

		2 $\mu$ ΔNEG											
		DAY 1			DAY 2			DAY 3			DAY 4		
		HAPLOID	MIXTURE	DIPLOID	HAPLOID	MIXTURE	DIPLOID	HAPLOID	MIXTURE	DIPLOID	HAPLOID	MIXTURE	DIPLOID
FIRST REP (n = 4)	<i>wild type</i>	4	0	0	1	3	0	0	1	3	1	1	2
	<i>swe1Δ</i>	1	2	1	0	0	4	0	0	4	0	0	4
	<i>mad2Δ</i>	0	0	4	0	0	4	0	0	4	0	0	4
SECOND REP (n = 4)	<i>wild type</i>	4	0	0	1	3	0	1		3	1	1	2
	<i>swe1Δ</i>	1	1	2	0	0	4	0	0	4	0	0	4
	<i>mad2Δ</i>	0	0	4	0	0	4	0	0	4	0	0	4

		empty vector											
		DAY 1			DAY 2			DAY 3			DAY 4		
		HAPLOID	MIXTURE	DIPLOID	HAPLOID	MIXTURE	DIPLOID	HAPLOID	MIXTURE	DIPLOID	HAPLOID	MIXTURE	DIPLOID
FIRST REP (n = 4)	<i>wild type</i>	2	0	0	-	-	-	-	-	-	2	0	0
	<i>swe1Δ</i>	2	0	0	-	-	-	-	-	-	2	0	0
	<i>mad2Δ</i>	2	0	0	-	-	-	-	-	-	2	0	0
SECOND REP (n = 4)	<i>wild type</i>	2	0	0	-	-	-	-	-	-	2	0	0
	<i>swe1Δ</i>	2	0	0	-	-	-	-	-	-	2	0	0
	<i>mad2Δ</i>	1	0	0	-	-	-	-	-	-	1	0	0

		2 $\mu$ ΔNEG (IN %)											
		DAY 1			DAY 2			DAY 3			DAY 4		
		HAPLOID	MIXTURE	DIPLOID	HAPLOID	MIXTURE	DIPLOID	HAPLOID	MIXTURE	DIPLOID	HAPLOID	MIXTURE	DIPLOID
FIRST REP (n = 4)	<i>wild type</i>	100	0	0	25	75	0	0	25	75	25	25	50
	<i>swe1Δ</i>	25	50	25	0	0	100	0	0	100	0	0	100
	<i>mad2Δ</i>	0	0	100	0	0	100	0	0	100	0	0	100
SECOND REP (n = 4)	<i>wild type</i>	100	0	0	25	75	0	25	0	75	25	25	50
	<i>swe1Δ</i>	25	25	50	0	0	100	0	0	100	0	0	100
	<i>mad2Δ</i>	0	0	100	0	0	100	0	0	100	0	0	100

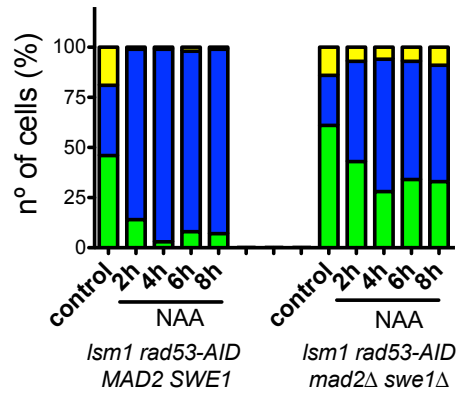
  

		2 $\mu$ ΔNEG ( AVERAGE, IN %)											
		DAY 1			DAY 2			DAY 3			DAY 4		
		HAPLOID	MIXTURE	DIPLOID	HAPLOID	MIXTURE	DIPLOID	HAPLOID	MIXTURE	DIPLOID	HAPLOID	MIXTURE	DIPLOID
AVERAGE	<i>wild type</i>	100	0	0	25	75	0	13	13	75	25	25	50
	<i>swe1Δ</i>	25	38	38	0	0	100	0	0	100	0	0	100
	<i>mad2Δ</i>	0	0	100	0	0	100	0	0	100	0	0	100

		2 $\mu$ ΔNEG ( SD, IN %)											
		DAY 1			DAY 2			DAY 3			DAY 4		
		HAPLOID	MIXTURE	DIPLOID	HAPLOID	MIXTURE	DIPLOID	HAPLOID	MIXTURE	DIPLOID	HAPLOID	MIXTURE	DIPLOID
SD	<i>wild type</i>	0	0	0	0	0	0	18	18	0	0	0	0
	<i>swe1Δ</i>	0	18	18	0	0	0	0	0	0	0	0	0
	<i>mad2Δ</i>	0	0	0	0	0	0	0	0	0	0	0	0

**Source data Figure 8a:** Quantification of the number of haploids, diploids and cells in which a mixed profile can be observed in wild type cells *mad2Δ* or *swe1Δ* cells transformed with the 2 $\mu$ ΔNEG. Two independent experiments were performed. Experiment 1 was carried out with 4 independent colonies for each background and also carried two candidates transformed with an empty vector that were measured only on day 1 and day 4. Experiment 2 was performed similarly but one of the spores of *mad2Δ* cells transformed with the empty vector were haploid was lost (contamination).



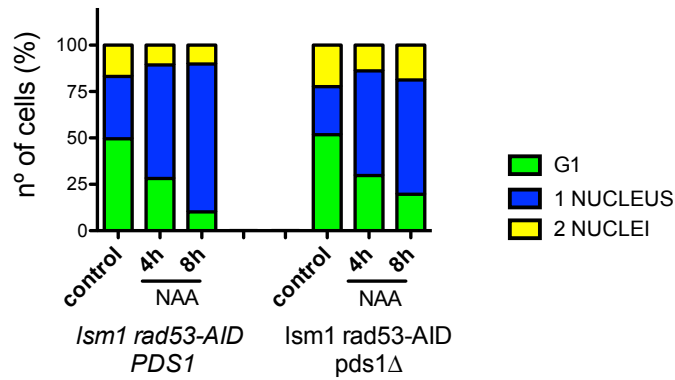
1ST EXP		<i>lsm1Δ rad53-AID</i>					<i>lsm1Δ rad53-AID swe1Δ mad2Δ</i>						
time in NAA (h)		0	2	4	6	8	time in NAA (h)		0	2	4	6	8
G1		46	14	3	8	7	G1		61	43	28	34	33
1 nucleus		35	85	96	90	92	1 nucleus		25	50	66	59	58
2 nuclei		19	1	1	2	1	2 nuclei		14	7	6	7	9
n		100	100	100	100	100	n		100	100	100	100	100
2ND EXP		<i>lsm1Δ rad53-AID</i>					<i>lsm1Δ rad53-AID swe1Δ mad2Δ</i>						
time in NAA (h)		0	2	4	6	8	time in NAA (h)		0	2	4	6	8
G1		50	17	8	4	11	G1		53	45	24	28	27
1 nucleus		41	80	90	95	84	1 nucleus		39	52	70	65	66
2 nuclei		9	3	2	1	5	2 nuclei		8	3	6	7	7
n		100	100	100	100	100	n		100	100	100	100	100

AVERAGE		<i>lsm1Δ rad53-AID</i>					<i>lsm1Δ rad53-AID swe1Δ mad2Δ</i>				
time in NAA (h)		0	2	4	6	8	0	2	4	6	8
G1		48	15,5	5,5	6	9	57	44	26	31	30
1 nucleus		38	82,5	93	92,5	88	32	51	68	62	62
2 nuclei		14	2	1,5	1,5	3	11	5	6	7	8

SD		<i>lsm1Δ rad53-AID</i>					<i>lsm1Δ rad53-AID swe1Δ mad2Δ</i>				
time in NAA (h)		0	2	4	6	8	0	2	4	6	8
G1		2,8	2,1	3,5	2,8	2,8	5,7	1,4	2,8	4,2	4,2
1 nucleus		4,2	3,5	4,2	3,5	5,7	9,9	1,4	2,8	4,2	5,7
2 nuclei		7,1	1,4	0,7	0,7	2,8	4,2	2,8	0,0	0,0	1,4

ANOVA test ( <i>lsm1Δ rad53-AID</i> vs <i>lsm1Δ rad53-AID swe1Δ mad2Δ</i> )					
time in NAA (h)	0	2	4	6	8
G1	ns	p<0.001	p<0.01	p<0.001	p<0.01
1 nucleus	ns	p<0.001	p<0.001	p<0.001	p<0.001
2 nuclei	ns	ns	ns	ns	ns

**Source data Figure 8b.** Raw data obtained in the two cell cycle kinetics performed to determine changes in the cell cycle distribution of *rad53-AID lsm1Δ* and *rad53-AID lsm1Δ mad2Δ swe1Δ* cells after treatment with NAA. Cells were fixed, stained with DAPI and classified according to morphology and number of nuclei using a 100x objective. The image on the top represents the numbers obtained in the second experiment, not included in the main text. p-values were obtained performing an ANOVA test, using Prism (5.0).



	<i>lsm1Δ rad53-AID</i>			<i>lsm1Δ rad53-AID pds1Δ</i>			<i>lsm1Δ rad53-AID</i>			<i>lsm1Δ rad53-AID pds1Δ</i>		
	RAW DATA			RAW DATA			%			%		
1st experiment	AS	4H NAA	8H NAA	AS	4H NAA	8H NAA	AS	4H NAA	8H NAA	AS	4H NAA	8H NAA
G1	53	29	12	58	28	22	50	28	10	52	30	20
bud, 1 nucleus	36	63	94	29	53	69	34	61	80	26	56	62
bud, two nuclei	18	11	12	25	13	21	17	11	10	22	14	19
n	107	103	118	112	94	112	100	100	100	100	100	100
2nd experiment	RAW DATA			RAW DATA			%			%		
G1	AS	4H NAA	8H NAA	AS	4H NAA	8H NAA	AS	4H NAA	8H NAA	AS	4H NAA	8H NAA
	76	49	20	41	45	35	44	32	18	44	41	30
bud, 1 nucleus	57	82	78	29	50	61	33	54	72	31	45	53
bud, two nuclei	41	20	11	23	15	20	24	13	10	25	14	17
n	174	151	109	93	110	116						

	t-test (paired, two tails)		
	AS	4H NAA	8H NAA
G1	0,386	0,379	0,070
bud, 1 nucleus	0,372	0,185	0,016
bud, two nuclei	0,367	0,421	0,058

	t-test (paired, one tail)		
	AS	4H NAA	8H NAA
G1	0,193	0,189	0,035
bud, 1 nucleus	0,186	0,092	0,008
bud, two nuclei	0,183	0,211	0,029

**Source data Figure 8-Figure Supplement 8b.** Raw data obtained in the two cell cycle kinetics performed to determine changes in the cell cycle distribution of *rad53-AID lsm1Δ* and *rad53-AID lsm1Δ pds1Δ* cells after treatment with NAA. Cells were fixed, stained with DAPI and classified according to morphology and number of nuclei using a 100x objective. The image on the top represents the numbers obtained in the second experiment, not included in the main text. P-values are indicated in the panel below..