

Table S1: Independent RT-PCR confirmation of microarray data

Gene ID	Microarray		RT-PCR	
	WT	Δ GCN5-A	WT	Δ GCN5-A
<i>Genes up-regulated in WT during alkaline stress</i>				
641.m01566	2.29	-1.06	1.5 \pm 0.03	-1.4 \pm 0.01*
541.m01237	3.29	1.52	2.4 \pm 0.05	1.3 \pm 0.08
641.m01498	7.4	2.0	2.8 \pm 0.08	1.3 \pm 0.1
76.m01548	7.01	5.24	-2.8 \pm 0.04	-3.6 \pm 0.09
<i>Genes with no significant change in WT during alkaline stress</i>				
41.m02959	1.35	2.05	1.07 \pm 0.07	1.5 \pm 0.7
49.m03159	1.2	2.38	-1.1 \pm 0.03	1.8 \pm 0.14
162.m00002	1.16	2.4	-1.25 \pm 0.06	1.4 \pm 0.6
641.m01597	-1.05	1.2	-2.1 \pm 0.03	-1.6 \pm 0.17*
<i>Genes down-regulated in WT during alkaline stress</i>				
20.m00368	-4.37	-3.7	-4.7 \pm 0.03	-8.3 \pm 0.09
46.m01600	-3.22	-2.74	-6.2 \pm 0.05	-3.7 \pm 0.09
55.m04769	-6.6	-6.31	-1.2 \pm 0.1	-4.5 \pm 0.1
641.m01514	-3.21	-3.24	-15.6 \pm 0.1	-3.8 \pm 0.3

Values represent fold-change in microarrays and fold change normalized to tubulin mRNA levels in RT-PCRs (\pm S.E. Δ Ct). WT = wild-type. Student's t-test was performed for RT-PCR data and p values were <0.05 except for two samples indicated with asterisks. With exception of 76.m01548, each gene tested reproduces the trend observed with the microarrays.