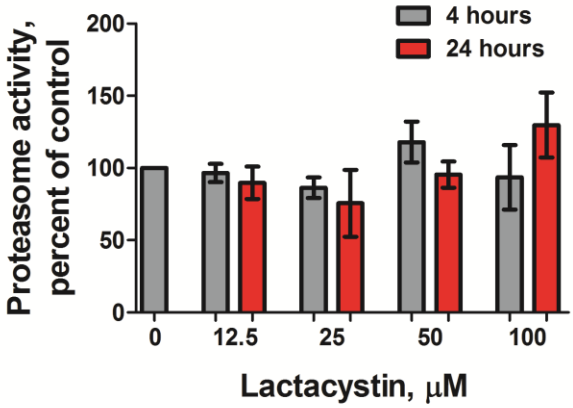
Table S1. **Proteomics analysis**. The file shows raw proteomics data of four sample sets treated with 0 or 150 µM polyphosphate for 3 hours. For proteins identified in each individual sample set the protein ID (Protein accession number), a description (taken from UniProt), length (amino acids), molecular weight (kDa), peptide spectrum matches (PSMs, number of spectra assigned to peptides that contributed to the inference of the protein), peptide sequences (number of different unique peptide sequences, or modified variants of sequences that were identified for the protein), percent sequence coverage (percentage of the protein sequence that was covered by the peptides identified for the protein), modifications observed, spectral counts (this measures the weighted count of peptide spectrum matches assigned to each protein for the particular sample), spectral index (a statistic calculated from the intensity of fragment ions in each spectrum assigned to a particular protein), and the ratio of the protein after polyphosphate stimulation relative to the no polyphosphate control. Consistently downregulated and upregulated proteins, and proteins downregulated or upregulated in 3 of the 4 assays are shown with the average fold change across the data sets. Phosphorylated Adrm1 as determined by ModLS is shown including the ID prob (probability supporting the localization of the phosphorylation to a peptide).

Click here to Download Table S1

A



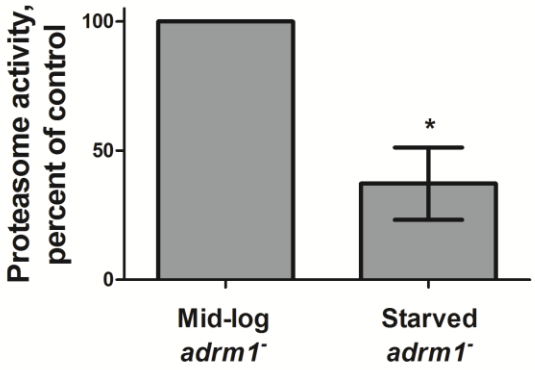
B

	Lactacystin (μM)		
	control	25uM	50uM
24hrs	-	-	-
32hrs	-	-	-
48hrs	-	-	-

Figure S1

Figure S1. Effect of lactacystin. A) Cells were incubated with the indicated amounts of lactacystin for 4 hours or 24 hours in HL5, and proteasome activity levels were measured and normalized to no Lactacystin controls. Values are mean ± SEM, n=4. **B)** Cells were incubated in 25% HL5 for 48 hours with the indicated amounts of lactacystin, and scored for the presence of aggregates at the indicated times. – indicates no aggregates observed in 4 of 4 independent assays

A



B

		25% HL5		30% HL5	
	hours	control	polyP	control	polyP
Ax2	18	-	-	-	-
	20	-	-	-	-
	24	-	+	-	-
adrm1⁻	18	-	-	-	-
	20	-	-	-	-
	24	+	+	-	-

Figure S2

Figure S2. Adrm1 response to starvation or polyphosphate. A) Proteasome activity of starved *adrm1*$^{-}$ cells (PBM for 4 hours) was measured and normalized to mid-log *adrm1*$^{-}$ controls. Values are mean ± SEM, n=4. * indicates $p < 0.05$, t test. **B)** Ax2 and *adrm1*$^{-}$ cells were incubated in 25% or 30% HL5 for 24 hours in the presence or absence of 150 µM polyphosphate, and were scored for the presence of aggregates at the indicated times. – indicates no aggregates and + indicates aggregates observed in 4 of 4 independent assays.

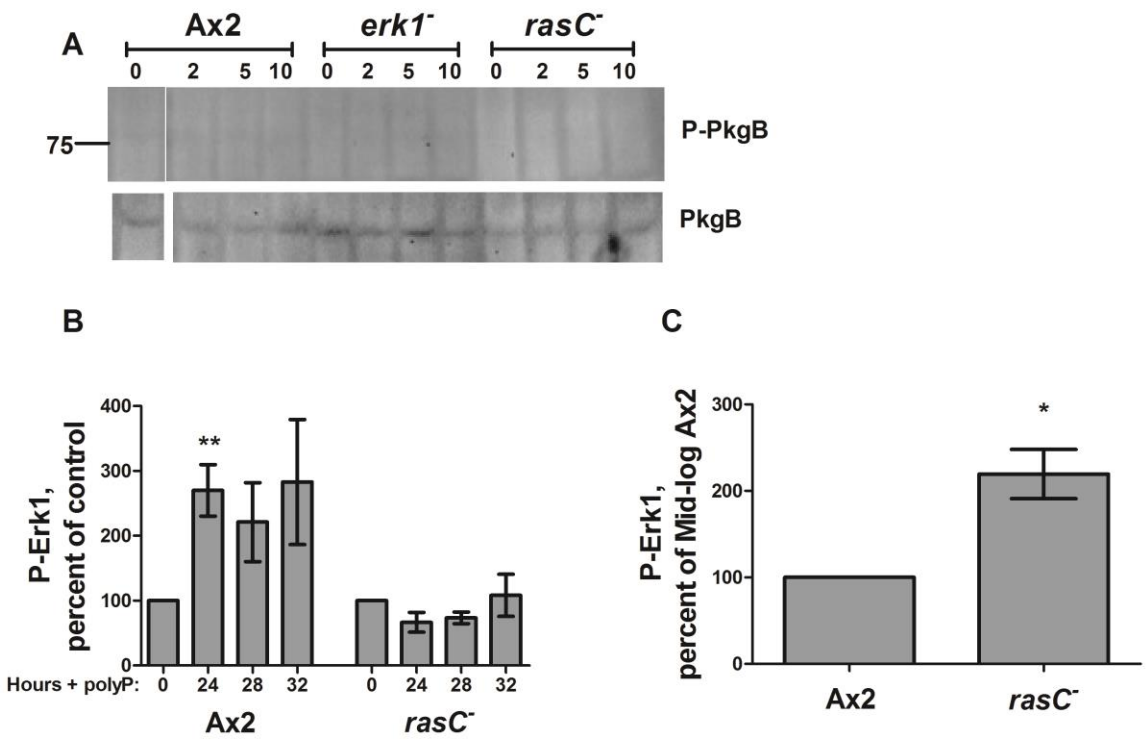


Figure S3

Figure S3. PkgB and Erk1 phosphorylation. A) The indicated cell lines were incubated with 150 µM polyphosphate for the indicated times, and phospho-PkgB levels were analyzed by western blot (Image representative of 3 blots). **B)** Ax2 and cells lacking RasC were incubated with 150 µM polyphosphate for the indicated times, and levels of phospho-Erk1 were measured and normalized to the no polyphosphate control. **C)** Basal levels of phospho-Erk1 were measured in mid-log *rasC*$^{-}$ cells and normalized to mid-log Ax2. All values are mean ± SEM, $n \geq 3$, * indicates $p < .05$ and ** $p < .01$ (paired t-tests).