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Supplementary Materials for

Genetic regulation of mitotic competence in G_0 quiescent cells

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The PDF file includes:

Other Supplementary Material for this manuscript includes the following:

(available at advances.sciencemag.org/cgi/content/full/4/8/eaat5685/DC1)

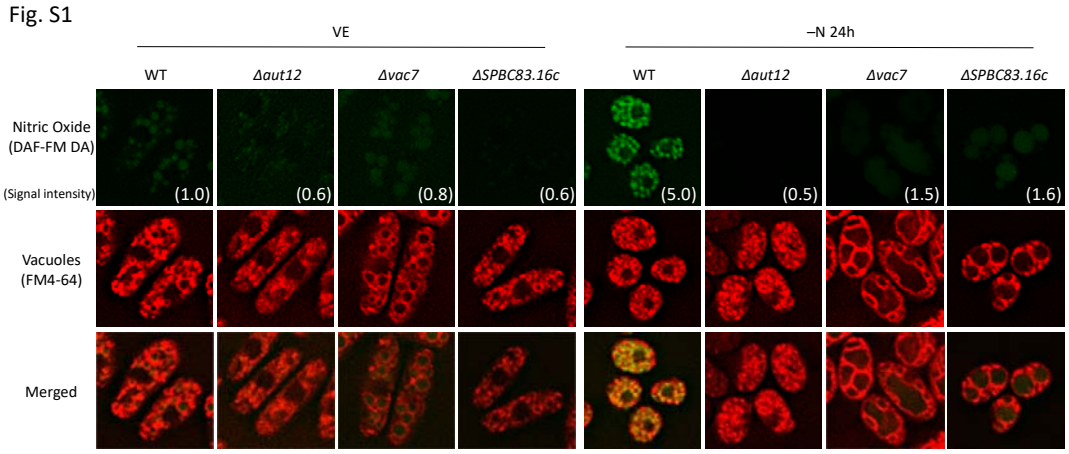


Fig. S1. Fluorescence images of nitric oxide (green, DAF-FM DA) and vacuoles (red, FM4-64) and merged images of indicated strains. Left columns show VE cells, and right columns show cells 24 hours after –N. Signal intensity of DAF-FM DA was quantified and shown in the images, proportional to WT VE cells.

Fig. S2

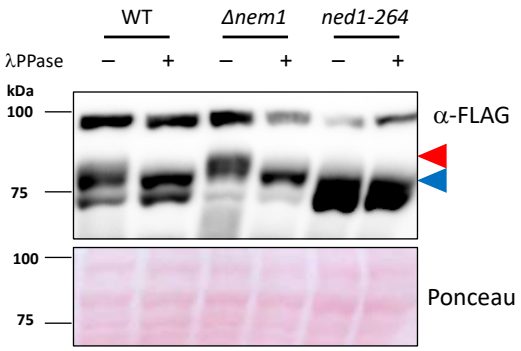


Fig. S2. A low-mobility band of Ned1-FLAG is phosphorylated. Western blot analysis of Ned1-FLAG-tagged strains of WT, Δ*nem1* and *ned1-264* was performed in a 6% Phos-tag gel. Samples were prepared from VE cells, treated with (+) or without (–) lambda protein phosphatase (λPPase). A low-mobility band (red arrowhead) increased its electrophoretic mobility (blue arrowhead) after λPPase treatment.

Fig. S3

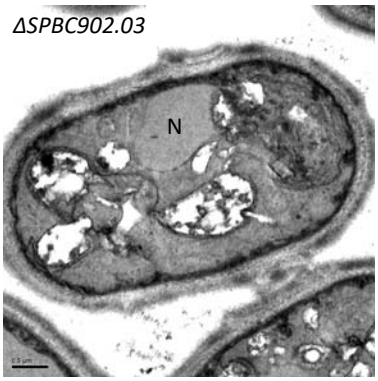


Fig. S3. Electron micrograph of Δ*SPBC902.03* at 24 hours after −N. N, nucleus.

Fig. S4

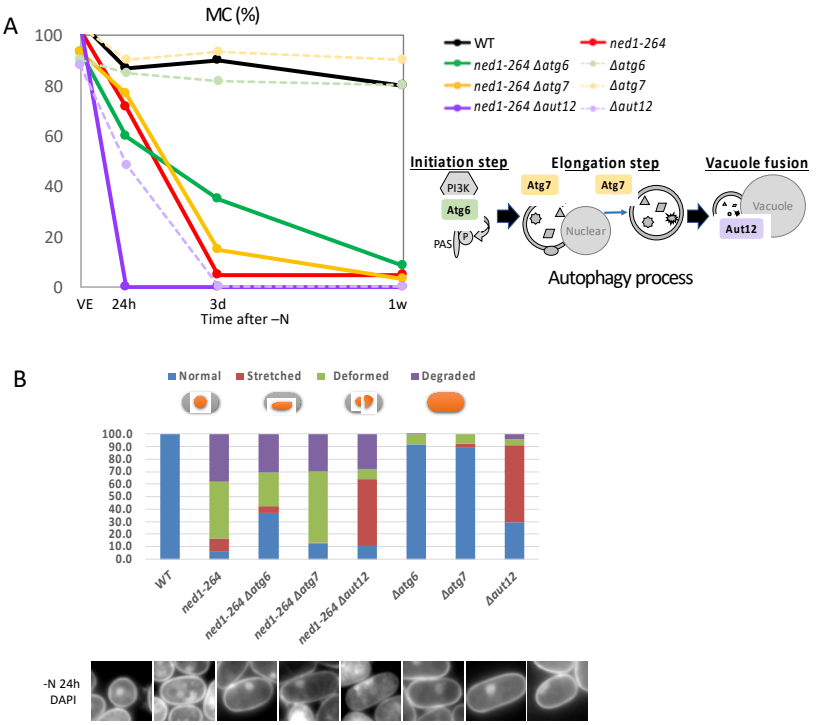


Fig. S4. *ned1-264* showed MC loss and deformed nuclei, which were rescued by deletions of autophagy genes. (**A**) MC graphs of the indicated strains. Diagram showing autophagy processes associated with these strains. (**B**) Percentages of DAPI-stained nuclear shapes found in indicated strains and DAPI images 24 hours after –N. 200 cells for each strain were counted.

Fig. S5

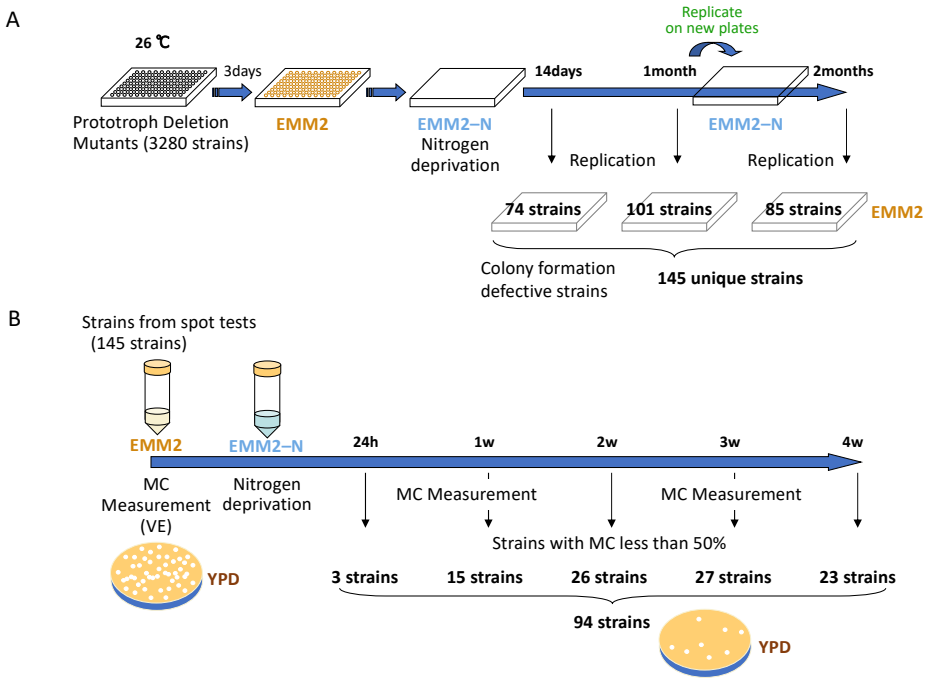
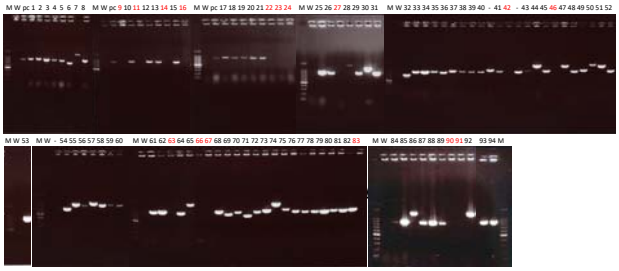


Fig. S5. Scheme of two screening procedures. (**A**) Spot tests of 3280 prototrophic deletion strains. Colony formation ability was tested after –N on agar plates for a maximum of 2 months. (**B**) MC measurements of selected strains from spot tests. MC was measured after –N using liquid medium for a maximum of 4 weeks.

Fig. S6

A 5' end check

cp5 – CPN10



cp5 – CPN1

PCR No.	Gene ID	Gene Name
1	SPAC10F6.16	mug134
2	SPAC11D3.15	SPAC11D3.15
3	SPAC11H11.01	sst6
4	SPAC144.02	iec1
5	SPAC144.04c	spe1
6	SPAC1486.01	sod2
7	SPAC17A5.14	exo2
8	SPAC17G6.05c	bro1
9	SPAC17G8.05	med20
10	SPAC17G8.06c	SPAC17G8.06c
11	SPAC1952.08c	SPAC1952.08c
12	SPAC1B3.16c	vht1
13	SPAC1D4.03c	aut12
14	SPAC1F8.02c	shu1
15	SPAC20G8.10c	atg6
16	SPAC22F8.12c	shf1
17	SPAC22H12.02	tfg3
18	SPAC23D3.09	arp42
19	SPAC25A8.01c	fit3
20	SPAC25A8.02	atg14
21	SPAC26A3.04	rpl2002
22	SPAC26A3.07c	rpl1101
23	SPAC29A4.18	prw1
24	SPAC31F12.01	zds1

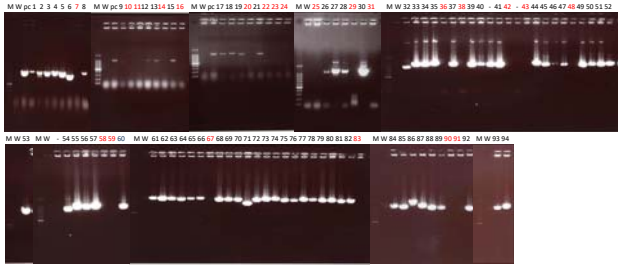
PCR No.	Gene ID	Gene Name
25	SPAC31G5.04	lys12
26	SPAC3A12.13c	hcr1
27	SPAC3F10.17	ltv1
28	SPAC4F10.04	ypa1
29	SPAC4F10.07c	atg13
30	SPAC4F8.01	did4
31	SPAC4G9.13c	vps26
32	SPAC57A10.14	sqf11
33	SPAC57A7.12	ssz1
34	SPAC589.07c	atg1801
35	SPAC630.05	ppp7
36	SPAC637.09	SPAC637.09
37	SPAC694.04c	SPAC694.04c
38	SPAC8F11.02c	dph3
39	SPAC9.13c	cwf16
40	SPAPB1A10.14	pof15
41	SPAPJ691.02	SPAPJ691.02
42	SPBC1347.08c	SPBC1347.08c
43	SPBC13G1.08c	ash2
44	SPBC13G1.12	did2
45	SPBC1685.01	pmp1
46	SPBC16C6.11	rpl3201
47	SPBC1711.04	mtd1
48	SPBC1718.03	ker1

PCR No.	Gene ID	Gene Name
49	SPBC18E5.04	rpl1001
50	SPBC18H10.07	wbp4
51	SPBC215.14c	vps20
52	SPBC21C3.02c	dep1
53	SPBC21C3.03	SPBC21C3.03
54	SPBC2D10.16	mhf1
55	SPBC2G2.03c	sbh1
56	SPBC365.16	SPBC365.16
57	SPBC3B8.10c	nem1
58	SPBC3B9.06c	atg3
59	SPBC3B9.11c	clf1
60	SPBC3B9.13c	rpp102
61	SPBC428.04	apq12
62	SPBC4B4.10c	atg5
63	SPBC4F6.06	kin1
64	SPBC56F2.11	met6
65	SPBC577.04	SPBC577.04
66	SPBC646.13	sds23
67	SPBC646.15c	pex16
68	SPBC6B1.05c	atg7
69	SPBC725.01	SPBC725.01
70	SPBC83.16c	SPBC83.16c
71	SPBC83.19c	SPBC83.19c
72	SPBC902.03	SPBC902.03

PCR No.	Gene ID	Gene Name
73	SPBC947.15c	nde1
74	SPBP8B7.13	vac7
75	SPBP8B7.16c	dbp2
76	SPCC11E10.06c	elp4
77	SPCC11E10.08	rik1
78	SPCC1393.08	SPCC1393.08
79	SPCC1672.06c	asp1
80	SPCC16C4.20c	hap2
81	SPCC1739.07	cti1
82	SPCC188.02	par1
83	SPCC24B10.06	SPCC24B10.06
84	SPCC24B10.11c	tho7
85	SPCC364.05	vps3
86	SPCC4G3.04c	coq5
87	SPCC622.12c	gdh1
88	SPCC663.14c	trp663
89	SPCC74.02c	ppn1
90	SPCC74.09	mug24
91	SPCC757.09c	rnc1
92	SPCC777.13	vps35
93	SPCC970.05	rpl3601
94	SPCP1E11.05c	are2

B 3' end check

cp3 – CPC3



cp3 – CPC1

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15	SPAC20G8.10c	atg6
16	SPAC22F8.12c	shf1
17	SPAC22H12.02	tfg3
18	SPAC23D3.09	arp42
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27	SPAC3F10.17	ltv1
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32	SPAC57A10.14	sqf11

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49	SPBC18E5.04	rpl1001
50	SPBC18H10.07	wbp4
51	SPBC215.14c	vps20
52	SPBC21C3.02c	dep1
53	SPBC21C3.03	SPBC21C3.03
54	SPBC2D10.16	mhf1
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59	SPBC3B9.11c	clf1
60	SPBC3B9.13c	rpp102
61	SPBC428.04	apq12
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63	SPBC4F6.06	kin1
64	SPBC56F2.11	met6

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87	SPCC622.12c	gdh1
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90	SPCC74.09	mug24
91	SPCC757.09c	rnc1
92	SPCC777.13	vps35
93	SPCC970.05	rpl3601
94	SPCP1E11.05c	are2

Fig. S6. PCR confirmation of gene deletion. M: Molecular weight DNA ladder. W: wild-type control. pc: positive control. (**A**) Deletion check of the 5′ end. Strains that failed to amplify with the first primer set (cp5-CPN10) were also tested with the second primer set (cp5-CPN1). Nine strains (11, 14, 22, 23, 27, 42, 67, 83, 90) failed to amplify with both primer sets, and they were removed from the list. (**B**) Deletion check of the 3′ end. Strains that failed to amplify with the first primer set (cp3-CPC3) were also tested with the second primer set (cp3-CPC1). There were eight strains (11, 14, 22, 23, 42, 67, 83, 90) that failed to amplify with both primer sets.

Table S1. Table of 85 GZE genes. Columns show classes, functional groups, strain names, human and budding yeast orthologs, MC (%) at the indicated time points, average cell length 24 hours after –N, cell number increment 24 hours after –N and major DNA peaks in VE and 24 hours after –N measured by FACS.

Table S2. List of cancer-related references for 85 GZE genes. More than 40% (36 of 85) of these genes are implicated in the etiology of various cancers.

Table S3. Strains that failed to backcross or grow. There were 175 unique strains excluded for viability failure (179 strains were listed, but 4 stains were duplicates of other versions), which is about 5% of all 3280 strains.