

Table I. *Effect of solute concentration on gene regulation*

	KCl concentration (M)				
	0.0625	0.125	0.25	0.5	1.0
Genes regulated in wild type ^a	279	623	841	1828	1396
Percent of genes that exhibited altered expression in <i>ssk1 ste11</i> ^b					
2-fold, 1 time point	34.8	77.2	86.4	54.2	40.1
2-fold, 2 time points	21.9	58.4	38.0	33.7	11.2
3-fold, 2 time points	10.0	20.2	11.5	7.28	1.79
Ave. fold induction in WT ^c	3.4	4.7	6.2	9.7	7.2
Ave. fold induction in <i>ssk1 ste11</i> ^c	1.6	1.4	1.5	4.1	4.6
Ssk1/Ste11-independent induction ^d	0.47	0.30	0.24	0.42	0.64
Pearson ρ ^e	0.43	0.22	0.25	0.73	0.83

Table I. Effect of solute concentration on gene expression. Wild-type and *ssk1 ste11* strains (IH4506 and IH4514, respectively) were each treated with five concentrations of KCl, as indicated. RNA was harvested at five time points for each. Because the transcriptional response was delayed with increasing solute concentration, we sampled the different cultures at different times: for 0.0625 M KCl, 0 (pre-treatment), 2.5, 5, 10 and 15 min; for 0.125 M KCl, 0 (pre-treatment), 5,

10, 20 and 30 min; for 0.25 M and 0.5 M KCl, 0 (pre-treatment), 10, 20, 30 and 40 min; and for 1.0 M, 0 (pre-treatment), 30, 60, 120 and 180 min.

^aGenes which showed an increase or decrease of >2-fold at two or more time points.

^bGenes which (1) are regulated in the wild-type strain (see footnote a above), and (2) exhibited altered regulation in the *ssk1 ste11* strain by a factor of at least 2- or 3-fold for at least one or two time points, as indicated.

^cThe average induction values (across all non-zero time points) for the top 1% of genes (59 or 60 genes) induced in the wild-type strain at each concentration of KCl.

^dThe average induction value for the *ssk1 ste11* strain divided by the average induction value for the wild-type strain for the genes described in footnote c.

^e ρ is the Pearson Correlation Coefficient (ρ) which measures the strength of linear relationships between two sets of data. In this case, the two data sets compared were the entire genome expression values for the entire time course for the wild-type and the *ssk1 ste11* mutant strains. A ρ value near 1.0 signifies a

positive correlation; ρ near zero indicates that there is little correlation between the two data sets.