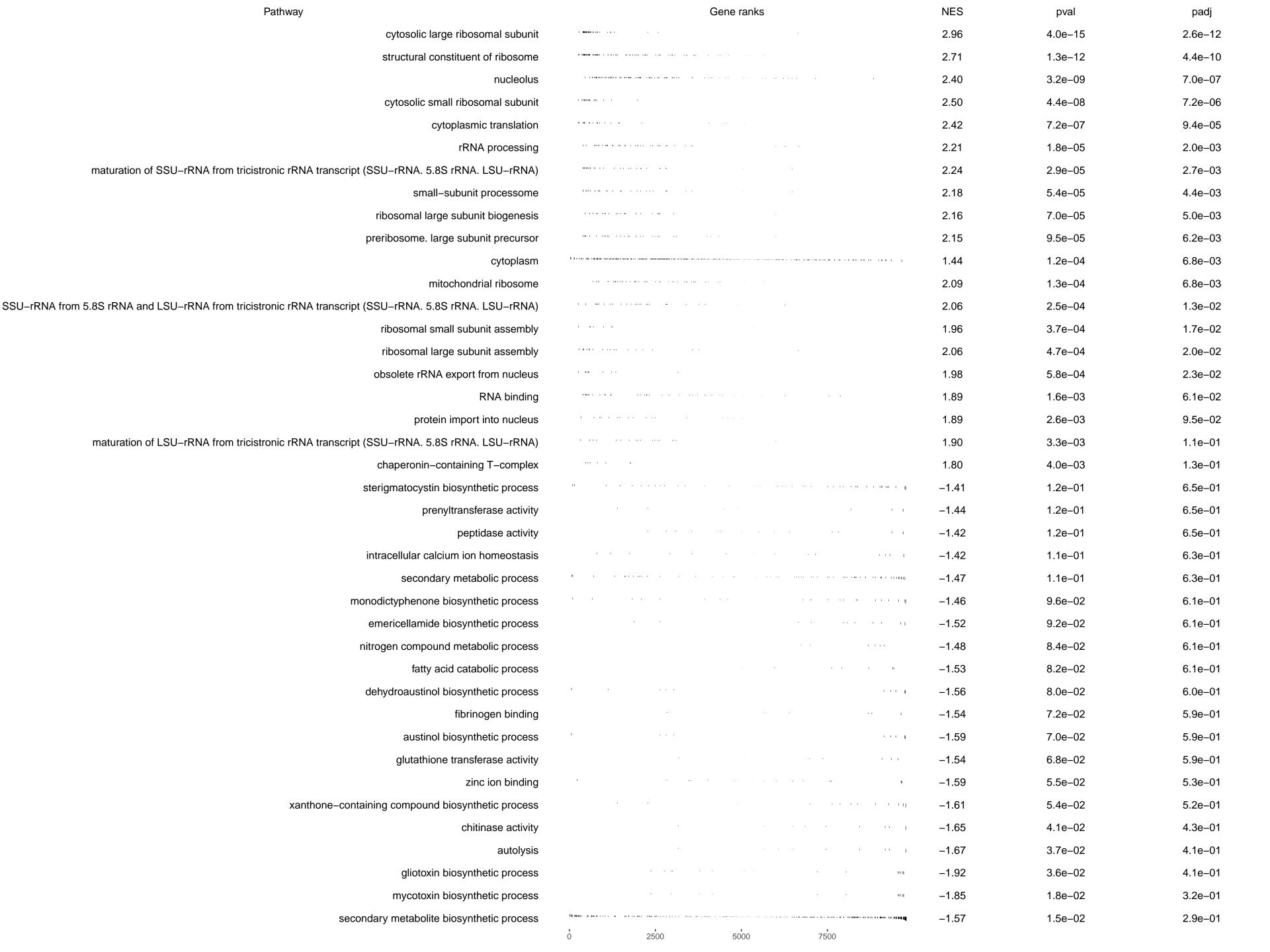
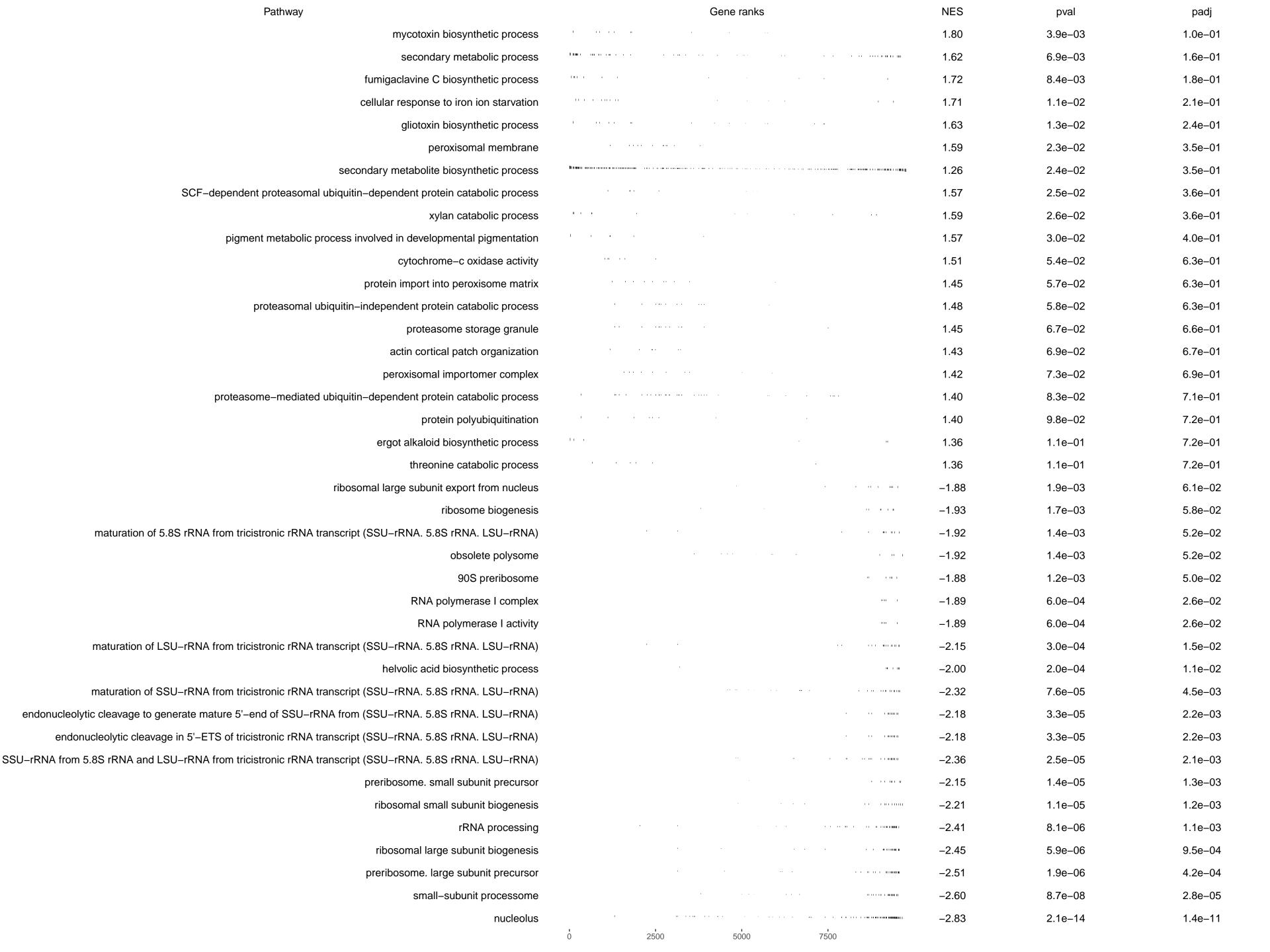
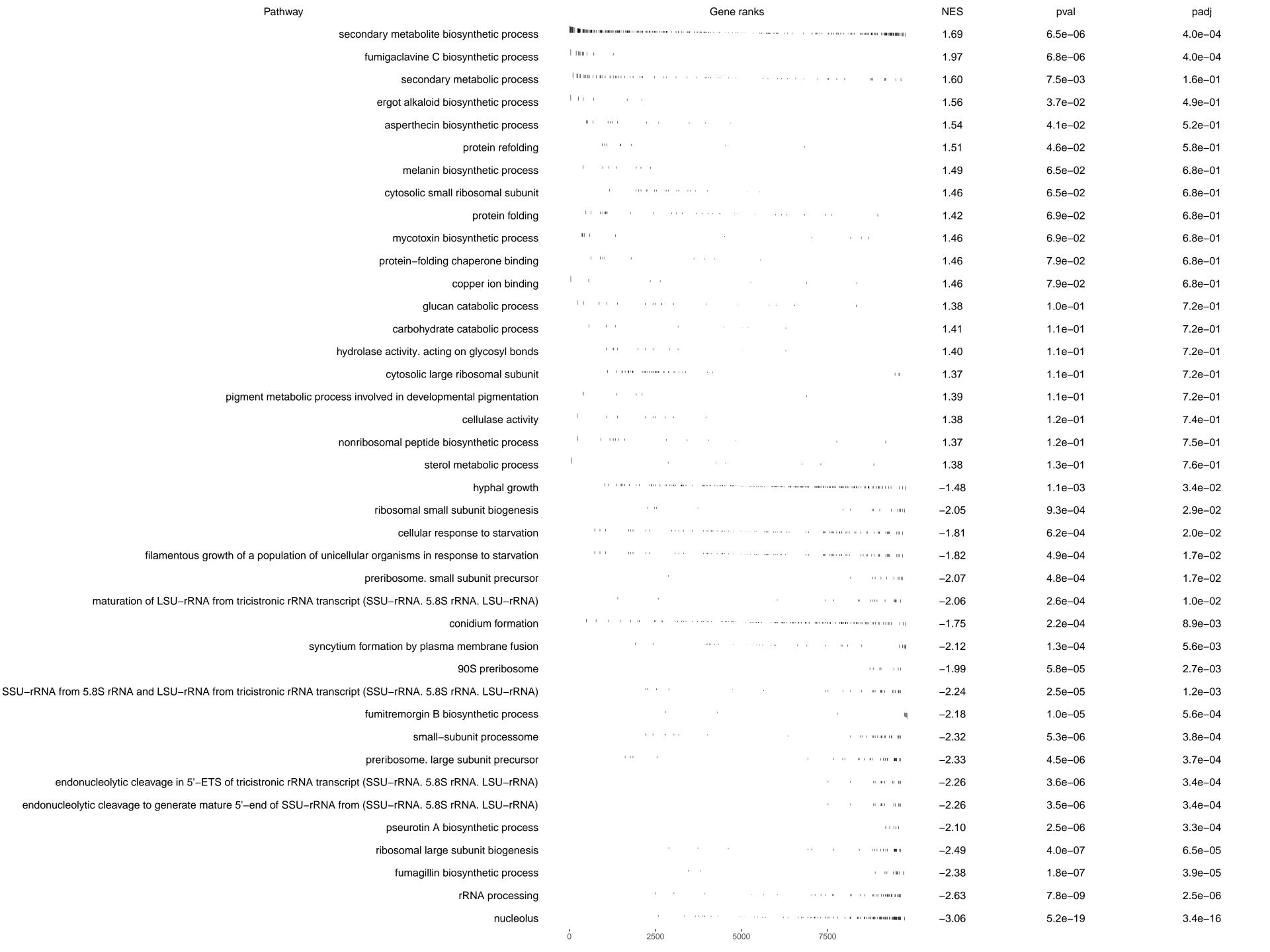
Pathway	Gene ranks	NES	pval	padj
fumigaclavine C biosynthetic process	Штип	1.83	5.6e-05	3.3e-03
secondary metabolite biosynthetic process	Marian 11: manuscrius in 1: 10: 1: 10: 10: 10: 10: 10: 10: 10: 1	1.38	7.5e-03	1.6e-01
ergot alkaloid biosynthetic process	True .	1.62	7.7e-03	1.6e-01
protein refolding	THE CONTRACTOR OF THE CONTRACT	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	I minimum and the contract of	1.33	9.2e-02	9.2e-01
asperthecin biosynthetic process		1.41	9.8e-02	9.2e-01
melanin biosynthetic process	l i i in	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	Total to the second of the sec	1.34	1.5e-01	9.8e-01
protein folding	For the first control of the control	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	To the term of the commence of the contract of	1.23	2.0e-01	1.0e+00
cellulase activity	To the contract of the contrac	1.29	2.0e-01	1.0e+00
xylan catabolic process		1.25	2.3e-01	1.0e+00
cytosolic large ribosomal subunit	T HHIIIIIIII I HIII I W II W II W II W I	1.18	2.5e-01	1.0e+00
obsolete nucleosome positioning	en e	-1.84	2.3e-03	7.2e-02
maturation of LSU-rRNA from tricistronic rRNA transcript (SSU-rRNA. 5.8S rRNA. LSU-rRNA)	t en	-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	To the first the second control of the secon	-1.44	1.1e-03	4.0e-02
maturation of SSU-rRNA from tricistronic rRNA transcript (SSU-rRNA. 5.8S rRNA. LSU-rRNA)	the community of the second of	-1.92	8.7e-04	3.5e-02
preribosome. small subunit precursor		-1.94	5.1e-04	2.2e-02
conidium formation	Harmonia de la companya della companya della companya de la companya de la companya della compan	-1.61	4.4e-04	2.0e-02
fumitremorgin B biosynthetic process	The second secon	-1.94	2.5e-04	1.2e-02
syncytium formation by plasma membrane fusion	THE CONTRACTOR OF THE CONTRACT	-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)	1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1	-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	The transfer of the second of	-2.20	2.0e-06	1.8e-04
ribosomal large subunit biogenesis	the state of the s	-2.32	1.7e-06	1.8e-04
pseurotin A biosynthetic process	•	-2.06	2.7e-07	4.4e-05
rRNA processing	ter en	-2.43	1.2e-08	2.7e-06
fumagillin biosynthetic process	· · · · · · · · · · · · · · · · · · ·	-2.54	1.6e-14	5.1e-12
nucleolus	the control of the co	-2.79	8.6e-19	5.6e-16
	0 2500 5000 7500			



Pathway	Gene ranks	NES	pval	padj
nucleolus	1. Name (1. 1. 1. 1. 1. 1. 1. 1. 1. 1. 1. 1. 1. 1	2.84	1.3e-18	8.2e-16
fumagillin biosynthetic process	N on-	2.48	1.1e-11	3.5e-09
rRNA processing	IMMETHEM TO THE TENED OF THE TE	2.48	1.1e-08	2.3e-06
ribosomal large subunit biogenesis	100 M (10310) ()	2.39	6.4e-07	1.0e-04
small-subunit processome		2.26	4.6e-06	5.6e-04
pseurotin A biosynthetic process		2.06	5.2e-06	5.6e-04
preribosome. large subunit precursor	100 H 100 H 1 1 1 1 1 1 1 1 1 1 1 1 1 1	2.22	1.0e-05	9.5e-04
SSU-rRNA from 5.8S rRNA and LSU-rRNA from tricistronic rRNA transcript (SSU-rRNA. 5.8S rRNA. LSU-rRNA)	MERCHANICA CONTRACTOR	2.15	1.8e-05	1.5e-03
endonucleolytic cleavage to generate mature 5'-end of SSU-rRNA from (SSU-rRNA. 5.8S rRNA. LSU-rRNA)		2.11	6.8e-05	4.9e-03
endonucleolytic cleavage in 5'-ETS of tricistronic rRNA transcript (SSU-rRNA. 5.8S rRNA. LSU-rRNA)		2.11	7.5e-05	4.9e-03
preribosome. small subunit precursor		2.03	8.2e-05	4.9e-03
maturation of SSU-rRNA from tricistronic rRNA transcript (SSU-rRNA. 5.8S rRNA. LSU-rRNA)	tin notice of the second of	2.01	2.1e-04	1.1e-02
ribosomal small subunit biogenesis	tentral and the second of the	1.92	1.3e-03	6.6e-02
filamentous growth of a population of unicellular organisms in response to starvation	THE COURT OF THE CONTROL OF THE CONT	1.61	2.6e-03	1.2e-01
hyphal growth	#1 HII - 11 1#1 / HIII HIIII HIIII HIIII HIIII HIIII HIIII HIIII HIII HIIII HIII	1.36	2.7e-03	1.2e-01
maturation of LSU-rRNA from tricistronic rRNA transcript (SSU-rRNA. 5.8S rRNA. LSU-rRNA)	una como en esta de la compansión de la co	1.86	3.1e-03	1.2e-01
syncytium formation by plasma membrane fusion	Microsoft Communication of the	1.80	3.3e-03	1.2e-01
conidium formation	To the contract the contract of the contract o	1.48	3.4e-03	1.2e-01
poly(A)+ mRNA export from nucleus	The first of the second of the	1.82	5.1e-03	1.7e-01
helvolic acid biosynthetic process		1.79	5.5e-03	1.7e-01
pigment biosynthetic process		-1.20	2.8e-01	1.0e+00
xylan catabolic process	The second of th	-1.21	2.7e-01	1.0e+00
protein folding	And the second of the second o	– 1.16	2.7e-01	1.0e+00
DNA-binding transcription factor activity. RNA polymerase II-specific		-1.24	2.4e-01	1.0e+00
proteasome core complex. alpha-subunit complex		-1.27	2.2e-01	1.0e+00
protein-folding chaperone binding	en e	-1.29	2.1e-01	1.0e+00
proteasome storage granule		-1.27	2.0e-01	1.0e+00
negative regulation of DNA-templated transcription		-1.32	1.7e-01	1.0e+00
proteasomal ubiquitin-independent protein catabolic process		-1.31	1.7e-01	1.0e+00
proteasome-mediated ubiquitin-dependent protein catabolic process	the second of th	-1.29	1.5e-01	1.0e+00
melanin biosynthetic process		-1.34	1.5e-01	1.0e+00
sterol metabolic process		-1.36	1.3e-01	1.0e+00
hydrolase activity. acting on glycosyl bonds		-1.38	1.2e-01	1.0e+00
copper ion binding		-1.42	9.6e-02	1.0e+00
protein refolding		-1.43	8.8e-02	1.0e+00
secondary metabolite biosynthetic process		−1.24	7.2e-02	9.5e-01
pigment metabolic process involved in developmental pigmentation		-1.46	6.5e-02	9.3e-01
asperthecin biosynthetic process		-1.49	5.4e-02	9.1e-01
ergot alkaloid biosynthetic process		-1.60	1.7e-02	3.6e-01
fumigaclavine C biosynthetic process		-1.71	7.9e-03	2.3e-01
	0 2500 5000 7500			





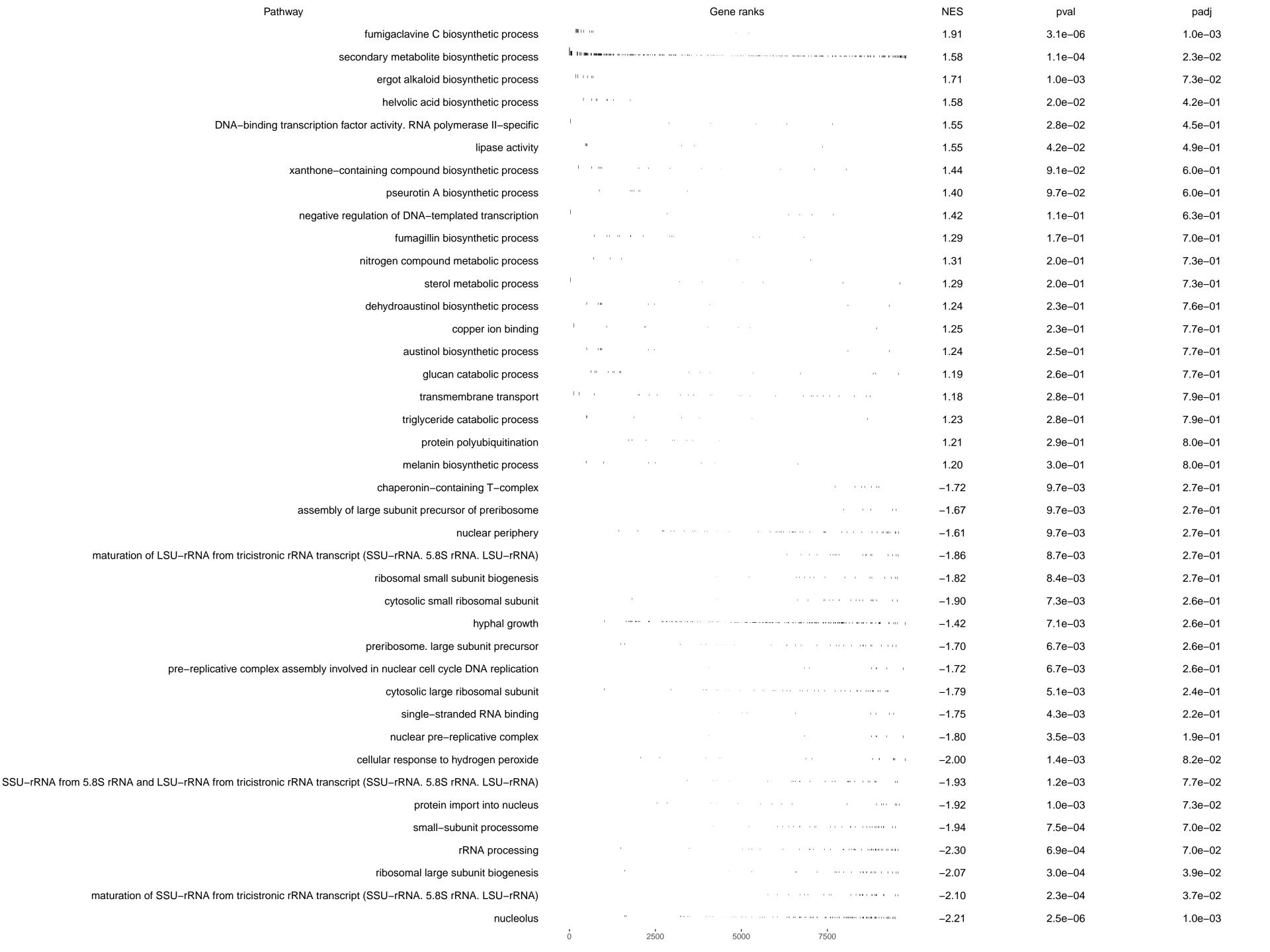
Pathway	Gene ranks	NES	pval	padj
nucleolus		3.30	2.2e-27	1.4e-24
rRNA processing	MINERALIZATION OF THE THEORY OF THE THE THEORY OF THE THE THEORY OF THE THE THEORY OF THE THE THE THEORY OF THE THEORY OF THE THEORY OF THE THE THE THE THE	2.84	9.8e-13	3.2e-10
structural constituent of ribosome	HI I I I I I I I I I I I I I I I I I I	2.69	5.7e-12	1.2e-09
preribosome. large subunit precursor	WIN (1) (1) (1) (1) (1) (1) (1) (1) (1) (1)	2.69	2.5e-11	4.0e-09
small-subunit processome	Hammar at a craw to c	2.64	1.6e-10	1.9e-08
ribosomal large subunit biogenesis	MHTTITE I I I I I I I I I I I I I I I I I	2.66	1.7e-10	1.9e-08
cytosolic large ribosomal subunit	I I II 11.100 MM1.000 *	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)	1881/H 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1	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)	THE COLUMN COLUM	2.46	3.5e-07	1.9e-05
endonucleolytic cleavage in 5'-ETS of tricistronic rRNA transcript (SSU-rRNA. 5.8S rRNA. LSU-rRNA)	MIN 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1	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)	MINI II .	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	en en la companya de la companya de La companya de la co	-1.38	1.3e-01	6.4e-01
intracellular iron ion homeostasis	en e	-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	en de la companya de La companya de la co	-1.41	1.1e-01	6.2e-01
glucan catabolic process	en e	-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	en e	-1.53	6.6e-02	4.7e-01
phosphatase activity		-1.50	6.4e-02	4.7e-01
apoptotic process	en e	-1.54	5.6e-02	4.3e-01
cellulase activity		– 1.57	4.6e-02	3.7e-01
cellular response to iron ion starvation	en e	-1.66	4.6e-02	3.7e-01
xanthone-containing compound biosynthetic process	en de la companya de La companya de la co	-1.66	4.1e-02	3.4e-01
pectin catabolic process		-1.88	4.0e-02	3.4e-01
mycotoxin biosynthetic process	en e	–1.85	2.8e-02	2.6e-01
gliotoxin biosynthetic process	en de la companya de	-1.94	1.8e-02	2.2e-01
secondary metabolite biosynthetic process	1 0 2500 5000 7500	– 1.57	5.8e-03	9.4e-02
	0 2500 5000 7500			

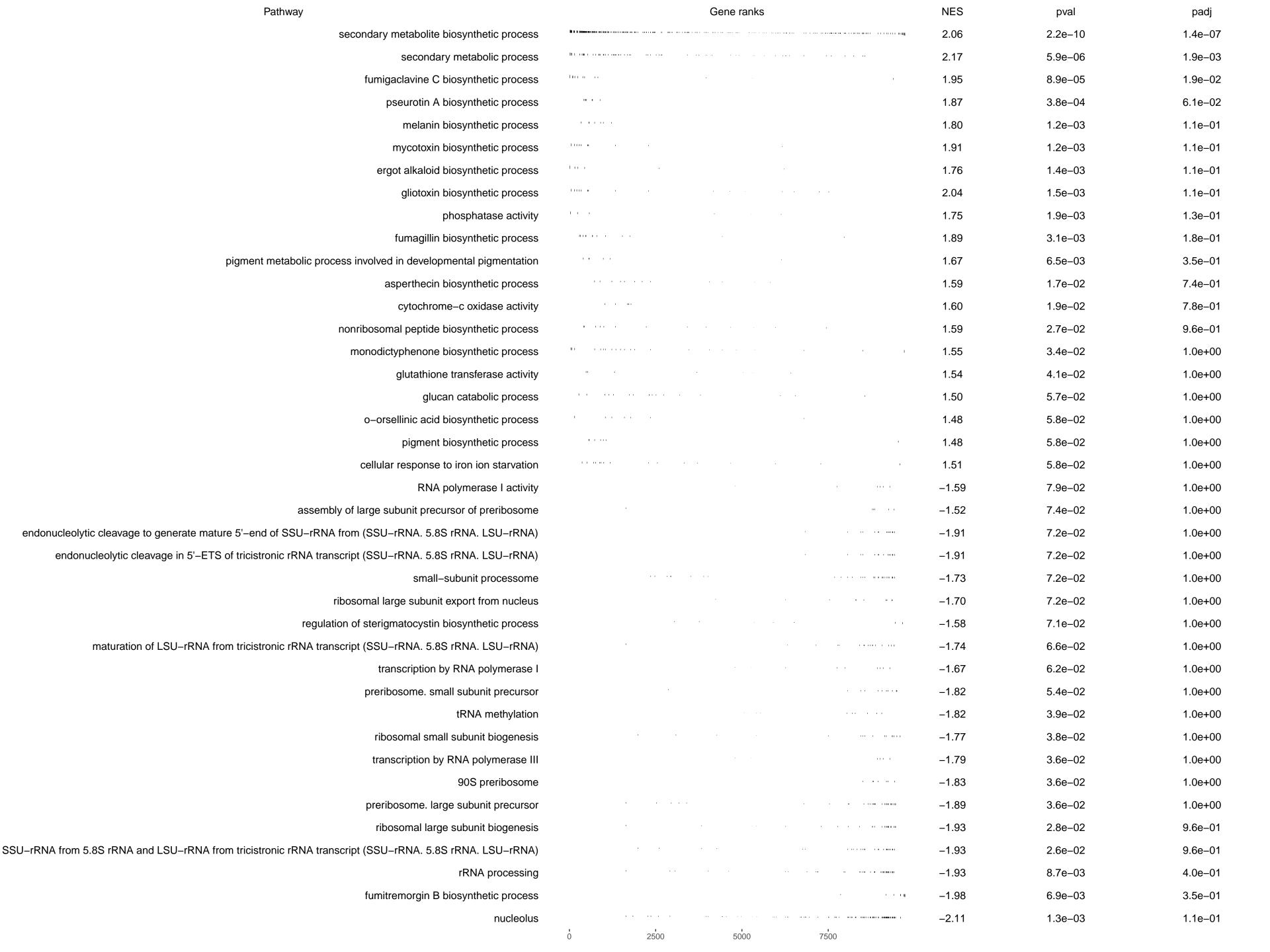
Pathway	Gene ranks	NES	pval	padj
fumigaclavine C biosynthetic process	l morno c	2.10	1.2e-06	7.8e-05
ergot alkaloid biosynthetic process	1 1:11	1.75	5.9e-04	2.0e-02
secondary metabolite biosynthetic process	1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1	1.50	1.8e-03	5.7e-02
secondary metabolic process	Пилинин писто по то се пинат по по по пр	1.62	1.0e-02	1.9e-01
protein folding	H-HHH	1.62	2.4e-02	3.5e-01
protein refolding	TI I III	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	To the control of the	1.51	4.6e-02	5.3e-01
pigment metabolic process involved in developmental pigmentation	The first of the f	1.39	9.0e-02	6.5e-01
cytosolic large ribosomal subunit	1 1 11 mm (minimum m) () () () () () () () () (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	The state of the s	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	territoria de la compansa de la comp	-1.99	7.2e-04	2.3e-02
maturation of SSU-rRNA from tricistronic rRNA transcript (SSU-rRNA. 5.8S rRNA. LSU-rRNA)	HILL COLUMN TO THE THEORY OF THE THE THEORY OF THE THEORY	-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)	t e e e e e e e e e e e e e e e e e e e	-2.05	1.4e-04	5.5e-03
ribosomal small subunit biogenesis	1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1	-2.10	8.8e-05	3.8e-03
conidium formation	TO THE THEORY OF THE THE THEORY OF THE THEORY OF THE THEORY OF THE THEORY OF THE THEOR	-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	tii t tii ii iiii iiii iiii iiii iiii	-2.40	5.9e-07	5.5e-05
ribosomal large subunit biogenesis	t to the second of the second	-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)	ti i i i i i i i i i i i i i i i i i i	-2.35	2.1e-07	2.7e-05
small-subunit processome	t i i i i i i i i i i i i i i i i i i i	-2.45	2.0e-07	2.7e-05
rRNA processing	t de la companya del companya de la companya del companya de la co	-2.63	3.3e-10	7.2e-08
fumagillin biosynthetic process	THII	-2.55	1.2e-11	3.8e-09
nucleolus	1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1	-3.13	3.6e-23	2.4e-20
	0 2500 5000 7500			

Pathway	Gene ranks	NES	pval	padj
secondary metabolite biosynthetic process	• Indiana	2.01	2.8e-06	1.8e-03
pseurotin A biosynthetic process	III .	1.83	3.4e-04	1.1e-01
helvolic acid biosynthetic process	THE TOTAL CONTRACTOR OF THE PROPERTY OF THE PR	1.82	9.8e-04	1.8e-01
cytosolic large ribosomal subunit	11 1 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2	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	num ,	2.02	1.7e-03	1.8e-01
preribosome. large subunit precursor		1.87	2.6e-03	1.9e-01
ribosomal large subunit biogenesis	MCC 1-111 - 100-1-101-1-1-1-1-1-1-1-1-1-1-1	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	t t to minimum to warrant or a contract of the	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	(10.0 to 10.10 to 10.0	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	Thus we exceed the second of t	1.63	1.6e-02	5.5e-01
monodictyphenone biosynthetic process	tion of the second of the seco	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	Element of the second of the s	-1.26	2.0e-01	1.0e+00
peroxisomal membrane	en de la companya de La companya de la co	-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	en e	-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	en e	-1.42	1.2e-01	1.0e+00
positive regulation of asexual sporulation resulting in formation of a cellular spore	en de la companya de La companya de la co	-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
	0 2500 5000 7500			

Pathway	Gene ranks	NES	pval	padj
cytosolic large ribosomal subunit	WE MAN I I	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	Marin	2.75	7.8e-11	1.3e-08
mitochondrial ribosome	II HEIM MILL IN MARKET IN A COLUMN CO	2.62	7.3e-09	9.5e-07
obsolete rRNA export from nucleus	11 111 1	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	The state of the contract of t	2.28	2.1e-05	1.4e-03
hyphal cell wall	Hamman and the second of the s	2.18	6.7e-05	3.9e-03
chaperonin-containing T-complex		2.00	1.1e-04	5.7e-03
mitochondrial membrane	# #1 HITHER TO COM CO.	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)	tman in the second of the seco	2.08	3.4e-04	1.4e-02
induction by symbiont of host defense response	tim is an experience of the second of the se	2.10	3.4e-04	1.4e-02
mitochondrial small ribosomal subunit		2.02	5.5e-04	2.1e-02
cell surface	MINISTER OF THE PROPERTY OF TH	1.69	6.4e-04	2.2e-02
mitotic spindle pole body	t mentantina and the control of the	2.04	6.6e-04	2.2e-02
ribosomal small subunit assembly	t man and the second	1.94	7.9e-04	2.6e-02
ribosomal large subunit assembly	MILITAR TO THE REPORT OF THE PROPERTY OF THE P	1.97	9.3e-04	2.8e-02
mycotoxin biosynthetic process	And the second of the second o	-1.56	7.0e-02	4.6e-01
glutathione transferase activity	And the second of the second o	-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	-1.70	4.7e-02	3.6e-01
emericellamide 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	r i i i i i i i i i i i i i i i i i i i	-1.67	2.0e-02	2.3e-01
prenyltransferase activity	$ ag{1}$	-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	n	-1.85	3.7e-03	7.4e-02
chitinase activity	n	-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
	0 2500 5000 7500			

Pathway	Gene ranks		pval	padj
secondary metabolite biosynthetic process	M (M) (M) (M) (M) (M) (M) (M) (M) (M) (M	1.63	2.4e-04	7.8e-02
positive regulation of secondary metabolite biosynthetic process	MIT I I I I I I I I I I I I I I I I I I	1.71	1.2e-02	1.0e+00
negative regulation of G2/M transition of mitotic cell cycle		1.70	1.2e-02	1.0e+00
asperfuranone biosynthetic process		1.66	1.8e-02	1.0e+00
shamixanthone biosynthetic process	Time to the second of the seco	1.59	3.2e-02	1.0e+00
cellular response to osmotic stress		1.57	4.2e-02	1.0e+00
membrane raft		1.55	4.9e-02	1.0e+00
prenyltransferase activity		1.50	5.7e-02	1.0e+00
cell wall-bounded periplasmic space		1.51	6.0e-02	1.0e+00
intracellular iron ion homeostasis		1.49	6.7e-02	1.0e+00
extracellular region	I was made a summer a construction of the cons	1.28	6.9e-02	1.0e+00
oxidoreductase activity		1.44	7.3e-02	1.0e+00
glutathione transferase activity		1.47	7.9e-02	1.0e+00
cellular response to hydrogen peroxide	To the control of the	1.43	8.4e-02	1.0e+00
glutathione metabolic process		1.45	8.7e-02	1.0e+00
asperthecin biosynthetic process	the many many control of the second of the s	1.42	8.9e-02	1.0e+00
protein homodimerization activity	(1, 2, 3, 3, 3, 3, 3, 3, 3, 3, 3, 3, 3, 3, 3,	1.41	8.9e-02	1.0e+00
syncytium formation by plasma membrane fusion	tom the second of the second o	1.41	9.1e-02	1.0e+00
fibrinogen binding		1.43	9.7e-02	1.0e+00
o-orsellinic acid biosynthetic process		1.43	9.9e-02	1.0e+00
U1 snRNP		-1.44	9.9e-02	1.0e+00
vesicle-mediated transport		-1.37	9.6e-02	1.0e+00
negative regulation of septation initiation signaling		-1.46	9.1e-02	1.0e+00
protein targeting to ER		-1.47	8.6e-02	1.0e+00
endoplasmic reticulum to Golgi vesicle-mediated transport	the transfer of the second of	-1.44	8.2e-02	1.0e+00
mitochondrial small ribosomal subunit	e e e e e e e e e e e e e e e e e e e	-1.51	8.1e-02	1.0e+00
chaperonin-containing T-complex		-1.50	6.8e-02	1.0e+00
mRNA 3'-end processing		-1.51	6.5e-02	1.0e+00
U4/U6 x U5 tri-snRNP complex		-1.52	6.2e-02	1.0e+00
poly(U) RNA binding		-1.56	4.9e-02	1.0e+00
RNA binding	Company of the compan	-1.56	4.6e-02	1.0e+00
mitochondrial ribosome	the state of the s	-1.57	4.2e-02	1.0e+00
cytoplasmic translation	the second of th	-1.79	3.3e-02	1.0e+00
protein glycosylation		-1.64	2.8e-02	1.0e+00
mitochondrial respiratory chain complex I assembly		-1.62	2.3e-02	1.0e+00
helvolic acid biosynthetic process		-1.70	1.5e-02	1.0e+00
obsolete rRNA export from nucleus		-1.73	1.0e-02	1.0e+00
cytosolic small ribosomal subunit	· (0.) (1.00)	-2.08	8.4e-03	1.0e+00
cytosolic large ribosomal subunit	Company of the second of the s	-2.23	1.2e-03	2.5e-01
structural constituent of ribosome		-2.28	1.8e-04	7.8e-02
	0 2500 5000 7500			

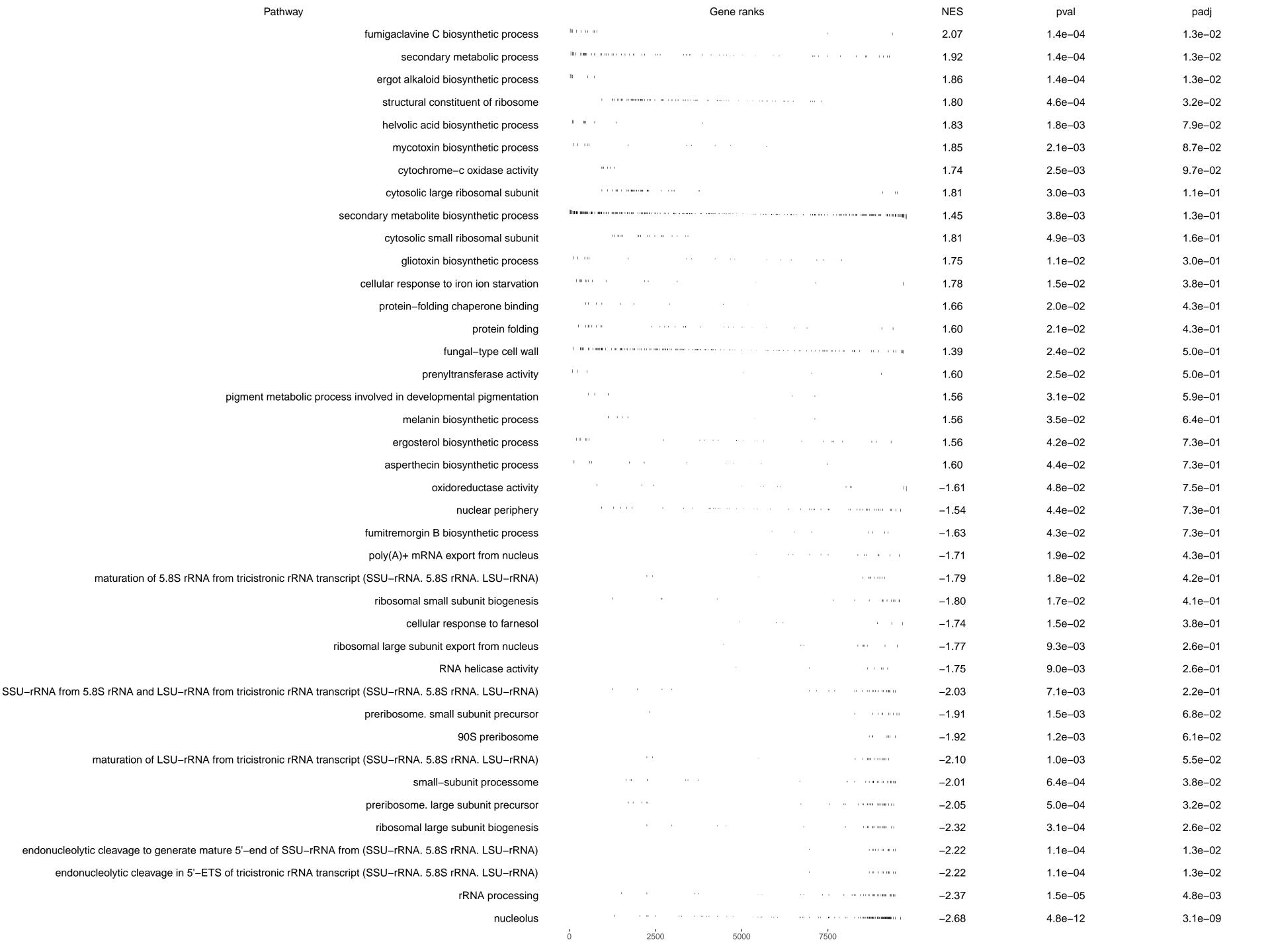




Pathway	Gene ranks	NES	pval	padj
intracellular anatomical structure	Immutum na materia station i com montes de la companya de la companya de la companya de la companya de la comp	1.73	8.7e-04	3.5e-02
cellular response to heat	If the contract of the contrac	1.66	5.2e-03	1.4e-01
cellular response to hydrogen peroxide	Here there is a second of the	1.64	1.2e-02	2.9e-01
cell adhesion	l e de la companya d	1.57	2.0e-02	4.0e-01
fungal-type cell wall	10 mm () m m ()	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	The state of the s	1.44	7.7e-02	8.9e-01
peroxisome	1.1	1.37	7.8e-02	8.9e-01
oxidoreductase activity	The first of the second of the	1.44	8.2e-02	9.0e-01
cellular response to pH		1.41	8.3e-02	9.0e-01
zinc ion binding	THE CONTRACTOR OF THE CONTRACT	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	0 101 11 10 10 1	1.37	1.2e-01	1.0e+00
glutathione metabolic process		1.36	1.3e-01	1.0e+00
protein homodimerization activity	The first of the second of the	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	The first manner of the first of the second	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	term of the second of the sec	-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)	e e e e e e e e e e e e e e e e e e e	-1.92	9.4e-04	3.5e-02
preribosome. large subunit precursor	e e e e e e e e e e e e e e e e e e e	-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	Control of the second of the s	-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 - 1 - H	-1.88	2.6e-05	1.8e-03
fumitremorgin B biosynthetic process	to the	-1.88	1.6e-05	1.3e-03
rRNA processing	And the second of the second o	-2.17	5.3e-06	4.9e-04
secondary metabolic process	l limitation de la company	-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	The second of th	-2.25	6.3e-08	1.4e-05
fumagillin biosynthetic process	en de la companya de	-2.24	3.2e-09	1.0e-06
nucleolus	1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1	-2.34	2.3e-10	1.5e-07
	0 2500 5000 7500			

Pathway	G	Sene ranks	NES	pval	padj
intracellular anatomical structure	MILT II III II I		2.01	3.9e-06	2.5e-03
cellular response to heat	Material Control of the Control of t		1.93	4.2e-04	9.2e-02
fungal-type cell wall	MITTELL MITTELL REPORT OF THE CO. T. C.		1.59	5.8e-04	9.4e-02
protein-folding chaperone binding	1 111 1		1.80	3.0e-03	3.9e-01
protein refolding	Military and the second of the		1.73	7.2e-03	7.8e-01
protein folding	11 1100 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1		1.70	1.3e-02	1.0e+00
cellular response to osmotic stress	I to a constant of the constan	· · · · · · · · · · · · · · · · · · ·	1.61	2.3e-02	1.0e+00
chromosome segregation			1.63	2.3e-02	1.0e+00
positive regulation of DNA-templated transcription	Leading to the second s		1.63	3.0e-02	1.0e+00
chromosome. centromeric region	total and the second second		1.54	3.6e-02	1.0e+00
regulation of fungal-type cell wall organization	11		1.52	3.8e-02	1.0e+00
mitotic spindle midzone	1 - 1 - 0 - 1 - 1 - 1 - 1 - 1 - 1 - 1 -		1.51	4.5e-02	1.0e+00
proteasome-mediated ubiquitin-dependent protein catabolic process	1 1 10 10 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1	the second of th	1.47	4.5e-02	1.0e+00
positive regulation of G2/M transition of mitotic cell cycle	The second of th		1.56	4.6e-02	1.0e+00
asperthecin biosynthetic process	THE CONTRACT OF	· · · · ·	1.51	5.4e-02	1.0e+00
protein homodimerization activity			1.51	6.0e-02	1.0e+00
negative regulation of G2/M transition of mitotic cell cycle	l .		1.50	6.9e-02	1.0e+00
protein import into peroxisome matrix			1.47	7.2e-02	1.0e+00
positive regulation of protein import into nucleus	The state of the s		1.46	7.3e-02	1.0e+00
actin cortical patch organization			1.43	8.0e-02	1.0e+00
TOR signaling			-1.40	1.3e-01	1.0e+00
rRNA processing		e e e e e e e e e e e e e e e e e e e	– 1.52	1.3e-01	1.0e+00
endonucleolytic cleavage to generate mature 5'-end of SSU-rRNA from (SSU-rRNA. 5.8S rRNA. LSU-rRNA)		e e e e e e e e e e e e e e e e e e e	-1.45	1.3e-01	1.0e+00
autolysis			-1.41	1.2e-01	1.0e+00
asperfuranone biosynthetic process			-1.48	1.1e-01	1.0e+00
emericellamide biosynthetic process	T T		–1.51	1.1e-01	1.0e+00
xanthone-containing compound biosynthetic process		· · · · · · · · · · · · · · · · · · ·	-1.56	1.0e-01	1.0e+00
90S preribosome		()	-1.47	9.3e-02	1.0e+00
o-orsellinic acid biosynthetic process			-1.48	9.1e-02	1.0e+00
fumitremorgin B biosynthetic process			–1.52	9.0e-02	1.0e+00
fumagillin biosynthetic process			-1.64	8.8e-02	1.0e+00
negative regulation of sexual sporulation resulting in formation of a cellular spore	to the second of		–1.68	8.5e-02	1.0e+00
dehydroaustinol biosynthetic process		и ц	–1.62	7.9e-02	1.0e+00
sexual sporulation resulting in formation of a cellular spore			–1.65	7.8e-02	1.0e+00
austinol biosynthetic process	1	и ц	–1.60	7.4e-02	1.0e+00
nucleolus			-1.49	6.4e-02	1.0e+00
oxidoreductase activity		en e	-1.77	5.3e-02	1.0e+00
helvolic acid biosynthetic process	•	· · · · · · · · · · · · · · · · · · ·	-1.70	2.0e-02	1.0e+00
regulation of DNA-templated transcription	l ll v v v v v v v v v v v v v v v v v		-1.88	8.5e-03	7.9e-01
secondary metabolite biosynthetic process	1 0 2500	5000 7500	– 1.82	7.9e-05	2.6e-02
	0 2500	3000 / 300			

Pathway	Gene ranks	NES	pval	padj
nucleolus	HINMAN MICHIGAN AND AND AND AND AND AND AND AND AND A	2.10	1.6e-06	1.0e-03
fumagillin biosynthetic process	Thurs are a second of the seco	2.10	6.0e-06	1.9e-03
pseurotin A biosynthetic process	BI II	1.89	1.7e-05	3.7e-03
ribosomal large subunit biogenesis	Therefore the second of the se	2.01	1.2e-04	1.6e-02
rRNA processing	1000 1110 m m x x x x x x x x x x x x x x x x x	2.00	1.2e-04	1.6e-02
prenyltransferase activity		1.83	2.2e-04	2.0e-02
fumitremorgin B biosynthetic process	1_{1} , \mathbf{n}_{2} , \mathbf{n}_{3}	1.88	2.3e-04	2.0e-02
secondary metabolite biosynthetic process		1.59	2.4e-04	2.0e-02
secondary metabolic process	Digital constants from a second of the constant of the constan	1.92	4.0e-04	2.9e-02
preribosome. large subunit precursor	I make to the first of the control o	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)	Town the second of the second	1.70	6.4e-03	3.2e-01
small-subunit processome	THE CONTRACT OF THE CONTRACT O	1.73	7.4e-03	3.4e-01
shamixanthone biosynthetic process		1.76	9.0e-03	3.9e-01
ribosomal small subunit biogenesis	The state of the second	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	the state of the s	-1.30	1.6e-01	1.0e+00
extrinsic component of membrane		-1.32	1.5e-01	1.0e+00
protein targeting to vacuole	en de la companya de	-1.35	1.5e-01	1.0e+00
actin cytoskeleton organization		-1.34	1.4e-01	1.0e+00
phagophore assembly site	en de la companya de La companya de la co	-1.35	1.4e-01	1.0e+00
proteasomal ubiquitin-independent protein catabolic process	en e	-1.37	1.3e-01	1.0e+00
SCF ubiquitin ligase complex		-1.37	1.2e-01	1.0e+00
cellular response to pH	en de la companya de La companya de la co	-1.37	1.2e-01	1.0e+00
obsolete integral component of Golgi membrane	en de la companya de	-1.39	1.1e-01	1.0e+00
actin cortical patch	the second secon	-1.40	1.1e-01	1.0e+00
negative regulation of DNA-templated transcription		-1.40	1.1e-01	1.0e+00
macroautophagy	ti de la companya de	-1.42	1.0e-01	1.0e+00
cellular response to hydrogen peroxide	en de la companya de La companya de la co	-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	11 i i i i i i i i i i i i i i i i i i	-1.34	8.7e-02	1.0e+00
cytosolic small ribosomal subunit	en e	-1.48	7.6e-02	1.0e+00
proteasome-mediated ubiquitin-dependent protein catabolic process	e de la composição de l	-1.53	6.6e-02	1.0e+00
peroxisome		-1.65	3.6e-02	8.7e-01
	0 2500 5000 7500			



Pathway	Gene ranks	NES	pval	padj
nucleolus	The manner of the contract of	3.20	4.0e-27	2.6e-24
fumagillin biosynthetic process		2.55	1.8e-12	5.7e-10
rRNA processing	HINTER CONTRACTOR OF THE CONTR	2.73	1.5e-11	3.2e-09
small-subunit processome	H I WICH H I I I I I I I I I I I I I I I I I	2.72	3.9e-11	6.3e-09
preribosome. large subunit precursor	The matter of the contract of	2.65	2.9e-10	3.8e-08
ribosomal large subunit biogenesis	HIND THE EXECUTION OF THE SECOND SECO	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)	WHI HILL I I I I I I I I I I I I I I I I	2.56	1.5e-08	1.4e-06
pseurotin A biosynthetic process	II	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)	HE TRUET IN THE CONTRACT OF TH	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	THE HEIGHT BUT I I TO THE WALL COME A SECOND OF THE WALL COME IN THE TAX OF THE PARTY OF THE PAR	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	reconstruction of the second s	-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	the second of th	-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	territoria de la companya de la comp	-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	n i i i	-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
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Pathway	Gene ranks	NES	pval	padj
nucleolus	Плитичности на при на 	2.56	5.1e-13	3.3e-10
fumagillin biosynthetic process	I m a second se	2.53	3.3e-12	1.1e-09
pseurotin A biosynthetic process	i i	2.10	2.9e-07	6.4e-05
rRNA processing	The second control of	2.27	1.1e-05	1.8e-03
ribosomal large subunit biogenesis	Table Cambridge Community of the Communi	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	THE THE COURT OF THE CONTRACT	1.94	1.3e-03	1.1e-01
preribosome. small subunit precursor		1.93	1.6e-03	1.2e-01
small-subunit processome	HTTL HE CONTROL OF THE CONTROL OF TH	1.88	2.3e-03	1.5e-01
poly(A)+ mRNA export from nucleus	I I i i i i i i i i i i i i i i i i i i	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	H I III I	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	Market 11 with 1 mark and 10 to 10 t	-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	ti di series de la companya de la c	-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	e de la companya del companya de la companya del companya de la co	-1.46	5.9e-02	1.0e+00
fumigaclavine C biosynthetic process	· · · · · · · · · · · · · · · · · · ·	-1.58	1.6e-02	6.1e-01
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