Supplementary information

Table S1: Yeast strains

Stain	Genotype	Origin
BY4741	MATa; his3Δ1; leu2Δ0; met15Δ0; ura3Δ0	Euroscarf (Brachmann et al,1998)
BY4743	MATa/MATα his3Δ1/his3Δ1; leu2Δ0 /leu2Δ0; met15Δ0/MET15; LYS2/lys2Δ 0; ura3Δ0/ura3Δ0	Euroscarf (Brachmann et al,1998)
tma108Δ/TMA108+	MATa/MATα his3Δ1/his3Δ1; leu2Δ0 /leu2Δ0; met15Δ0/MET15; LYS2/lys2Δ 0; ura3Δ0/ura3Δ0: TMA108::KanMX4/ TMA108::KanMX4	Euroscarf (Brachmann et al,1998)
tma108Δ/Δ	MATa/MATα his3Δ1/his3Δ1; leu2Δ0 /leu2Δ0; met15Δ0/MET15; LYS2/lys2Δ 0; ura3Δ0/ura3Δ0: TMA108::KanMX4/ TMA108	Euroscarf (Brachmann et al,1998)
tma7Δ/Δ	MATa/MATα his3Δ1/his3Δ1; leu2Δ0 /leu2Δ0; met15Δ0/MET15; LYS2/lys2Δ 0; ura3Δ0/ura3Δ0: TMA7::KanMX4/ TMA7::KanMX4	Euroscarf (Brachmann et al,1998)
tma19Δ/Δ	MATa/MATα his3Δ1/his3Δ1; leu2Δ0 /leu2Δ0; met15Δ0/MET15; LYS2/lys2Δ 0; ura3Δ0/ura3Δ0: TMA19::KanMX4/ TMA19::KanMX4	Euroscarf (Brachmann et al,1998)
tma22Δ/Δ	MATa/MATα his3Δ1/his3Δ1; leu2Δ0 /leu2Δ0; met15Δ0/MET15; LYS2/lys2Δ 0; ura3Δ0/ura3Δ0: TMA22::KanMX4/ TMA22::KanMX4	Euroscarf (Brachmann et al,1998)
tm46Δ/Δ	MATa/MATα his3Δ1/his3Δ1; leu2Δ0 /leu2Δ0; met15Δ0/MET15; LYS2/lys2Δ 0; ura3Δ0/ura3Δ0: TMA46::KanMX4/ TMA46::KanMX4	Euroscarf (Brachmann et al,1998)
tae1Δ/Δ	MATa/MATα his3Δ1/his3Δ1; leu2Δ0 /leu2Δ0; met15Δ0/MET15; LYS2/lys2Δ 0; ura3Δ0/ura3Δ0: TAE1::KanMX4/ TAE1::KanMX4	Euroscarf (Brachmann et al,1998)
tae2Δ/Δ	MATa/MATα his3Δ1/his3Δ1; leu2Δ0 /leu2Δ0; met15Δ0/MET15; LYS2/lys2Δ 0; ura3Δ0/ura3Δ0: TAE2::KanMX4/ TAE2::KanMX4	Euroscarf (Brachmann et al,1998)
tma20Δ/Δ	MATa/MATα his3Δ1/his3Δ1; leu2Δ0 /leu2Δ0; met15Δ0/MET15; LYS2/lys2Δ 0; ura3Δ0/ura3Δ0: TMA20::KanMX4/ TMA20::KanMX4	Euroscarf (Brachmann et al,1998)
rpl38Δ/Δ	MATa/MATα his3Δ1/his3Δ1; leu2Δ0 /leu2Δ0; met15Δ0/MET15; LYS2/lys2Δ 0; ura3Δ0/ura3Δ0: RPL38::KanMX4/ RPL38::KanMX4	Euroscarf (Brachmann et al,1998)
rps7aΔ/Δ	MATa/MATα his3Δ1/his3Δ1; leu2Δ0 /leu2Δ0; met15Δ0/MET15; LYS2/lys2Δ 0; ura3Δ0/ura3Δ0: RPS7A::KanMX4/ RPS7A::KanMX4	Euroscarf (Brachmann et al,1998)
Tma108-PA	MATa; his3Δ1; leu2Δ0; met15Δ0; ura3Δ0, TMA108-ProtA-His5	This study*[1]
Rpl16A-PA	MATa; his3Δ1; leu2Δ0; met15Δ0; ura3Δ0, RPL16A-ProtA-His5	This study*[1]
Tma46-PA	MATa; his3Δ1; leu2Δ0; met15Δ0; ura3Δ0, TMA46-ProtA-His5	This study*[1]
Scp160-PA	MATa; his3Δ1; leu2Δ0; met15Δ0; ura3Δ0, SCP160-ProtA-His5	This study*[1]
Tma108(MAMQN)-PA	MATa; his3Δ1; leu2Δ0; met15Δ0; ura3Δ0, tma108(E296Q)-ProtA-His5	This study*[2]

*[1]Strains tagged at their C terminus were obtained from BY4741 strain, after classical procedure of Lithium acetate transformation, by homologous recombination with ProtA-His5 cassette amplified from pBXA (Rout et al., 2000 , provided by M. Rout, The Rockefeller, University, New York, NY).

*[2] Genomic DNA of Tma108-PA strain was used to amplify a fragment of TMA108 fused with the ProtA-His5 sequence and carrying the desired mutation added in the forward primer (AGTGACATGGCAATG**C**AGAACTTTGGTATGATCACC) used for the PCR. This mutagenesis cassette was used to modify by homologous recombination TMA108 locus in BY4741 strain. DNA sequencing of TMA108 locus allowed identifying a mutant strain among the 24 clones obtained on the selective plate after the transformation.

Table S2: Plasmids and derived strains

BY4743 strain was transformed with pRS416 derived plasmid pTMA108 and pGTG.

pRS416 derivatived plasmid (origin)	Inserted sequence	Experiment
pTMA108 (origin: This study)	TMA108(-840→3559) PGK1 terminator	Functionnal complementation
PGTG (origin: This study)	GAL1 promotor TMA108(-11→3559) 13myc tag (C terminal) PGK1 terminator	Tma108 overexpression

Tma108-PA strain was transformed with the following pRS416 derived plasmids

pRS416 derivatived plasmid (Origin)	Inserted sequence	Experiment
pZMYA7 (This study)	ZWF1 promotor ASN1(1-1717)-13myc PGK1 terminator	Search of signals required for Tma108 recruitment
pZMYA7M1 (This study)	ZWF1 promotor ASN1(1-1717)-13myc with mutated ATG PGK1 terminator	
pZMYA11 (This study)	ZWF1 promotor ASN1(105-1717)-13myc PGK1 terminator	
pZLG (Garcia et al., embor, 2010)	ZWF1 promotor LacZ PGK1 terminator	
pZLGpn42 (This study)	ZWF1 promotor ASN1(1-35)-LacZ PGK1 terminator	

pZFG pn4 (Garcia et al., embor, 2010)	ZWF1 promotor ATP2(1-1533)-ZTag PGK1 terminator	
pZFGpn4M2 (Garcia et al., embor, 2010)	ZWF1 promotor ATP2(1-1533)-ZTag with frameshift PGK1 terminator	
pZFGpn14 (Garcia et al., embor, 2010)	ZWF1 promotor ATP2(99-1533)-ZTag PGK1 terminator	

Table S3: Oligonucleotides used for quantitative PCR

Gene	**ORF**	**Oligonucléotide Name**	**Sequence 5' →3'**
ATP1	YBL099W	Q_ATP1for	GGGTAGAGTTGTCGACGCTTTAGG
ATP1	YBL099W	Q_ATP1rev	TGACCTCTACCGATAGGGACC
ATP15	YPL271W	Q_ATP15for	GTCTGCCTGGAGGAAAGCTGG
ATP15	YPL271W	Q_ATP15rev	GAGTGGGTTCAGAAGCTGCAG
ATP16	YDL004W	Q_ATP16for	CCTGCCTGCTAAGTCAGGACG
ATP16	YDL004W	Q_ATP16rev	GCGAGTCTGGTTGAACTGTTGC
ATP17	YDR377W	Q_ATP17for	GTTCGGCACCAAATGCCAAGC
ATP17	YDR377W	Q_ATP17rev	GCCACAATGGTTTACCACTAGC
ATP18	YML081C-A	Q_ATP18for	GAAAAGATTCCCTACCCCTATCC
ATP18	YML081C-A	Q_ATP18rev	GCGAATCTGGGATTTCTTGGATC
ATP19	YOL077W-A	Q_ATP19for	CTATCCCTCCACACCAACTAGC
ATP19	YOL077W-A	Q_ATP19rev	CGCATCTTGCTTTTCCGAATGTTTC
ATP2	YJR121W	Q_ATP2for	GTGGTGCAGGTGTCGGTAAGAC
ATP2	YJR121W	Q_ATP2rev	ACGGTACAAGTCATTACCTTCTC
ATP20	YPR020W	Q_ATP20for	CCAGTGGGTTGGTTTCTAAAGC
ATP20	YPR020W	Q_ATP20rev	TTAGAGCAAAGTTTAGGCTCTGC
ATP3	YBR039W	Q_ATP3for	AAGAAGATGGATGAAGCAGAGCAG
ATP3	YBR039W	Q_ATP3rev	CCTTATCAGAGGTGATAGCAAC
ATP4	YPL078C	Q_ATP4for	ACTGTTGAACTTGAAAGCGAAGC
ATP4	YPL078C	Q_ATP4rev	GACTGAACTCTGGAGATGACAG
ATP5	YDR298C	Q_ATP5for	GTGAGATTGTTCGGTGTTGAGG
ATP5	YDR298C	Q_ATP5rev	CTGTCCTTCAATGACAATGCAGG
ACT1	YFL039C	Q_ACTfor	GGTTGCTGCTTTGGTTATTG
ACT1	YFL039C	Q_ACTrev	GACCCATACCGACCATGATAC
TPM2	YIL138C	Q_TPM2for	CGAGCAACTCGACAGTGAAGTGG
TPM2	YIL138C	Q_TPM2rev2	ATCCATTGCTTCCTTCAGTTTGG
JEN1	YKL217W	Q_jen1for	CGAGATTTACGTCCTTACTGC
JEN1	YKL217W	Q_jen1rev	GAGCGACTGATACTGAAACG
FLR1	YBR008C	Q_FLR1for	CGTGGCAATGTGTGTCTGCTGGTGCCT
FLR1	YBR008C	Q_FLR1rev	CCAATGCACTCGAGCAGTCCAACCA

ASN1	YPR145W	S1_asn1for	GACTGTGACACTATCACTGC
ASN1	YPR145W	Q_asn1rev	CGATTAAAGAGGAGTCCAAACC
VMA1	YDL185W	S1_vma1	GAGGTACAATCACTTGGATTGC
VMA1	YDL185W	Q_vma1rev	CCTGGAATACATGTCGTACCACC
ASN1-Myc	/	Q_ASN1for	CCAACCACAAAAGAGGCTTTCTGG
ASN1-Myc	/	Q_ASN1mycrev	GCTTTTGTTCACCGTTAATTAATTCG
LacZ	/	Q_LacZfor	CGTCACGAGCATCATCCTCTGC
LacZ	/	Q_lacZrev	GTCGCACAGCGTGTACCACAGC
ATP2-Ztag	/	Q_lacZpn4for	GGACACCGTTGCCTCGTTCAAAGC
ATP2-Ztag	/	Q_lacZpn4rev	GCTCATCCGCCACATATCCTGATC

Table S4: Proteins used for multiple alignment

M1 metallopeptidases		
Name	**Specie**	**Accession number**
TMA108 [Translation Machinery associated factor 108]	*Saccharomyces cerevisiae*	NP_012129.1
APE2 [Aminopeptidase yscII]	*Saccharomyces cerevisiae*	NP_012765.3
AAP1 [Arginine/alanine amino peptidase]	*Saccharomyces cerevisiae*	NP_011913
PSA [puromycin-sensitive aminopeptidase]	*Homo sapiens*	NP_006301.3
AP-Q [aminopeptidase Q]	*Homo sapiens*	NP_776161.3
Ap-N [aminopeptidase N]	*Homo sapiens*	AAA51719.1
TRH-DE [thyrotropin-releasing hormone degrading enzyme]	*Homo sapiens*	EAW97281.1
Ap-A [aminopeptidase A]	*Homo sapiens*	CAP09201.1
ERAP1 [endoplasmic reticulum aminopeptidase 1]	*Homo sapiens*	NP_057526.3
ERAP2 [endoplasmic reticulum aminopeptidase 2]	*Homo sapiens*	XP_011541846.1
ePepN [E. coli Aminopeptidase N]	*Escherichia coli*	P04825
IRAP [oxytocinase/insulin-responsive aminopeptidase]	*Homo sapiens*	CAB94753.1
LTA4H [Human Leukotriene A4 Hydrolase]	*Homo sapiens*	3U9W
Ap-B [aminopeptidase B]	*Homo sapiens*	CAC14047.1
RNPEP-L1 [arginyl aminopeptidase-like 1]	*Homo sapiens*	NP_060696.4
TMA108 orthologues		
Specie		**Accession number**
Saccharomyces bayanus		AACG02000025
Zygosaccharomyces rouxii		*XP_002496293*
Kluyveromyces lactis		*XP_454307*
Lachancea thermotolerans		*XP_002555415*
Saccharomyces kluyveri		*AACE03000003*
Ashbya gossypii		*NP_985281*
Candida glabrata		*XP_449140*
Naumovozyma castellii		*XP_003675117*
Vanderwaltozyma polyspora		*XP_001647329*
Kazachstania africana		*XP_003959375*
Debaryomyces hansenii		*XP_457134*
Scheffersomyces stipitis		*XP_001383787*

Millerozyma farinosa	*XP_004204526*
Meyerozyma guilliermondii	*EDK39075*
Spathaspora passalidarum	*EGW30536*
Candida tropicalis	*XP_002548472*
Clavispora lusitaniae	*XP_002616570*

Mass spectrometry procedure

Digestion was performed overnight at 37°C in the presence of 12.5 µg/ml of sequencing grade trypsin (Promega, Madison, Wi, USA). Digests were analyzed by a LTQ Velos Orbitrap (Thermo Fisher Scientific, San Jose, CA) coupled to an Easy nano-LC Proxeon system (Thermo Fisher Scientific, San Jose, CA). Chromatographic separation of peptides was performed with the following parameters: column Easy Column Proxeon C18 (10 cm, 75 µm i.d., 120 Å), 300nl/min flow, gradient rising from 95 % solvent A (water - 0.1% formic acid) to 25% B (100 % acetonitrile, 0.1% formic acid) in 20 min, then to 45% B in 40 min and finally to 80% B in 10 min. Peptides were analyzed in the Orbitrap in full ion scan mode at a resolution of 30,000 and a mass range of 400-1800 m/z. Fragments were obtained with a collision-induced dissociation (CID) activation with a collisional energy of 40%, an activation Q of 0.25 for 10 ms, and analyzed in the LTQ. MS/MS data were acquired in a data dependent mode in which 20 most intense precursor ions were isolated, with a dynamic exclusion of 20 seconds and an exclusion mass width of 10 ppm. Data were processed with Proteome Discoverer 1.4 software (Thermo Fisher scientific, San Jose, CA) coupled to an in-house Mascot search server (Matrix Science, Boston, MA; version 2.4.1). The mass tolerance of fragment ions was set to 7 ppm for precursor ions and 0.5 Dalton for fragments. The following modifications were considered in mass calculation: oxidation (M), phosphorylations (STY), acetylation (Nterm, K), deamidation (NQ). The maximum number of missed cleavages was limited to 2 for trypsin digestion. MS/MS data were searched against the SwissProt database with the S.cerevisiae taxonomy.