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