

Table 1. Putative coiled-coil regions used in this study

Construct*	Systematic Name	Yeast Proteome	Region used [†]	Dimer score [‡]	Interactions [§]
1	YFL008W	SMC1	159–497 [¶]	0.99	A, B
2	YFL008W	SMC1	688–929 [¶]	0.99	A, B
3	YFL008W	SMC1	688–1076 [¶]	0.99	A, B
4	YDL181W	INH1	37–84	0.99	A, B
5	YHL010C	YHL010C	477–560	0.96	A
6	YKL179C	YKL179C	44–113	0.62	
7	YKL179C	YKL179C	159–222	0.63	
8	YKL179C	YKL179C	217–354	0.63	A
9	YKL179C	YKL179C	382–455	0.96	
10	YKL179C	YKL179C	484–548	0.60	A
11	YLR131C	ACE2	171–253	0.95	A
12	YDR499W	YDR499W	76–152	0.93	
13	YLL026W	HSP104	447–519	0.93	
14	YHL009C	YAP3	144–220	0.93	
15	YDR184C	ATC1	235–293	0.93	
16	YDL072C	YDL072C	156–202	0.92	B
17	YMR117C	SPC24	24–136 [¶]	0.92	A
18	YMR117C	SPC24	72–136	0.92	A, B
19	YLR190W	YLR190W	280–347	0.92	
20	YLR190W	YLR190W	342–400	0.28	A, B
21	YCL029C	BIK1	178–409 [¶]	0.92	B
22	YCL029C	BIK1	346–409	0.92	
23	YBR057C	MUM2	169–236	0.92	
24	YBR057C	MUM2	233–294	0.24	B
25	YBR057C	MUM2	310–365	0.31	
26	YKL050C	YKL050C	481–547	0.92	B
27	YKL023W	YKL023W	143–228	0.92	
28	YOL069W	NUF2	124–449 [¶]	0.91	A, B
29	YCL024W	YCL024W	520–583	0.91	
30	YLR314C	CDC3	427–516	0.91	B
31	YJL036W	SNX4	330–394	0.90	
32	YOR195W	SLK19	277–821 [¶]	0.90	A, B
33	YNL079C	TPM1	1–198	0.90	A
34	YIL138C	TPM2	1–160	0.90	A, B
35	YPL146C	YPL146C	307–380	0.90	
36	YLL021W	SPA2	267–410	0.89	B
37	YGR059W	SPR3	439–505	0.89	B
38	YLR429W	CRN1	589–650	0.89	A, B
39	YCR086W	YCR086W	7–86	0.88	B
40	YIR018W	YAP5	61–148	0.87	A

41	YHR158C	KEL1	770–1163 [¶]	0.87	A, B	
42	YHR158C	KEL1	959–1092	0.54	B	
43	YHR158C	KEL1	770–971 [¶]	0.87	A, B	
44	YHR158C	KEL1	1078–1163 [¶]	0.27	A	
45	YLR319C	BUD6	584–641	0.86		
46	YMR124W	YMR124W	480–546	0.85		
47	YMR124W	YMR124W	803–863	0.48	A, B	
48	YDR379W	RGA2	606–686	0.85	A, B	
49	YGL086W	MAD1	61–333 [¶]	0.49	A, B	
50	YGL086W	MAD1	379–598 [¶]	0.85		
51	YJL114W	(TY4B)	30–125	0.83	A, B	
52	YJL113W	(TY4A)	30–125	0.83	A, B	
53	YDR200C	YDR200C	444–547	0.83		
54	YDL074C	YDL074C	118–183	0.44		
55	YDL074C	YDL074C	118–635 [¶]	0.83	A, B	
56	YGL075C	MPS2	145–227	0.83	A, B	
57	YGL066W	YGL066W	264–334	0.83		
58	YNL271C	BNI1	696–807	0.81		
59	YNL271C	BNI1	1517–1578	0.83		
60	YPR049C	YPR049C	676–865 [¶]	0.83		
61	YNL272C	SEC2	11–178 [¶]	0.83	A, B	
62	YDL099W	YDL099W	173–290	0.86	A, B	
63	YOR326W	MYO2	575–1101 [¶]	0.84	B	
64	YOR326W	MYO2	575–1192 [¶]	0.84		
65	YLR238W	YLR238W	354–419	0.46		
66	YIR017C	MET28	111–185	0.82	B	
67	YGR285C	ZUO1	285–372	0.82		
68 [¶]	YLR045C	STU2	681–775	0.81		
69	YFR031C	SMC2	159–398 [¶]	0.28	A	
70	YFR031C	SMC2	774–958 [¶]	0.82	A, B	
71	YAL011W	YAL011W	182–277	0.82	B	
72	YAL035W	YAL035W	73–251 [¶]	0.72		
73	YAL047C	SPC72	91–155	0.20	B	
74	YAL047C	SPC72	335–471 [¶]	0.10	B	
75	YAL047C	SPC72	566–621	0.44		
76	YBL063W	KIP1	701–758	0.74		
77	YBR211C	AME1	189–248	0.76	B	
78	YDL087C	LUC7	113–166	0.20	A	
79	YDL126C	CDC48	750–800	0.05		
80	YDR150W	NUM1	103–303 [¶]	0.66	A, B	
81	YDR159W	SAC3	677–747	0.48		
82	YDR218C	SPR28	369–422	0.73		
83	YDR251W	PAM1	346–531 [¶]	0.79		
84	YDR285W	ZIP1	182–357 [¶]	0.79	A	
85	YDR285W	ZIP1	388–761 [¶]	0.66	A	
86	YDR295C	YDR295C	439–655 [¶]	0.74	A, B	

87	YDR356W	NUF1	135–803 [¶]	0.60		
88	YDR507C	GIN4	539–645	0.78	A	
89	YEL043W	YEL043W	214–392 [¶]	0.80	A, B	
90	YEL061C	CIN8	543–670	0.59	A, B	
91	YEL061C	CIN8	873–931	0.06	A	
92	YER149C	PEA2	249–416 [¶]	0.76	A, B	
93	YGL216W	KIP3	431–482	0.04		
94	YGR089W	YGR089W	762–936 [¶]	0.75	A, B	
95	YGR130C	YGR130C	422–782 [¶]	0.74	A	
96	YGR142W	BTN2	255–331	0.80		
97	YHR107C	CDC12	356–407	0.67	A, B	
98	YJL074C	SMC3	107–518 [¶]	0.50	A, B	
99	YJL074C	SMC3	751–1050 [¶]	0.75	A, B	
100	YJL187C	SWE1	289–339	0.10		
101	YJR035W	RAD26	75–146	0.77	A	
102	YJR076C	CDC11	348–414	0.31	A	
103	YJR083C	YJR083C	70–135	0.78	A, B	
104	YJR112W	NNF1	59–187 [¶]	0.78	A	
105	YJR112W	NNF1	113–187	0.78	A	
106	YKL042W	SPC42	47–150	0.81	A, B	
107	YKL113C	RAD27	80–138	0.36		
108	YKR054C	DYN1	469–524	0.26	A	
109	YKR054C	DYN1	3249–3318	0.20	A, B	
110	YKR054C	DYN1	3522–3620 [¶]	0.63	A, B	
111	YLR045C	STU2	681–775	0.81		
112	YLR086W	SMC4	382–684 [¶]	0.80	A, B	
113	YLR086W	SMC4	834–1275 [¶]	0.69	A	
114	YLR200W	YKE2	1–51	0.77		
115	YLR200W	YKE2	55–113	0.71	B	
116	YLR200W	YKE2	1–113 [¶]	0.77		
117	YLR212C	TUB4	401–457	0.21		
118	YLR254C	YLR254C	1–134	0.73	A	
119	YLR309C	IMH1	117–828 [¶]	0.77		
120	YLR454W	YLR454W	1070–1128	0.30	B	
121	YLR454W	YLR454W	1878–1949	0.78	B	
122	YML072C	YML072C	924–985	0.77		
123	YMR029C	YMR029C	14–82	0.73		
124	YMR065W	KAR5	302–438 [¶]	0.16	A	
125	YMR192W	YMR192W	552–707 [¶]	0.75	A	
126	YMR198W	CIK1	190–374 [¶]	0.72	B	
127	YMR294W	JNM1	86–235 [¶]	0.26		
128	YNL084C	END3	277–349	0.72	B	
129	YNL153C	GIM3	62–128	0.73	B	
130	YNL225C	CNM67	166–461 [¶]	0.73		
131	YNL250W	RAD50	200–538 [¶]	0.74	B	
132	YNL250W	RAD50	730–1115 [¶]	0.74	A, B	

133	YOL145C	CTR9	484–528	0.77		
134	YOR058C	ASE1	478–540	0.29		
135	YOR127W	RGA1	585–668	0.76	A	
136	YOR269W	PAC1	74–140	0.78	A, B	
137	YPL018W	CTF19	27–100	0.78	B	
138	YPL115C	BEM3	39–104	0.79		
139	YPL155C	KIP2	495–554	0.43	A	
140	YPL155C	KIP2	495–702 [¶]	0.43	A, B	
141	YPL242C	IQG1	741–810	0.78		
142	YPL255W	BBP1	309–368	0.15		
143	YPR141C	KAR3	84–384 [¶]	0.47	A, B	
144	YER016W	BIM1	161–229	0.33		
145	YGL093W	SPC105	583–714 [¶]	0.12	B	
146	YIL144W	TID3	361–690 [¶]	0.69	A, B	
147	YIL144W	TID3	511–690 [¶]	0.69	A, B	
148	YPL124W	NIP29	1–52	0.44	A	
149	YPL124W	NIP29	124–180	0.09	A, B	
150	YPL124W	NIP29	1–180 [¶]	0.44	A, B	
151	YER018C	SPC25	4–76	0.01	B	
152	YJR060W	CBF1	272–331	0.10		
153	YDR201W	SPC19	1–44	0.23		
154	YDR201W	SPC19	61–164 [¶]	0.23	B	
155	YDR201W	SPC19	1–164 [¶]	0.23	A, B	
156	YEL009C	GCN4	227–281	0.72		
157	YER111C	SWI4	856–927	0.23		
158	YER111C	SWI4	926–974	0.08		
159	YDR146C	SWI5	169–232	0.83	A	
160	YLR182W	SWI6	553–645	0.68		
161	YOL004W	SIN3	468–517	0.08		
162	YOL004W	SIN3	892–922	0.01		
163	YNL103W	MET4	591–650	0.57	A, B	

From the Yeast Proteome Database, Version 9.46A (1).

*DNA corresponding to each putative coiled-coil region was subcloned into the pGAD-C1 and pGBDU-C1 vectors (2) to yield two plasmids denoted p(Construct)A and p(Construct)B, respectively (see *Materials and Methods*).

[†]Amino acid sequences encoded by two-hybrid plasmids used in this study. Primers were chosen using **primer3** (see *Materials and Methods*) to lie within a region corresponding to up to 42 nucleotides adjacent to the ends of the predicted coiled coil and up to 20 nucleotides into the predicted coiled-coil sequence.

[‡]Coiled-coil scores for the regions denoted at left were calculated using the program MULTICOIL (3).

[§] Activation-domain fusion constructs that interact in the two-hybrid assay are denoted A.
DNA-binding-domain constructs that interact are denoted B.

[¶] Denotes a region predicted to contain multiple coiled coils.

^{||} Construct 68 is identical to 111.

References

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