

## Supplementary Materials Legends

### **S1 Fig. Neither *rpc128-1007*, nor *maf1Δ* are auxotrophic for glutamate.**

Yeast strains MB159-4D (WT), *maf1Δ* and *rpc128-1007* were grown overnight in rich medium supplemented with 2% glucose. The cells were washed twice with minimal medium supplemented with 2% glucose without glutamate or glutamine and diluted to appropriate  $D_{600}$ . Cells dilutions were spotted on solid synthetic minimal medium supplemented with 2% glucose and basics amino acids either without (A) or with addition of 100 mg/L glutamate and incubated at 30°C for 2 days. Growth curves (C) for tested strains were measured in the same media (minimal medium supplemented with 2% glucose and basics amino acids without or with the addition of glutamate) at 30°C for several hours. Experiments were carried out for two independent biological replicates.

### **S2 Fig. Real-time quantitative PCR analyses of *LEU3* gene transcript.**

Slight increase in *LEU3* transcript levels was observed in *rpc128-1007* in glucose medium. Opposite effect was observed on glycerol-based rich medium. Maf1 deficiency cause 2-fold decrease in *LEU3* mRNA levels, when grown non-fermentative carbon source and reduced in glucose-based rich medium. Yeast cells were grown in 2% glucose (YPD) or 2% glycerol (YPGly) rich medium at 30°C until an  $D_{600} \approx 1.0$ . SYBER-Green based Real-Time PCR was performed. The expression level of each target PCR product was normalized to reference genes transcript levels: *U2* spliceosomal RNA (*U2*) and small cytosolic RNA (*SCR1*). The means + standard deviations of the relative expression levels from three independent biological replicates are shown. The value of basal gene expression level of WT strain was assumed as 1.0. Asterisks (\*) indicate  $P$ -values  $\leq 0.05$  determined by t-student test.

### **S1 Table. Mean value for triplicate experiments of fermentative capacity assay of WT and *maf1Δ* cells.**

Results are expressed in mM / g dry weight. 'C-limited' stands for 'carbon-limited conditions'.

**S2 Table. The list of 8 proteins involved in oxidative stress with higher abundance in *maf1Δ* and lowered quantity in *rpc128-1007* mutant in comparison to wild-type reference strain under high glucose conditions according to global proteomics.**

**S3 Table.** The list of 18 proteins regulated by RPN4 that are part of 26S proteasome and its core complex, 20S proteasome, with lowered abundance in *rpc128-1007* mutant in comparison to wild-type reference strain under high glucose conditions according to global proteomics.

**S4 Table.** The list of 73 proteins involved in ribosome biogenesis with lowered abundance in *rpc128-1007* mutant in comparison to wild-type reference strain under high glucose conditions according to global proteomics.

**S1 Table**

Ethanol [mM / g dry weight]	
WT	15.52365
<i>maf1</i> Δ	16.20646
WT C-limited	72.9832
<i>maf1</i> Δ C-limited	84.02746

**S2 Table**

ORF	Protein function
<i>CTT1</i>	Cytosolic catalase.
<i>GAD1</i>	Glutamate decarboxylase.
<i>YPR1</i>	NADPH-dependent aldo-keto reductase.
<i>GRX2</i>	Cytoplasmic glutaredoxin.
<i>RCK2</i>	Protein kinase involved in response to

	oxidative stress.
<i>AHP1</i>	Thiol specific peroxiredoxin.
<i>TRR1</i>	Cytoplasmic thioredoxin reductase.
<i>TSA1</i>	Cytoplasmic thioredoxin peroxidase.

**S3 Table**

ORF	Protein function
<i>RPN5</i>	Subunit of the 26S proteasome lid complexes.
<i>RPN6</i>	26S proteasome non-ATPase regulatory subunit.
<i>RPN9</i>	
<i>RPN10</i>	Non-ATPase base subunit of the 19S RP of the 26S proteasome.
<i>RPN11</i>	Metalloprotease subunit of 19S regulatory particle and part of 26S proteasome lid that couples the deubiquitination and degradation of proteasome substrates.
<i>CIC1</i>	Protein that interacts with proteasome components and has a potential role in proteasome substrate specificity.
<i>UBP6</i>	Ubiquitin-specific protease that is situated in the base subcomplex of the 26S proteasome.
<i>SCL1</i>	Alpha 1 subunit of the 20S proteasome that is involved in the degradation of ubiquitinated substrates.
<i>RPT1</i>	ATPase of the 19S regulatory particle of the 26S proteasome.
<i>RPT3</i>	
<i>PUP1</i>	Beta 2 subunit of the 20S proteasome that is endopeptidase with trypsin-like activity that cleaves after basic residues.
<i>RPN2</i>	Subunit of the 26S proteasome and a substrate of the N-acetyltransferase Nat1p.
<i>PRE3</i>	Beta 1 subunit of the 20S proteasome.
<i>PRE4</i>	Beta 7 subunit of the 20S proteasome.
<i>PRE7</i>	Beta 6 subunit of the 20S proteasome.

<i>PRE9</i>	Alpha 3 subunit of the 20S proteasome.
<i>PRE10</i>	Alpha 7 subunit of the 20S proteasome.
<i>PUP2</i>	Alpha 5 subunit of the 20S proteasome.

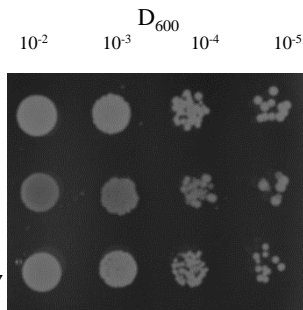
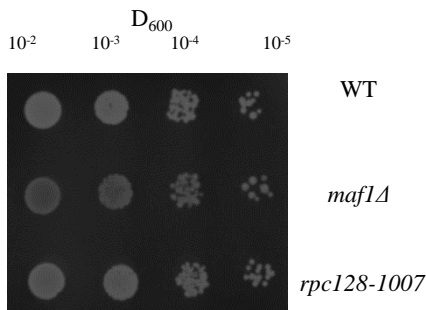
S4 Table

ORF	Protein function
<i>RPS1, RPS2, RPS3, RPS4B, RPS5, RPS6B, RPS7B, RPS9A, RPS9B, RPS11B, RPS12, RPS13, RPS14B, RPS17B, RPS18B, RPS19B, RPS24B, RPS25A, RPS26A, RPS27B, RPS29B, RPS31</i>	Protein component of the small (40S) ribosomal subunit.
<i>RPL1B, RPL2B, RPL3, RPL4A, RPL4B, RPL6A, RPL6B, RPL7A, RPL7B, RPL8B, RPL10, RPL11B, RPL12B, RPL13A, RPL13B, RPL14B, RPL15A, RPL16B, RPL17B, RPL18B, RPL19B, RPL20B, RPL21A, RPL23B, RPL24A, RPL24B, RPL26B, RPL27A, RPL28, RPL31A, RPL32, RPL33A, RPL33B, RPL34A, RPL35B, RPL36A, RPL37B, RPL38, RPL39, RPL42B, RPL43B</i>	Ribosomal 60S subunit protein.
<i>RPP0</i>	Ribosomal protein involved in interaction between translational elongation factors and the ribosome.

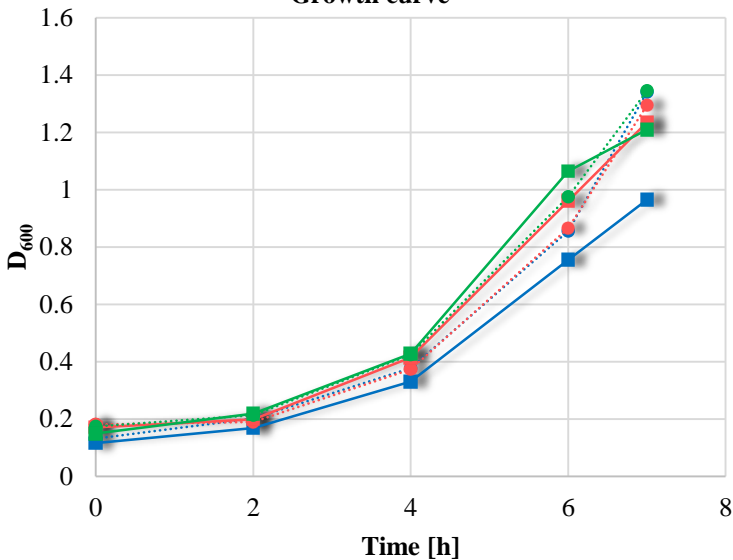
<i>MRT4</i>	Protein involved in mRNA turnover and ribosome assembly.
<i>NOPI</i>	Component of the small subunit processome complex, which is required for processing of pre-18S rRNA.
<i>NOPI2</i>	Nucleolar protein involved in pre-25S rRNA processing, involved in biogenesis of large 60S ribosomal subunit.
<i>HMO1</i>	rDNA-binding component that regulates transcription from RNA polymerase I promoters.
<i>NSR1</i>	Required for pre-rRNA processing and ribosome biogenesis.
<i>ARB1</i>	ATPase of the ATP-binding cassette (ABC) family; involved in 40S and 60S ribosome biogenesis.
<i>SAS10</i>	Involved in production of 18S rRNA and assembly of small ribosomal subunit.
<i>RPP2B</i>	Ribosomal protein P2 beta; a component of the ribosomal stalk.
<i>ASCI</i>	Core component of the small (40S) ribosomal subunit, required to prevent frameshifting at ribosomes stalled at repeated CGA codons.

**A.** Synthetic minimal medium supplemented with 2% glucose and amino acids without glutamate or glutamine

**B.** Synthetic minimal medium supplemented with 2% glucose and 100 mg/L glutamate



**C.** **Growth curve**



.....●..... WT (+Gln)  
 .....●..... *maf1Δ* (+Gln)  
 .....●..... *rpc128-1007* (+Gln)

—■— WT  
 —■— *maf1Δ*  
 —■— *rpc128-1007*

*LEU3*

