













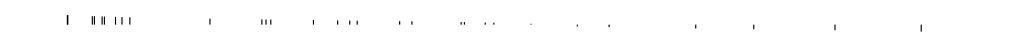









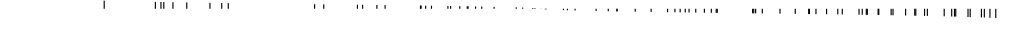

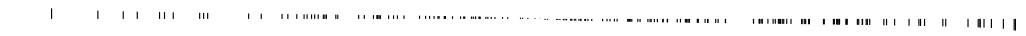






















































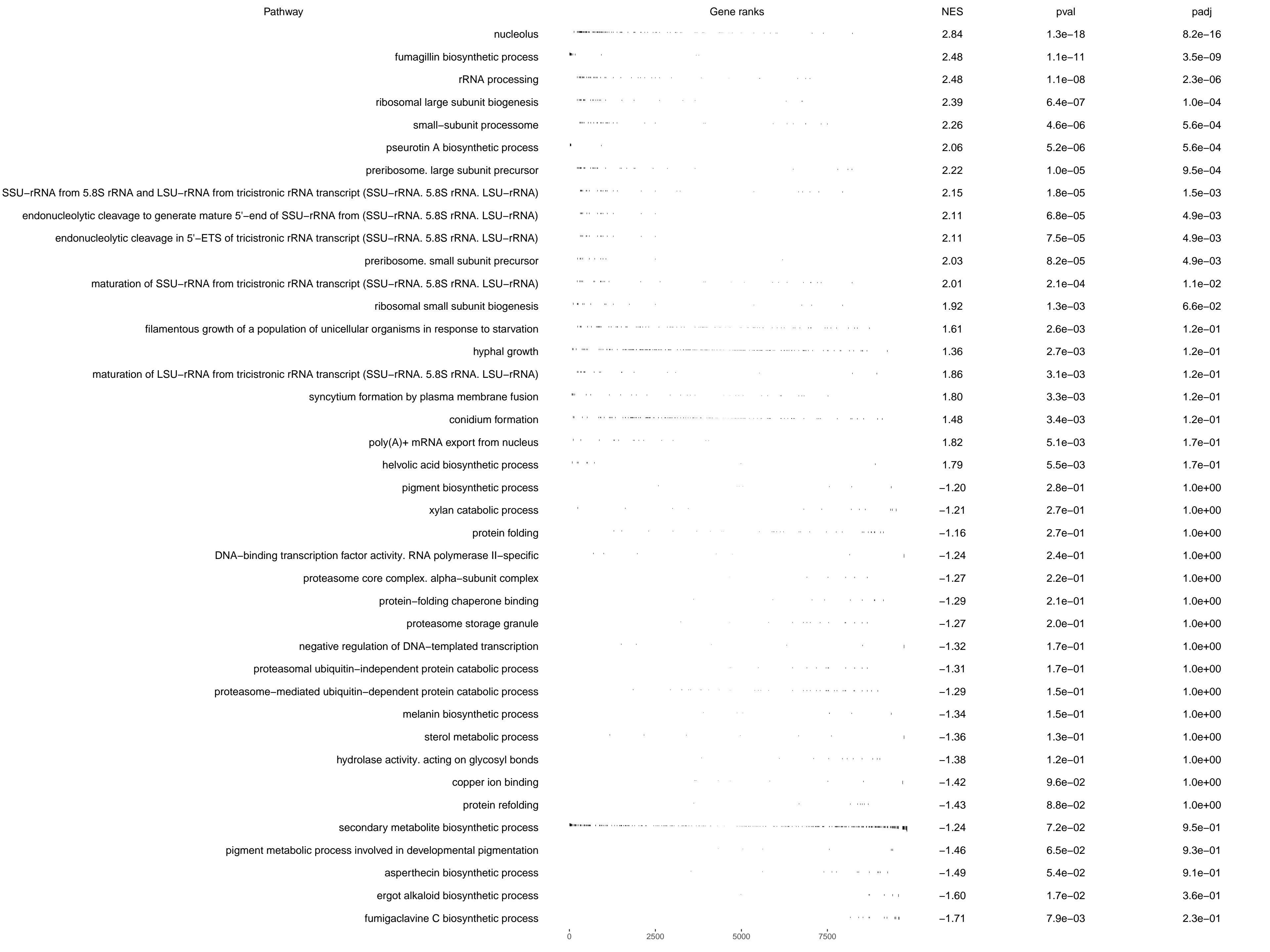
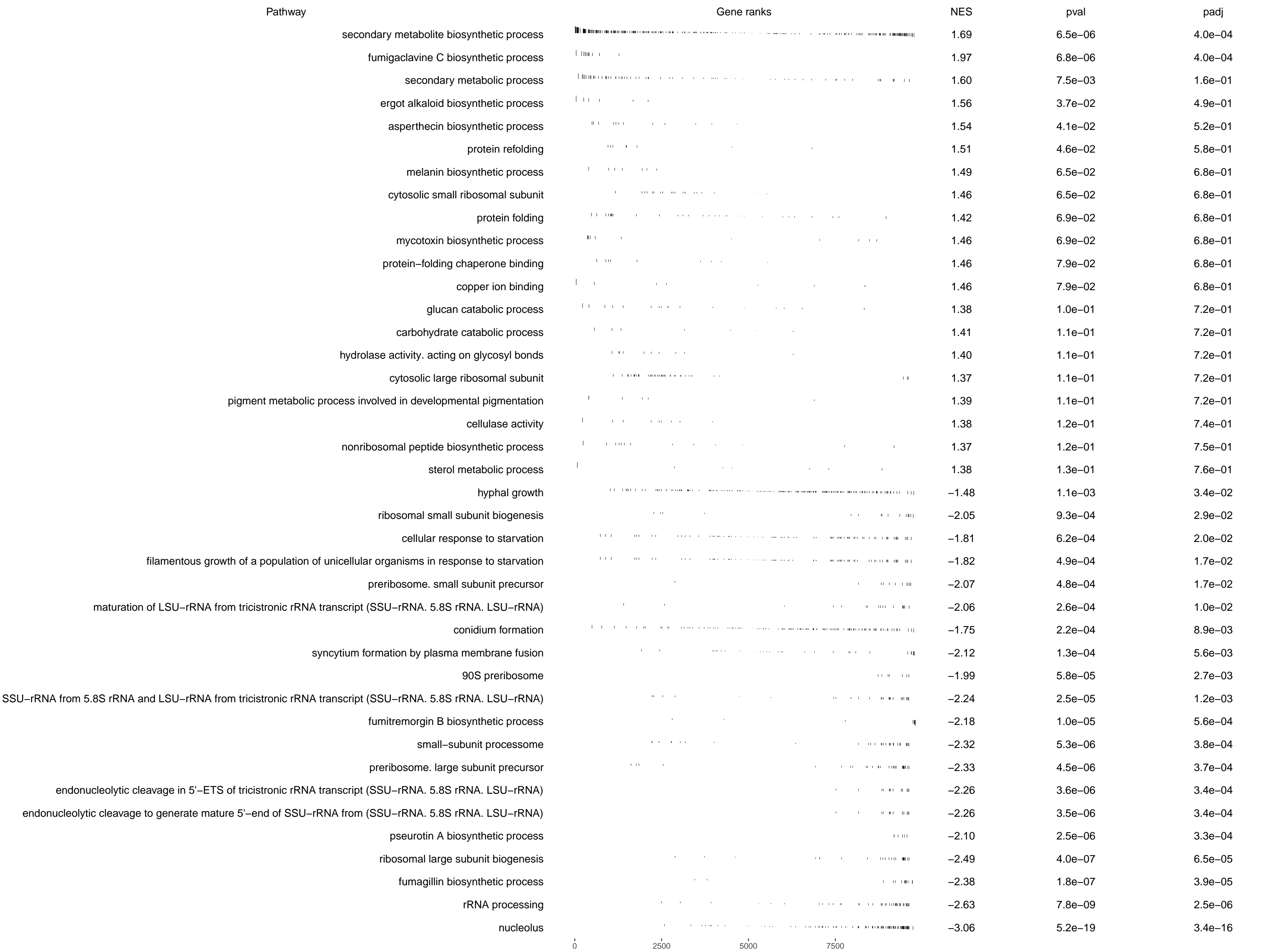












































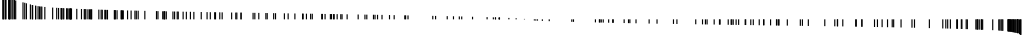
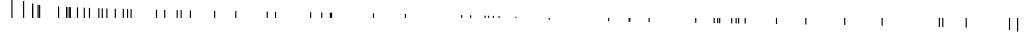

















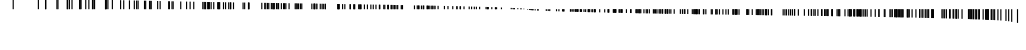


















Pathway	Gene ranks	NES	pval	padj
fumigaclavine C biosynthetic process		1.83	5.6e−05	3.3e−03
secondary metabolite biosynthetic process		1.38	7.5e−03	1.6e−01
ergot alkaloid biosynthetic process		1.62	7.7e−03	1.6e−01
protein refolding		1.57	2.2e−02	3.8e−01
copper ion binding		1.50	6.2e−02	7.3e−01
hydrolase activity. acting on glycosyl bonds		1.48	7.2e−02	8.0e−01
secondary metabolic process		1.33	9.2e−02	9.2e−01
asperthecin biosynthetic process		1.41	9.8e−02	9.2e−01
melanin biosynthetic process		1.42	1.1e−01	9.2e−01
pigment metabolic process involved in developmental pigmentation		1.38	1.3e−01	9.4e−01
protein–folding chaperone binding		1.34	1.4e−01	9.6e−01
sterol metabolic process		1.37	1.5e−01	9.7e−01
proteasomal ubiquitin–independent protein catabolic process		1.34	1.5e−01	9.8e−01
protein folding		1.28	1.8e−01	1.0e+00
negative regulation of DNA–templated transcription		1.33	1.8e−01	1.0e+00
proteasome core complex. alpha–subunit complex		1.34	1.8e−01	1.0e+00
proteasome–mediated ubiquitin–dependent protein catabolic process		1.23	2.0e−01	1.0e+00
cellulase activity		1.29	2.0e−01	1.0e+00
xylan catabolic process		1.25	2.3e−01	1.0e+00
cytosolic large ribosomal subunit		1.18	2.5e−01	1.0e+00
obsolete nucleosome positioning		−1.84	2.3e−03	7.2e−02
maturation of LSU–rRNA from tricistronic rRNA transcript (SSU–rRNA. 5.8S rRNA. LSU–rRNA)		−1.91	1.8e−03	5.8e−02
cellular response to starvation		−1.59	1.2e−03	4.0e−02
filamentous growth of a population of unicellular organisms in response to starvation		−1.68	1.1e−03	4.0e−02
hyphal growth		−1.44	1.1e−03	4.0e−02
maturation of SSU–rRNA from tricistronic rRNA transcript (SSU–rRNA. 5.8S rRNA. LSU–rRNA)		−1.92	8.7e−04	3.5e−02
preribosome. small subunit precursor		−1.94	5.1e−04	2.2e−02
conidium formation		−1.61	4.4e−04	2.0e−02
fumitremorgin B biosynthetic process		−1.94	2.5e−04	1.2e−02
syncytium formation by plasma membrane fusion		−1.98	1.2e−04	6.7e−03
SSU–rRNA from 5.8S rRNA and LSU–rRNA from tricistronic rRNA transcript (SSU–rRNA. 5.8S rRNA. LSU–rRNA)		−2.17	2.2e−05	1.4e−03
endonucleolytic cleavage in 5'–ETS of tricistronic rRNA transcript (SSU–rRNA. 5.8S rRNA. LSU–rRNA)		−2.18	6.7e−06	4.8e−04
endonucleolytic cleavage to generate mature 5'–end of SSU–rRNA from (SSU–rRNA. 5.8S rRNA. LSU–rRNA)		−2.18	6.2e−06	4.8e−04
small–subunit processome		−2.20	2.0e−06	1.8e−04
preribosome. large subunit precursor		−2.20	2.0e−06	1.8e−04
ribosomal large subunit biogenesis		−2.32	1.7e−06	1.8e−04
pseurotin A biosynthetic process		−2.06	2.7e−07	4.4e−05
rRNA processing		−2.43	1.2e−08	2.7e−06
fumagillin biosynthetic process		−2.54	1.6e−14	5.1e−12
nucleolus		−2.79	8.6e−19	5.6e−16

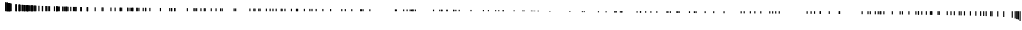







































	Pathway	Gene ranks	NES	pval	padj
SSU–rRNA from 5.8S rRNA and LSU–rRNA from tricistronic rRNA transcript (SSU–rRNA. 5.8S rRNA. LSU–rRNA)	cytosolic large ribosomal subunit		2.96	4.0e–15	2.6e–12
	structural constituent of ribosome		2.71	1.3e–12	4.4e–10
	nucleolus		2.40	3.2e–09	7.0e–07
	cytosolic small ribosomal subunit		2.50	4.4e–08	7.2e–06
	cytoplasmic translation		2.42	7.2e–07	9.4e–05
	rRNA processing		2.21	1.8e–05	2.0e–03
	maturation of SSU–rRNA from tricistronic rRNA transcript (SSU–rRNA. 5.8S rRNA. LSU–rRNA)		2.24	2.9e–05	2.7e–03
	small–subunit processome		2.18	5.4e–05	4.4e–03
	ribosomal large subunit biogenesis		2.16	7.0e–05	5.0e–03
	preribosome. large subunit precursor		2.15	9.5e–05	6.2e–03
	cytoplasm		1.44	1.2e–04	6.8e–03
	mitochondrial ribosome		2.09	1.3e–04	6.8e–03
	SSU–rRNA from 5.8S rRNA and LSU–rRNA from tricistronic rRNA transcript (SSU–rRNA. 5.8S rRNA. LSU–rRNA)		2.06	2.5e–04	1.3e–02
	ribosomal small subunit assembly		1.96	3.7e–04	1.7e–02
	ribosomal large subunit assembly		2.06	4.7e–04	2.0e–02
	obsolete rRNA export from nucleus		1.98	5.8e–04	2.3e–02
	RNA binding		1.89	1.6e–03	6.1e–02
	protein import into nucleus		1.89	2.6e–03	9.5e–02
	maturation of LSU–rRNA from tricistronic rRNA transcript (SSU–rRNA. 5.8S rRNA. LSU–rRNA)		1.90	3.3e–03	1.1e–01
	chaperonin–containing T–complex		1.80	4.0e–03	1.3e–01
	sterigmatocystin biosynthetic process		–1.41	1.2e–01	6.5e–01
	prenyltransferase activity		–1.44	1.2e–01	6.5e–01
	peptidase activity		–1.42	1.2e–01	6.5e–01
	intracellular calcium ion homeostasis		–1.42	1.1e–01	6.3e–01
	secondary metabolic process		–1.47	1.1e–01	6.3e–01
	monodictyphenone biosynthetic process		–1.46	9.6e–02	6.1e–01
	emericellamide biosynthetic process		–1.52	9.2e–02	6.1e–01
	nitrogen compound metabolic process		–1.48	8.4e–02	6.1e–01
	fatty acid catabolic process		–1.53	8.2e–02	6.1e–01
	dehydroaustinol biosynthetic process		–1.56	8.0e–02	6.0e–01
	fibrinogen binding		–1.54	7.2e–02	5.9e–01
	austinol biosynthetic process		–1.59	7.0e–02	5.9e–01
	glutathione transferase activity		–1.54	6.8e–02	5.9e–01
	zinc ion binding		–1.59	5.5e–02	5.3e–01
	xanthone–containing compound biosynthetic process		–1.61	5.4e–02	5.2e–01
	chitinase activity		–1.65	4.1e–02	4.3e–01
	autolysis		–1.67	3.7e–02	4.1e–01
	gliotoxin biosynthetic process		–1.92	3.6e–02	4.1e–01
	mycotoxin biosynthetic process		–1.85	1.8e–02	3.2e–01
	secondary metabolite biosynthetic process		–1.57	1.5e–02	2.9e–01
					



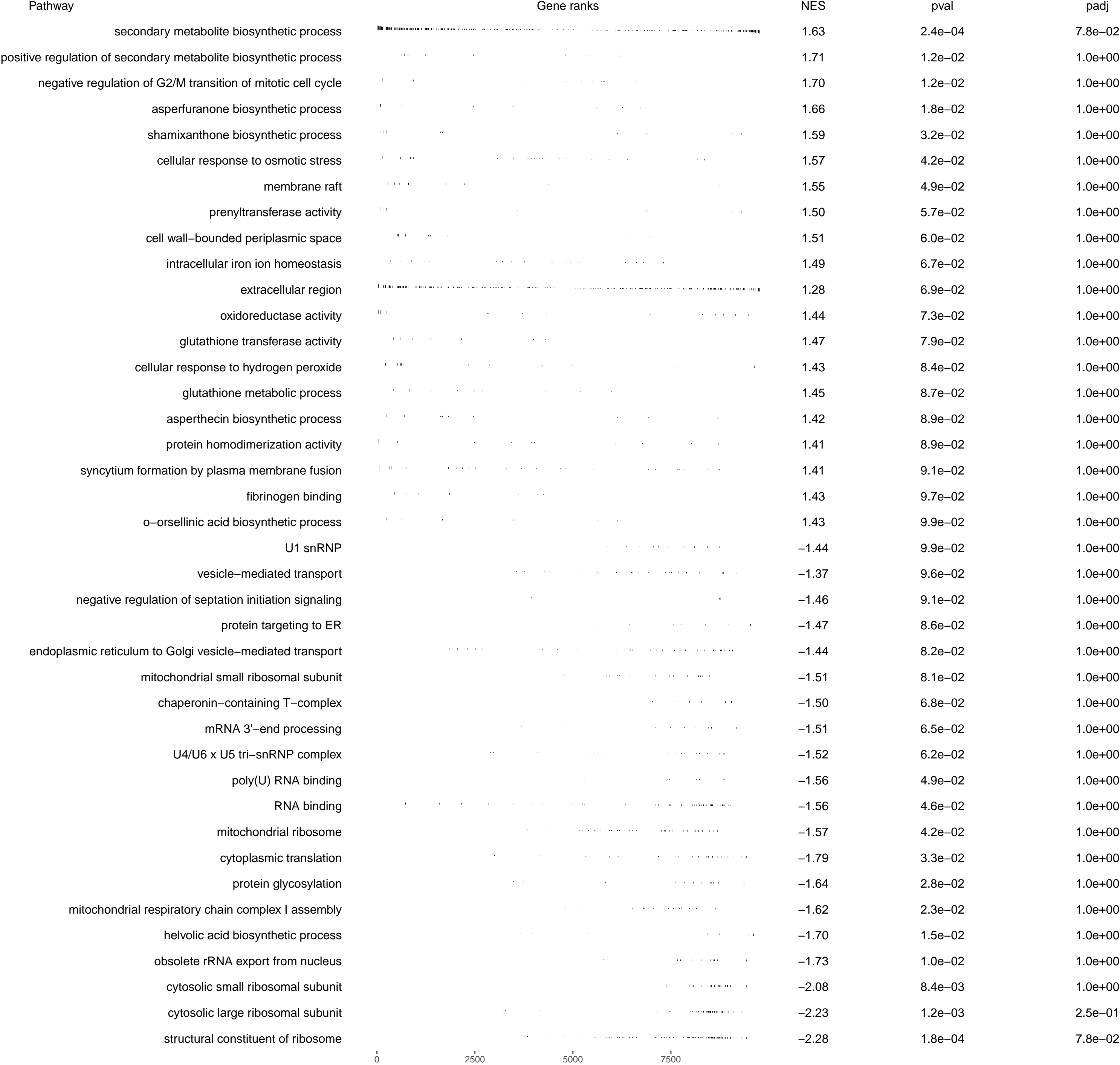


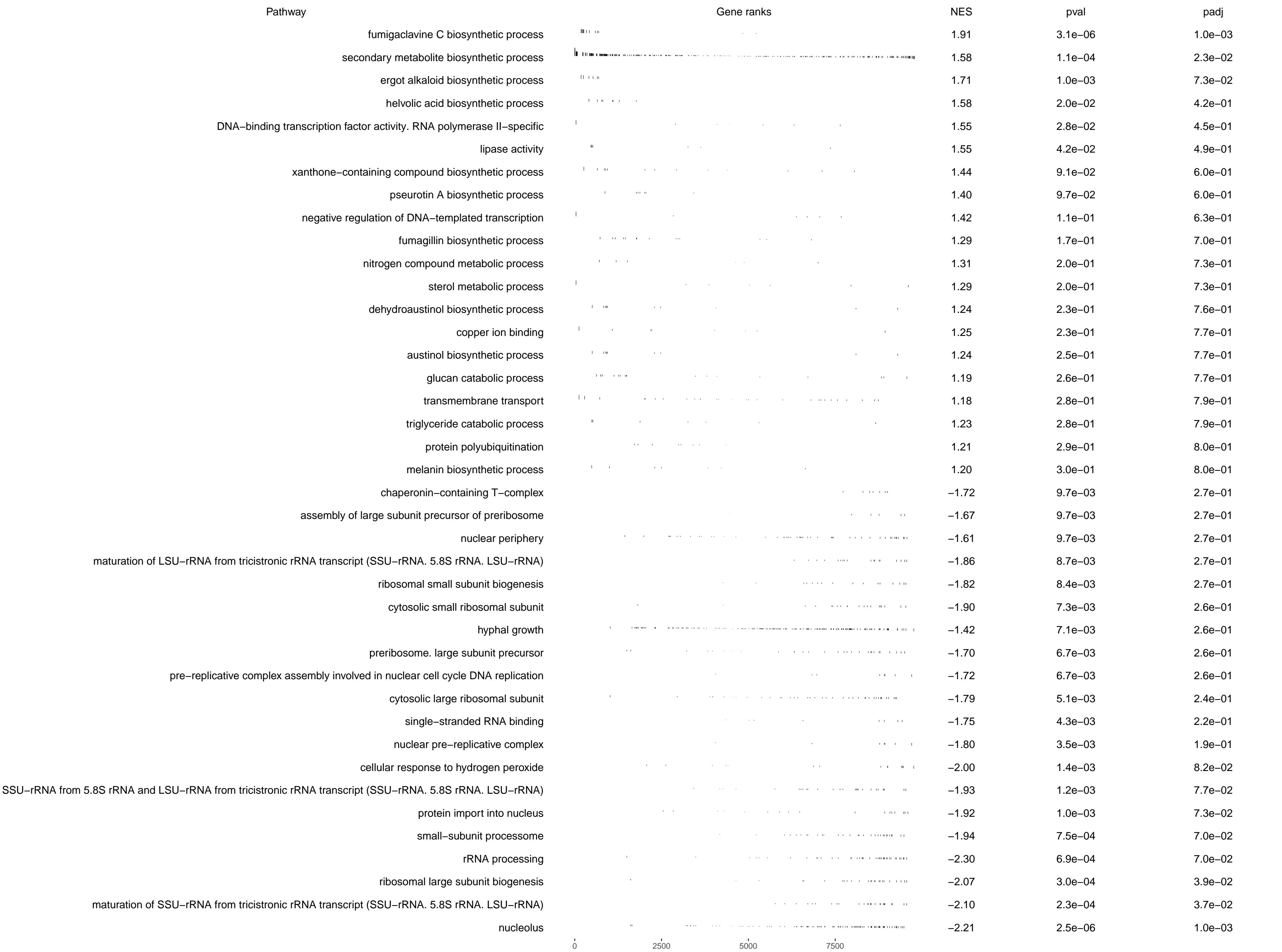
Pathway	Gene ranks	NES	pval	padj
nucleolus		3.30	2.2e−27	1.4e−24
rRNA processing		2.84	9.8e−13	3.2e−10
structural constituent of ribosome		2.69	5.7e−12	1.2e−09
preribosome. large subunit precursor		2.69	2.5e−11	4.0e−09
small-subunit processome		2.64	1.6e−10	1.9e−08
ribosomal large subunit biogenesis		2.66	1.7e−10	1.9e−08
cytosolic large ribosomal subunit		2.62	2.2e−09	1.9e−07
SSU-rRNA from 5.8S rRNA and LSU-rRNA from tricistronic rRNA transcript (SSU-rRNA. 5.8S rRNA. LSU-rRNA)		2.61	2.3e−09	1.9e−07
maturation of SSU-rRNA from tricistronic rRNA transcript (SSU-rRNA. 5.8S rRNA. LSU-rRNA)		2.55	3.8e−08	2.8e−06
maturation of LSU-rRNA from tricistronic rRNA transcript (SSU-rRNA. 5.8S rRNA. LSU-rRNA)		2.46	3.5e−07	1.9e−05
endonucleolytic cleavage in 5'-ETS of tricistronic rRNA transcript (SSU-rRNA. 5.8S rRNA. LSU-rRNA)		2.41	3.5e−07	1.9e−05
endonucleolytic cleavage to generate mature 5'-end of SSU-rRNA from (SSU-rRNA. 5.8S rRNA. LSU-rRNA)		2.41	3.6e−07	1.9e−05
mitochondrial ribosome		2.34	6.8e−07	3.4e−05
preribosome. small subunit precursor		2.35	9.2e−07	4.3e−05
ribosomal small subunit biogenesis		2.35	8.0e−06	3.5e−04
ribosomal large subunit assembly		2.30	1.2e−05	4.8e−04
maturation of 5.8S rRNA from tricistronic rRNA transcript (SSU-rRNA. 5.8S rRNA. LSU-rRNA)		2.26	5.0e−05	1.8e−03
cytosolic small ribosomal subunit		2.26	5.1e−05	1.8e−03
RNA polymerase I activity		1.95	1.9e−04	6.1e−03
RNA polymerase I complex		1.95	1.9e−04	6.1e−03
intracellular calcium ion homeostasis		−1.38	1.3e−01	6.4e−01
intracellular iron ion homeostasis		−1.36	1.3e−01	6.4e−01
glutathione transferase activity		−1.40	1.2e−01	6.3e−01
austinol biosynthetic process		−1.39	1.2e−01	6.3e−01
secondary metabolic process		−1.48	1.1e−01	6.2e−01
nucleotide-excision repair		−1.41	1.1e−01	6.2e−01
glucan catabolic process		−1.43	9.8e−02	6.0e−01
autolysis		−1.48	7.9e−02	5.2e−01
obsolete cellular carbohydrate catabolic process		−1.47	7.6e−02	5.2e−01
chitinase activity		−1.50	6.7e−02	4.7e−01
monodictyphenone biosynthetic process		−1.53	6.6e−02	4.7e−01
phosphatase activity		−1.50	6.4e−02	4.7e−01
apoptotic process		−1.54	5.6e−02	4.3e−01
cellulase activity		−1.57	4.6e−02	3.7e−01
cellular response to iron ion starvation		−1.66	4.6e−02	3.7e−01
xanthone-containing compound biosynthetic process		−1.66	4.1e−02	3.4e−01
pectin catabolic process		−1.88	4.0e−02	3.4e−01
mycotoxin biosynthetic process		−1.85	2.8e−02	2.6e−01
gliotoxin biosynthetic process		−1.94	1.8e−02	2.2e−01
secondary metabolite biosynthetic process		−1.57	5.8e−03	9.4e−02

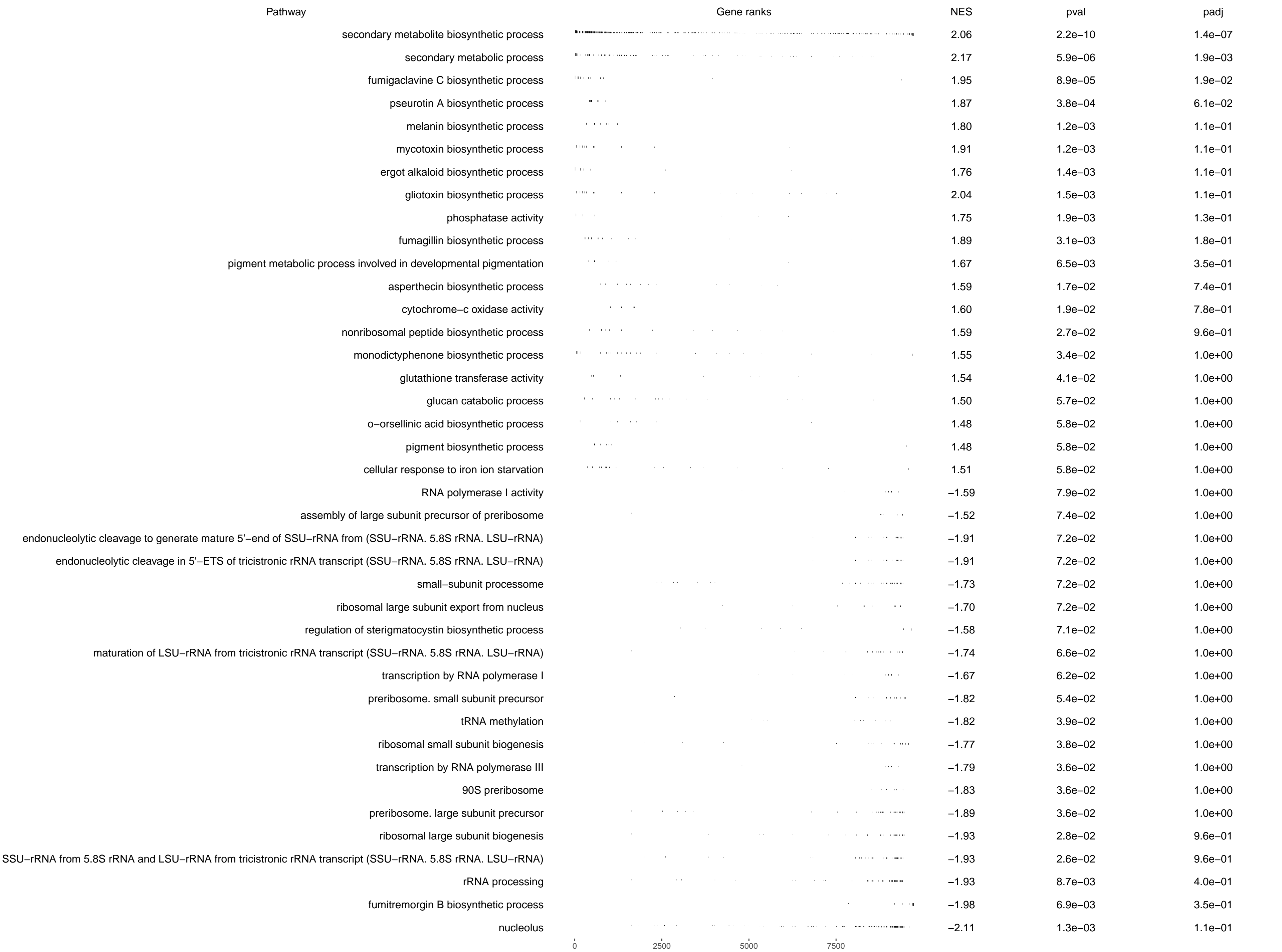
Pathway	Gene ranks	NES	pval	padj
fumigaclavine C biosynthetic process		2.10	1.2e-06	7.8e-05
ergot alkaloid biosynthetic process		1.75	5.9e-04	2.0e-02
secondary metabolite biosynthetic process		1.50	1.8e-03	5.7e-02
secondary metabolic process		1.62	1.0e-02	1.9e-01
protein folding		1.62	2.4e-02	3.5e-01
protein refolding		1.59	2.8e-02	3.8e-01
cytosolic small ribosomal subunit		1.55	4.0e-02	4.9e-01
protein-folding chaperone binding		1.53	4.2e-02	5.1e-01
asperthecin biosynthetic process		1.51	4.6e-02	5.3e-01
pigment metabolic process involved in developmental pigmentation		1.39	9.0e-02	6.5e-01
cytosolic large ribosomal subunit		1.35	1.0e-01	6.5e-01
hydrolase activity. acting on glycosyl bonds		1.40	1.0e-01	6.6e-01
proteasomal ubiquitin-independent protein catabolic process		1.39	1.0e-01	6.6e-01
cellular response to iron ion starvation		1.33	1.4e-01	7.6e-01
cytochrome-c oxidase activity		1.31	1.6e-01	8.2e-01
copper ion binding		1.32	1.7e-01	8.5e-01
proteasome core complex. alpha-subunit complex		1.30	1.8e-01	8.7e-01
cellulase activity		1.30	1.9e-01	8.9e-01
negative regulation of DNA-templated transcription		1.29	1.9e-01	8.9e-01
sterol metabolic process		1.29	1.9e-01	9.0e-01
maturation of 5.8S rRNA from tricistronic rRNA transcript (SSU-rRNA. 5.8S rRNA. LSU-rRNA)		-1.91	2.2e-03	6.1e-02
nucleus		-1.23	2.2e-03	6.1e-02
syncytium formation by plasma membrane fusion		-1.99	7.2e-04	2.3e-02
maturation of SSU-rRNA from tricistronic rRNA transcript (SSU-rRNA. 5.8S rRNA. LSU-rRNA)		-2.04	3.8e-04	1.4e-02
90S preribosome		-2.03	3.1e-04	1.2e-02
maturation of LSU-rRNA from tricistronic rRNA transcript (SSU-rRNA. 5.8S rRNA. LSU-rRNA)		-2.05	1.4e-04	5.5e-03
ribosomal small subunit biogenesis		-2.10	8.8e-05	3.8e-03
conidium formation		-1.76	7.1e-05	3.3e-03
preribosome. small subunit precursor		-2.19	2.3e-05	1.1e-03
fumitremorgin B biosynthetic process		-2.14	1.8e-05	9.6e-04
pseurotin A biosynthetic process		-2.18	2.1e-06	1.2e-04
endonucleolytic cleavage to generate mature 5'-end of SSU-rRNA from (SSU-rRNA. 5.8S rRNA. LSU-rRNA)		-2.32	9.2e-07	6.7e-05
endonucleolytic cleavage in 5'-ETS of tricistronic rRNA transcript (SSU-rRNA. 5.8S rRNA. LSU-rRNA)		-2.32	9.1e-07	6.7e-05
preribosome. large subunit precursor		-2.40	5.9e-07	5.5e-05
ribosomal large subunit biogenesis		-2.41	3.4e-07	3.7e-05
SSU-rRNA from 5.8S rRNA and LSU-rRNA from tricistronic rRNA transcript (SSU-rRNA. 5.8S rRNA. LSU-rRNA)		-2.35	2.1e-07	2.7e-05
small-subunit processome		-2.45	2.0e-07	2.7e-05
rRNA processing		-2.63	3.3e-10	7.2e-08
fumagillin biosynthetic process		-2.55	1.2e-11	3.8e-09
nucleolus		-3.13	3.6e-23	2.4e-20

Pathway	Gene ranks	NES	pval	padj
secondary metabolite biosynthetic process		2.01	2.8e-06	1.8e-03
pseurotin A biosynthetic process		1.83	3.4e-04	1.1e-01
helvolic acid biosynthetic process		1.82	9.8e-04	1.8e-01
cytosolic large ribosomal subunit		2.03	1.1e-03	1.8e-01
maturation of SSU-rRNA from tricistronic rRNA transcript (SSU-rRNA. 5.8S rRNA. LSU-rRNA)		1.91	1.5e-03	1.8e-01
fumagillin biosynthetic process		2.02	1.7e-03	1.8e-01
preribosome. large subunit precursor		1.87	2.6e-03	1.9e-01
ribosomal large subunit biogenesis		1.84	2.7e-03	1.9e-01
small-subunit processome		1.84	3.1e-03	1.9e-01
cytosolic small ribosomal subunit		1.79	3.6e-03	1.9e-01
SSU-rRNA from 5.8S rRNA and LSU-rRNA from tricistronic rRNA transcript (SSU-rRNA. 5.8S rRNA. LSU-rRNA)		1.71	3.7e-03	1.9e-01
rRNA processing		1.81	3.8e-03	1.9e-01
asperfuranone biosynthetic process		1.71	6.6e-03	3.1e-01
structural constituent of ribosome		1.83	1.0e-02	4.3e-01
nucleolus		1.89	1.0e-02	4.3e-01
o-orsellinic acid biosynthetic process		1.63	1.3e-02	4.9e-01
ribosomal small subunit biogenesis		1.64	1.5e-02	5.5e-01
secondary metabolic process		1.63	1.6e-02	5.5e-01
monodictyphenone biosynthetic process		1.68	1.7e-02	5.5e-01
preribosome. small subunit precursor		1.65	1.9e-02	5.7e-01
DNA-directed DNA polymerase activity		-1.26	2.0e-01	1.0e+00
xylan catabolic process		-1.26	2.0e-01	1.0e+00
peroxisomal membrane		-1.26	2.0e-01	1.0e+00
protein deneddylation		-1.29	1.9e-01	1.0e+00
sulfate assimilation		-1.30	1.9e-01	1.0e+00
proteasomal ubiquitin-independent protein catabolic process		-1.30	1.8e-01	1.0e+00
COP9 signalosome		-1.31	1.8e-01	1.0e+00
mitotic actomyosin contractile ring. intermediate layer		-1.33	1.7e-01	1.0e+00
proteasome storage granule		-1.29	1.7e-01	1.0e+00
positive regulation of G2/M transition of mitotic cell cycle		-1.34	1.6e-01	1.0e+00
vacuolar transport		-1.36	1.6e-01	1.0e+00
fatty acid beta-oxidation		-1.36	1.5e-01	1.0e+00
Arp2/3 protein complex		-1.40	1.3e-01	1.0e+00
Arp2/3 complex-mediated actin nucleation		-1.40	1.3e-01	1.0e+00
fatty acid metabolic process		-1.42	1.2e-01	1.0e+00
positive regulation of asexual sporulation resulting in formation of a cellular spore		-1.40	1.2e-01	1.0e+00
negative regulation of sexual sporulation resulting in formation of a cellular spore		-1.48	1.0e-01	1.0e+00
protein autophosphorylation		-1.48	9.0e-02	1.0e+00
septin ring assembly		-1.53	7.3e-02	1.0e+00
fumitremorgin B biosynthetic process		-1.92	2.0e-03	1.8e-01

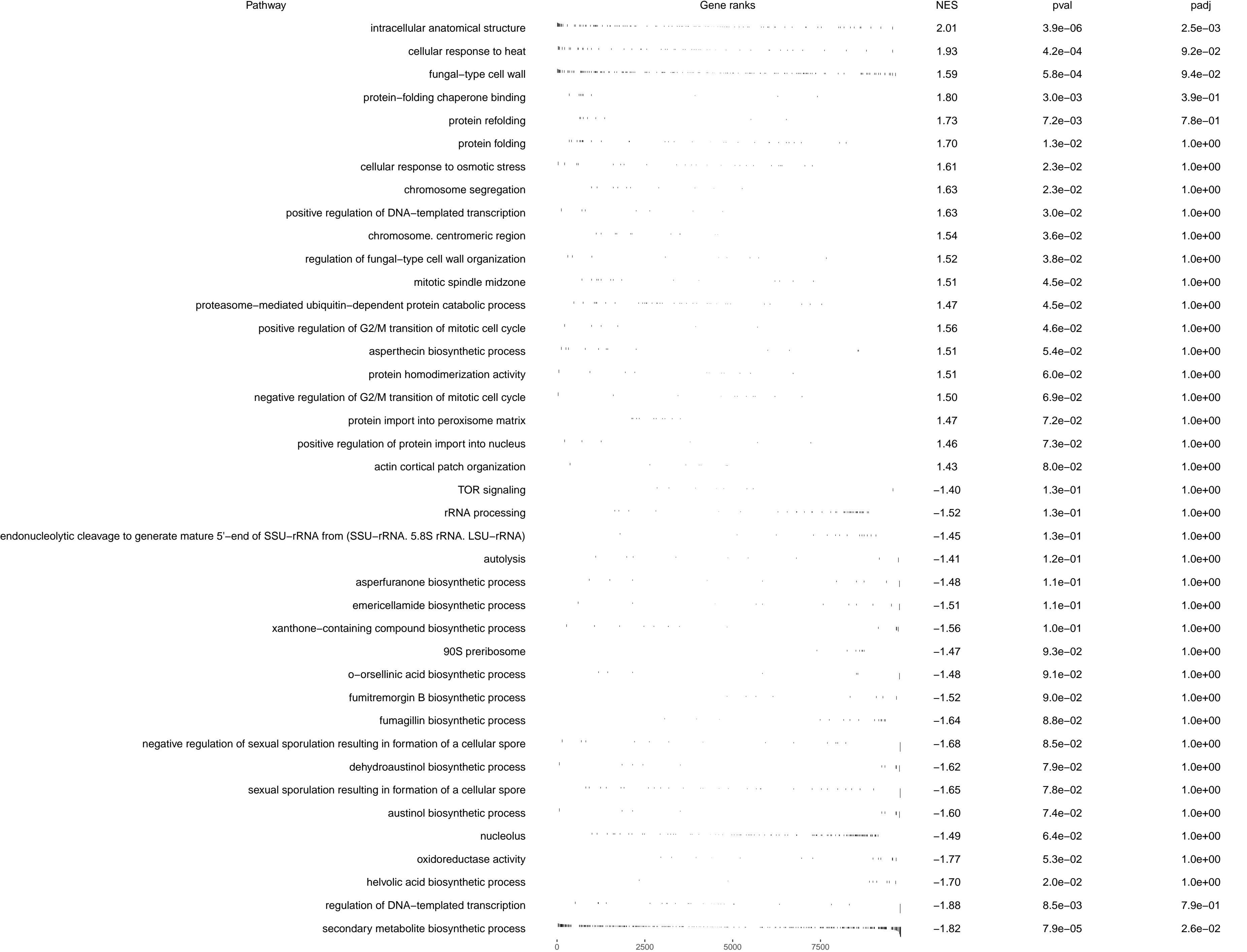
Pathway	Gene ranks	NES	pval	padj
cytosolic large ribosomal subunit		3.48	7.3e−27	4.7e−24
structural constituent of ribosome		3.32	3.3e−22	1.1e−19
cytosolic small ribosomal subunit		2.80	8.4e−13	1.8e−10
cytoplasmic translation		2.75	7.8e−11	1.3e−08
mitochondrial ribosome		2.62	7.3e−09	9.5e−07
obsolete rRNA export from nucleus		2.45	1.0e−08	1.1e−06
RNA binding		2.43	3.5e−06	2.8e−04
fungal biofilm matrix		2.13	1.4e−05	1.0e−03
mitochondrial large ribosomal subunit		2.28	2.1e−05	1.4e−03
hyphal cell wall		2.18	6.7e−05	3.9e−03
chaperonin-containing T-complex		2.00	1.1e−04	5.7e−03
mitochondrial membrane		1.87	2.4e−04	1.2e−02
eukaryotic translation initiation factor 3 complex		2.01	2.9e−04	1.3e−02
maturation of SSU-rRNA from tricistronic rRNA transcript (SSU-rRNA. 5.8S rRNA. LSU-rRNA)		2.08	3.4e−04	1.4e−02
induction by symbiont of host defense response		2.10	3.4e−04	1.4e−02
mitochondrial small ribosomal subunit		2.02	5.5e−04	2.1e−02
cell surface		1.69	6.4e−04	2.2e−02
mitotic spindle pole body		2.04	6.6e−04	2.2e−02
ribosomal small subunit assembly		1.94	7.9e−04	2.6e−02
ribosomal large subunit assembly		1.97	9.3e−04	2.8e−02
mycotoxin biosynthetic process		−1.56	7.0e−02	4.6e−01
glutathione transferase activity		−1.50	6.4e−02	4.4e−01
negative regulation of sexual sporulation resulting in formation of a cellular spore		−1.68	5.6e−02	4.1e−01
sexual sporulation resulting in formation of a cellular spore		−1.70	4.7e−02	3.6e−01
emerice llamide biosynthetic process		−1.72	3.9e−02	3.1e−01
regulation of DNA-templated transcription		−1.77	3.4e−02	3.0e−01
fumitremorgin B biosynthetic process		−1.67	2.0e−02	2.3e−01
prenyltransferase activity		−1.64	2.0e−02	2.3e−01
helvolic acid biosynthetic process		−1.70	1.7e−02	2.2e−01
o-orsellinic acid biosynthetic process		−1.66	1.7e−02	2.2e−01
sterigmatocystin biosynthetic process		−1.70	1.5e−02	2.0e−01
asperfuranone biosynthetic process		−1.74	1.3e−02	1.8e−01
syncytium formation by plasma membrane fusion		−1.80	5.8e−03	1.0e−01
monodictyphenone biosynthetic process		−1.87	5.2e−03	9.6e−02
austinol biosynthetic process		−1.84	4.1e−03	8.0e−02
autolysis		−1.85	3.7e−03	7.4e−02
chitinase activity		−1.85	3.6e−03	7.4e−02
dehydroaustinol biosynthetic process		−1.84	1.7e−03	4.1e−02
secondary metabolic process		−1.80	1.1e−03	3.2e−02
secondary metabolite biosynthetic process		−1.79	1.3e−08	1.2e−06







































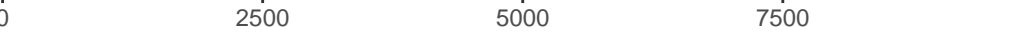



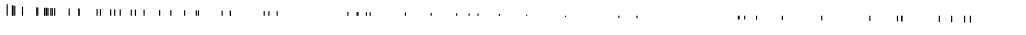















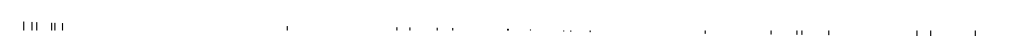


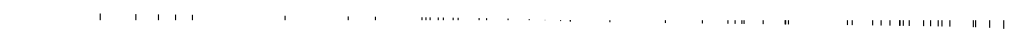
















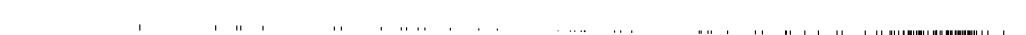




















































































Pathway	Gene ranks	NES	pval	padj
intracellular anatomical structure		1.73	8.7e−04	3.5e−02
cellular response to heat		1.66	5.2e−03	1.4e−01
cellular response to hydrogen peroxide		1.64	1.2e−02	2.9e−01
cell adhesion		1.57	2.0e−02	4.0e−01
fungal-type cell wall		1.39	3.3e−02	5.5e−01
nucleotide-excision repair		1.47	6.4e−02	8.2e−01
negative regulation of G2/M transition of mitotic cell cycle		1.46	6.6e−02	8.2e−01
SCF ubiquitin ligase complex		1.44	7.7e−02	8.9e−01
peroxisome		1.37	7.8e−02	8.9e−01
oxidoreductase activity		1.44	8.2e−02	9.0e−01
cellular response to pH		1.41	8.3e−02	9.0e−01
zinc ion binding		1.43	8.6e−02	9.2e−01
phagophore assembly site		1.40	9.5e−02	9.8e−01
cellular response to farnesol		1.39	1.0e−01	1.0e+00
protein histidine kinase activity		1.38	1.1e−01	1.0e+00
piecemeal microautophagy of the nucleus		1.37	1.2e−01	1.0e+00
glutathione metabolic process		1.36	1.3e−01	1.0e+00
protein homodimerization activity		1.35	1.3e−01	1.0e+00
membrane raft		1.34	1.4e−01	1.0e+00
asexual sporulation resulting in formation of a cellular spore		1.23	1.6e−01	1.0e+00
endonucleolytic cleavage in 5'–ETS of tricistronic rRNA transcript (SSU–rRNA. 5.8S rRNA. LSU–rRNA)		−1.76	2.7e−03	8.5e−02
ribosomal small subunit biogenesis		−1.81	2.7e−03	8.5e−02
endonucleolytic cleavage to generate mature 5'–end of SSU–rRNA from (SSU–rRNA. 5.8S rRNA. LSU–rRNA)		−1.76	2.6e−03	8.5e−02
shamixanthone biosynthetic process		−1.82	9.6e−04	3.5e−02
SSU–rRNA from 5.8S rRNA and LSU–rRNA from tricistronic rRNA transcript (SSU–rRNA. 5.8S rRNA. LSU–rRNA)		−1.92	9.4e−04	3.5e−02
preribosome. large subunit precursor		−1.98	7.1e−04	3.1e−02
helvolic acid biosynthetic process		−1.76	6.5e−04	3.0e−02
cytosolic large ribosomal subunit		−1.91	4.6e−04	2.3e−02
mitochondrial ribosome		−1.92	2.2e−04	1.2e−02
ribosomal large subunit biogenesis		−2.06	1.2e−04	6.9e−03
maturation of SSU–rRNA from tricistronic rRNA transcript (SSU–rRNA. 5.8S rRNA. LSU–rRNA)		−2.10	2.7e−05	1.8e−03
pseurotin A biosynthetic process		−1.88	2.6e−05	1.8e−03
fumitremorgin B biosynthetic process		−1.88	1.6e−05	1.3e−03
rRNA processing		−2.17	5.3e−06	4.9e−04
secondary metabolic process		−2.07	4.4e−06	4.8e−04
prenyltransferase activity		−1.92	3.6e−06	4.7e−04
small–subunit processome		−2.28	1.3e−06	2.1e−04
structural constituent of ribosome		−2.25	6.3e−08	1.4e−05
fumagillin biosynthetic process		−2.24	3.2e−09	1.0e−06
nucleolus		−2.34	2.3e−10	1.5e−07



Pathway	Gene ranks	NES	pval	padj
nucleolus		2.10	1.6e−06	1.0e−03
fumagillin biosynthetic process		2.10	6.0e−06	1.9e−03
pseurotin A biosynthetic process		1.89	1.7e−05	3.7e−03
ribosomal large subunit biogenesis		2.01	1.2e−04	1.6e−02
rRNA processing		2.00	1.2e−04	1.6e−02
prenyltransferase activity		1.83	2.2e−04	2.0e−02
fumitremorgin B biosynthetic process		1.88	2.3e−04	2.0e−02
secondary metabolite biosynthetic process		1.59	2.4e−04	2.0e−02
secondary metabolic process		1.92	4.0e−04	2.9e−02
preribosome. large subunit precursor		1.90	8.2e−04	5.4e−02
SSU−rRNA from 5.8S rRNA and LSU−rRNA from tricistronic rRNA transcript (SSU−rRNA. 5.8S rRNA. LSU−rRNA)		1.81	3.0e−03	1.8e−01
preribosome. small subunit precursor		1.67	6.1e−03	3.2e−01
maturation of LSU−rRNA from tricistronic rRNA transcript (SSU−rRNA. 5.8S rRNA. LSU−rRNA)		1.70	6.4e−03	3.2e−01
small−subunit processome		1.73	7.4e−03	3.4e−01
shamixanthone biosynthetic process		1.76	9.0e−03	3.9e−01
ribosomal small subunit biogenesis		1.71	9.9e−03	4.0e−01
endonucleolytic cleavage in 5'−ETS of tricistronic rRNA transcript (SSU−rRNA. 5.8S rRNA. LSU−rRNA)		1.73	1.2e−02	4.5e−01
maturation of 5.8S rRNA from tricistronic rRNA transcript (SSU−rRNA. 5.8S rRNA. LSU−rRNA)		1.72	1.3e−02	4.5e−01
endonucleolytic cleavage to generate mature 5'−end of SSU−rRNA from (SSU−rRNA. 5.8S rRNA. LSU−rRNA)		1.72	1.3e−02	4.5e−01
helvolic acid biosynthetic process		1.65	1.6e−02	5.3e−01
proteasome core complex. beta−subunit complex		−1.34	1.6e−01	1.0e+00
cytoplasm to vacuole targeting by the Cvt pathway		−1.30	1.6e−01	1.0e+00
extrinsic component of membrane		−1.32	1.5e−01	1.0e+00
protein targeting to vacuole		−1.35	1.5e−01	1.0e+00
actin cytoskeleton organization		−1.34	1.4e−01	1.0e+00
phagophore assembly site		−1.35	1.4e−01	1.0e+00
proteasomal ubiquitin−independent protein catabolic process		−1.37	1.3e−01	1.0e+00
SCF ubiquitin ligase complex		−1.37	1.2e−01	1.0e+00
cellular response to pH		−1.37	1.2e−01	1.0e+00
obsolete integral component of Golgi membrane		−1.39	1.1e−01	1.0e+00
actin cortical patch		−1.40	1.1e−01	1.0e+00
negative regulation of DNA−templated transcription		−1.40	1.1e−01	1.0e+00
macroautophagy		−1.42	1.0e−01	1.0e+00
cellular response to hydrogen peroxide		−1.45	9.5e−02	1.0e+00
late endosome to vacuole transport		−1.42	8.9e−02	1.0e+00
cellular response to farnesol		−1.45	8.9e−02	1.0e+00
intracellular anatomical structure		−1.34	8.7e−02	1.0e+00
cytosolic small ribosomal subunit		−1.48	7.6e−02	1.0e+00
proteasome−mediated ubiquitin−dependent protein catabolic process		−1.53	6.6e−02	1.0e+00
peroxisome		−1.65	3.6e−02	8.7e−01

Pathway	Gene ranks	NES	pval	padj
fumigaclavine C biosynthetic process		2.07	1.4e-04	1.3e-02
secondary metabolic process		1.92	1.4e-04	1.3e-02
ergot alkaloid biosynthetic process		1.86	1.4e-04	1.3e-02
structural constituent of ribosome		1.80	4.6e-04	3.2e-02
helvolic acid biosynthetic process		1.83	1.8e-03	7.9e-02
mycotoxin biosynthetic process		1.85	2.1e-03	8.7e-02
cytochrome-c oxidase activity		1.74	2.5e-03	9.7e-02
cytosolic large ribosomal subunit		1.81	3.0e-03	1.1e-01
secondary metabolite biosynthetic process		1.45	3.8e-03	1.3e-01
cytosolic small ribosomal subunit		1.81	4.9e-03	1.6e-01
gliotoxin biosynthetic process		1.75	1.1e-02	3.0e-01
cellular response to iron ion starvation		1.78	1.5e-02	3.8e-01
protein-folding chaperone binding		1.66	2.0e-02	4.3e-01
protein folding		1.60	2.1e-02	4.3e-01
fungal-type cell wall		1.39	2.4e-02	5.0e-01
prenyltransferase activity		1.60	2.5e-02	5.0e-01
pigment metabolic process involved in developmental pigmentation		1.56	3.1e-02	5.9e-01
melanin biosynthetic process		1.56	3.5e-02	6.4e-01
ergosterol biosynthetic process		1.56	4.2e-02	7.3e-01
asperthecin biosynthetic process		1.60	4.4e-02	7.3e-01
oxidoreductase activity		-1.61	4.8e-02	7.5e-01
nuclear periphery		-1.54	4.4e-02	7.3e-01
fumitremorgin B biosynthetic process		-1.63	4.3e-02	7.3e-01
poly(A)+ mRNA export from nucleus		-1.71	1.9e-02	4.3e-01
maturation of 5.8S rRNA from tricistronic rRNA transcript (SSU-rRNA. 5.8S rRNA. LSU-rRNA)		-1.79	1.8e-02	4.2e-01
ribosomal small subunit biogenesis		-1.80	1.7e-02	4.1e-01
cellular response to farnesol		-1.74	1.5e-02	3.8e-01
ribosomal large subunit export from nucleus		-1.77	9.3e-03	2.6e-01
RNA helicase activity		-1.75	9.0e-03	2.6e-01
SSU-rRNA from 5.8S rRNA and LSU-rRNA from tricistronic rRNA transcript (SSU-rRNA. 5.8S rRNA. LSU-rRNA)		-2.03	7.1e-03	2.2e-01
preribosome. small subunit precursor		-1.91	1.5e-03	6.8e-02
90S preribosome		-1.92	1.2e-03	6.1e-02
maturation of LSU-rRNA from tricistronic rRNA transcript (SSU-rRNA. 5.8S rRNA. LSU-rRNA)		-2.10	1.0e-03	5.5e-02
small-subunit processome		-2.01	6.4e-04	3.8e-02
preribosome. large subunit precursor		-2.05	5.0e-04	3.2e-02
ribosomal large subunit biogenesis		-2.32	3.1e-04	2.6e-02
endonucleolytic cleavage to generate mature 5'-end of SSU-rRNA from (SSU-rRNA. 5.8S rRNA. LSU-rRNA)		-2.22	1.1e-04	1.3e-02
endonucleolytic cleavage in 5'-ETS of tricistronic rRNA transcript (SSU-rRNA. 5.8S rRNA. LSU-rRNA)		-2.22	1.1e-04	1.3e-02
rRNA processing		-2.37	1.5e-05	4.8e-03
nucleolus		-2.68	4.8e-12	3.1e-09

Pathway	Gene ranks	NES	pval	padj
nucleolus		3.20	4.0e-27	2.6e-24
fumagillin biosynthetic process		2.55	1.8e-12	5.7e-10
rRNA processing		2.73	1.5e-11	3.2e-09
small-subunit processome		2.72	3.9e-11	6.3e-09
preribosome. large subunit precursor		2.65	2.9e-10	3.8e-08
ribosomal large subunit biogenesis		2.61	2.5e-09	2.8e-07
SSU-rRNA from 5.8S rRNA and LSU-rRNA from tricistronic rRNA transcript (SSU-rRNA. 5.8S rRNA. LSU-rRNA)		2.56	1.5e-08	1.4e-06
pseurotin A biosynthetic process		2.11	3.2e-08	2.6e-06
endonucleolytic cleavage in 5'-ETS of tricistronic rRNA transcript (SSU-rRNA. 5.8S rRNA. LSU-rRNA)		2.35	6.8e-08	4.4e-06
endonucleolytic cleavage to generate mature 5'-end of SSU-rRNA from (SSU-rRNA. 5.8S rRNA. LSU-rRNA)		2.35	6.8e-08	4.4e-06
maturation of SSU-rRNA from tricistronic rRNA transcript (SSU-rRNA. 5.8S rRNA. LSU-rRNA)		2.45	1.6e-07	9.6e-06
preribosome. small subunit precursor		2.29	6.7e-07	3.4e-05
ribosomal small subunit biogenesis		2.35	6.9e-07	3.4e-05
maturation of LSU-rRNA from tricistronic rRNA transcript (SSU-rRNA. 5.8S rRNA. LSU-rRNA)		2.25	1.2e-05	5.7e-04
conidium formation		1.79	1.7e-05	7.6e-04
ribosome biogenesis		2.02	1.0e-04	4.2e-03
90S preribosome		1.93	1.7e-04	6.3e-03
filamentous growth of a population of unicellular organisms in response to starvation		1.74	3.7e-04	1.3e-02
hyphal growth		1.52	5.5e-04	1.8e-02
maturation of 5.8S rRNA from tricistronic rRNA transcript (SSU-rRNA. 5.8S rRNA. LSU-rRNA)		1.97	7.2e-04	2.2e-02
proteasome core complex. alpha-subunit complex		-1.35	1.5e-01	7.2e-01
protein refolding		-1.33	1.5e-01	7.2e-01
actin cortical patch organization		-1.36	1.4e-01	7.2e-01
proteasome storage granule		-1.32	1.4e-01	7.2e-01
peroxisomal membrane		-1.33	1.4e-01	7.2e-01
carbohydrate catabolic process		-1.38	1.2e-01	6.8e-01
copper ion binding		-1.40	1.2e-01	6.7e-01
cellulase activity		-1.39	1.1e-01	6.7e-01
proteasomal ubiquitin-independent protein catabolic process		-1.37	1.1e-01	6.7e-01
protein-folding chaperone binding		-1.42	1.0e-01	6.4e-01
xylan catabolic process		-1.41	9.6e-02	6.2e-01
protein folding		-1.38	9.5e-02	6.2e-01
proteasome-mediated ubiquitin-dependent protein catabolic process		-1.38	8.7e-02	6.0e-01
pigment metabolic process involved in developmental pigmentation		-1.44	8.2e-02	5.8e-01
secondary metabolic process		-1.37	6.3e-02	5.0e-01
hydrolase activity. acting on glycosyl bonds		-1.52	5.2e-02	4.4e-01
ergot alkaloid biosynthetic process		-1.57	3.7e-02	3.5e-01
asperthecin biosynthetic process		-1.64	3.3e-02	3.3e-01
secondary metabolite biosynthetic process		-1.36	1.8e-02	2.1e-01
fumigaclavine C biosynthetic process		-2.00	1.2e-04	4.5e-03

Pathway	Gene ranks	NES	pval	padj
nucleolus		2.56	5.1e-13	3.3e-10
fumagillin biosynthetic process		2.53	3.3e-12	1.1e-09
pseurotin A biosynthetic process		2.10	2.9e-07	6.4e-05
rRNA processing		2.27	1.1e-05	1.8e-03
ribosomal large subunit biogenesis		2.16	8.6e-05	1.1e-02
endonucleolytic cleavage to generate mature 5'-end of SSU-rRNA from (SSU-rRNA. 5.8S rRNA. LSU-rRNA)		2.02	4.8e-04	4.5e-02
endonucleolytic cleavage in 5'-ETS of tricistronic rRNA transcript (SSU-rRNA. 5.8S rRNA. LSU-rRNA)		2.02	4.9e-04	4.5e-02
preribosome. large subunit precursor		1.94	1.3e-03	1.1e-01
preribosome. small subunit precursor		1.93	1.6e-03	1.2e-01
small-subunit processome		1.88	2.3e-03	1.5e-01
poly(A)+ mRNA export from nucleus		1.86	3.8e-03	2.3e-01
protein transmembrane transporter activity		1.79	6.3e-03	3.4e-01
ribosomal small subunit biogenesis		1.74	7.3e-03	3.7e-01
obsolete nucleosome positioning		1.79	8.3e-03	3.7e-01
maturation of LSU-rRNA from tricistronic rRNA transcript (SSU-rRNA. 5.8S rRNA. LSU-rRNA)		1.70	8.8e-03	3.7e-01
SSU-rRNA from 5.8S rRNA and LSU-rRNA from tricistronic rRNA transcript (SSU-rRNA. 5.8S rRNA. LSU-rRNA)		1.74	9.0e-03	3.7e-01
cellular response to starvation		1.36	1.8e-02	6.4e-01
90S preribosome		1.70	2.6e-02	8.3e-01
fumitremorgin B biosynthetic process		1.62	2.6e-02	8.3e-01
filamentous growth of a population of unicellular organisms in response to starvation		1.38	2.7e-02	8.3e-01
proteasome-mediated ubiquitin-dependent protein catabolic process		-1.16	2.8e-01	1.0e+00
protein targeting to membrane		-1.23	2.7e-01	1.0e+00
proteasome core complex. beta-subunit complex		-1.23	2.7e-01	1.0e+00
proteasome core complex. alpha-subunit complex		-1.23	2.7e-01	1.0e+00
proteasome storage granule		-1.24	2.4e-01	1.0e+00
secondary metabolite biosynthetic process		-1.12	2.4e-01	1.0e+00
proteasomal ubiquitin-independent protein catabolic process		-1.26	2.3e-01	1.0e+00
cellulase activity		-1.27	2.3e-01	1.0e+00
DNA-binding transcription factor activity. RNA polymerase II-specific		-1.29	2.2e-01	1.0e+00
protein folding		-1.23	2.1e-01	1.0e+00
negative regulation of DNA-templated transcription		-1.33	1.7e-01	1.0e+00
sterol metabolic process		-1.34	1.7e-01	1.0e+00
protein-folding chaperone binding		-1.33	1.7e-01	1.0e+00
cytosolic large ribosomal subunit		-1.26	1.7e-01	1.0e+00
ergot alkaloid biosynthetic process		-1.41	1.1e-01	1.0e+00
asperthecin biosynthetic process		-1.38	1.1e-01	1.0e+00
copper ion binding		-1.40	9.9e-02	1.0e+00
hydrolase activity. acting on glycosyl bonds		-1.38	9.8e-02	1.0e+00
protein refolding		-1.46	5.9e-02	1.0e+00
fumigaclavine C biosynthetic process		-1.58	1.6e-02	6.1e-01