Supplemental Data

Duf89 abets lncRNA control of fission yeast phosphate homeostasis via its antagonism of precocious lncRNA transcription termination

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Figures S1, S2, S3, S4, S5, S6, S7, and S8

Sample	Total Paired Reads	Mapped Reads
WT (1)	21,449,706	20,980,488 (98%)
WT (2)	23,888,710	23,365,656 (98%)
WT (3)	22,670,827	22,083,962 (97%)
*duf89*Δ (1)	23,636,442	23,165,432 (98%)
*duf89*Δ (2)	21,921,106	21,455,434 (98%)
*duf89*Δ (3)	22,457,455	21,769,307 (97%)

Figure S1. RNA-seq read counts for triplicate biological replicates.

Sample pairs	Pearson Coefficient
WT (1) vs (2)	0.977
WT (2) vs (3)	0.978
WT (1) vs (3)	0.987
*duf89*Δ (1) vs (2)	0.984
*duf89*Δ (2) vs (3)	0.985
*duf89*Δ (1) vs (3)	0.985

Figure S2. RNA-seq data reproducibility between biological replicates.

gene	log2 change	function
*tgp1**	2.87	glycerophosphodiester transporter
SPBPB2B2.06c*	2.34	extracellular 5'-nucleotidase
*ecl3**	2.06	extender of chronological lifespan protein
*pho1**	1.73	acid phosphatase
*pfl3**	1.57	flocculin
spn5	1.35	meiotic septin
*pho84**	1.30	inorganic phosphate transporter
num1	1.24	cortical anchoring factor for dynein
cao2	1.21	copper amine oxidase-like protein
SPCC1884.01	1.17	
SPBC25B2.08*	1.12	
*nap1**	1.10	histone H2A-H2B chaperone
new25	1.04	SAP domain containing protein
SPBC26H8.11c	1.01	acyl-coenzyme A thioesterase
*mfs3**	1.01	spermidine transmembrane transporter

Figure S3. Transcription profiling identifies genes up-regulated in the absence of Duf89. List of 15 annotated protein-coding genes that were up-regulated at least two-fold in *duf89*Δ cells, 9 of which (indicated by asterisks) were also up-regulated at least two-fold in *aps1*Δ cells. The log2 fold changes versus wild-type are shown.

gene	log2 change	function
SPBC23G7.13c*	–2.25	urea transmembrane transporter
SPCC70.08c*	–2.03	methyltransferase
*ght5**	–1.91	glucose/fructose:proton symporter
hsp9	–1.70	heat shock protein
SPAC15E1.02c*	–1.53	DUF1761 family protein
SPBC1271.07c*	–1.51	N-acetyltransferase
*rtc3**	–1.48	SBDS family protein
SPAC637.03*	–1.45	DUF1774 family protein
*ubp11**	–1.36	ubiquitin C-terminal hydrolase
*ssa1**	–1.35	heat shock protein
SPAC26H5.09c*	–1.34	oxidoreductase
SPAC11D3.19*	–1.33	
*aca1**	–1.32	azetidine-2-carboxylic acid acetyltransferase
eno102	–1.29	enolase
str1	–1.28	siderophore-iron transporter
SPBC1271.08c	–1.23	
aes1	–1.20	phenazine biosynthesis PhzF protein
*srx1**	–1.20	sulfiredoxin
ecl1	–1.18	extender of chronological lifespan protein
mug106	–1.18	
SPACUNK4.17	–1.11	
*fip1**	–1.04	plasma membrane iron permease
mmf1	–1.00	mitochondrial matrix protein

Figure S4. List of 23 annotated protein-coding genes that were down-regulated at least two-fold in *duf89*Δ cells, 14 of which (61%, denoted by asterisks) were also down-regulated at least two-fold in *aps1*Δ cells.

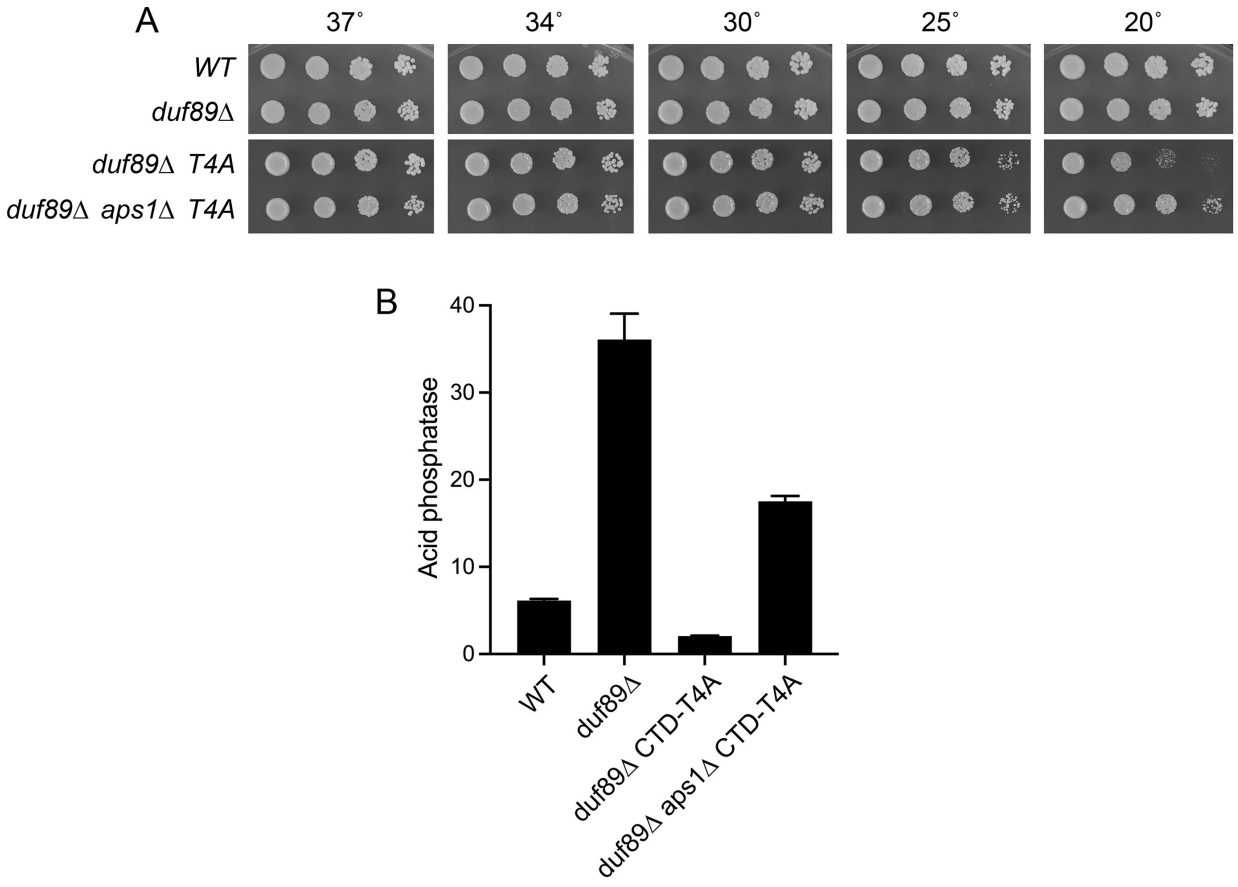

Figure S5. Lethality of *duf89Δ aps1Δ* is rescued by *CTD-T4A*. (A) *S. pombe* cells with indicated genotypes were spot tested for growth at the temperatures specified. (B) The indicated strains were grown in liquid culture at 30°C and assayed for acid phosphatase activity.

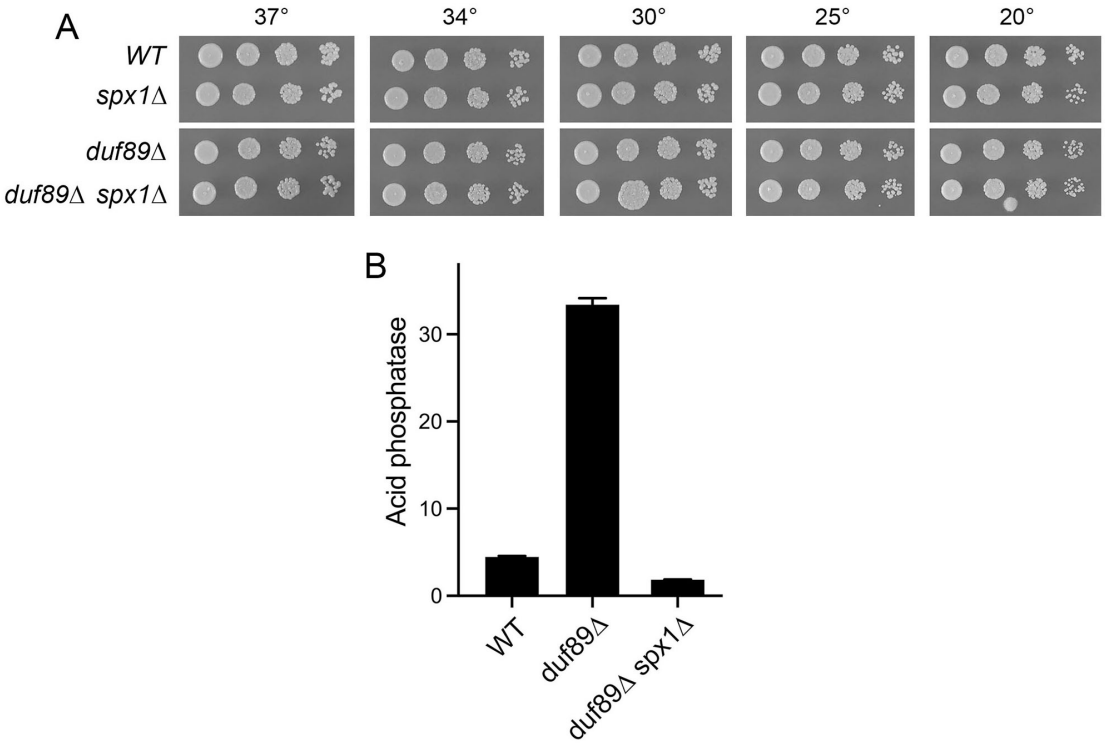

Figure S6. Derepression of *pho1* expression by *duf89*Δ depends on Spx1. (A) *S. pombe* cells with indicated genotypes were spot tested for growth at the temperatures specified. (B) The indicated strains were grown in liquid culture at 30°C and assayed for acid phosphatase activity.

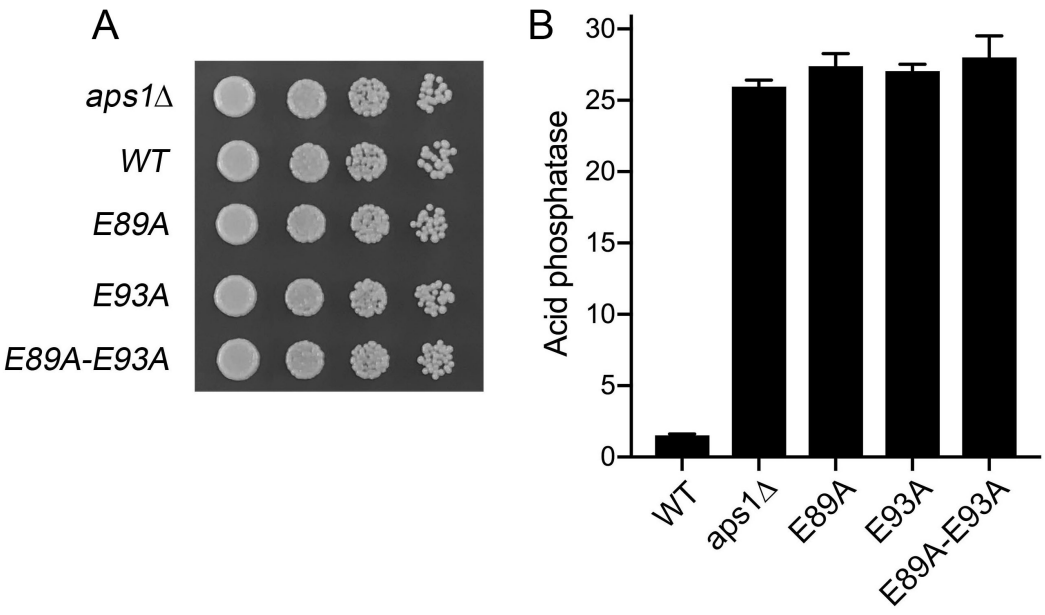

Figure S7. Pyrophosphatase activity of Aps1 is required for its function in *pho1* regulation.
(A) Fission yeast strains with the *aps1* genotypes indicated at left were spot tested for growth on YES agar at 30˚C. (B) Wild-type, *aps1*Δ, *aps1-E89A*, *aps1-E93A*, and *aps1-(E89A-E93A)* strains were assayed for acid phosphatase activity.

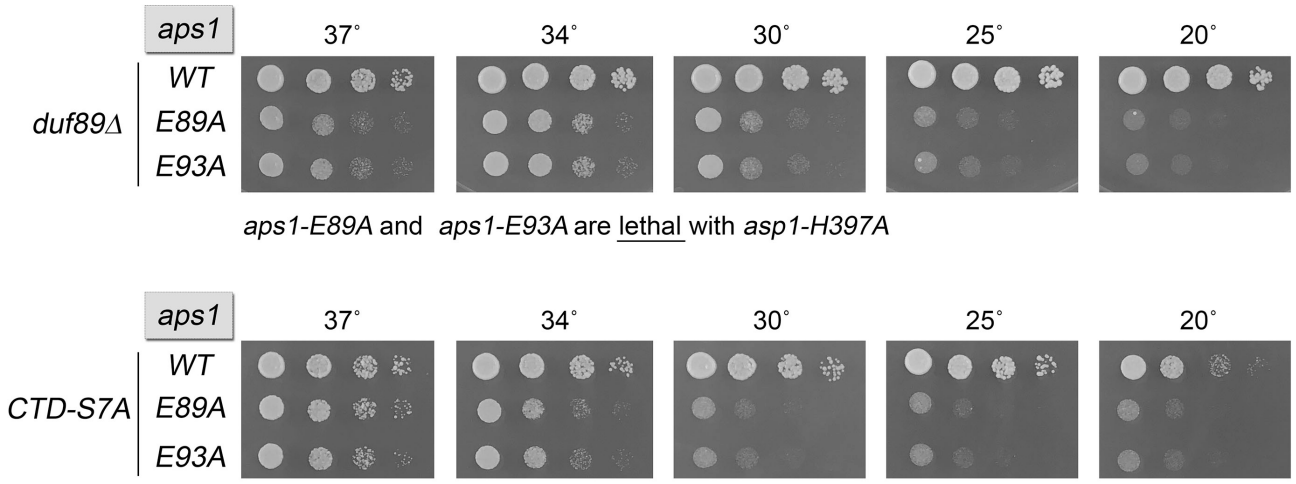

Figure S8. Mutational synergies of Aps1 pyrophosphatase active site mutants. *S. pombe duf89*Δ (top) and *CTD-S7A* (bottom) strains with the indicated *aps1* genotypes were spot tested for growth on YES agar at the temperatures specified.