Tma108, a putative M1 aminopeptidase, is a specific nascent-chain associated protein in *Saccharomyces cerevisiae. Delaveau et al.*

Description of the additional information

Supplementary methods
Supplementary information for material and method section.

Supplementary Table 1
Yeast strains

Supplementary Table 2
Plasmids and derived strains

Supplementary Table 3
Oligonucleotides used for quantitative PCR

Supplementary Table 4
Proteins used for multiple alignment

Supplementary Table 5
Fig. 1b additional information: Microarray log2 data of mitochondrial extraction experiments

Supplementary Table 6
Fig. 2 additional information: Protein detected with MS analysis in Tma108 immunoprecipitations

Supplementary Table 7
Fig. 3 additional information: Microarray log2 data of Tma128, Scp160, Tma46 and Rpl16a immunoprecipitation experiments

Supplementary Table 8
Fig. 3 additional information: Tma108, Scp160 and Tma46 targets identified with Limma analysis of microarrays data

Supplementary Table 9
Fig. 3 additional information: Microarray enrichment analysis for Gene Ontology compartment

Supplementary Table 10
Fig. 3 additional information: Microarray enrichment analysis for Gene Ontology function

Supplementary Table 11
Fig. 3 additional information: Microarray enrichment analysis for Pfam domains

Supplementary Table 12

Fig. 5 additional information: Protein detected with MS analysis in Tma108, Scp160, Tma108 and Rpl16a immunoprecipitations

Supplementary Data 1
Fig. 4 additional information: Full annotated alignment of Tma108 with M1 aminopeptidases

Supplementary Figure 1
Protein score distribution obtained in mass spectrometry analysis of immunoprecipitation experiments

Supplementary Figure 2
Phylogenic tree showing Tma108, Aap1 et Ape2 orthologues in *Saccharomycetaceae.*

Supplementary Figure 3
Tma108 positioning in a phylogenic tree of M1 aminopeptidases

Supplementary Figure 4
Hypothesis to explain the impact of Tma108 on *ATP2* mRNA localization to mitochondria

Supplementary Figure 5
ATP2 mRNA localization phenotype and functional complementation of Tma108 deletion

Supplementary Figure 6
Surexpression of Tma108 induces a delocalization of ATP2 mRNA

Supplementary Figure 7
Tma108 recognize the N-terminal part of the nascent peptide: control and additional experiments

Supplementary Figure 8
Tma108 deletion does not impact the steady state level of the global proteome