

## Supplemental Data

### **A conserved SET-domain methyltransferase, Set11, modifies ribosomal protein Rpl12 in fission yeast**

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#### **SUPPLEMENTAL FIGURE LEGENDS**

##### **Supplemental Figure S1. LC-MS/MS analysis of Rpl12 derived from wild-type and $\Delta set11$ strains.**

Rpl12 in wild-type (*set11*<sup>+</sup>) or  $\Delta set11$  mutant cells was isolated by reverse-phase chromatography, digested with GluC, and analyzed using a Finnigan LTQ spectrometer. (A and B) Base peak, ion chromatogram for a 20-min separation of digested Rpl12 peptides for the wild-type (A) and  $\Delta set11$  strains (B). Elution time and detected *m/z* of representative peaks are indicated. A peak for the peptide fragment spanning residues 1-8 is indicated by “\*.” MS spectra of the Rpl12 peptide detected at 8.27 min for wild-type and at 8.03 min for the  $\Delta set11$  strain are depicted on the right. The experimental mass calculated from the mean *m/z* of MH<sup>2+</sup> and the theoretical mass of the corresponding peptide are also shown to the right of the MS spectrum. (C) MSMS spectrum of the peptide fragment spanning residues 61-82 for the wild-type strain is depicted. The observed *y* and *b* ions and the fragment map are shown.

**Supplemental Table S1** *S. pombe* strains used in this study

Strain	Genotype	Source
SPYB109	<i>h<sup>90</sup> ade6-M216 leu1-32 ura4-D18</i>	This study
SPYB221	<i>h<sup>90</sup> ade6-M216 leu1-32 ura4-D18 Δset11::kan<sup>R</sup></i>	This study
SPYB881	<i>h<sup>90</sup> ade6-M216 leu1-32 ura4-D18 set11ΔNHSP</i>	This study
SPYB885	<i>h<sup>90</sup> ade6-M216 leu1-32 ura4-D18 set11ΔGE-Y</i>	This study
SPYB820	<i>h<sup>90</sup> ade6-M216 leu1-32 ura4-D18 Δset11::hyg<sup>R</sup></i>	This study
SPYB1279	<i>h<sup>90</sup> ade6-M216 leu1-32 ura4-D18 Δrpl1202::ura4<sup>+</sup></i>	This study
SPYB1282	<i>h<sup>90</sup> ade6-M216 leu1-32 ura4-D18 Δrpl1202::ura4<sup>+</sup> Δset11::hyg<sup>R</sup></i>	This study
SPYB739	<i>h<sup>90</sup> ade6-M210 leu1-32 ura4DS/E Δset11::kan<sup>R</sup> pREP1-EGFP-set11<sup>+</sup></i>	This study
SPYB733	<i>h<sup>90</sup> ade6-M210 leu1-32 ura4DS/E pREP1-EGFP-set11<sup>+</sup></i>	This study
SPYB200	<i>h<sup>90</sup> ade6-M216 his2 leu1-32 ura4DS/E pREP1</i>	This study
SPYB760	<i>h<sup>90</sup> ade6-M216 his2 leu1-32 ura4DS/E pREP1-set11<sup>+</sup></i>	This study
SPYB1369	<i>h<sup>90</sup> ade6-M210 leu1-32 ura4-D18 rpl1202<sup>+</sup>-3HA- kan<sup>R</sup> pREP1</i>	This study
SPYB1371	<i>h<sup>90</sup> ade6-M210 leu1-32 ura4-D18 rpl1202<sup>+</sup>-3HA- kan<sup>R</sup> pREP1-set11<sup>+</sup></i>	This study
SPYB1225	<i>h<sup>90</sup> ade6-M210 leu1-32 ura4-D18 rpl1202<sup>+</sup>-EGFP-kan<sup>R</sup></i>	This study
SPYB1232	<i>h<sup>90</sup> ade6-M210 leu1-32 ura4-D18 rpl1202<sup>+</sup>-EGFP-kan<sup>R</sup> Δset11::hyg<sup>R</sup></i>	This study

**Supplemental Table S2** Summary for LC-MS analysis of Rpl12ab K39 and K40

Total methyl group	Methyl group		Number of observed peptides	
	K39	K40	Wild type	<i>Δset11</i>
1Me	1	0	0	0
	0	1	1	1
2Me	2	0	43	32
	0	2	17	13
	1	1	1	5
6Me	3	3	5	7

