Strain	Description of deleted gene	dieldrin IC30 (690 µM) Ratio SEM		p-value to WT	dieldrin IC30 (690 µM) + 5mM leucine Ratio SEM		p-value to no leucine	Human homolog of deleted gene
	nd phosphatases	Natio			Natio		leucille	gene
oca1∆	Tyrosine phosphatase	0.389	0.043	***	0.884	0.042	**	
ssk2∆	MAPKKK of the HOG1 mitogen-activated signaling pathway	0.787	0.007	***	0.949		***	MAP3K4
ssk1∆	Cytoplasmic response regulator	0.854		***	0.990		*	
cka1∆	Alpha catalytic subunit of casein kinase 2	0.888	0.004	***	ND	ND	NA	CSNK2A1
gcn2∆	Protein kinase; initiates starvation response	0.907	0.054	NS	1.203	0.046	*	EIF2AK4
ptc6∆	Mitochondrial type 2C protein phosphatase	0.909	0.021	**	ND	ND	NA	PPM1K
Downstre	,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,							
sap155∆	Required for function of the Sit4p protein phosphatase	0.927	0.022	*	0.915	0.027	NS	PPP6R1
sit4∆	Type 2A-related serine-threonine phosphatase	0.957	0.020	NS	0.957	0.022	NS	PPP6
sap4∆	Required for function of the Sit4p protein phosphatase	1.036	0.017	NS	1.007	0.019	NS	
Transcript	tion activators/repressors							
imp2∆'	Transcriptional activator; maintains ion homeostasis	0.373	0.091	**	ND	ND	NA	
spt8∆	Subunit of the SAGA transcriptional regulatory complex	0.470	0.016	***	0.825	0.017	***	
mot3∆	Transcriptional repressor	0.633	0.015	***	ND	ND	NA	
gat1∆	Transcriptional activator for nitrogen catabolite repression genes	1.027	0.013	NS	0.9833	0.019	NS	
Autophag	y (48H treatment)							
atg13∆	Required for vesicle formation during autophagy	0.933	0.023	*	0.947	0.026	NS	ATG13
atg12∆	Ubiquitin-like modifier involved in autophagy and Cvt pathway	0.993	0.015	NS	1.023	0.034	NS	APG12
atg5∆	Involved in autophagy and the Cvt pathway	1.010	0.012	NS	0.987	0.023	NS	ATG5
Other								
pdr5∆	Multidrug transporter	0.314	0.040	***	0.486	0.037	*	ABCG2
opi3∆	Phospholipid methyltransferase	0.711	0.045	**	ND	ND	NA	PEMT
bre5∆	Ubiquitin protease cofactor	0.714	0.030	***	ND	ND	NA	
ufd2∆	Ubiquitin chain assembly factor (E4)	0.746	0.061	*	ND	ND	NA	UBE4B
yen1∆	Holliday junction resolvase	0.754	0.027	***	ND	ND	NA	GEN1
sac3∆	Nuclear pore-associated protein	0.757	0.035	**	ND	ND	NA	МСМЗАР
tim18∆	Component of the mitochondrial TIM22 complex	0.775	0.024	***	ND	ND	NA	
par32∆	Unknown function; phosphorylated upon rapamycin treatment	0.787	0.062	*	ND	ND	NA	
cnb1∆	Calcineurin B; the regulatory subunit of calcineurin	0.913	0.008	**	0.908	0.016	NS	PPP3R1
thi3∆	Role in branched chain amino acid degradation	0.941	0.014	**	ND	ND	NA	HACL1
pda1∆	E1 alpha subunit of the pyruvate dehydrogenase complex	0.969	0.028	NS	ND	ND	NA	PDHA1

Table S2. Confirming dieldrin sensitivity for various strains by flow cytometry. A list of strains not shown in the main text that were tested for sensitivity to dieldrin. Ratios are defined as relative growth to a wild-type GFP strain between treated and control cultures. Statistically significant differences between wild-type and mutant strains as well as non-leucine and leucine treated strains were determined by Student's t-test, where ***=p<0.001, **=p<0.01, and *=p<0.05. ND=not determined, NA=not applicable, NS=not significant.

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