

Supplementary Figures and Tables

Fig. S1 Rec12-binding in *rad50S* versus *rad50* wild type

The graph shows the ratios of real time PCR product at *ura4A* from chromatin precipitated with an antibody against Rec12_{myc} versus PCR product from total chromatin. The chromatin was isolated from *rad50S* and *rad50*⁺ strains during meiotic progression in a *pat1-114* mutant. The *rad50S* experiment was performed four times, the *rad50*⁺ experiment once. Error bars indicate the standard error of the mean (SEM).

Fig. S2 Location of genetic markers on chromosome I

Vertical lines indicate the physical location of the genetic markers listed in Supplementary Table II, the gray box indicates the centromere, and the bar stands for 500 kb.

Fig. S3 Correlation of Rec12-binding with chromosome features

The Rec12-binding ratios are the averaged coefficients of the amounts of immunoprecipitated DNA to input DNA (red dots) from two (ORF probes) or four (intergenic probes) independent experiments, and are plotted in log₂ scale (y-axis) against a 250 kb region on chromosome II (300 Mb to 550 Mb). The units on the x-axis are in kb. The red curve shows a moving average over two probes of Rec12-binding ratios. Only concordant data sets are shown.

a. Inverse correlation of Rec12-binding with GC content per probe

The GC contents of 229 ORF and intergenic probes in percentage are plotted against the chromosomal location and are given as blue dots. The genomic average of 35.4% is set to the log₂ value of 0 for Rec12-binding ratio. The blue curve represents a moving average of GC content over two adjacent probes.

b. Inverse correlation of Rec12-binding with origins of replication.

The average log₂ values of stalled replication forks in meiosis (after hydroxyurea treatment) versus a reference ratio (Heichinger et al. 2006) of 186 ORF and intergenic probes are plotted against the chromosomal locations, and are given as blue dots. A moving average over two adjacent probes is represented by the blue curve.

- c. Some Rec12-binding peaks are close to cohesin binding sites.

The \log_2 values of the averaged and to our microarray architecture transformed, Rec8 binding ratio (see Material and Methods, (Ding et al. 2006)) of 227 ORF and intergenic probes are plotted against the respective chromosomal location, and are given as blue dots. The blue curve represents a moving average of Rec8 binding ratio over two probes.

Fig. S4 Distance between Rec12-binding hotspots and Rec8 binding peaks

A histogram of the classified distances between Rec8 peaks (with \log_2 value above 0.5) and the nearest Rec12-binding hotspot is given. The distances were measured and arranged into categories of 0–55 bp, 56-524 bp, 525-993 bp, 994-1463 bp, 1464-1932 bp, and 1933-2404 bp, respectively. The average distance of each category is given above the bar. The y-axis gives the number of representatives per category.

Table S1 The 144 Rec12-binding hotspots (ChIPOTIe)

Chr	Probe name	Probe start	Probe end	Average Rec12-binding ratio ^a	ChIPOTIe peak ^b			Low complexity gene-free regions ^c	Gene-free regions ^c	Gene-free region lengths [kb]	Non-protein coding genes ^d
					log ₂ of average ratio	Start	Length				
1	<i>C212.11</i>	1	5662	3.18	1.67	500	5750	2.0E-09			
1	<i>ght3</i>	83836	85503	5.38	2.43	83500	2500	3.6E-11	x	5	<i>ncRNA.76</i>
1	chr1.38.1	97436	98498	14.17	3.82	97000	2000	1.1E-31			
1	<i>C1F5.02</i>	293160	294638	4.11	2.04	292750	1500	4.6E-07			
1	<i>C2F7.09c</i>	549668	551143	3.64	1.86	550250	500	2.0E-05			
1	<i>C3H8.05c</i>	594877	598177	3.28	1.72	595500	2250	3.7E-04			
1	chr1.279.2	661189	662618	4.01	2	661750	500	1.1E-06	x	6	
1	<i>ural</i>	740200	746934	3.33	1.73	740250	6250	1.3E-04			
1	<i>C1A6.04c</i>	1075677	1077518	3.57	1.84	1076250	2000	3.6E-06		x	3.4
1	<i>rad31: uba4</i>	1199359	1200519	3.28	1.71	1201000	250	2.1E-05			
1	<i>PB17E12.10c</i>	1282314	1283435	2.81	1.49	1282000	1000	4.6E-06			
1	<i>pas1</i>	1363471	1364706	2.41	1.27	1363000	1250	8.2E-04	x	4.4	<i>ncRNA.86</i>
1	<i>pof1</i>	1373966	1375783	5.33	2.41	1373500	2000	5.1E-11			
1	<i>C20G8.09c</i>	1416442	1419650	5.12	2.36	1417000	2250	2.4E-10			
1	<i>C23H4.17c</i>	1577754	1578812	3.52	1.82	1577500	1000	4.5E-04			<i>ncRNA.80/.81</i>
1	<i>C23H4.01c</i>	1609062	1611899	3.73	1.9	1609750	1750	9.6E-06			
1	<i>C343.04c</i>	1644833	1646534	4.74	2.25	1645250	1000	3.8E-09			
1	<i>C343.06c</i>	1650512	1651657	4.67	2.22	1650250	1000	1.6E-05			
1	<i>meu5</i>	1793493	1795872	3.55	1.83	1794250	1250	4.0E-05			
1	chr1.832.1	1951884	1953529	6.24	2.64	1951500	2750	1.0E-13		x	8.3

1	<i>C9G1.05</i>	1977802	1979961	3.24	1.7	1978500	1000	5.2E-04				
1	<i>C17H9.06c</i>	2015106	2017038	3.31	1.73	2015750	1000	3.0E-04				
1	<i>noc1: tip1</i>	2090687	2092072	2.75	1.46	2091750	250	5.7E-04				
1	<i>C631.02</i>	2108840	2111023	3.46	1.79	2108500	2250	5.8E-05				
1	<i>php3</i>	2146581	2147288	5.12	2.36	2147250	500	2.2E-07				
1	<i>C23C11.14</i>	2159712	2160875	5.07	2.34	2159250	1750	3.2E-10				
1	<i>ypt3</i>	2216715	2217657	2.36	1.24	2217500	250	8.0E-04				
1	<i>C13G7.04c</i>	2301422	2303692	2.84	1.5	2301500	500	2.4E-06				
1	chr1.1018.1	2373271	2374071	7.20	2.85	2374000	750	5.0E-10				
1	chr1.1066.1	2482992	2483886	4.66	2.22	2483500	1000	1.2E-11				
1	<i>apl6</i>	2503877	2506164	3.59	1.84	2504500	2250	1.5E-07				
1	<i>C25H1.02</i>	2526817	2528211	3.76	1.91	2527500	250	7.8E-06				
1	<i>tif33</i>	2581120	2583876	4.48	2.16	2581000	2500	2.8E-08				
1	chr1.1123.1	2609899	2610376	4.33	2.11	2609750	1250	2.7E-05				
1	<i>C4F8.11</i>	2658944	2661484	3.61	1.85	2659500	1500	2.6E-05				
1	<i>C3F10.15c</i>	2849829	2850101	2.52	1.33	2850000	750	2.1E-04				
1	chr1.1355.2	3159791	3161158	11.71	3.55	3159500	2250	6.0E-27				
1	<i>dmc1: dmp1</i>	3383232	3384304	3.70	1.89	3384750	250	2.2E-06				
1	<i>C3H5.11</i>	3414039	3415396	3.86	1.95	3413750	1250	3.5E-06				
1	<i>car1: sod1</i>	3551052	3552632	4.34	2.12	3550750	2500	1.3E-08				
1	chr1.1523.1	3576564	3577267	5.54	2.47	3576250	1750	7.3E-17		x	7.9	
1	<i>fat1</i>	3717706	3721863	2.95	1.56	3717750	500	2.2E-04				
1	chr1.1605.1	3766386	3767771	2.54	1.35	3767500	1000	6.5E-04				
1	chr1.1606.3	3773024	3774850	2.64	1.4	3774500	1000	3.0E-04				
1	chr1.1607.2	3776322	3777706	3.55	1.83	3776000	1250	6.1E-07				
1	<i>pB18E9.05c</i>	3987548	3987820	4.60	2.2	3987500	1250	8.6E-18				
1	<i>P15E9.02c</i>	3992778	3993344	3.15	1.66	3992500	1000	1.5E-05		x	2.5	
1	<i>prl53</i>	4009072	4009581	7.96	2.99	4008750	2500	2.3E-38				<i>ncRNA.49/.53/.63</i>

1	<i>C19G12.08</i>	4057858	4059189	4.47	2.16	4058500	250	3.0E-08				
1	<i>C19G12.17c</i>	4079838	4081850	4.91	2.29	4079250	3250	3.4E-18				
1	<i>C1F7.03</i>	4220901	4223033	3.58	1.84	4220750	2000	3.2E-05				
1	chr1.1795.1	4230633	4231792	4.32	2.11	4231250	250	9.3E-08				
1	<i>c23D3.01</i>	4338147	4339370	4.86	2.28	4338750	250	1.6E-09				
1	<i>C23D3.13c</i>	4368606	4373611	3.38	1.76	4369250	4000	1.6E-04				
1	<i>C9E9.09c</i>	4454459	4455970	5.22	2.39	4454000	2500	8.1E-11				
1	<i>mei2</i>	4511939	4514191	5.36	2.42	4510250	6000	2.3E-19	x		2.7	
1	chr1.1916.3	4517080	4518483	26.28	4.72	4516750	2250	1.7E-49				<i>ncRNA.130</i>
1	<i>kfp3: krp1</i>	4707814	4709857	3.17	1.66	4708500	1000	9.9E-04				
1	chr1.2005.1	4734647	4735138	10.70	3.42	4734250	1500	8.3E-16				
1	<i>C1782.01</i>	4755906	4760945	6.14	2.62	4755750	5750	1.8E-22				
1	<i>grx1</i>	4875168	4875858	6.24	2.64	4875000	1000	1.9E-08				
1	<i>bgs3</i>	4884897	4890377	3.57	1.84	4884500	5500	6.2E-08		x	3.5	
1	<i>C26F1.05</i>	5175878	5176225	4.84	2.28	5175500	250	9.4E-05				
1	chr1.2203.1	5181931	5182906	11.48	3.52	5181500	1750	3.6E-20				
1	chr1.2258.1	5330799	5331444	4.27	2.09	5330750	1250	6.6E-10				
1	<i>C4D7.02c</i>	5353505	5354571	2.98	1.58	5353250	1000	8.6E-04				
1	<i>pop2: sud1</i>	5356030	5358141	2.56	1.36	5357750	1000	2.4E-05				
1	<i>C922.02c</i>	5472460	5475447	3.68	1.88	5472000	3000	1.0E-07				
1	<i>C922.06</i>	5486270	5487046	3.80	1.92	5487000	750	7.1E-05				
2	<i>ght4</i>	158455	160128	5.11	2.35	158000	2750	2.6E-10				
2	<i>C660.17c</i>	234534	235148	6.18	2.63	232000	3750	1.6E-30				<i>ncRNA.101/.102</i>
2	chr2.103.1	339029	340273	32.14	5.01	338750	2250	1.5E-47	x		3.3	<i>ncRNA.103</i>
2	<i>exo70</i>	418219	420376	3.18	1.67	419000	1000	9.1E-04				
2	<i>C902.02c</i>	484849	487860	3.93	1.98	484500	3000	1.9E-06				
2	<i>C902.05c</i>	493062	494555	8.20	3.04	492750	2500	5.4E-19				
2	chr2.187.1	527542	527970	16.40	4.04	527250	1250	1.4E-35				<i>ncRNA.133/.134</i>

2	chr2.270.1	745225	745674	3.58	1.84	745000	750	5.3E-06				
2	<i>C577.05c</i>	758466	759097	3.22	1.69	758750	1000	1.7E-04				
2	<i>dsk1</i>	827079	828713	2.51	1.33	826750	500	6.6E-04				
2	<i>C36.02c</i>	838452	840185	5.78	2.53	838000	2750	2.3E-12	x		4.2	
2	<i>C409.03</i>	1138956	1139430	5.66	2.5	1139000	250	1.5E-05				
2	chr2.437.1	1154617	1155535	3.85	1.94	1154250	1000	2.1E-10	x		4.5	
2	chr2.493.1	1271792	1272899	4.13	2.04	1271500	1000	6.9E-05				
2	chr2.508.2	1308267	1309559	8.25	3.04	1308000	2250	3.8E-40				
2	<i>C83.11</i>	1530191	1531531	3.16	1.66	1531250	1000	6.1E-04				
2	chr2.642.1	1600667	1601007	2.58	1.37	1600250	1000	1.4E-05				
2	chr2.651.2	1623014	1624892	4.05	2.02	1622750	2750	1.1E-09				
2	chr2.651.4	1627072	1628985	4.15	2.05	1626750	2750	1.2E-10				
2	<i>C11G11.01</i>	1759607	1760202	3.32	1.73	1760250	500	1.1E-05				
2	<i>C1E8.05</i>	1972714	1973667	2.37	1.25	1973250	1000	8.5E-04				
2	chr2.857.1	2096062	2096221	6.03	2.59	2095750	1000	3.2E-13				
2	chr2.867.1	2116146	2116328	4.56	2.19	2116000	1000	1.7E-08				
2	<i>matmi: c1711.01</i>	2134386	2134514	2.76	1.46	2134250	500	6.2E-04				
2	<i>rec15</i>	2163342	2163933	5.57	2.48	2163000	1500	1.7E-17				
2	<i>C15C4.04c</i>	2244631	2246259	3.59	1.84	2245250	750	3.0E-05				
2	<i>C21H7.01c</i>	2253536	2255206	3.45	1.79	2254250	500	9.4E-05				
2	<i>C21D10.09c</i>	2428367	2433388	5.58	2.48	2428000	6000	9.1E-12				<i>ncRNA.107</i>
2	<i>C29A10.02</i>	2538021	2539827	16.96	4.08	2537750	3000	9.8E-57				
2	<i>cad1: hmt2</i>	2590900	2592279	3.08	1.62	2591000	500	1.6E-04				
2	chr2.1078.1	2621114	2621524	2.66	1.41	2621250	500	4.7E-04				
2	chr2.1208.1	2941560	2941863	2.77	1.47	2941500	750	9.6E-06				
2	<i>ral2</i>	3222146	3223981	4.01	2.01	3222750	750	9.9E-07				
2	<i>C25H2.14</i>	3251999	3253047	2.46	1.3	3251500	1000	2.4E-04				

2	<i>ncd10</i>	3352648	3354614	4.95	2.31	3352250	3000	7.7E-10				
2	<i>ptr2</i>	3407636	3409492	3.01	1.59	3406500	1750	3.0E-10				
2	<i>C887.13c</i>	3567624	3568987	2.53	1.34	3567250	750	7.3E-04				
2	<i>C13G1.05</i>	3736592	3738704	7.37	2.88	3736750	2500	7.3E-17				
2	<i>mcm6: mis5</i>	3882118	3884796	2.97	1.57	3882250	500	3.9E-04				
2	<i>C26H8.04c</i>	3950985	3955475	4.70	2.23	3951750	3250	5.0E-09				
2	chr2.1694.1	4038771	4039964	30.11	4.91	4038500	2000	1.1E-27				
2	<i>C342.04</i>	4210098	4211079	5.12	2.35	4209750	1000	7.5E-07				
2	<i>C8E4.07c</i>	4423213	4427064	4.10	2.04	4424000	2750	4.9E-07				
2	<i>C8E4.01c</i>	4446052	4447770	3.70	1.89	4446750	1750	6.1E-07		x	4	
3	<i>P20C8.02c</i>	31185	31520	4.84	2.28	30750	500	3.7E-05				
3	<i>meu3RC</i>	41985	42728	5.78	2.53	41500	1750	4.7E-08				<i>ncRNA.07</i>
3	<i>C757.12</i>	73483	75360	3.85	1.95	74250	750	3.5E-06				
3	<i>C613.02</i>	82860	84353	7.96	2.99	82500	1750	2.2E-18				<i>ncRNA.22</i>
3	<i>C613.07</i>	91686	92723	3.60	1.85	92250	500	4.8E-05				
3	<i>C330.12c</i>	135957	136499	4.02	2.01	135500	500	1.3E-06				
3	<i>C320.02c</i>	174183	176159	4.78	2.26	174750	1750	2.8E-09				
3	<i>ght5</i>	212313	213953	4.34	2.12	212000	4000	8.6E-16	x		5.4	
3	chr3.82.1	228381	229858	2.87	1.52	228000	1000	1.1E-07		x	4.4	
3	<i>C553.07c</i>	293444	295010	3.13	1.65	293000	750	8.5E-08				
3	<i>mob2</i>	508053	509308	2.85	1.51	509000	1000	3.1E-05				
3	<i>C1393.07c</i>	806262	808855	5.00	2.32	806000	3500	5.7E-10				
3	chr3.408.1	814299	814847	3.76	1.91	814000	1500	4.3E-10	x		3.8	
3	<i>C16A11.03c</i>	872348	874056	4.00	2	873000	750	1.1E-06				
3	chr3.535.1	1094047	1095508	4.53	2.18	1093750	4000	3.6E-27				
3	chr3.531.1	1098451	1100186	2.79	1.48	1098000	1000	1.2E-06				
3	chr3.537.2	1100240	1101968	3.23	1.69	1099750	2750	1.6E-10				
3	chr3.538.2	1105308	1106766	3.45	1.79	1105000	2500	4.9E-06				

3	<i>C1322.05c</i>	1294976	1296814	5.43	2.44	1294500	2000	2.6E-11				
3	chr3.703.1	1541440	1541899	3.27	1.71	1541500	1000	1.5E-08				
3	chr3.848.2	1871661	1872676	3.61	1.85	1869000	4250	6.5E-07				
3	chr3.865.1	1929106	1930756	6.49	2.7	1928750	1500	1.9E-14				
3	<i>C4F11.05</i>	2011402	2011689	5.01	2.32	2011000	1250	3.3E-08				<i>ncRNA.30/.124</i>
3	<i>wtf1</i>	2018617	2020188	3.31	1.73	2018500	2250	3.0E-04				
3	<i>C1739.01</i>	2026479	2028230	2.82	1.5	2027750	1000	2.0E-07				
3	chr3.905.1	2042561	2044209	7.62	2.93	2042250	2500	1.6E-17				
3	<i>C1620.12c</i>	2168699	2170486	4.23	2.08	2168250	1750	3.2E-13				
3	chr3.963.1	2173192	2173549	6.91	2.79	2173250	1000	1.5E-13				
3	chr3.980.1	2217827	2218900	16.98	4.09	2217500	2000	1.6E-36				
3	<i>C1494.08c</i>	2342459	2343283	4.89	2.29	2343250	250	1.1E-04				
3	<i>meu19</i>	2419951	2420699	3.65	1.87	2420250	2000	2.0E-11				<i>ncRNA.29</i>

^a The Rec12-binding ratio (immunoprecipitated DNA to input DNA) was determined for ORF probes (two experiments) and intergenic probes (four experiments)

^b Peaks were computed by the ChIPOTie algorithm (Buck et al. 2005) with the following parameters: 1000 bp sliding window, 250 bp steps. The log₂ value of the average Rec12-binding ratio over peak length, peak start, peak length, and p-value are given.

^c As annotated in (Wood et al. 2002).

^d Non-protein coding genes as described in (Watanabe et al. 2002)

Table S2 Genetic length of different intervals on chromosome I

Interval ^a	Distance in kb	Colonies tested	P1 ^b	P2 ^b	R1 ^b	R2 ^b	R1 + R2 in %	cM ^c	cM/kb	mean cM/kb ± SEM ^d
<i>sod2::ura4 - lys3-37</i>	478	448	162	122	83	81	36.6	65.9	0.14	0.16±0.01
	478	448	167	103	101	77	39.7	79.2	0.17	
	478	448	153	117	104	74	39.7	79.2	0.17	
<i>lys3-37 - ura1-61</i>	209	448	181	190	41	36	17.2	21.1	0.10	0.12±0.01
	209	447	171	195	42	39	18.1	22.5	0.11	
	209	448	166	185	45	52	21.7	28.4	0.14	
<i>ura1-61 - pro1-1</i>	267	448	164	150	56	78	29.9	45.6	0.17	0.14±0.02
	267	448	173	155	49	71	26.8	38.4	0.14	
	267	448	176	174	50	48	21.9	28.8	0.11	
<i>pro1-1 - ade3-58</i>	323	448	140	138	85	85	38.0	71.1	0.22	0.19±0.02
	323	448	136	161	81	70	33.7	56.1	0.17	
	323	448	146	150	78	74	33.9	56.8	0.18	
<i>lys1-131 - his1-102</i>	565	448	120	115	105	108	47.6	150.7	0.27	0.27
<i>lys1-131 - cdc1-7</i>	276	448	143	118	93	94	41.7	90.0	0.33	0.34
	276	448	140	116	91	101	42.9	97.3	0.35	
<i>cdc1-7 - his1-102</i>	289	448	147	138	67	96	36.4	65.0	0.23	0.21
	289	448	147	152	64	85	33.3	54.7	0.19	
<i>his1-102 - leu2-120</i>	136	448	208	178	25	37	13.8	16.2	0.12	0.12
<i>leu2-120 - lys7-2</i>	57	448	209	182	31	26	12.7	14.7	0.26	0.26

^a The location of the markers is given in Fig. S2

^b P1 and P2 have the same genotypes like the parents, R1 (wt/wt) and R2 (mutant/mutant) represent recombinants

^c Genetic Distance: $d = -50 \cdot \ln[1 - 2 \cdot (R1 + R2) / (P1 + P2 + R1 + R2)]$

^d SEM: standard error of the mean

Table S3 Observed distribution of Rec12-binding versus random redistribution in the intervals on chromosome I

Correlation of genetic distance in intervals on chromosome I with the sum of	Pearson r	p-value	r ²
observed Rec12-binding ratios ^a	0.94	0.0002	0.89
randomly redistributed Rec12-binding ratios ^a , set 1	0.96	0.0001	0.91
set 2	0.68	0.04	0.46
set 3	0.84	0.0048	0.70
set 4	0.74	0.02	0.54
set 5	0.61	0.08	0.37
set 6	0.90	0.0011	0.80
set 7	0.75	0.02	0.57
set 8	0.89	0.0014	0.79
set 9	0.92	0.0004	0.85
set 10	0.83	0.01	0.69
set 11	0.75	0.02	0.57
set 12	0.83	0.01	0.69
set 13	0.74	0.02	0.55
set 14	0.71	0.03	0.50
set 15	0.70	0.03	0.50
set 16	0.58	0.10	0.34
set 17	0.83	0.01	0.69
set 18	0.71	0.03	0.50
set 19	0.65	0.06	0.43
set 20	0.82	0.01	0.67

^a The Rec12-binding ratios (observed or randomly redistributed) were added up over the length of the genetic intervals, divided by the sum of measured probe lengths in the intervals, and correlated with recombination frequencies (cM/kb) (Table S2).

Table S4 Rec12-binding hotspots per chromosomes

	Sum of probe lengths in Mb	Number of Rec12-binding hotspots ^a	Average Rec12-binding ratio \pm SEM ^b	Average distance between Rec12-binding hotspots in kb
chr I	5.4	69	1.18 \pm 0.01	78
chr II	4.4	44	1.24 \pm 0.02	100
chr III	2.3	31	1.16 \pm 0.02	74
all	12.0	144	1.20 \pm 0.01	84

^a Hotspots were determined by the ChIPOTIe algorithm (Buck et al. 2005) with a 1000 bp sliding window and 250 bp steps (Table S1).

^b The average Rec12-binding ratio per probe and chromosome is given. SEM = Standard error of the mean

Table S5 Co-localization of Rec12-binding hotspots (HS) with Rec8 binding sites on chromosome II

	Pairs tested	Spearman r	P-value	Significant
Rec12-binding HS ^a	49	-0.18	0.23	No
Rec12-binding ratio > 1 ^b	334	0.013	0.80	No
Rec12-binding ratio > 0.8 ^b	463	0.160	0.001	Yes

^a The Rec12-binding ratios of the probes from the ChIPOTIe hotspots (Table S1) were correlated with the transformed Rec8-binding ratios on the same probes on chromosome II (see Material and Methods).

^b To include also less pronounced Rec12-binding sites, log₂ values of Rec12-binding ratios over 1 or over 0.8 were used for correlation analysis with the corresponding Rec8-binding ratios on chromosome II.

Table S6 Probability of occurrence of Rec8-binding peaks in Rec12-binding peak windows

Chromosome ^a	Cut-off values for \log_2 of Rec8-binding ratios	Rec8 peak width [bp] ^b	Number of Rec8 Peaks ^c	Average Rec8 peak distance [bp] ^d	% occurrence of Rec8 peaks in Rec12 peak windows ^e
II	0.5	3'000	419	10'467	47.8
III	0.5	3'000	122	10'536	47.5
II	0.8	2'500	276	15'890	31.4
III	0.8	2'500	84	15'303	32.7

^a The Rec8-binding data for chromosome II measured on an Affimetrix ChIP contained gaps, and most of the data for the right arm of chromosome III was missing (Ding et al. 2006).

^b Conservative peak widths were assumed, based on measured average width.

^c Number of peaks with a Rec8 binding ratio above 0.5 (or 0.8, respectively) and a maximal peak width of 3'000 bp (or 2'500 bp, respectively).

^d The lengths of covered Affimetrix probes were added together and divided by the number of Rec8 peaks

^e A window around a Rec12-binding ratio peak of 5000 bp was assumed.

References

- Buck MJ, Nobel AB, Lieb JD (2005) ChIPOTle: a user-friendly tool for the analysis of ChIP-chip data. *Genome Biol* 6:R97
- Ding DQ, Sakurai N, Katou Y, Itoh T, Shirahige K, Haraguchi T, Hiraoka Y (2006) Meiotic cohesins modulate chromosome compaction during meiotic prophase in fission yeast. *J Cell Biol* 174:499-508
- Heichinger C, Penkett CJ, Bähler J, Nurse P (2006) Genome-wide characterization of fission yeast DNA replication origins. *Embo J* 25:5171-5179
- Watanabe T, Miyashita K, Saito TT, Nabeshima K, Nojima H (2002) Abundant poly(A)-bearing RNAs that lack open reading frames in *Schizosaccharomyces pombe*. *DNA Res* 9:209-215
- Wood V, Gwilliam R, Rajandream MA, Lyne M, Lyne R, Stewart A, Sgouros J, Peat N, Hayles J, Baker S, Basham D, Bowman S, Brooks K, Brown D, Brown S, Chillingworth T, Churcher C, Collins M, Connor R, Cronin A, Davis P, Feltwell T, Fraser A, Gentles S, Goble A, Hamlin N, Harris D, Hidalgo J, Hodgson G, Holroyd S, Hornsby T, Howarth S, Huckle EJ, Hunt S, Jagels K, James K, Jones L, Jones M, Leather S, McDonald S, McLean J, Mooney P, Moule S, Mungall K, Murphy L, Niblett D, Odell C, Oliver K, O'Neil S, Pearson D, Quail MA, Rabbinowitsch E, Rutherford K, Rutter S, Saunders D, Seeger K, Sharp S, Skelton J, Simmonds M, Squares R, Squares S, Stevens K, Taylor K, Taylor RG, Tivey A, Walsh S, Warren T, Whitehead S, Woodward J, Volckaert G, Aert R, Robben J, Grymonprez B, Weltjens I, Vanstreels E, Rieger M, Schafer M, Muller-Auer S, Gabel C, Fuchs M, Dusterhoft A, Fritz C, Holzer E, Moestl D, Hilbert H, Borzym K, Langer I, Beck A, Lehrach H, Reinhardt R, Pohl TM, Eger P, Zimmermann W, Wedler H, Wambutt R, Purnelle B, Goffeau A, Cadieu E, Dreano S, Gloux S, Lelaure V, Mottier S, Galibert F, Aves SJ, Xiang Z, Hunt C, Moore K, Hurst SM, Lucas M, Rochet M, Gaillardin C, Tallada VA, Garzon A, Thode G, Daga RR, Cruzado L, Jimenez J, Sanchez M, del Rey F, Benito J, Dominguez A, Revuelta JL, Moreno S, Armstrong J, Forsburg SL, Cerutti L, Lowe T, McCombie WR, Paulsen I, Potashkin J, Shpakovski GV, Ussery D, Barrell BG, Nurse P (2002) The genome sequence of *Schizosaccharomyces pombe*. *Nature* 415:871-880

Fig. S1, Ludin et al.

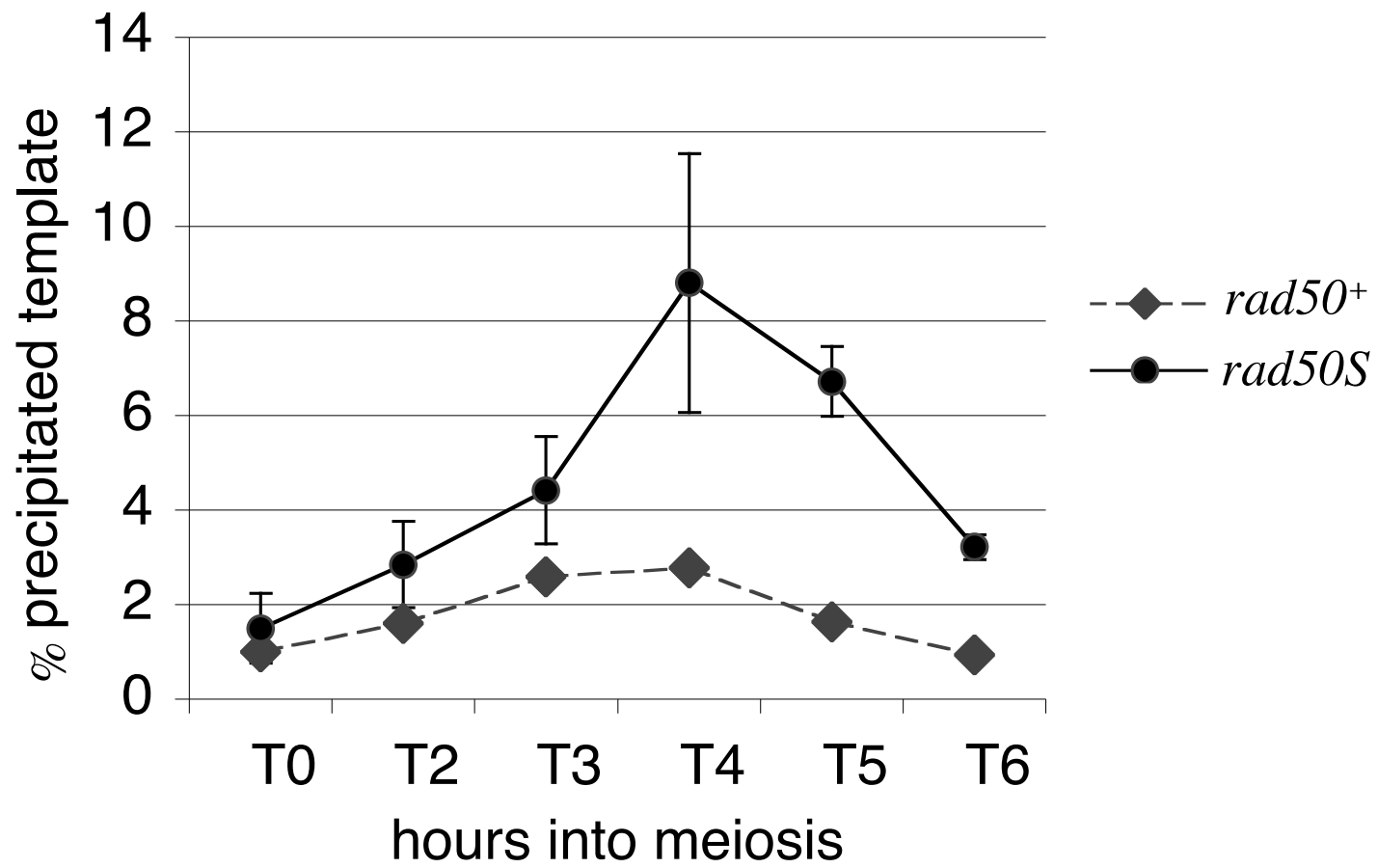


Fig. S2, Ludin et al.

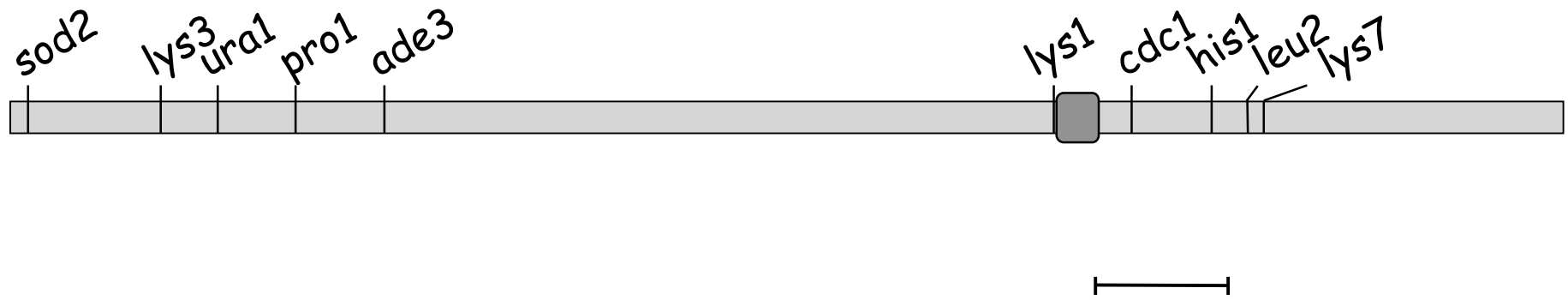


Fig. S3, Ludin et al.

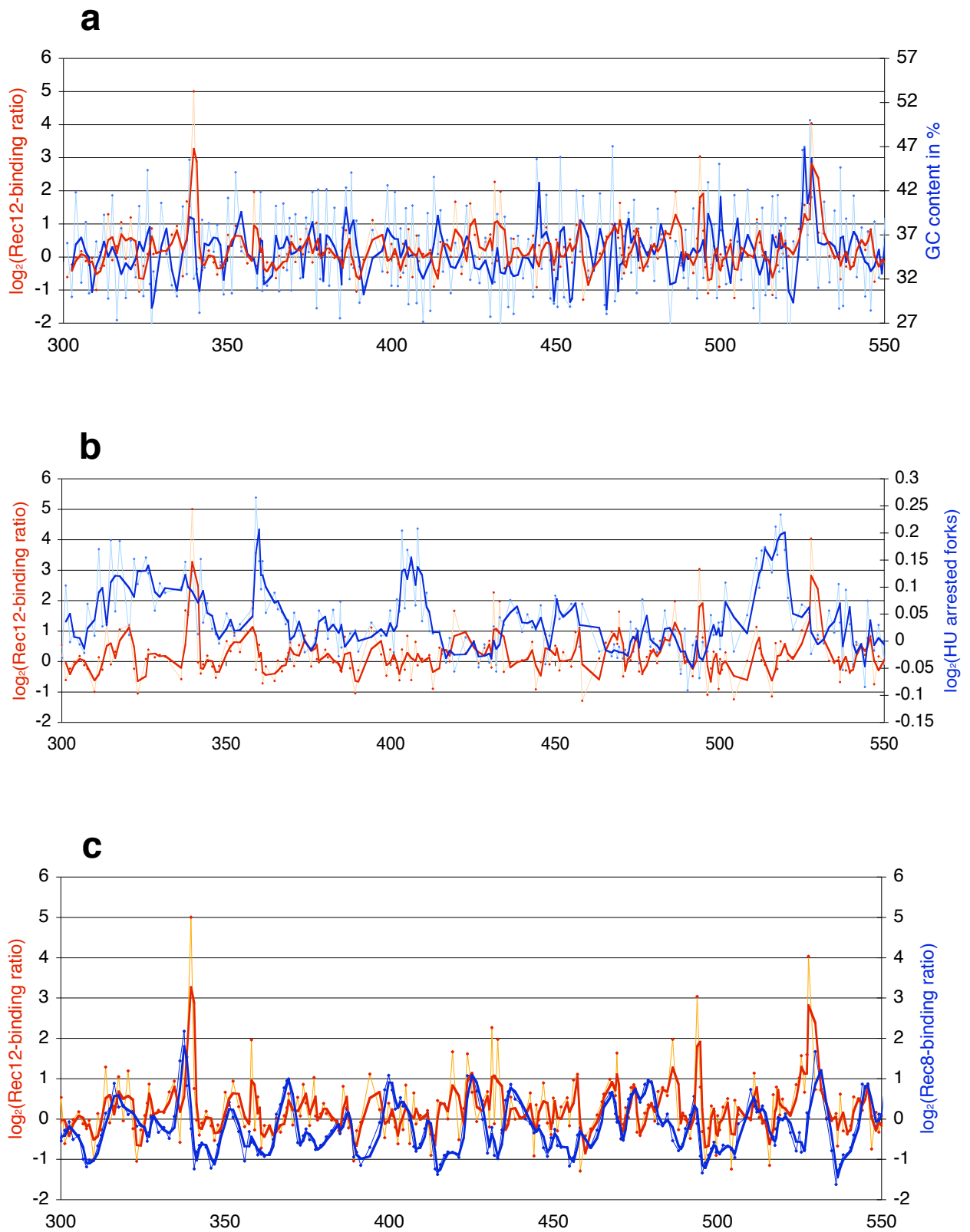


Fig. S4, Ludin et al.

