

Supplementary Table 2. Desiccation tolerance of mutant strains carrying deletions in genes identified as beneficial by phenomics (a), significantly differently expressed in the transcriptomics study (b (up) or (down) regulated), or selected based on biological function (c)¹.

Selection criteria	Mutant	Affected protein function/annotation	Phenomics, fold under-representation ²	Survival (%)	SD (%)
Intolerant deletion mutants (<10% survival of desiccation)					
a	<i>cox16Δ</i>	assembly of cytochrome c oxidase	-510	8	1
b (up)	<i>dcs1Δ</i>	hydrolase	NI	3	1
a, b (up)	<i>rim15Δ</i>	glucose-repressible protein kinase	-264	6	1
c	<i>snf1Δ</i>	serine/threonine protein kinase	NI	4	1
c	<i>snf4Δ</i>	protein kinase activator of Snf1p complex	NI	6	1
a	<i>tdh1Δ</i>	glyceraldehyde-3-phosphate dehydrogenase	-3	2	1
Deletion mutants severely affected (10-34% survival of desiccation)					
a	<i>bck1Δ</i>	MAPKKK of the cell integrity pathway	-52	17	1
b (up)	<i>bcy1Δ</i>	regulatory subunit of PKA	NI	27	3
a, b (up)	<i>blm10Δ</i>	nuclear assembly and regulation of proteasome	-11	16	1
a	<i>cat8Δ</i>	transcription factor	-8	24	1
a	<i>hap2Δ</i>	transcription factor	-111	13	1
a	<i>kre1Δ</i>	cell wall glycoprotein	-11	34	8
a	<i>ksp1Δ</i>	putative serine/threonine protein kinase	-39	26	1
c	<i>mig1Δ</i>	transcription factor; glucose repression	NI	27	1
a	<i>mir1Δ</i>	mitochondrial phosphate carrier	-18	14	1
a	<i>opi3Δ</i>	phospholipid methyltransferase	-19	29	2
a	<i>ptk2Δ</i>	putative serine/threonine protein kinase	-143	13	1
a	<i>ras2Δ</i>	regulates nitrogen starvation response etc.	-40	10	1
a	<i>rhr2Δ</i>	DL-glycerol-3-phosphatase	-46	22	1
a	<i>sel1Δ</i>	ER-associated protein degradation	-23	34	1
a	<i>sin3Δ</i>	DNA binding subunit of histone deacetylase	-5	27	3
c	<i>sir2Δ</i>	histone deacetylase	NI	24	1
Deletion mutants moderately affected (35-60% survival of desiccation)					
a	<i>fbp26Δ</i>	fructose-2,6-bisphosphatase	-166	38	1
c	<i>gts1Δ</i>	zinc-finger protein; regulates cell cycle, cell size	NI	36	1
c	<i>hnm1Δ</i>	choline permease	NI	41	1
c	<i>hvk2Δ</i>	hexokinase PII	NI	57	2
b (up)	<i>ino1Δ</i>	inositol-1-phosphate synthase	NI	35	2
c	<i>kss1Δ</i>	MAP kinase; filamentous growth	NI	59	2

<i>a, b (up)</i>	<i>msn2Δ</i>	transcription factor	-3	40	1
<i>a, b (down)</i>	<i>msn4Δ</i>	transcription factor	-3.9	58	2
<i>c</i>	<i>rad1Δ</i>	single-stranded DNA endonuclease	NI	59	4
<i>a</i>	<i>sak1Δ</i>	upstream kinase for the Snf1 complex	-34	46	6
<i>c</i>	<i>sip1Δ</i>	beta-subunit of the Snf1 complex	NI	37	1
<i>c</i>	<i>sip4Δ</i>	transcription factor; regulated by Snf1	NI	49	2
<i>c</i>	<i>sod1Δ</i>	Cu, Zn superoxide dismutase	NI	56	2
<i>c</i>	<i>sod2Δ</i>	Mn-containing superoxide dismutase	NI	48	1
<i>a, b (up)</i>	<i>tcb1Δ</i>	calcium/lipid binding protein	-4	36	3
<i>c</i>	<i>tsl1Δ</i>	trehalose biosynthesis	NI	35	3
<i>c</i>	<i>tpk1Δ</i>	subunit of cytoplasmic PKA	NI	39	2
<i>a</i>	<i>ubi4Δ</i>	ubiquitin, essential for stress response	-87	49	3
<i>a, b (up)</i>	<i>yak1Δ</i>	serine-threonine protein kinase	-166	35	3
<i>b (up)</i>	<i>yap1Δ</i>	transcription factor, oxidative stress	NI	57	3
Deletion mutants not adversely affected (>60% survival of desiccation)					
<i>b (up)</i>	<i>agp1Δ</i>	amino acid uptake	NI	75	1
<i>b (up)</i>	<i>ald3Δ</i>	aldehyde dehydrogenase; stress induced	NI	65	1
<i>b (up)</i>	<i>avt1Δ</i>	amino acid vacuolar transporter	NI	70	1
<i>c</i>	<i>bmh1Δ</i>	14-3-3 protein	NI	86	1
<i>c</i>	<i>bmh2Δ</i>	14-3-3 protein	NI	64	1
<i>c</i>	<i>cnb1Δ</i>	calcineurin B; regulates Crz1	NI	74	3
<i>b (up)</i>	<i>ctt1Δ</i>	cytosolic catalase	NI	67	3
<i>c</i>	<i>crz1Δ</i>	transcription factor, stress response	NI	71	4
<i>b (up)</i>	<i>ecm29Δ</i>	major component of the proteasome	NI	74	1
<i>c</i>	<i>elm1Δ</i>	serine/threonine protein kinase	NI	65	1
<i>a</i>	<i>fps1Δ</i>	glycerol efflux	-25	65	2
<i>b (down)</i>	<i>fus3Δ</i>	MAP kinase, mating	NI	67	1
<i>c</i>	<i>gal83Δ</i>	beta-subunit of the Snf1 kinase complex	NI	61	3
<i>b (up)</i>	<i>gap1Δ</i>	amino acid permease	NI	62	2
<i>b (up)</i>	<i>glo1Δ</i>	monomeric glyoxalase I	NI	69	6
<i>b (up)</i>	<i>gpd1Δ</i>	glycerol biosynthesis	NI	66	3
<i>c</i>	<i>gpd2Δ</i>	glycerol biosynthesis	NI	73	1
<i>c</i>	<i>gre1Δ</i>	hydrophilin of unknown function	NI	61	5
<i>b (up)</i>	<i>gre2Δ</i>	methylglyoxal reductase	NI	72	1
<i>b (up)</i>	<i>gre3Δ</i>	aldose reductase	NI	70	1
<i>a</i>	<i>hog1Δ</i>	MAP kinase	-24	63	3
<i>c</i>	<i>hom2Δ</i>	aspartic beta semi-aldehyde dehydrogenase	NI	69	2
<i>c</i>	<i>hor2Δ</i>	DL-glycerol-3-phosphatase	NI	67	4
<i>c</i>	<i>hot1Δ</i>	transcription factor	NI	65	2
<i>c</i>	<i>hsp104Δ</i>	heat shock protein; disaggregase	NI	73	8
<i>c</i>	<i>hsp12Δ</i>	stress response protein	NI	72	3
<i>b (down)</i>	<i>inm1Δ</i>	inositol biosynthesis	NI	71	3

c	<i>mbp1Δ</i>	transcription factor; G1 to S regulation	NI	79	1
c	<i>msb2Δ</i>	osmosensor	NI	64	2
a	<i>msn1Δ</i>	transcription factor	-7	62	1
b (down)	<i>nop6Δ</i>	hydrophilin of unknown function	NI	80	2
c	<i>nth1Δ</i>	neutral trehalase	NI	69	3
a	<i>pbs2Δ</i>	MAP kinase kinase	-28	66	1
b (up)	<i>pma2Δ</i>	plasma membrane H ⁺ /ATPase	NI	62	4
b (up)	<i>pns1Δ</i>	putative choline transporter	NI	66	5
c	<i>reg1Δ</i>	regulatory subunit of protein phosphatase 1	NI	95	7
b (up), c	<i>reg2Δ</i>	regulatory subunit of protein phosphatase 1	NI	81	1
c	<i>rlm1Δ</i>	transcription factor	NI	62	3
c	<i>rpd3Δ</i>	histone deacetylase	NI	62	3
b (up)	<i>sfa1Δ</i>	formaldehyde detoxification	NI	75	1
c	<i>sho1Δ</i>	osmosensor	NI	62	2
c	<i>sip18Δ</i>	unknown function; induced by osmostress	NI	70	2
c	<i>sip2Δ</i>	beta subunit of the Snf1 complex; ageing-related	NI	64	5
a	<i>skn7Δ</i>	transcription factor; stress response	-7.8	71	3
c	<i>sko1Δ</i>	transcription factor; stress response	NI	66	2
a	<i>slt2Δ</i>	MAP kinase; CWI, cell cycle progression	-32	78	1
c	<i>smk1Δ</i>	MAP kinase, sporulation	NI	73	6
c	<i>smp1Δ</i>	putative transcription factor, osmostress	NI	67	3
a	<i>ssk1Δ</i>	signal transduction; MAPKKK for Hog1	-4	61	1
c	<i>stb5Δ</i>	transcription factor; binds Sin3	NI	69	8
c	<i>ste11Δ</i>	MAPKK kinase; osmostress, pheromone resp.	NI	66	6
c	<i>stf2Δ</i>	regulation of mitochondrial F1F0-ATP synthase	NI	69	1
b (up)	<i>stl1Δ</i>	glycerol/H ⁺ symporter	NI	64	6
c	<i>swi4Δ</i>	transcription factor	NI	64	3
c	<i>tdh2Δ</i>	glyceraldehyde-3-phosphate dehydrogenase	NI	68	4
a	<i>tdh3Δ</i>	glyceraldehyde-3-phosphate dehydrogenase	-3	68	2
c	<i>tos3Δ</i>	protein kinase activator of Snf1 complex	NI	60	1
b (up), c	<i>tpk2Δ</i>	subunit of cytoplasmic PKA	NI	60	1
c	<i>tpk3Δ</i>	subunit of cytoplasmic PKA	NI	72	2
b (up)	<i>ynl195cΔ</i>	hypothetical protein, mitochondrial	NI	69	1
b (up)	<i>ypr115w</i> Δ	hypothetical protein, cytoplasm	NI	72	2
c	<i>zap1Δ</i>	transcription factor	NI	79	1

1: Strains derived from BY4741 were grown individually to the post-diauxic phase of growth in YEPD media before drying. The proportion of cells surviving desiccation was measured as detailed in the Methods, and the mean and standard deviation (SD) of three replicate experiments is shown. Survival of the parental strain BY4741 was 70% +/-6%. Includes the data from Supplementary table 1.

2: NI = not identified as under-represented