

Supplementary Materials: A WDR Gene Is a Conserved Member of a Chitin Synthase Gene Cluster and Influences the Cell Wall in *Aspergillus nidulans*

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Table S1. Locus numbers for *chs* and WDR genes in fungal species showing collinear *chs*-WDR genes. Asterisk indicates probable wrong annotation predicting the *chs* fused to the WDR gene.

Species	<i>chs</i> (Locus id)	WDR (Locus id)
<i>Fusarium graminearum</i>	FG10619.1	FG10616.1
<i>Neurospora crassa</i>	NCU09324	NCU09325
<i>Penicillium chrysogenum</i>	Pc12g02600	Pc12g02590
<i>Byssoschlamys spectabilis</i>	GAD94253*	GAD94253*
<i>Coccidioides immitis</i>	CIMG_08766	CIMG_08764
<i>Uncinocarpus reesii</i>	UREG_02708	UREG_02705
<i>Paracoccidioides lutzii</i>	PAAG_04862	PAAG_04865
<i>Arthroderma otae</i>	MCYG_02610	MCYG_02611
<i>Trichophyton verrucosum</i>	TRV_03668	TRV_03670
<i>Sclerotinia sclerotiorum</i>	SS1G_04263	SS1G_04255
<i>Marssonina brunnea</i>	MBM_06183	MBM_06185
<i>Pyrenophora tritici-repentis</i>	PTRG_07569	PTRG_07571
<i>Setosphaeria turcica</i>	estExt_Genewise1.C_200184	estExt_Genewise1.C_200186
<i>Bipolaris zeicola</i>	e_gw1.170.42.1	e_gw1.170.30.1
<i>Phaeosphaeria nodorum</i>	SNOG_04257	SNOG_04254
<i>Leptosphaeria maculans</i>	LEMA_P024060.1	LEMA_P024040.1
<i>Colletotrichum gloeosporioides</i>	CGGC5_7101	CGGC5_7102
<i>Verticillium albo-atrum</i>	VDBG_05981	VDBG_05983
<i>Chaetomium thermophilum</i>	CTHT_0059710	CTHT_0059720
<i>Podospora anserina</i>	PODANSg5938	PODANSg5939
<i>Myceliophthora thermophila</i>	MYCTH_2296388	MYCTH_2296384
<i>Aspergillus nidulans</i>	ANID_01555	ANID_10216
<i>Aspergillus versicolor</i>	Aspve1_0079582	Aspve1_0123502
<i>Aspergillus sydowii</i>	Aspsy1_0143806	Aspsy1_0055743
<i>Aspergillus flavus</i>	AFL2G_00575	AFL2G_00574
<i>Aspergillus oryzae</i>	AO090005000579	AO090005000578
<i>Aspergillus terreus</i>	ATEG_07757	ATEG_07758
<i>Aspergillus carbonarius</i>	Acar5010_211936	Acar5010_510790
<i>Aspergillus clavatus</i>	ACLA_059050	ACLA_059060
<i>Neosartorya fischeri</i>	NFIA_098390	NFIA_098400
<i>Aspergillus fumigatus</i>	Afu8g05630	Afu8g05640
<i>Aspergillus glaucus</i>	Aspgl1_0125048	Aspgl1_0035139
<i>Aspergillus wentii</i>	Aspwe1_0119338	Aspwe1_0118846
<i>Aspergillus niger</i>	An09g02290	An09g02280
<i>Aspergillus acidus</i>	Aspfo1_0144304	Aspfo1_0051389
<i>Aspergillus brasiliensis</i>	Aspbr1_0032516	Aspbr1_0198343
<i>Aspergillus tubingensis</i>	Asptu1_0136299	Asptu1_0392309
<i>Aspergillus zonatus</i>	Aspzo1_0016743	Aspzo1_0133145
<i>Aspergillus kawachii</i>	Aspka1_0179037	Aspka1_0179039
<i>Aspergillus aculeatus</i>	Aacu16872_031285	Aacu16872_053227
<i>Aspergillus ruber</i>	gm1.7455_g	gm1.7454_g
<i>Puccinia graminis</i>	PGTG_10666	PGTG_10670
<i>Cryptococcus gattii</i>	CGB_F4460C	CGB_F4440C
<i>Cryptococcus neoformans</i>	CNF01610	CNF01630
<i>Ustilago maydis</i>	UM04290.1	UM04291.1

Table S2. *Arabidopsis* and poplar orthologs of FPWD with details on their tissue expression.

Gene	Expression
AT1G78070	not in database
AT1G36070	mature embryo, stem
Potri.002G094100, POPTR_0002s09470	root
Potri.005G168600, POPTR_0005s16680	xylem & root
AT1G55680	seed & pollen
AT3G13340	seed & other
Potri.011G168600, POPTR_0011s17160	root (catkin)
Potri.006G000500, POPTR_0006s00270	root & seedling
Potri.001G471800, POPTR_0001s47580	root (catkin)
AT5G56190	pollen
Potri.002G233700, POPTR_0002s23480	not in database
Potri.014G147400, POPTR_0014s14460	male catkin & root

Table S3. Fungal species showing conserved genomic association WDR-*bf* gene. Asterisk indicates probable wrong annotation predicting the WDR gene fused to the *bf* gene.

Organism	WDR (Locus id)	<i>bf</i> Gene (Locus id)
<i>Aspergillus nidulans</i>	AN10216	AN10219
<i>Aspergillus versicolor</i>	Aspve1_0123502	Aspve1_0079584
<i>Aspergillus niger</i>	An15g04470	An15g04480
<i>Aspergillus acidus</i>	Aspfo1_0061227	Aspfo1_0219095
<i>Aspergillus carbonarius</i>	Acar5010_510790	Acar5010_010551
<i>Aspergillus brasiliensis</i>	Aspbr1_0032637	Aspbr1_0198466
<i>Aspergillus clavatus</i>	ACLA_059060	ACLA_059070
<i>Neosartorya fischeri</i>	NFIA_098400	NFIA_098410
<i>Aspergillus fumigatus</i>	Afu8g05640	Afu8g05650
<i>Aspergillus tubingensis</i>	Asptu1_0048296	Asptu1_0156027
<i>Aspergillus wentii</i>	Aspwe1_0118846	Aspwe1_0045178
<i>Aspergillus kawachii</i>	Aspka1_0180599	Aspka1_0180600
<i>Aspergillus sydowii</i>	Aspsy1_0055743*	Aspsy1_0055743*
<i>Aspergillus flavus</i>	AFL2G_00574	AFL2G_00573
<i>Aspergillus oryzae</i>	AO090005000578	AO090005000577
<i>Aspergillus aculeatus</i>	Aacu16872_053227	Aacu16872_044768
<i>Aspergillus glaucus</i>	Aspgl1_0035139	Aspgl1_1516651
<i>Aspergillus zonatus</i>	Aspzo1_0133145	Aspzo1_0097766
<i>Penicillium chrysogenum</i>	Pc12g02590	Pc12g02580
<i>Coccidioides immitis</i>	CIMG_08764	CIMG_08762
<i>Uncinocarpus reesii</i>	UREG_02705	UREG_02704
<i>Arthroderma otae</i>	MCYG_02611	MCYG_02612
<i>Aspergillus ruber</i>	gm1.7454_g	estExt_Genemark1.C_310069
<i>Puccinia graminis</i>	PGTG_10670	PGTG_10672

Table S4. Sequence of primers used in the study.

Name	Sequence (5'→3')
WD Southern Fwd	TTGCCGCGTGAGCCTGAAGTCTTGCCATT
WD Southern Rev	TGTGGCGAGATTTGTTGAAGTAACCGTTCT
WD Upstream Fwd	GAGGGTGGGATAAGGCGAAAGAGGAGTT
WD Upstream Rev	GTCTTGTGAACGAAACCGCGAAGATTCC
WD Downstream Fwd	GCTGGCTAGAGTTGCAGAACGATCTGCT
WD Downstream Rev	AAACCCGCACCTCCACCTCCACCTCCAG
Ribochimera Fwd	GGGGAATCTTCGCGGTTTCGTTTCAAGACCGTACGTAGTGTAGATTCA GGCACATTGAAGCG
Ribochimera Rev	CCAGCAGATCGTTTCTGCAACTCTAGCCAGCCTGCCATGACTACTAGGT GGTGCTATCATT
WD nested Fwd	CTACGTCGTTGTTTCTTCAATCATCAAA
WD nested Rev	TTTGAGGTGCGTCTGGATCGGGAGCTAG
CPS1 Fwd	ACGATCGAAACCATCCTGAC
CPS1 Rev	CGGCTTAGCATTCTTCAGC
rpl3 Fwd	TTCTCGCAAGACTCACAAG
rpl3 Rev	TTGTGGTTGCAAGAGGTACG
act Fwd	ATTGAGCACGGTGTGTGCAC
act Rev	GTTGGACTTGGGATTGATGG
rpl37 Fwd	CGCCACAACAAAACCTCACAC
rpl37 Rev	TCTCGCTCCAGTTGTACTTGC
pkcA Fwd	AACCGGTCTTCTGACAATGC
pkcA Rev	ACCTGGTTGCCTTTGTTCTG
wcsB Fwd	CATCTTCTTCTCGCAAAGC
wcsB Rev	AAGATCCGTTGGACAAGGTG
wcsA Fwd	TCATTGGTGTGTGGGTCTG
wcsA Rev	AGTCTTGCGACATGGGTTTG
FPWD Fwd	ACCATGAAAACGGCTGTAGG
FPWD Rev	TTCCACTCCCTTGGTTTCAG
bf Fwd	TTCTCCGAAGACTCCAATC
bf Rev	TCCTCGTCGATGTCATCTTG

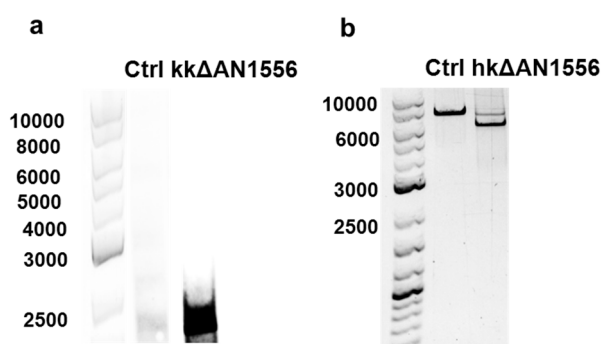
**Figure S1.** Molecular characterization of *hkΔAN1556*: (a) Southern blotting analysis; and (b) PCR on SAA.111 (Ctrl) and *hkΔAN1556*. The size of the band hybridizing with the probe in the transformed line is 2572 bp. The sizes of the PCR bands are 7408 and 6204 bp.



Figure S2. Phenotypes in liquid culture of control and *hkΔAN1556* mycelia. The formation of big irregular clumps is evident in *hkΔAN1556*.

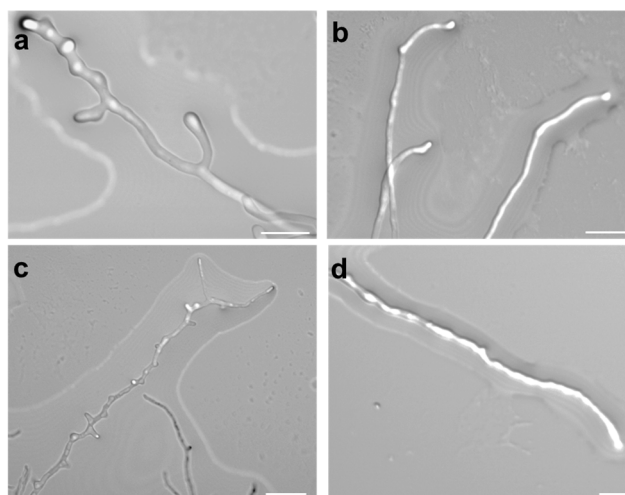


Figure S3. Differential interference contrast pictures of the four diploids showing the presence of non-straight, vacuolated hyphae: (a) diploid D1; (b) diploid D2; (c) diploid D3; and (d) diploid D4. Scale bars refer to 10 μm .

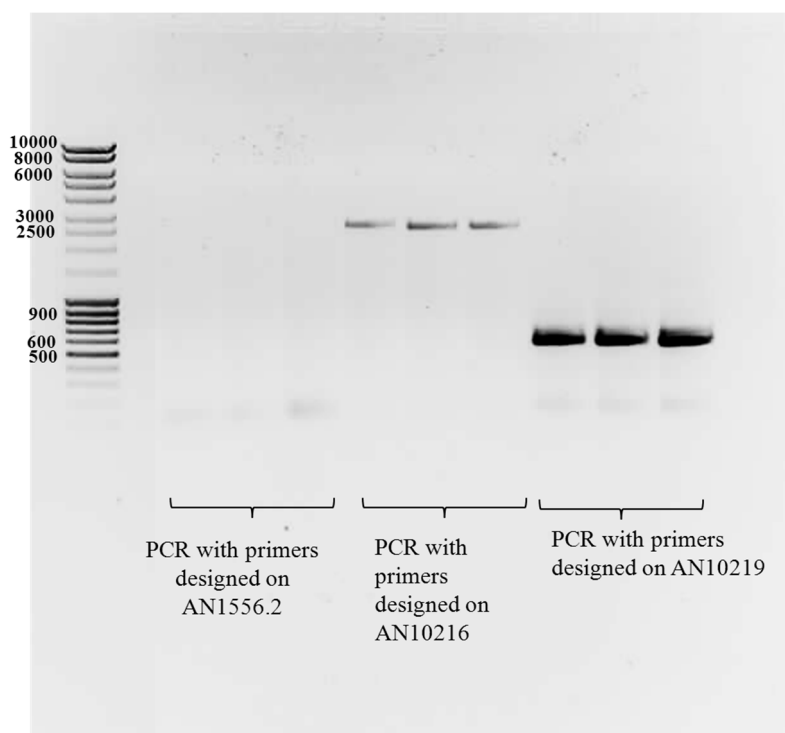


Figure S4. PCR on cDNA confirming the reannotation of the *FPWD* locus, AN10216. The primers are designed to amplify the full-length genes. The PCR product is 2484 bp for AN10216 and 543 bp for AN10219.

ANID_10219	1	-----	-----
CIMG_08762	1	-----	-----
estExt Genemark1	1	DGPPQSSGYGGGGSYGGPSYGGSSGGHGGHGGPPHGSSGGYGGPPQSSGYGG---GDSYG	
MCYG_02612	1	-----	-----
UREG_02704	1	-----	-----
Pcl2g02580	1	-----GYGSN-----	-----EGYGNQNQ---GYGN-NNNNSYG
Aspzol_0097766	1	-----	-----
AFL2G_00573	1	NDRPS-QGYGGD-SYN-----	DRPSHGNQGGYNDRPS-SGYGG---DSYG
Aspvel_0079584	1	-----	-----
Aspgll_1516651	1	-----	-----GGYGG---GDSYG
Anl5g04480	1	-----	-----
Aspfol_0219095	1	-----	-----
Acar5010_010551	1	-----	-----
Aspbrl_0198466	1	-----	-----
ACLA_059070	1	-----	-----
NFIA_098410	1	-----	-----
Afu8g05650	1	-----	-----
Asptul_0156027	1	-----	-----
Aspwe1_0045178	1	-----	-----
Aspkal_0180600	1	-----	-----
AO090005000577	1	NDRPS-QGYGGD-SYN-----	DRPSHGNQGGYNDRPS-SGYGG---DSYG
Aacu16872_044768	1	-----GGYGGEQSYG---SQGGSYGG-GPQGGSYGGSQGGYGGEQG-GSYGGGPQGGSYG	
consensus	1	-----	-----
ANID_10219	1	-----	MS-LQNLIVDAV---K--
CIMG_08762	1	-----	MSNYSRPPNPAEYC-GGG
estExt Genemark1	58	G----GSSGGYGGPP-----	QSSGYG-GGDSYGGPSYC-G--
MCYG_02612	1	-----	MS-YNDTQHRGEA-G--
UREG_02704	1	-----	-----
Pcl2g02580	25	G----SGGGYGNSN-----	DAYGNQNQC-N--
Aspzol_0097766	1	-----	-----
AFL2G_00573	40	GRPSHGNQGGYNDRP-----	SSGYG-GDSYNDRPSHC-N--
Aspvel_0079584	1	-----	MS-FQNLIVAGAV---K--
Aspgll_1516651	11	G----PSSGGHGGPP-----	QSSGYG-GGDSYGGPSYC-G--
Anl5g04480	1	-----	MS-FSNLISSALEQ-A--
Aspfol_0219095	1	-----	MS-FSNLISSALEQ-A--
Acar5010_010551	1	-----	MS-FSNLISSALEQ-A--
Aspbrl_0198466	1	-----	MS-FSNLISSALEQ-A--
ACLA_059070	1	-----	MS-LSNFIQDAISCAT--
NFIA_098410	1	-----	MS-FSNLIQDALSC-H--
Afu8g05650	1	-----	MS-FSNLIQDALSC-H--
Asptul_0156027	1	-----	MS-FSNLISSALEQ-A--
Aspwe1_0045178	1	-----	-----
Aspkal_0180600	1	-----	MS-FSNLISSALEQ-A--
AO090005000577	40	GRPSHGNQGGYNDRP-----	SSGYG-GDSYNDRPSHC-N--
Aacu16872_044768	51	G----GPQGGYGGPQGGYGGEQGGYQQQHHHQQHHQQQGGYS	EGGSYGGGPQC-G--
consensus	61	-----	ms y n l a v g
ANID_10219	13	-SHFDKDDDKD-----	-----
CIMG_08762	18	SSGANYDPRADFSQS-----	QPYQQQ-----SQYQC
estExt Genemark1	87	SSGSHGGPSH-GSS-----	GGYGG
MCYG_02612	15	-----YYNP-----	-----
UREG_02704	1	-----	-----
Pcl2g02580	45	-YG---RQESH-G-----	GGYG
Aspzol_0097766	1	-----	MSY-----NGYNG
AFL2G_00573	72	-QGGYNDRPSS-GYGCDSYNDRPSHGNQGGYNDRPSHGGNQG	GGYGGGGSYNDTSYNAPPP
Aspvel_0079584	13	-DHFNQDSGHS-GNQC-----	-----
Aspgll_1516651	40	SSGSHGGPSH-GSSGGY-----	GNSSGGYGG
Anl5g04480	15	-TSHS-----SG-----	SG
Aspfol_0219095	15	-TSGSHSSSSG-GYSG-----	G-----GGYGG
Acar5010_010551	14	-----GLSCG-----	G-----
Aspbrl_0198466	15	-TSGNHNSSSGGGYGGS-----	GGYGG
ACLA_059070	16	-GHNNENNSSY-GNNPSYGN-----	-----
NFIA_098410	15	-GHSNNNNNRH-DND-----	-----
Afu8g05650	15	-SHSN-NNSRH-DNN-----	-----
Asptul_0156027	15	-TSGSHSSSSG-GYSG-----	GGY-G
Aspwe1_0045178	1	-----MASND-YYNQ-----	NSYGG
Aspkal_0180600	15	-TSGSHSSSSG-GYSG-----	GGYGG
AO090005000577	72	-QGGYNDRPSS-GYGCD-----	-----YNDTSYNAPPP
Aacu16872_044768	103	-SYG--GEPSY-GSQGSY-----	G-----GGSNN
consensus	121	s s g g	gy g

Figure S5. Cont.

ANID_10219	23	-----	DLKPALSHASA-NASS	---
CIMG_08762	46	G----SGGY-NYDPAFS	-----	N-AVKQAKYHNSG-REDD
estExt_Genemark1	105	S----SQGH-GRHSDS	-----	D-D-FNPPALSHAQS-SGGS
MCYG_02612	19	-----GDL-SLNQ--D	-----	Q-AVRQAQYHKNG-REDH
UREG_02704	1	-----	-----	-----
Pc12g02580	57	N----NSSS-HHSNYND	-----	D-N-DYSGAAMHAQE-HHSN
Aspzol_0097766	9	G--GA-SASY--YDNNN	-----	D-FS-----D-ELRGAAQHAER-GHSA
AFL2G_00573	130	S----HGGY-HNSNPSS	-----	H-GFSD-----S-DVSPALAHAAQHSDDS
Aspvel_0079584	28	-----	-----	N-----QFDLNGAASHAST-H-SS
Aspg11_1516651	65	S----SQGH-GHHSDS	-----	D-D-LNPPALSHAQS-SGGS
An15g04480	24	-----SGSY-D	-----	P-EFSSAQHHAQA-HESS
Aspfol_0219095	36	G----GGSY-D	-----	P-EFSSAQHHAQS-HESS
Acar5010_010551	20	N----NSNY-D	-----	P-EFSSAHSHAQS-HHASYNQ
Aspbr1_0198466	36	NYGGNESGSY-D	-----	P-EFSSAQHHAQS-HESS
ACLA_059070	34	-----NPSY-STNPPPSHNPNSAPFAN	-----	D-DFNPALRYAES-HSNT
NFIA_098410	28	-----	-----	N-----D-DFNPAVRYAES-HTNT
Afu8g05650	27	-----	-----	Y-----D-EFNPAVRYAES-HANT
Asptul_0156027	34	N----SGSY-D	-----	P-EFSSAQHHAQS-HESS
Aspwe1_0045178	16	G---H-GHSYGD	-----	D-DFSSAAHHAQA-HESS
Aspkal_0180600	35	G----GGSY-D	-----	P-EFSSAQHHAQS-HESS
AO090005000577	99	S----HGGY-HNSNPSS	-----	H-GFSD-----S-DVSPALAHAAQHSDDS
Aacu16872_044768	123	N----EGNY-GHNPPHQ	-----	NPSYGGGRPSYD-DVASATSHAESHAGT
consensus	181	g y	df a haqs h ss	
ANID_10219	38	-----	E-D--SNLFSQALSFTNQKSEG	----
CIMG_08762	74	-----DE	-----	D-DEESGFEKKALSFTSEHKDRF
estExt_Genemark1	134	-----	G-D--SSLFSSALSFTKDKKKK	----
MCYG_02612	43	-----ED	-----	D-D--SSLFSKAMSF LGDNKEKL
UREG_02704	1	-----	-----	-----
Pc12g02580	86	-----	E-D--TSLFSSALNFKDRKNND	----
Aspzol_0097766	40	-----P	-----	D-S--SSLFGEAVSFTQGRASEYMSGGG
AFL2G_00573	164	-----	S-D--SSLFSTALNFKDKQGRS	----
Aspvel_0079584	45	-----	E-D--SSLFSQALKFVQERN-S-G	----
Aspg11_1516651	94	-----	G-D--SSLFSSALSFTKDKKKK	----
An15g04480	45	-----	G-D--SSLFSSALGFLSDRKSQY	----
Aspfol_0219095	58	-----	S-D--SSLFSSALGFLSDRKSQY	----
Acar5010_010551	45	GGYGNQGGYSDDQGRDYSYQGGGGGSGSGS	S--S-D--SSLFSTALSFTSSRKSQY	----
Aspbr1_0198466	63	-----	S-D--SSLFSSALSFTSDRKNQY	----
ACLA_059070	72	-----	SSND--SSLFTSALSFTLNENKHRF	----
NFIA_098410	45	-----	S-D--FSLFTSALSFTLNENKHL	----
Afu8g05650	44	-----	S-D--SSLFTSALSFTLNENKHL	----
Asptul_0156027	56	-----	S-D--SSLFSSALGFLSDRKSQY	----
Aspwe1_0045178	40	-----S	E-D--SSLFSSALSFTKDRQSQY	----
Aspkal_0180600	57	-----	S-D--SSLFSSALGFLSDRKSQY	----
AO090005000577	133	-----	S-D--SSLFSTALNFKDKRGRS	----
Aacu16872_044768	163	-----	G-S--SDLEQKALGYITNRHSSS	----
consensus	241		d sslfssalsfl drk	
ANID_10219	58	---V-QD--DIDEEQAVNAHRRYEQG	-----	GNMDSKDFGAGAAQALKMF
CIMG_08762	98	---GQE-DIDEEQVVGAAHQALYGG-GQQQQQ	QQAERKHDADFLNGAALQALKMF	
estExt_Genemark1	154	---DYKND-EINDNEMVSAHQSLYGS-G	-----	GSDDRKHDSNSVGMGAAMQALKMF
MCYG_02612	65	---GRE-DIDEEQKVVNSHQKLYGD	-----	V-DDRNEKHGAESLGSAGAAQALKMFL
UREG_02704	1	---MVGAHQALYGG	-----	QHE-GGDRGKVDADFLGSGAALQALKMF
Pc12g02580	106	---D--DN-DVDEEKAAAHQAAMYGS	-----	GSSNEKHDSNTVGAGAAMQALKMF
Aspzol_0097766	66	GGGS-SGP-AVDENQMVQAHAQAVYQG	G-S--	QGGGQCHSSETLGAGAAMQALKMF
AFL2G_00573	184	---S--SP-DIDEDQMVSQHQQLYND	-----	NDSSKAHDSNSLGAGAAMQALKMF
Aspvel_0079584	64	---S-DH--DVDEEHAVNSHRRYEQG	-----	GNMDSRDMGAGAAMQALKMF
Aspg11_1516651	114	---DYKND-EVNDDEMVSAAHQSLY-N-G	-----	GSDDRKHDSNSVGMGAAMQALKMF
An15g04480	65	---S-EQP-DIDEEHLVQSHQQLYNG	GGG-GY	GQEQQCHDSKSLGAGAAMQALKMF
Aspfol_0219095	78	---S-EQP-DIDEEHLVQSHQRLYNG	G----	GE-QQQCHDSSSLGAGAAMQALKMF
Acar5010_010551	96	---E-EQP-DVDEEHMVQSHQALYNN	-----	QDEGQCHDSKSLGAGAAMQALKMF
Aspbr1_0198466	83	---S-EQP-DIDEEHLVQSHQALYNG	GGGGGY	GGGEQCHDSKSLGAGAAMQALKMF
ACLA_059070	94	---S-DDRADLNEADVRAHQSLYNN-NGGNE	---	GQGGQGRHDAGSLGAGAALQALKLF
NFIA_098410	65	---S-NDN-DINEQEMIAHQSLYGG	-----	GESERRHDSSSVGAGAAMQALKMF
Afu8g05650	64	---S-NDN-DINEQEMIAHQSLYDG	-----	RDSEERRHDSSSVGAGAAMQALKMF
Asptul_0156027	76	---S-EQP-DIDEEHLVQSHQRLYNN	GGG--YG	GQEQQCHDSSSLGAGAAMQALKMF
Aspwe1_0045178	61	---S-HHE-EIDENEVSSHQSLYNN	-----	EDDGRSHDSKSLGSGAALQALKMF
Aspkal_0180600	77	---S-EQP-DIDEEHLVQSHQRLYNG	G----	GEQQQCHDSSSLGAGAAMQALKMF
AO090005000577	153	---S--SP-DIDEDQMVSQHQQLYND	-----	NDSSKAHDSNSLGAGAAMQALKMF
Aacu16872_044768	183	---EDDDD-DIDESQMVQSHQAVYNSHEG	-----	AGQQQCHDSKTLGAGAAMQALKMF
consensus	301	s didee vvnsHq lyn	g hds slGaGAAMQALKMF	

Figure S5. Cont.

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ANID_10219      98 ---NSSSG--QETGG-----GK-DKNAFI GMAMAQA AKMWE EKA-CKG-EASGDKQSAI
CIMG_08762     149 ---TSGEG--QQS-Q--TG--GH-DQNKLI GLAMAQA GLWDQQN-QQG-NVATDKQSVI
estExt_Genemark1 201 ---TSSDS--GSG-SGSSS--GGM DKNKLI GLAMSQA GDLWEKKN-SGG-QASGDKQSAV
MCYG_02612     111 NDGNKNQG--QNQ-S--QG--GG-DQNKLI GMAMAQA GKMWEQKN-QEG-RVDTDKQTAV
UREG_02704      39 ---SSGEG--RQS-Q--SG--GH-DQNKLI GLAMAQA GLWDQQN-QQG-QVATDKQSAI
Pc12g02580     150 ---AGGNE--SSG-SSG---GGM DKNKLI GLAMAQA GLWDEKNGSGG-DVSGDKQSAV
Aspzol_0097766  116 ---GSG---SSG-S-----SG-SMNEFI GMAMSQA CNLWDQHS-ASG-SVAGSKQSAI
AFL2G_00573     228 ---SSGQS--GGS-S-----GG-DQNAFI GMAMSQA AKLWEQKN-SGG-NVTDDKQSAV
Aspvel_0079584  104 ---NSGSG--GASGG-----GQ-DKNAFI GLAMAQA SKMWE EKN-CKG-EASGDKQSAV
Aspgl1_1516651  160 ---SSDS--GSG-SGSSSSS GGM DKNKLI GLAMSQA GDLWEKKN-SGG-QASGDKQSAV
An15g04480     115 ---TSG---GGG-S-----SG-DKNEFI GMAMAQA SKLWE EKS-GSG-NVSGDKQSAV
Aspfo1_0219095  123 ---TSGG--GGS-S-----GG-DKNEFI GMAMAQA SKLWE EKA-GSG-NVSGDKQSAV
Acar5010_010551 141 ---TSG---SGG-S-----SG-DKNEFI GMAMAQA SKLWDQKS-GSG-SVAGDKQSAI
Aspbr1_0198466  134 ---TSGGGSSGSS-S-----GG-DKNEFI GMAMAQA SKLWDQKS-GSG-NVSGDKQSAI
ACLA_059070     145 ---TTSSE--GEK-S-----GM-SKDAFI GLAMAQA KLFEEKE-CKG-EVSGDKQSAI
NFIA_098410     110 ---TSSSE--GEK-S-----GM-DKNAFI GLAMAQA KMFEEKE-AKG-EVNGDKQSAI
Afu8g05650     109 ---TSSSE--GEK-S-----GM-DKNAFI GLAMAQA KMFEEKE-AKG-EVNGDKQSAI
Asptul_0156027  126 ---TSGGG--GGS-S-----GG-DKNEFI GMAMAQA SKLWE EKA-GSG-NVSGDKQSAV
Aspwe1_0045178  106 ---TGGGGSSGGS-G-----GM-DKNEFI GLAMSQA GLWEQKQ-QSSGNNVSGDKQSAI
Aspkal_0180600  123 ---TSGGG--GGS-S-----GG-DKNEFI GMAMAQA SKLWE EKA-GSG-NVSGDKQSAV
AO090005000577 197 ---SSGQS--GGS-S-----GG-DQNAFI GMAMSQA AKLWEQKN-SGG-NVTDDKQSAV
Aacu16872_044768 232 ---TSGSG--GSG-SSSGS--GG--KNEFI GLAMAQA SKLWE EKS-SGG-LASGDKQSAI
consensus      361   tsg   g t s       gg dkn fI GmAmAQAaklweek   gsG nvsgdKQsai

ANID_10219      144 NQAAEMAFKMYLKSQMSG---SECTGG-----
CIMG_08762     196 NSAAKMALKMYLKNQAGGGGALGGLGG-----LGG-----LASGVS
estExt_Genemark1 251 NSAAEMALKMYMKSNGSG---SGTG---
MCYG_02612     161 NMAAQYALKMYLKGQMGGGSTGMGGLGGGLALISSALGGGGGHQQQQQQSGLAALAGAL-
UREG_02704      86 NSAAKMALKMYLKNQSGG---KLGCVGG-----LGG-----LAGSL-
Pc12g02580     199 NSAAEMALKMYMKNQMSG---GGS---
Aspzol_0097766  159 NSAAEMALKMYMKSQSGG---LGGTGG-----
AFL2G_00573     273 NKAEMALKMYMKSQSGG---SSGSGG-----
Aspvel_0079584  150 NQAAEMAFKMYMKSESG---SSGTGG-----
Aspgl1_1516651  212 NSAAEMALKMYMKNGSG---SGTG---
An15g04480     158 NSAAEMAFKMYMKSQSGG---SSGTGG-----
Aspfo1_0219095  167 NSAAEMAFKMYMKSQSGG---SSGTGG-----
Acar5010_010551 184 NSAAEMAFKMYMKSQSGG---SSGTGG-----
Aspbr1_0198466  181 NSAAEMAFKMYMKSQSGG---SSGTGG-----
ACLA_059070     190 NSAAEMALKMYMKSQGG---MSGTGG-----
NFIA_098410     155 NAAEMALKMYLKSGGG---MAGTGG-----
Afu8g05650     154 NAAEMALKMYLKSGGG---MTGTGG-----
Asptul_0156027  171 NSAAEMAFKMYMKSQSGG---SSGTGG-----
Aspwe1_0045178  154 NNAEMALKMYMKSQGG---IGGTGG-----
Aspkal_0180600  168 NSAAEMAFKMYMKSQSGG---SSGTGG-----
AO090005000577 242 NKAEMALKMYMKSQSGG---SSGSGG-----
Aacu16872_044768 280 NQAAEMALKMYMKSQSGG---SSGTGG-----
consensus      421 NsAAemAlKMYmKsqgsG   ssgtGG

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Figure S5. Cont.

ANID_10219	168	-----P-----G--G-----LMSLASKFL-K-----
CIMG_08762	233	GGG-----Q--S--G--G-SG--LGLAKKFL-----
estExt_Genemark1	275	-----PSSSSGGAS-G-----LMSLASKFM-----
MCYG_02612	220	-GGSGGQQQQQQQQQQ--S---G-A-SN-LNMASKLL-CRGCQVVTY
UREG_02704	119	-GG-----Q--S--G--G-SG--LFDLAKKFF-----
Pc12g02580	223	-----G-----G-----LMSLASKFL-----
Aspzol_0097766	183	-----P-----A--G-----LMSLASKFL-----
AFL2G_00573	297	-----P-----A-----LMNLAKKFLSK-----
Aspvel_0079584	174	-----P-----S--G-----LMGLASKFL-K-----
Aspgll_1516651	236	-----PSSSSGGAS-G-----LMSLASKFM-----
An15g04480	182	-----P-----A--A-----LMSLASKFL-----
Aspfol_0219095	191	-----P-----G--A-----LMSLASKFL-----
Acar5010_010551	208	-----P-----A--G-----LMSLASKFL-----
Aspbri_0198466	205	-----P-----A--A-----LMSLASKFL-----
ACLA_059070	214	-----P-----G--G-----LMSLASKFM-----
NFIA_098410	179	-----P-----GGG-----LQLASKFL-----
Afu8g05650	178	-----P-----G--G-----LQLASKFL-----
Asptul_0156027	195	-----P-----G--A-----LMSLASKFL-----
Aspwei_0045178	178	-----P-----G--GGASGL--LMSLASKFL-----
Aspkal_0180600	192	-----P-----G--A-----LMSLASKFL-----
AO090005000577	266	-----P-----A-----LMNLAKKFLSK-----
Aacu16872_044768	304	-----P-----A--G-----LMSLASKFL-----
consensus	481	p g g LmslAsKfl

Figure S5. Alignment of Bf proteins from different ascomycetes. The alignment was done with Boxshade (www.ch.embnet.org/software/BOX_form.html). Black shading, identical amino acids; gray shading, similar amino acids.