

Table S1. **Strain list**

Strains	Genotype
AY2571	<i>h⁹⁰ ade6-M210 or M216 leu1-32 ura4-D18 mes1::LEU2^(e) lys1::Pnda3-GFP-atb2^(h)</i>
AY296-2C	<i>h⁹⁰ ade6-M210 leu1-32 ura4-D18 mad2::ura4^(a) rec12-152::LEU2^(h) lys1::Pnda3-GFP-atb2⁺</i>
AY296-2D	<i>h⁹⁰ ade6-M210 leu1-32 ura4-D18 rec12-152::LEU2 lys1::Pnda3-GFP-atb2⁺</i>
AY296-3D	<i>h⁹⁰ ade6-M210 leu1-32 ura4-D18 mad2::ura4⁺ lys1::Pnda3-GFP-atb2⁺</i>
AY296-17A	<i>h⁹⁰ ade6-M210 leu1-32 ura4-D18 lys1::Pnda3-GFP-atb2⁺</i>
AY319-1A	<i>h⁹⁰ ade6-M216 leu1-32 lys1-131 ura4-D18 sid4::GFP-kan^(l) cen2(D107)::kan⁻ura4⁺-lacO^(l) his7::Pdis1-GFP-lacI-NLS^(k)</i>
AY319-24C	<i>h⁹⁰ ade6-M210 or M216 leu1-32 lys1-131 ura4-D18 rec12-152::LEU2 sid4::GFP-kan⁻ cen2(D107)::kan⁻ura4⁺-lacO his7::Pdis1-GFP-lacI-NLS</i>
AY333-1C	<i>h⁹⁰ ade6-M216 leu1-32 lys1-131 ura4-D18 sid4::GFP-kan⁻ ade8[::kan⁻ura4⁺-lacO]^(l) his7::Pdis1-GFP-lacI-NLS</i>
AY338-7A	<i>h⁹⁰ ade6-M210 leu1-32 lys1-131 ura4-D18 sid4::GFP-kan⁻ sod2.proximal[::kan⁻ura4⁺-lacO]^(l) his7::Pdis1-GFP-lacI-NLS</i>
AY340-3A	<i>h⁹⁰ ade6-M210 or M216 leu1-32 lys1-131 ura4-D18 rec12-152::LEU2 sid4::GFP-kan⁻ ade8[::kan⁻ura4⁺-lacO] his7::Pdis1-GFP-lacI-NLS</i>
AY343-10B	<i>h⁺ ade6-M210 leu1-32 mad2::GFP-kan^(m)</i>
AY348-2D	<i>h⁺ leu1-32 lys1-131 rec12-152-LEU2 mad2::GFP-kan⁻</i>
AY354-5B	<i>H⁻ leu1-32 lys1-131 ura4-D18 rec12-152-LEU2 sad1::DsRed-LEU2⁽ⁿ⁾</i>
AY359-3B	<i>h⁺ leu1-32 lys1-131 ura4-D18 mad2::ura4⁺ rec12-152::LEU2 ade8[::kan⁻ura4⁺-lacO] his7::Pdis1-GFP-lacI-NLS</i>
AY361-1A	<i>h⁹⁰ ade6-M210 leu1-32 ura4-D18 rec8::ura4^(a) lys1::Pnda3-GFP-atb2⁺</i>
AY368-2C	<i>h⁹⁰ leu1-32 ura4-D18 or DS/E clr4::ura4^(a) lys1::Pnda3-GFP-atb2⁺</i>
AY370-2B	<i>h⁻ leu1-32 ura4-D18 mad2::ura4⁺ rec12-152::LEU2 sid4::GFP-kan⁻ ade8[::kan⁻ura4⁺-lacO] his7::Pdis1-GFP-lacI-NLS</i>
AY373-8B	<i>h⁹⁰ ade6-M210 leu1-32 lys1-131 ura4-D18 rec8::ura4⁺ sid4::GFP-kan⁻ cen2(D107)::kan⁻ura4⁺-lacO his7::Pdis1-GFP-lacI-NLS</i>
AY378-1A	<i>h⁻ leu1-32 lys1-131 ura4-D18 sid4::GFP-kan⁻ ade6[::kan⁻ura4⁺-lacO]^(l) his7::Pdis1-GFP-lacI-NLS</i>
AY378-2C	<i>h⁺ leu1-32 lys1-131 ura4-D18 sid4::GFP-kan⁻ ade6[::kan⁻ura4⁺-lacO] his7::Pdis1-GFP-lacI-NLS</i>
AY379-6A	<i>h⁹⁰ ade6-M210 leu1-32 ura4-D18 or DS/E rec12-152::LEU2 clr4::ura4⁺ lys1::Pnda3-GFP-atb2⁺</i>
AY385-4C	<i>h⁹⁰ ade6-M210 or M216 leu1-32 ura4-D18 or DS/E clr4::ura4⁺ mad2::ura4⁺ lys1::Pnda3-GFP-atb2⁺</i>
AY388-1B	<i>h⁹⁰ ade6-M210 leu1-32 lys1-131 ura4-D18 rec12-152::LEU2 sid4::GFP-kan⁻ sod2.proximal[::kan⁻ura4⁺-lacO] his7::Pdis1-GFP-lacI-NLS</i>
AY398-2C	<i>h⁹⁰ ade6-M216 leu1-32 lys1-131 ura4-D18 cdc13::GFP-LEU2</i>
AY398-21A	<i>h⁹⁰ ade6-M210 leu1-32 lys1-131 ura4-D18 rec12-152-LEU2 cdc13::GFP-LEU2</i>
AY395-14A	<i>h⁻ leu1-32 lys1-131 ura4-D18 rec12-152::LEU2 mad2::ura4⁺ sod2.proximal[::kan⁻ura4⁺-lacO] his7::Pdis1-GFP-lacI-NLS</i>
AY395-15C	<i>h⁺ leu1-32 lys1-131 ura4-D18 rec12-152::LEU2 mad2::ura4⁺ sid4::GFP-kan⁻ sod2.proximal[::kan⁻ura4⁺-lacO] his7::Pdis1-GFP-lacI-NLS</i>
AY401-5A	<i>h⁺ leu1-32 lys1-131 ura4-D18 rec12-152::LEU2 sid4::GFP-kan⁻ ade6[::kan⁻ura4⁺-lacO] his7::Pdis1-GFP-lacI-NLS</i>
AY401-5B	<i>h⁻ leu1-32 lys1-131 ura4-D18 rec12-152::LEU2 sid4::GFP-kan⁻ ade6[::kan⁻ura4⁺-lacO] his7::Pdis1-GFP-lacI-NLS</i>
AY402-2B	<i>h⁺ leu1-32 lys1-131 ura4-D18 rec12-152::LEU2 mad2::ura4⁺ ade6[::kan⁻ura4⁺-lacO] his7::Pdis1-GFP-lacI-NLS</i>
AY402-8A	<i>h⁻ leu1-32 lys1-131 ura4-D18 rec12-152::LEU2 mad2::ura4⁺ sid4::GFP-kan⁻ ade6[::kan⁻ura4⁺-lacO] his7::Pdis1-GFP-lacI-NLS</i>
AY413-2D	<i>h⁺ ade6-M210 leu1-32 lys1-131 ura4-D18 or DS/E clr4::ura4⁺ sid4::GFP-kan⁻ cen2(D107)::kan⁻ura4⁺-lacO his7::Pdis1-GFP-lacI-NLS</i>
AY413-9C	<i>h⁻ ade6-M210 leu1-32 lys1-131 ura4-D18 or DS/E clr4::ura4⁺ sid4::GFP-kan⁻ cen2(D107)::kan⁻ura4⁺-lacO his7::Pdis1-GFP-lacI-NLS</i>
AY417-5A	<i>h⁹⁰ ade6-M210 leu1-32 ura4-D18 slp1-362^(a) lys1::Pnda3-GFP-atb2⁺</i>
AY418-2C	<i>h⁹⁰ ade6-M210 or M216 leu1-32 ura4-D18[β] slp1-362 rec12-152::LEU2 mad2::ura4⁺ lys1::Pnda3-GFP-atb2⁺</i>
AY437-4D	<i>h⁹⁰ ade6-M210 leu1-32 ura4-D18 clr4::kan^(p) fzf1::ura4^(h) lys1::Pnda3-GFP-atb2⁺</i>
AY441-3B	<i>h⁹⁰ ade6-M210 leu1-32 lys1-131 ura4-D18 cdc13::GFP-LEU2^(h) fzf1::ura4⁺</i>
AY441-19A	<i>h⁹⁰ ade6-M210 leu1-32 ura4-D18 cdc13::GFP-LEU2 rec12::kan^(h) fzf1::ura4⁺</i>
AY442-15A	<i>h⁹⁰ ade6-M210 or M216 leu1-32 ura4-D18 rec12-152::LEU2 clr4::kan⁻ fzf1::ura4⁺ lys1::Pnda3-GFP-atb2⁺</i>
AY445-1D	<i>h⁹⁰ ade6-M210 leu1-32 ura4-D18 fzf3::kan^(h) lys1::Pnda3-GFP-atb2⁺</i>
FY13046 ^(e)	<i>h⁻ leu1-32 nda3-KM311M</i>
GT260	<i>h⁹⁰ ade6-M216 leu1-32 ura4-D18 mis6::GFP-LEU2⁽ⁿ⁾ lys1::Pnda3-mDsRed-atb2^(v)</i>
HR649 ^(b)	<i>h⁺ his2 leu1-32 lys1-131 ura4-D18 sad1::DsRed-LEU2</i>
HA516 ^(c)	<i>h⁻ ura4-D18 nuf2::DsRed-ura4^(w)</i>
KSP3351	<i>h⁹⁰ ade6-M210 leu1-32 ura4-D18 fzf1::ura4⁺ rec12-152::LEU2 lys1::Pnda3-GFP-atb2⁺</i>
KSP3361	<i>h⁹⁰ ade6-M210 leu1-32 ura4-D18 fzf2::ura4^(k) rec12-152-LEU2 lys1::Pnda3-GFP-atb2⁺</i>
KSP3362	<i>h⁹⁰ ade6-M210 leu1-32 ura4-D18 slp1-362 rec12-152-LEU2 lys1::Pnda3-GFP-atb2⁺</i>
KSP3381	<i>h⁹⁰ ade6-M210 leu1-32 ura4-D18 fzf3::kan⁻ rec12-152-LEU2 lys1::Pnda3-GFP-atb2⁺</i>
KSP3403	<i>h⁹⁰ ade6-M216 leu1-32 ura4-D18 fzf1::ura4⁺ lys1::Pnda3-GFP-atb2⁺</i>
KSP3481	<i>h⁹⁰ ade6-M210 leu1-32 ura4-D18 fzf2::ura4⁺ lys1::Pnda3-GFP-atb2⁺</i>
KSP3502	<i>h⁹⁰ ade6-M210 leu1-32 ura4-D18 Prad21-slp1::kan^(v) lys1::Pnda3-GFP-atb2⁺</i>
KSP3512	<i>h⁹⁰ ade6-M210 or M216 leu1-32 ura4-D18 slp1-mr63^(a) rec12-152::LEU2 lys1::Pnda3-GFP-atb2⁺</i>
KJ3401	<i>h⁹⁰ ade6-M210 leu1-32 ura4-D18 slp1-362 fzf1::ura4⁺ lys1::Pnda3-GFP-atb2⁺</i>
KJ362-5B	<i>h⁹⁰ ade6-M210 leu1-32 ura4-D18 slp1-362 mes1::LEU2 lys1::Pnda3-GFP-atb2⁺</i>
KJ362-9B	<i>h⁹⁰ ade6-M216 leu1-32 ura4-D18 fzf1::ura4⁺ mes1::LEU2 lys1::Pnda3-GFP-atb2⁺</i>
KJ380B-5D	<i>h⁹⁰ ade6-M210 leu1-32 ura4-D18 slp1-mr63 clr4::kan⁻ lys1::Pnda3-GFP-atb2⁺</i>
MA071 ^(d)	<i>h⁻ leu1-32 ura4-D18 mad2::GFP-kan⁻</i>
RT3981	<i>h⁹⁰ ade6-M216 leu1-32 ura4-D18 cdc13::GFP-LEU2 lys1::Pnda3-mDsRed-atb2⁺</i>
RT3982	<i>h⁹⁰ ade6-M210 leu1-32 ura4-D18 rec12-152-LEU2 cdc13::GFP-LEU2 lys1::Pnda3-mDsRed-atb2⁺</i>
SAY502-3A	<i>h⁹⁰ ade6-M216 leu1-32 lys1-131 ura4-D18 rec8::ura4⁺ cdc13::GFP-LEU2</i>

Strains used in figures. Figure 1: (A and B) AY296-17A; (D–G) cen2: AY319-1A; (F) ade6: AY378-1A X AY378-2C; ade8: AY333-1C; sod2: AY338-7A; (H) GT260; (I) RT3981. Figure 2: (A) AY319-24C; (B) AY296-2D; (C) Wt: AY296-17A; mad2: AY296-3D; rec12: AY296-2D; rec12 mad2: AY296-2C; rec12 slp1-mr63: KSP3512; fzf1: KSP3403; rec12 fzf1: KSP3351; (D) RT3982; (E) Wt: AY333-1C, AY378-1A X AY378-2C, and AY338-7A; rec12: AY340-3A, AY401-5A X AY401-5B, and AY388-1B; rec12 mad2: AY370-2B X AY359-3B, AY402-2B X AY402-8A, and AY395-15C X AY395-14A. Figure 3: (A and B) rec8: AY373-8B; clr4: AY413-2D X AY413-9C; (C–E) Wt: AY296-17A; rec8: AY361-1A; rec8 mad2: AY366-1A; clr4: AY368-2C; clr4 mad2: AY385-4C; clr4 slp1-mr63: KSP380B-5D; rec12: AY296-2D; clr4 rec12: AY379-6A; fzf1: KSP3403; rec12 fzf1: KSP3351; rec12 clr4 fzf1: AY442-15A; rec12 fzf1: AY437-4D. Figure 4: Wt: RT3981; rec12: RT3982; fzf1: AY441-3B; rec12 fzf1: AY441-19A. Figure 5: mes1: AY2571; mes1 slp1: KSP362-5B; mes1 fzf1: KSP362-9B. Figure S1: (A) RT3981; (B and C) Wt: AY398-2C; rec12: AY398-21A; rec8: SAY502-3A; fzf1: AY441-3B; rec12 fzf1: AY441-19A. Figure S2: Wt: AY296-17A; slp1-362: AY417-5A; Prad21-slp1: KSP3362; slp1-362 rec12: AY418-2C; slp1-362 rec12 mad2: KJ3401; fzf2: KSP3481; fzf3: AY445-1D; rec12 fzf2: KSP3361; rec12 fzf3: KSP3381; mes1: AY2571; mes1 slp1: KSP362-5B; mes1 fzf1: KSP362-9B. Figure S3: (A) MA071 X HR649 and HA516 X AY343-10B; (B) AY348-2D X AY354-5B; (C) PJ69-4A; (D) FY13046.

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^dProvided by Takashi Toda, London Research Institute.

^eProvided by Chikashi Shimoda, Osaka City University, Osaka, Japan; Kishida, M., T. Nagai, Y. Nakaseko, and C. Shimoda. 1994. *Curr. Genet.* 25:497–503.

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¹³Provided by M. Molnar, National Institute of Information and Communications Technology, Kobe, Japan. Present address is Department of Microbial Biotechnology and Cell Biology, University of Debrecen, Debrecen, Hungary.

¹⁴This study. The *fzr3+* gene was deleted by direct integration of a PCR-generated fragment at the *fzr3+* locus.

¹⁵This study. See Materials and methods.

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Table S2. **Parameters of meiotic centromere movements in various strains**

		Wild type		rec12	rec8	clr4
		Meiosis I	Meiosis II	Meiosis I	Meiosis II	Meiosis II
Velocities (V $\mu\text{m}/\text{min} \pm \text{SD}$)	P	0.60 ± 0.47 (100)	0.34 ± 0.22 (106)	nd	nd	0.37 ± 0.21 (101)
	AP	0.59 ± 0.39 (97)	0.31 ± 0.16 (114)	nd	nd	0.36 ± 0.22 (96)
	P and AP	nd	nd	0.55 ± 0.39 (162)	0.39 ± 0.23 (202)	0.36 ± 0.22 (197)
	Anaphase	0.84 ± 0.52 (26)	0.84 ± 0.40 (29)	nd	nd	0.66 ± 0.33 (35)
Durations (t [min] \pm SD)	P	1.40 ± 0.57 (72)	1.15 ± 0.39 (85)	nd	nd	1.36 ± 0.66 (69)
	AP	1.30 ± 0.52 (77)	1.25 ± 0.43 (87)	nd	nd	1.30 ± 0.60 (69)
	P and AP	nd	nd	1.50 ± 0.86 (123)	1.37 ± 0.64 (130)	1.33 ± 0.63 (138)
	N	1.15 ± 0.37 (20)	1.51 ± 0.91 (47)	1.33 ± 0.62 (27)	1.36 ± 0.70 (47)	1.38 ± 0.65 (55)
Frequencies (%)	Anaphase	1.69 ± 0.70 (16)	1.32 ± 0.48 (22)	nd	nd	nd
	Individual centromeres					
		(220)	(291)	(198)	(282)	(273)
	P	45.5	36.4	nd	nd	37
	AP	44.1	37.1	nd	nd	35.2
	P and AP	89.5	73.6	81.8	71.6	72.2
	N	10.5	24.4	18.2	28.4	27.8
	Bi-oriented centromere pairs					
		(108)	(145)			(133)
	P-P	8.3	9.7	nd	nd	15
AP-AP	5.6	10.3	nd	nd	9	
P-AP	67.6	35.9	nd	nd	32.3	
P-N or AP-N	16.7	37.9	nd	nd	31.6	
N-N	1.9	6.2	nd	nd	12	

Movements of bioriented homologous (meiosis I) or sister (meiosis II) centromeres during phase II were analyzed every minute. The movements of individual centromeres were classified into the four categories in relation to the spindle pole to which the centromere appeared to be attached: Anaphase, anaphase poleward movement; AP, movement away from the pole; N, indeterminate or no movement; P, nonanaphase poleward movement. Movements of pairs of bioriented homologous or sister centromeres were further categorized as follows: P-P, both centromeres move toward the poles; AP-AP, both centromeres move away from the poles; P-AP, one of the centromeres moves toward the pole while the other centromere moves away from the pole (coordinate movements); P-N or AP-N, only one of the centromeres moves toward or away from the pole; N-N, both centromeres show indeterminate or no movements. P and AP movements were not distinguished in rec12 and rec8, as it was difficult to determine the poleward or antipoleward movement due to the lack of centromere biorientation. In analysis of the wild type, 9 spindles in 9 cells and 11 spindles in 7 cells were examined for MI and MII, respectively. In analyses of rec12, rec8, and clr4, 4 spindles in 4 cells, 9 spindles in 5 cells, and 10 spindles in 6 cells were examined, respectively. In the rec12 analysis, only cells with apparent phase II were analyzed. Numbers in parenthesis show number of examined movements. nd, not determined; SD, standard deviation.