	98	108	118	128	138
Ab	LLAIQSAC	KHGVRIPWVI	EVALMMGSSIT		AKLRVRMVELGQDVP
Aca	LLLCIQSACN	TKSIKLPWE	TI <mark>AELMGG</mark> SIS	DGAITQHL	TKL <mark>RARLEKEGE</mark> QVP
Acl	LLTVQSVCN	KNNIKIPWA	EVATTMGHNVS	EGAIV <mark>Q</mark> HL	AKVRLRRLEAGKDVP
Ad	LLCIQSACS	AKGIKLPWE	AVAELMGGSIS	DGAIT <mark>Q</mark> HL	TKL <mark>RAKLEKEGEH</mark> VP
Af	LLTVQSVC	INQSIK <mark>I</mark> PWS	EVASTMKNNVT	EGAIV <mark>Q</mark> HL	AKLRTRRVDAGKEVP
Ag	LLAIQSAC	KCNIRIPWI	EVALMMGSNIT	<mark>DGAIIQ</mark> HL	AKLRIRMVELGQDVP
An	LLTVQSVCN	TKSIKIPWA	EVANTMGHNVT	EGAIV <mark>Q</mark> HL	AKL <mark>R</mark> SRRVSADKAVP
Aor	LLTVQSVCN	INQSIK <mark>IPWS</mark>	EVASTMKNNVT	EGAIV <mark>Q</mark> HL	AKL <mark>RTRRVDAGKE</mark> VP
Aot	LLAIQSAC	I <mark>KHGVR</mark> VPWGI	EVANMMQNNI T	DGAIV <mark>Q</mark> HL	AKL <mark>RTRMVEAGME</mark> VP
At	LLTIQSVCN	IKNSVKIPWA	EVAKTMGHNVT	EGAIV <mark>Q</mark> HL	AKL <mark>R</mark> SRRVQSDKAVP
Bf	FILNMVYEFF	RRSEITIPWD	K <mark>IAHRQRPG</mark> SS	GAAAM <mark>Q</mark> HV	NKLREILITEGHLVP
Cg	LLNMQYELV	QAGVE I PYDI	RIAHRLRPGSS	GSAIS <mark>Q</mark> FL	GRTRERLVAEGHLVP
Ch	ILLNLMYEAS	SIKGIKLPMD	AVAHRTHCGAS	GQSLI <mark>Q</mark> WL	ARERKNMLKQGRMCP
Ci	LLSIQYACN	IAAGIKIPWGI	N <mark>VATLMG</mark> NNIT	EGAIV <mark>Q</mark> HL	AKL <mark>RARMEEEGIR</mark> VP
Cm	LLHLHYECI	RHKIVLPWD	SIAHRLHPGSS	GAAVV <mark>Q</mark> HL	NRVR <mark>KELIREGHL</mark> VP
Cp	LLSIQYACN	IAAGIKIPWGI	NVATLMGNNIT	EGAIV <mark>Q</mark> HL	AKL <mark>RARMEEEGIR</mark> VP
Gg	LLINTLYQAS	SIQ <mark>GHK</mark> LSMD2	AIAHRTHCGAS	<mark>G</mark> QSLI <mark>Q</mark> HL	ARERRKILKRGRMAP
Gl	LMLHVQYECQ	Q <mark>RQGVQ</mark> IPWDI	XVVHRLSPGSS	GATAQ <mark>Q</mark> HL	NKIRDILVGEGHMVP
Mac	LLHIHYECS	S <mark>RHKLQ</mark> LPWD2	AIAHRFHPGSS	GAAIIQHI	NRL <mark>RREVLVEGHL</mark> VP
Man	LLHIHYECS	S <mark>RHKLQ</mark> LPWD2	AIAHRFHPGSS	GAAIIQHI	NRL <mark>RREVLVEGHL</mark> VP
Mo	VMMHLQYECS	SRHKIELPWD	AIAHRLHPGST	GGAVVQHL	GRLRSQLIVEGHLVP
Nc	LLHIQYECS	SRYRVD I PWD	SIAHRLHPGST	GSAIH <mark>Q</mark> HL	NRLRSHLIAEGHLVP
Nd	LLHIQYECS	RYRVD I PWD	SIAHRLHPGST	GSAIH <mark>Q</mark> HL	NRLRSHLIAEGHLVP
Nf	LLTIQSVCN	ITKNVKIPWAI	OVASTMGHNVT	DGAIV <mark>Q</mark> HL	SKL <mark>R</mark> SRRVEGGKVVP
Nh	LLQVLVYECN	IRAKIRLPWD	Q <mark>VAHR</mark> LNPGSS	GSSIIQWL	GRNRNDLIAEGHIVP
Nt	LLHIQYECS	SRYRVD I PWD	SIAHRLHPGST	GSAIHQHL	NRLRSHLIAEGHLVP
Pb	LLSIQSAC	ISLAIKLPWQI	EIAALMGGSIS	DSAIVQHL	TKLRARMEESGASVP
Pd	LLLAIQYACN	IKSSVKIPWKI	EVAEVMGEKFT	EGAIVQHL	SKL <mark>RTKREE</mark> QDKPNP
Pm	LLTIQSVCN	IKEGVRLPWAI	EV <mark>AKSMG</mark> NNVT	' <mark>DGAIIQ</mark> HL	AKL <mark>RIRRVEKNKQ</mark> VP
Sm	LLHIQYECS	SRYRVD I PWD:	SI <mark>AHRLHPG</mark> ST	GSAIHQHL	NRL <mark>RGHLIAEGHLV</mark> P
Ss	LILHIVFECF	RADINLPWD	XIAHRLCPGSS	GAAAQQYI	NKMRDVLITEGHLVP
Tre	VLHCLIYEME	LMDMRVSWDI	NIAHRLRPGTS	GSSL <mark>K</mark> QYI	HRSRNGLVSEGHVVA
Tru	LLSIQSAC	KCGVRIPWI	EVALMMGSNIT	<mark>DGAIIQ</mark> HL	AKLR <mark>VRMVELGQD</mark> VP
Ts	LLTIQSVCN	IREGVKI PWAI	EV <mark>AKSMG</mark> NNVT	EGAIIQHL	AKL <mark>RVRRVEKNK</mark> QVP
Tve	LLAIQSAC	KCGVRI PWVI	EVALMMGSSIT	DGAIIQHL	AKLRVRMVELGQDVP
Tvi	LLHIHYECA	RHKVNVPWD2	AIAHRLHPGSS	GQAVLQHV	NRLRKELLSEGHMVP
Ur	LLSIQSACN	ISAGIRIPWA	QVAEIMGEKIT	EGAIV <mark>Q</mark> HL	AKL <mark>RSRMEGDGI</mark> PVP

Figure S1 Conserved region in SAD-4 homologs. Positions are relative to *N. crassa* SAD-4. Strain names and sequence accession numbers are listed in Table S2.

_	10 20 30 40 50 60 70 80 90 10 	00
Cg Mt		-
Nc Nd	MSPKKAEPDAVAWPLIGCRLDAGIOIIMIGHEALR-KPOVHFVNASRREVDPAT- 	-
Nt Pa	MSPKKAEPEAVAWPLBGRLEVEIOIMIBHEALR-KPQIHFADASRHEVDPVT- MPPKKKKALIIKATPKGRLKASSTESTKGKATATTSTKKTHAASKASKDNDDSLVKFPQBKCFPLBIOOLR-KPSIHFMNVEKAVIPGYTNDKG	;
Sm Tt		-
Ca	110 120 130 140 150 160 170 180 190 20	00
Mt	TWSLSFYPDDPKSRDRSCHRLYEKMASVDPAAAAAMRYERQTRLGQLPFKKLRAPVDYERDLVVLDFRKCKGR	-
NC Nd	WELVLKSKNKK-GDTSGYRLIENIQDVARDSPVAREAILKSALQPLLPIPVRPN-DWCKIDAATDIVVFEFGVDKSG	-
Nt Pa	WKLDLKSRSKKK@DTSGYHLVENIQDVARDSPVRABAILKSALQPLLLPIPVRPNNDWRKIDAATDLVVFEFSVDKSG	-
Sm Tt	WTVALKARDKS-SDTSGYRLLNNMEDIARSFPVAAEVMRKNILEPHRLPLMPVPKEGSWSIDAATDLVVIEFDRDKSG	-
	210 220 230 240 250 260 270 280 290 30	00
Cg Mt	TLGYLHPDNQILNPTGSAFDANAVAMQLEKIQKVAVVWNDQQPLCHDSSNNFRCPDPSSPVHEPHRNWCMCPEELFGLLNCFPELRQFYL	5
Nc Nd	KLWLWHPRNQLVDLNPLASHIHSRRVREDLKGIRKVAFVYGGNKQPQAGSSESVFQCLQHHNRGHARQKFCPEELLGFIYQLSDTETVY KLWLWHPRNQLVDLIPLASHIDSSKIRKDLKDVRKVAFVYGGKKQPSAGSSESVFQCLQQHTGRHWRRKFCPEELLGFIYQLSNTEAVY	r 7
Nt Pa	KLWLWHPRNQLVDLNPLASHIDSRQVRKDLRGIRKVAFVYGGNKQPSAGSSESVFQCLQHHNGRHSGQKFC ZELLGFIYQLSDIEAVYI VDYEDDELSTDAGESTLEDEGENKKSSVEGTETPCGMADLKKVQVVYKOSSOPTCAKONTVEOCCTHVDGSTVPHGNWMCDDEVAGETDSMCGTEVIJ	-
Sm	KRRFWHPRNRVYTSTQDVDAIRHQLEGIRKRKHASWQFCPEELLGFIYQLSHVEAVY	
Τt	VFGYFHGVNQILNPAGGLFNSNNLAAKFSNIQKVALKYSQKHHTAHSIRANFKCPK-VTDEHVKHQQWHMCPEEVCGFLNCFPSLKEF	
	310 320 330 340 350 360 370 380 390 40 ••••• •••• •••• •••• •••• •••• •••• •	00
Cg Mt	310 320 330 340 350 360 370 380 390 40 KG-YFAGTYPTEHPTNKTPFYGISTLYIPLHHSDALPAFGFPNNPNTNHHHHHHPPHHPTTSPGFPFALQDLHDMHDMLAAVADHFFLDRLPPQHS LIPLGKKTNPQQLHVEDLIEDTYKFNDQHLYEVFHGRGRSFVHAGQLRSWEGRNHESNDNELSVFQLSPHRVHPSMLEMLRELRDDSFLADDVETLPEAE	00
Cg Mt Nc	310 320 330 340 350 360 370 380 390 40 	50
Cg Mt Nc Nd Nt	310 320 330 340 350 360 370 380 390 40 KG-YFAGTYPTEHPTNKTPFYGISTLYIPLHHSDALPAFGFPNNPNTNHHHHHHPPPHHPTTSPGPFPALQDLHDMHDMLAAVADHFFLDRLPPQUS LIPLGKKTNPQQLHVEDLIEDTYKNDQHLYPVFHGRGRSFVHAGQLRSWEGRNHESNDNELSVFQLSPHRVHPSMLEMLRELADDSFLADDVETLPEAE ILHDRVNAKAVTNYAASYFSVTVPAATRNTFGLKTFYSTTRSYITVPLPSYGIGPVLHATWKTKDRIWPHGPSPPLVNAAREAAIARPPDSRERRYTEHV ILHHRVNKKPVTNYAASYFSVPAATRNTFGLKTFYSTTRSYITVPLPSYEIGPVFHATWKTKDRIWPHGPSPPLVNAAREAAMARPSDSRERRYTEHV	50 5 7 7 7
Cg Mt Nc Nt Pa Sm	310 320 330 340 350 360 370 380 390 40 	500 5 7 7 7
Cg Mt Nd Nt Pa Sm Tt	310 320 330 340 350 360 370 380 390 40 KG-YFAGTYPTEHPTNKTPFYGISTLYIPLHHSDALPAFGFPNNPNTNHHHHHHPPPHHPTTSPGPFPALQDLHDMHDMLAAVADHFFLDRLPPQHS LIPLGKKTNPQQLHVEDLIEDTYKFNDQHLYPVHGRGRSFVHAGQLRSWEGRNHESNDDELSVFQLSPHRVHPSMLEMLRELRDDSFLADDVETLPEAE ILHDRVNAKAVTNYAASYFSVTVPAATRNTFGLKTFYSTTRSYITVPLPEYQIGPVHATWKTKDRIWPHGPSPPLVNAAREAAIARPPDSRERLYAEHV ILHHRVNAKAVTNYAASYFTVTVPAATRNTFGLKTFYSTTRSYITVPLPEYQIGPVHATWKTKDRIWPHGPSPPLVNAAREAAIARPPDSRERLYTEHV ILHHRVNKKPVTNYAASYFSVPAATRNTFGLKTFYSTTRSYITVPLPSYEIGPVFHATWKTKDRIWPHGPSPPLVNAAREAAMARPDSRERRYTEHV VQVPKGSREDRERLEIYRRWFSTSESNPPVSSQFNHDLLLT- ILKARINTKVVKEYATSYFSIPAAIRNSFGFETFYSTTRSYUTVPLPSYTIGPVYHATWKTKDCVWPEKPLPVLIKIARASAATLPPDSKEKQYAEHT	500 5 7 7 7 7 7 7 7
Cg Mt Nd Nt Pa Sm Tt	310 320 330 340 350 360 370 380 390 40 KG-YFAGTYPTEHPTNKTPFYGISTLYIPLHHSDALPAFGFPNNPNTNHHHHHHPPPHHPTTSPGPFPALQDLHDMHDMLAAVADHFFLDRLPPQHS LIPLGKKTNPQQLHVEDLIEDTYKFNDQHLYPVFHGRGRSFVHAGQLRSWEGRNHESNDNELSVFQLSPHRVHPSMLEMLRELRDDSFLADDVETLPEAE ILHDRVNAKAVTNYAASYFSVTVPAATRNTFGLKTFYSTTRSYITVPLPSYGIGPVHATWKTKDRIWPHGPSPPLVNAAREAANARPSDSRERLYAEHV ILHHRVNAKAVTNYAASYFSVTVPAATRNTFGLKTFYSTTRSYITVPLPSYGIGPVHATWKTKDRIWPHGPSPLVNAAREAANARPSDSRERRYTEHV ILHHRVNKKVVTVYAASYFSVPAATRNTFGLKTFYSTTRSYITVPLSYEIGPVFHATWKTKDRIWPHGPSPPLVNAAREAAMARPSDSRERRYTEHV ILHHRVNKKVVTVAASYFSVPAATRNTFGLKTFYSTTRSYITVPLSYEIGPVFHATWKTKDVIWPHGPSPPLVNAVREAAMARPSDSRERRYTEHV ILHHRVNKKVVTVAASYFSVPAATRNTFGLKTFYSTTRSYITVPLSYEIGPVFHATWKTKDVIWPHGPSPPLVNAVREAAMARPSDSREGRYVEHV VQUPKGSREDRERLEIYRWFSTSESWPPVSSQFHHDLLLT- ILKARINTKVVKEYATSYFSIPAAIRNSFGFETFYSTTRSYTVPLPSYTIGPVYHATWKTKDCVWPEKPLPVLIKIARASAATLPPDSKEKQYAEHT V	500 5 7 7 7 7 7 7 7 7 7 7 7 7 7 7 7 7 7
Cg Mt Nd Nt Pa Sm Tt	310 320 330 340 350 360 370 380 390 40 KG-YFAGTYPTEHPTNKTPFYGISTLYIPLHHSDALPAFGFPNNPNTNHHHHHHPPHHPTTSPGPFPALQDLHDMHDMLAAVADHFFLDRLPPQHS LIPLGKKTNPQQLHVEDLIEDTYKFNDQHLYEVFHGRGRSFVHAGQLRSWEGRNESNDNELSVFQLSPHRVHPSMLEMLRELRDDSFLADDVETLPEAE ILIPLGKKNPQQLHVEDLIEDTYKFNDQHLYEVFHGRGRSFVHAGQLRSWEGRNESNDNELSVFQLSPHRVHPSMLEMLRELRDDSFLADDVETLPEAE ILHDRVNAKAVTNYAASYFSVTVPAATRNTFGLKTFYSTTRSYITVPLPSYEIGEVFHATWKTKDRIWPHGPSPPLVNAAREAAIARPPDSRERLYAEHV ILHHRVNKKAVTNYAASYFSVPAATRNTFGLKTFYSTTRSYITVPLPSYEIGEVFHATWKTKDRIWPHGPSPPLVNAVREAAMARPSDSRERRYTEHV ILHHRVNKKPVTNYAASYFSVPAATRNTFGLKTFYSTTRSYITVPLPSCEIGEVFHATWKTKDRIWPHGPSPPLVNAVREAAMARPSDSRERRYTEHV VVQVPKGSREDRERLEIYRRWFSTSESWPPVSSQFNHDLLLT	500 5 7 7 7 7 7 7 7 7 7 7 7 7 7 7 7 7 7
Cg Mt Nd Nt Pa Sm Tt Cg Mt Nc	310 320 330 340 350 360 370 380 390 40 KG-YFAGTYPTEHPTNKTPFYGISTLYIPLHHSDALPAFGFPNNPNTNHHHHHHPPPHPTTSPGPFPALQDLHDMHDMLAAVADHFFLDRLPPQHS LIPLCKKNNPQQLAVEDLIEDTYKFNDQHLYPVHGRGRSFVHAGQLRSWEGRNHESNDELSVFQLSPHRVHSMLEMLRELRDDSFLADDVETLPAE ILHDRVNAKAVTNYAASYFSVTVPAATRNTFGLKTFYSTTRSYITVPLPSYGIGPVLHATWKTKDRIWHGPSPPLVNAAREAAIARPPDSRERLYAEHV ILHHRVNKKAVTNYAASYFSVTVPAATRNTFGLKTFYSTTRSYITVPLPSYEIGPVFHATWKTKDRIWHGPSPPLVNAAREAAIARPPDSRERLYAEHV ILHHRVNKKPVTNYAASYFSVPAATRNTFGLKTFYSTTRSYITVPLPSYEIGPVFHATWKTKDRIWHGPSPPLVNAAREAAMARPDSRERRYTEHV VQVPKGSREDRERLEIYRWFSTSESWPPVSSQFNHDLLLT- ILKARINTKVVKEYATSYFSIPAAIRNSFGFETFYSTTRSYITVPLPSYTIGPVYHATWKTKDCVWPEKPLPVLIKIARASAATLPPDSKEGRYVEHV VQUPKGSREDRERLEIYRWFSTSESWPPVSSQFNHDLLLT- ILKARINTKVVKEYATSYFSIPAAIRNSFGFETFYSTRSYVTVPLPSYTIGPVYHATWKTKDCVWPEKPLPVLIKIARASAATLPPDSKEKQYAEHT V	500 5 7 7 7 7 7 7 7 7 7 7 7 7 7 7 7 7 7
Cgt Ncd Nta Smt Cgt Ncd Nt	310 320 330 340 350 360 370 380 390 40 KG-YFAGTYPTEHPTNKTPFYGISTLYIPLHKSDALPAFGFPNNPNTNHHHHHHPPPHPTTSPGPFPALQDLHDMHDMLAAVADHFFLDRLPPQUS 1	
Cgt NN NN PS T CM tcd NN PS T	310 320 330 340 350 360 370 380 390 40 KG-YFAGTYPTEHPTNKTPFYGISTLYIPLHHSDALPAFGFPNNPNTNHHHHHHPPPHPTTSPGPFPALQDLHDMHDMLAAVADHFFLDRLPPQHS LIPLGKKTNPQQLHVEDLIEDTXKFNDQHLYPVHGRGRSFVHAGQLRSWEGRNHESNDNELSVFQLSPHRVHPSMLEMLRELRDDSFLADUVETLPEAE ILHDRVNAKAVTNYAASYFSVTVPAATRNTFGLKTFYSTTRSYITVPLPSYQIGPVLHATWKTKDRIWPHGPSPPLVNAREAAIARPPDSRERRYTEN ILHHRVNKKAVTNYAASYFSVTVPAATRNTFGLKTFYSTTRSYITVPLPSYEIGPVFHATWKTKDRIWPHGPSPPLVNAREAAIARPPDSRERRYTEN ILHHRVNKKAVTNYAASYFSVTVPAATRNTFGLKTFYSTTRSYITVPLPSYEIGPVFHATWKTKDRIWPHGPSPPLVNAREAAMARPDSRERRYTEN ILHHRVNKKPVTNYAASYFSVPAATRNTFGLKTFYSTTRSYITVPLPSCEIGPVFHATWKTKDRIWPHGPSPPLVNAREAAMARPDSREGRYVEHV VQVPKGSREDRERLEIYRWFSTSESNPPVSSQFNHDLLLT- ILKARINTKVVKEYATSYFSIPAAIRNSFGFETFYSTTRSYVTVPLPSYTIGPVYHATWKTKDCVWPEKPLPVLIKIARASAATLPPDSKEKQYAEHT V	
Cgt Ncd NN Pam Tt CMtcd tam Tt	310 320 330 340 350 360 370 380 390 40 KG-YFAGTYPTEHPTNKTPFYGISTLYIPLHHSDALPAFGFPNNPNTNHHHHHHHPPEHPTTSPGPFPALQDLHDMHDMLAAVADHFFLDRLPPQBS LIPLGKKNNPQQLHVEDLIEDTYKPNQHIYPVFHGRGRSFVHAGQLRSWEGNHESNDNELSVFQLSPHRVHPSMLEMLRELDDSFLADDVETLPEAE LIHDRVNAKAVTNYAASYFSVTVPNATRNTFGLKTFYSTTRSYIPVPLPEYQIGPVLHATWKTKDRIWPRGPSPPLVNAREAAIARPPDSRERLYAEHV ILHHRVNAKAVTNYAASYFSVTVPDATRNTFGLKTFYSTTRSYITVPLPESYEIGPVFHATWKTKDRIWPRGPSPPLVNAREAAIARPPDSRERLYAEHV ILHHRVNKKPVTNYAASYFS-VPAATRNTFGLKTFYSTTRSYITVPLPSYEIGPVFHATWKTKDRIWPRGPSPPLVNAVREAAMARPDSREGRYVEHV VVQVPKGSREDRERLEIYRWFSTSESWPPVSQFNNDLLLT- ILKARINTKVVKEYATSYFS-IPAAIRNSFGFETFYSTTRSYTVPLPSYTIGPVYHATWKTKDCVWPEKPLPVLIKIARASAATLPPDSKERQYAEHT V	
C M N N N P S T C M N C M T A M N N P S T C M N N P S T T T C M T A M T	310 320 330 340 350 360 370 380 390 40 KG-YFAGTYPTEHPTNKTPFYGISTLYIPLHHSDALPAFGFPNNPNTNHHHHHHHPPPHHPTTSPGFPFALQDLHDMHDMLAAVADHFFLDRLPPQUS LIPLGKKTNPQQLHVEDLIEDTYKFNDQHLYPVFHGRGRSFVHAQQLRSWEGNHESNDNELSVFQLSPHRVHSMLRELRDDSFLADDVETLPEAE LIHDRVNAKAVTNYAASYFSVTVPAATRNTFGLKTFYSTTRSYITVPLPEYQIGPVHATWKTKDRIWPHOPSPPLVNAREAAIAAPPDSRERLYAEHV ILHHRVNAKAVTNYAASYFSVTVPAATRNTFGLKTFYSTTRSYITVPLPEYQIGPVHATWKTKDRIWPHOPSPPLVNAREAAIAAPPDSRERLYAEHV ILHHRVNKKPVTNYAASYFSVPAATRNTFGLKTFYSTTRSYITVPLPESVEIGPVHATWKTKDRIWPHOPSPPLVNAREAAIAAPPDSREGRYVEHV VVQVPKGSREDRERLEIYRRWFSTSESWPPVSQFNHDLLLT- ILKARINTKVVKEYATSYFSIPAAIRNSFGFETFYSTTRSYITVPLPSYTIGPVHATWKTKDCVWPEKPLPVLIKIARASAATLPPDSKEKQYAEHT 410 420 430 440 450 460 470 480 490 50 RYVGPSEYRLERAAREKLVFGVLVAVGREKKSPGPDIETSNPT RVLSGKYKLSRKERENLVFGVLQCKT- RKLSGLADALHHCKEVWRLVLEMIQURADQDTPLSPDWPLPIPPQTNTA@FRTLKQHHRQRYNLENFTKERRDNLEFGMLLMVDETAVFKSQKNQSD RKLSHLAHKLDHHEEVYLLVAEMISIRARDONTPLSPDWPLPIPPPQVNTAQFRTLKQHHKQRYNLENFTKERRDNLEFGMLLMVDETAVFKSQKNQSA RKLSHLAHKLDHHEEVYLLVAEMIQURADQNIPUSADYEWPDPPPPLVNTARFKAHKQHRRQNNLENFTKERRDNLEFGMLLMVDETAVFKSQKNQSA RKLSHLSRKLNHRDKVSPLVSEVIRQMRADQNIPVSADYEWPDPPPPLVNTARFKAHKQHRRDYNLDNFTKERRDNLEFGMLLMVDETAVFKSQKNQSA RKLSHLSRKLNHRDKVSPLVSEVIRQMRADQNIPVSADYEWPDPPPPLVNTARFKAHKQHRRDYNLDNFTKERRDNLEFGMLLMVDAAPAVSKKGGEK	
Cgt NN NN Smt CM tcd NN Pam T Cg	310 320 330 340 350 360 370 380 390 40 KG-YFAGTYPTEHPTNKTPFYGISTLYIPLHESDALPAFGFPNNPNTNHHHHHHHHHHPPPHHPTTSPGPFPALQDLEDMHDMLAAAADHFFLDRLPPQHS LIPLGKKTNPQQLHVEDLIEDTYKFNDQHLYPVHGRGRSFVHAGQLRSWEGRNHESNDELSVFQLSPHRVHPSMLEMLRELRDDSFLADDVETLDDAPE LIPLGKKTNPQQLHVEDLIEDTYKFNDQHLYPVHGRGRSFVHAGQLRSWEGRNHESNDELSVFQLSPHRVHPSMLEMLRELRDDSFLADDVETLDAPE LIHRVNKAAVTNYAASYFFVTVPAATRNTFGLKTFYSTTRSYITVPLPEYQIGPVHATWKTKDRIWPHGPSPPLVNAAREAAMARPDSRERRYTEHV LIHHRVNKKPVTNYAASYFF VQVPKGSREDRERLEIYRRWFSTSESWPPVSSQFNHDLLLT	
CMNcdtamt gttcdtamt gttcdt CMNNPST CMNNNPST CMNc	310 320 330 340 350 360 370 380 390 40 KG-YFAGYYPTEHPTNKTPFYGISTLYIPLHRSDALPAGOFNNPNTNHHHHHHHPPPHPTTSPGPFPALQDLHDMIDMLAAVADHPTDRLP-PQIS 1	
CMtcdtamt Gttcdtamt CMNNNPST CMNCdtamt	310 320 330 340 350 360 370 380 390 40 KG-YPAGTYPTEHPTNKTPFYGISTLYIPLHSDALPAPGPNNPNTNHHHHHHPPPHPTTSPGPFPALQDLHDMHDMLAAVADHFFLDRLPPQ18 ILFLGKKTNPQ0LHYEDLIEDTXKFNDGHLYPVHGRGRSFVHAQ0LRSWEGNHESNDHELSVPQLSPHRVHPSMLEMLRELRDSFLADUVETLPEAE ILHDRVNAKAVTNYAASYFSVTVPAATRNTFGLKTFYSTTRSVITVPLPSVEGNHESNDHELSVPQLSPHRVHPSMLEMLRELRDSFLADUVETLPEAE ILHHRVNKKAVTNYAASYFSVTVPAATRNTFGLKTFYSTTRSVITVPLPSVEIGPVPHATWKTKDRIWPHOPSSPPLVNAREAAMARPSDSRERITEN VQVPKGSREDRERLEIYRWFSTSESWPPVSQFNHDLLLT ILHARNNKVKEYATSYFSDAATRNTFGLKTFYSTTRSVITVPLPSVEIGPVPHATWKTKDCWPEKPLPVLIKIARASAATLPPDSREGVEH VQVPKGSREDRERLEIYRWFSTSESWPPVSSQFNHDLLLT ILKARINTKVVKEYATSYFSDAATRNFFGEFFFYSTTRSVTVPLPSVTIGPVHATWKTKDCWPEKPLPVLIKIARASAATLPPDSREGVEH V	
CMNNNPST CMNNNPST CMNNNPA	310 320 330 340 350 360 370 380 390 440 KG-YFAGTYPTENPTWEDULEDTYKNDQHLYEDTHGERGRSTUNACQLRSWEGRNHESNDNELSUFQLSPHENDULAAVADHPFLDRLDDSFELADUETLPEAR ILHORVNAKAVTNYAASYFSUTUPAATRNTFGLKTFYSTTRSYTTVDLPSVEIGPULATWKTKDRIWPHGPSPPLUNAAREAATARPDSRERLYAEHU ILHBRUNAKAVTNYAASYFSUTUPAATRNTFGLKTFYSTTRSYTTVDLPSVEIGPULATWKTKDRIWPHGPSPPLUNAAREAATARPDSRERLYAEHU ILHRRUNAKAVTNYAASYFSUTUPAATRNTFGLKTFYSTTRSYTTVDLPSVEIGPULATWKTKDRIWPHGPSPPLUNAAREAATARPDSRERRTTEHU ILHRRUNAKAVTNYAASYFSUTUPAATRNTFGLKTFYSTTRSYTTVDLPSVEIGPUHATWKTKDRIWPHGPSPPLUNAAREAAMARPSDSRERRTTEHU ILHRRUNAKAVTNYAASYFSVPAATRNTFGLKTFYSTTRSYTTVDLPSCEIGPUHATWKTKDRIWPHGPSPPLUNAVERAAMARPSDSRERRTTEHU VQUPKGSREDRELEIYRWFSTSSEWPUSSQFNHDLLLT	

Figure S2 Alignment of SAD-5 homologs. Strain names and sequence accession numbers are listed in Table S2.



Figure S3 *sad-4* and *sad-5* mutants appear normal during the vegetative phase. *sad-4*^{$^{\Delta}$} and *sad-5*^{$^{\Delta}$} strains have normal mycelial morphology (A and C) and growth (B and D).



Figure S4 Crosses homozygous for $sad-4^{\Delta}$ produce fewer ascospores. (A and B) No differences in perithecial development and abundance were detected between $sad-4^{\Delta}$ (F5-32 × P17-62) and control (F5-23 × P3-08) crosses. Bars, 500 µm. (C and D) *sad-4*–null crosses produce more aborted (bubble) asci. Bars, 100 µm.

Purpose	Primer	Sequence (5' to 3')
sad-4 [∆] ::hph confirmation	NCU01591-294825F	TGGCATGAGACTGGCATCTGAG
	NCU01591-299764R	GCAGAAGCGGAAGACATGTCAAG
<i>sad-5</i> [∆] :: <i>hph</i> confirmation	NCU06147-438124F	GACCATGGCCACGACTACAGCTAC
	NCU06147-442142R	ATATGAGACCTGCGCGCTAGCCAAC
rfp-sad-4 construction	NCU01591-296360F*NotI	GTCTAGCGGCCGCGATCATATCAAG
	NCU01591-298299R*Spel	CCAGACTAGTCTTCCGAATACTAAAATG
gfp-sad-5 construction	NCU06147-E	TCTGCGGAACAATATGAACAACCTG
	NCU06147-F	AGGACAACCCTCCACTCGCAAAG
	NCU06147-G	AGGCTCGAACTCCCGACCTCA
	NCU06147-H	CCGCTTCACGGGCTGCGTTGAC
	NCU06147-NGFP1	GCAGCCTGAATGGCGAATGGACGCGCAGCTGAGACGAGGTGCCGAAAG
	NCU06147-NGFP2	CAGGAGCGGGTGCGGGTGCTGGAGCGATGAGTCCCAAAAAGGCCGAGCCTGAC
sad-1 cDNA amplification	SAD1-4489F	ATGCTCATCTGGCGACAGCAGATG
	SAD1-4796R	TTCTCTTTCATGTCGAATGTTTCCC
sad-4 cDNA amplification	NCU01591-296801F	CTGGTGTAGCCGTTGTGGTTCG
	NCU01591-298048R	GCGTCGAAGGCAGGAACTTGAT
sad-5 cDNA amplification	NCU06147-F2-TH	CGCTTTCGTTTACGGTGGGAAC
	NCU06147-R2-TH	GGCCAGATGCGATCCTTTGTCT
actin cDNA amplification	ACT-507F	CGTTGGTCGTCCCCGTTATCATG
	ACT-811R	TGGGAGCCTCGGTAAGAAGGACG

Table S1 Primers used in this study

Table S2 Sequences used in this study

Protein	Abbreviation ¹	Accession # ²	Strain
SAD-4	Ab	XM_003014454.1	Arthroderma benhamiae CBS 112371
	Aca	XM_001539307.1	Ajellomyces capsulatus NAm1
	Acl	XM_001267850.1	Aspergillus clavatus NRRL 1
	Ad	XM_002623645.1	Ajellomyces dermatitidis SLH14081
	Af	XM_002377995.1	Aspergillus flavus NRRL3357
	Ag	XM_003173571.1	Arthroderma gypseum CBS 118893
	An	XM_001395616.2	Aspergillus niger CBS 513.88
	Aor	XM_001826292.2	Aspergillus oryzae RIB40
	Aot	XM_002844811.1	Arthroderma otae CBS 113480
	At	XM_001218470.1	Aspergillus terreus NIH2624
	Bf	CCD55484.1	Botryotinia fuckeliana
	Cg	XP_001228162.1	Chaetomium globosum CBS 148.51
	Ch	CCF43159.1	Colletotrichum higginsianum
	Ci	XM_001242382.1	Coccidioides immitis RS
	Cm	EGX93189.1	Cordyceps militaris CM01
	Ср	XM003069573.1	Coccidioides posadasii C735 delta SOWgp
	Gg	EFQ30009.1	Glomerella graminicola M1.001
	GI	EHK98895.1	Glarea lozoyensis 74030
	Mac	EFY84375.1	Metarhizium acridum CQMa 102
	Man	EFY96871.1	Metarhizium anisopliae ARSEF 23
	Мо	XM_360623.1	Magnaporthe oryzae 70-15
	Nc	BK006474	Neurospora crassa OR74A
	Nd	102414 ³	Neurospora discreta 8579 mat A
	Nf	XM_001260425.1	Neosartorya fischeri NRRL 181
	Nh	XP_003051566.1	Nectria haematococca mpVI 77-13-4
	Nt	EGO56400.1	Neurospora tetrasperma FGSC 2508
	Pb	XM_002789947.1	Paracoccidioides brasiliensis Pb01
	Pd	EKV11485.1	Penicillium digitatum PHI26
	Pm	XM_002149363.1	Penicillium marneffei ATCC 18224
	Sm	$XP_{003350666.1}^{4}$	Sordaria macrospora k-hell
	Ss	XP_001597890.1	Sclerotinia sclerotiorum 1980
	Tre	EGR52832.1	Trichoderma reesei QM6a
	Tru	XM_003235041.1	Trichophyton rubrum CBS 118892
	Ts	XM_002484729.1	Talaromyces stipitatus ATCC 10500
	Tve	XM_003019899.1	Trichophyton verrucosum HKI 0517
	Tvi	EHK24463.1	Trichoderma virens Gv29-8
	Ur	XM_002544541.1	Uncinocarpus reesii 1704
SAD-5	Cg	XP_001227787.1	Chaetomium globosum CBS 148.51
	Mt	XP_003665043.1	Myceliophthora thermophila ATCC 42464
	Nc	BK006779	Neurospora crassa OR74A
	Nd	62731 ³	Neurospora discreta 8579 mat A
	Nt	EGO55361.1	Neurospora tetrasperma FGSC 2508
	Sm	XP_003344714.1	Sordaria macrospora k-hell
	Ра	XP_001905702.1	Podospora anserina S mat+
	Tt	XP_003654540.1 ⁵	Thielavia terrestris NRRL 8126

¹Abbreviations are used in Figures S1 and S2. ²GenBank accession numbers are listed unless otherwise stated. ³*N. discreta* database at DOE-JGI (http://genome.jgi-psf.org/). ⁴A putative intron was removed from its ORF. ⁵This sequence is incomplete.

Table S3 Small RNA sequencing and alignment data

	$r^{\Delta} \times r^{+}$	$r^{\Delta}4^{\Delta} \times r^{+}4^{\Delta}$	$r^{\Delta}5^{\Delta} \times r^{\dagger}5^{\Delta}$	$r^{+} \times r^{+}$
Raw reads	58,558,484	31,162,221	31,162,221	36,467,267
≥14 nt after adapter trimming	55,022,756	26,001,036	22,318,233	32,655,370
Homology with the genome	51,641,029	24,578,034	20,920,863	30,650,403
18-30 nt long	33,392,504	15,763,605	14,098,686	20,701,772
No mismatches	30,016,594	14,093,205	12,738,940	18,758,512

Shown are numbers of small RNA reads after each processing step. See Figure 6 for cross information.