Supplemental Table S1. Sequences of primers used for quantitative real-time as well as sizes and melting temperatures of amplicons. Primer sets were designed using Primer Express™ from Applied Biosystems. All used primers were obtained from DNA technology.

Gene	Upstream primer (5`→3`)	Downstream primer (5`→3`)	T_M (°C)	Product size (bp)
ACT1	GAA ACT TTC AAC GTT CCA GCC TT	AGG ACA AAA CGG CTT GGA TG	79	52
CHO1	CGA AAA TGA CGG GTA TGC CT	CTT CTG CTT AAT GTG CCA CCA A	79	51
CHO2	CTT TCA AAC CAC CTG TAA CCC AC	TTG GAT CGA AAA GCG AAC G	79	51
CKA2	CTC CAT GGG CAT AAT GCA CA	TCA ATC ATG ACA TTC TGA GGC TTT	78	51
CTT1	CGT TGG TGG TGA AAG TGG TAC A	ACA CCT CTT GGG TCT CTT GCA	81	51
DDR2	CTG TCT TCG GCC TCG CTA CT	TGG TGT TGG ATG CGT TTT GA	80	51
ELO1	TCG CTT CCA GCC AAA GGA T	CTC AAA GGC TGC TTC CCA AC	80	51
ERG11	CGC TAA GTT GGC AGA TGT TTC AG	GTA GTC AAA TGA GCG TAA GCA GCT	79	51
FAS1	CTT GCC AGG TAC TAT CAC GCA C	GCA CGG ACG GAA GCA GAA	81	51
FAS2	ACC AGT TGA TGA CAA GGA CGT TAA G	TCT AGG ATT GAT GTT TCA TAC TTG GC	76	51
GPD1	TCA AGG TTG CTA GGC TAA TGG C	CAC ATT CCC AGG CGT CCT TA	80	51
HSP12	ACA AGG TCG CTG GTA AGG TTC A	CTT GGA AGA CAC CCT TGT TGT CT	80	51
HSP26	GGA CCA TGA CAA CAA CTA CGA GTT	GCT TTT GAC ACC AGG AAC CAC	79	52
HSP104	AGG ATT CTG GAT AGC GCC TTA GT	GTA ACG CTT GGC TAA TTG AGC A	80	51
INO1	GCT GAG CAT GAG GGT ACA TTC A	TTG TCC CGA CTT GAG ATC GTC	81	51
INO2	GTT ACC CAC AAA CAC AGC AGA TG	CCT TCC CTC GTG GTG AAC TC	81	51
INO4	AGC GAT CCC GTA CAA GAA CAA	CTC CTT CGG TAC TAA ATC CCG AAT	78	54
OLE1	TAG GTA AGG ACG CTA CCA AGG C	TTG AGT GAC GGT AGA CAC CAC C	80	51
OPI1	CAA GCT GAA CAT GTC CAT CGA	TGC AAG CAC GTT ACA AGC CT	79	51
OPI3	AAC AAC CCC ATG TAC CAG GGT	AAG GGC TAT GCC CAA GAA GG	80	51
PEP4	GCT GAG GCT ACC AGC GAG C	CAT CGA ACT TGC CAA ATG CA	82	52
PIS1	AGA CGG AAC CAT GGC AAG AA	ACG GCA CCC AGA CTG GAA	80	51
PSD1	TTC AGC AAC GAC GCA GTT CT	CAG CAG CTT TGG CAC GAT C	81	51
PSD2	AGG AAG GAC ACC ACG ACG AG	GGT ACC GCT GAG CTT CAA TTG	79	52
TDH1	GTT TCC CAT GAC GAC AAG GA	GGT AGC GAT CTT GAC ACC ATC AA	79	51
HAC1	CCC ACT CTG CGA CGA TAT AGC	ACC TGA CTG CGC TTC TGG AT	79	91

Supplemental Table S2. A list of some of the most upregulated and downregulated genes obtained in response to Acb1p depletion. Fold- upregulation and downregulation of genes in response to Acb1p depletion are represented by positive- and negative values, respectively. Each value is an average of results obtained from two microarrays (dye reversal). Wild type and Acb1p depleted cells were grown in YPD media.

GeneID	Gene	Function	Process	Fold change[a] ± S.D.
Stress response				
ydr001c	NTH1	neutral trehalase (alpha,alpha-trehalase)	response to stress; trehalose catabolism	3.9 ± 0.83
yll039c	UBI4	ubiquitin	response to stress; protein deubiquitination; protein monoubiquitination; protein polyubiquitination	3.6 ± 0.96
ymr251w-a	HOR7	hyperosmolarity-responsive protein	response to stress	5.6 ± 1.3
yol052c-a	DDR2	heat shock protein DDRA2	response to stress	6.9 ± 0.71
Lipid metabolism				
ygl001c	ERG26	C-3 sterol dehydrogenase (C-4 decarboxylase)	ergosterol biosynthesis	-1.6 ± 0.08
ygl055w	OLE1	stearoyl-CoA desaturase	fatty acid desaturation; mitochondrion inheritance	1.9 ± 0.75
ygr037c	ACB1	acyl-coenzyme-A-binding protein(diazepam binding inhibitor)	fatty acid metabolism; long- chain fatty acid transport	-11.5 ± 2.5
ygr177c	ATF2	alcohol O-acetyltransferase	steroid metabolism	-1.7 ± 0.49
ykl182w	FAS1	fatty-acyl-CoA synthase, beta chain	fatty acid biosynthesis	1.6 ± 0.25
ylr056w	ERG3	C-5 sterol desaturase	ergosterol biosynthesis	-1.9 ± 0.15
ynr016c	ACC1	acetyl-CoA carboxylase	fatty acid biosynthesis	1.6 ± 0.33
ypl028w	ERG10	acetyl-CoA C-acetyltransferase, cytosolic	ergosterol biosynthesis	1.6 ± 0.14
ypl117c	IDI1	isopentenyl-diphosphate delta-isomerase	ergosterol biosynthesis	1.8 ± 0.72
ypl170w	DAP1	similarity to C.elegans LIM homeobox protein	sterol metabolism	2.5 ± 0.37
ypl231w	FAS2	fatty-acyl-CoA synthase, alpha chain	fatty acid biosynthesis	1.8 ± 0.17
Protein sorting				
ynl044w	YIP3	protein of unknown function	ER to Golgi transport	1.7 ± 0.35
ynl263c	YIF1	Slh1p Interacting Factor	ER to Golgi transport	1.7 ± 0.12
yor216c	RUD3	suppressor of USO1-1 transport defect	ER to Golgi transport	-2.1 ± 0.18
Proteolysis				
ypl154c	PEP4	aspartyl protease	vacuolar protein catabolism; cellular response to starvation; sporulation; microautophagy	1.8 ± 0.14
C-compound and Carbohydrate metabolism				
ydl022w	GPD1	glycerol-3-phosphate dehydrogenase (NAD+), cytoplasmic	intracellular accumulation of glycerol	6.4 ± 1.8
yjl052w	TDH1	glyceraldehyde-3-phosphate dehydrogenase 1	glycolysis; gluconeogenesis	4.8 ± 0.16
Sphingolipid/ceramide metabolism				
ykl004w	AUR1	aureobasidin-resistance protein	sphingolipid metabolism	2.3 ± 0.68
Transporters/permeases				
ydr497c	ITR1	myo-inositol permease, major	myo-inositol transport	2.2 ± 0.16
ygl077c	HNM1	choline permease	choline transport	2.4 ± 0.59
ygl255w	ZRT1	high-affinity zinc transport protein	high-affinity zinc ion transport	-2.8 ± 0.64
ylr130c	ZRT2	low affininty zinc transporter	low-affinity zinc ion transport	-1.8 ± 0.59
ymr243c	ZRC1	zinc- and cadmium resistance protein	zinc ion transport; cobalt ion transport; zinc ion homeostasis; glutathione metabolism	-1.7 ± 0.10
ynl055c	POR1	mitochondrial outer membrane porin	aerobic respiration; ion transport; mitochondrion organization and biogenesis	2.2 ± 0.72
Phospholipid metabolism				
yer026c	CHO1	CDP-diacylglycerol serine O-phosphatidyl-transferase	phosphatidylserine biosynthesis	1.8 ± 0.24
ygr157w	CHO2	phosphatidylethanolamine N-methyltransferase	phosphatidylcholine biosynthesis	1.8 ± 0.51
yjr073c	OPI3	methylene-fatty-acyl-phospholipid synthase	phosphatidylcholine biosynthesis	2.9 ± 0.68
Protein folding				
ycl043c	PDI1	protein disulfide-isomerase precursor	protein folding	2.2 ± 0.17
yjl034w	KAR2	nuclear fusion protein	response to unfolded protein	1.9 ± 0.98
ylr350w	ORM2	strong similarity to ORM1	response to unfolded protein	2.8 ± 0.43

[a] Positive values correspond to gene expression that is negatively affected by *ACB1* (increased in Acb1p depleted cells). Negative values correspond to gene expression that is positively affected by *ACB1* (decreased in Acb1p depleted cells). S.D. indicates standard deviation of two independent experiments.

Supplementary data S3. Distribution of PI species in Y700 *pGAL-ACB1* and Y700 cells.

Strain	Molecular species[1] 28:0	30:0	30:1	32:0	32:1	34:1	34:2	36:1
YPD media								
Y700[2]	0.12 ± 0.03	0.20 ± 0.07	0.02 ± 0.01	1.28 ± 0.06	0.19 ± 0.02	3.40 ± 0.49	0.67 ± 0.002	1.15 ± 0.33
Percent[3]	1.6 ± 0.56	2.8 ± 1.18	0.3 ± 0.05	17.1 ± 1.02	2.6 ± 0.04	45.2 ± 1.64	9.0 ± 0.94	15.1 ± 2.77
Y700 *pGAL-ACB1*[2]	0.82 ± 0.25	0.87 ± 0.13	0.43 ± 0.13	1.74 ± 0.26	1.24 ± 0.04	1.89 ± 0.19	1.68 ± 0.34	0.63 ± 0.01
Percent[3]	8.3 ± 2.89	8.8 ± 1.65	4.4 ± 1.51	17.6 ± 1.97	12.6 ± 0.10	19.1 ± 1.18	16.9 ± 2.74	6.3 ± 0.16
SC media (+ ino.)[4]								
Y700[2]	0.18 ± 0.16	0.36 ± 0.33	0.04 ± 0.05	1.98 ± 1.55	0.38 ± 0.33	2.99 ± 2.42	0.49 ± 0.39	0.75 ± 0.58
Percent[3]	2.4 ± 0.27	4.5 ± 0.75	0.5 ± 0.25	26.9 ± 1.04	4.9 ± 0.44	40.2 ± 0.07	6.6 ± 0.16	10.3 ± 0.56
Y700 *pGAL-ACB1*[2]	0.45 ± 0.37	0.44 ± 0.29	0.22 ± 0.16	1.11 ± 0.97	0.92 ± 0.64	1.17 ± 0.91	0.95 ± 0.69	0.27 ± 0.22
Percent[3]	7.5 ± 0.61	7.8 ± 0.94	3.8 ± 0.18	17.8 ± 2.95	16.2 ± 1.48	19.9 ± 0.37	16.5 ± 0.87	4.6 ± 0.19
SC media (- ino.)[5]								
Y700[2]	0.05 ± 0.06	0.11 ± 0.08	0.01 ± 0.01	0.51 ± 0.46	0.06 ± 0.06	0.66 ± 0.63	0.07 ± 0.07	0.17 ± 0.19
Percent[3]	2.8 ± 0.57	7.4 ± 2.17	0.6 ± 0.01	31.3 ± 3.48	3.4 ± 0.003	37.8 ± 0.46	3.8 ± 0.31	8.1 ± 3.23
Y700 *pGAL-ACB1*[2]	0.39 ± 0.41	0.61 ± 0.63	0.22 ± 0.23	0.74 ± 0.65	0.51 ± 0.45	0.66 ± 0.53	0.40 ± 0.37	0.18 ± 0.19
Percent	9.0 ± 2.25	14.6 ± 2.52	5.2 ± 1.14	19.8 ± 1.65	13.4 ± 0.78	18.9 ± 3.98	10.6 ± 0.46	4.1 ± 1.02

[1] Only molecular species constituting 3 % or more, in at least one of the used growth conditions, are shown.
[2] The $^{12}C/^{13}C$ ratio between ion counts for each individual ^{12}C-species and one selected ^{13}C-specie in each lipid class.
[3] Percent that each species constitute of the total phospholipid class.
[4] SC media supplemented with 0.2 mM inositol.
[5] SC media without inositol.

Supplementary data S4. Distribution of PC species in Y700 *pGAL-ACB1* and Y700 cells.

Strain	Molecular species[1] 28:1	30:1	30:2	32:1	32:2	34:1	34:2	36:2
YPD media								
Y700[2]	0.14 ± 0.01	0.20 ± 0.01	0.12 ± 0.02	0.53 ± 0.18	2.69 ± 0.12	0.44 ± 0.04	4.15 ± 0.26	0.89 ± 0.18
Percent[3]	1.5 ± 0.20	2.1 ± 0.01	1.2 ± 0.07	5.4 ± 1.48	28.0 ± 0.87	4.5 ± 0.11	43.1 ± 0.53	9.2 ± 1.20
Y700 *pGAL-ACB1*[2]	0.31 ± 0.10	0.21 ± 0.07	0.54 ± 0.07	0.28 ± 0.11	3.71 ± 0.75	0.20 ± 0.02	3.30 ± 0.73	0.59 ± 0.21
Percent[3]	3.2 ± 0.37	2.2 ± 0.24	5.6 ± 0.52	2.8 ± 0.50	38.2 ± 0.70	2.1 ± 0.26	33.9 ± 0.01	6.0 ± 0.83
SC media (+ ino.)[4]								
Y700[1]	0.13 ± 0.09	0.12 ± 0.005	0.14 ± 0.08	0.40 ± 0.25	3.36 ± 1.43	0.32 ± 0.22	4.68 ± 2.31	0.40 ± 0.07
Percent[3]	1.2 ± 0.29	1.3 ± 0.59	1.4 ± 0.14	3.8 ± 0.69	34.3 ± 2.29	3.0 ± 0.77	46.9 ± 0.47	4.4 ± 1.39
Y700 *pGAL-ACB1*[2]	0.23 ± 0.08	0.22 ± 0.12	0.45 ± 0.18	0.29 ± 0.12	3.80 ± 1.33	0.28 ± 0.33	3.12 ± 0.43	0.40 ± 0.01
Percent[3]	2.5 ± 0.16	2.3 ± 0.56	4.8 ± 0.50	3.1 ± 0.36	41.1 ± 1.58	2.6 ± 2.75	34.9 ± 6.23	4.6 ± 1.48
SC media (- ino.)[5]								
Y700[2]	0.16 ± 0.06	0.84 ± 0.59	0.07 ± 0.003	2.95 ± 0.87	2.94 ± 0.94	2.21 ± 0.96	3.31 ± 0.86	0.46 ± 0.20
Percent[3]	1.2 ± 0.03	5.8 ± 2.42	0.5 ± 0.20	22.0 ± 1.00	21.9 ± 0.49	16.1 ± 1.64	24.9 ± 2.08	3.3 ± 0.34
Y700 *pGAL-ACB1*[2]	0.37 ± 0.07	0.60 ± 0.07	0.57 ± 0.06	1.14 ± 0.23	4.45 ± 1.22	0.58 ± 0.28	4.44 ± 0.41	0.58 ± 0.03
Percent[3]	2.8 ± 0.01	4.6 ± 0.37	4.3 ± 0.35	8.7 ± 0.13	33.5 ± 2.95	4.2 ± 1.34	33.9 ± 3.23	4.4 ± 0.63

[1] Only molecular species constituting 3 % or more, in at least one of the used growth conditions, are shown.
[2] The $^{12}C/^{13}C$ ratio between ion counts for each individual ^{12}C-species and one selected ^{13}C-specie in each lipid class.
[3] Percent that each species constitute of the total phospholipid class.
[4] SC media supplemented with 0.2 mM inositol.
[5] SC media without inositol.

Supplementary data S5. Distribution of PE species in Y700 *pGAL-ACB1* and Y700 cells.

Strain	Molecular species[1] 32:1	32:2	34:1	34:2	36:1	36:2	38:0	38:2
YPD media								
Y700[2]	0.38 ± 0.04	0.61 ± 0.17	1.02 ± 0.11	3.28 ± 0.39	0.19 ± 0.08	1.39 ± 0.24	0.39 ± 0.54	0.15 ± 0.12
Percent[3]	5.0 ± 0.76	8.1 ± 2.62	13.5 ± 2.13	43.4 ± 7.5	2.4 ± 0.93	18.3 ± 2.15	5.0 ± 6.86	2.0 ± 1.41
Y700 *pGAL-ACB1*[2]	0.60 ± 0.22	1.83 ± 0.69	0.66 ± 0.08	3.98 ± 0.38	0.08 ± 0.02	1.04 ± 0.32	0.65 ± 0.90	0.11 ± 0.08
Percent[3]	6.3 ± 2.33	19.2 ± 7.22	6.9 ± 0.85	41.7 ± 3.87	0.8 ± 0.26	10.9 ± 3.41	6.8 ± 9.45	1.2 ± 0.89
SC media (+ ino.)[4]								
Y700[2]	0.42 ± 0.37	0.71 ± 0.63	0.82 ± 0.68	2.70 ± 2.13	0.17 ± 0.13	1.79 ± 1.63	0.65 ± 0.51	0.43 ± 0.28
Percent[3]	5.2 ± 0.29	8.6 ± 0.82	10.4 ± 0.02	34.4 ± 1.67	2.3 ± 0.22	21.5 ± 2.67	8.5 ± 0.63	6.1 ± 1.53
Y700 *pGAL-ACB1*[2]	0.24 ± 0.16	0.75 ± 0.53	0.25 ± 0.28	2.07 ± 1.31	0.10 ± 0.10	1.02 ± 0.69	0.58 ± 0.32	0.34 ± 0.11
Percent[3]	4.2 ± 0.05	12.9 ± 1.03	3.6 ± 2.69	37.1 ± 0.95	1.6 ± 0.69	18.0 ± 0.42	10.8 ± 1.42	6.9 ± 2.61
SC media (- ino.)[5]								
Y700[2]	0.52 ± 0.47	0.42 ± 0.29	1.08 ± 0.83	1.74 ± 1.20	0.44 ± 0.35	0.83 ± 0.64	0.40 ± 0.19	0.27 ± 0.11
Percent[3]	7.9 ± 2.14	7.1 ± 0.27	17.6 ± 1.14	29.5 ± 1.07	7.2 ± 0.72	13.6 ± 1.05	7.4 ± 2.12	5.2 ± 1.88
Y700 *pGAL-ACB1*[2]	0.60 ± 0.54	1.06 ± 1.11	0.91 ± 0.86	2.83 ± 2.43	0.32 ± 0.29	1.36 ± 1.05	0.77 ± 0.49	0.42 ± 0.18
Percent[3]	5.2 ± 1.37	10.7 ± 4.16	7.0 ± 2.16	34.0 ± 3.48	2.7 ± 0.93	17.9 ± 0.54	11.0 ± 1.69	6.7 ± 2.20

[1] Only molecular species constituting 3 % or more, in at least one of the used growth conditions, are shown.
[2] The $^{12}C/^{13}C$ ratio between ion counts for each individual ^{12}C-species and one selected ^{13}C-specie in each lipid class.
[3] Percent that each species constitute of the total phospholipid class.
[4] SC media supplemented with 0.2 mM inositol.
[5] SC media without inositol.

Supplementary data S6. Distribution of PG species in Y700 *pGAL-ACB1* and Y700 cells.

Strain	Molecular species[1] 28:0	30:1	32:1	32:2	34:1	34:2	36:1	36:2
YPD media								
Y700[2]	0.12 ± 0.08	0.18 ± 0.08	1.41 ± 0.66	0.56 ± 0.03	4.21 ± 0.33	1.75 ± 0.03	0.44 ± 0.11	0.45 ± 0.11
Percent[3]	1.2 ± 0.64	1.8 ± 0.51	14 ± 4.72	5.8 ± 0.54	43.2 ± 3.00	18.0 ± 2.33	4.5 ± 0.50	4.5 ± 0.43
Y700 *pGAL-ACB1*[2]	0.16 ± 0.08	0.46 ± 0.06	1.07 ± 0.10	1.18 ± 0.08	1.32 ± 0.27	1.77 ± 0.18	0.19 ± 0.05	0.69 ± 0.10
Percent[3]	2.0 ± 1.07	5.8 ± 1.15	13.2 ± 0.39	14.5 ± 0.02	16.5 ± 4.42	21.8 ± 0.79	2.4 ± 0.48	8.5 ± 0.69
SC media (+ ino.)[4]								
Y700[2]	0.28 ± 0.15	0.53 ± 0.58	2.21 ± 2.46	1.38 ± 1.72	4.14 ± 4.30	2.09 ± 2.24	0.44 ± 0.50	0.59 ± 0.52
Percent[3]	3.4 ± 2.46	3.9 ± 0.29	15.4 ± 2.48	8.1 ± 4.53	31.8 ± 0.78	15.4 ± 0.80	2.9 ± 0.71	5.3 ± 1.62
Y700 *pGAL-ACB1*[2]	0.11 ± 0.11	0.20 ± 0.24	0.57 ± 0.80	0.51 ± 0.55	1.35 ± 1.36	0.95 ± 0.62	0.16 ± 0.14	0.30 ± 0.01
Percent[3]	2.0 ± 0.14	3.1 ± 1.65	6.4 ± 9.08	8.8 ± 1.99	24.8 ± 1.86	22.9 ± 10.3	3.0 ± 0.17	10.8 ± 10.7
SC media (- ino.)[5]								
Y700[2]	0.84 ± 0.82	0.84 ± 0.68	7.34 ± 5.28	1.10 ± 1.03	11.5 ± 8.91	2.43 ± 1.22	0.43 ± 0.33	1.18 ± 0.40
Percent[3]	2.6 ± 1.02	2.9 ± 0.34	26.4 ± 0.33	3.6 ± 1.08	40.1 ± 2.66	9.7 ± 2.67	1.5 ± 0.07	6.4 ± 6.11
Y700 *pGAL-ACB1*[2]	0.52 ± 0.62	1.26 ± 1.30	2.62 ± 2.09	2.88 ± 3.10	4.11 ± 3.24	4.00 ± 2.99	0.43 ± 0.46	1.27 ± 0.29
Percent[3]	2.1 ± 1.66	5.9 ± 2.25	14.2 ± 0.23	13.0 ± 6.19	22.4 ± 0.67	22.3 ± 1.87	2.0 ± 0.87	11.1 ± 10.5

[1] Only molecular species constituting 3 % or more, in at least one of the used growth conditions, are shown.
[2] The $^{12}C/^{13}C$ ratio between ion counts for each individual ^{12}C-species and one selected ^{13}C-specie in each lipid class.
[3] Percent that each species constitute of the total phospholipid class.
[4] SC media supplemented with 0.2 mM inositol.
[5] SC media without inositol.

Supplementary data S7. Distribution of PS species in Y700 *pGAL-ACB1* and Y700 cells.

Strain	Molecular species[1] 28:0	28:2	32:1	32:2	34:1	34:2	38:1	38:2
YPD media								
Y700[2]	0.08 ± 0.006	0.28 ± 0.02	0.63 ± 0.11	0.26 ± 0.05	3.30 ± 0.06	2.47 ± 0.05	0.09 ± 0.06	0.16 ± 0.17
Percent[3]	1.0 ± 0.02	3.5 ± 0.09	7.9 ± 0.90	3.3 ± 0.43	41.6 ± 1.64	31.2 ± 1.07	1.1 ± 0.65	1.9 ± 2.04
Y700 *pGAL-ACB1*[2]	0.16 ± 0.06	0.10 ± 0.01	0.72 ± 0.17	0.75 ± 0.17	1.15 ± 0.18	2.30 ± 0.07	0.07 ± 0.01	0.10 ± 0.03
Percent[3]	2.7 ± 1.20	1.6 ± 0.05	11.6 ± 1.67	12.1 ± 1.70	18.6 ± 1.20	37.2 ± 2.13	1.1 ± 0.33	1.6 ± 0.36
SC media (+ ino.)[4]								
Y700[2]	0.22 ± 0.09	0.57 ± 0.45	0.76 ± 0.62	0.29 ± 0.17	2.06 ± 1.33	1.48 ± 1.07	0.18 ± 0.06	0.57 ± 0.28
Percent[3]	3.3 ± 0.45	7.9 ± 2.26	10.3 ± 3.53	4.3 ± 0.10	29.6 ± 3.37	20.8 ± 4.34	3.3 ± 2.68	11.4 ± 10.5
Y700 pGAL-ACB1[2]	0.18 ± 0.10	0.18 ± 0.11	0.42 ± 0.21	0.02 ± 0.003	1.30 ± 0.30	0.01 ± 0.01	0.26 ± 0.08	0.55 ± 0.14
Percent[3]	3.9 ± 1.11	3.9 ± 1.36	9.0 ± 2.21	9.9 ± 2.32	11.9 ± 5.10	29.5 ± 1.79	6.3 ± 3.49	13.2 ± 6.83
SC media (- ino.)[5]								
Y700[2]	0.22 ± 0.11	0.82 ± 0.82	1.53 ± 1.52	0.37 ± 0.34	2.63 ± 2.43	1.85 ± 1.68	0.22 ± 0.09	0.45 ± 0.32
Percent[3]	2.9 ± 1.05	8.3 ± 2.82	15.4 ± 5.13	3.9 ± 0.81	27.9 ± 5.62	19.7 ± 3.61	4.2 ± 4.41	9.6 ± 11.3
Y700 pGAL-ACB1[2]	0.32 ± 0.14	0.46 ± 0.43	1.43 ± 1.10	1.17 ± 1.11	1.60 ± 0.92	3.13 ± 2.76	0.22 ± 0.06	0.63 ± 0.39
Percent[3]	3.5 ± 1.06	4.0 ± 1.44	13.3 ± 1.54	9.9 ± 3.87	16.3 ± 2.31	27.6 ± 7.71	3.0 ± 2.65	9.7 ± 10.4

[1] Only molecular species constituting 3 % or more, in at least one of the used growth conditions, are shown.
[2] The $^{12}C/^{13}C$ ratio between ion counts for each individual ^{12}C-species and one selected ^{13}C-specie in each lipid class.
[3] Percent that each species constitute of the total phospholipid class.
[4] SC media supplemented with 0.2 mM inositol.
[5] SC media without inositol.

Supplementary data S8. Distribution of PA species in Y700 *pGAL-ACB1* and Y700 cells.

Strain	Molecular species[1] 28:1	30:1	32:1	32:2	34:1	34:2	36:1	36:2
YPD media								
Y700[2]	0.16 ± 0.05	0.52 ± 0.30	1.73 ± 1.10	1.29 ± 1.15	5.55 ± 0.05	5.85 ± 0.16	1.29 ± 0.06	1.86 ± 0.16
Percent[3]	0.8 ± 0.18	2.5 ± 1.25	8.5 ± 4.63	6.3 ± 5.13	28.5 ± 3.59	30.0 ± 4.32	6.6 ± 0.47	9.6 ± 1.91
pGAL-ACB1[2]	0.09 ± 0.12	0.26 ± 0.02	1.38 ± 0.44	2.06 ± 0.46	2.69 ± 0.13	8.35 ± 0.27	0.44 ± 0.11	1.88 ± 0.53
Percent[3]	0.5 ± 0.61	1.4 ± 0.16	7.5 ± 2.60	11.2 ± 2.78	14.5 ± 1.10	45.0 ± 0.18	2.3 ± 0.51	10.1 ± 2.56
SC media (+ ino.)[4]								
Y700[2]	0.60 ± 0.68	0.58 ± 0.27	2.48 ± 1.85	1.50 ± 0.63	3.78 ± 2.37	3.78 ± 1.91	0.71 ± 0.30	0.43 ± 0.10
Percent[3]	3.0 ± 2.80	3.6 ± 0.01	14.1 ± 4.99	9.3 ± 0.35	22.2 ± 4.51	22.9 ± 1.39	4.4 ± 0.12	2.8 ± 0.67
pGAL-ACB1[2]	0.77 ± 0.35	0.60 ± 0.40	1.43 ± 0.81	1.84 ± 1.31	1.18 ± 0.95	3.89 ± 2.78	0.23 ± 0.07	1.00 ± 0.55
Percent[3]	5.9 ± 0.49	4.3 ± 0.68	10.5 ± 0.52	12.9 ± 2.97	8.0 ± 2.89	27.3 ± 6.31	1.9 ± 0.47	7.4 ± 0.18
SC media (- ino.)[5]								
Y700[2]	0.14 ± 0.03	0.47 ± 0.43	3.15 ± 2.41	1.10 ± 0.58	4.81 ± 3.45	2.79 ± 1.75	0.43 ± 0.12	0.06 ± 0.03
Percent[3]	1.2 ± 0.59	2.9 ± 1.17	21.1 ± 3.40	8.1 ± 1.16	32.9 ± 3.23	19.8 ± 0.33	3.4 ± 1.33	0.5 ± 0.13
pGAL-ACB1[2]	1.13 ± 0.51	0.95 ± 0.67	1.83 ± 0.40	2.45 ± 1.47	1.80 ± 0.98	4.16 ± 2.22	0.55 ± 0.34	0.07 ± 0.09
Percent[3]	7.1 ± 0.35	5.5 ± 1.41	12.2 ± 3.52	14.8 ± 1.84	11.0 ± 0.68	25.5 ± 1.22	3.3 ± 0.50	0.3 ± 0.43

[1] Only molecular species constituting 3 % or more, in at least one of the used growth conditions, are shown.
[2] The $^{12}C/^{13}C$ ratio between ion counts for each individual ^{12}C-species and one selected ^{13}C-specie in each lipid class.
[3] Percent that each species constitute of the total phospholipid class.
[4] SC media supplemented with 0.2 mM inositol.
[5] SC media without inositol.