SUPPLEMENTARY MATERIAL.

Fission yeast SWI/SNF and RSC complexes show compositional and functional differences from budding yeast

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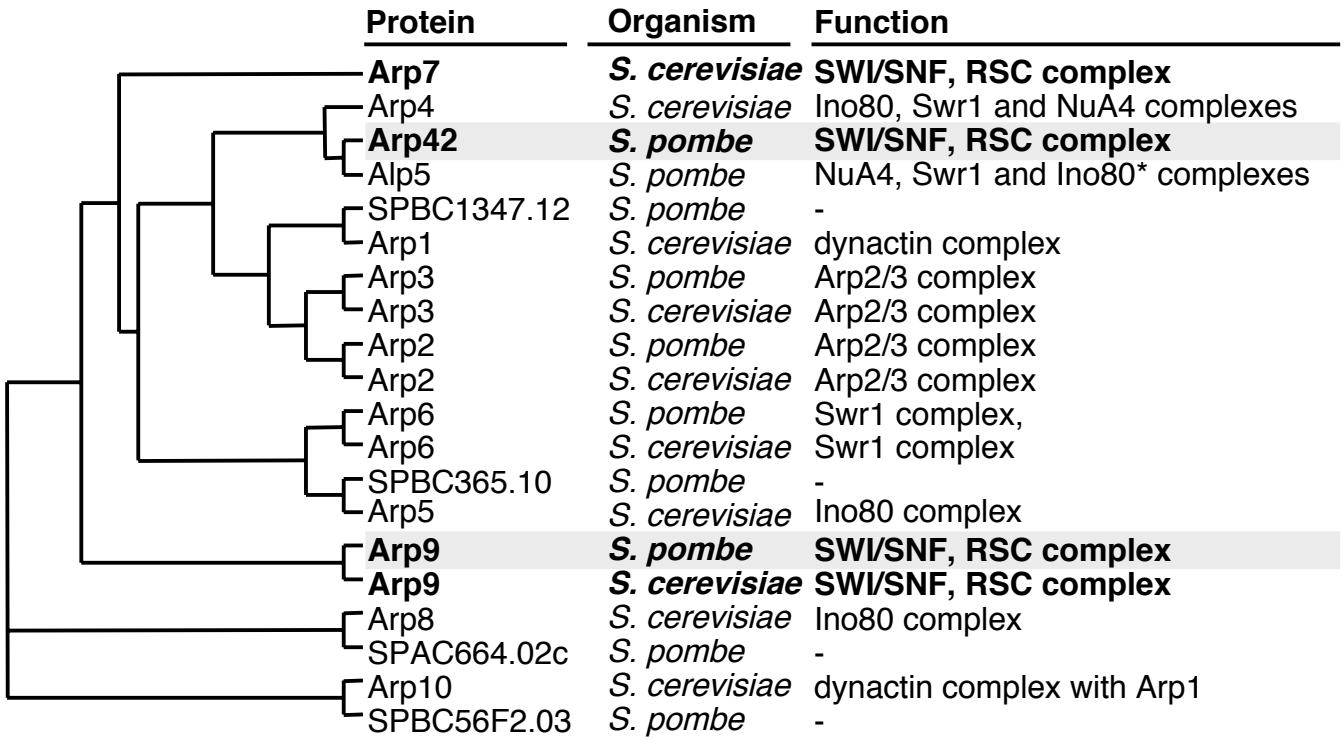
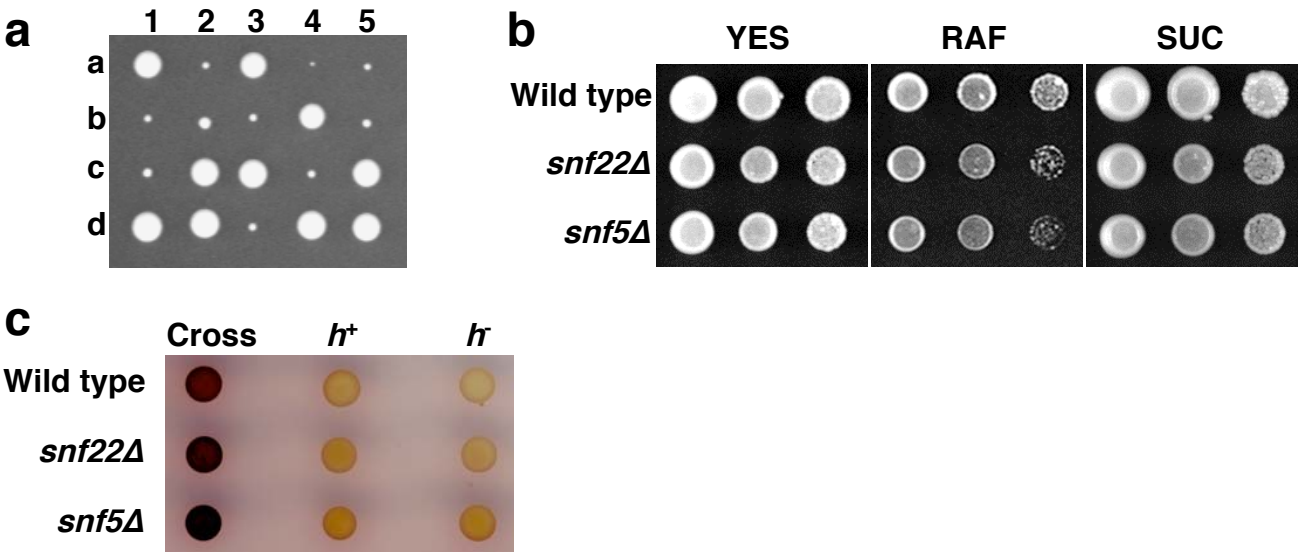


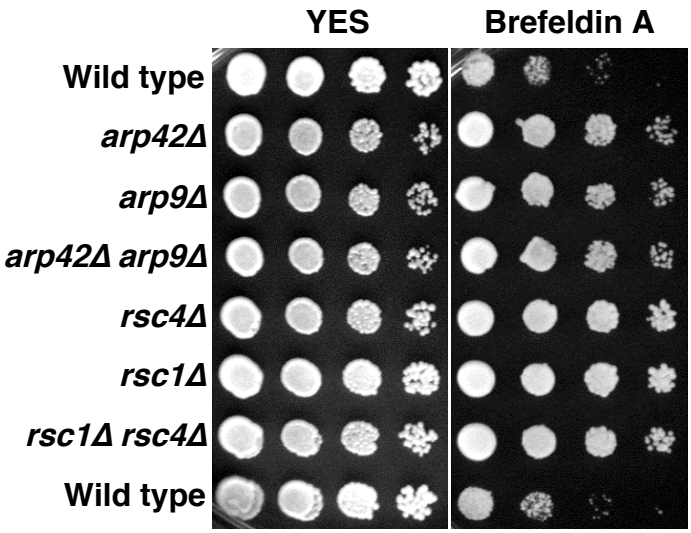
Supplementary Figure 1. *S. pombe* actin related protein (ARP) family. A dendrogram showing relatedness of the ten *S. pombe* and *S. cerevisiae* ARPs. *S. pombe* does not contain a gene encoding an Arp7 homolog but does contain two apparent Arp4 paralogs, named Alp5 and Arp42. ARPs present in SWI/SNF and RSC are highlighted in bold with the *S. pombe* complexes shaded in grey boxes. Putative function or association of each ARP is indicated where applicable. The tree was constructed by the neighbor-joining method with ClustalX[4].



Supplementary Figure 2. Deletion analysis of *S. pombe* SWI/SNF and RSC genes (**a**) The *S. pombe rsc58*Δ mutant displays a severe growth phenotype. Shown are progeny after sporulation and tetrad dissection of a *rsc58*$^{+}$/*rsc58*Δ diploid. The four progeny of each tetrad are labeled a-d. The small colonies are *rsc58*Δ and the large colonies are *rsc58*$^{+}$. (**b** and **c**) *S. pombe* SWI/SNF mutants do not display phenotypes characteristic of *S. cerevisiae* SWI/SNF mutants. In contrast to phenotypes noted for *S. cerevisiae* SWI/SNF mutants *S. pombe snf22*Δ and *snf5*Δ mutants display wildtype growth on media containing sucrose or raffinose as the sole carbon source (**b**). (**c**) *S. pombe snf22*Δ/*snf22*Δ and *snf5*Δ/*snf5*Δ mutants display normal sporulation although a small proportion of asci have incorrect spore number (data not shown). Iodine staining of mating plates is shown. As a negative control, staining of the *h*$^{+}$ and *h*$^{-}$ parent strains is also shown.

	SYSTEMATIC	Protein	Arp42:TAP		Arp9:TAP		no tag
			Exp 1	Exp 2	Exp 1	Exp 2	
RSC	SPAC1250.01	Snf21	116	93	108	97	0
	SPBC4B4.03	Rsc1	52	43	54	41	0
	SPBC1703.02	Rsc9	55	49	46	44	0
	SPBC1734.15	Rsc4	44	34	46	31	0
	SPCC16A11.14	Sfh1	22	15	20	17	0
	SPAC1F3.07c	Rsc58	22	21	19	21	0
	SPCC1281.05	Rsc7	24	20	25	19	0
Shared	SPAC17G6.10	Ssr1	45	37	49	35	0
	SPAC23H3.10	Ssr2	37	35	36	31	0
	SPAC23G3.10c	Ssr3	47	44	48	38	0
	SPBP23A10.05	Ssr4	30	29	31	28	0
	SPAC1071.06	Arp9	37	25	37	34	0
	SPAC23D3.09	Arp42	31	30	33	30	0
Swi/Snf	SPCC1620.14c	Snf22	54	41	39	41	0
	SPBC30B4.04c	Sol1	28	27	24	28	0
	SPAC2F7.08c	Snf5	22	16	20	18	0
	SPBC26H8.09c	Snf59	29	29	22	25	0
	SPAC23G3.07c	Snf30	9	8	6	7	0
	SPAC22H12.02	Tfg3	1	2	0	2	0
Ino80	SPAC29B12.01	Ino80	0	0	0	0	0
	SPBC365.10	Arp5	0	0	0	0	0
	SPAC664.02C	Arp8	0	0	0	0	0
	SPBC28F2.11	(Nhp10)	0	0	0	0	0
Swr1	SPAPB8E5.09	Rvp1	1	0	0	0	1
	SPBC83.08	Rvp2	0	0	1	0	0
	SPBP23A10.08*	Alp5	0	0	0	0	0
	SPBC32H8.12c*	actin	19	9	21	10	11
	SPAC11E3.01c	Swr1	0	0	0	0	0
	SPCC550.12	Arp6	0	0	0	0	0
	SPBP35G2.13C	Swc2	0	0	0	0	0
	SPAC9G1.13C*	Swc4	0	0	0	0	0
	SPCC576.13	Swc5	0	0	0	0	0
	SPAC17G8.07*	(Yaf9)	0	0	0	0	0
	SPBC29A3.05	(Vps71)	0	0	0	0	0
NuA4	SPAC637.12C	Mst1	0	0	0	0	0
	SPCC1795.08C	(Eaf1)	0	0	0	0	0
	SPAC23H4.12	Alp13	0	0	0	0	0
	SPAC6F6.09	(Eaf6)	0	0	0	0	0
	SPBC16A3.19	Eaf7	0	0	0	0	0
	SPCC830.05C	Epl1	0	0	0	0	0
	SPBC1709.11C	Png2	0	0	0	0	0
	SPBP16F5.03C	Tra1	0	0	0	0	0

Supplementary Figure 3. The *S. pombe* actin related proteins Arp42 and Arp9 are specific to the SWI/SNF and RSC chromatin remodeling complexes. Mass-spectrometry analysis of duplicate Arp42-TAP and Arp9-TAP purifications are shown. The number of unique peptides identified in the mass-spectra for the respective protein for each purification is shown. To illustrate specificity of Arp42 and Arp9, various proteins predicted to be members of the *S. pombe* chromatin remodeling or modifying complexes known to contain ARPs, namely NuA4, Swr1 and Ino80, are shown. The name of the respective complex is indicated on the left. Asterisks represent proteins that are also putative components of the NuA4 complex.



Supplementary Figure 4. *S. pombe* RSC mutants show brefeldin A resistance. Wild type (FWP52), *arp42*Δ (FWP239), *arp9*Δ (FWP240), *arp42*Δ *arp9*Δ (FWP249), *rsc1*Δ (FWP234), *rsc4*Δ (FWP242), and *rsc1*Δ *rsc4*Δ (FWP250) strains were grown in liquid YES medium to stationary phase, subjected to 10-fold serial dilutions, and spotted onto solid YES medium containing 10 μg ml^{-1} brefeldin A.

Supplementary Table 1. Summary of BLASTP analysis of the *S. pombe* protein set searching for RSC (a) and SWI/SNF (b).

(a)

***S. cerevisiae* RSC complex**			***S. pombe* BLASTP top hit(s)[1]**			
protein	**systematic**	**size (aa)**	**protein**	**systematic**	**size (aa)**	**e-value**
Sth1	YIL126W	1359	**Snf21**	**SPAC1250.01**	**1199**	**7E-262**
			Snf22	SPCC1620.14c	1680	3E-253
Rsc1	YGR056W	928	**Rsc1**	**SPBC4B4.03**	**803**	**1E-56**
Rsc2	YLR357W	889	**Rsc1**	**SPBC4B4.03**	**803**	**1E-58**
Rsc3	YDR303C	885		SPAPB1A11.04c	697	2E-06
Rsc30	YHR056C	832	Moc3	SPAC821.07c	497	2E-05
Rsc4	YKR008W	625	**Rsc4**	**SPBC1734.15**	**542**	**3E-17**
Rsc9	YML127W	581	**Rsc9**	**SPBC1703.02**	**780**	**1E-23**
Rsc8	YFR037C	557	**Ssr2**	**SPAC23H3.10**	**503**	**4E-73**
			Ssr1	**SPAC17G6.10**	**527**	**5E-64**
Rsc58	YLR033W	502		SPBC215.07c	568	6E-02
Rsc6	YCR052W	483	**Ssr3**	**SPAC23G3.10c**	**425**	**5E-15**
Arp7	YPR034W	477	**Arp42**	**SPAC23D3.09**	**430**	**4E-27**
Arp9	YMR033W	467	**Arp9**	**SPAC1071.06**	**523**	**3E-21**
Rsc7	YMR091C	435	**Rsc7**	**SPCC1281.05**	**390**	**2E-46**
Sfh1	YLR321C	426	**Sfh1**	**SPCC16A11.14**	**418**	**1E-33**
Rtt102	YGR275W	186	Swr1	SPAC2H10.03c	1288	7E-02
Ldb7	YBL006C	145		No hits, E < 0.01		
Htl1	YCR020W-B	78	Mde1	SPBC31F10.08	209	3E-02

(b)

***S. cerevisiae* SWI/SNF complex**			***S. pombe* BLASTP top hit(s)[1]**			
protein	**systematic**	**size (aa)**	**protein**	**systematic**	**size (aa)**	**e-value**
Snf2	YOR290C	1703	**Snf22**	**SPCC1620.14c**	**1680**	**6E-279**
			Snf21	SPAC1250.01	1199	2E-231
Swi1	YPL016W	1314	**Sol1**	**SPBC30B4.04c**	**865**	**7E-24**
Snf5	YBR289W	905	**Snf5**	**SPAC2F7.08c**	**632**	**8E-45**
Swi3	YJL176C	825	**Ssr2**	**SPAC23H3.10**	**503**	**9E-60**
			Ssr1	**SPAC17G6.10**	**527**	**3E-51**
Swp82	YFL049W	623	Rsc7	SPCC1281.05	390	1E-11
Snf12	YNR023W	566	**Ssr3**	**SPAC23G3.10c**	**425**	**1E-22**
Arp7	YPR034W	477	**Arp42**	**SPAC23D3.09**	**430**	**4E-27**
Arp9	YMR033W	467	**Arp9**	**SPAC1071.06**	**523**	**3E-21**
Snf6	YHL025W	332		No hits E < 0.01		
Taf14	YPL129W	244	**Tfg3**	**SPAC22H12.02**	**241**	**3E-48**
Rtt102	YGR275W	186	Swr1	SPAC2H10.03c	1288	7E-02
Snf11	YDR073W	169	-	SPBC660.06	273	1E-03

[1] Bold indicates that the protein was subsequently identified as a component of the respective complex.

Supplementary Table 2. Deletion analysis of *S. pombe* SWI/SNF and RSC genes and comparison to *S. cerevisiae*

S. pombe		***S. cerevisiae***	
subunit[a]	deletion phenotype	ortholog	deletion phenotype
Snf22	viable	Snf2	viable
Snf5	viable	Snf5	viable
Sol1	viable	Swi1	viable
Tfg3	viable	Taf14	viable
Snf59	viable	Swp82	viable
Snf30	viable		
Ssr1	inviable	Swi3[b], Rsc8[c]	*swi3Δ* viable, *rsc8Δ* inviable
Ssr2	inviable	Swi3[b], Rsc8[c]	*swi3Δ* viable, *rsc8Δ* inviable
Ssr3	inviable	Snf12[b], Rsc6[c]	*snf12Δ* viable, *rsc6Δ* inviable
Ssr4	inviable		
Arp42	viable		
Arp9	viable	Arp9	inviable or sick[d]
Snf21	inviable	Sth1	inviable
Sfh1	inviable	Sfh1	inviable
Rsc9	inviable	Rsc9	inviable
Rsc7	inviable	Rsc7	viable
Rsc1	viable	Rsc1, Rsc2	double mutant inviable
Rsc4	viable	Rsc4	inviable
Rsc58	viable	Rsc58	inviable

[a]The top group of subunits in the unshaded boxes is in *S. pombe* SWI/SNF, the middle shaded group is shared between SWI/SNF and RSC, and the bottom unshaded group is in *S. pombe* RSC.

[b]Part of *S. cerevisiae* SWI/SNF.

[c]Part of *S. cerevisiae* RSC.

[d]The null phenotype depends upon the genetic background[1].

Supplementary Table 3. Mass-spectrometry analysis of RSC and SWI/SNF purifications in the presence or absence of Arp42 and Arp9. Shared components are within grey box with RSC-specific subunits above and SWI/SNF-specific subunits below. This analysis also indicated that no other *S. pombe* ARP or actin substitute for either *arp42*Δ or *arp9*Δ. The 10 *S. pombe* ARPs and actin(Act1) are shown in red.

	RSC (Snf21-TAP)				SWI/SNF (Snf21-TAP)				controls	
	350 mM NaCl		150 mM NaCl		350 mM NaCl		150 mM NaCl		350	150
protein	*arp+*	*arp*Δ	*arp+*	*arp*Δ	*arp+*	*arp*Δ	*arp+*	*arp*Δ		
Snf21	103[a]	123	130	109	10	7	9	9	2	1
Rsc1	44	45	53	47	0	0	0	1	0	0
Rsc9	50	47	60	45	2	3	0	1	0	0
Rsc4	35	36	46	36	0	0	0	0	0	0
Sfh1	16	15	20	20	1	0	0	0	1	0
Rsc58	17	18	23	22	1	0	0	0	0	1
Rsc7	21	24	27	21	0	0	0	0	1	1
Ssr1	39	46	44	38	42	44	38	40	1	0
Ssr2	37	38	39	31	32	33	29	38	0	2
Ssr3	50	50	52	46	40	40	40	41	0	0
Ssr4	27	27	32	26	20	20	24	26	0	1
Arp9	**24**	**0**	**31**	**0**	**25**	**1**	**23**	**3**	**2**	**1**
Arp42	**29**	**0**	**30**	**0**	**30**	**0**	**23**	**0**	**0**	**1**
Snf22	0	1	0	0	96	90	99	97	0	0
Sol1	0	0	0	0	38	40	40	50	0	0
Snf5	0	0	0	0	47	35	39	33	0	0
Snf59	0	0	0	0	62	60	52	54	0	0
Snf30	0	0	0	0	20	18	17	12	0	0
Tfg3	0	0	0	0	9	9	5	11	0	0
Alp5	0	0	0	0	0	0	0	0	0	0
Arp1	0	0	0	0	0	0	0	0	0	0
Arp2	0	0	0	0	0	0	0	0	0	0
Arp3	0	0	0	0	0	0	0	0	0	0
Arp5	0	0	0	0	0	0	0	0	0	0
Arp6	0	0	0	0	0	0	0	0	0	0
Arp8	0	0	0	0	0	0	0	0	0	0
Arp10	0	0	0	0	0	0	0	0	0	0
Act1	25	19	21	22	28	25	34	23	25	9

[a]Number of unique peptides for the respective protein.

Supplementary Table 4. Microarray data of SWI/SNF mutants showing the fold-change in mRNA levels for the hexose and iron transporter genes and their known repressors (in blue).

gene	*snf22*Δ	*snf5*Δ	Description
fip1^{+}	4.3	3.2	Iron permease FTR1 family
frp1^{+}	15.0	10.4	Ferric reductase transmembrane component
fio1^{+}	2.5	2.2	iron transport multicopper oxidase
str1^{+}	2.2	2.1	Siderophore iron transporter
str2^{+}	1.7	1.5	Siderophore iron transporter
str3^{+}	8.1	14.1	Siderophore iron transporter
ght1^{+}	2.5	2.9	hexose transporter
ght2^{+}	2.0	1.6	hexose transporter
ght3^{+}	5.3	4.4	hexose transporter
ght4^{+}	11.4	10.3	hexose transporter
ght5^{+}	3.6	3.7	hexose transporter
ght6^{+}	4.3	3.0	hexose transporter
ght7^{+}	0.9	1.3	hexose transporter
ght8^{+}	3.4	2.5	hexose transporter
fep1^{+}	0.9	1.0	GATA transcription factor iron repressor
scr1^{+}	1.4	1.3	Mig1/CreA-like carbon catabolite repressor
tup11^{+}	1.1	1.1	transcriptional corepressor
tup12^{+}	1.2	1.2	transcriptional corepressor

Supplementary Table 5. *S. pombe* strains used in this study

Strain	Genotype	Source
FWP52	*h⁺ leu1-32 ade6-m216*	Lab stock
FWP165	*h⁺ ura4-D18 leu1-32 ade6-m216*	Lab stock
FWP172	*h⁻ ura4-D18 leu1-32 ade6-m210*	Lab stock
FWP253	*h⁺ fep1::ura4⁺ ura4-D18 leu1-32 ade6-M210 his7-366*	Pelletier *et al*[2]
FWP197	*h⁻ tup11::ura4⁺ tup12::ura4⁺ ura4-D18 leu1-32*	Janoo *et al*[3]
FWP218	*h⁺ snf21⁺-TAP::KANMX6 ura4-D18 leu1-32 ade6-m216*	This study
FWP219	*h⁺ snf22⁺-TAP::KANMX6 ura4-D18 leu1-32 ade6-m216*	This study
FWP220	*h⁺ snf5⁺-TAP::KANMX6 ura4-D18 leu1-32 ade6-m216*	This study
FWP221	*h⁺ sfh1⁺-TAP::KANMX6 ura4-D18 leu1-32 ade6-m216*	This study
FWP222	*h⁺ snf59⁺-TAP::KANMX6 ura4-D18 leu1-32 ade6-m216*	This study
FWP223	*h⁺ snf30⁺-TAP::KANMX6 ura4-D18 leu1-32 ade6-m216*	This study
FWP224	*h⁺ rsc7⁺-TAP::KANMX6 ura4-D18 leu1-32 ade6-m216*	This study
FWP225	*h⁺ rsc1⁺-TAP::KANMX6 ura4-D18 leu1-32 ade6-m216*	This study
FWP226	*h⁺ arp42⁺-TAP::KANMX6 ura4-D18 leu1-32 ade6-m216*	This study
FWP227	*h⁺ arp9⁺-TAP::KANMX6 ura4-D18 leu1-32 ade6-m216*	This study
FWP287	*h⁺*	This study
FWP289	*h⁺ snf22⁺-TAP::KANMX6*	This study
FWP228	*h⁺/h⁻ snf21::ura4⁺ ura4-D18 /ura4-D18 leu1-32/leu1-32 ade6m216/ade6-m210*	This study
FWP229	*h⁺ snf22::ura4⁺ ura4-D18 leu1-32 ade6-m216*	This study
FWP230	*h⁻ snf22::ura4⁺ ura4-D18 leu1-32 ade6-m210*	This study
FWP231	*h⁺ snf5::ura4⁺ ura4-D18 leu1-32 ade6-m216*	This study
FWP232	*h⁻ snf5::ura4⁺ ura4-D18 leu1-32 ade6-m210*	This study
FWP233	*h⁺/h⁻ sfh1::ura4⁺ ura4-D18 /ura4-D18 leu1-32/leu1-32 ade6-m216/ade6-m210*	This study
FWP234	*h⁺ rsc1::ura4⁺ ura4-D18 leu1-32 ade6-m216*	This study
FWP235	*h⁺/h⁻ rsc7::ura4⁺ ura4-D18 /ura4-D18 leu1-32/leu1-32 ade6-m216/ade6-m210*	This study
FWP236	*h⁺/h⁻ ssr1::ura4⁺ ura4-D18 /ura4-D18 leu1-32/leu1-32 ade6-m216/ade6-m210*	This study
FWP237	*h⁺/h⁻ ssr2::ura4⁺ ura4-D18 /ura4-D18 leu1-32/leu1-32 ade6-m216/ade6-m210*	This study
FWP238	*h⁺/h⁻ ssr3::ura4⁺ ura4-D18 /ura4-D18 leu1-32/leu1-32 ade6-m216/ade6-m210*	This study
FWP239	*h⁺ arp42::ura4⁺ ura4-D18 leu1-32 ade6-m210*	This study
FWP240	*h⁺ arp9::ura4⁺ ura4-D18 leu1-32 ade6-m210*	This study
FWP241	*h⁺/h⁻ ssr4::ura4⁺ ura4-D18 /ura4-D18 leu1-32/leu1-32 ade6-m216/ade6-m210*	This study
FWP242	*h⁺ rsc4::ura4⁺ ura4-D18 leu1-32 ade6-m216*	This study
FWP243	*h⁺/h⁻ rsc9::ura4⁺ ura4-D18 /ura4-D18 leu1-32/leu1-32 ade6-m216/ade6-m210*	This study
FWP244	*h⁺ rsc58::ura4⁺ ura4-D18 leu1-32 ade6-m216*	This study
FWP245	*h⁺ sol1::ura4⁺ ura4-D18 leu1-32 ade6-m216*	This study
FWP246	*h⁺ tfg3::ura4⁺ ura4-D18 leu1-32 ade6-m216*	This study
FWP247	*h⁺ snf59::ura4⁺ ura4-D18 leu1-32 ade6-m216*	This study
FWP248	*h⁺ snf30::ura4⁺ ura4-D18 leu1-32 ade6-m216*	This study
FWP249	*h⁺ arp42::ura4⁺ arp9::ura4⁺ ura4-D18 leu1-32 ade6-m210*	This study
FWP250	*h⁺ rsc1::ura4⁺ rsc4::ura4⁺ ura4-D18 leu1-32 ade6-m216*	This study
FWP251	*h⁺ snf21⁺-TAP::KANMX6 arp42::ura4⁺ arp9::ura4⁺ ura4-D18 leu1-32 ade6-m210*	This study
FWP252	*h⁺ snf22⁺-TAP::KANMX6 arp42::ura4⁺ arp9::ura4⁺ ura4-D18 leu1-32 ade6-m216*	This study

Supplementary Table 6. Oligonucleotide primers used in this study.

Gene	Name	Sequence	Description
snf21^{+}	FO3577	TGTTTGTTTTTTATTTCAATAATAACGACCTGGAAATCGTCTATTTATGTGGTAATTTGGATTTTTGATCACAAATCGCCAGGGTTTTCCCAGTCACGAC	Deletion-For
	FO3578	AACAAAAAAAAAGACAATCTGTGTTTTTATGAGACTTCAGCACTTGCATCTATAGTAGTTCAAAAAAAGCAATTAATAGCGGATAACAATTTCACACAGGA	Deletion-Rev
	FO3569	AGGATGGCACATTAGCAACGCTTCGCGGAATGGAGGCGGAGGCTACATCGCAATTGGAAGACAGAATTGAAAATGAGGCTCGGATCCCCGGGTTAATTAA	TAP-For
	FO3570	AAAAAACAAAAAAAAAGACAATCTGTGTTTTTATGAGACTTCAGCACTTGCATCTATAGTAGTTCAAAAAAAGCAATTAATGAATTCGAGCTCGTTTAAAC	TAP-Rev
snf22^{+}	FO3579	TCCATTTGTACGTTGAGGGTTTTCGGTCATTGTTGTTGTAATATTGATTTGCGATTTACTAAAACACATTTCTCCGCGCCAGGGTTTTCCCAGTCACGAC	Deletion-For
	FO3580	CCTCACCTAACAAAATGTACCAAAATATTATAAACAAGGCATTAAAATAAAACGACAAAAGGTAAAACGTTAGTCCAGCGGATAACAATTTCACACAGGA	Deletion-Rev
	FO3571	TACCGTTGGATTCTGGTATAGTAAGCGCCGAAGATGACAAAGTTATTACTTATGAAGATTCTTCTTCTTCTTATTCGGAGCGGATCCCCGGGTTAATTAA	TAP-For
	FO3572	TAGTCCTCACCTAACAAAATGTACCAAAATATTATAAACAAGGCATTAAAATAAAACGACAAAAGGTAAAACGTTAGTCCGAATTCGAGCTCGTTTAAAC	TAP-Rev
snf5^{+}	FO3581	AAGAATGACACCGATATATGATATTCTTTCTAATAACATTTGCACTTAAACGAATCTTTACTTTTTTTTTAAATCTCGCCAGGGTTTTCCCAGTCACGAC	Deletion-For
	FO3582	CTGGTCCGTCGAGCTATCCATAACGTGAGTCAAATCTTGATTATGGTCTTTGATAAAGATTCTTCCAAAATTGTATAGCGGATAACAATTTCACACAGGA	Deletion-Rev
	FO3573	ATTTCCATATCCACTTGTTGTCAAGCTCGCATCAACAAAAAAAGGAGGTGAGAATGAATACGGTTTTGGATAGAAATACTCGGATCCCCGGGTTAATTAA	TAP-For
	FO3574	GAAACTGGTCCGTCGAGCTATCCATAACGTGAGTCAAATCTTGATTATGGTCTTTGATAAAGATTCTTCCAAAATTGTATGAATTCGAGCTCGTTTAAAC	TAP-Rev
sfh1^{+}	FO3583	CCAACTGTAAATTGACTTGCGGCTTACATAGTGTTTTTTGGCATACTTGTGCAAACTACCGACTTCACAATTTACACGCCAGGGTTTTCCCAGTCACGAC	Deletion-For
	FO3584	TTCTCCATTAAATTCGTCTCCTTAAAACACGACTAATGAACATCAAATACATCAGTCCATTAGAGTAAAACATCTTAGCGGATAACAATTTCACACAGGA	Deletion-Rev
	FO3575	ACAAATCATTGTGCAATGCTTGTGGTGTTGCATATGCTAAAACAGGACAATTGCCATATTGGAGAAAATCTCTATACACTCGGATCCCCGGGTTAATTAA	TAP-For
	FO3576	GACCTTCTCCATTAAATTCGTCTCCTTAAAACACGACTAATGAACATCAAATACATCAGTCCATTAGAGTAAAACATCTTGAATTCGAGCTCGTTTAAAC	TAP-Rev
rsc1^{+}	FO4016	TGATATACCCCGTTAAAAATCTTACGAACAAGGTACGGGTACGTCTTCCACGAAAACACCAAGAAAATCCATCAGTGAGACGCCAGGGTTTTCCCAGTCA	Deletion-For

	FO4017	ATATACATTATTAGGTTCTAAAAATCTTCAAATCTATCACAATATTTGTTTTCTAAAAATCACAGTGAGTAATTTTCACTAGCGGATAACAATTTCACAC	Deletion-Rev
	FO3575	ACAAATCATTGTGCAATGCTTGTGGTGTTGCATATGCTAAAACAGGACAATTGCCATATTGGAGAAAATCTCTATACACTCGGATCCCCGGGTTAATTAA	TAP-For
	FO3576	GACCTTCTCCATTAAATTCGTCTCCTTAAAACACGACTAATGAACATCAAATACATCAGTCCATTAGAGTAAAACATCTTGAATTCGAGCTCGTTTAAAC	TAP-Rev
rsc7^{+}	FO4018	AAAAAGCAATTTTTAACACAGTGCTATTCAGTACGATAAGATTGAACTGTTTATGGAATAAACACCTTGCAATTAAAGTACGCCAGGGTTTTCCCAGTCA	Deletion-For
	FO4019	TGATAAATGACTGTATACAATCTGAAAATTAATATTATAAAACATCCAAAACAAAATAGGATTAAAAGAAAACGAGCACTAGCGGATAACAATTTCACAC	Deletion-Rev
	FO3575	ACAAATCATTGTGCAATGCTTGTGGTGTTGCATATGCTAAAACAGGACAATTGCCATATTGGAGAAAATCTCTATACACTCGGATCCCCGGGTTAATTAA	TAP-For
	FO3576	GACCTTCTCCATTAAATTCGTCTCCTTAAAACACGACTAATGAACATCAAATACATCAGTCCATTAGAGTAAAACATCTTGAATTCGAGCTCGTTTAAAC	TAP-Rev
ssr1^{+}	FO4020	TGCATTTTATTGACGTGAAGCTTTTAAAGCCCTTGGCGTTGAGGATTTTGTAAATATTATACTAGACTCTAACACCACAACGCCAGGGTTTTCCCAGTCA	Deletion-For
	FO4021	ATTAAGATAAGATAAAAAAAAAATTCATTTAAATAAAAGCCTAATAAATTTTTATCCGATAAGCATATTAGTTGAGATTAAGCGGATAACAATTTCACAC	Deletion-Rev
ssr2^{+}	FO4022	TTACAACTTAAAAACAACTTAATTTTGTGGGTATTACATTTTTTTCGTGAGTGGACTATTCAAAAATCAGACCTTCACGACGCCAGGGTTTTCCCAGTCA	Deletion-For
	FO4023	TACATATATATATGTCTATAAAAACTAGATAGCCAAAAGAACTTCATGCAGAATACAAATTTGAATTTGGTGAACCTAACAGCGGATAACAATTTCACAC	Deletion-Rev
ssr3^{+}	FO4024	ACGTCCACCAAATATCGAAGATTATTGATCGGTTCGGATTGCCGCATATTTGAGAGGAGCTTGAATAAGGACAGCTTATCCGCCAGGGTTTTCCCAGTCA	Deletion-For
	FO4025	AATTTGTAAATAATATACACGTTTGTGACACACGCAGGAATATACCGTTGCTTTCTACTGGTAACGTAGTAATAGTCTATAGCGGATAACAATTTCACAC	Deletion-Rev
arp42^{+}	FO4031	ATACTAAACTATTTACATAGACATGGGTAAGTGCGGTTAATCAACCATAATATGTGTTGAGACGAAGACAATGGCATGAACGCCAGGGTTTTCCCAGTCA	Deletion-For
	FO4026	TGCGAGATTTCGTAAATTTATTTTATACTCTCTTGGGTTTTGAAGACTTTATTTTTTGTGAGCAAATAACACAGGCGGATAGCGGATAACAATTTCACAC	Deletion-Rev
	FO5236	TTCAACATTTGTGGGTATCTAAGCAAGAGTACGATGAAGTAGGTGTTGACAGAGCTTTGTTTGTTGAGAAAAGATGCAAGCGGATCCCCGGGTTAATTAA	TAP-For
	FO5237	ATGCGAGATTTCGTAAATTTATTTTATACTCTCTTGGGTTTTGAAGACTTTATTTTTTGTGAGCAAATAACACAGGCGGAGAATTCGAGCTCGTTTAAAC	TAP-Rev
arp9^{+}	FO4027	AGATTAGTGAGTAGTATGACTTGTATCGTAAACCACAATTCATCCATAGCACAACCAAAGCAATCGGTTTGGGAAAACGACGCCAGGGTTTTCCCAGTCA	Deletion-For

	FO4028	AAGTACCTTTCGCACGAGTCAATTGATTTCTTAAAATACCGT GACAGGCAATTAAACTTTTATGTGATGAACGAGAGTAAAGC GGATAACAATTTCACAC	Deletion-Rev
	FO5238	TTAATGAATCTGTATCTTCCCATTATGTTACACTTGAGGAATA TGCCCAACATGGACCCACAGCGATTCATACAAAGCAACGGA TCCCCGGGTTAATTAA	TAP-For
	FO5239	AAGTACCTTTCGCACGAGTCAATTGATTTCTTAAAATACCGT GACAGGCAATTAAACTTTTATGTGATGAACGAGAGTAAGAAT TCGAGCTCGTTTAAAC	TAP-Rev
ssr4^{+}	FO4029	AACAAAGCCAAAACTTCTGCATCTTGATAGATATGAGTAAGT TGTACCATCCAAAACTTACATATAATTAAAATCAACAACGCC AGGGTTTTCCCAGTCA	Deletion-For
	FO4030	TAAAGTAGGACGTACGTACTTTTCAAATCTTCTTTCTGATTA GCCTCAACATGTTTTTTCTATACTACACTTTAAATCTTAGCGG ATAACAATTTCACAC	Deletion-Rev
rsc4^{+}	FO4285	CAGTCGCAAGCGGACCTAATTAAAGTTGATATACTCTATTCA TTGTACATAAACGTTGCAATATAATAAATTATTTAAAACGCCA GGGTTTTCCCAGTCACGAC	Deletion-For
	FO4286	TGTACATATTTCAAACGAATGATACCATTTATTTTAATTCCTT GTATTAATACATTTTGTCTCTATCCAAAAAGTGTAGCAGCGG ATAACAATTTCACACAGGA	Deletion-Rev
rsc9^{+}	FO4911	CCACTTAGTATTTCGAAAAGTTGTGAAAGGTTTCGTTATACT ACTTTTGACCACCTACTTACTTTACGACGCGCGCTTCACGC CAGGGTTTTCCCAGTCA	Deletion-For
	FO4912	ATATGAAAAGTGATGTCGAGATGCTTGACCTTAGCAATGAG ATTTAAAAGACATGTTATGACTATCGAGCCATCCAAAATAGC GGATAACAATTTCACAC	Deletion-Rev
rsc58^{+}	FO4913	TCTGGGCATATTTTGAGTATTTGAAACGCATTACCGTTATCC GGCCTTTTTTGATAGCAATTCGTAAAACAAACTCGGCACGC CAGGGTTTTCCCAGTCA	Deletion-For
	FO4914	TATATATATGTATGTATATACATCTATTAATTAGTTAAACTAAA ATCTTTAAGTAACACCATGGAAATAGAGAACGAATTAGCGGA TAACAATTTCACAC	Deletion-Rev
sol1^{+}	FO4915	CCAAGCGCCTTAGACGTTAATATATTGAAACGTGTATTTTAA GGTCCCTTTACTCTTTGTTTGATTTAGTATGAGGAATCCGCC AGGGTTTTCCCAGTCA	Deletion-For
	FO4916	GACAATATACATACAGAAACGCATCAGATTAACTAGAATGAA GACAAAAATATTAAACGTTTGGAAAATTATCTACAAATAGCG GATAACAATTTCACAC	Deletion-Rev
taf14^{+}	FO4917	GCCCGATATCTCTTCTCACGACTCGCTAAGCGTCTTCTATCC ATATATTTTTCGTCCTCATATACATTGATTTAAGAATACGCCA GGGTTTTCCCAGTCA	Deletion-For
	FO4918	CAGTCTTCAGGAAAAAAGTAGAATGGGGAAACTAACGCTTC TCCCTTAAAGTAGGCTGCACAAAACTGCAATGCTCTTAAAGC GGATAACAATTTCACAC	Deletion-Rev
snf59^{+}	FO4919	AATTAGGTACAAGTCTATAAAATCACGCTTGGTTTTGGAATT GATATTCGTAACATTTTCGTTTGACACCAACTTTTCTTCGCC AGGGTTTTCCCAGTCA	Deletion-For
	FO4920	ACCAATAGCAACTAGCCTAAATCCACTTGATCGAAAATATGA TAGCTCAGCAATGCAATTAATAATTTTTAATATAAAGTAGCG GATAACAATTTCACAC	Deletion-Rev
	FO3968	TCATGAGGACAAGAAATCTAAGGAAAGAAGCAAGGTTAAGT TATTATACAAAATTACGAGGTGTCAACAGATCTGTTTCACGG ATCCCCGGGTTAATTAA	TAP-For

	FO3969	ACCAATAGCAACTAGCCTAAATCCACTTGATCGAAAATATGA TAGCTCAGCAATGCAATTAATAATTTTTAATATAAAGTGAATT CGAGCTCGTTTAAAC	TAP-Rev
snf30^{+}	FO4921	ACAAGAAGTTACAACAAATTTTTTAAAAAAACTGGTTATTTAA GTTATATCTCCTTTTTAAGTTAACTACGTTTGTAATACGCCAG GGTTTTCCCAGTCA	Deletion-For
	FO4922	TTACGTTTAGATAAATGATCAATTAAAACATAAAATTACAGGA CATAGCTTTTCTATATCATAAACTTCAAAAACACCACAGCGG ATAACAATTTCACAC	Deletion-Rev
	FO3970	GTTTTTTTGATTCACAACAAGCTCAAGTTCAGGCTCGAGCAT TGATGCAAAGATATCAACAGGGGATGGAATTTAACAAACGG ATCCCCGGGTTAATTAA	TAP-For
	FO3971	TTACGTTTAGATAAATGATCAATTAAAACATAAAATTACAGGA CATAGCTTTTCTATATCATAAACTTCAAAAACACCACGAATTC GAGCTCGTTTAAAC	TAP-Rev
fip1^{+}	FO6125	GTCGGAGTTGGTGTCCACTT	ChIP
	FO6126	GCCAATGTCCTTTGTCTCGT	ChIP
str3^{+}	FO6127	GCTAATCAGTAACCAGGGTTGT	ChIP
	FO6128	CACCGCGGTTAAGAAGCTC	ChIP
frp1^{+} 3'	FO5994	CTTCCAGACTTCGGAGTGAA	ChIP
	FO5995	TTTCCAAAAGCAAACGGAGT	ChIP
frp1^{+}	FO5990	TGTACAAAGCCTCCCCTCTG	ChIP
	FO5991	GCCGCTTCCGCTATACACTA	ChIP
pex7^{+}	FO6270	TCCCACCCTTATCGAAGCTA	ChIP
	FO6271	GCGAAGCTTGTTTCCTCAAC	ChIP
obr1^{+}	FO6272	ACCCAAAGTCCCCCACTTAG	ChIP
	FO6273	CAAACCGATTTTGTGCTTGA	ChIP
pho1^{+}	FO6282	TGGTTCGGGACACATTTACA	ChIP
	FO6283	CACAAACGAAACCAACAACG	ChIP
spo3^{+}	FO4013	GTGCGCTTCAATGAGTTAACACTC	ChIP
	FO4014	AGTGTGGGGAAACTTTTATTAATC	ChIP
hcs1^{+}	FO6129	GCGAATTGTTCACTTGTCCA	ChIP
	FO6130	TCATACGTTCACGTTTCTCG	ChIP
	FO5758	CTCGTGTTGTACACTCCCAAT	RT-PCR
	FO5759	CTTCCAAACGACCAATCTTGC	RT-PCR
ght3^{+}	FO5113	GAAGAATTCATTGAAAATGCT	RT-PCR
	FO5764	TCTAGAACTGCCTCGCTATCA	RT-PCR
ght4^{+}	FO5115	ACGTTTTATCGAAAATGCAGA	RT-PCR
	FO5765	CCTCATGAAACTAGTCACTTCC	RT-PCR
ght5^{+}	FO5117	TCTAGCAATGACATTAGTTCC	RT-PCR
	FO5766	AAATGCAGCGAGTGAGACAAG	RT-PCR

Supplementary references.

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