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Nc -----MASTGVSQPAKLVAVTTLHKLTEDLKSTSLSP-----ERDKALELKVYGRDPRNADPI-----FTKCGIETLTKHAFDS
Pa -----MNAKAKIPVAKLDVAKVQLLGSLEDELETSSLAPQRWFIIPAALBIASNKFEIGRESLLEBLKTYGRDPNCADPI-----FTKEGITLTVRHAFDS
Mg -----MLNNTLTKGTDKLLDLKHHNLSSQ-----ERDAALEQLKVYGRDPRDAPPI-----FTKEGISTLAHSHDFG
Fg -----MALPAPAGLPTGTDKLEYKELINDLEDLNELELDP-----DRAAVLDQKHLTRDPIINADPL-----YTBEGISTLLRHAYDK
Ss MSISSTRTSLSQCLTGEAKLADVTNIYVSLKADLENISSLPH-----ORDALLEQLKVYGRDPRADPI-----FTREGIETLSKHAFNS
An -----MDLRILQSGEKLQOVTKLLNSLEKDLKNSLNSA-----ORTQILLOLRQYGTSPDNAGPI-----YSRKGIEITLSKVCIDG
Hc -----MATPALVVEVTSCLNAEKTAAQFGSRGS-----WEQNINLEINFLGLOFQONNSR-----IRGEGKTRG
Bc MSISARTSLSQELTGKAKLTDVTKIVBSLKEDELEKISLLEPH-----ORDALLEQLKVYGRDPRNADPI-----FTKEGIEITLSKHAFNS
Sj -----MPDSKSTVDLLSFERDNGSFVPTICSKINLLKPTAWELSAN-----LIEIAVSLKELRKKSRPKDACQKISNALDWTLVLAERAFVSKLRNSA
Yl -----MIGHLHLYDITYTISLLEHNPVQYHFSPPKMSKKTAYEDFQS-----EPQDPLICCALKMSLTTAQAWTCIG-----GISAADDIATHVLDG

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Nc PSETTSRNALRVLGNAMLLIPETQRQRFVLDLGYEAKACEKLN--DNWDEFLAARVIFSTYGTIVDLAKLIDBHHLAESVANLARHARSRISEHAKNKIKPDPME
Pa TSVNTRSRGALRILCNLILLPEPQRQRFVDTGYAAKASEKLE--DNSDDEFLVARLLISTYNTNIDLPKLIQOHGLADSIANHLARHAKRISSTNR-STTANPMD
Mg SDDTTSRNALRCLANAMLLPSSRQELVDLGYHIKAKALAS--DSWDEFLVSRVLMLANARNINHEILITOHGLAELIARLESMMRFLP----DEDSSPNTME
Fg PSTKSAADARRVLANAMVLTVTVDIFVNKGFAPNAQOGLNG--GSFDDEFLNSRILFLSTYGTIKVDLKKLIDDEKLADRISENLARHAK----ESKAKSDPMQ
Ss PSKFTSRNALRCLANALLKPDTRQTLVTLGYDAKACTLLKDRNGSVVDEFLSRIIFLITYGTTININLIDHCHLADATSHNLANHARLHNAKQKVKQLDPM
An ETTDVRHAALRCVANALLDSNMROLFVDTCGKGRLEAMLK--DSSBHEMVISRILFLSTYDININFDLNNHSLGDNINYOILRHSKQPKSGR--PLSQVD
Hc -----CHAIKTKITCOQYKNSSSFSKSVNTECDLE--BNSDDEFLASRLFLFLATYDIDDFKLDIDNNLGEYINNHYRHSKRFKARKK--KLDQMD
Bc PSKFTSRNALRCLANALLKPDTRQTLVGSYDERACALLKDRIASVDEFLSRIIFLITYGTTININLIDQCHLADITSHNLANHDKLHSAKQKKTROLDPME
Sj HSLELIRLIVNVLVNPMSQRIASLFSNSAFDEESFQNSACQIALRLFLLCVGENDEDRWTFRITPEGLQALGIVVNNLSTEPVSASVLDLRLRAY
Yl SLDEASTLNLAATVSNQYFLLRQYITSATKAPKLVNWAATTPDTERGKMCRRILELCSSEIRIEGLNVATLAKGLEBLGLTDLQDLQBLKQKQKLLQLHREIL

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Nc LMAIGETLRLFFNVTSKCPKSLDCFTAAVPHIVTLLSLDIPPKKTPPLESPLSPLVNALMNLKLDSEARSCLYPKDAPSSLAELKITLLDLSIKAYS-DOELD
Pa PMALBETLKLITFNVSCHSPNHLASHEPALPHIITILCSIDLPSHTKTPGPFPGPAVNALNLDLSPTAKYLYLDPSSPSSFDRLIKLISLSTIKAYK-NPDLE
Mg GMALSETLKMFPVAVLRFQGOSTRBACAGHILTLICQRPLE--AESVLDPPFGPLINALCTLDLEDEAITNLFPERDPSLVTSLRISILDRALSEKNGMDD
Fg DMALVESAKLLFNVTYCPDKSSFSATAPHLVALLLKQDIS--QTKPLDPPVGFIFINALANLVDGSDCQKSIHPEDEPKVVSRLISILDPAAMKNVP-DNQLD
Ss DMALAESLKLFLNITFCPCRNSSFSQALPHILSILDKREI--PNTPLESPISQLINLTLNLFLEDPCNIVLFPANPHSHVYCKFLELLDHSINBYK-DEELE
An ELAFTDTLKLVFNIAKLFQDLAPITFSPSTPYIFKILSRIDILPLKPLDGLGLTLLNCLSTLLENKKNKPYDGNPIFFPTFNQCNVDKLNILDQAVSAYE-PSELE
Hc ELALSETLKLIFNITINBYHIVDAPSPSPHILKILSRILITPEPLQAPVNYLINSLLNLDLEAKKSKHFCTNPLPKFDQNCNVDKLNILDQAVAMHK-POHLE
Bc DMALGS-----PNNVVEKFINLLDHSINBYK-DEELE
Sj AVGSKDKPKSSTAQLSPEFVIQLWKETGTRDPSYTSNTSWHIVNALVLPLQNLTSSSLYQITDIALTALDVLPLKGIQLLEAGNASFKVNFASVVELTAKELE
Yl SGFVCLITVYKTVREDQEKQTSSELKQIVPHVLTIAQNP-----BLLYPCPIISCRPMAVESQKLFVYLETLEVOIKQVLCATYPTDIALA---QLL

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Nc ATVIPLVCLISSIYENAPASPVRDFIRKSLLPSEERHNKVLGKGDTPAKLLANMTPNPLAPBFARAVSHLLFNVSQDKANKFVENIGYGYASGFLFQNNIPV-
Pa QIVIPLYCALSTVYEHAPAS--VKQSIKCALLPTEKDRALGKADTLQGHLLKNWNSPEAPELCKATAHLYFDLSNRDPHKFVKNVGYGYASGFLFQNNISFTPE
Mg PTMTVLAGSLCIIIEAEP--VRISMCAQLLPTDEDKVEVLGSTELESPLSKLLKMTNMAPKSRKAIHLLFLGLSDRDAGKVFVKVGYGYASGFLFEENIPVPOS
Fg ATVSPLLGVISSVYKHAADS--SKKYIREKLLPTEEDRKEVLGKGDALSAKLLQNFNPLAPSIVGTVITCHLLYDLSNDANKFVENVGYGFASGFLFQNNIPVPS
Ss QLVSPLLTLIRRYEYEGPSE--VHKFLQIRLLPSDKD-----HASTFVQNLGYGFASGFLFQNNIPVPE
An TKATPLFHTLVITHEVADPG--PRKYMOWLLLEDNDRDRPTGQSDTSSKLLKLSMTHVAN-LKVAISELMFVLSCKNABSLTNIGYGFAGLLASRGMDIPKS
Hc SLAVPLLTLLRKLVSFAPEG--PKKYMFWLLLEDNDHDLPIGKSNLTLSSRLLRLSSTPVAPSLREGISALMFELSAGSDAIDFVNVNMGYGFAGLLASRGMDIPVPE
Bc QLVSPLLTLIRKANEIGPSE--VHOFMCIQLLPSDKDREQVGRGESLSARLQOLSTSPMAPOVRESISALLFELSADKASTFVHNLGYGFASGFLFQNNIPVPE
Sj VRSPLLLALLQNVKINDTO--TCRLLESRLPSEADRSASLAFSGSLPSRLLRLVIPCFLQPOQAHLIYSLCRENAKVLDTIGYGFASGILRVCCBETDST
Yl YGLAPLVPVVTVDGABPAR---EILCRVFLPSDEDRKEAIGKTKSIPSRLLKVIIEEPFQDCFLVNEAQVLCENKDKFTDAILGAYAGYLTFGAASSAS

* * *
Nc EGLCGDAKKGESSQACQSS-----RAVNPITGQFLDTEFTFDPPEMTEEEKEREAERLTVLFRERAKLGIIVNENPVAKAQEGRFEELPDDYEDSD-
Pa ELNKGGETVECEDEGVREI--KRFINPITGQFLDTEFVSELPEMTEDEKEREERLTVLFRERAKLQGTGILDVONPVEQAMREGRFEELPDDK-
Mg ALAS-----EGASCSTMQ--GRAVNPITGQFLDAEKLSLIPMPSOEBEKEEAERLTVLFRERLKKITGVVDVONPVEKAFQEGRFEELPDDKEDDENKVKVEQK
Fg ASDPG-----S--QKQVNPVITGQHVDAKPVDEPEMTEEEKEREAERLTVLFRERLKNITGVVDVONPVEBAMREGRFEELPDDKEDVEEIE-
Ss ALEAWSKENDNDGKARSSHDSGKAVNPITGQFLHAEKIDMPMPSOEBEKEERAEKLFVLLK---KNGIITAKNPEBALQGRFEELPDDKEDSD-
An ACEAFATN-----SCLNPNINPITGQFWAAEKEDTGPMTKEEKEREAERLTVLFRERAKANGILGVENPVQALREGRFEELPDSSE-
Hc AKEAFSTS-----AGGLDPMNINPITGQFWDAEPQDGGPEMTEEEKEREAERLTVLFRERLKATGVVDVNPVSAALQGRFEELG-
Bc AFEAWSTENDKNGKARPSQDSGKAVNPITGQFLHAEKIDMPMPSOEBEKEEREAERLTVLFRERLKNITTAANPMEBALQGRFEELPDDKEDSD-
Sj VSKDSLFSG-----LSTATADNVNIPITGQFTSEKPP--VPEMSEEEKEREAERLTVLFRERLKNITGVENPVKKAVERSCLFENSNNDNA-
Yl GPASNISGFG-----YDKVITGQKLTPELQELKKEQECIS--AMSPBEKEREAELMYLNLNRMRELGIIVNFHPHRAAQESGRFEEL-

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Figure S2 RIC8 homologs in other fungi. ClustalW (<http://www.ch.embnet.org/software/ClustalW.html>) was used to align RIC8 sequences from *Neurospora crassa* (Nc; NCU02788.3), *Podospora anserina* (Pa; Pa_1_3900), *Magnaporthe grisea* (Mg; MGG_14008), *Fusarium graminearum* (Fg; FSG_01511), *Sclerotinia sclerotiorum* (Ss; SS1G_02787.1), *Aspergillus nidulans* (An; AN1661.3), *Histoplasma capsulatum* (Hc; HCAG_03335.1), *Botrytis cinerea* (Bc; BC1G_02317.1), *Schizosaccharomyces japonicus* (Sj; SJAG_02027), *Yarrowia lipolytica* (Yl; ACCESSION# XP_505953). Shading indicates identical (black) and similar (grey) amino acid residues (http://www.ch.embnet.org/software/BOX_form.html).