## **Supplemental Tables**

Name	Sequence	Purpose	
I vuille	Sequence	rupose	
oli 2078	AATACTCGAGTTAGTTGTCTTTGCAGTTTC	Rvs. ALA2 stop ( <i>XhoI</i> )	
oli 2953	GTAGAGACTGCAGCTTTAGATGGTCAAACTGATCTCAA AACAAGAGTG	Fwd ala2E159Q	
oli 2954	CACTCTTGTTTTGAGATCAGTTTGACCATCTAAAGCTGC AGTCTCTAC	Rvs ala2E159Q	
oli 2390	ATTGCATGCATGTACCCATACGATGTTCCAGATTACGCT GAATTTTCTTCCGAAGAACTTGTGG	Fwd ALA2 start ( <i>SphI</i> , HA-tag)	
oli3422	GAATTCTTATGAAGCGTTTTGTGTACATTAACG	Fwd on ALA2 start ( <i>BamHI</i> )	
oli3423	GAGCTCTTAGTTGTCTTTGCAGTTTCTGG	Rvs ALA2 stop	

## Supplemental Table S2. List of plasmids used in this study.

Plasmid	Description	Source or
		Reference <sup>#</sup>
pRS423-GAL	HIS3-based S. cerevisiae expression vector	[1]
pRS426-GAL	URA3-based S. cerevisiae expression vector	[1]
pMP3157	Modified pRS423-GAL containing an RGSH10-thrombin	[2]
	cleavage-3gly motif on the EcoRI side of the polylinker	
pMP3395	ALA2 in pMP3157	[3]
pMP2766	HA-ala2D381N in pRS423-GAL	[4]
pMP3836	FLAG-ALIS5 in pRS426-GAL	This study
pMP3681	Modified pRS423-GAL containing RGSH10-ALA2	This study
	and FLAG-ALIS5	
pMP3464	HA-ala2E159Q in pRS423-GAL	This study
pMP4131	FLAG-ala2E159Q in pRS423-GAL	This study

## <sup>#</sup>Reference list to Supplemental Table S2:

- 1 Burgers, P. M. J. (1999) Overexpression of Multisubunit Replication Factors in Yeast. Methods 18, 349-355.
- 2 Costa, S. R. R., Marek, M., Axelsen, K. B., Theorin, L., Pomorski, T. G. and Lopez-Marques, R. L. (2016) Role of post-translational modifications at the -subunit ectodomain in complex association with a promiscuous plant P4-ATPase. Biochem. J. 473, 1605–1615.
- 3 Poulsen, L. R., López-Marqués, R. L., Pedas, P. R., McDowell, S. C., Brown, E., Kunze, R., Harper, J. F., Pomorski, T. G. and Palmgren, M. (2015) A phospholipid uptake system in the model plant Arabidopsis thaliana. Nat. Commun. 6, 7649.
- 4 López-Marqués, R. L., Poulsen, L. R., Hanisch, S., Meffert, K., Buch-pedersen, M. J., Jakobsen, M. K., Pomorski, T. G. and Palmgren, M. G. (2010) Intracellular targeting signals and lipid specificity determinants of the ALA/ALIS P4-ATPase complex reside in the catalytic ALA alpha-subunit. Mol. Biol. Cell **21**, 791–801.

	Digitonin <sup>1</sup>		DDM <sup>2</sup>	
Protein	Peptides identified	Sequence coverage [%]	Peptides identified	Sequence coverage [%]
ALA2	93	73.2	62	55.6
ALIS5	34	66.9	17	40.9
Ssa1p	60	83.3	42	65.7
Tom40p	30	95.3	12	53.2
Fet4p	29	46.7	22	33.9
Tom22p	13	72.4	1	11.2
Kar2p	56	60.4	43	48.2
Rps31p/Ubi4p	11	60.5	6	35.5
Rpl2ap	30	79.5	16	64.6
Rpp0p	18	52.6	9	30.4
Hsc82p	52	70.4	29	38.3
Rpl4ap	27	75.4	18	50.3
Ssb1p	39	52.5	28	50.2
Rpl16bp	38	72.8	12	45.7
Por1p	24	68.2	14	62.5
Rpl8bp	22	94.0	21	64.1
Pma1p	28	73.4	28	32.8
Yos9p	23	46.7	9	18.5
Pdr12p	61	50.0	31	24.2

**Supplemental Table S3.** Proteins which co-purify with the ALA2-ALIS5 complex identified by mass spectrometry.

<sup>1</sup>Yeast membranes co-expressing FLAG-ALIS5 and His<sub>10</sub>-tagged ALA2 were solubilized with 1% (w/v) digitonin and subjected to anti-FLAG affinity chromatography followed by ESI mass spectrometry analysis.

<sup>2</sup>Yeast membranes co-expressing FLAG-ALIS5 and  $His_{10}$ -tagged ALA2 were solubilized with 0.8% (w/v) DDM and subjected to anti-FLAG affinity chromatography followed by ESI mass spectrometry analysis.