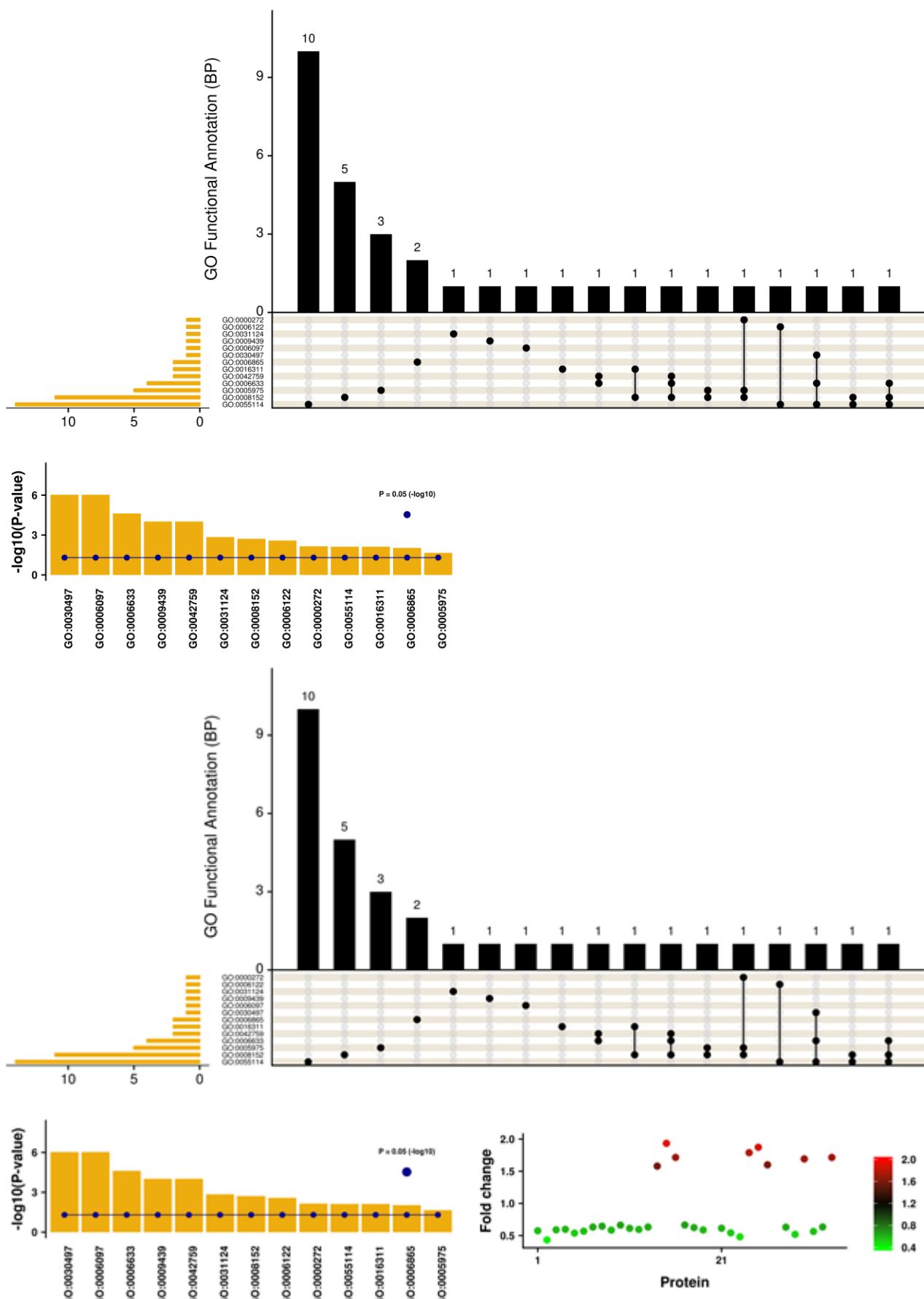


Figure S10 UpSet plot



Phosphoproteome under NaCl (1 M) stress

Figure S11 Circular network

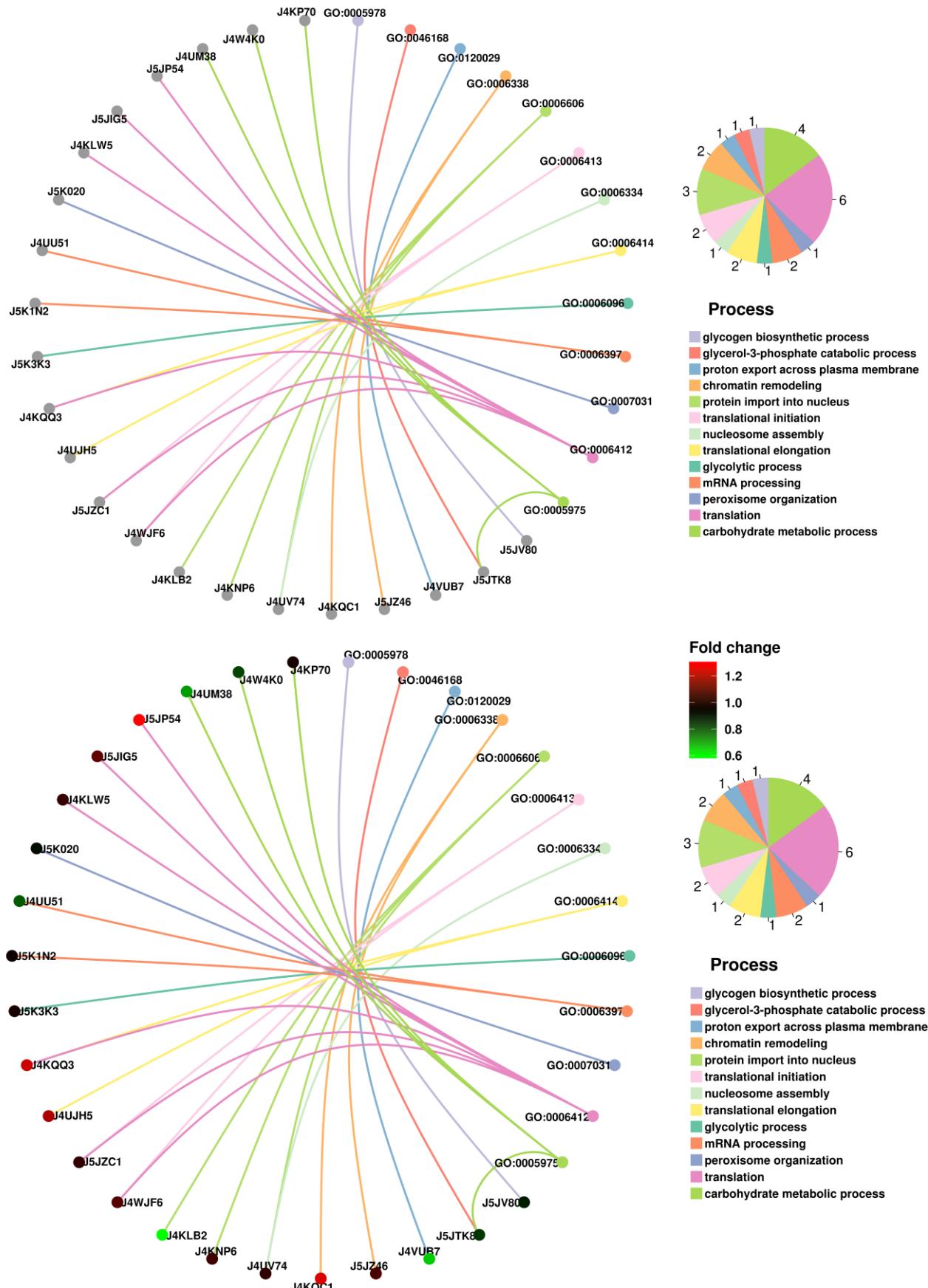


Figure S12 Random network

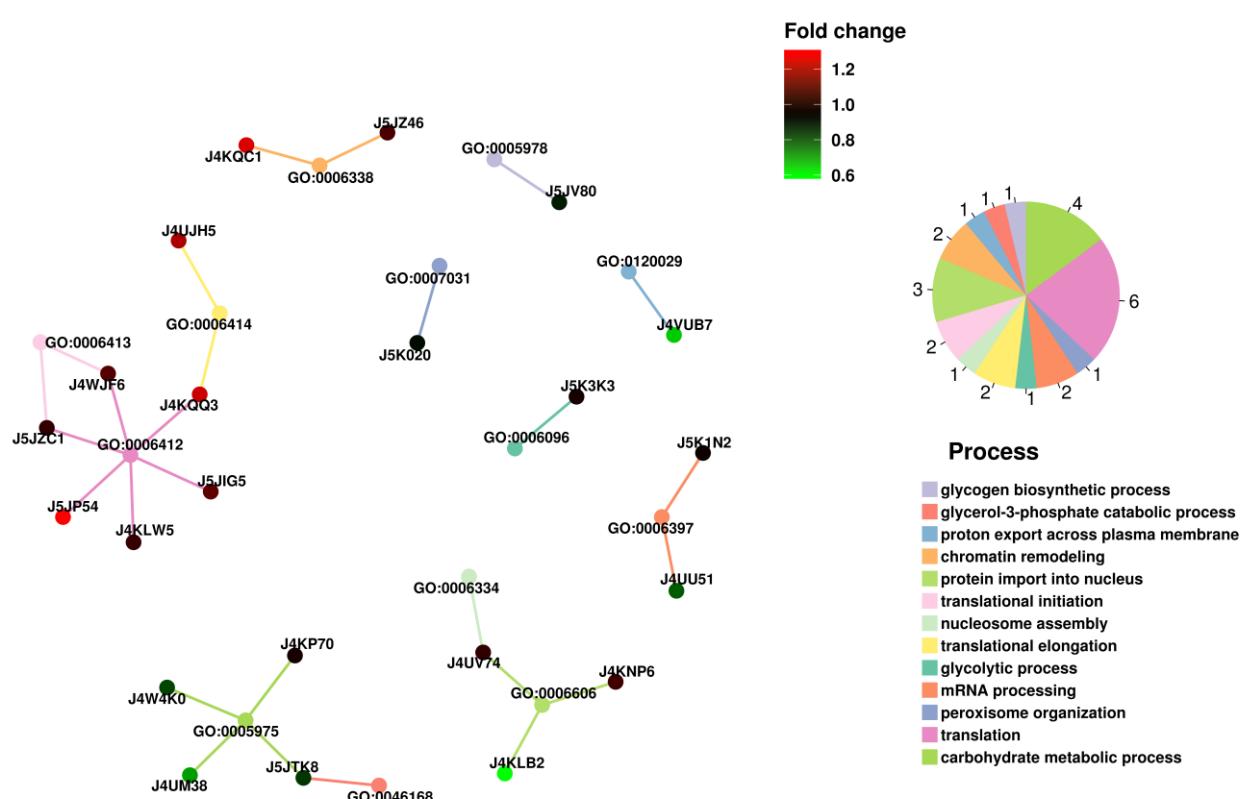
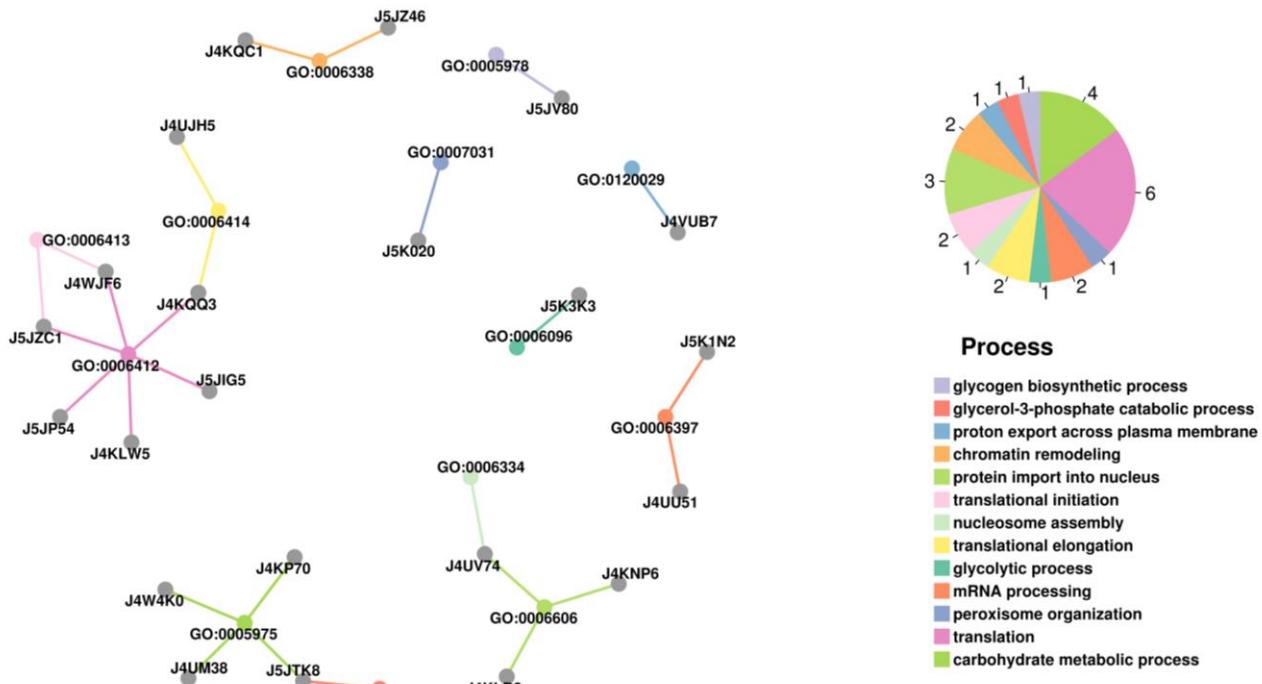


Figure S13 Chord plot

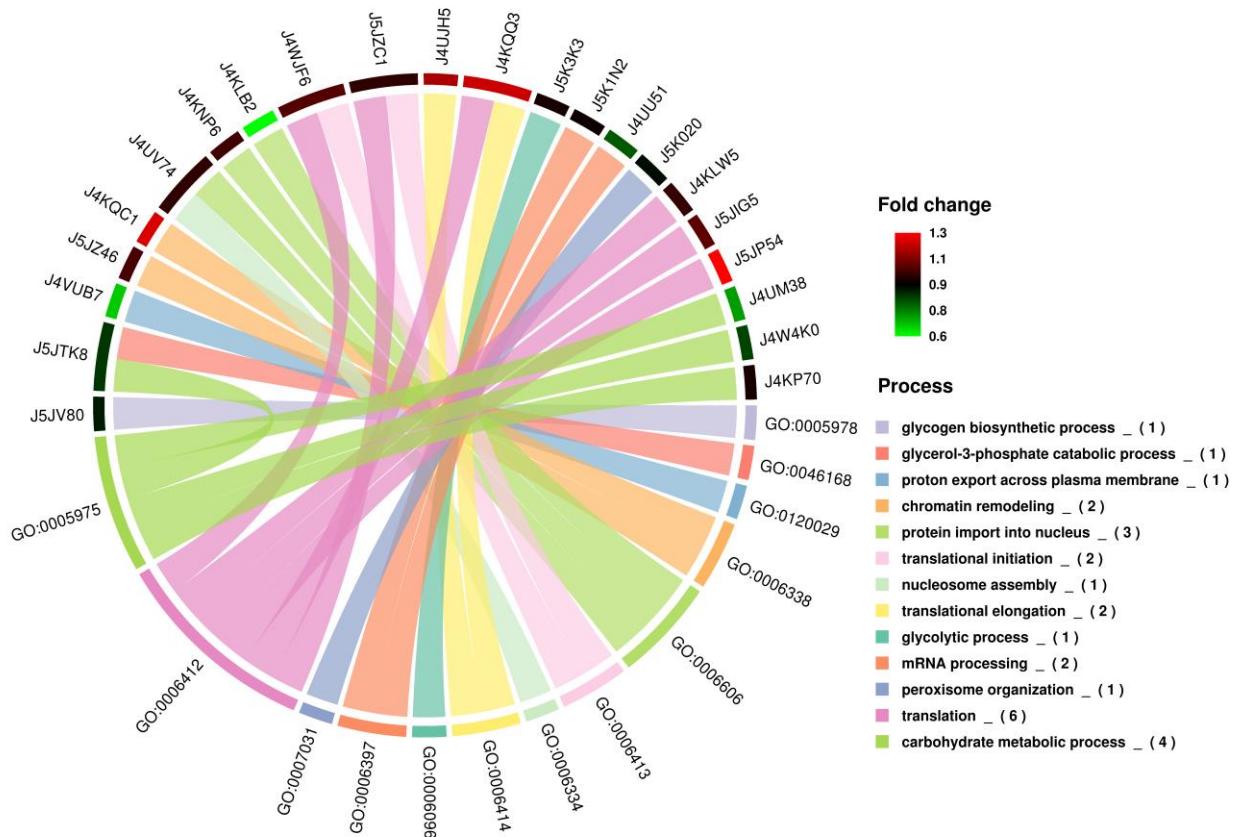
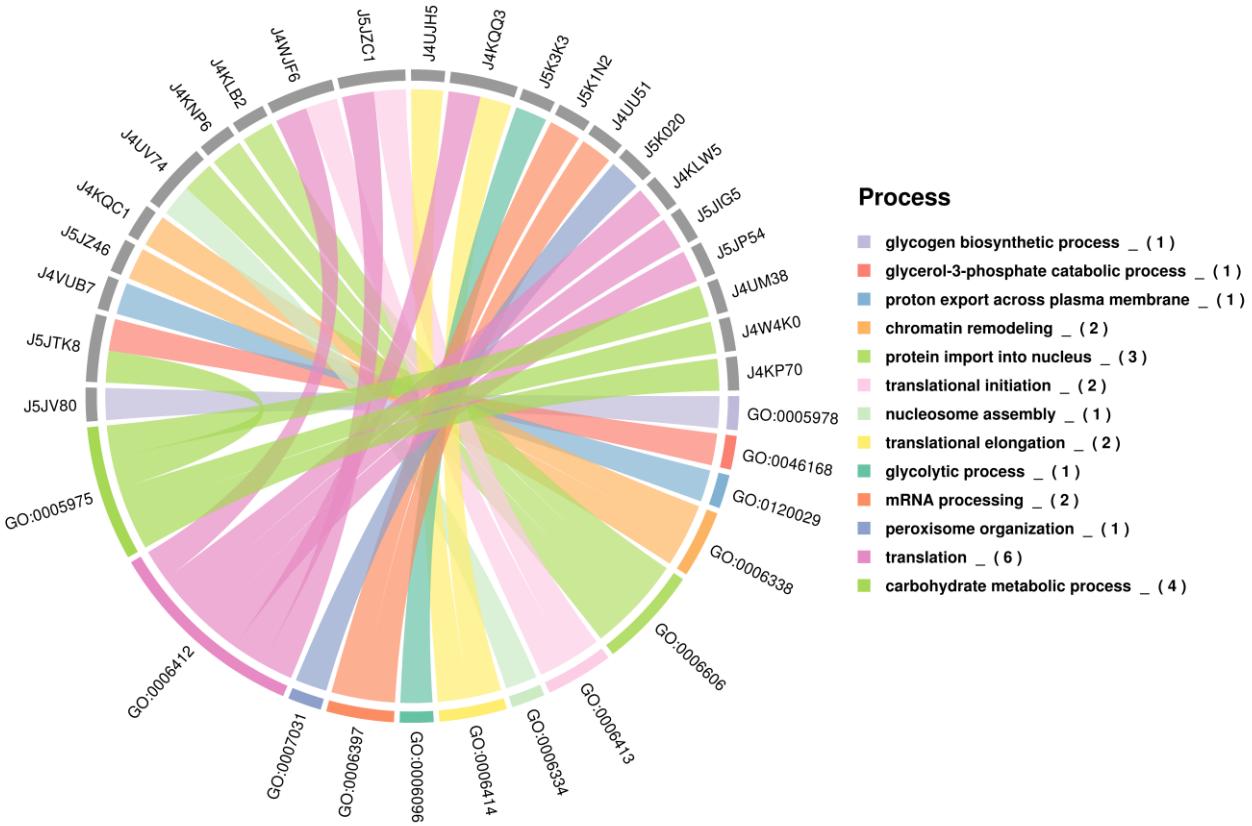
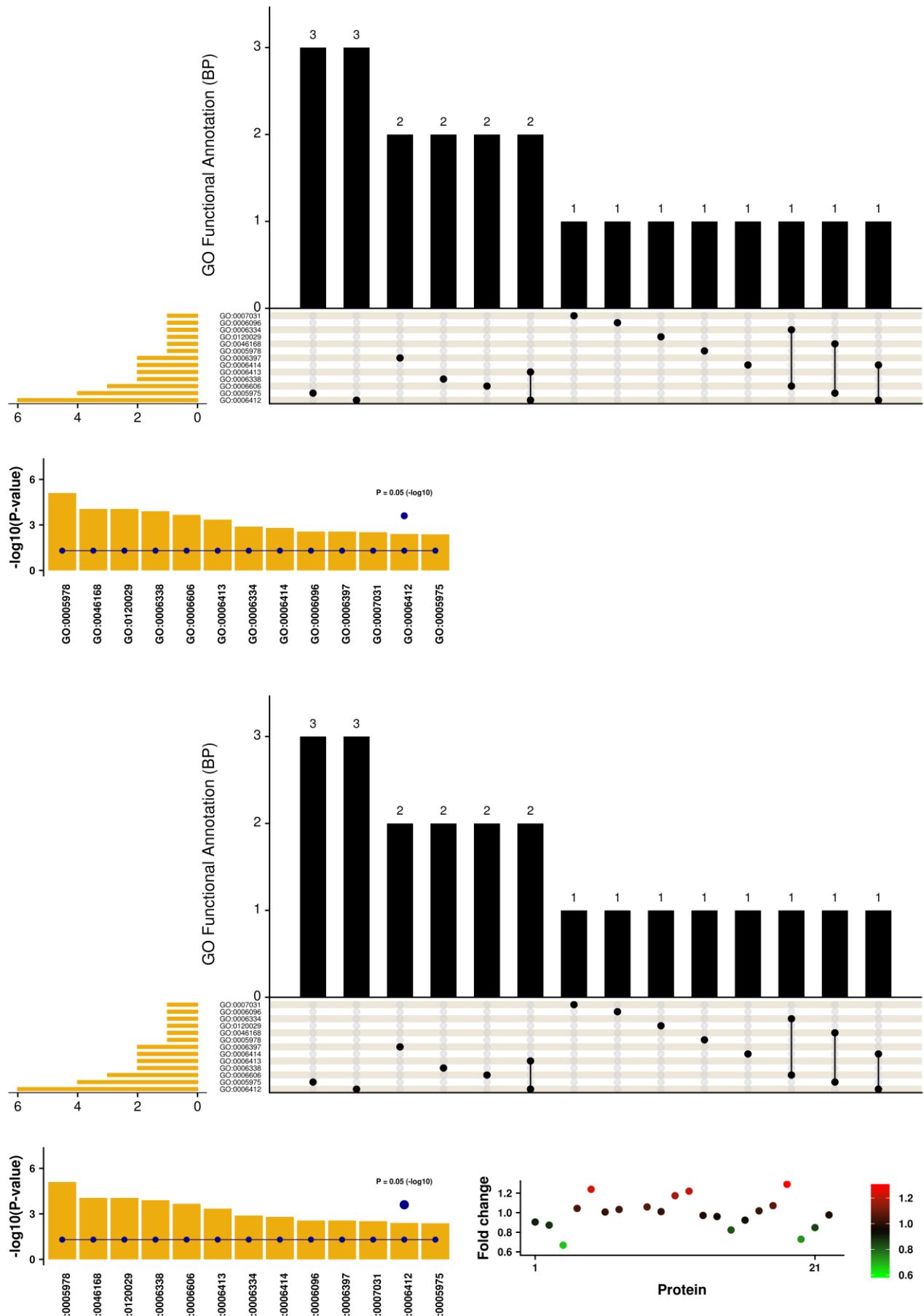


Figure S14 UpSet plot



Proteome under H₂O₂ (3 Mm) stress

Figure S15 Circular network

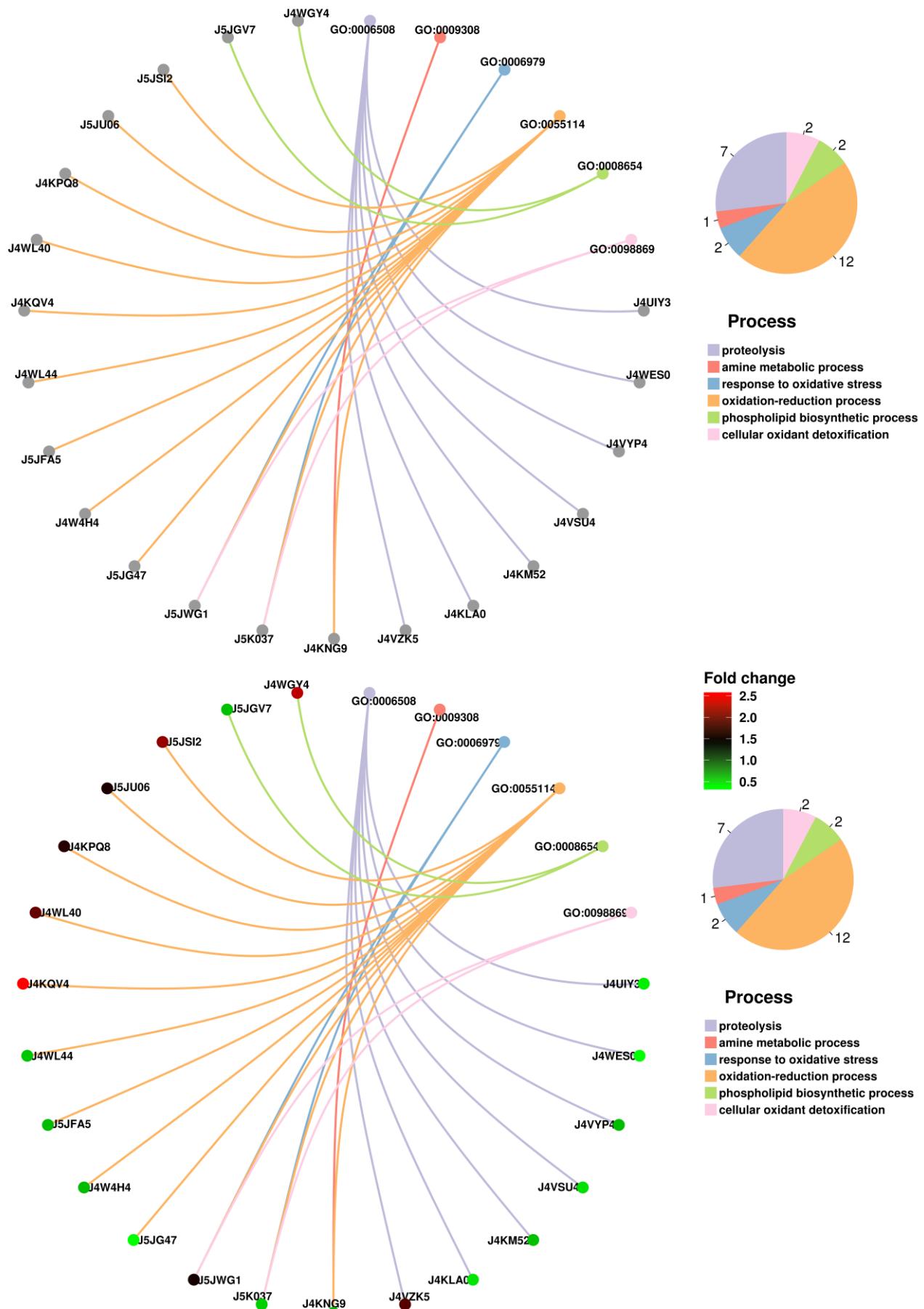


Figure S16 Random network

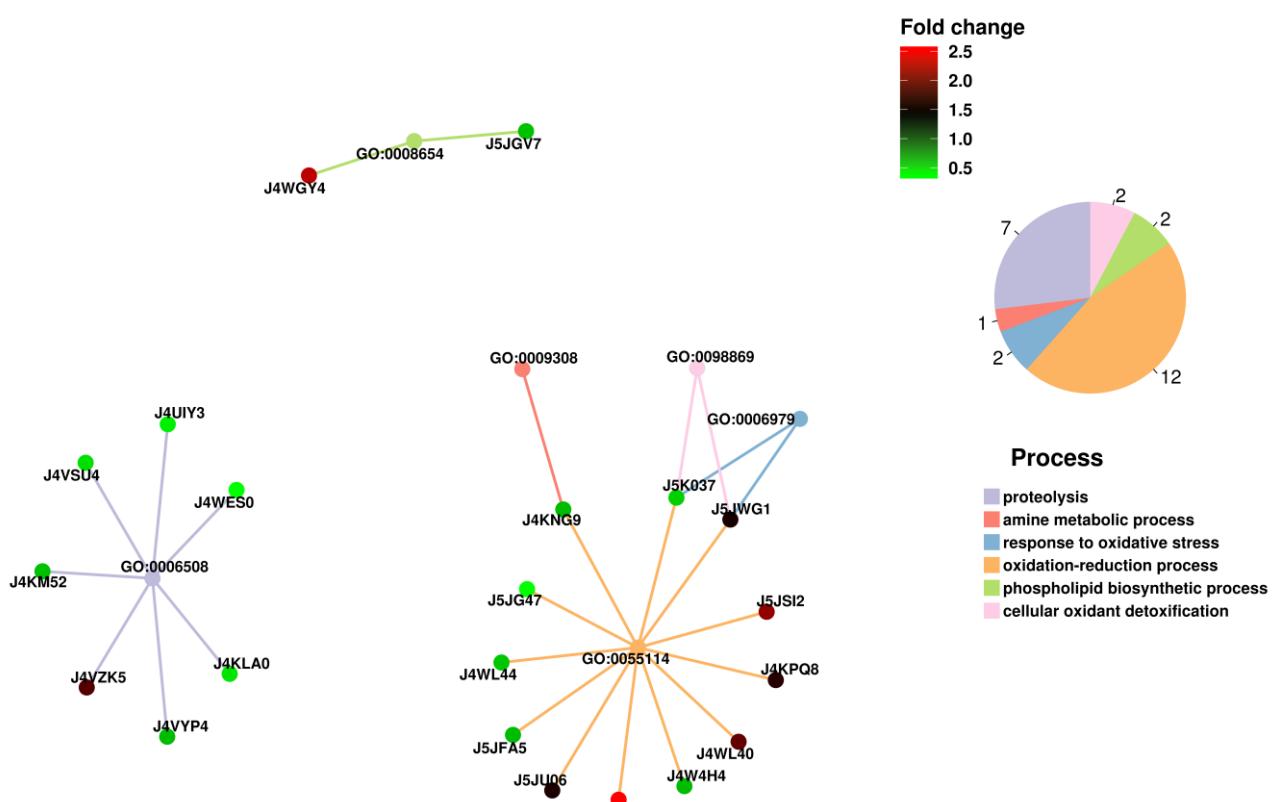
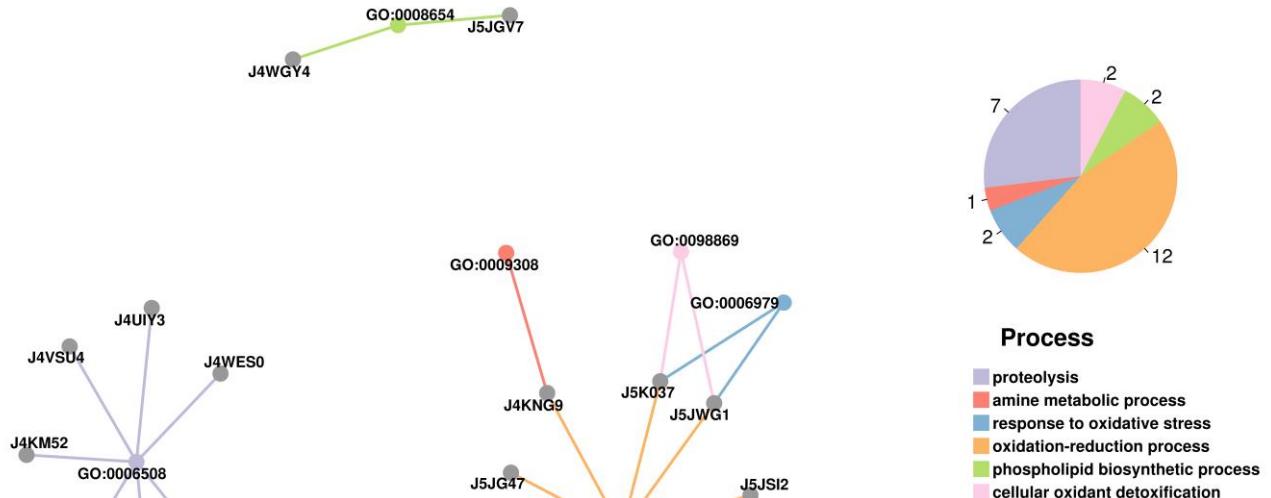


Figure S17 Chord plot

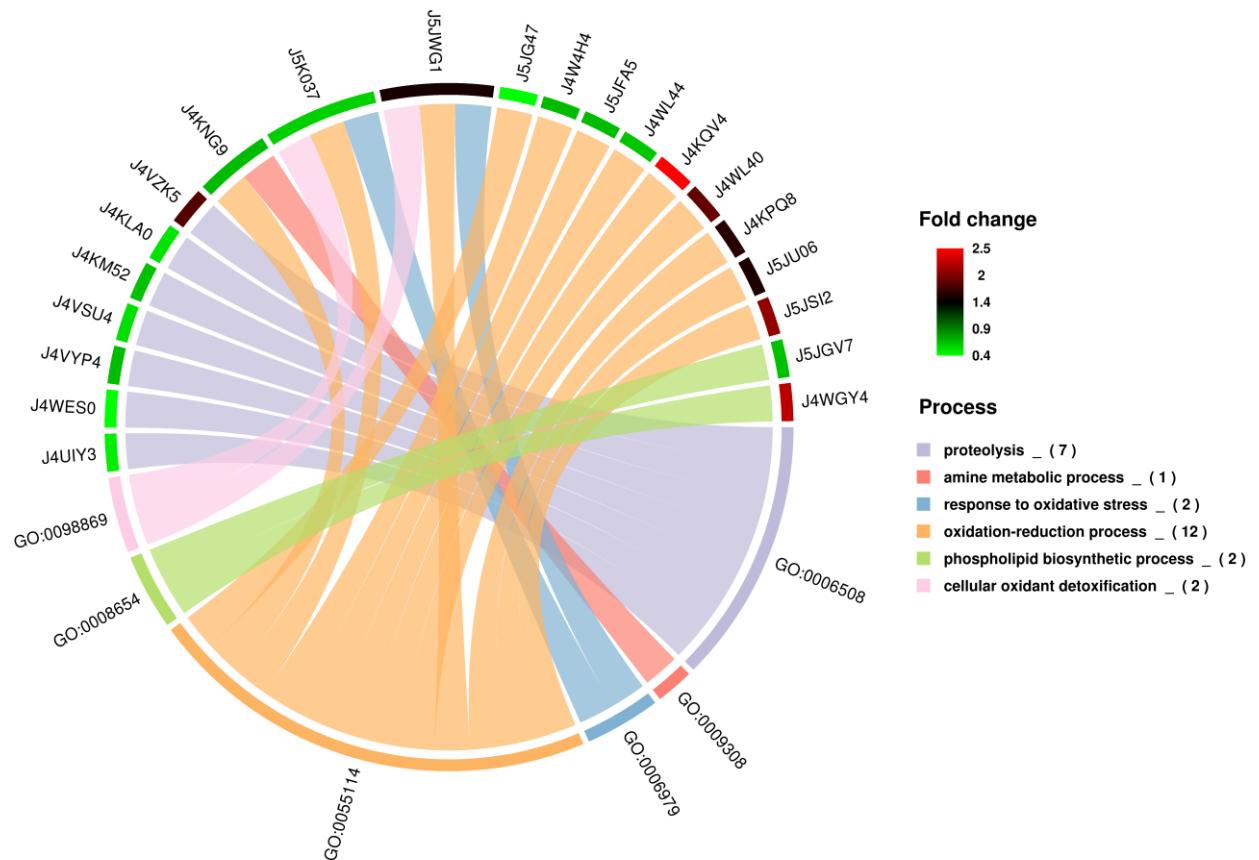
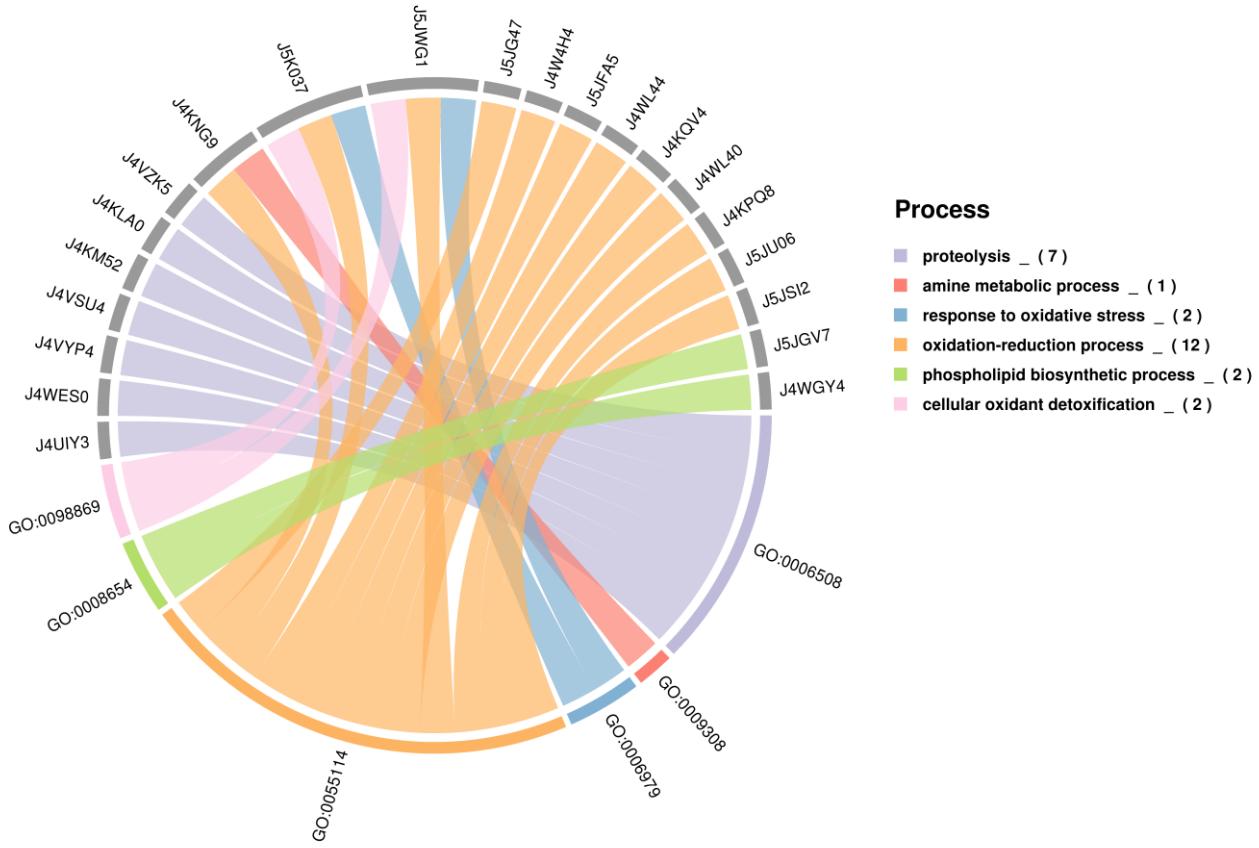
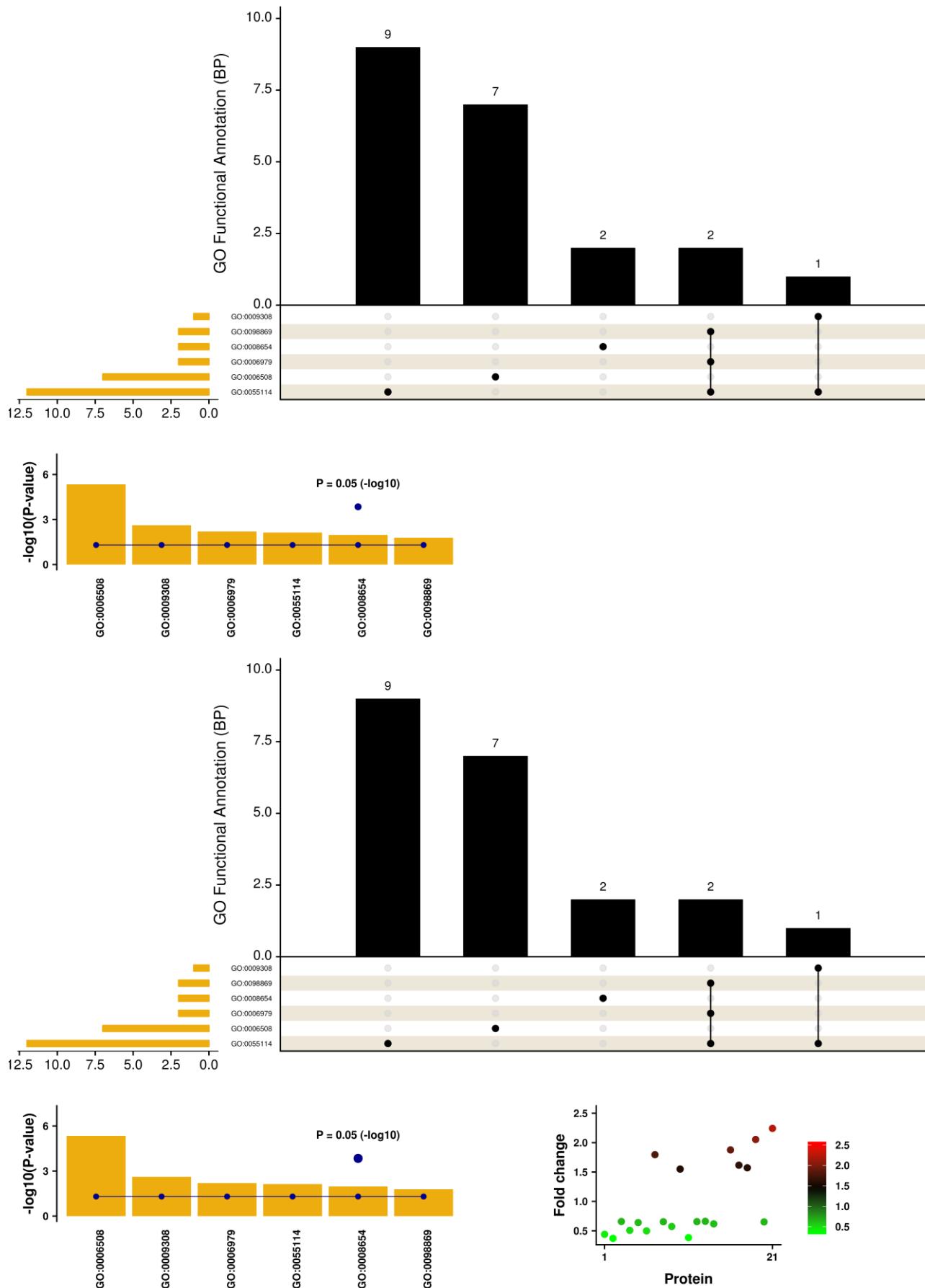


Figure S18 UpSet plot



Phosphoproteome under H₂O₂ (3 Mm) stress

Figure S19 Circular network

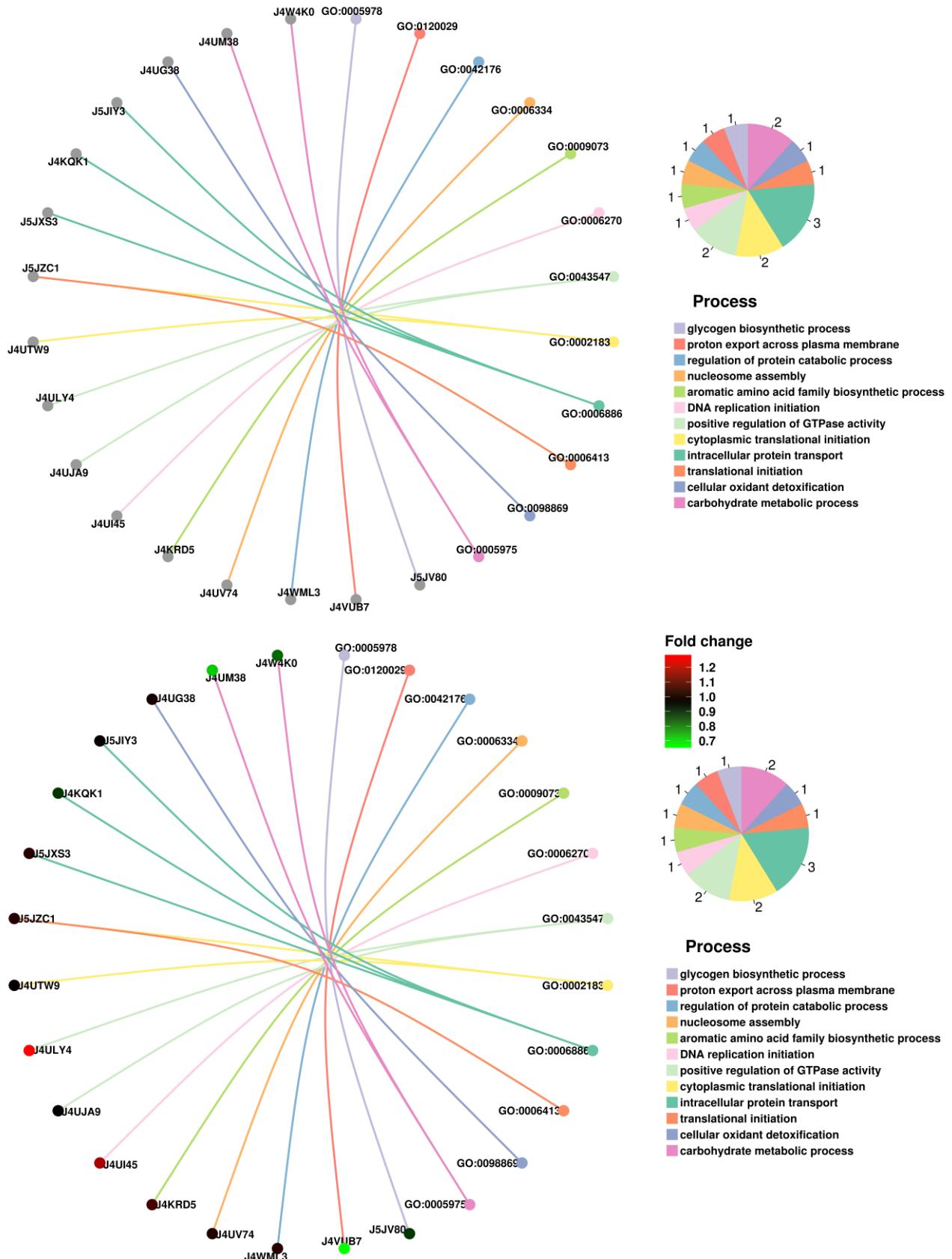


Figure S20 Random network

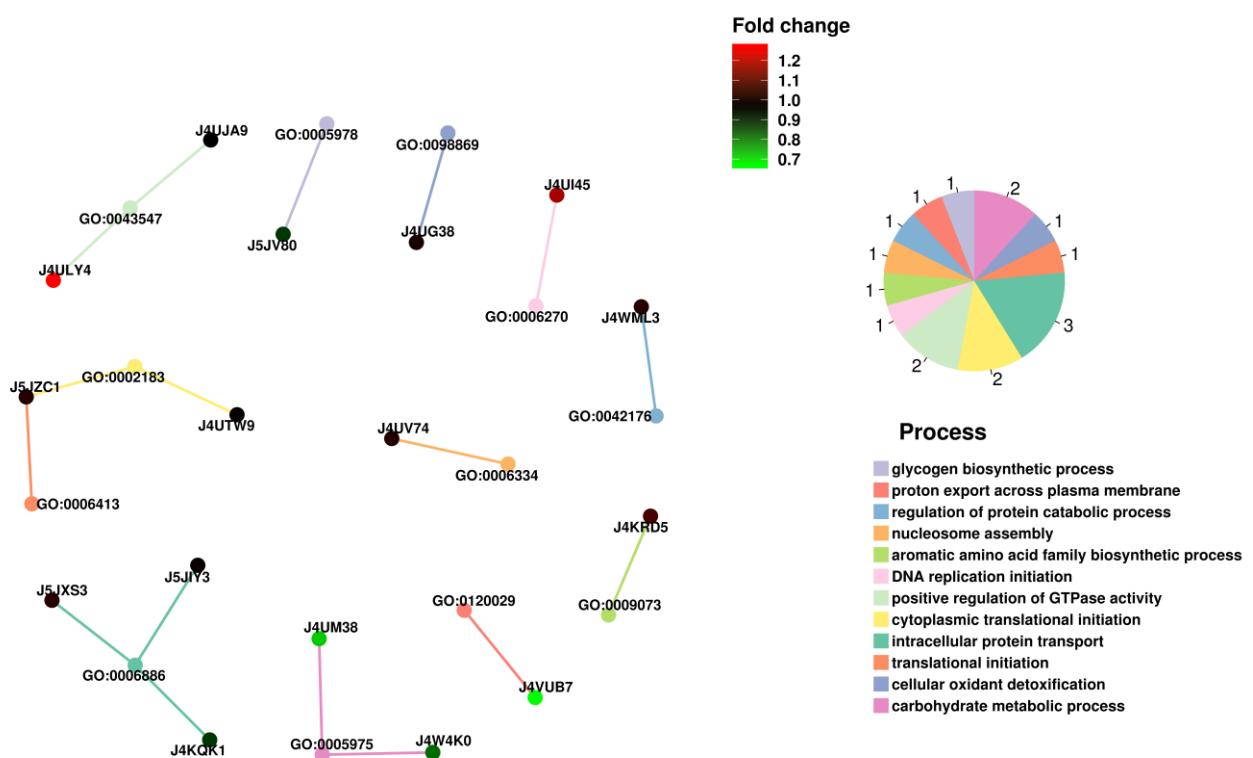
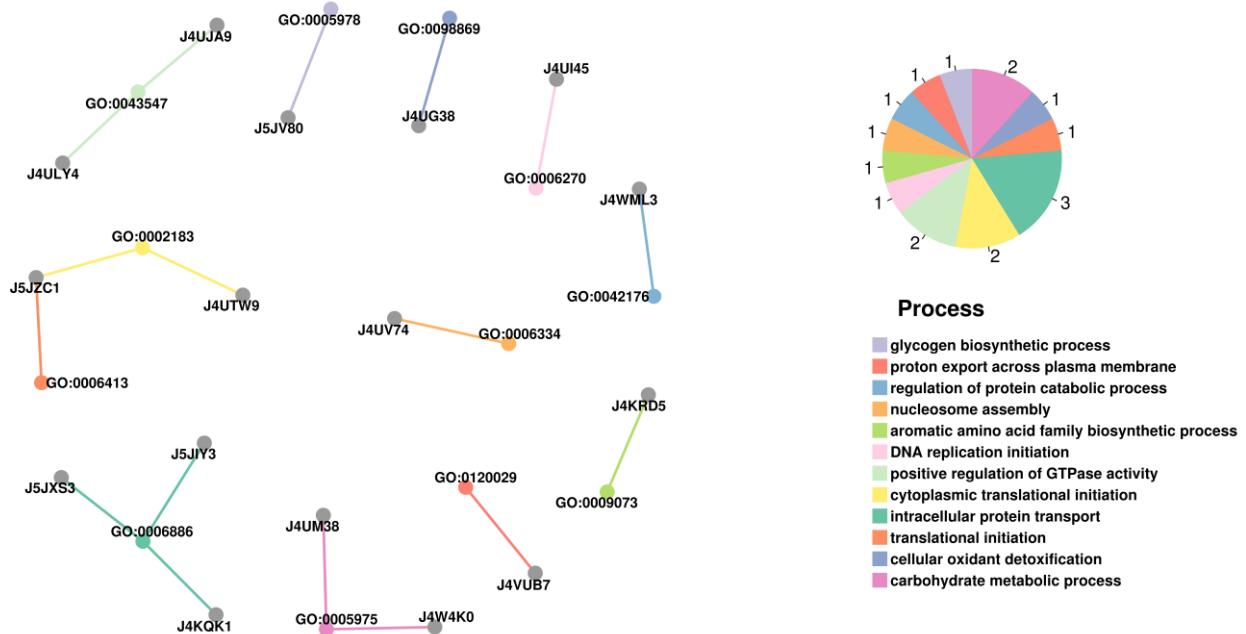


Figure S21 Chord plot

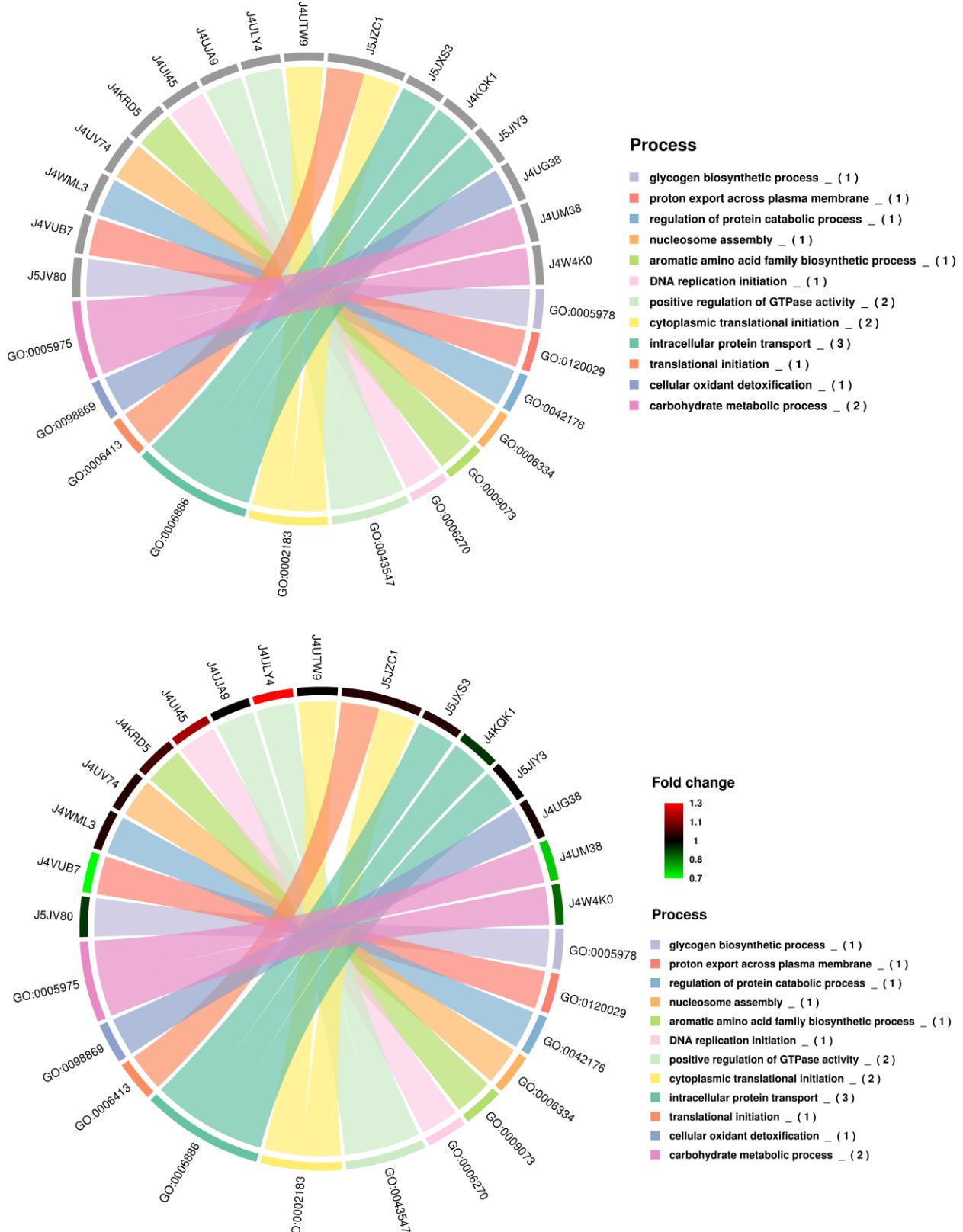
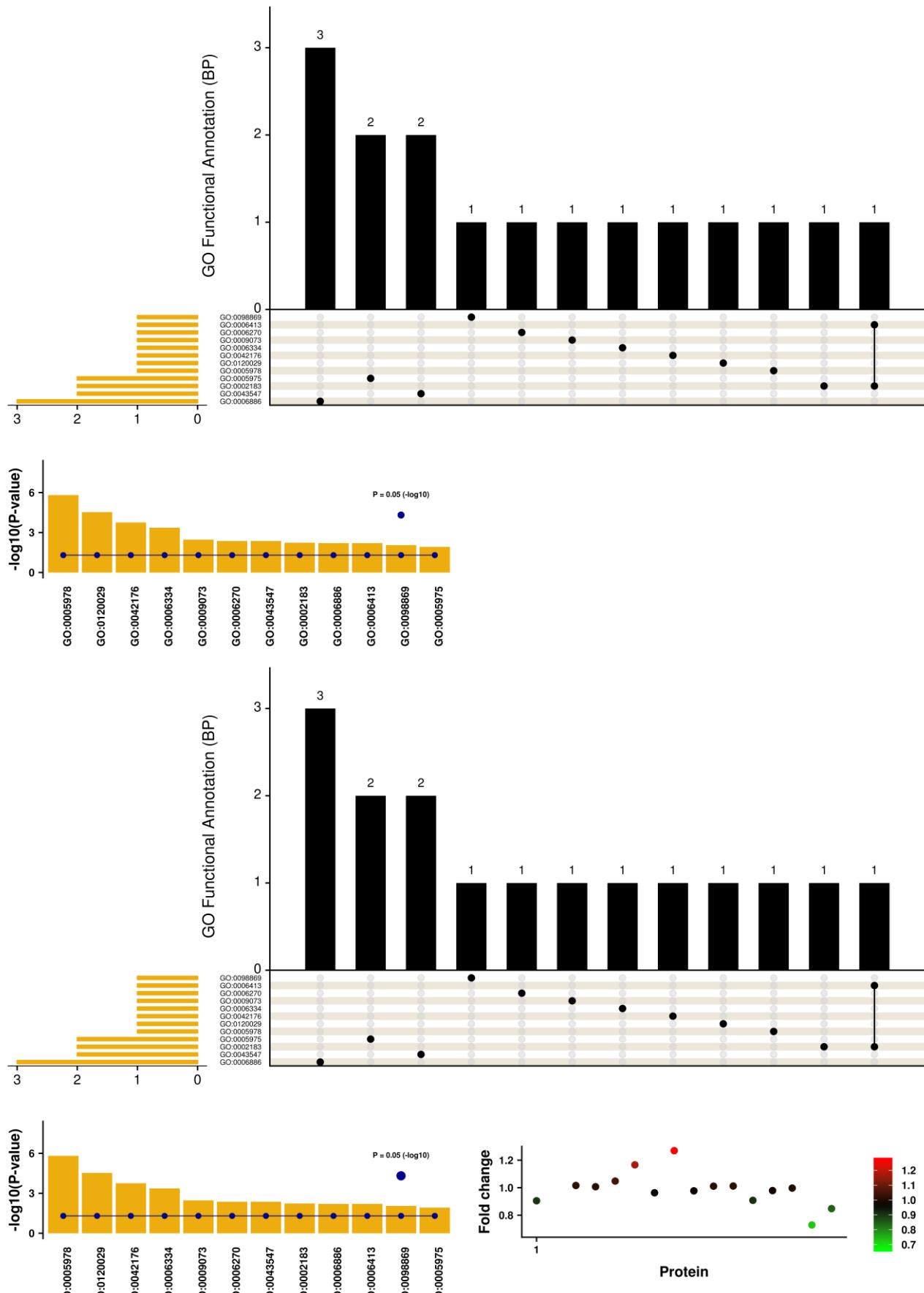


Figure S22 UpSet plot



Comparison and advantages of GOmics over others functional enrichment analysis tools

Figure S15

