

**Table S2. Functional Annotations of the modules identified by WGCNA**  
(Modules M8, M9 and M11 have no significant association)

Module ID	Category	Description	Number of genes	q-value
M1	GO_BP_TERM	siderophore transport	7	2,4E-2
	KEGG	mRNA surveillance pathway	14	2,1E-2
M2	GO_BP_TERM	regulation of transcription, DNA-templated	79	4,1E-10
	GO_BP_TERM	transcription, DNA-templated	75	7,5E-8
	GO_BP_TERM	positive regulation of transcription from RNA polymerase II promoter	36	3,2E-5
	GO_BP_TERM	fungal-type cell wall organization	24	1,0E-2
	KEGG	MAPK signaling pathway - yeast	15	2,8E-5
	KEGG	Meiosis - yeast	19	6,2E-3
	KEGG	Protein processing in endoplasmic reticulum	15	5,8E-3
M3	GO_BP_TERM	ribosome biogenesis	124	1,2E-101
	GO_BP_TERM	rRNA processing	117	8,5E-89
	GO_BP_TERM	rRNA methylation	40	1,9E-31
	GO_BP_TERM	ribosomal large subunit biogenesis	34	3,1E-25
	GO_BP_TERM	maturation of SSU-rRNA from tricistronic rRNA transcript (SSU-rRNA, 5.8S rRNA, LSU-rRNA)	37	2,1E-23
	GO_BP_TERM	endonucleolytic cleavage in ITS1 to separate SSU-rRNA from 5.8S rRNA and LSU-rRNA from tricistronic rRNA transcript (SSU-rRNA, 5.8S rRNA, LSU-rRNA)	29	3,4E-22
	GO_BP_TERM	maturation of LSU-rRNA from tricistronic rRNA transcript (SSU-rRNA, 5.8S rRNA, LSU-rRNA)	27	6,2E-22
	GO_BP_TERM	endonucleolytic cleavage in 5'-ETS of tricistronic rRNA transcript (SSU-rRNA, 5.8S rRNA, LSU-rRNA)	23	1,2E-18
	GO_BP_TERM	endonucleolytic cleavage to generate mature 5'-end of SSU-rRNA from (SSU-rRNA, 5.8S rRNA, LSU-rRNA)	22	1,1E-16
	GO_BP_TERM	maturation of 5.8S rRNA from tricistronic rRNA transcript (SSU-rRNA, 5.8S rRNA, LSU-rRNA)	16	1,0E-13
	GO_BP_TERM	ribosomal large subunit assembly	21	5,1E-13
	GO_BP_TERM	tRNA transcription from RNA polymerase III promoter	13	1,7E-9
	GO_BP_TERM	ribosomal small subunit biogenesis	16	1,7E-9
	GO_BP_TERM	termination of RNA polymerase III transcription	12	5,9E-9
	GO_BP_TERM	methylation	25	8,7E-9
	GO_BP_TERM	RNA secondary structure unwinding	14	5,1E-8
	GO_BP_TERM	tRNA methylation	12	1,0E-6
	GO_BP_TERM	transcription elongation from RNA polymerase III promoter	12	1,0E-6
	GO_BP_TERM	transcription from RNA polymerase III promoter	12	4,6E-6
	GO_BP_TERM	tRNA processing	22	4,4E-6
	GO_BP_TERM	translational initiation	15	3,3E-5
	GO_BP_TERM	tRNA modification	13	3,2E-5
	GO_BP_TERM	translation	43	4,4E-5
	GO_BP_TERM	cytoplasmic translation	28	1,3E-4
	GO_BP_TERM	regulation of translational initiation	9	1,9E-4
	GO_BP_TERM	assembly of large subunit precursor of preribosome	7	2,0E-4
	GO_BP_TERM	U4 snRNA 3'-end processing	8	2,9E-4

	Category	Description	Number of genes	q-value
M3 (cont'd)	GO_BP_TERM	transcription from RNA polymerase I promoter	9	4,1E-4
	GO_BP_TERM	ribosomal large subunit export from nucleus	10	4,2E-4
	GO_BP_TERM	nuclear polyadenylation-dependent tRNA catabolic process	8	4,4E-4
	GO_BP_TERM	ribosomal subunit export from nucleus	7	6,7E-4
	GO_BP_TERM	nuclear polyadenylation-dependent rRNA catabolic process	8	1,6E-3
	GO_BP_TERM	formation of translation preinitiation complex	8	1,6E-3
	GO_BP_TERM	polyadenylation-dependent snoRNA 3'-end processing	7	2,9E-3
	GO_BP_TERM	nuclear polyadenylation-dependent mRNA catabolic process	7	2,9E-3
	GO_BP_TERM	maturation of SSU-rRNA	7	2,9E-3
	GO_BP_TERM	nuclear polyadenylation-dependent CUT catabolic process	6	2,9E-3
	GO_BP_TERM	snRNA pseudouridine synthesis	5	3,2E-3
	GO_BP_TERM	exonucleolytic trimming to generate mature 3'-end of 5.8S rRNA from tricistronic rRNA transcript (SSU-rRNA, 5.8S rRNA, LSU-rRNA)	7	8,3E-3
	GO_BP_TERM	ribosomal small subunit assembly	8	1,2E-2
	GO_BP_TERM	rRNA modification	5	1,2E-2
	GO_BP_TERM	maturation of LSU-rRNA	6	1,6E-2
	GO_BP_TERM	RNA processing	8	2,7E-2
	GO_BP_TERM	nuclear mRNA surveillance of mRNA 3'-end processing	4	2,9E-2
	GO_BP_TERM	ncRNA polyadenylation	4	2,9E-2
	GO_BP_TERM	nuclear polyadenylation-dependent snoRNA catabolic process	4	2,9E-2
	GO_BP_TERM	nuclear polyadenylation-dependent snRNA catabolic process	4	2,9E-2
	GO_BP_TERM	nucleoside metabolic process	6	2,9E-2
	KEGG	Ribosome biogenesis in eukaryotes	38	7,0E-21
	KEGG	RNA polymerase	16	1,4E-9
	KEGG	Pyrimidine metabolism	21	1,6E-7
	KEGG	RNA transport	22	2,6E-6
	KEGG	Purine metabolism	21	1,7E-5
	M4	KEGG	Biosynthesis of antibiotics	37
KEGG		Metabolic pathways	74	4,1E-4
KEGG		Biosynthesis of secondary metabolites	41	3,6E-4
KEGG		Biosynthesis of amino acids	23	5,1E-4
KEGG		Lysine biosynthesis	6	1,4E-2
KEGG		2-Oxocarboxylic acid metabolism	9	3,2E-2
M5	GO_BP_TERM	proteasome-mediated ubiquitin-dependent protein catabolic process	10	2,6E-5
	GO_BP_TERM	ubiquitin-dependent protein catabolic process	10	1,7E-4
	GO_BP_TERM	protein folding	10	2,1E-3
	GO_BP_TERM	DNA replication	9	2,4E-3

	Category	Description	Number of genes	q-value
M5 (cont'd)	GO_BP_TERM	positive regulation of proteasomal protein catabolic process	4	5,0E-3
	GO_BP_TERM	'de novo' protein folding	4	5,0E-3
	GO_BP_TERM	protein refolding	5	5,3E-3
	GO_BP_TERM	nucleotide-excision repair	6	5,4E-3
	GO_BP_TERM	ER-associated ubiquitin-dependent protein catabolic process	7	5,9E-3
	GO_BP_TERM	reciprocal meiotic recombination	7	8,8E-3
	GO_BP_TERM	protein catabolic process	5	9,8E-3
	GO_BP_TERM	proteasome regulatory particle assembly	4	1,8E-2
	GO_BP_TERM	positive regulation of RNA polymerase II transcriptional preinitiation complex assembly	4	2,1E-2
	KEGG	Proteasome	14	4,2E-13
	KEGG	DNA replication	6	4,6E-3
	KEGG	Mismatch repair	5	5,6E-3
	KEGG	Base excision repair	4	3,8E-2
	M6	GO_BP_TERM	trehalose biosynthetic process	5
GO_BP_TERM		carbohydrate metabolic process	12	3,0E-3
KEGG		Starch and sucrose metabolism	11	6,0E-8
KEGG		Biosynthesis of secondary metabolites	16	5,0E-3
KEGG		Biosynthesis of antibiotics	13	8,8E-3
KEGG		Metabolic pathways	24	1,5E-2
KEGG		Carbon metabolism	8	4,9E-2
M7	GO_BP_TERM	cellular amino acid biosynthetic process	11	7,7E-5
	GO_BP_TERM	histidine biosynthetic process	4	2,3E-2
	GO_BP_TERM	arginine biosynthetic process	4	2,1E-2
	GO_BP_TERM	biosynthetic process	5	3,0E-2
	KEGG	Biosynthesis of secondary metabolites	16	1,5E-5
	KEGG	Biosynthesis of amino acids	10	1,8E-4
	KEGG	Metabolic pathways	20	7,0E-4
	KEGG	Histidine metabolism	4	3,9E-3
M10	GO_BP_TERM	cell cycle	12	1,4E-5
	GO_BP_TERM	cell division	10	1,6E-5
	GO_BP_TERM	mitotic nuclear division	8	1,0E-4
	GO_BP_TERM	mitotic sister chromatid cohesion	5	3,2E-4
	GO_BP_TERM	morphogenesis checkpoint	3	3,3E-3
	KEGG	Cell cycle - yeast	11	4,9E-10
	KEGG	Meiosis - yeast	7	2,0E-4
	M12	GO_BP_TERM	ribosome biogenesis	17
GO_BP_TERM		rRNA processing	12	5,2E-7
GO_BP_TERM		maturation of SSU-rRNA from tricistronic rRNA transcript (SSU-rRNA, 5.8S rRNA, LSU-rRNA)	7	7,8E-5
GO_BP_TERM		rRNA methylation	6	4,2E-4
GO_BP_TERM		endonucleolytic cleavage in 5'-ETS of tricistronic rRNA transcript (SSU-rRNA, 5.8S rRNA, LSU-rRNA)	4	1,2E-2

	Category	Description	Number of genes	q-value
M12 (cont'd)	GO_BP_TERM	endonucleolytic cleavage to generate mature 5'-end of SSU-rRNA from (SSU-rRNA, 5.8S rRNA, LSU-rRNA)	4	1,1E-2
	KEGG	Ribosome biogenesis in eukaryotes	7	1,6E-5
M13	GO_BP_TERM	methionine biosynthetic process	4	3,7E-2
	GO_BP_TERM	cellular amino acid biosynthetic process	5	4,2E-2
	GO_BP_TERM	sulfate assimilation	3	2,9E-2