

Supplemental Table S2. Yeast strains used in this study.

Strain	Genotype	Growth	Source	Reference
EBY.VW4000	(<i>MATa Δhxt1-17Δgal2 Δstl1 Δagt1 Δmph2 Δmph3 leu2-3,112 ura3-52 trp1-289 his3-1 MAL2-8S SUC2</i>)	No growth on glucose but normal growth on maltose.	Eckhard Boles	Wieczorke <i>et al.</i> , 1999*
YBR241C	MATa his3Δ1 leu2Δ0 met15Δ0 ura3Δ0 ybr241c::KanMX4.	Moderate growth defect on minimal media, NaCl or lactate); Moderate growth defect on YPD after 60 generations	ATCC 4003381	Giaever <i>et al.</i> (2000) Warringer <i>et al.</i> (2003) http://www.yeastgenome.org/
YDR387C	MATa his3Δ1 leu2Δ0 met15Δ0 ura3Δ0 ydr387c::KanMX4.	No growth defect on minimal medium, but moderate growth defect on YPD after 20 and 60 generations	ATCC 4004223	Giaever <i>et al.</i> (2000) Warringer <i>et al.</i> (2003). http://www.yeastgenome.org/
RGT2/YDL138W	MATa his3Δ1 leu2Δ0 met15Δ0 ura3Δ0 ΔRGT2.	Moderate growth defect on YPD after 20 generations; severe growth defect on minimal media; and severe growth defect on YPD after 60 generations	ATCC 4003836	Giaever <i>et al.</i> (2000) Warringer <i>et al.</i> (2003) http://www.yeastgenome.org/

Giaever *et al.* (2000) Functional profiling of the *Saccharomyces cerevisiae* genome.

Nature 418, 387-391.

Warringer *et al.* (2003) High-resolution yeast phenomics resolves different physiological features in the saline response. PNAS, 100: 15724-15729

Wieczorke *et al.*, 1999*. Concurrent knock-out of at least 20 transporter genes is required to block uptake of hexoses in *Saccharomyces cerevisiae*. FEBS Lett. 464, 123-128.