Supplemental Information

Red1 Promotes the Selective Elimination of Meiosis-Specific Transcripts in Growing Fission Yeast

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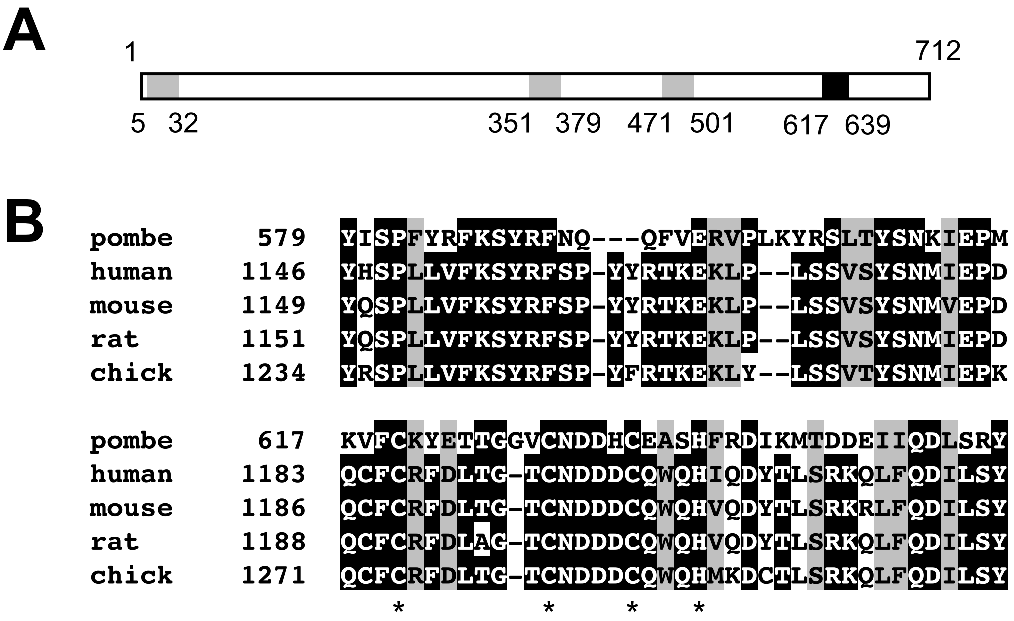
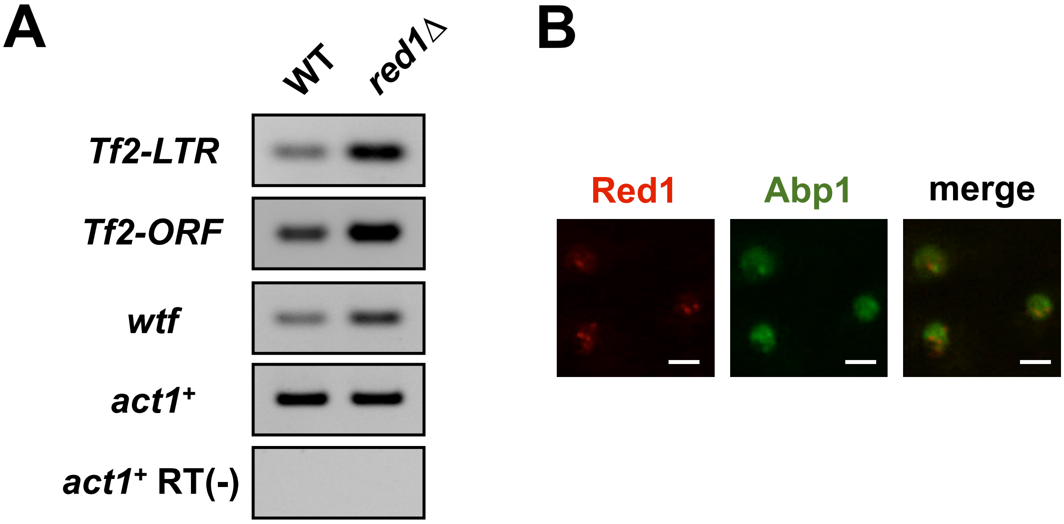
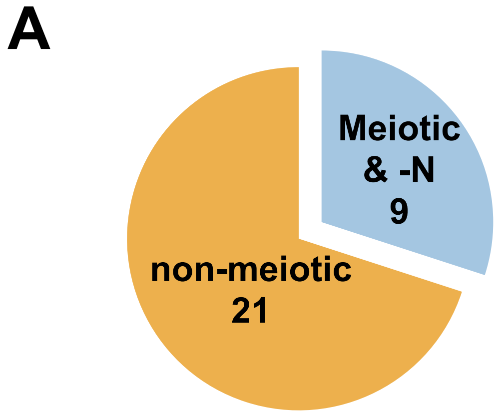


Supplementary Figure S1 A multiple alignment of Zn-finger domains of Red1 and Red1 homologs. **(A)** Schematic representation of Red1 protein. The gray and black boxes represent the coiled-coil domain and the CCCH-type Zn-finger domain, respectively. **(B)** The amino acid sequences of Zn-finger domains in Red1 (NP_594850) and Red1 homologs in human (NP_659419), mouse (NP_001028433), rat (XP_235146), and chicken (XP_416097) were aligned by Basic ClustalW alignment (http://insilico.ehu.es/clustalw/). The asterisks indicate the conserved cysteine and histidine residues in the Zn-finger. The black and gray shades indicate identical and similar amino acid residues, respectively.

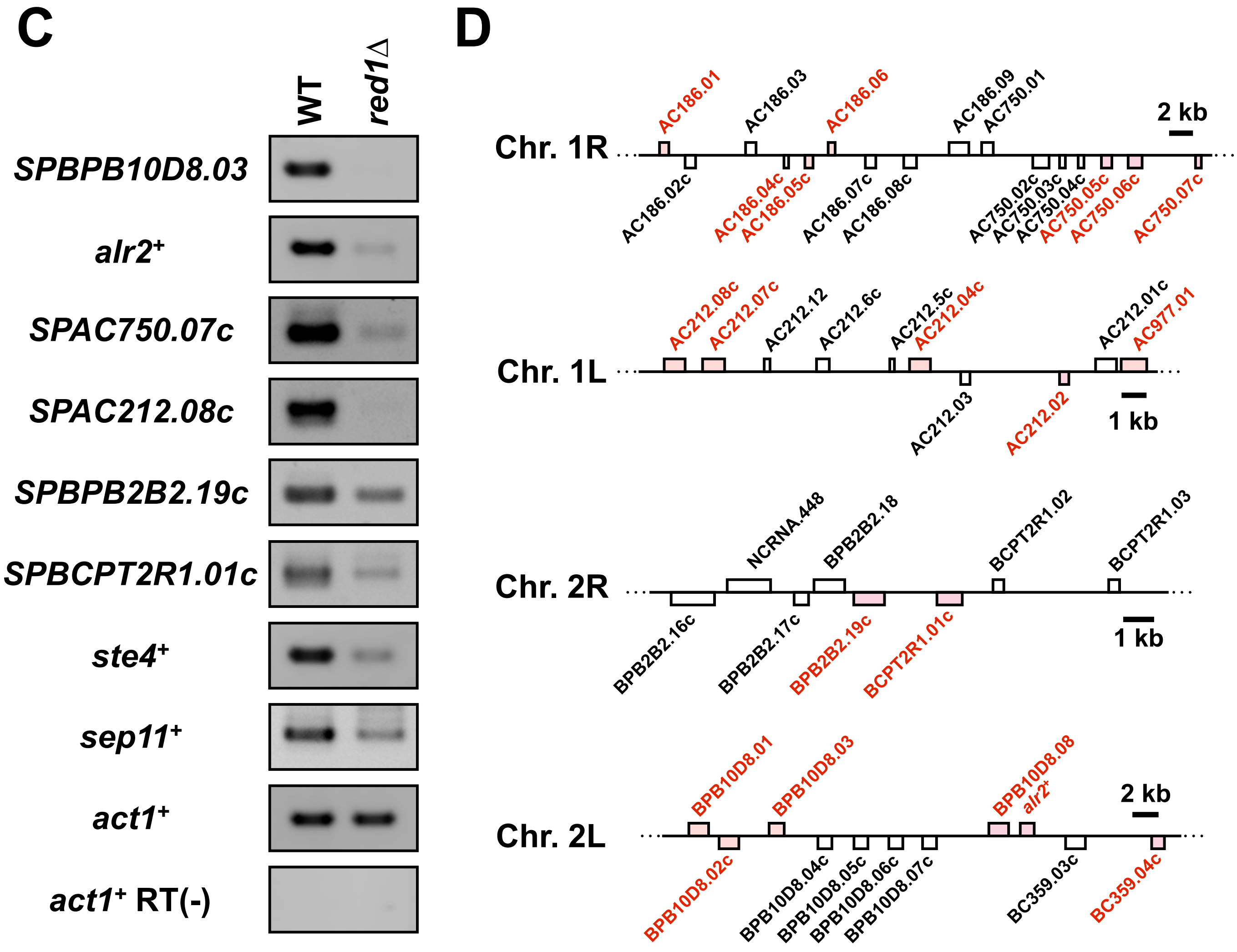


Supplementary Figure S2 Red1 and CENP-B proteins coordinate to suppress transposons. **(A)** RT-PCR of *Tf2-LTR*, *Tf2-ORF*, and *wtf* RNAs derived from transposable elements. These transcripts are significantly increased in *red1*Δ cells. **(B)** Localization patterns of Red1 and Abp1. Fluorescent microscopy demonstrates that Red1-tdTomato does not co-localize with the GFP-tagged CENP-B protein, Abp1 in growing fission yeast. Bars, 2 μm.

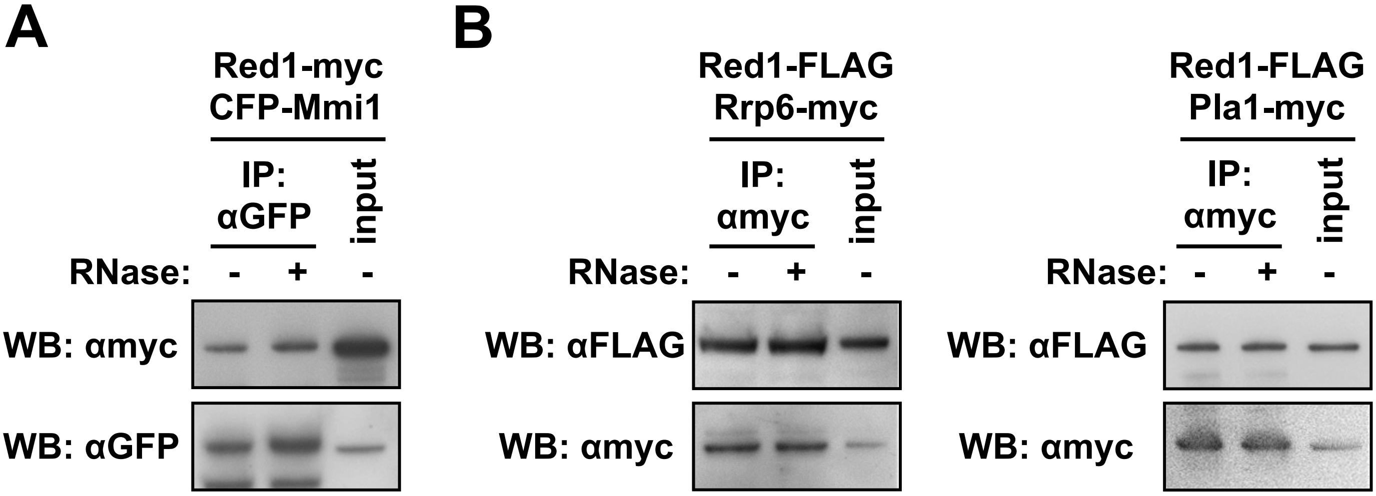


B

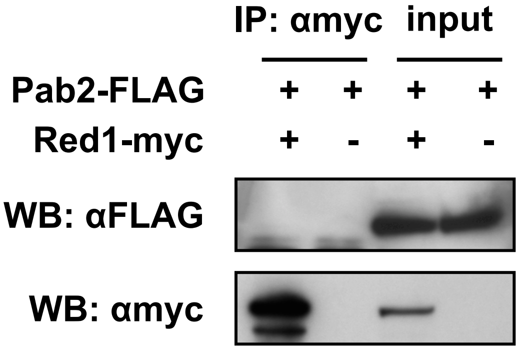
gene name	relative decrease
SPBPB10D8.03	0.036
alr2$^+$	0.039
SPAC750.07c	0.077
SPBPB10D8.02c	0.078
SPAC212.08c	0.086
SPBC359.04c	0.120
SPBPB10D8.01	0.158
SPAC17A2.11	0.212
SPCC330.03c	0.2133
SPAC212.04c	0.261



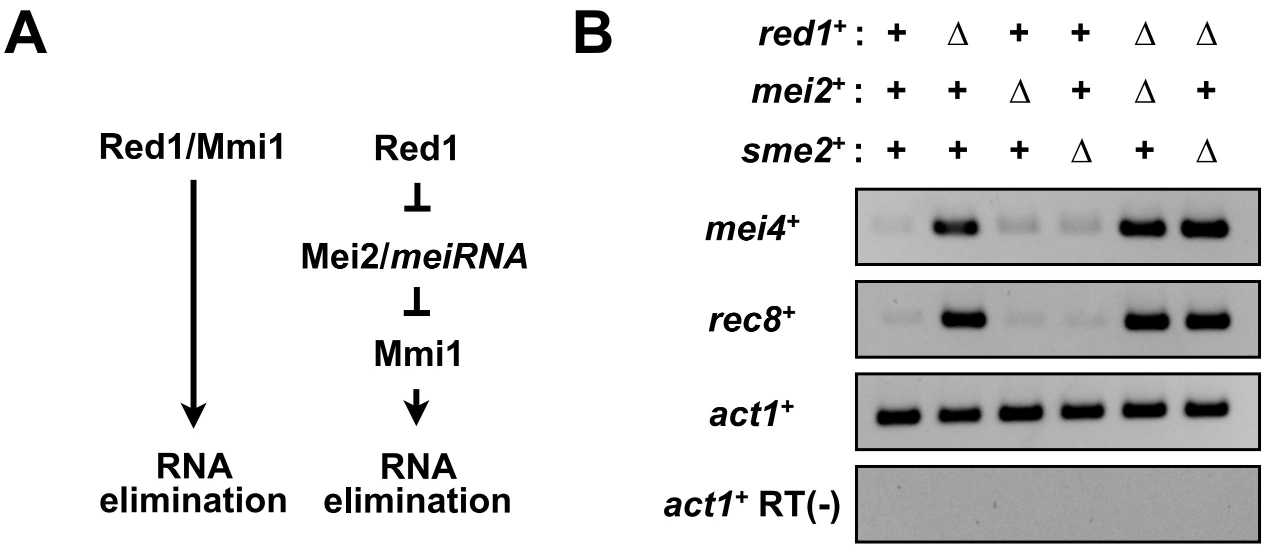
Supplementary Figure S3 Red1 is required for relatively small number of genes. **(A)** Pie chart of decreased mRNAs (total 30 genes) in *red1*Δ cells. These downregulated mRNAs were classified into two categories, meiotic and non-meiotic genes. **(B)** List of the 10 most decreased genes in *red1*Δ. **(C)** Expression of various subtelomeric, *ste4*$^+$, and *sep11*$^+$ mRNAs in wild-type and *red1*Δ strains. The results obtained from the expression array were confirmed by conventional RT-PCR analyses. **(D)** Schematic representation of subtelomeric loci of chromosomes 1 and 2, in which the genes decreased in *red1*Δ are relatively enriched. The genes decreased in *red1*Δ are shown by red letters and boxes.



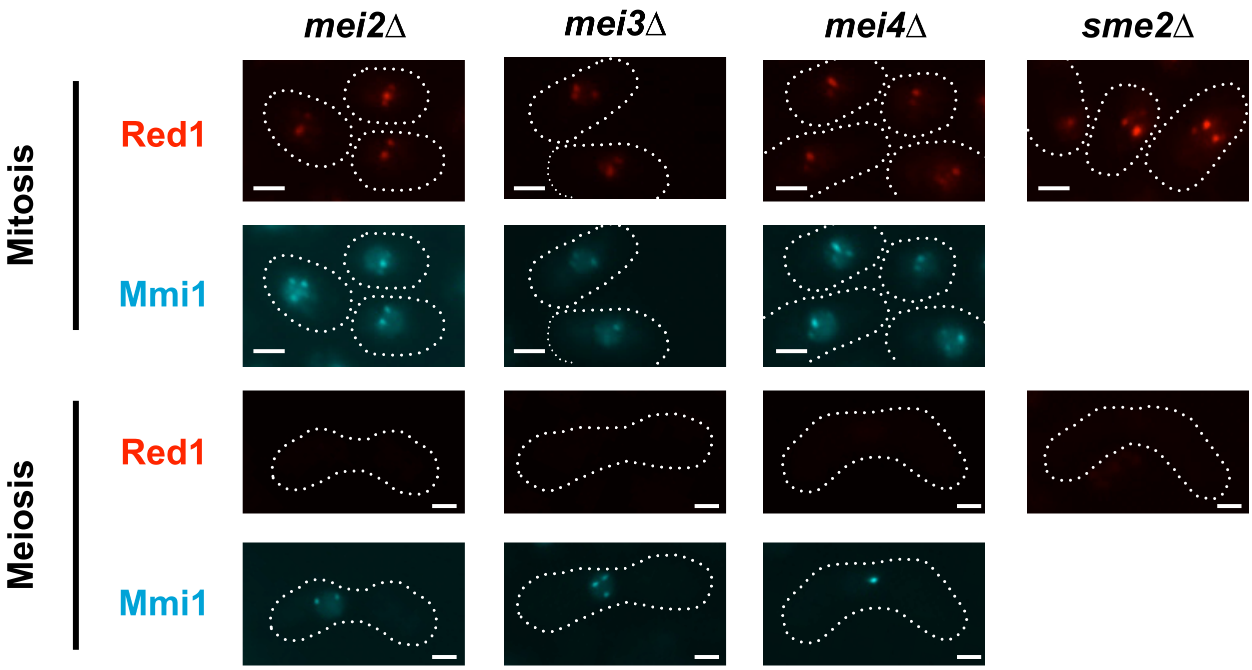
Supplementary Figure S4 Red1 interactions with Mmi1/Rrp6/Pla1 are not sensitive to RNase treatent. Total cell extracts prepared from a strain expressing Red1-myc/CFP-Mmi1, Red1-FLAG/Rrp6-myc, and Red1-FLAG/Pla1-myc were subjected to immunoprecipitation using the indicated antibodies. Immuno-protein complexes recovered by proteinA/G agarose were treated with both RNase A and RNase T1, followed by western blotting.



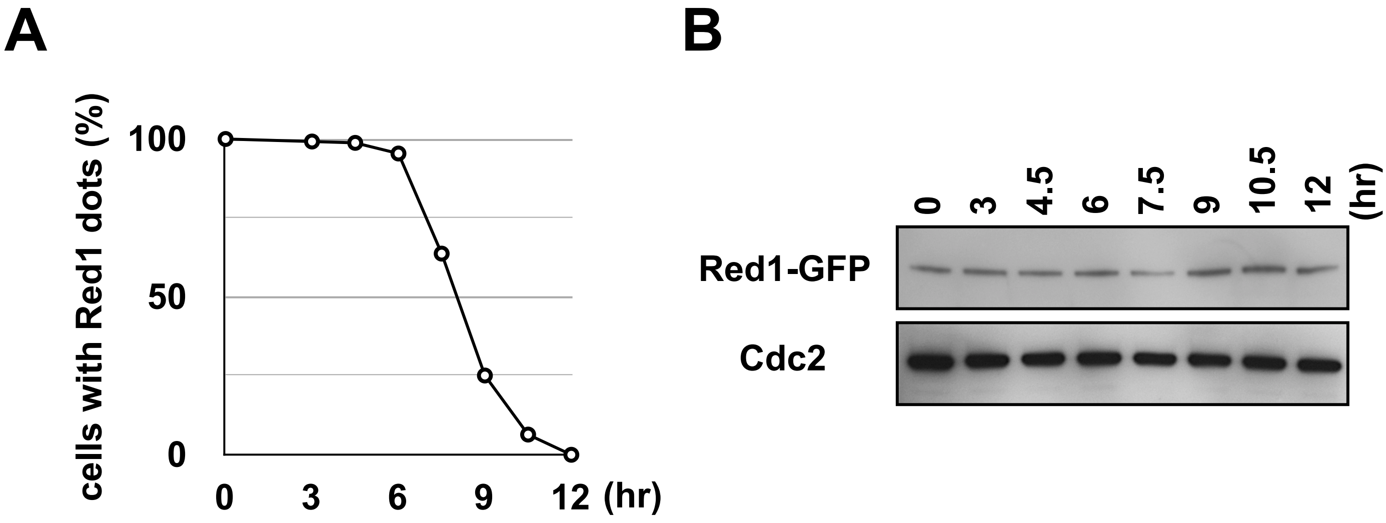
Supplementary Figure S5 Pab2 does not co-immunoprecipitate with Red1 in mitotic cells. Total cell extracts prepared from a strain expressing Pab2-FLAG and Red1-myc/Pab2-FLAG were subjected to immunoprecipitation, followed by western blotting. Red1 does not interact with Pab2 under our experimental conditions.



Supplementary Figure S6 Red1 downregulates meiotic mRNAs independently of Mei2 and *meiRNA*. **(A)** Two possible pathways for meiotic mRNA elimination. One possibility is that Red1 and Mmi1 promote DSR-mediated RNA decay. The other possibility is that Red1 inhibits Mei2/*meiRNA*, and then Mmi1 facilitates the selective removal of meiotic mRNAs. **(B)** The expression levels of *mei4*$^+$ and *rec8*$^+$ mRNAs in mitotic wild-type, *red1*Δ, *mei2*Δ, *sme2*Δ, *red1*Δ*mei2*Δ, and *red1*Δ*sme2*Δ cells analysed by RT-PCR indicate that the accumulation of these mRNAs is also observed in *red1*Δ*mei2*Δ and *red1*Δ*sme2*Δ cells.



Supplementary Figure S7 Red1 disappears independently of *mei2*$^+$/*mei3*$^+$/*mei4*$^+$/*sme2*$^+$ during meiosis. *mei2*Δ, *mei3*Δ, or *mei4*Δ cells expressing Red1-tdTomato/CFP-Mmi1 and *sme2*Δ cells expressing Red1-tdTomato were cultured in rich media at 30°C for vegetative growth or nitrogen-starved media at 26°C to induce meiosis. Representative images of each strain are shown, and the shapes of cells are indicated with white dotted lines. Bars, 2 μm.



Supplementary Figure S8 Loss of Red1 foci in response to the pheromone signaling does not accompany the change in Red1 protein level. *h*$^-$ cells carrying *lys1*$^+$*::matPc* and Red1-GFP were cultured in liquid EMM without nitrogen at 26^{o}C to activate the pheromone signaling. The percentage of cells with Red1 foci (**A**) and Red1-GFP levels (**B**) were monitored by microscopic analyses and western blotting, respectively.

Table SI. List of *S. pombe* strains used in this study

Strain	Genotype	Source
ay449	*h^{90} leu1 ura4D18 ade6-M216 LEU2-CFP-mmi1*	Yamamoto M
FY7354	*h^{90} leu1 ura4D18 mei4-HA::LEU2*	NBRP
FY12806	*h^{90} leu1-32 ura4D18 ade6-M210*	NBRP
FY13293	*h^{90} leu1 ura4D18 ade6-M210 mei2Δ::ura4^{+}*	NBRP
FY13308	*h^{90} leu1 ura4D18 ade6-M210 sme2Δ::ura4^{+}*	NBRP
FY16231	*h^{-} leu1 mei4-P572*	NBRP
FY16846	*h^{-} lys3 mcp5-9myc-3UTR-lys3^{+}*	NBRP
SP238	*h^{90} leu1-32 ura4D18 ade6-M210 red1-tdTomato::kan^{r}*	this study
SP253	*h^{90} leu1-32 ura4D18 ade6-M210 red1Δ::kan^{r}*	this study
SP286	*h^{90} leu1 ura4D18 ade6-M216 red1-tdTomato::kan^{r} LEU2-CFP-mmi1*	this study
SP558	*h^{90} leu1-32 ura4D18 ade6-M210 red1-tdTomato::kan^{r} sme2Δ::ura4^{+}*	this study
SP568	*h^{90} leu1-32 ura4D18 ade6-M210 red1-GFP::kan^{r}*	this study
SP571	*h^{90} leu1-32 ura4D18 ade6-M210 red1-FLAG::kan^{r}*	this study
SP573	*h^{+}/h^{-} leu1-32/leu1-32 ura4D18/ura4D18 his3^{+}/his3D1 ade6-M210/ade6-M216 arg3^{+}/arg3D4 red1Δ::kan^{r}/red1Δ::kan^{r}*	this study
SP583	*h^{-} leu1-32 ura4D18 ade6-M216 pat1-114 red1-tdTomato::kan^{r}*	this study
SP590	*h^{-} leu1-32 ura4DS/E ade6-M216 lys1^{+}-ura4-mei4DSR::kan^{r}*	this study
SP591	*h^{+}/h^{-} leu1-32/leu1-32 ura4D18/ura4D18 his3^{+}/his3D1 ade6-M210/ade6-M216 arg3^{+}/arg3D4*	this study
SP599	*h^{90} leu1-32 ura4D18 ade6-M210 rrp6Δ::kan^{r}*	this study
SP613	*h^{90} leu1-32 ura4D18 ade6-M216 red1-tdTomato::kan^{r} LEU2-CFP-mmi1 mei2Δ::ura4^{+}*	this study
SP616	*h^{90} leu1-32 ura4D18 ade6-M216 red1Δ::kan^{r} mei4Δ::hyg^{r}*	this study
SP618	*h^{-} leu1-32 ura4DS/E ade6-M216 lys1^{+}-ura4-mei4DSR::kan^{r} red1Δ::hyg^{r}*	this study
SP624	*h^{-} leu1-32 ura4DS/E ade6-M216 lys1^{+}-ura4-mei4DSR::kan^{r} mmi1-619::nat^{r}*	this study
SP636	*h^{90} leu1-32 ura4D18 ade6-M210 red1*$^{\mathrm{H637I}}$*-GFP::kan^{r}*	this study
SP652	*h^{90} leu1-32 ura ade6-M210 red1-tdTomato::kan^{r} LEU2-CFP-mmi1 mei3Δ::LEU2*	this study
SP659	*h^{90} leu1-32 ura4D18 ade6-M210 red1-tdTomato::kan^{r} LEU2-CFP-mmi1 mei4Δ::ura4^{+}*	this study
SP674	*h^{90} leu1 ura4D18 ade6-M210 red1Δ::kan^{r} mei2Δ::ura4^{+}*	this study
SP676	*h^{90} leu1 ura4D18 ade6-M210 red1Δ::kan^{r} sme2Δ::ura4^{+}*	this study
SP754	*h^{90} leu1-32 ura4D18 ade6-M216 red1-myc::kan^{r}*	this study
SP827	*h^{90} leu1-32 ura4D18 ade6-M216 red1-tdTomato::kan^{r} pcf11-GFP::kan^{r}*	this study
SP892	*h^{90} leu1-32 ura4D18 ade6-M216 red1-myc::kan^{r} LEU2-CFP-mmi1*	this study
SP893	*mat1Msmt0 leu1-32 ura4D18 ade6-M216 red1-tdTomato::kan^{r} abp1-GFP::kan^{r}*	this study
SP898	*h^{90} leu1-32 ura4D18 ade6-M216 red1Δ::hyg^{r} rep1Δ::kan^{r}*	this study
SP955	*h^{90} leu1-32 ura4D18 ade6-M216 red1-myc::kan^{r} LEU2-CFP-mmi1 mei4Δ::ura4^{+}*	this study
SP972	*h^{90} leu1-32 ura4D18 ade6-M210 pab2-FLAG::kan^{r}*	this study
SP981	*h^{-} lys1^{+}::matPc pat1-114 red1-tdTomato::kan^{r}*	this study
SP1008	*h^{-} leu1 mei4-P572 red1Δ::kan^{r}*	this study
SP1009	*h^{90} leu1-32 ura4? ade6? mei4-HA::LEU2 red1Δ::hyg^{r}*	this study
SP1020	*h^{90} leu1-32 ura4D18 ade6-M216 red1-tdTomato::kan^{r} rrp6-GFP::kan^{r}*	this study
SP1022	*h^{90} leu1-32 ura4D18 ade6? red1-myc::kan^{r} pab2-FLAG::kan^{r}*	this study
SP1024	*h^{90} leu1-32 ura4D18 ade6-M210 red1-FLAG::kan^{r} rrp6-myc::kan^{r}*	this study
SP1050	*h^{90} leu1-32 ura4D18 ade6-M210 red1-tdTomoto::kan^{r} pla1-GFP::kan^{r}*	this study
SP1052	*h^{90} leu1-32 ura4D18 ade6-M210 red1-FLAG::kan^{r} pla1-myc::kan^{r}*	this study
SP1078	*h^{-} leu1? ura4? ade6-M210 mcp5-9myc-3UTR-lys3^{+} red1Δ::kan^{r}*	this study

Table SI. List of *S. pombe* strains used in this study (continued)

Strain	Genotype	Source
SP1111	*h*$^-$ *leu1 mei4-P572 mmi1Δkan*^{r}	this study
SP1163	*h*^{90} *leu1-32 ura4D18 ade6-M216 red1-tdTomato::kan*^{r} *pab2-GFP::kan*^{r}	this study
SP1167	*h*^{90} *leu1-32 ura4D18 ade6-M210 red1Δ::hyg*^{r} *rrp6Δ::kan*^{r}	this study
SP1208	*h*^{90} *leu1 ura4D18 ade6-M216 red1-tdTomato::kan*^{r} *LEU2-CFP-mmi1 fus1Δ::hyg*^{r}	this study
SP1227	*h*$^-$ *lys1*$^+$*::matPc pat1-114 red1-tdTomato::kan*^{r} *mei2Δ::hyg*^{r}	this study
SP1318	*h*$^-$ *lys1*$^+$*::matPc pat1-114 red1-GFP::kan*^{r}	this study

Table SII. List of genes upregulated in *red1*Δ cells

Systematic ID	Name	Product	Classification	Mmi1 regulated	Pab2 regulated
SPAC6G9.13c	*bqt1*$^+$	bouquet formation protein Bqt1	early	Yes[A, C]	-
SPAC1002.06c	*bqt2*$^+$	bouquet formation protein Bqt2	early	-	-
SPBC2G2.09c	*crs1*$^+$	meiosis specific cyclin Crs1	early	Yes[A, C]	-
SPAC1093.06c	*dhc1*$^+$	dynein heavy chain	early	Yes[C]	-
SPBC646.17c	*dic1*$^+$	dynein intermediate chain	early	Yes[C]	Yes[B]
SPAC458.04c	*dil1*$^+$	dynein intermediate light chain Dil1	early	Yes[A, C]	-
SPBC1718.02	*hop1*$^+$	linear element associated protein Hop1	early	Yes[C]	-
SPBC582.06c	*mcp6*$^+$	horsetail movement protein Hrs1/Mcp6	early	Yes[C]	Yes[B]
SPAC13A11.03	*mcp7*$^+$	meiosis specific coiled-coil protein	early	Yes[C]	-
SPCC1223.12c	*meu10*$^+$	GPI anchored cell surface protein	early	Yes[C]	Yes[B]
SPAC222.15	*meu13*$^+$	Tat binding protein-interacting protein (TBPIP) homolog	early	Yes[C]	Yes[B]
SPAP27G11.08c	*meu32*$^+$/*mug11*$^+$	sequence orphan	early	Yes[A, C]	Yes[B]
SPCC11E10.03	*mug1*$^+$	dynactin complex subunit	early	Yes[A, C]	Yes[B]
SPAC57A10.04	*mug10*$^+$	Rho guanine nucleotide exchange factor	early	Yes[C]	Yes[B]
SPAC17A5.18c	*mug19*$^+$/*rec25*$^+$	meiotic recombination protein Rec25	early	Yes[A, C]	Yes[B]
SPBC216.02	*mug21*$^+$/*mcp5*$^+$	cortical anchoring factor for dynein	early	Yes[C]	-
SPBC31F10.05	*mug37*$^+$	sequence orphan	early	Yes[C]	-
SPCC1393.07c	*mug4*$^+$	sequence orphan	early	-	Yes[B]
SPBC577.05c	*mug41*$^+$/*rec27*$^+$	meiotic recombination protein	early	-	-
SPBP8B7.04	*mug45*$^+$	sequence orphan	early	Yes[C]	Yes[B]
SPAC14C4.08	*mug5*$^+$	sequence orphan	early	-	-
SPAC32A11.01	*mug8*$^+$	conserved fungal protein	early	Yes[C]	Yes[B]
SPCC70.09c	*mug9*$^+$	conserved fungal protein	early	Yes[A, C]	-
SPAC22F3.03c	*rdh54*$^+$	ATP-dependent DNA helicase Rdh54	early	-	Yes[B]
SPAC25G10.04c	*rec10*$^+$	meiotic recombination protein Rec10	early	Yes[B, C]	Yes[B]
SPCC550.16c	*rec11*$^+$	meiotic cohesin complex subunit Rec11	early	Yes[C]	-
SPBC1711.14	*rec15*$^+$	meiotic recombination protein Rec15	early	-	-
SPBC29A10.14	*rec8*$^+$	meiotic cohesin complex subunit Rec8	early	Yes[A, C]	Yes[B]
SPBC2D10.06	*rep1*$^+$	MBF transcription factor complex subunit Rep1	early	-	-
SPBC119.14	*rti1*$^+$	Rad22 homolog Rti1	early	-	-
SPBC29A10.02	*spo5*$^+$	meiotic RNA-binding protein 1	early	Yes[A, C]	Yes[B]
SPAC27D7.13c	*ssm4*$^+$	p150-Glued	early	Yes[A, C]	Yes[B]
SPAC22H10.13	*zym1*$^+$	metallothionein	early	-	-
SPAC6C3.05	-	sequence orphan	early	-	-
SPAC2E1P3.02c	*amt3*$^+$	ammonium transporter Amt3	middle	-	-
SPAC1006.04c	*mcp3*$^+$/*mug7*$^+$	sequence orphan	middle	-	-
SPBC32H8.11	*mei4*$^+$	meiotic forkhead transcription factor Mei4	middle	Yes[A, C]	-
SPAC1556.06	*meu1*$^+$/*meu2*$^+$	sequence orphan	middle	Yes[A, C]	Yes[B]
SPCPJ732.03	*meu15*$^+$	sequence orphan	middle	-	-
SPAC1A6.08c	*mug125*$^+$	sequence orphan	middle	-	-
SPAC23C4.07	*mug22*$^+$/*tht2*$^+$	meiotically upregulated gene Mug22	middle	Yes[C]	Yes[B]
SPBC32H8.06	*mug93*$^+$	TPR repeat protein, meiotically spliced	middle	-	-
SPBC1271.06c	*mug96*$^+$	sequence orphan	middle	Yes[C]	-
SPBC16E9.17c	*rem1*$^+$	meiosis-specific cyclin Rem1	middle	-	-
SPAC20H4.11c	*rho5*$^+$	Rho family GTPase Rho5	middle	-	-
SPAC22F8.05	-	alpha,alpha-trehalose-phosphate synthase	middle	-	-
SPBPB2B2.07c	-	S. pombe specific DUF999 protein family 7	middle	-	-

Table SII. List of genes upregulated in *red1*Δ cells (continued)

Systematic ID	Name	Product	Classification	Mmi1 regulated	Pab2 regulated
SPCC417.12	-	carboxylesterase-lipase family protein	middle	-	-
SPCC794.04c	-	membrane transporter	middle	-	-
wtf-pseudo	-	wtf1, 2, 3, 6, 8, 15, 17, 23, 24, and/or 25 (cannot be distinguished)	middle	-	-
SPAC869.07c	*mel1*$^+$	alpha-galactosidase, melibiase	late	-	-
SPAC1002.19	*urg1*$^+$	GTP cyclohydrolase II	late	-	-
SPAC14C4.01c	-	DUF1770 family protein	late	-	-
SPAC1F7.06	-	ThiJ domain protein	late	-	-
SPAC23C11.06c	-	hydrolase	late	-	-
SPAC23H3.15c	-	sequence orphan	late	-	-
SPAC4H3.03c	-	glucan 1,4-alpha-glucosidase	late	-	-
SPAC869.06c	-	HHE domain cation binding protein	late	-	-
SPACUNK4.17	-	NAD binding dehydrogenase family protein	late	-	-
SPBP4G3.03	-	PI31 proteasome regulator related	late	-	-
SPCC737.04	-	S. pombe specific UPF0300 family protein 6	late	-	-
SPAC20G4.03c	*hri1*$^+$	eIF2 alpha kinase Hri1	transient	-	-
SPBPB2B2.06c	-	phosphoprotein phosphatase	transient	-	-
SPAP8A3.04c	*hsp9*$^+$	heat shock protein	continuous	-	-
SPBC365.12c	*ish1*$^+$	LEA domain protein	continuous	-	-
SPBC16E9.16c	*lsd90*$^+$	Lsd90 protein	continuous	-	-
SPBC56F2.06	*mug147*$^+$	sequence orphan	continuous	-	-
SPCC338.12	*pbi2*$^+$	proteinase B inhibitor Pbi2	continuous	-	-
SPAC19G12.09	-	NADH/NADPH dependent indole-3-acetaldehyde reductase AKR3C2	continuous	-	-
SPAC25B8.18	-	mitochondrial electron carrier	continuous	-	-
SPAC6B12.03c	-	HbrB family protein	continuous	-	-
SPAPJ691.02	-	yippee-like protein	continuous	-	-
SPBC8E4.02c	-	sequence orphan	continuous	Yes[C]	-
SPCC70.04c	-	sequence orphan	continuous	-	-
SPBC23G7.17c	*mat3-m*	mating-type M-specific polypeptide Mi 2	delayed	-	-
SPAPB8E5.05	*mfm1*$^+$	M-factor precursor Mfm1	delayed	-	-
SPBC1347.12	*arp1*$^+$	actin-like protein Arp1, forming a complex with mug1/ssm4	unassigned	Yes[C]	-
SPCC645.02	*gep4*$^+$	mitochondrial matrix PGP phosphatase involved in cardiolipin biosynthesis	unassigned	-	-
SPAC14C4.03	*mek1*$^+$	Cds1/Rad53/Chk2 family protein kinase Mek1	unassigned	Yes[B, C]	Yes[B]
SPBC14C8.05c	*meu17*$^+$	glucan-alpha-1,4-glucosidase, probably middle gene	unassigned	-	-
SPAC6B12.16	*meu26*$^+$	conserved fungal protein	unassigned	Yes[A, C]	-
SPAC57A7.11	*mip1*$^+$	WD repeat protein, Raptor homolog Mip1	unassigned	-	-
SPAC15E1.07c	*moa1*$^+$	meiotic cohesin complex associated protein Moa1	unassigned	Yes[C]	-
SPAC167.06c	*mug143*$^+$	sequence orphan, probably middle gene	unassigned	-	-
SPAC13D6.01	*pof14*$^+$	F-box protein Pof14	unassigned	-	-
SPAC1F8.03c	*str3*$^+$	siderophore-iron transporter	unassigned	-	-
SPAC458.07	*tfa1*$^+$	transcription factor TFIIE alpha subunit Tfa1	unassigned	-	-
SPAC1142.09	-	dubious	unassigned	-	-
SPAC16E8.16	-	transcription factor TFIIB	unassigned	-	-
SPAC1A6.11	-	dubious	unassigned	-	-
SPAC1D4.01	-	human c9orf78 ortholog	unassigned	-	-
SPAC1F3.08c	-	dubious	unassigned	-	-
SPAC1F8.02c	-	sequence orphan	unassigned	-	-
SPAC22H10.06c	-	dubious	unassigned	-	-

Table SII. List of genes upregulated in *red1*Δ cells (continued)

Systematic ID	Name	Product	Classification	Mmi1 regulated	Pab2 regulated
SPAC23C11.10	-	human c16orf57 ortholog	unassigned	-	-
SPAC27F1.10	-	sequence orphan	unassigned	-	-
SPAC29E6.07	-	sequence orphan	unassigned	-	Yes[B]
SPAC2G11.05c	-	BRO1 domain protein	unassigned	-	Yes[B]
SPAC637.03	-	conserved fungal protein	unassigned	-	-
SPAC9E9.17c	-	dubious	unassigned	-	-
SPAP27G11.11c	-	dubious	unassigned	-	-
SPAPB1A11.02	-	esterase/lipase	unassigned	-	-
SPBC13G1.15c	-	sequence orphan	unassigned	-	-
SPBC1711.15c	-	sequence orphan	unassigned	-	-
SPBC1921.04c	-	dubious	unassigned	-	-
SPBC27.05	-	dubious	unassigned	-	-
SPBC336.05c	-	S-adenosylmethionine-dependent methyltransferase	unassigned	-	-
SPBC530.02	-	membrane transporter	unassigned	-	-
SPBC83.19c	-	sequence orphan	unassigned	Yes[C]	-
SPBC8D2.12c	-	mitochondrial translational activator of cytochrome C oxidase I	unassigned	-	-
SPBPB2B2.03c	-	pseudo-very degraded permease	unassigned	Yes[C]	-
SPBPB2B2.04	-	pseudo-very degraded transporter	unassigned	Yes[C]	-
SPCC1442.11c	-	sequence orphan	unassigned	-	-
SPCC191.04c	-	dubious	unassigned	-	-
SPCC2H8.02	-	inorganic phosphate transporter	unassigned	-	-
SPCC569.04	-	sequence orphan	unassigned	-	-
SPCC622.05	-	dubious	unassigned	-	-
SPAC1348.13	-	similar to fragment of cox1 intron protein	unassigned	-	-
SPBC354.11c	-	dubious	unassigned	-	-
SPBC8D2.02c	-	vacuolar sorting protein Vps68	unassigned	-	-
SPCC417.11c	-	glutamate-1-semialdehyde 2,1-aminomutaseaminotransferase	unassigned	-	-
SPCC663.06c	-	short chain dehydrogenase	unassigned	-	-
wtf	-	wtf1, 5, 9, 17, and/or 21 (cannot be distinguished)	unassigned	-	-
	Yes[A]	Harigaya et al., (2006) Nature 442(7098): 45-50.			
	Yes[B]	St-Andre et al., (2010) J. Biol. Chem. 285(36): 27859-27868.			
	Yes[C]	this study and our unpublished data			

Table SIII. List of genes downregulated in *red1*Δ cells

Systematic ID	Name	Product	Classification	Mmi1 regulated
SPAC750.06c	-	S. pombe specific DUF999 protein family 4	middle	-
SPAC212.04c	-	S. pombe specific DUF999 family protein 1	middle	-
SPAC212.02	-	sequence orphan	middle	-
SPBPB2B2.19c	-	S. pombe specific 5Tm protein family	late	-
SPAC977.01	-	S. pombe specific 5Tm protein family	late	-
SPAC977.16c	*dak2*$^{+}$	dihydroxyacetone kinase	delayed	-
SPAC513.03	*mfm2*$^{+}$	M-factor precursor	delayed	Yes^{A}
SPAC1565.04c	*ste4*$^{+}$	adaptor protein	delayed	-
SPBC359.02	*alr2*$^{+}$	alanine racemase	unassigned	-
SPAC57A10.03	*cyp1*$^{+}$	cyclophilin	unassigned	-
SPAC11D3.05	*mfs2*$^{+}$	MFS family membrane transporter	unassigned	-
SPAC5D6.05	*sep11*$^{+}$	mediator complex subunit	unassigned	-
SPCC330.03c	-	NADPH-hemoprotein reductase	unassigned	-
SPBC359.01	-	amino acid permease	unassigned	-
SPBPB10D8.03	-	pseudogene transporter	unassigned	-
SPBPB10D8.02c	-	arylsulfatase	unassigned	-
SPBPB10D8.01	-	cysteine transporter	unassigned	-
SPBCPT2R1.01c	-	S. pombe specific DUF999 protein family 9	unassigned	-
SPBC530.07c	-	TENA/THI family protein	unassigned	-
SPBC359.04c	-	cell surface glycoprotein, DIPSY family	unassigned	-
SPBC1348.04	-	methyltransferase	unassigned	Yes^{A}
SPAC977.15	-	dienelactone hydrolase family	unassigned	-
SPAC750.07c	-	S. pombe specific GPI anchored protein family 1	unassigned	-
SPAC56F8.13	-	dubious	unassigned	-
SPAC212.08c	-	GPI anchored protein	unassigned	-
SPAC212.07c	-	pseudogene	unassigned	-
SPAC186.06	-	ER unfolded protein response protein	unassigned	Yes^{A}
SPAC186.05c	-	human TMEM165 homolog	unassigned	Yes^{A}
SPAC186.01	-	cell surface glycoprotein, DIPSY family	unassigned	-
SPAC17A2.11	-	sequence orphan	unassigned	-
	Yes^{A}	our unpublished data		