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Sp Npr2      MEYSEEGWMDQADSFPRLLAIFFALFDPLGGPIVACEAPAGSVTNVDGGKNCLLPFETI
Hs NPRL2     -----MGSGCRIECIEFFSEFHPTLGPKITYQVPEDFIS-----RELFDTV
              .  * : .***: *. *  ** : : . * . : :                * : * :

Sp Npr2      SDYVIPKRELCNKTITVCTNHYQVIGHPIISIGSNYERNALIFNMCMIFHEEEDSACYIP
Hs NPRL2     QVYIITKPELQNKLITVTAMEKKLIGCPVCI EHKKYSRNALLFNLGFVCDAAKTCALEP
              .  * : * . * ** * * * * : . : ** * : * . * : * : * : * : * : * : *

Sp Npr2      LVKRLARNLEVLKQIHYISDLNKRPIFSVIEQILEDMNNFCECMIQLDDQNSINIKLF
Hs NPRL2     IVKLAGYLTTLEESSFVSMEEKQKLPIMTILLEELNASGRCTLPIDESNTIHLKVI
              : * : * * * . * * : : * : : : : : : : * : * * . * : * : * : * : * :

Sp Npr2      PVFSPPTVKS FHPILT AQLDLLMDKNWDMTVQKVYPFINGINSVQRI AELANVSYRSC
Hs NPRL2     EQRPDPVVAQEYDVPVFTKDKEDFFNSQWDLTTQQILPYIDGFRHIQKISAEADVELNLV
              * . * . . : . * : * * : : : : : * : * . * : * : * : * : * : * .

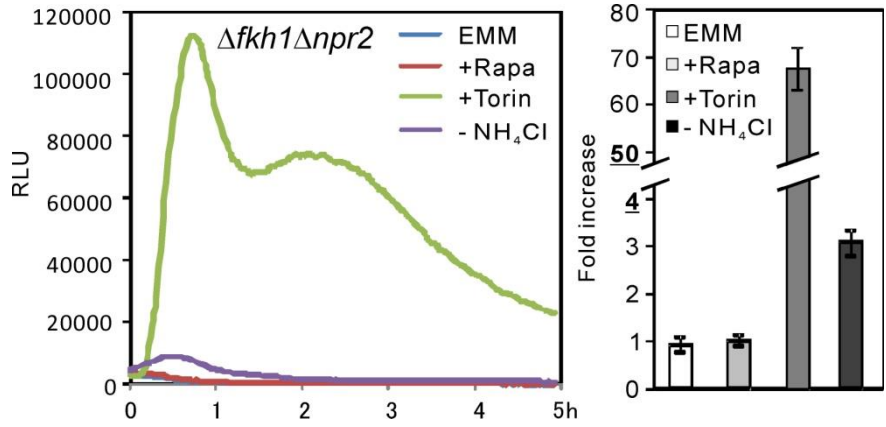
Sp Npr2      QKCMHFLLYYGCLIIADIFGFHNIYAMTTNAPNLLQDPDFQRECTAYVSTNSSNAKNVTF
Hs NPRL2     RIAIQNLLYYGVVTLVSI LQSNVYCPKQVQDLVDDKSLGEACLSYVTKQG—HKRASL
              : . : : : * * * * : : . * : * * * . * . : : * : * . * * * : : . * : :

Sp Npr2      ATIFKLYCSLRQGLRVKDWNNENKEIFKGLDVRRLISFGTIKGLIYRVHKYPYLERRTMR
Hs NPRL2     RDVFQLYCSLSPGTTVRDLIGRHPQQLQHVDERKLIQFGLMKNLIRRLQKYPVRVTR—
              : * : * * * * * * * * . * . : : : : * * * * * * * * * * * * * * *

Sp Npr2      NNLTEEEKLLGLLDGKHDFDEL CVTLKKS PKV V NEM IAGLGDACFIYV
Hs NPRL2     —EEQSHPARLYTGCHSYDEICCKTGMSYHELDERLENDPNI IICWK
              * : . : . * * * * * : * . * : * : : . : : :

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**Figure S1** Alignment of protein sequences of *Schizosaccharomyces pombe* (Sp) Npr2 with related proteins from humans (Hs) NPRL2. Sequence alignment was performed using the CLUSTALW program. Asterisks indicate identical amino acids, colons indicate strictly conserved amino acids and dots indicate conserved amino acids.



**Figure S2** The *fkh1* deletion abolished rapamycin-induced reporter activity in  $\Delta npr2$  cells. The  $\Delta fkh1\Delta npr2$  cells harboring the reporter vector pKB8527 were grown to exponential phase, and assayed as described in Figure 4A. Standard deviations of ratio are from three independent experiments, and each sample was analyzed in triplicate.

**Table S1 Fission yeast strains used in this study**

Strain	Genotype	Reference
HM123	<i>h<sup>-</sup> leu1-32</i>	Our stock
KP456	<i>h<sup>-</sup> leu1-32 ura4-D18</i>	Our stock
KP928	<i>h<sup>+</sup> his2 leu1-32 ura4-D18</i>	Our stock
KP207	<i>h<sup>+</sup> his2 leu1-32</i>	Our stock
KP91087	<i>h<sup>+</sup> leu1-32 ade6 ura4-D18 tsc2::KanMX<sub>4</sub></i>	(KIM <i>et al.</i> 2010)
KP90390	<i>h<sup>+</sup> leu1-32 ade6 ura4-D18 npr2::KanMX<sub>4</sub></i>	(KIM <i>et al.</i> 2010)
KP93006	<i>h<sup>+</sup> leu1-32 ade6 ura4-D18</i>	(KIM <i>et al.</i> 2010)
KP5131	<i>h<sup>-</sup> leu1-32 tsc2::KanMX<sub>4</sub></i>	This study
KP5236	<i>h<sup>+</sup> leu1-32 npr2::KanMX<sub>4</sub></i>	This study
KP5080	<i>h<sup>-</sup></i>	This study
KP5128	<i>h<sup>-</sup> tsc2::KanMX<sub>4</sub></i>	This study
KP5237	<i>h<sup>-</sup> npr2::KanMX<sub>4</sub></i>	This study
KP5395	<i>h<sup>-</sup> ura4-D18 tsc2::ura4<sup>+</sup></i>	(MATSUMOTO <i>et al.</i> 2002)
KP5482	<i>h<sup>-</sup> leu1-32 tor2-287</i>	(HAYASHI <i>et al.</i> 2007)
KP5734	<i>h<sup>+</sup> tor2-287</i>	This study
KP5637	<i>h<sup>+</sup> tor2-287 tsc2::KanMX<sub>4</sub></i>	This study
KP5579	<i>h<sup>+</sup> tor2-287 npr2::KanMX<sub>4</sub></i>	This study
KP5875	<i>h<sup>-</sup> tor2<sup>S1837E</sup>::KanMX</i>	(NAKASHIMA <i>et al.</i> 2010)
KP5873	JUP1350 <i>h<sup>90</sup> tor2<sup>L1310P</sup>::KanMX</i>	(URANO <i>et al.</i> 2007)
KP5874	JUP1352 <i>h<sup>90</sup> tor2<sup>E2221K</sup>::KanMX</i>	(URANO <i>et al.</i> 2007)

KP5490	<i>h<sup>+</sup>ura4-D18 tsc2::ura4<sup>+</sup> npr2::KanMX<sub>4</sub></i>	This study
KP5750	<i>h<sup>-</sup> leu1-32 ura4-D18 cat1::ura4<sup>+</sup></i>	This study
KP6029	<i>h<sup>-</sup> ura4-D18 cat1::ura4<sup>+</sup> tsc2::KanMX<sub>4</sub></i>	This study
KP6031	<i>h<sup>+</sup> ura4-D18 cat1::ura4<sup>+</sup> npr2::KanMX<sub>4</sub></i>	This study
KP6033	<i>h<sup>+</sup> ura4-D18 tor2-287 cat1::ura4<sup>+</sup></i>	This study
KP6034	<i>h<sup>+</sup> ura4-D18 cat1::ura4<sup>+</sup></i>	This study
KP2233	<i>h<sup>+</sup> leu1-32 his2 ura4-D18 fkh1::ura4<sup>+</sup></i>	(Sio <i>et al.</i> 2005)
KP5585	<i>h<sup>-</sup> leu1-32 ura4-D18 fkh1::ura4<sup>+</sup> npr2::KanMX<sub>4</sub></i>	This study
KP5855	<i>h<sup>-</sup> leu1-32 ura4-D18 tsc2::ura4<sup>+</sup> npr2::KanMX<sub>4</sub></i>	This study
KP5859	<i>h<sup>+</sup> ura4-D18 Cat1-GFP:ura4<sup>+</sup></i>	This study
KP5822	<i>h<sup>+</sup> ura4-D18 npr2::KanMX<sub>4</sub> Cat1-GFP:ura4<sup>+</sup></i>	This study
KP5826	<i>h<sup>+</sup> ura4-D18 tsc2::KanMX<sub>4</sub> Cat1-GFP:ura4<sup>+</sup></i>	This study
KP5955	<i>h<sup>+</sup> ura4-D18 tor2-287 Cat1-GFP:ura4<sup>+</sup></i>	This study
KP5903	<i>h<sup>-</sup> gtr1::KanMX<sub>6</sub></i>	(VALBUENA <i>et al.</i> 2012)
KP5904	<i>h<sup>-</sup> ura4-D18 gtr2::ura4<sup>+</sup></i>	(VALBUENA <i>et al.</i> 2012)
KP5914	<i>h<sup>+</sup> ura4-D18 tor2-287</i>	This study
KP5968	<i>h<sup>+</sup> ura4-D18 gtr2::ura4<sup>+</sup> tor2-287</i>	This study
KP5974	<i>h<sup>+</sup> ura4-D18 gtr2::ura4<sup>+</sup> npr2::KanMX<sub>4</sub></i>	This study
KP6385	<i>h<sup>-</sup> ura4-D18 tor2-287 npr2::KanMX<sub>4</sub> Cat1-GFP:ura4<sup>+</sup></i>	This study
KP6366	<i>h<sup>-</sup> npr2::natMX<sub>6</sub></i>	This study
KP6402	<i>h<sup>-</sup> npr2::natMX<sub>6</sub> tor2<sup>S1837E</sup>:KanMX</i>	This study

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**Table S2 Binding of Npr2 with components of the SEA complex in fission yeast**

Budding yeast gene	Homolog in fission yeast	Product	Binding with Npr2
<i>SEH1</i>	SPAC15F9.02	nucleoporin Seh1	ND
<i>SEA1/IML1</i>	SPBC26H8.04c	DEP domain protein, human ortholog DEPDC5	+
<i>SEA2</i>	SPAC4F8.11	WD repeat protein, human family WDR24	+
<i>SEA3</i>	SPAC11E3.05	ubiquitin-protein ligase E3, human ortholog WDR59	+
<i>SEA4</i>	SPAC12G12.01c/ SPAC630.02	ubiquitin-protein ligase E3	+
<i>NPR3</i>	SPBC543.04/Npr3	Npr2/3 complex subunit Npr3	+

ND indicates not determined.

+ indicates the binding with Npr2 was demonstrated based on the *S. pombe* predicted protein interaction database ([www.bahlerlab.info/PInt](http://www.bahlerlab.info/PInt)).