

Supplementary Figure S4

	WALKER A	WALKER B	
<i>Y.lipolyt.</i> (60)	PE--PIAGVKKTIIVVSSAKGGVGKSTVSNVNTALSIA--KRGLRVGLLDVDFGSPISPTMFGLSG---EPRMT-HEGK-----LTPMS		
<i>N.crassa</i> (37)	PQKRRIKKNVDKVIIVVSSAKGGVGKSTIAANLALSLS--RLGYTTCILDDIDLFGPSIPTFNLSSPSLSPSLN-PHNQ-----LPLPT		
<i>C.albicans</i> (46)	PIRQKIPNVSNIILISSAKGGVGKSTVSNVNTALALN--SLGKKVGLLDADIFGSPISPKLMLNKG---EPRLS-SSGK-----LPLSL		
<i>H.sapiens</i> (58)	PKQKPIEGVKQVIVVSSAKGGVGKSTTAVNLALALAANDSSKATGLLDVDFVYGPSVPMNLK--GN-PELSSQSNL-----MRPIL		
<i>G.gallus</i> (65)	PKQKPIEGVKQVIVVSSAKGGVGKSTTAVNLALALAANDSAKEVGLLDADIDYGPSIPKMLNLK--GN-PELTPKNL-----MRPLK		
<i>X.trop.</i> (58)	PKQKPIPGVKHVIVVSSAKGGVGKSTTAVNLALGLTAAASDQVKAIVGLLDADVYGPSIPRMLNLK--GN-PEVSNKNL-----MPLIF		
<i>D.rerio</i> (66)	PKQKPIAGVKEVIVVSSAKGGVGKSTTAVNLALGLMANEQSKLVGLLDADVDFGPSVPMNLK--GN-PELTKENL-----MRPLV		
<i>D.melano.</i> (34)	PKQKPIICVQDLIVVSSAKGGVGKSTVAVNFAFCSIAKL--GKRVGLLDGDFGPTIPLLMNVH--GE-PVVNDKNL-----MPEPQ		
<i>S.purpur.</i> (31)	PKREPIPGVKNTILVSSAKGGVGKSTTAVNVALGIAAIEQNANVGLLDADVDFGPSIPRMLNLQ--GKEPDIDKNNQ-----LTPLR		
<i>D.discoid.</i> (48)	VTKVAIEGCKNIIVVSSAKGGVGKSTCAVNIALGLS-SHNLS-VGLLDVDFVYGPSIPLMLDLKN-HEKPFNTNELNQ-----MPLIQ		
<i>O.lucimar</i> (29)	PLPPSIASCARVFAVASAKGGVGKSTTCVNIATAVA--RLGHR--VALLDADVYGPSVPTLMLRLS---GQPVVDADGR-----MTPME		
<i>A.thaliana</i> (34)	TTELRLHGVKDIIVVSSAKGGVGKSTTAVNLAVALKANKCELK--IGLLDADVYGPSVPMNLK--GE-PVVNDKNL-----MPEVE		
<i>L.major</i> (3)	FSRVSPVGVKRVITICSAKGGVGKSTTSVNVALLAKN--MGHSVGLVDADITGPSIPTMMGVSSQVETRYVAGSDR-----FCBPM		
<i>T.brucei</i> (5)	FSRVAIPGVKHVITLCSAKGGVGKSTCSVNVALLAKN--IGFNVGVVDADITGPSIPTMMGVSSQVETRYVAGSDR-----FABPT		
<i>T.vaginal.</i> (29)	GRKALP-CIGRIIMTTSCKGGVGKSTVALNTALALQK--AGMRVGLFDADIDYGPSVPTMLNTEG---KPLYSDAEGN-----FITPE		
<i>P.tetrau.</i> (109)	PKKQPIICVQDLIVVSSAKGGVGKSTTAVNLFATSLQK--LGFNVGIFDADVYGPSLPTLMLNTEG---KPLYSDAEGN-----FITPE		
<i>T.thermo.</i> (110)	KKRQLENVKKIIVVSSAKGGVGKSTVAVNLFATSLQK--QGHKVGIFDADIDYGPSIPTLMLNKEN---AILQAPEDRPK---EITPE		
<i>P.yoelii</i> (109)	-RKKNIKKIENIILVYSCKGGVGKSTTAVNLFATSLQK--QGATVGLLDADIDYGPSLPTLMLNTEG---KPLYSDAEGN-----FITPE		
<i>O.lucimar</i> (144)	ETVEGLRRVRHIIVVSSAKGGVGKSTTAVNLFATSLQK--MGAKVGLLDADVYGPSLPTLMLNTEG---KPLYSDAEGN-----FITPE		
<i>A.thal.</i> (144)	QLPFGLSRISNIIVVSSAKGGVGKSTVAVNLFATSLQK--MGARVGLFDADVYGPSLPTLMLNTEG---KPLYSDAEGN-----FITPE		
			MRP signature
<i>Y.lipolytica</i>	KFETIQVMSMGFLVDPN--KAVAVRGLLVQKALEQLLQDVWDG--TLDVLMVDLPPGTGDVQLTITACTVKIDGAIIVSTPQDVALVDVV		
<i>N.crassa</i>	SYGVKTMSTIGYLLGSED--SALVWRGPMILKAIQQLLHEVDWVSHPSLDVLMVDLPPGTGDVQLTITACTVKIDGAIIVSTPQDVALVDVV		
<i>C.albicans</i>	NYGVQVTSMGYLIDEK--QAITWRGLMVMKALQQLLFEVEWS--PIDYLVVDMPPGTGDVQLTITACTVKIDGAIIVSTPQDVALVDVV		
<i>H.sapiens</i>	NYGIACMSMGFLVEESE--PVVWRGLMVMASIEKLLRQVDWG--QLDYLVDMPPGTGDVQLTITACTVKIDGAIIVSTPQDVALVDVV		
<i>G.gallus</i>	NYGIACMSMGFLVEEAA--PVVWRGLMVMASIEKLLRQVDWG--QLDYLVDMPPGTGDVQLTITACTVKIDGAIIVSTPQDVALVDVV		
<i>X.tropicalis</i>	NYGIRCMSMGFLVEETA--PIVWRGLMVMASIEKLLRQVDWG--QLDYLVDMPPGTGDVQLTITACTVKIDGAIIVSTPQDVALVDVV		
<i>D.rerio</i>	NFGIPICMSIGFLVEDVA--PIVWRGLMVMASIEKLLRQVDWG--QLDYLVDMPPGTGDVQLTITACTVKIDGAIIVSTPQDVALVDVV		
<i>D.melanogaster</i>	NYNVKCLSMGMLTPVET--SVIWRGLMVMASIEKLLRQVDWG--QLDYLVDMPPGTGDVQLTITACTVKIDGAIIVSTPQDVALVDVV		
<i>S.purpuratus</i>	NFGIPICMSIGFLVEEKS--PVVWRGLMVMASIEKLLRQVDWG--QLDYLVDMPPGTGDVQLTITACTVKIDGAIIVSTPQDVALVDVV		
<i>D.discoideum</i>	NYGIKCMSMGFLVNEED--PIIWRGLMVMASIEKLLRQVDWG--QLDYLVDMPPGTGDVQLTITACTVKIDGAIIVSTPQDVALVDVV		
<i>O.lucimarinus</i>	NHGVRCQSMGFLMKPGA--AATWRGLMVMASIEKLLRQVDWG--QLDYLVDMPPGTGDVQLTITACTVKIDGAIIVSTPQDVALVDVV		
<i>A.thaliana</i>	NYGVKCMSMGFLLEKDA--PLVWRGLMVMASIEKLLRQVDWG--QLDYLVDMPPGTGDVQLTITACTVKIDGAIIVSTPQDVALVDVV		
<i>L.major</i>	NFGIPICMSIGFLVPEDE--AIAVRGLMVMASIEKLLRQVDWG--QLDYLVDMPPGTGDVQLTITACTVKIDGAIIVSTPQDVALVDVV		
<i>T.brucei</i>	NFGIPICMSIGFLVPHDE--AIAVRGLMVMASIEKLLRQVDWG--QLDYLVDMPPGTGDVQLTITACTVKIDGAIIVSTPQDVALVDVV		
<i>T.vaginalis</i>	NYGMPTVSVGYGIGPKM--AMLVKGPVIGKVIISDFLRNAIWP--ELDYLVDMPPGTGDVQLTITACTVKIDGAIIVSTPQDVALVDVV		
<i>P.tetraurelia</i>	FNGLVKTMSYGYASGNQK---AIIIRGPMVSSIVVQLVQQTQWQ--NLDYLVDMPPGTGDVQLTITACTVKIDGAIIVSTPQDVALVDVV		
<i>T.thermophilus</i>	YEGKTMMSYGFAR--KK---AIIIRGPMVSSIVVQLVQQTQWQ--NLDYLVDMPPGTGDVQLTITACTVKIDGAIIVSTPQDVALVDVV		
<i>P.yoelii</i>	YKNNKLSYAYIKDKQLGFASRGPINELISEFVHNVNWG--VLDYLVDMPPGTGDVQLTITACTVKIDGAIIVSTPQDVALVDVV		
<i>O.lucimarinus</i>	YEGKTMMSYGFAR--KK---AIIIRGPMVSSIVVQLVQQTQWQ--NLDYLVDMPPGTGDVQLTITACTVKIDGAIIVSTPQDVALVDVV		
<i>A.thaliana</i>	YMGVKKLSYGFAGQGRA---IMRGPVMSGLINQLLTTTEWG--ELDYLVDMPPGTGDVQLTITACTVKIDGAIIVSTPQDVALVDVV		
			C C
<i>Y.lipolytica</i>	RGIDLFEKTYTKVLGLVONMSVFCVCPNHNHETHIFGVD--GAVSKAKSRGLGVGNVPLD-PQCSQSDKCV (287)		
<i>N.crassa</i>	KGVNMFRRKVDIPILGLVONMSVFCVCPNHNHETHIFGVD--EGVTKVCEEMDMFELGDVPLH-PSIGEDGGRCKP (273)		
<i>C.albicans</i>	KGITMFKNIPIPLGLVONMSVFCVCPNHNHETHIFGVD--GAERVALENNLKVSSIPIN-EEICVQSDKCV (275)		
<i>H.sapiens</i>	KCAEMFRVHVPLGLVONMSVFCVCPNHNHETHIFGVD--GARKLAQTLGLEVLGDIPLH-LNIREASDTCQP (289)		
<i>G.gallus</i>	KCTEMFRKVHVPVGLVONMSVFCVCPNHNHETHIFGVD--GVRDLAKTLGLDVLGDIPLH-VTIRETCDSCQP (296)		
<i>X.tropicalis</i>	RCAEMFRKVNVPVGLVONMSVFCVCPNHNHETHIFGVD--GARRLAESLGFDIIGDIPLH-INIRETSDQCRP (289)		
<i>D.rerio</i>	RCAEMFRKVNVPVGLVONMSVFCVCPNHNHETHIFGVD--GAKELAQTLGVELLGDIPLR-LNIRETSDMQCP (297)		
<i>D.melanogaster</i>	KCAEMFRKVNVPVGLVONMSVFCVCPNHNHETHIFGVD--DSRIS-SLPRKLSLPLD-SRLIREGSDSCVP (258)		
<i>S.purpuratus</i>	KCAEMFRKVNVPVGLVONMSVFCVCPNHNHETHIFGVD--GVHGVAKEMCLDVLGAVIVSILDARKGAEMFKK (270)		
<i>D.discoideum</i>	RGVNMFKKVEVPLGLVONMSVFCVCPNHNHETHIFGVD--GAKNTAKKMGINFGLDVPILH-LQIRETSDSCVP (279)		
<i>O.lucimarinus</i>	RGIDMFGKVNTEVGVVENMAYFCVCPNHNHETHIFGVD--GARATAAERGVEFAEVPLD-ATIRESDSCVP (257)		
<i>A.thaliana</i>	RGVNMFKKVEVPLGLVONMSVFCVCPNHNHETHIFGVD--GARRTAAKLLKLGDIPLH-MSIREGSDSCVP (264)		
<i>L.major</i>	RGIDMFAAVNAPVGLVONMSVFCVCPNHNHETHIFGVD--GVARAAEELGVPLGDIPLH-SRIMQDTEGCV (236)		
<i>T.brucei</i>	RGIDMFAAVNAPVGLVONMSVFCVCPNHNHETHIFGVD--GVKATAEELGVPLGDIPLH-GEVFPQ-QRIMSDTEGCV (236)		
<i>T.vaginalis</i>	RNFDMFKKLVKVPVGLVONMSVFCVCPNHNHETHIFGVD--GAANLSKKYVPLGDIPLH-GEVFPQ-QRIMSDTEGCV (259)		
<i>P.tetraurelia</i>	KGITMFDVVKVPLGLVONMSVFCVCPNHNHETHIFGVD--YMNMLQKQFCIATAVSIPIYG-DISKYSDELSP (341)		
<i>T.thermophila</i>	KGITMFDVVKVPLGLVONMSVFCVCPNHNHETHIFGVD--YMNMLQKQFCIATAVSIPIYG-DISKYSDELSP (346)		
<i>P.yoelii</i>	KGITMFDVVKVPLGLVONMSVFCVCPNHNHETHIFGVD--DIKSLQKQISKIYEFYFH-PLVSKNVNNTD (465)		
<i>O.lucimarinus</i>	KGVNMFRRKVDIPILGLVONMSVFCVCPNHNHETHIFGVD--ICEYQVGNLQMPILV-PEISAGSDTCRP (326)		
<i>A.thaliana</i>	KGVNMFRRKVDIPILGLVONMSVFCVCPNHNHETHIFGVD--VVKQFCIPIHFDLPLR-PTLSASGSDGTP (372)		

Alignment of the relatively well conserved parts of IND1 and HCF101, that are predicted by SMART (Letunic et al., 2006) to correspond to the 3D structure of the nucleotide binding domain. The IND1 from *Y.lipolytica* and the HCF101 from *A.thaliana* are underlined. The alignment was created with ClustalX (Thompson et al., 1997), positions with strongly conserved (black: 100% similarity) or less strongly conserved (grey, white letters: >80% similarity; grey, black letters: >60% similarity) residues are

highlighted with GeneDoc (Nicholas et al., 1997). The Walker A motif and the Walker B motif are indicated, as well as the MRP signature and two cysteines that are conserved at the C-terminus and that correspond to the essential CxxC motif in position 201-204 of Cfd1. These cysteines have apparently been lost in HCF101 and its close relative from the algae *O. lucimarinus*, as they are present in sequences from the Alveolates (*P. tetraurelia* and *P. yoelii*) that are monophyletic with HCF101 (see Supplementary Figure S1). Note furthermore that the cysteine pair is not universally conserved within the IND1 group, as one of the cysteines has been replaced by an aspartate in the *O. lucimarinus* sequence.

Letunic I., Copley, R.R., Pils, B., Pinkert, S., Schultz, J. and Bork, P. (2006) SMART 5: domains in the context of genomes and networks. *Nucleic Acids Res.* **34**(Database issue), D257-260.

Nicholas, K.B., Nicholas H.B. Jr. and Deerfield, D.W. II. (1997) GeneDoc: Analysis and visualization of genetic variation, *EMBNEW.NEWS* **4**, 14.

Thompson, J.D., Gibson, T.J., Plewniak, F., Jeanmougin, F. and Higgins, D.G. (1997) The ClustalX windows interface: flexible strategies for multiple sequence alignment aided by quality analysis tools. *Nucleic Acids Res.*, **24**, 4876-4882.