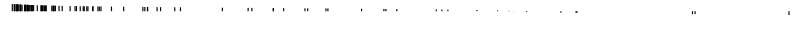
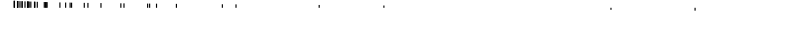



































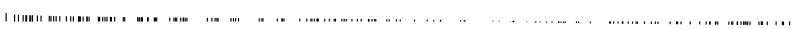




Pathway	Gene ranks	NES	pval	padj
nucleolus		3.30	2.2e−27	1.4e−24
rRNA processing		2.84	9.8e−13	3.2e−10
structural constituent of ribosome		2.69	5.7e−12	1.2e−09
preribosome. large subunit precursor		2.69	2.5e−11	4.0e−09
small-subunit processome		2.64	1.6e−10	1.9e−08
ribosomal large subunit biogenesis		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