

Supplemental Figure S1: Putative GPI-anchor synthesis pathway in *C.graminicola*. The figure was drawn by referring to *S.cerevisiae*. The GPI-anchor synthesis pathway proteins in *S.cerevisiae* and the corresponding homologous proteins found in *C.graminicola* are shown. Number 1 to 12 indicated the biosynthetic steps. GlcNH₂, Glucosamine; GlcNAc, N-Acetyl-Glucosamine; Man, Mannose; EtN-P, phosphorylethanolamine; inositol-P, phosphatidylinositol.

MCD4_Saccharomyces_cerevisiae	MWNKSTITLAVVVFHLLHNSIFDIYFVSFVHSGSWQSTPTP.....PARRSEILVVDGLRAGTTFCKVTHF.....VSGKTEPLAFFRSVNNNAHGSHTMPTESRPGHV	109
MCD4_Aspergillus_nidulans	MARLGSTGFLTLAVVFHLLHNSIFDIYFVSFVHSGSWQSTPTP.....GSEAPARRVLDVADGLRAGTTFELTDDPLPEESNGDDLTFFAPFIRSVLSHGTGGSHTMPTESRPGHV	119
MCD4_Magnaporthe_oryzae	..MSRSGRFMAVAVVFHLLHNSIFDIYFVSFVHSGSWQSTPTP.....SKPAPARRVLDVADGLRAGTTFELTDDPLPEESNGDDLTFFAPFIRSVLSHGTGGSHTMPTESRPGHV	116
MCD4_Fusarium_graminearum	MAGSSRGCFMAVAVVFHLLHNSIFDIYFVSFVHSGSWQSTPTP.....HVKPAPARRVLDVADGLRAGTTFELTDDPLPEESNGDDLTFFAPFIRSVLSHGTGGSHTMPTESRPGHV	119
MCD4_Colletotrichum_graminicola	MAVSSAGFLAVAVVFHLLHNSIFDIYFVSFVHSGSWQSTPTP.....HVKPAPARRVLDVADGLRAGTTFELTDDPLPEESNGDDLTFFAPFIRSVLSHGTGGSHTMPTESRPGHV	118
Consensus	r v fhl y sifdiyf sp v gm pa rl l v dg lrad f p lap rs v t g sht r ptesrpghv	
MCD4_Saccharomyces_cerevisiae	AIACGYEDVSAYTCKKKNPNVNFDSFNKSHHTSSGSPDILNKHKPSSENNKTFWVVDHTDFDTGSSIEHFAVVRHLDQTHNSTLNSLDYBHTGKGNVFFLHLGLDTPRH	229
MCD4_Aspergillus_nidulans	AIACGYEDVSAYTCKKKNPNVNFDSFNKSHHTSSGSPDILNKHKPSSENNKTFWVVDHTDFDTGSSIEHFAVVRHLDQTHNSTLNSLDYBHTGKGNVFFLHLGLDTPRH	238
MCD4_Magnaporthe_oryzae	AIACGYEDVSAYTCKKKNPNVNFDSFNKSHHTSSGSPDILNKHKPSSENNKTFWVVDHTDFDTGSSIEHFAVVRHLDQTHNSTLNSLDYBHTGKGNVFFLHLGLDTPRH	235
MCD4_Fusarium_graminearum	AIACGYEDVSAYTCKKKNPNVNFDSFNKSHHTSSGSPDILNKHKPSSENNKTFWVVDHTDFDTGSSIEHFAVVRHLDQTHNSTLNSLDYBHTGKGNVFFLHLGLDTPRH	238
MCD4_Colletotrichum_graminicola	AIACGYEDVSAYTCKKKNPNVNFDSFNKSHHTSSGSPDILNKHKPSSENNKTFWVVDHTDFDTGSSIEHFAVVRHLDQTHNSTLNSLDYBHTGKGNVFFLHLGLDTPRH	237
Consensus	a iag yedvsav gwk npvnfds fn s ht s gspdil mf ga p vd y edf ld vf f l r d vffhlhlg dt gh	
MCD4_Saccharomyces_cerevisiae	RPYSAEYIDNMYVDDQIPILIDKVNKGFAADKTAFTADHGMSAGSHGDGHEINTRTPLVAGAGINNK.....VHNPFVSNYNTENMSSIKENDVQAGFASMSVLDVNVME	345
MCD4_Aspergillus_nidulans	RPYSAEYIDNMYVDDQIPILIDKVNKGFAADKTAFTADHGMSAGSHGDGHEINTRTPLVAGAGINNK.....VHNPFVSNYNTENMSSIKENDVQAGFASMSVLDVNVME	358
MCD4_Magnaporthe_oryzae	RPYSAEYIDNMYVDDQIPILIDKVNKGFAADKTAFTADHGMSAGSHGDGHEINTRTPLVAGAGINNK.....VHNPFVSNYNTENMSSIKENDVQAGFASMSVLDVNVME	355
MCD4_Fusarium_graminearum	RPYSAEYIDNMYVDDQIPILIDKVNKGFAADKTAFTADHGMSAGSHGDGHEINTRTPLVAGAGINNK.....VHNPFVSNYNTENMSSIKENDVQAGFASMSVLDVNVME	357
MCD4_Colletotrichum_graminicola	RPYSAEYIDNMYVDDQIPILIDKVNKGFAADKTAFTADHGMSAGSHGDGHEINTRTPLVAGAGINNK.....VHNPFVSNYNTENMSSIKENDVQAGFASMSVLDVNVME	356
Consensus	rpys ey n k d f d taf ftdhgms gshgdghe ntrtp l v g g p d w l r dv qad a im l g p	
MCD4_Saccharomyces_cerevisiae	RKQVSGFHAIDGKESFLAHVNRARSLELTLVDEEVI.DSOFVKEVFKVEK..SHSHYLEIETLQRSEGENVLEQDANTFLTESMQITSGVLYLVNVPFRTITVVE	462
MCD4_Aspergillus_nidulans	TRVQGVSELEVVDGTPREDAALAAATQVLENNVKEGHHK.AALLRYRPFEPPLAS...DYGNASARQLAMKDLIDRGFY..EALHTSAPATAPATAGVLYLVNVPFRTITVVE	472
MCD4_Magnaporthe_oryzae	ANVGVHPPELTAANKREAEITVYAGQGLEVYVVEKKKQSQPKYKALAGGAGNSRGIEERVAARRLIDGQNH..EALHSAPAHKVGSGVLYLVNVPFRTITVVE	473
MCD4_Fusarium_graminearum	ANVGVHPPELTAANKREAEITVYAGQGLEVYVVEKKKQSQPKYKALAGGAGNSRGIEERVAARRLIDGQNH..EALHSAPAHKVGSGVLYLVNVPFRTITVVE	470
MCD4_Colletotrichum_graminicola	ANVGVHPPELTAANKREAEITVYAGQGLEVYVVEKKKQSQPKYKALAGGAGNSRGIEERVAARRLIDGQNH..EALHSAPAHKVGSGVLYLVNVPFRTITVVE	469
Consensus	n vg p k a n le y vk i ai l l gl yl ty w f r t g	
MCD4_Saccharomyces_cerevisiae	FVGHPFFSFIIFKSPFLIENVDDQKASPLSHAVGSGICLGNWILFYQGSFNFNMLLPFLYFWSYFTNSVLRGKIEFPGTSPKWRVLTITISIIIVGEG...EVVGFFHMTF	578
MCD4_Aspergillus_nidulans	YVGHTAYALTIVLHVLHGASESDRTT.ASIFSESSVILVDFSVLYQGSFNRVLDGFPFLIFWEEVFARAKAFHAG.....RAG.....ALLLPKRD..	561
MCD4_Magnaporthe_oryzae	YVGHTAYALTIVLHVLHGASESDRTT.MGLAATAVILVDFASFIASGPTTPARAFPPVFWEEVYARQSLVQGRLLFAHIFKPGVLSASFVLAAYTVAVTVLAGVIRSEVL	592
MCD4_Fusarium_graminearum	YVGHTAYALTIVLHVLHGASESDRTT.LGSAFTLSVLVDFSSFTISRSFPAHDAFFPVLVFWEEVYARQSLVQGRLLFAHIFKPGVLSASFVLAAYTVAVTVLAGVIRSEVL	589
MCD4_Colletotrichum_graminicola	YVGHTAYALTIVLHVLHGASESDRTT.LGSAFTLSVLVDFSSFTISRSFPAHDAFFPVLVFWEEVYARQSLVQGRLLFAHIFKPGVLSASFVLAAYTVAVTVLAGVIRSEVL	588
Consensus	gw l sp y y p w r g r	
MCD4_Saccharomyces_cerevisiae	TLITNLIAEYFICQVREISVN.....ILNITISVLSTFIDCAVLDLNLHSLHLILILSKAFYAKIHSRINSY.....TATPGLISIAAMLAVTRRSVISGLIQ	682
MCD4_Aspergillus_nidulansHNSVVDIDITPYCGAFMLLTGLLWLFDEILGTS..HOPAVSRKGSNIMGICLGMVLLILVITRSVISGLIQ	638
MCD4_Magnaporthe_oryzae	TCGLTGLAFWASYSIGIFQHEAALAGTWFVSCLMGTFLLKCNBNDLHLICGALMVVIGLTVLSLESFVRDSSDTPFPVKRHNVSALYAGLGVILAMLVTRSVIAIRAKK	712
MCD4_Fusarium_graminearum	TCGLTGLAFWASYSIGIFQHEAALAGTWFVSCLMGTFLLKCNBNDLHLICGALMVVIGLTVLSLESFVRDSSDTPFPVKRHNVSALYAGLGVILAMLVTRSVIAIRAKK	709
MCD4_Colletotrichum_graminicola	TCGLTGLAFWASYSIGIFQHEAALAGTWFVSCLMGTFLLKCNBNDLHLICGALMVVIGLTVLSLESFVRDSSDTPFPVKRHNVSALYAGLGVILAMLVTRSVIAIRAKK	700
Consensus	tlvylaaftwmtvlgftrhsnvlavvffaclvmvftllpamgsbvpvlvacitamaaigmalvwedkllsrp.....alpaalaltgvvlgillalilvtrssalssqakl	
MCD4_Saccharomyces_cerevisiae	GLRERSCVACMIIFPVFLVFMILHYRKNKNKVRDLIILTFASFSILTISSESLFVFLFSPYVMVQMEIEN.....KIKEMNKQDEN.....WL	771
MCD4_Aspergillus_nidulans	GLRERSCVACMIIFPVFLVFMILHYRKNKNKVRDLIILTFASFSILTISSESLFVFLFSPYVMVQMEIEN.....KIKEMNKQDEN.....WL	756
MCD4_Magnaporthe_oryzae	GLRERSCVACMIIFPVFLVFMILHYRKNKNKVRDLIILTFASFSILTISSESLFVFLFSPYVMVQMEIEN.....KIKEMNKQDEN.....WL	831
MCD4_Fusarium_graminearum	GLRERSCVACMIIFPVFLVFMILHYRKNKNKVRDLIILTFASFSILTISSESLFVFLFSPYVMVQMEIEN.....KIKEMNKQDEN.....WL	815
MCD4_Colletotrichum_graminicola	GLRERSCVACMIIFPVFLVFMILHYRKNKNKVRDLIILTFASFSILTISSESLFVFLFSPYVMVQMEIEN.....KIKEMNKQDEN.....WL	811
Consensus	glp q g s p pn y rl lt p l l t i s e l f y f w e r q vt l	
MCD4_Saccharomyces_cerevisiae	QVLNVSILCFEIQCAFFTCGNWASGSFSLSVSGILHFGHLMGALMLMLIFSGHSTCHLNLHNFKYDTTSSLTISMSSILSGFYLTPEGSWLIGSTISNVCIHLS	891
MCD4_Aspergillus_nidulans	SDARVALFFELQCAFFTCGNWASGSFSLSVSGILHFGHLMGALMLMLIFSGHSTCHLNLHNFKYDTTSSLTISMSSILSGFYLTPEGSWLIGSTISNVCIHLS	876
MCD4_Magnaporthe_oryzae	TDARVALFFELQCAFFTCGNWASGSFSLSVSGILHFGHLMGALMLMLIFSGHSTCHLNLHNFKYDTTSSLTISMSSILSGFYLTPEGSWLIGSTISNVCIHLS	951
MCD4_Fusarium_graminearum	SDARVALFFELQCAFFTCGNWASGSFSLSVSGILHFGHLMGALMLMLIFSGHSTCHLNLHNFKYDTTSSLTISMSSILSGFYLTPEGSWLIGSTISNVCIHLS	935
MCD4_Colletotrichum_graminicola	ADARVALFFELQCAFFTCGNWASGSFSLSVSGILHFGHLMGALMLMLIFSGHSTCHLNLHNFKYDTTSSLTISMSSILSGFYLTPEGSWLIGSTISNVCIHLS	931
Consensus	r llq aff tgn as s fs l sv r p f p g ll lk p s g l l sd l ff egswl ig ti a	
MCD4_Saccharomyces_cerevisiae	SLERMLILEVLGHVLLKNVITQDKTKKTQ.....	919
MCD4_Aspergillus_nidulans	CTFVAGLEFLSEVFISVDVFLGRLTDAITAS..VDFIVNGIISKQGDVNPVGVEDK	929
MCD4_Magnaporthe_oryzae	CVFVALLGVSTLFAVGKVSSEGRSGGRRD..ADAKVAPTRSNQKTATKALDG.	1003
MCD4_Fusarium_graminearum	CVFVALLGVSTLFAVGKVSSEGRSGGRRD..AALTSASPKDEPVPVAGAE.	981
MCD4_Colletotrichum_graminicola	CVFVALLGVSTLFAVGKVSSEGRSGGRRD..TANGCTPLTATKA.	985
Consensus	f le	

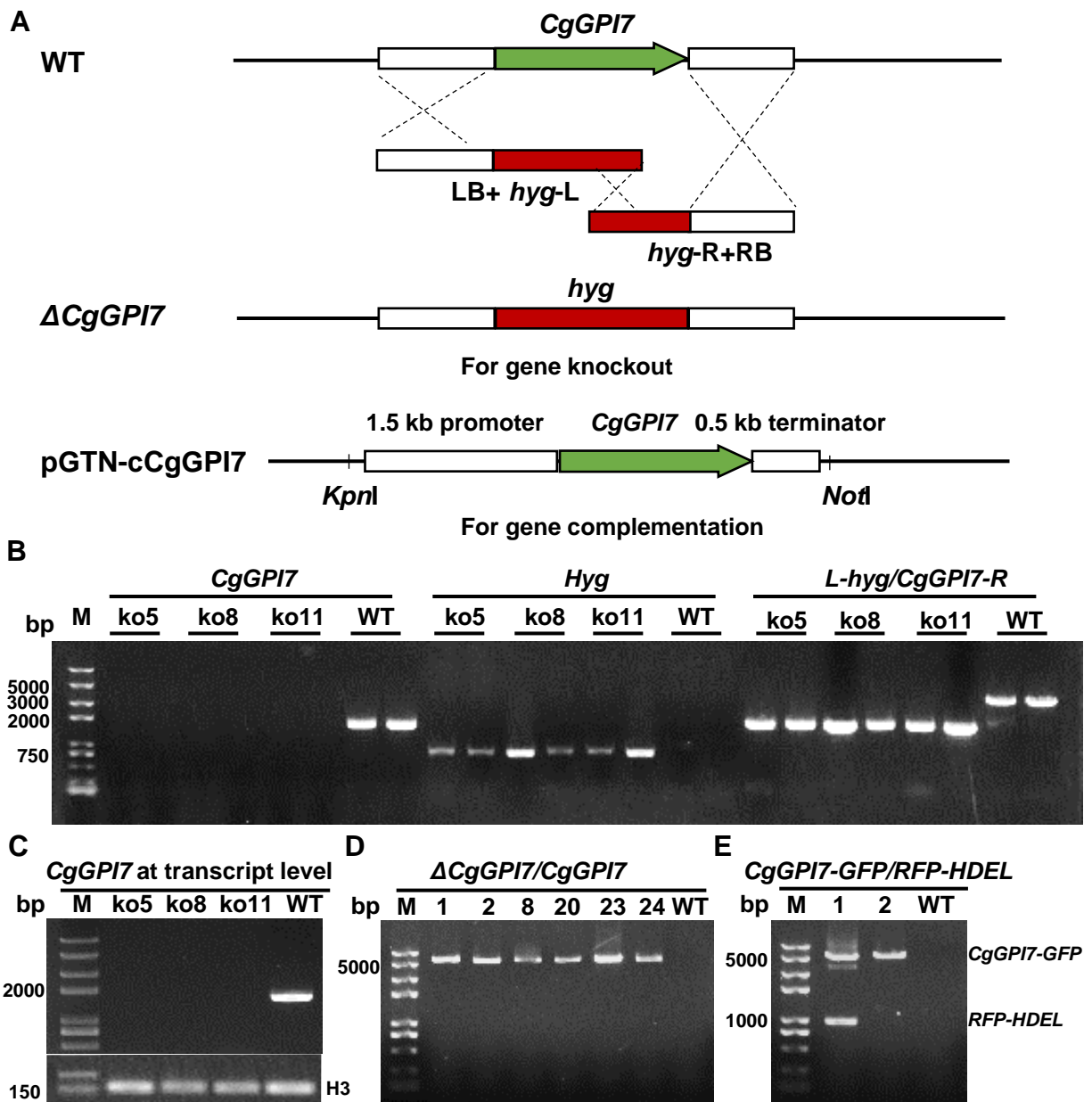
Supplemental Figure S2: Multiple alignment of MCD4 from different fungi species. Homologous proteins of MCD4 from 5 different fungi species and performed multiple alignment. Total sequence identity is 67.09%.

GPI7_Saccharomyces_cerevisiaeMNLKQFTCLSCAQLLALLIFAFRRFRIVITTSKQDPQDR..DLQRDRFQQLVFVITDALRSDFLSDQISHFNN.....VHGLWNTFSAAGHSFANPPTVAFPRR	105
GPI7_Aspergillus nidulansMVHHLVLVANVLFIAVIVSLGFFFRFSLICSHATFSFED....RFRVRGAVIVFVVVLAASDVIVNNSGFLTQSPIDFRSRLRSRFRFRAHSGSVVAFRA	108
GPI7_Magnaporthe oryzae	MQPNEELRLATVLLIANVIFLAFITKGFRRFSLKSVKVOVLGLSPFDFADRLICQAVVVDALASDVIVSSESGFFFTQ.....SLIRNRNLSRFRFRAHSGSVVAFRA	114
GPI7_Fusarium graminearum	MVPSHNSLRLTLLIANLIPASIVVFNLCFFRFFRFLFAEFSLDF..GSPFNAPDRLLFVVQALRSDEVVYSDSGSEYVQ.....SLIRNRNLSRFRFRAHSGSVVAFRA	112
GPI7_Colletotrichum graminicola	.MSFRYGGFGLATLLIVANILFLAIVTERTFFFRFVFLVGLHAKYETLDY..GPPRAAPDRLLFVVQDALF.....RLIRNRNLSRFRFRAHSGSVVAFRA	96
Consensus f ffp k g f f dalr g a t a ptvt pr k	
GPI7_Saccharomyces_cerevisiae	STTGSFSGFDMILVAQDIDNDSEHSMGLFIQHNN..TRFVGDDTWLKLFPQWGFAPFHSFFSDFTVNNVNTNIPGRUFQEWAMDVAILHYLGLDGHIGHRGSPRSKF	224
GPI7_Aspergillus nidulans	AMTGSFSGFDMILNARSSTSTSLAYOCQWLRKAKGE.QQVVMGDDTWLKLFPQWMSRSRSGTTSFFVSDFTVNNVNRHHDDELVTG..LWSGMILHYLGLDGHIGHRGSPRSY	224
GPI7_Magnaporthe oryzae	AITGSFSGFDMILNINCEDESSGASOCQWLRKAKAKATGKLVGGDDTWLKLFPD.TDRACGCSFFVADFTVNNVNRHITPLENN..LWNTLVHYLGLDGHIGHRGSPRSY	231
GPI7_Fusarium graminearum	SMTGSFSGFDMILNIDGCDTSSDASOCQWLRKAKHAKGKLLVGGDDTWLKLFPN.TDRSGGTSFFVADFTVNNVNRNIAPLENN..LWGLMVHYLGLDGHIGHRGSPSN	229
GPI7_Colletotrichum graminicola	AITGSFSGFDMILNIDGADTSSDASOCQWLRKAKAGELAMVGGDDTWLKLFPD.TDRSGGTSFFVADFTVNNVNRHITPLEND..LWSTLVHYLGLDGHIGHRGSPSSH	213
Consensus	ttgs psf d ln s l d wl q gddtwklfp f d t sffv dft vd nvtr l w hylgldhighk gp s	
GPI7_Saccharomyces_cerevisiae	MAAPGCMGSLIKSYIDVLEHEDDDDTLICVSDRCMNLNHNHSGSAGETSAGLSSFRACQARFESQVNYTLPINASPDWNQFVLETGGLDVFPTAALHSAFPMSSVGLHIG	344
GPI7_Aspergillus nidulans	AVPSGCMGSLIAQVVRAMEQEAELGSTIFILGCDRMRMDNHCSSAGETSAGLSSFRACQSLGAG.....RESFVNATHELOQTVVGLDVFPTAALHSAFPMSSVGLHIG	337
GPI7_Magnaporthe oryzae	MLPSGCMGSLIVETISATESQALGSTVLVVGCDHGRADNHCSSAGETSAGLSSFRACQALONG.....VPMMPVEDEQTVVGLDVFPTAALHSAFPMSSVGLHIG	344
GPI7_Fusarium graminearum	MLPSGCMGSLIVETLEAMKTFPHLSTLVLVLCGDHGNADNHCSSAGETSAGLSSFRACQPKDESDYVGLDVFPTAALHSAFPMSSVGLHIG	342
GPI7_Colletotrichum graminicola	MYPSGCMGSLIKRIVSAMOTQSHMSSALLVLGCDHGNADNHCSSAGETSAGLSSFRACQALORN.....LSAPAAFKDESDYVGLDVFPTAALHSAFPMSSVGLHIG	326
Consensus	m k emd gdhgm gnhg ss gets l f spk v q d pt l g p n g i	
GPI7_Saccharomyces cerevisiae	GFQLLR...NKLASKKFMELKLS.DHRGEVALGDFTA.....EDYITKMYTIOETL.....TKSATNYYPLLLAFVGL...FLIITITAILVGLR.YS.PDFWQ	435
GPI7_Aspergillus nidulans	BFNMMHLGSRIRLLACNKKQLNALKEITYPHNFGDDTLF.ASCYDSDPRGPDGALANAAQAGELHQYGADAAADDIVQVTEIESALLRFRSSQEVMSAASNMRLYLLICITAG	456
GPI7_Magnaporthe oryzae	GFPPFWRSRRDKTOLLNNAKQIGIVEATYCGDKLTSSLF..DEICVHGKSAMGVLACENKKILETAG...DEVTSDFRDAEVPVPTVAVLEAAGQIMSSMASNMOKKLKQSMV	459
GPI7_Fusarium graminearum	GFPPFWKTSQIQIIVNNARQIINIVTAATGSELDFSKSS..VDPCALEQTEINELACENKINKEA...HVLAAGDNLGQSLDEMSONLRRAGDLMSSMASNMOKKLIYQQAIAA	456
GPI7_Colletotrichum graminicola	GFPPFWDRNDQVOLIRNARQIRKVVVATGPEMGTATTSAREACAGPDQDAQELACENHRVNDAL...KNMDGQAGELPINLEAMSKVLSKAGDLMSSMASNMOKKLHICAVAI	452
Consensus	fl n sss eee w w t wn gqk w	
GPI7_Saccharomyces cerevisiae	LTVS.....SLSVLVSIIIGVSTFASFPFEESSGSHDGNVITAFSAVP.LFVVLNVLIIVR....WFIMMACVSNHNNNSORFIYS.VVMSNLLNQNSWNRKCL	532
GPI7_Aspergillus nidulans	LAVLFSFIVTIVKALSHNFRFLFTTGVLGLGDMRASSV..EEECQFVWGTGFTPIGHVRSIRLQAPQAGATYLLPAAILAISHFRRNRNQTGQAPAEPOIARIYLPSSRINMALL	576
GPI7_Magnaporthe oryzae	CRIGTLGVPVLLGD.EPRFVPLGSLIRGLKSNMSSVIVV...EFTFAMLAIVIGPRRLVFGSARLAGEIIVSVGLMALLNNQTCOKPAGCPDITWILFKPSFTILLFCL	578
GPI7_Fusarium graminearum	IAAVASAMVVVSLGAHRRQILPFPALLTLAAGAMVASSVVEECQFVWGTGFTPIGHVRSIRLQAPQAGATYLLPAAILAISHFRRNRNQTGQAPAEPOIARIYLPSSRINMALL	573
GPI7_Colletotrichum graminicola	LATG....SLVFG..ARLSLPLILAIAVAVGVMMPSAVVEEHRHNNVTTSAWLGILAKHMQTTRPIKT..LLSLLLALTATPISNNQTCOKPAGCPDITWILFKPSFTILLFCL	553
Consensus sss eee w w t wn gqk w	
GPI7_Saccharomyces cerevisiae	NMLTFLVIMAS.AGFOVLFHIVTITVLVGLCFTYKISLIVNGQAEIPFMHDLAKIDFAPTESNIVLARVFGQAWIVVRSIRLVLTCLKVLKNKNYLIKDMKVITILLMFQTSSQN	651
GPI7_Aspergillus nidulans	IVVTYADVCLHMDNIS...SLIWRLLCLAVTAMCFTFLVFAESPELNLNETTIOVTATFMDGITTVLYARVAMGGIATVLMFLIMRNGKLP.....IKGQLFREALTLFLLTQSR	686
GPI7_Magnaporthe oryzae	ILVTVFVYVRELLRGESCLPTIPNTIGTTTIVLAALSFLKAFITYEESPEIVFG.FAOTLLKFTAGASINBARAVFGGLAVGATVIFSMVTKLP..RSNKATGSATLHLHFLFAMTQSR	696
GPI7_Fusarium graminearum	ITLGMMLSFRLARLKSLPSLASTSITSVLLMSAYSPKLDFTSEDAPELVVG.FAKSLNDLLVQCSINBARATFLLLSLLFGYGIYRSFTGG..LRNMWQGSAYLFFHLYTIFGMTQSR	690
GPI7_Colletotrichum graminicola	VSLTFLFLVQILRLGLFRALAVATSATLALSFTFKVAFNEDAPELVVG.VPATLNALIQSLSVTRATVFAGVATAAYSTYLTLSNP..RVEARHTSPILLHLITLLATQSR	670
Consensus l ar	
GPI7_Saccharomyces cerevisiae	ICQFVFLQILESQIFYFQVIFPTASTSTSKIYFSNLVDEILNFRFSGGGGNSGSHDGNVITAFSAVP.LFVVLNVLIIVR....WFIMMACVSNHNNNSORFIYS.VVMSNLLNQNSWNRKCL	766
GPI7_Aspergillus nidulans	VTVVFILFPRF....LQKALTWNNNSAE...VTLSLGLAIAHFGGSAAGSDGNVITAFSAVP.LFVVLNVLIIVR....WFIMMACVSNHNNNSORFIYS.VVMSNLLNQNSWNRKCL	787
GPI7_Magnaporthe oryzae	ATNIPVLELLD....VIFKVTSSQPTREE.....LSTITLLAPFAPFGCGGNSGSHDGNVITAFSAVP.LFVVLNVLIIVR....WFIMMACVSNHNNNSORFIYS.VVMSNLLNQNSWNRKCL	801
GPI7_Fusarium graminearum	ATNIPVLELLD....VIFKVTSSQPTREE.....LSTITLLAPFAPFGCGGNSGSHDGNVITAFSAVP.LFVVLNVLIIVR....WFIMMACVSNHNNNSORFIYS.VVMSNLLNQNSWNRKCL	795
GPI7_Colletotrichum graminicola	VTVNPLLLFT....FQLPFTASLLSLPA....LSTTSLGLAIAHFGGSAAGSDGNVITAFSAVP.LFVVLNVLIIVR....WFIMMACVSNHNNNSORFIYS.VVMSNLLNQNSWNRKCL	781
Consensus l q ff fgg n is dl ay g vg l n a w	
GPI7_Saccharomyces cerevisiae	SKLPAPTVOICFGTCILDAVVRHBLFMSVFSRKLDCFLGNFVMGLN...GWLPEALCAL	829
GPI7_Aspergillus nidulans	HTALLTPHASICLTSVMAACTALHBLFMSVFSRKLDCFLGNFVMGLN...GWLPEALCAL	847
GPI7_Magnaporthe oryzae	HVTVLMTFASVGAHMACTVHBLFMSVFSRKLDCFLGNFVMGLN...GWLPEALCAL	866
GPI7_Fusarium graminearum	VYALQTLFVSATVALVMACTVHBLFMSVFSRKLDCFLGNFVMGLN...GWLPEALCAL	860
GPI7_Colletotrichum graminicola	HVGHMLTFTACSVAFTHVAGEAIRHBLFMSVFSRKLDCFLGNFVMGLN...GWLPEALCAL	846
Consensus m ac r hlf v v fspk y w l	

Supplemental Figure S3: Multiple alignment of GPI7 from different fungi species. Homologous proteins of GPI7 from 5 different fungi species and performed multiple alignment. Total sequence identity is 57.15%.

GPI13_Saccharomyces_cerevisiaeMDEKTIKSISSNDKIIYKS.....RIKKFKNKHFYIILLVITAILQFIHAF	53
GPI13_Magnaporthe_oryzae	MPSSPKTPAATGGKTPOTHTAASKTSFATQDYKATAAQFAAKKLKEADAKAKARAEAPTEQIEAKSRINALQKEQAKLRDALEGRSSRARFESRWTTVFWFWVIFTHAAGILVE	120
GPI13_Colletotrichum_graminicolaMPQOKAS.RAKAPPP.P.ADYKATAEQYAKAKRKQEMEEASRLPEEQAEKERAMLE.....KQRAVFESRRKDAYERRWWTVGFWAMMCLHAGVCAF	94
GPI13_Fusarium_graminearumMAKPKAKPKAQOQTPO.TEHQKIAEQWAKARARAAQOTANARFLGPPADENVEVLE.....QRREALDQRKRSNKRNRWAAGFWVVLAIHALCML	96
GPI13_Aspergillus_nidulansMSSRNSSTDAFNRK.G.....LLNSSECESDPPPTQAKMLSHMQSRTAIKSLKD.....DHVEKLER.EFKYKHLSSLGVFVITILLVVEHFE	87
Consensusi f	
GPI13_Saccharomyces_cerevisiae	RFPLSRLVLDNIS.....SQNETSKLIPPRARVILVLDALRGSRAEVNESHSHNYLNMYHNILSYDSFISDKDASSLAFPIADPPPTQRLK	148
GPI13_Magnaporthe_oryzae	SGPLSLGSLLESSELAFFIAVLPMNGLIGIKDWKRGTFDGGCWHEHNSRVAIVLDIAIUSOFVW.....VDDQAEIHNAAFHMRKTEKFNNAFSEPIADPPPTQRLK	234
GPI13_Colletotrichum_graminicola	SGPLSLGSLLESSELAFFIAVLPMNGLIGIKDWKRGTFDGGCWHEHNSRVAIVLDIAIUSOFVW.....VDDQAEIHNAAFHMRKTEKFNNAFSEPIADPPPTQRLK	200
GPI13_Fusarium_graminearum	SGPLSLGSLLESSELAFFIAVLPMNGLIGIKDWKRGTFDGGCWHEHNSRVAIVLDIAIUSOFVW.....VDDQAEIHNAAFHMRKTEKFNNAFSEPIADPPPTQRLK	201
GPI13_Aspergillus_nidulans	SGPLSLGSLLESSELAFFIAVLPMNGLIGIKDWKRGTFDGGCWHEHNSRVAIVLDIAIUSOFVW.....VDDQAEIHNAAFHMRKTEKFNNAFSEPIADPPPTQRLK	198
Consensus	t gfil r vl s p f a idalr df p a i fiadppt t qrlkg	
GPI13_Saccharomyces_cerevisiae	LTGGLPTFFLAGNSRQCTV.BEDNLSKQILHNKTVKFGDGTWMLHPHFLS.NDSFFLSNVNVDLITVNGVMDYFHDHQQDK..LENDVMIGHYLCQDGHGNYGPGHFTREKQ	265
GPI13_Magnaporthe_oryzae	LTGGLPTFFLAGNSRQCTV.BEDNLSKQILHNKTVKFGDGTWMLHPHFLS.NDSFFLSNVNVDLITVNGVMDYFHDHQQDK..LENDVMIGHYLCQDGHGNYGPGHFTREKQ	354
GPI13_Colletotrichum_graminicola	LTGGLPTFFLAGNSRQCTV.BEDNLSKQILHNKTVKFGDGTWMLHPHFLS.NDSFFLSNVNVDLITVNGVMDYFHDHQQDK..LENDVMIGHYLCQDGHGNYGPGHFTREKQ	320
GPI13_Fusarium_graminearum	LTGGLPTFFLAGNSRQCTV.BEDNLSKQILHNKTVKFGDGTWMLHPHFLS.NDSFFLSNVNVDLITVNGVMDYFHDHQQDK..LENDVMIGHYLCQDGHGNYGPGHFTREKQ	321
GPI13_Aspergillus_nidulans	LTGGLPTFFLAGNSRQCTV.BEDNLSKQILHNKTVKFGDGTWMLHPHFLS.NDSFFLSNVNVDLITVNGVMDYFHDHQQDK..LENDVMIGHYLCQDGHGNYGPGHFTREKQ	318
Consensus	lttg lptf d gs f g i edn ql gddtw lf s nvwdl tvd gv wd gh lg dh gh yyp h m k	
GPI13_Saccharomyces_cerevisiae	QAGSGLDNLKSGIDDTLLVYGDHGMDSKCHGCSQDGYEARLWMYSSRRPFG..RTNPFYSAPATKAPSTNIDIVLITALLIPIDNNLPGCTPEFAFGKGDAGGDAIAA	383
GPI13_Magnaporthe_oryzae	QAGSGLDNLKSGIDDTLLVYGDHGMDSKCHGCSQDGYEARLWMYSSRRPFG..RTNPFYSAPATKAPSTNIDIVLITALLIPIDNNLPGCTPEFAFGKGDAGGDAIAA	472
GPI13_Colletotrichum_graminicola	QAGSGLDNLKSGIDDTLLVYGDHGMDSKCHGCSQDGYEARLWMYSSRRPFG..RTNPFYSAPATKAPSTNIDIVLITALLIPIDNNLPGCTPEFAFGKGDAGGDAIAA	438
GPI13_Fusarium_graminearum	QAGSGLDNLKSGIDDTLLVYGDHGMDSKCHGCSQDGYEARLWMYSSRRPFG..RTNPFYSAPATKAPSTNIDIVLITALLIPIDNNLPGCTPEFAFGKGDAGGDAIAA	439
GPI13_Aspergillus_nidulans	QAGSGLDNLKSGIDDTLLVYGDHGMDSKCHGCSQDGYEARLWMYSSRRPFG..RTNPFYSAPATKAPSTNIDIVLITALLIPIDNNLPGCTPEFAFGKGDAGGDAIAA	436
Consensus	q d i idd tllv gdhgmd g hgg s de l ys r v qddiv l ll g pip nllg pi e	
GPI13_Saccharomyces_cerevisiae	...RISQQLKQKDTMQIHENDEILEPLAKNISNTPTSPDEKFKVLG.....HKYKVEQCTQBLWAFEDFYYSIATGILLATSLVILISITKLIPSIYVN.....	478
GPI13_Magnaporthe_oryzae	SRVAAGLRKRSSSVFAARCTAAGSGPGT..PAEVWSSAAIAIATAGAKKO..KLQHAYSLFAQYCAETALICGLWAFEDFYSIMLILGNMALGLMALILYARDSDDTAGSPAVEMDD	588
GPI13_Colletotrichum_graminicola	SRVTAAGLRKRSSSVFAARCTAAGSGPGT..PAEVWSSAAIAIATAGAKKO..KLQHAYSLFAQYCAETALICGLWAFEDFYSIMLILGNMALGLMALILYARDSDDTAGSPAVEMDD	549
GPI13_Fusarium_graminearum	SRVTAAGLRKRSSSVFAARCTAAGSGPGT..PAEVWSSAAIAIATAGAKKO..KLQHAYSLFAQYCAETALICGLWAFEDFYSIMLILGNMALGLMALILYARDSDDTAGSPAVEMDD	546
GPI13_Aspergillus_nidulans	LNSSQKPKKQQAARNSSESGNSGS...MEYNETARQWQAHGHRPNPKFSVSNINAYKQYRRTIQAARLWAFEDFYSIMLILGNMALGLMALILYARDSDDTAGSPAVEMDD	542
Consensusy g q l c lwa fd gi l f s n s t	
GPI13_Saccharomyces_cerevisiaeQMPVEIPGIIIMVLVNLCPHFIFY..VYQPSFVDQFQWFTLLATGIIITCYITIPRYNNIWIAMALGETIADYSRVIAWMTIHALLENSEK	576
GPI13_Magnaporthe_oryzae	LDIAEKKELEIAVNRKQDVSRHLERKLVQSALVSLGPAALG..VAAQTLMWLGSKTTIGITIDTSIIAVLAALVGVGRKFTALB...SSVAGSLSVTVVVSQSGPSSNSK	702
GPI13_Colletotrichum_graminicola	LDIAEKKELEIQGVQ..ADAATSYKTLHKVILITAILGAVPGAAVG..AGYSIFTCPQDLYVALAGAAVSAVGVLFVSYGFC.KTFRNMLP...NTFGKHLAVTVVSQSGPSSNSK	660
GPI13_Fusarium_graminearum	LDIAEKKELELSFK..ENDPEIEDNFKNKALGMDPKILFTVSV..LTAVGMYRQPIEGVLVALVVLFMAGLSSELHEAG.KTILNVFP...SFGGMMAVTVTVVSQSGPSSNSK	657
GPI13_Aspergillus_nidulansRTLLTGPLSRVGLGSILGALVGTLMAILGLTEIKVLELSALLAAGSICGASVAIFGSS.QRLSLPLP...NSLGLMLAILTVVSQSGPSSNSK	635
Consensusa w f s n s t	
GPI13_Saccharomyces_cerevisiae	IWEBSLWELSLSTGMLTYEFVFLPKRQSTALLTATISEKEGTTSGVNPSTANSNYLPTFRAPLILSGVSHAVLIITFIDHSMITICREGEYVCHIFNN...QNNSSMMWGLCFL	693
GPI13_Magnaporthe_oryzae	IWEBSLWELSLSTGMLTYEFVFLPKRQSTALLTATISEKEGTTSGVNPSTANSNYLPTFRAPLILSGVSHAVLIITFIDHSMITICREGEYVCHIFNN...QNNSSMMWGLCFL	787
GPI13_Colletotrichum_graminicola	IWEBSLWELSLSTGMLTYEFVFLPKRQSTALLTATISEKEGTTSGVNPSTANSNYLPTFRAPLILSGVSHAVLIITFIDHSMITICREGEYVCHIFNN...QNNSSMMWGLCFL	745
GPI13_Fusarium_graminearum	IWEBSLWELSLSTGMLTYEFVFLPKRQSTALLTATISEKEGTTSGVNPSTANSNYLPTFRAPLILSGVSHAVLIITFIDHSMITICREGEYVCHIFNN...QNNSSMMWGLCFL	742
GPI13_Aspergillus_nidulans	IWEBSLWELSLSTGMLTYEFVFLPKRQSTALLTATISEKEGTTSGVNPSTANSNYLPTFRAPLILSGVSHAVLIITFIDHSMITICREGEYVCHIFNN...QNNSSMMWGLCFL	720
Consensus	iwed i f tfg r l yh f ras creeq c t s w l	
GPI13_Saccharomyces_cerevisiae	MEFTHACTGCVYNNLSQYQAAHFNHNVFLRQICLNFVHSSTLSNNSAVIA..IPFLRDITIFKFTLRRIAGFSLSNVNVHMLWPLCKINIHNT.....DVKSH	797
GPI13_Magnaporthe_oryzae	VLAHSTVTKAMYPPTREGLAPRAGLVLRIITFLCSPKALDAYDNSGNPTISAPLEGLKLSLSVLAQVILAIQVILAFVAFYVAPPLVSLITTPF.....NPGRA	895
GPI13_Colletotrichum_graminicola	VLAHSTVTKAMYPPTREGLAPRAGLVLRIITFLCSPKALDAYDNSGNPTISAPLEGLKLSLSVLAQVILAIQVILAFVAFYVAPPLVSLITTPF.....NPGRA	848
GPI13_Fusarium_graminearum	VLAHSTVTKAMYPPTREGLAPRAGLVLRIITFLCSPKALDAYDNSGNPTISAPLEGLKLSLSVLAQVILAIQVILAFVAFYVAPPLVSLITTPF.....NPGRA	846
GPI13_Aspergillus_nidulans	VLAHSTVTKAMYPPTREGLAPRAGLVLRIITFLCSPKALDAYDNSGNPTISAPLEGLKLSLSVLAQVILAIQVILAFVAFYVAPPLVSLITTPF.....NPGRA	836
Consensus	lp s a wi l w a a	
GPI13_Saccharomyces_cerevisiae	EATILGNTIYSEFFLIVNVLISILFNKPAQLSYFIMCNLLSLEITILKLR..ENIIGIHALCLLSYOHFFGTGHCATIPSWMDIGISEKVEITFEETATILNLNHPGHIL	915
GPI13_Magnaporthe_oryzae	QIVDVGQNAHARYLIDPMLISALIIITFVFGGALAIMMCMLSLABIIMNITPATSPIGETAILLASFFHFTGHCQALSSQWDAASVPLFSIRYRSPSLVALNLNHPASHFL	1015
GPI13_Colletotrichum_graminicola	QIVDVGQNAHARYLIDPMLISALIIITFVFGGALAIMMCMLSLABIIMNITPATSPIGETAILLASFFHFTGHCQALSSQWDAASVPLFSIRYRSPSLVALNLNHPASHFL	966
GPI13_Fusarium_graminearum	QIVDVGQNAHARYLIDPMLISALIIITFVFGGALAIMMCMLSLABIIMNITPATSPIGETAILLASFFHFTGHCQALSSQWDAASVPLFSIRYRSPSLVALNLNHPASHFL	964
GPI13_Aspergillus_nidulans	QIVDVGQNAHARYLIDPMLISALIIITFVFGGALAIMMCMLSLABIIMNITPATSPIGETAILLASFFHFTGHCQALSSQWDAASVPLFSIRYRSPSLVALNLNHPASHFL	956
Consensus	t g n g i n kp q e d lgp l f tqhg s qw f p in f	
GPI13_Saccharomyces_cerevisiae	VSLVHLITLWQOPDVILKPQTLGR.....IVSCSGILLTYNTLCSFPIVTHRRHLMWKHICRRFIFASLSITVQLVTFGFIASFASGRLIKIHIDFHK	1017
GPI13_Magnaporthe_oryzae	AAAGLGLLLWKVNPFRKGLLGLVSA.....RVLAVEVVYFAVQSAAMAHARRHLMYRVESPRFMAAAVLLVDLAVIFVSLFGFRSNTLAISEVEGVA	1115
GPI13_Colletotrichum_graminicola	AAAGLGLLLWKVNPFRKGLLGLVSA.....RVLAVEVVYFAVQSAAMAHARRHLMYRVESPRFMAAAVLLVDLAVIFVSLFGFRSNTLAISEVEGVA	1065
GPI13_Fusarium_graminearum	AAAGLGLLLWKVNPFRKGLLGLVSA.....RVLAVEVVYFAVQSAAMAHARRHLMYRVESPRFMAAAVLLVDLAVIFVSLFGFRSNTLAISEVEGVA	1063
GPI13_Aspergillus_nidulans	AAAGLGLLLWKVNPFRKGLLGLVSA.....RVLAVEVVYFAVQSAAMAHARRHLMYRVESPRFMAAAVLLVDLAVIFVSLFGFRSNTLAISEVEGVA	1067
Consensus	l lw 1 w rrlhm f prf l w	

Supplemental Figure S4: Multiple alignment of GPI13 from different fungi species. Homologous proteins of GPI13 from 5 different fungi species and performed multiple alignment. Total sequence identity is 55.08%.



Supplemental Figure S5: Gene knockout and complementation of *CgGPI7* in *C.graminicolla*. (A) The *CgGPI7* gene knockout and complementation schematics. Gene knockout through a split-marker approach. And gene complementation by native promoter. (B) Verification of three *CgGPI7* knockout mutants by PCR. *CgGPI7* gene fragments couldn't be amplified in $\Delta CgGPI7$ mutants. Hygromycin resistance gene fragments could be amplified in $\Delta CgGPI7$ mutants. In situ amplification shown the smaller bands were amplified in $\Delta CgGPI7$ mutants which contain the replaced *hyg* fragments.(C) Verification of *CgGPI7* knockout mutants at the transcriptional level. (D) Verification of *CgGPI7* gene complementation strains by PCR. The fusion fragments contain native promoter, ORF and terminator of *CgGPI7* were amplified in complementation strains using the vector primer. (E) Verification of *CgGPI7*-GFP and RFP-HDEL co-transformant strains by PCR. There are two bands including *RFP-HDEL* and *CgGPI7*-GFP can be amplified in correct strain by same vector primer.