Supporting Information

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PNAS PNAS

	Species		I	DCL		
	S. cerevisiae	DID	D	_	ΙI	EL
	S. paradoxus	DID	A D	L	ΚI	EL
	S. mikatae	DID	A D	L	KI	EL
	S. bayanus	DID	A D I	L	ΚI	EI
	A. gossypii	EID	A D I	L	I	QI
	K. lactis	EIE	T D	L	I	DM
	S. kluyveri	DID	A D	L	Ι	GM
	L. thermotolerans	DID	A D	L	I	GM
	K. waltii	DID	A D	L	I	GM
н	P. pastoris	DID	A D	L	D V C	B P M
d	V. polyspora	DID	A D I	L	KI	EI
Group	Z. rouxii	DID	A D I	L	KI	EL
6	C. glabrata	DID	A D	L	ΚI	EL
	S. castellii	DID	A D I	L	KI	DI
	D. hansenii	DID	SE	L	KI	DM
	C. guilliermondii	DID	SE	L	KI	DM
	S. stipitis	NID	SE	L	KI	DM
	L. elongisporus	NID	SE	L	KI	DM
	C. parapsilosis	NID	SE	L	KI	DM
	C. albicans	DID	SE	L	ΟI	DM
	C. tropicalis	DFD	SE	L	ΟI	DM
	C. dubliniensis	DID	SE	L	ΟI	DM
	C. lusitaniae	DID	SE	L	RI	DM
	Y. lipolytica	TID	E	L	GI	DI
	N. crassa	DID	E	L	GI	DI
	M. oryzae	DID	E	L	GI	DT
	S. sclerotiorum	DID	E	L	GI	DT
	B. fuckeliana	DID	E	L	GI	DT
	A. nidulans	DID	E		AI	ET
	A. fumigates	DID	E			ΕI
	N. fischeri	DID	E	L	AI	EI
	A. oryzae	DID	E		-	ΕT
	A. niger	DID	E			ΕT
	A. flavus	DID	E		AI	EI
	A. clavatus	DID	E		-	ΕT
	P. chrysogenum	DID	E			ΕT
븝	C. immitis	DID	E		AI	DI
Group II	P. nodorum	DID	E		-	ΕT
no	S. japonicas	DID	E		_	DI
Gr	S. octosporus	DID	E		GI	DI
	S. pombe	DID	D E			DI
	C. neoformans	DID	E			DI
	L. bicolor	DID	D		<u> </u>	DI
	C. cinerea		A D /			DI
	U. maydis	DID	E		GI	DI
	M. globosa	DID			-	DI
	T. stipitatus		E		-	EI
	A. capsulatus	DID	E		AII	EI
	A. terreus		E	_		EI
	C. globosum	DID) E			DI
	P. anserine	DID	E		GI	DI
	G. zeae	DID	E		GI	DI
	P. marneffei	DID	DE E	L	AII	DI

Fig. S1. IDCL sequence of PCNA from 53 fungal species retrieved from the fungal orthogroup database (http://www.yeastgenome.org/cgi-bin/blast-fungal.pl). Residues that are differentially conserved between group I and group II sequences (red and blue, respectively; Fig. 2) are colored according to Lesk (1). Small nonpolar residues (G, A, S, T) are highlighted in yellow, hydrophobic residues (C, V, I, L, P, F, Y, M, W) are highlighted in green, polar residues (N, Q, H) are highlighted in magenta, negatively charged residues (D, E) are highlighted in red, and positively charged residues (K, R) are highlighted in blue.

1. Lesk A (2008) Introduction to Bioinformatics (Oxford Univ Press, Oxford).

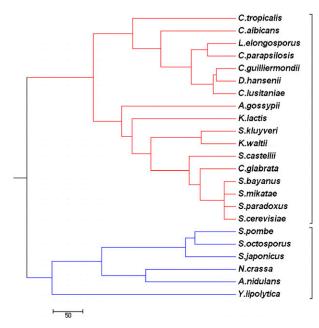


Fig. 52. PCNA protein phylogenetic tree indicating that PCNA sequences diverged into two main branches, separating those same species that are contained in group I and group II (Fig. 2*B*).

Species												C	2 – t	erm	ina	l sec	que	nce	of I	PCN	Α											
S.cerevisiae	R	L	S	S	Е	А	Ρ	Α	L	F	Q	F	D	L	Κ	-	S	G	F	L	Q	F	F	L	A	Ρ	Κ	F	Ν	D	Е	E
S.castelii	R	L	S	S	Е	А	Ρ	Α	L	F	Q	F	D	L	S	-	S	G	F	L	Q	F	F	L	А	Ρ	Κ	F	D	D	Е	E
K.waltii	Κ	L	S	А	Е	Т	Ρ	Α	L	F	Е	F	G	L	Q	-	S	G	Y	L	Q	F	F	L	Α	Ρ	Κ	F	Ν	Е	Е	E
K.lactis	Κ	L	S	Е	Е	Α	Ρ	Α	L	F	Q	F	D	I	S	-	S	G	Ν	L	Q	F	Y	L	A	Ρ	Κ	F	D	Е	Е	E
S.kluyveri	Κ	L	S	A	Е	Т	Ρ	Α	L	F	Е	F	K	L	Q	-	S	G	Y	L	Q	F	F	L	Α	Ρ	Κ	F	Ν	Е	Е	E
A.gossypii	Κ	L	S	A	D	Т	Ρ	Α	L	F	Q	F	N	L	D	G	A	G	Н	L	Q	Y	F	L	A	Ρ	K	F	Ν	E	E	E
C.lusitaniae	Κ	L	А	D	Κ	Т	Ρ	Α	L	F	Е	Y	K	L	D	А	G	G	Y	L	R	F	Y	L	А	Ρ	Κ	F	D	Е	D	D
D.hansenii	Κ	L	А	D	Κ	Т	Ρ	Α	L	F	Е	Y	Κ	L	D	А	G	G	Y	L	R	F	Y	L	А	Ρ	Κ	F	D	Е	D	D
C.tropicalis	Κ	М	A	D	Κ	Т	Ρ	Α	L	F	Е	F	K	М	Е	S	G	G	Y	L	R	Y	Y	L	А	Ρ	Κ	F	D	D	Е	E
C.albicans	Κ	L	А	D	Κ	Т	Ρ	Α	L	F	Е	F	K	М	Q	S	G	G	Y	L	R	F	Y	L	А	Ρ	Κ	F	D	D	D	E
C.parapsilosis	Κ	L	Α	D	Κ	Т	Ρ	Α	L	F	Е	F	K	L	D	V	G	G	Y	L	R	F	Y	L	Α	Ρ	Κ	F	D	Е	D	E
Y.lipolytica	G	М	S	S	Е	V	Ρ	Ι	М	V	Е	Y	L	L	Р	-	Ν	G	Y	L	R	F	Y	L	А	Ρ	Κ	Ι	G	D	Е	D
A.nidulans	S	L	S	Q	Е	V	Ρ	L	L	V	Е	Y	G	L	G	-	S	G	Н	L	R	F	Y	L	А	Ρ	Κ	V	Ν	W	_	-
N.crassa	С	L	S	Ν	Е	V	Ρ	L	L	V	Е	Y	Ν	I	S	А	S	S	Y	L	R	F	Y	L	A	Ρ	Κ	Ι	G	D	Е	E
S.pombe	S	М	S	Ν	D	V	Ρ	L	L	V	Е	Y	K	М	Е	-	S	G	F	L	R	F	Y	L	Α	Ρ	Κ	Ι	g	Е	Е	D

Fig. S3. Sequence alignment of the C-terminal region of PCNA derived from species shown in Fig. 2 indicates changes mainly in five amino acids (highlighted in colors) that are differentially conserved between group I and group II sequences (red and blue, respectively). The correlated changes between the C-terminal and the IDCL regions can indicate coevolution between these regions of PCNA (Fig. 2). Fungal species were assigned to group I or group II according to their PCNA IDCL sequence (Fig. 1 and Fig. S1). Residues that are differentially conserved between the two groups are colored according to Lesk (1). Small nonpolar residues (G, A, S, T) are highlighted in yellow, hydrophobic residues (C, V, I, L, P, F, Y, M, W) are highlighted in green, polar residues (N, Q, H) are highlighted in magenta, negatively charged residues (D, E) are highlighted in red, and positively charged residues (K, R) are highlighted in blue.

1. Lesk A (2008) Introduction to Bioinformatics (Oxford Univ Press, Oxford).

Α			C	dc	9						в			U	ng	1					
S. cerevisiae	к	Q	A	т	L	А	R	F	F	Т	Scerevisiae	Κ	Q	т	т	1	Е	D	F	F	G
A. gossypii	ĸ	Q	A	т	L	G	R	F	F	т	Klactis	т	К	V	L	V	т	D	F	F	к
Klactis	к	Q	L	т	L	D	G	F	L	R	Lthermotolerans	К	Q	к	т	L	м	E	F	F	G
L. thermotolerans	к	Q	A	т	L	A	K	F	F	S	Ppastoris	к	Q	к	L	L	S	D	F	F	P
Ppastoris	G	Q	Q	S	L	N	R	F	F	S	Vpolyspora	R	R	V	т	L	Е	D	F	F	S
V. polyspora	к	Q	A	т	L	A	R	F	F	S	Zrouxii	к	F	V	т	T.	Е	D	F	F	S
Z. rouxii	к	Q	A	т	L	A	к	F	F	S	Cglabrata	к	Q	V	т	1	Е	E	F	F	S
Cglabrata	R	Q	A	т	L	A	R	F	F	S	Mguilliermondii	к	Р	к	т	1	т	D	F	F	R
Dhansenii	Q	Q	Q	S	L	A	R	F	F	S	Dhansenii	к	S	к	L	1	т	D	F	F	Q
Sstipitis	R	Q	Q	S	1	G	R	F	F	G	Calbicans	к	R	v	F	L	т	D	F	F	R
M. guilliermondii	Q	Q	Q	S	1	A	R	F	F	G	Ctropicalis	к	R	1	L	1	т	D	F	F	S
Lelongisporus	Q	Q	Q	т	L	G	R	F	F	G	Cdubliniensis	к	R	V	L	1	т	D	F	F	R
Calbicans	к	Q	Q	S	L	Α	R	F	F	G	Clusitaniae	K	Ρ	к	L	1	т	E	F	F	Α
C. tropicalis	к	Q	Q	S	L	A	R	F	F	Ρ	Ncrassa	Q	N	G	Ν	1	м	S	F	F	G
C. dubliniensis	к	Q	Q	S	L	A	R	F	F	G	Panserina	К	Q	G	S	1	м	S	F	F	G
Clusitaniae	Е	Q	Q	S	1	L	R	F	F	G	Moryzae	Q	N	А	S	1	т	S	F	F	Α
Ncrassa	Р	S	R	G	L	E	Y	F	F	Α	Fgraminearum	Α	D	G	Ν	1	Α	S	F	F	Α
Panserina	Α	т	к	G	1	Q	Y	F	F	Α	Ssclerotiorum	Α	N	G	S	1	т	S	F	F	G
Moryzae	т	Q	Q	т	к	L	S	F	Α	т	Bfuckeliana	А	N	G	S	L	т	S	F	F	G
Fgraminearum	Ρ	Α	К	G	L	Е	Y	F	F	S	Anidulans	т	Ν	G	S	1	т	S	F	F	G
Afumigatus	R	V	R	s	1	A	S	F	F	Q	Afumigatus	Α	N	G	S	1	т	S	F	F	G
Nfischeri	R	V	R	S	1	A	S	F	F	Q	Nfischeri	Α	N	G	S	1	т	S	F	F	G
Aoryzae	R	N	R	S	1	A	S	F	F	Q	Aniger	Α	N	G	S	1	т	S	F	F	G
Aniger	R	S	R	s	1	A	S	F	F	Q	Aclavatus	А	Ν	G	S	1	т	S	F	F	G
Aflavus	R	Ν	R	s	1	Α	S	F	F	Q	Cimmitis	S	Ν	G	т	1	т	S	F	F	G
Aclavatus	P	F	R	S	1	Α	S	F	F	Q	Cposadasii	S	N	G	т	1	т	S	F	F	G
											Ureesii	Ρ	Ν	Q	Т	L	т	S	F	F	к
											Pnodorum	Α	Ν	G	S	1	т	Α	F	F	G
											Spombe	K	Q	Ρ	R	L	D	Ν	F	F	к

Fig. 54. PIP box sequence of Cdc9 (A) and Ung1 (B), PCNA partners from a variety of different fungal species. Sequences were retrieved from the KEGG orthology database (http://www.genome.jp/kegg/). Fungal species were assigned to group I (red) or group II (blue) according to their PCNA IDCL sequences (Fig. S1). Residues that are differentially conserved between the two groups are colored according to Lesk (1). Small nonpolar residues (G, A, S, T) are highlighted in yellow, hydrophobic residues (C, V, I, L, P, F, Y, M, W) are highlighted in green, polar residues (N, Q, H) are highlighted in magenta, negatively charged residues (D, E) are highlighted in red, and positively charged residues (K, R) are highlighted in blue.

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Α			Po	513	32						в			Ra	ad	27						
S. cerevisiae	к	Q	G	т	L	Е	S	F	F	к	S. cerevisiae	G	1	Q	G	R	L	D	G	F	F	Q
A. gossypii	v	Q	S	S	L	м	N	F	F	к	A. gossypii	G	V	Q	G	R	L	D	S	F	F	ĸ
K. lactis	S	Q	R	т	L	Е	s	F	F	G	Klactis	G	V	Q	к	R	L	D	S	F	F	к
Vpolyspora	к	Q	R	S	1	Е	G	F	F	к	Lthermotolerans	G	V	Q	G	R	L	D	G	F	F	к
Zrouxii	т	Q	G	т	L	Е	S	F	F	к	Ppastoris	G	т	Q	G	R	L	D	к	F	F	V
Dhansenii	т	Q	S	S	L	м	Ν	F	F	к	Vpolyspora	G	V	Q	G	R	L	D	G	F	F	Q
Sstipitis	т	Q	т	Ν	L	м	S	F	F	G	Zrouxii	G	V	Q	V	R	L	D	G	F	F	Q
Mguilliermondii	т	Q	L	S	L	м	Ν	F	F	G	Cglabrata	G	V	Q	G	R	L	D	G	F	F	к
Lelongisporus	т	Q	S	S	L	м	S	F	F	G	Dhansenii	G	V	Q	G	R	L	D	G	F	F	Q
Calbicans	к	Q	S	S	L	м	S	F	F	G	Sstipitis	G	V	Q	G	R	L	D	G	F	F	S
Ctropicalis	R	Q	Α	S	L	м	D	F	F	G	Mguilliermondii	G	V	Q	G	R	L	D	G	F	F	S
Cdubliniensis	к	Q	S	S	L	м	Ν	F	F	G	Lelongisporus	G	1	Q	G	R	L	D	G	F	F	т
Clusitaniae	к	Q	Α	S	L	м	S	F	F	G	Calbicans	G	V	Q	G	R	L	D	G	F	F	к
Ylipolytica	к	Q	S	S	L	м	S	F	F	к	Ctropicalis	G	V	Q	G	R	L	D	S	F	F	т
Ncrassa	G	Q	G	Ν	1	м	S	F	F	S	Cdubliniensis	G	V	Q	G	R	L	D	G	F	F	к
Moryzae	G	Q	G	Ν	1	м	S	F	F	S	Clusitaniae	G	V	Q	G	R	L	D	G	F	F	т
Fgraminearum	G	Q	G	Ν	1	м	S	F	F	S	Ylipolytica	к	Р	Q	A	R	L	D	G	F	F	к
Ssclerotiorum	G	Q	G	S	Т	м	S	F	F	G	Ncrassa	s	Q	Q	Α	R	1	Е	G	F	F	к
Bfuckeliana	G	Q	G	Ν	1	м	Α	F	F	G	Panserina	S	Q	Q	S	R	1	Е	G	F	F	к
Anidulans	G	Q	G	Ν	1	м	S	F	F	G	Moryzae	S	Q	Q	Q	R	L	Е	G	F	F	к
Afumigatus	G	Q	G	Ν	1	м	S	F	F	S	Fgraminearum	S	Q	Q	A	R	L	Е	G	F	F	к
Nfischeri	G	Q	G	Ν	Т	м	S	F	F	s	Ssclerotiorum	S	Q	Q	Α	R	L	Е	G	F	F	к
Aoryzae	G	Q	G	Ν	1	м	s	F	F	G	Anidulans	Α	Q	Q	S	R	L	Е	G	F	F	к
Aflavus	G	Q	G	Ν	1	м	S	F	F	G	Afumigatus	Α	Q	Q	S	R	L	Е	G	F	F	к
Aclavatus	G	Q	G	Ν	1	м	S	F	F	S	Nfischeri	Α	Q	Q	S	R	L	Е	G	F	F	к
Pchrysogenum	G	Q	G	Ν	1	М	S	F	F	G	Aoryzae	Α	Q	Q	S	R	L	Е	G	F	F	к
Cimmitis	G	Q	G	S	1	м	s	F	F	G	Aniger	Α	Q	Q	S	R	L	Е	G	F	F	к
Cposadasii	G	Q	G	S	1	м	S	F	F	G	Aflavus	Α	Q	Q	S	R	L	Е	G	F	F	к
Ureesii	S	Q	G	S	1	м	S	F	F	G	Aclavatus	Α	Q	Q	S	R	L	Е	G	F	F	к
Pnodorum	G	Q	G	S	1	Α	s	F	F	к	Pchrysogenum	Α	Q	Q	S	R	L	Е	G	F	F	к
Tmelanosporum	G	Q	G	S	1	Ν	s	Y	F	F	Cimmitis	A	Q	Q	S	R	L	Е	G	F	F	к
Spombe	Q	Q	к	S	1	м	S	F	F	G	Cposadasii	Α	Q	Q	S	R	L	Е	G	F	F	к
Cneoformans	G	Q	s	т	L	м	G	F	F	к	Ureesii	Α	Q	Q	S	R	L	Е	G	F	F	к
Lbicolor	G	Q	к	S	L	A	Ν	F	F	G	Pnodorum	Α	Q	Q	S	R	L	Е	G	F	F	к
Umaydis	G	Q	Q	S	L	Ν	S	F	F	т	Tmelanosporum	N	Т	Q	A	R	V	Ν	D	F	F	к
											Spombe	1	Ρ	Q	G	R	L	D	S	F	F	к
											Cneoformans	ĸ	Q	Q	G	R	L	D	G	F	F	Т
											Lbicolor	ĸ	Q	Q	G	R	L	D	G	F	F	S
											Ccinerea	ĸ	Q	Q	G	R	L	D	G	F	F	Т
											Scommune	ĸ	Q	Q	G	R	L	D	G	F	F	Ţ
											Umaydis	ĸ	Q	Q	G	R	L	D	G	F	F	Т
											Ecuniculi	G	Т	Q	G	R	L	D	С	F	1	т

Fig. S5. PIP box sequence of Pol32 (*A*) and Rad27 (*B*) partners from a variety of different fungal species. Sequences were retrieved from the KEGG orthology database (http://www.genome.jp/kegg/). Fungal species were assigned to group I (red) or group II (blue) according to their PCNA IDCL sequence (Fig. S1). Residues that are differentially conserved between the two groups are colored according to Lesk (1). Small nonpolar residues (G, A, S, T) are highlighted in yellow, hydrophobic residues (C, V, I, L, P, F, Y, M, W) are highlighted in green, polar residues (N, Q, H) are highlighted in magenta, negatively charged residues (D, E) are highlighted in blue.

1. Lesk A (2008) Introduction to Bioinformatics (Oxford Univ Press, Oxford).

Α			Μ	lsł	13						В			Μ	sh	6					
S. cerevisiae	G	Q	Р	т	I.	S	R	F	F	K	S. cerevisiae	к	Q	S	S	L	L	S	F	F	S
Agossypii	Q	Q	P	т	1	S	R	F	F	ĸ	Agossypii	к	Q	A	т	L	м	S	F	F	K
Klactis	Y	Q	P	т	1	S	н	F	F	к	K. lactis	к	Q	A	т	I.	S	S	F	F	ĸ
L. thermotolerans	Y	Q	P	A	1	S	ĸ	F	F	к	L. thermotolerans	к	Q	A	S	V	L	S	F	F	S
Vpolyspora	к	Q	P	V	1	S	R	F	F	к	P. pastoris	Ν	Q	P	S	V	F	S	F	F	k
Z. rouxii	V	Q	P	т	1	S	к	F	F	к	V. polyspora	к	Q	S	S	L	м	S	F	F	5
Cglabrata	к	Q	A	S	1	S	R	F	F	к	Zrouxii	к	Q	т	т	L	L	S	F	F	5
D. hansenii	G	Q	R	S	1	S	н	F	F	к	C. glabrata	к	Q	S	т	L	L	S	F	F	5
C. albicans	R	Q	S	т	L	S	R	F	F	т	S. stipitis	к	Q	S	S	L	м	S	F	F	k
C. tropicalis	A	S	1	V	D	т	G	V	F	R	M. guilliermondii	R	Q	L	S	L	м	S	F	F	k
C. dubliniensis	R	Q	S	т	L	S	R	F	F	т	L. elongisporus	Q	Q	S	т	L	м	S	F	F	k
C. lusitaniae	R	Q	к	S	1	S	S	F	F	т	Calbicans	К	Q	S	S	L	м	D	F	F	k
Y. lipolytica	K	Q	A	т	L	S	R	F	F	ĸ	C. tropicalis	к	Q	т	S	L	M	D	F	F	k
N. crassa	к	Q	A	S	1	S	S	F	F	т	C. dubliniensis	к	Q	S	S	L	м	D	F	F	k
P. anserina	K	Q	S	S	L	Т	S	F	F	т	C. lusitaniae	к	Q	S	S	L	M	S	F	F	k
M. oryzae	K	Q	A	S	L	L	G	F	F	т	Y. lipolytica	ĸ	Q	Q	S	v	L	S	F	F	k
F. graminearum	K	Q	Q	S	L	т	S	F	F	т	N. crassa	R	Q	S	S	1	L	G	F	F	5
S. sclerotiorum	т	Q	ĸ	S	1	S	S	F	F	т	P. anserina	к	Q	Q	S	1	L	G	F	F	S
B. fuckeliana	т	Q	к	S	1	S	S	F	F	A	M. oryzae	к	Q	A	S	1	L	G	F	F	A
A. nidulans	ĸ	Q	P	т	i.	S	S	F	F	т	F. graminearum	K	Q	R	S	i.	v	S	F	F	5
A. fumigatus	ĸ	Q	Q	т	1	S	S	F	F	т	S. sclerotiorum	N	Q	A	S	1	L	G	F	F	S
N. fischeri	K	Q	Q	т	1	S	S	F	F	т	A. nidulans	N	Q	К	S	1	L	G	F	F	C
A. oryzae	K	Q	P	T	i	S	S	F	F	T	A. fumigatus	N	Q	R	S	î.	Ē	G	F	F	C
A. niger	K	Q	S	т	L	A	S	F	F	Т	N. fischeri	N	Q	R	S	1	L	G	F	F	C
A. flavus	K	Q	P	Т	ī	S	S	F	F	т	A. oryzae	N	Q	к	S	i.	L	G	F	F	C
A. clavatus	ĸ	Q	P	т	1	S	S	F	F	т	A. niger	N	Q	к	S	1	L	G	F	F	C
P. chrysogenum	K	Q	A	S	i.	S	S	F	F	т	A. flavus	N	Q	к	S	i.	Ē	G	F	F	C
C. immitis	Q	Q	P	т	1	S	S	F	F	G	A. clavatus	N	Q	К	S	1	L	G	F	F	C
C. posadasii	Q	Q	P	т	1	S	S	F	F	G	P. chrysogenum	S	Q	к	S	1	L	G	F	F	C
U. reesii	Q	Q	P	T	i	S	S	F	F	S	C. immitis	G	Q	ĸ	S	i	L	G	F	F	C
T. melanosporum	K	Q	R	M	i.	S	S	F	F	A	C. posadasii	G	Q	К	S	1	Ē	G	F	F	C
C. neoformans	Q	Q	P	S	L	D	S	F	F	K	P. nodorum	N	Q	к	S	i.	L	G	F	F	0
P. placenta	ĸ	Q	P	м	ī	S	S	F	F	S	S. pombe	ĸ	Q	ĸ	т	L	F	G	F	F	5
U. maydis	G	õ	A	S	i	s	A	F	F	ĸ	Cneoformans	ĸ	ã	A	Ť	Ē	A	A	F	F	d
	-	-		-		-					L. bicolor	ĸ	Q	K	s	L	ĸ	S	F	F	5
											C. cinerea	ĸ	Q	ĸ	S	L	M	S	F	F	A
											Scommune	ĸ	ã	ĸ	т	L	L	N	F	F	Ť
											U. maydis	ĸ	Q	S	s	L	L	G	F	F	s
											M. globosa	ĸ	Q	т	s	L	1	G	F	F	5

Fig. S6. PIP box sequence of Msh3 (A) and Msh6 (B) partners from a variety of different fungal species. Sequences were retrieved from the KEGG orthology database (http://www.genome.jp/kegg/). Fungal species were assigned to group I (red) or group II (blue) according to their PCNA IDCL sequence (Fig. S1). Residues that are differentially conserved between the two groups are colored according to Lesk (1). Small nonpolar residues (G, A, S, T) are highlighted in yellow, hydrophobic residues (C, V, I, L, P, F, Y, M, W) are highlighted in green, polar residues (N, Q, H) are highlighted in magenta, negatively charged residues (D, E) are highlighted in red, and positively charged residues (K, R) are highlighted in blue.

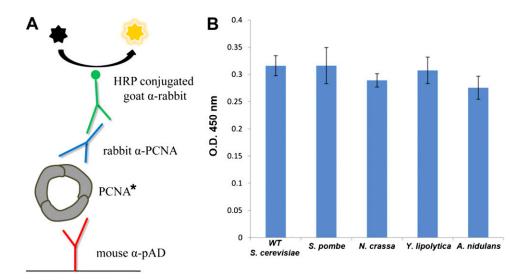
1. Lesk A (2008) Introduction to Bioinformatics (Oxford Univ Press, Oxford).

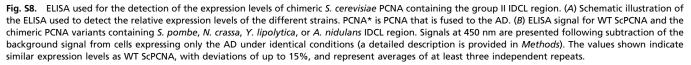
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	Rad27	PIP	Cdc9	PIP	Rfc1	PIP	Pol32	PIP	Msh6	PIP	Ung1	PIP	Msh3	PIP
S. cerevisiae														
S. paradoxus					1				1					
S. mikatae						T T			1	1				1
S. bayanus					1				1	1				
S. kluyveri					T									
S. castellii	1	1				1								
Agossypii		i												
Klactis											1			i i
thermotolerans														
K. waltii														
Ppastoris						1							1	
Vpolyspora					1				1	1				1
Zrouxii														
C. glabrata					T									
Dhansenii					T									
S. stipitis	1				1	1				1				
M. guilliermondii														
L. elongisporus						1								
C. parapsilosis						1								
Calbicans														
Ctropicalis														
Cdubliniensis													1	İL.
C. lusitaniae								-					-	
C. guilliermondii	1													
Y. lipolytica						1	1				1			
V. crassa					1	i r								il.
P. anserina	·		-			1					-	_	-	
M. oryzae	1						-		1	1	1			
Fgraminearum						1 -								+
S. sclerotiorum		1	-				-							11 -
B. fuckeliana														
A. nidulans						- i	-				1			Ì
A. fumigatus								-				-		
N. fischeri					1	-						-		1
A. oryzae						1							-	
A. niger														
Aflavus											1			
							-							
Aclavatus	Ŷ	L LL												
Pchrysogenum													1	
Cimmitis C. posadasii														
U. reesii							-							-
							-	-	1			_	-	
Pnodorum									 1					
Tmelanosporum													-	
S. octosporus														
S. japonicas								-						
Spombe														
C. neoformans			_											
P. placenta														
bicolor														
M. pemiciosa														
C. cinerea														
Scommune	J													
Umaydis	Ļ										<u></u>			
M. globosa														

Fig. S7. Analysis of PCNA partners containing a PIP box that facilitates interaction with the IDCL region of PCNA. The data are presented as a heat map, where the presence of a partner or conserved PIP box is depicted in green and its absence is presented in bright red. Fungal species were assigned to group I (red) or group II (blue) according to their PCNA IDCL sequence (Fig. S1).

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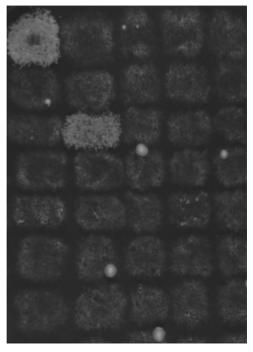


Fig. S9. Screening of a *Ylpcna* random mutant library for mutants that can complement the *ScPCNA (POL30)* deletion in *S. cerevisiae*. A typical agar plate containing 5-FOA was used to examine the function of the *Ylpcna* mutants as the sole source of PCNA in *S. cerevisiae*. Two mutants that can complement the *pol30* mutation and facilitate growth of *S. cerevisiae* are clearly observed on the plate. Using this screening approach, 2,500 mutants were examined to identify variants that can function in *S. cerevisiae*.

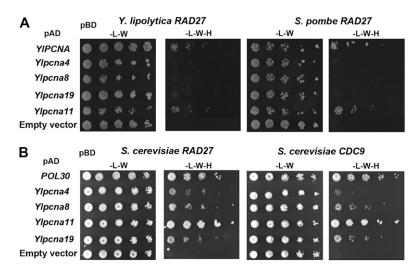


Fig. S10. Yeast two-hybrid analysis of the Ylpcna mutants from the directed evolution experiment with RAD27 orthologs from S. pombe and Y. lipolytica (A) and RAD27 and CDC9 from S. cerevisiae (B). Interactions with all partners are detected only in YlPCNA and Ylpcna11 that combine sequence motifs from YlPCNA and ScPCNA (Fig. 6).

Table S1.	Y2H	analysis	of	SpPCNA	(PCN1)	and	YIPCNA	interactions	with S.	cerevisiae	PCNA
partners											

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			S. cerevis	siae PCNA p	artners*		
Chimeric PCNA	Pol32	Rad27	Rad30	Cdc9	Msh6	Ung1	Rrm3
ScPCNA (POL30)	++++	+++	+++	++++	+++	++++	+
SpPCNA (PCN1)	++++	+++	+++	++++	+++++	++++	++++
YIPCNA	++++	+++	+++	++++	+++	++++	++
pcn1-POL30-IDCL	++++	+++	+++	++++	+++	++++	+
Ylpcna-POL30-IDCL	++++	+++	+++	++++	+	++++	+

*WT or PCNA mutants were fused to the pAD, and the different partners were fused to the pBD. Each Y2H strain was spotted in five dilutions (e.g., Fig. 5), and the interactions were scored according to the growth of the different dilutions on selective plates lacking histidine (–, no growth; +, growth observed at first serial dilution; + +, growth observed at second serial dilution; +++, growth observed at third serial dilution; +++, growth observed at fourth serial dilution).

Table S2. Y2H analysis of evolved Ylpcna mutants

	S. ce	<i>revisiae</i> P	CNA par	tners	5. p	ombe PC	NA part	ners	Y. lij	po <i>lytica</i> P partners	
	Pol32	Rad27	Cdc9	Ung1	Pol32	Rad27	Cdc9	Ung1	Pol32	Rad27	Ung1
POL30	++++	++++	++++	++++	_	-	-	_	_	_	_
Ylpcna4	-	+++	+	+++	-	-	-	-	-	-	-
Ylpcna8	+++	+++	+++	+++	-	-	-	-	-	-	-
Ylpcna11	++++	++++	++++	++++	+	+	+	+	+	+	ND
Ylpcna19	+++	+++	+++	+++	-	-	-	-	-	-	-

POL30 or *Ylpcna* mutants were fused to the pAD, and the different partners were fused to the pBD. Each Y2H strain was spotted in five dilutions (e.g., Fig. 6), and the interactions were scored according to the growth of the different dilutions on selective plates lacking histidine (–, no growth; +, growth observed at first serial dilution; +++, growth observed at second serial dilution; +++, growth observed at third serial dilution; ++++, growth observed at first serial dilution; ++++, growth observed at third serial dilution; ++++, growth observed at third serial dilution; ++++, growth observed at first serial dilution; ++++, growth observed at third serial dilution; ++++, growth observed at first serial dilution; ++++, growth observed at third serial dilution; ++++, growth observed at first serial dilution; ++++, growth observed at third serial dilution; ++++, growth observed at first serial dilution; ++++, growth observed at third serial dilution; ++++, growth observed at first serial dilution; ++++, growth observed at third serial dilution; ++++, growth observed at first serial dilution; +++, growth observed at first serial dilution; ++++, growth observed a

Table S3. Sequences of oligonucleotides used in this study

PNAS PNAS

DNA oligonucleotide sequence 5'-3'

fr-pRS-PCNA	TTTCACTCACAGCAACAAGCAGCAAGCACTAAGTACGCAGTCAAAAGAGAGAAAAAATGTT AGAAGCAAAATTTGAAGAAGCATC
rev-pRS-PCNA	GTTTTTTTTGTTTATTATTTTAGTATACAACTATATAGATAATTTACATTTTATTC TTCG TCATTAAATTTAGGAGCC
fr-waltii-IDCL	GATATTGATGCGGATTTTCTGGATATTGAAGGCATGCAGTACGACTCCACCCTGTCATTG
rev-waltii-IDCL	TACCCGCTTTAACTAGACAAACTACGCCTATAACTACAACTACAATTTCAGAGAGTATTCCGCTATAC
fr-gossypii-IDCL	GAAATTTATGCGGATTTTCTGGAAATTGATCAGATTCAGTACGACTCCACCCTGTCATTG
rev-gossypii-IDCL	AATCTGATCAATTTCCAGAAAATCCGCATAAATTTCCATCAATTTCAGAGAGTATTCGGCTATAC
fr-hansenii-IDCL	GATATTGATAGCGAATTTCTGAAAATTGATGATATGCAGTACGACTCCACCCTGTCATTG
rev-hansenii-IDCL	CATATCATCAATTTTCAGAAATTCGCTATCAATATCCAATTTCAGAGAGTATTCGGCTATAC
fr-albicans-IDCL	GATATTGATAGCGAATTTCTGCAGATTGATGATATGCAGTACGACTCCACCCTGTCATTG
rev-albicans-IDCL	TACCTACTATAAGTCGACAAACTTTCGCTATAACTACAACTACAACTACAGAGAGTATTCCGCTATAC
fr-crassa-IDCL	GATATTGATCAGGAACATCTGGGCATTCCGGATACCCAGTACGACTCCACCCTGTCATTG
rev-crassa-IDCL	GGTATCCGGAATGCCCAGATGTTCCTGATCAATATCCATCAATTTCAGAGAGTATTCGGCTATAC
fr-nidulans-IDCL	GATATTGATCAAGAACATCTTGCTATTCCTGAAACTCAGTACGACTCCACCCTGTCATTG
rev-nidulans-IDCL	AGTTTCAGGAATAGCAAGATGTTCTTGATCAATATCCATCAATTTCAGAGAGTATTCGGCTATAC
fr-lipolytica-IDCL	ACCATTGATCAGGAACATCTGGGCATTCCGGATACCCAGTACGACTCCACCCTGTCATTG
rev-lipolytica-IDCL	GGTATCCGGAATGCCCAGATGTTCCTGATCAATGGTCATCAATTTCAGAGAGTATTCGGCTATAC
fr-pombe-IDCL	GACATTGATCAAGAACACTTGGGTATACCAGATATCCAGTACGACTCCACCCTGTCATTG
rev-pombe-IDCL	GATATCTGGTATACCCAAGTGTTCTTGATCAATGTCCATCAATTTCAGAGAGTATTCGGCTATAC
fr-pAD-PCNA	CCAAACCCAAAAAAAGAGATCGAATTAATGTTAGAAGCAAAATTTGAAGAAGCATC
rev-pAD-PCNA	CACTATAGGGCTCTAGAGTCGACTAATACTCTCGAGTTATTCTTCGTCATTAAATTTAGGAGCC
fr-pcn1-pRS	TTCACTCACAGCAAGCAAGCAAGCACTAAGTACGCAGTCAAAAGAGAGAAAAAATGCTTGAAGCTAGATTTCAGCAG
rev-pcn1-pRS	GTTTTTTTTGTTTATTATTTTAGTATACAACTATATAGATAATTTACATCTACTCCTCATCCTCCTCACC
fr-pcn1-pol30-IDCL	GATATCGATGCTGATTTCTTAAAGATTGAAGAATTAGAATACGATGCTACTATTACTATGCCTG
rev-pcn1-pol30-IDCL	TAATTCTTCAATCTTTAAGAAATCAGCATCGATAATCGTCCATTAATTTAACATCATAATCAGAGATCC
fr-pombe-pol32-pBD	AGTTGACTGTATCGCCGGAATTCGCCCGGGCCTCGAGCCCGATGGATG
fr-pcn1-pRS	TTCACTCACAGCAACAAGCAGCAAGCACTAAGTACGCAGTCAAAAGAGAGAAAAAATGCTTGAAGCTAGATTTCAGCAG