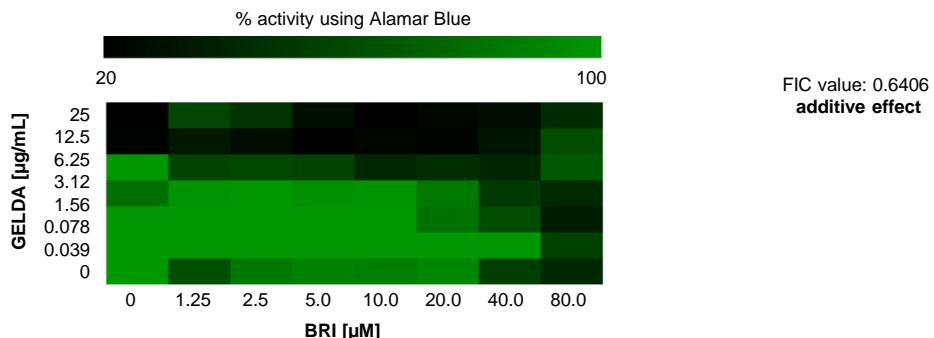
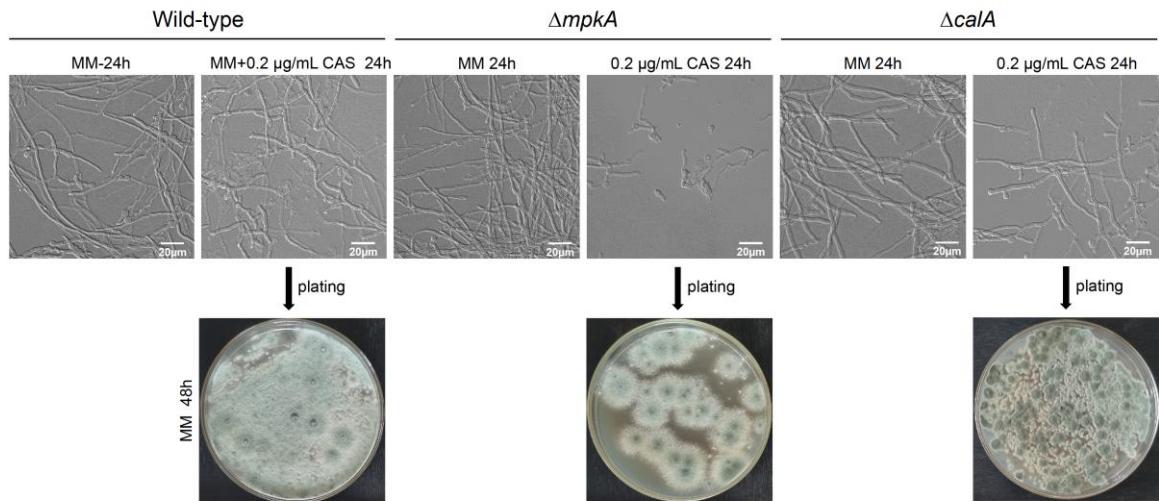


Supplementary Figure S1 – BRI and GELDA display na additive effect Against *A. fumigatus*



Supplementary Figure S1- The Fractional Inhibitory Concentration (FIC) index for BRI+GELDA. The heat map was generated by measurement of the metabolic activity using Alamar blue. The % of activity is based on *A. fumigatus* grown for 48 h at 37°C in the absence of BRI (ranging from 0-80 μ M) and GELDA (ranging from 0-25 μ g/mL). Results show the average of three independent experiments.

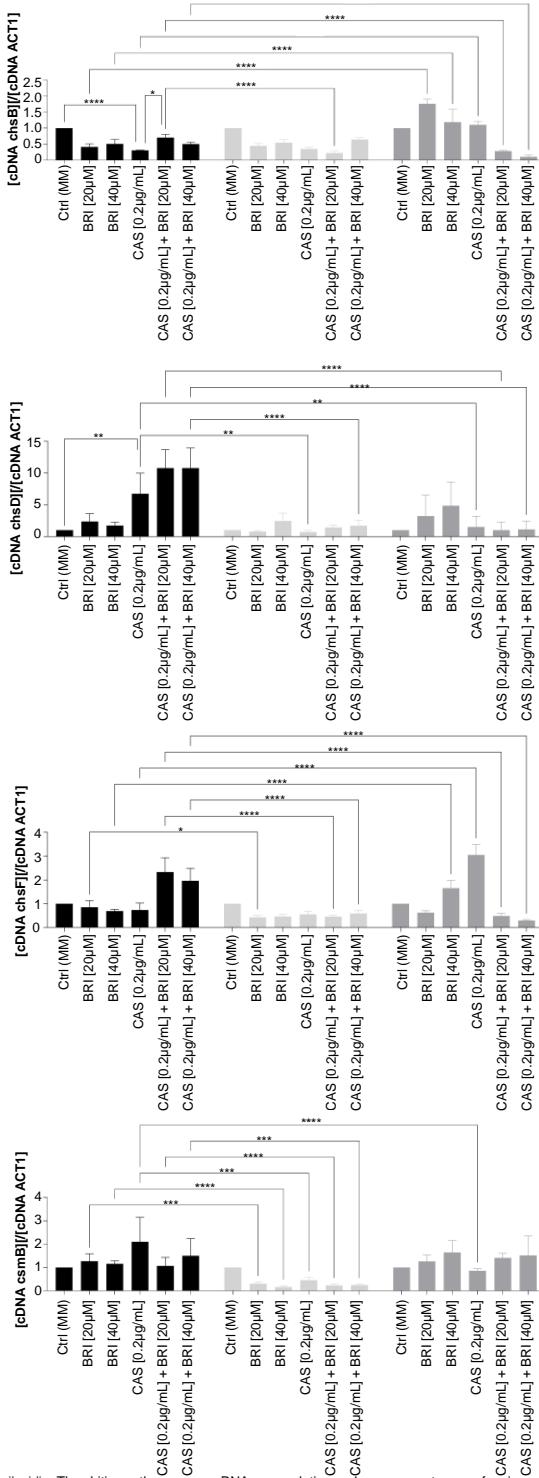
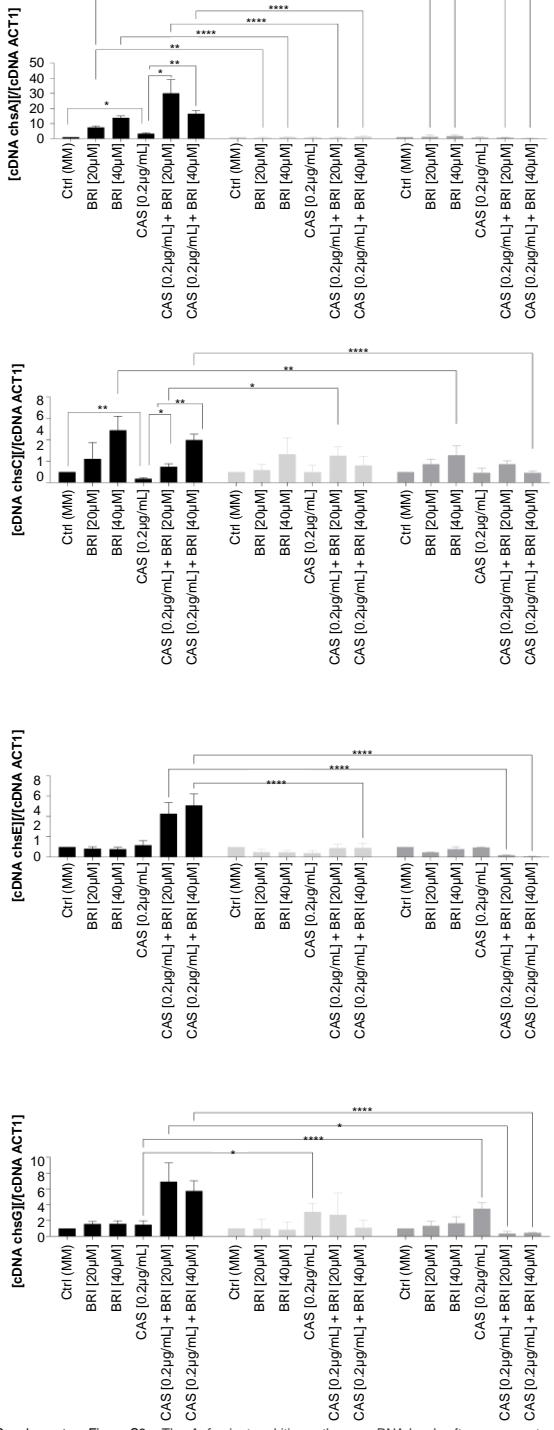
Supplementary Figure S2 - Caspofungin displays a fungistatic activity against the wild-type, $\Delta mpkA$, and $\Delta calA$ strains



Supplementary Figure S2 – Caspofungin displays a fungistatic activity against the wild-type, $\Delta mpkA$, and $\Delta calA$ strains. The wild-type, $\Delta mpkA$, and $\Delta calA$ (2×10^3 conidia) were grown for 24 h in 200 μ l liquid minimal medium (MM) supplemented or not with caspofungin 0.2 μ g/ml for 24 h at 37°C. The 200 μ l were plated on solid MM and Incubated for 48 hs at 37°C. The experiment was repeated independently 3 times and presented similar results.

Supplementary Figure S3 – The *A. fumigatus* chitin synthases mRNA levels after exposure to caspofungin and brilacidin.

■ wild-type
 □ $\Delta mpkA$
 ▨ $\Delta calA$



Supplementary Figure S3 – The *A. fumigatus* chitin synthases mRNA levels after exposure to caspofungin and brilacidin. The chitin synthase gene mRNA accumulation under exposure to caspofungin and brilacidin was measured in the wild-type, $\Delta mpkA$ and $\Delta calA$ strains. After 24h of growth at 37°C in MM, the mycelia were transferred to minimal medium (MM) containing (or not) CAS, BRI or combination of both drugs for 60 min. The Tukey's test are pre-test; * $p < 0.05$, ** $p < 0.005$, *** $p < 0.0005$, **** $p < 0.0001$.

* $p < 0.05$
 ** $p < 0.005$
 *** $p < 0.0005$
 **** $p < 0.0001$

Supplementary Table S1 - BRI+VOR cannot overcome *A. fumigatus* VOR-resistance

Strain	Mechanism of VOR ^R	MIC VOR [µg/ml]	MIC BRI [µM]	VOR [µg/ml]		BRI [µM]	0.5 µg/ml VOR		2 µg/ml VOR		
				0.5	2		20	20 µM BRI	40 µM BRI	20 µM BRI	40 µM BRI
WT	WT	2	>80	---	---	+	---	---	---	---	---
CYP-15-184	TR34/L98H	8	>80	+	+	+	+	+	+	+	+
CYP-15-190	TR34/L98H	8	>80	+	+	+	+	+	+	+	+
CYP-15-192	TR34/L98H	4	>80	+	+	+	+	+	+	+	+
CYP-15-195	TR34/L98H	8	>80	+	+	+	+	+	+	+	+
CYP-15-202	TR34/L98H	8	>80	+	+	+	+	+	+	+	+
CYP-15-212	TR34/L98H	8	>80	+	+	+	+	+	+	+	+
CYP-15-213	TR34/L98H	4	>80	+	+	-	+	+	+	+	+
CYP-15-215	Unknown	8	>80	+	+	-	+	+	+	+	+
CYP-15-220	TR34/L98H	4	>80	+	+	+	+	+	+	+	+
CYP-15-221	TR34/L98H	8	>80	+	+	+	+	+	+	+	+
CYP-15-222	TR34/L98H	4	>80	+	+	+	+	+	+	+	+
CYP-15-224	Unknown	8	>80	+	+	+	+	+	+	+	+
CYP-15-225	Unknown	8	>80	+	+	+	+	+	+	+	+
CYP-15-226	TR34/L98H	4	>80	+	+	+	+	+	+	+	+
CYP-15-228	TR34/L98H	4	>80	+	+	+	+	+	+	+	+
CYP-15-229	TR34/L98H	8	>80	+	+	+	+	+	+	+	+
CYP-15-230	TR34/L98H	8	>80	+	+	+	+	+	+	+	+
CYP-15-231	TR34/L98H	4	>80	+	+	+	+	+	+	+	+
CYP-15-75	Unknown	8	>80	+	+	+	+	+	+	+	+
CYP-15-108	Unknown	8	>80	+	+	+	+	+	+	+	+
CYP-15-109	Unknown	>8	>80	---	---	+	---	---	---	---	---
CYP-15-147	Unknown	8	>80	+	+	+	-	-	+	+	+
F14946	Unknown	8	>80	+	+	+	+	+	+	+	+
20089320	Unknown	8	>80	+	+	+	+	+	+	+	+

Obs.: 1) VOR=voriconazole; BRI=Brilacidin. (+): no inhibition; (-): partial inhibition; and (---) total inhibition;

2) In the experiment, one strain (CYP15-15-109) was totally inhibited by VOR, showing Wild Type response; also, one strain (CYP15-15-147) was partially inhibited by VOR 0.5 µg/ml+BRI but the inhibition was not seen at VOR 2.0 µg/ml+BRI.

Supplementary Table S2. Protein kinase inhibitors analysed in this study

COMPOUND NAME	TARGET KINASE	PKI [20 µM]	PKI [20 µM] + BRI [20 µM]	SMILES	molecular weight (MW)
PF +3758309	PAK3	++	++	CC1=NC2=C(SC=C2)C(NC3=NNC4=C3CN(C(N[C@H](C5=CC=CC=C5)CN(C)C)=O)C4(C)C)=N1	490.634
FRAX597		++	++	CCN1C2=NC(=NC=C2C=C(C1=O)C3=C(C=C(C=C3)C4=CN=CS4)Cl)NC5=CC=C(C=C5)N6CCN(CC6)C	558.108
FRAX486		++	+	C1C=CC(Cl)=C(C2=CC3=CN=C(NC4=CC(F)=C(N5CCNCC5)C=C4)N=C3N(CC2=O)C=C1	513.403
G5555		++	++	CNC1=NC=C2C=C(C3=C(C=C(C4=CC=CC(C)=N4)C=C3)Cl)C(N(C2=N1)C[C@H](C5OC[C@H](CO5)N)=O	492.966
GW300660X	PRKAA1	++	++	NS(=O)(=O)c1ccc(NN=C2/C(=O)Nc3ccc(cc23)C(=O)NCCc2c[nH]cn2)cc1	453.482
GW296115X		++	++	COc1ccc2[nH]c3c4[nH]c5ccc(OC)cc5c4c4C(=O)NC(=O)c4c3c2c1	385.378
GW416981X		++	++	CC(C)COC(=O)c1ccc2NC(=O)C(=C/Nc3ccc(cc3)S(N)(=O)=O)c2c1	415.469
GW290597X		++	++	NS(=O)(=O)c1ccc(NN=C2/C(=O)Nc3ccc(cc23)C(=O)NCCCh2ccncc2)cc1	467.509
CHIR +99021	GSK3A	++	++	N#CC(C=N1)=CC=C1NCCNC2=NC=C(C3=NC(C)=CN3)C(C4=CC=C(Cl)C=C4Cl)=N2	465.347
SB 216763		++	++	Clc1ccc(c(Cl)c1)C1=C(C(=O)NC1=O)c1cn(C)c2cccc12	371.222
LY2090314		++	++	O=C(N1)C(C2=CN=C3N2C=CC=C3)=C(C4=CN5C6=C4C=C(F)C=C6CN(C7=CCCCC7)=O)CC5)C1=O	512.543
AZD1080		++	++	OC(NC1=C2C=C(C#N)C=C1)=C2C3=NC=C(CN4CCOCC4)C=C3	334.378
AZD +8055	MTOR	++	++	C[C@H]1COCCN1C2=NC(=NC3=C2C=CC(=N3)C4=CC(=C(C=C4)OC)C(=O)N5CCOC[C@H]5C	465.552
vistusertib		++	++	C[C@H]1COCCN1C2=NC(=NC3=C2C=CC(=N3)C4=CC(=C(C=C4)C(=O)N5CCOC[C@H]5C	462.552
Torin 2		++	++	C1=CC(=CC(=C1)N2C(=O)C=CC3=CN=C4C=CC(=CC4=C32)C5=CN=C(C=C5)N)C(F)(F)F	432.404
CC +115		++	++	CCN1C(=O)CNC2=NC=C(N=C21)C3=C(N=C(C=C3)C4=NC=NN4)C	336.358
D4476	CSNK1G2	++	++	C1COC2=C(O1)C=CC(=C2)C3=C(NC(=N3)C4=CC=C(C=C4)C(=O)N)C5=CC=CC=N5	398.421
NK +258		++	++	CN(C)C(C=C1)=NN2C1=NC=C2C3=CC=CC(OC(F)(F)F)=C3	322.289
PP121	STK25	++	+	C1CCC(C1)N2C3=C(C(=N2)C4=CN=C5C(=C4)C=C5)C(=NC=N3)N	319.371
BX +795		++	++	O=C(NCCCNC1=C(C=NC(NC2=CC=CC(=NC(N3CCCC3)=O)=C2)=N1)I)C4=CC=CS4	591.472
SCH772984	MAPK3 (ERK1)	++	++	C1CN(CC1C(=O)NC2=CC3=C(C=C2)NN=C3C4=CC=NC=C4)CC(=O)N5CCN(CC5)C6=CC=C(C=C6)C7=NC=CC=N7	587.686
GW305074X		++	++	Oc1c(Br)cc(C=C2C(=O)Nc3ccc(l)cc23)cc1Br	520.942
XMD8 +92		++	++	CCOC1=C(C=CC(=C1)N2CCC(CC2)O)NC3=NC=C4C(=N3)N(C5=CC=C=C5C(=O)N4C)C	474.563
GW300657X		++	++	NS(=O)(=O)c1ccc(NN=C2/C(=O)Nc3ccc(cc23)C(=O)NCC2ccncc2)cc1	450.478
PF +4708671	RPS6KB2	++	++	CCC1=CN=CN=C1N2CCN(CC2)CC3=NC4=C(N3)C=C(C=C4)C(F)(F)F	390.412
LY +2584702		++	++	CC1=CC=C(C=C1)S(=O)(=O)O.CN1C=C(N=C1C2CCN(CC2)C3=NC=NC4=C(NC(=N4)C5=CC(=C(C=C5)F)C(F)(F)F	617.626
AT7867		++	++	C1CNCCC1(C2=CC=C(C=C2)C3=CNN=C3)C4=CC=C(C=C4)Cl.Cl.Cl	410.775
VX +745	MAPK11	++	++	C1=CC(=C(C(=C1)Cl)C2=C3C=CC(=NN3C=NC2=O)SC4=C(C=C(C=C4)F)Cl	436.268
AKI00000001a		++	++	FC(C=C1)=CC(F)=C1C2=C(C=C3)=NN4C3=NN=C4C(O)(C)C(N(CCC5)C5=N2	396.4
AKI00000067a		++	++	FC(C=C1)=CC(F)=C1C2=C(C=C3)=NN4C3=NN=C4C(C)C(N(C=O5)C5=N2	379.369
GSK223810A		++	++	COc1cc2c(Nc3cccc(NC(=O)c4cccc4)c3)ncnc2cc1OCCCN1CCOCC1	513.596

ralimetinib			CC(C)(C)CN1C2=C(C=CC(=N2)C3=C(N=C(N3)C(C)(C)C)C4=CC=C(C=C 612.746 4)F)N=C1N.CS(=O)(=O)O.CS(=O)(=O)O	
TAK +715	CSNK1E	++ ++	CCC1=NC(=C(S1)C2=CC(=NC=C2)NC(=O)C3=CC=CC=C3)C4=CC=CC(399.517 =C4)C	
PF +670462		++ ++	C1CCC(CC1)N2C=NC(=C2C3=NC(=NC=C3)N)C4=CC=C(C=C4)F.Cl.Cl 410.323	
CK1 +IN +1		++ ++	C1=CC=C2C(=C1)C=CC(=C2F)C3=NC(=C(N3)C4=CC=NC=C4)C5=CC= 383.4 C(C=C5)F	
PF +5006739		++ ++	C1CN(CCC1N2C=NC(=C2C3=NC(=NC=C3)N)C4=CC=C(C=C4)F)CC5=N 419.463 OC=C5	
MK +8353	MAPK1		CC(C)OC1=NC=C(C=C1)C2=NNC3=C2C=C(C=C3)NC(=O)[C@ @]4(CC[N 691.859 (C4)CC(=O)N5CCC(=CC5)C6=CC=C(C=C6)C7=NN(C=N7)C)SC	
PHA +767491	CDC7	++ ++	C1CNC(=O)C2=C1NC(=C2)C3=CC=NC=C3 213.239	
XL413		++ ++	C1C[C@H](NC1)C2=NC3=C(C(=O)N2)OC4=C3C=C(C=C4)Cl 289.721	
LY3177833		++ ++	C[C@ @]1(C2=C(C=C(C=C2)C3=CNN=C3)C(=O)N1)C4=NC=NC=C4F 309.303	
refametinib	MAP2K2	++ ++	COC1=CC(=C(C(=C1NS(=O)(=O)C2(CC2)C[C@ @H](CO)O)NC3=C(C=C(572.337 C=C3)I)F)F	
selumetinib		++ ++	CN1C=NC2=C1C=C(C(=C2F)NC3=C(C=C(C=C3)Br)Cl)C(=O)NOCCO 457.686	
SR +3677	CAMK1G	++ ++	O=C(C3COC(C=CC=C4)=C4O3)NC1=CC=C(C2=CNN=C2)C=C1OCCN(481.378 C)C.Cl.Cl	
CX +4945	CSNK2A2	++ ++	C1=CC(=CC(=C1)Cl)NC2=NC3=C(C=CC(=C3)C(=O)O)C4=C2C=CN=C4 349.776	
SGC +CK2 +1	CSNK2A2	++ ++	CC1=CC=C(NC2=NC3=C(C#N)C=NN3C(NC4CC4)=C2)C=C1NC(CC)=O 375.435	
TTP 22		++ ++	CC(C=C1)=CC=C1C2=CSC3=NC=NC(SCCC(O)=O)=C32 330.4	
Sorafenib	MAPK13	++ ++	CNC(=O)C1=NC=CC(=C1)OC2=CC=C(C=C2)NC(=O)NC3=CC(=C(C=C3) 464.83 Cl)C(F)(F)F	
5 +iodo tubercidin	MAP2K3	++ ++	O[C@H]1[C@H](N2C=C(I)C3=C(N)N=CN=C32)O[C@H](CO)[C@H]1O 392.148	
SB +216385		++ ++	Nc1nccc(n1)+c1c(ncn1CCCN1CCOC C1)+c1ccc(F)cc1 382.442	
SB +203580	PRKCA	++ ++	CS(=O)C1=CC=C(C=C1)C2=NC(=C(N2)C3=CC=NC=C3)C4=CC=C(C=C 377.442 4)F	
enzastaurin		++ ++	CN1C=C(C2=CC=CC=C21)C3=C(C(=O)NC3=O)C4=CN(C5=CC=CC=C5 515.615 4)C6CCN(CC6)CC7=CC=CC=N7	
darovasertib		++ ++	CC1(CCN(CC1)C2=C(N=CC=C2)NC(=O)C3=NC(=CN=C3N)C4=C(C=CC 472.474 =N4)C(F)(F)N	
GW461487A		++ ++	Cl.Cc1cccc2c(c(nn12)+c1ccc(F)cc1)+c1ccncc1 339.8	
UNC +ALM +33		++ ++	CC1=CC2=NC(C3=CC=C(F)C=C3)=C(C4=CC=NC=C4)N2C=C1 303.339	
UNC +ALM +39		++ ++	CC(C=N1)=CN2C1=C(C3=CC=NC=C3)C(C4=CC=C(F)C=C4)=N2 304.327	
UNC +ALM +16		++ ++	CC(C=C1)=NN2C1=C(C3=CC=NC=C3)C(C4=CC=C(F)C=C4)=N2 304.327	
UNC +ALM +87		++ ++	FC1=CC=C(C2=C(C3=CC=NC=C3)N4C(SC(C)=C4)=N2)C=C1 309.367	
GW434756X		++ ++	Fc1ccc(cc1)+c1nn2cccc2c1+c1ccncc1 289.31	

++: growth ≥ 80% compared to no treatment

+: growth ≤ 60% compared to no treatment

Supplementary Table S3. Susceptibility of phosphatase and kinase mutants to brilacidin

Strain	CAS [0.25 µg/mL]	BRI [20 µM]
Reference strains		
CEA17 (wild-type; A1160)	+	+
Afs35 (wild-type; A1159)	+	+
phosphatase null mutants		
$\Delta pphA$ (<i>Afu5g12010</i>)	+	+
$\Delta sitA$ (<i>Afu6g11470</i>)	+	+
$\Delta ppzA$ (<i>Afu2g03950</i>)	+	+
$\Delta pptA$ (<i>Afu5g06700</i>)	+	+
$\Delta ptcA$ (<i>Afu1g15800</i>)	+	+
$\Delta ptcB$ (<i>Afu1g09280</i>)	+	+
$\Delta ppmA$ (<i>Afu8g04580</i>)	+	+
$\Delta ptcD$ (<i>Afu5g13740</i>)	+	+
$\Delta ptcE$ (<i>Afu2g03890</i>)	+	+
$\Delta ptcF$ (<i>Afu1g06860</i>)	+	+
$\Delta ptcG$ (<i>Afu5g13340</i>)	+	+
$\Delta ptcH$ (<i>Afu4g00720</i>)	+	+
$\Delta nemA$ (<i>Afu1g09460</i>)	+	+
$\Delta psrA$ (<i>Afu1g04790</i>)	+	+
$\Delta ppsA$ (<i>Afu5g11690</i>)	+	+
$\Delta dspD$ (<i>Afu2g02760</i>)	+	+
$\Delta cdcA$ (<i>Afu3g12250</i>)	+	+
$\Delta dspA$ (<i>Afu1g13040</i>)	+	+
$\Delta dspB$ (<i>Afu1g03540</i>)	+	+
$\Delta ptpB$ (<i>Afu3g10970</i>)	+	+
$\Delta pypA$ (<i>Afu4g04710</i>)	+	+
$\Delta ltpA$ (<i>Afu2g01880</i>)	+	+
$\Delta yphA$ (<i>Afu4g07000</i>)	+	+
$\Delta ptyA$ (<i>Afu6g06650</i>)	+	+
$\Delta calA$ (<i>Afu5g09360</i>)	+	-
kinases null mutants		
$\Delta mpkA$	-	-
$\Delta mpkB$	+	+
$\Delta mpkC$	+	+
$\Delta sakA$	+	+
$\Delta sakA; \Delta mpkC$	+	+

+: sensitivity similar to wild-type

-: more sensitive than the wild-type

Supplementary Table S4. Strains used in this work

<i>Aspergillus fumigatus</i> strains	Genotype	Reference
CEA17 (A1160)	akuB (KU80) Δ ;pyrG1 MAT1-1	1
Af293	wild-type	2
Δ pphA	Δ pphA::pyrG, akuB (KU80) Δ , MAT1-1	3
Δ sitA	Δ sitA::pyrG, akuB (KU80) Δ , MAT1-1	3
Δ ppzA	Δ ppzA::pyrG, akuB (KU80) Δ , MAT1-1	3
Δ pptA	Δ pptA::pyrG, akuB (KU80) Δ , MAT1-1	3
Δ ptcA	Δ ptcA::pyrG, akuB (KU80) Δ , MAT1-1	3
Δ ptcB	Δ ptcB::pyrG, akuB (KU80) Δ , MAT1-1	3
Δ ppmA	Δ ppmA::pyrG, akuB (KU80) Δ , MAT1-1	3
Δ ptcD	Δ ptcD::pyrG, akuB (KU80) Δ , MAT1-1	3
Δ ptcE	Δ ptcE::pyrG, akuB (KU80) Δ , MAT1-1	3
Δ ptcF	Δ ptcF::pyrG, akuB (KU80) Δ , MAT1-1	3
Δ ptcG	Δ ptcG::pyrG, akuB (KU80) Δ , MAT1-1	3
Δ ptcH	Δ ptcH::pyrG, akuB (KU80) Δ , MAT1-1	3
Δ nemA	Δ nemA::pyrG, akuB (KU80) Δ , MAT1-1	3
Δ psrA	Δ psrA::pyrG, akuB (KU80) Δ , MAT1-1	3
Δ ppsA	Δ ppsA::pyrG, akuB (KU80) Δ , MAT1-1	3
Δ dspD	Δ dspD::pyrG, akuB (KU80) Δ , MAT1-1	3
Δ cdcA	Δ cdcA::pyrG, akuB (KU80) Δ , MAT1-1	3
Δ dspA	Δ dspA::pyrG, akuB (KU80) Δ , MAT1-1	3
Δ dspB	Δ dspB::pyrG, akuB (KU80) Δ , MAT1-1	3
Δ ptpB	Δ ptpB::pyrG, akuB (KU80) Δ , MAT1-1	3
Δ ypyA	Δ ypyA::pyrG, akuB (KU80) Δ , MAT1-1	3
Δ ltpA	Δ ltpA::pyrG, akuB (KU80) Δ , MAT1-1	3
Δ yphA	Δ yphA::pyrG, akuB (KU80) Δ , MAT1-1	3
Δ ptyA	Δ ptyA::pyrG, akuB (KU80) Δ , MAT1-1	3
Δ calA	Δ calA::pyrG, akuB (KU80) Δ , MAT1-1	3
Δ mpkC	Δ mpkC::prtA	4
Δ sakA	Δ sakA::hph	4
Δ mpkA	Δ mpkA::hph	5
Δ mpkB	Δ akuBmpkB::ptrA; prtA+	6
Δ sakA; Δ mpkC	Δ mpkC::prtA Δ sakA::hph	7
Afs35 (A1159)	akuA::loxP	8
CYP-15-75	clinical isolate	9
CYP-15-108	clinical isolate	9
CYP-15-109	clinical isolate	9
CYP-15-147	clinical isolate	9
20089320	clinical isolate	9
CYP-15-184	clinical isolate	Katrien Lagrou lab
CYP-15-190	clinical isolate	Katrien Lagrou lab
CYP-15-192	clinical isolate	Katrien Lagrou lab
CYP-15-195	clinical isolate	Katrien Lagrou lab
CYP-15-202	clinical isolate	Katrien Lagrou lab
CYP-15-212	clinical isolate	Katrien Lagrou lab
CYP-15-213	clinical isolate	Katrien Lagrou lab
CYP-15-215	clinical isolate	Katrien Lagrou lab
CYP-15-220	clinical isolate	Katrien Lagrou lab
CYP-15-221	clinical isolate	Katrien Lagrou lab
CYP-15-222	clinical isolate	Katrien Lagrou lab

CYP-15-224	clinical isolate	Katrien Lagrou lab
CYP-15-225	clinical isolate	Katrien Lagrou lab
CYP-15-226	clinical isolate	Katrien Lagrou lab
CYP-15-228	clinical isolate	Katrien Lagrou lab
CYP-15-229	clinical isolate	Katrien Lagrou lab
CYP-15-230	clinical isolate	Katrien Lagrou lab
CYP-15-231	clinical isolate	Katrien Lagrou lab
F14946	clinical isolate	Gustavo Goldman lab
CM7555	clinical isolate	Gustavo Goldman lab
DPL1033	clinical isolate	David Perlin lab
MD24053	clinical isolate	David Perlin lab
<i>Candida spp.</i> strains	Genotype	Reference
<i>C. auris</i> 467/2015	clinical isolate	Arnaldo Colombo lab
<i>C. auris</i> 468/2015	clinical isolate	Arnaldo Colombo lab
<i>C. auris</i> 469/2015	clinical isolate	Arnaldo Colombo lab
<i>C. auris</i> 470/2015	clinical isolate	Arnaldo Colombo lab
<i>C. auris</i> 474/2015	clinical isolate	Arnaldo Colombo lab
<i>C. albicans</i> DPL1006	clinical isolate; CAS ^R	David Perlin lab
<i>C. albicans</i> DPL1007	clinical isolate; CAS ^R	David Perlin lab
<i>C. albicans</i> DPL1009	clinical isolate; CAS ^R	David Perlin lab
<i>C. albicans</i> DPL1010	clinical isolate; CAS ^R	David Perlin lab
<i>C. albicans</i> DPL1011	clinical isolate; CAS ^R	David Perlin lab
<i>Cryptococcus neoformans</i>	Genotype	Reference
H99 (ATCC 208821)	wild-type	ATCC database
Mucorales fungi		
<i>R. oryzae</i> 99-892	Lung isolate	Fungus Testing Laboratory at the University of Texas Health Sciences Center at San Antonio (UTHSCSA)
<i>R. delemar</i> 99-880	Brain isolate	Fungus Testing Laboratory at the University of Texas Health Sciences Center at San Antonio (UTHSCSA)
<i>L. corymbifera</i>	clinical isolate from DEFEAT Mucor	Ibrahim laboratory
<i>M. circinelloides f. jenssenii</i> UTHSCSA DI15-131	clinical isolate	Fungus Testing Laboratory at the University of Texas Health Sciences Center at San Antonio (UTHSCSA)

References

- Da Silva Ferreira ME, Kress MR, Savoldi M, Goldman MH, Härtl A, Heinekamp T, Brakhage AA, Goldman GH. 2006. The akuB(KU80) mutant deficient for nonhomologous end joining is a powerful tool for analysing pathogenicity in *Aspergillus fumigatus*.
- Pain A, Woodward J, Quail MA, Anderson MJ, Clark R, Collins M, Fosker N, Fraser A, Harris D, Larke N, Murphy L, Humphray S, O'Neil S, Pertea M, Price C, Rabbinowitsch E, Rajandream MA, Salzberg S, Saunders D, Seeger K, Sharp S, Warren T, Denning DW,
- Winkelströter LK, Dolan SK, Fernanda Dos Reis T, Bom VL, Alves de Castro P, Hagiwara D, Alowni R, Jones GW, Doyle S, Brown NA, Goldman GH. Systematic Global Analysis of Genes Encoding Protein Phosphatases in *Aspergillus fumigatus*. *G3* (Bethesda). 2015
- Hagiwara D., Suzuki S., Kamei K., Gono T., Kawamoto S. The role of AtfA and HOG MAPK pathway in stress tolerance in conidia of *Aspergillus fumigatus*. *Fungal Genet. Biol.* 2014;73:138–149.
- Valiante V., Jain R., Heinekamp T., Brakhage A.A. The MpKα MAP kinase module regulates cell wall integrity signaling and pyomelanin formation in *Aspergillus fumigatus*. *Fungal Genet. Biol.* 2009;46(12):909–918.
- Manfioli AO, Siqueira FS, dos Reis TF, Van Dijck P, Schrevens S, Hoefgen S, Föge M, Straßburger M, de Assis LJ, Heinekamp T, Rocha MC, Janevska S, Brakhage AA, Malavazi I, Goldman GH, Valiante V. 2019. Mitogenactivated protein kinase cross-talk
- Bruder Nascimento A.C., Dos Reis T.F., de Castro P.A., Hori J.I., Bom V.L., de Assis L.J., Goldman G.H. Mitogen activated protein kinases SakA (HOG1) and MpKc collaborate for *Aspergillus fumigatus* virulence. *Mol. Microbiol.* 2016;100:841–859.
- FGSC, Fungal Genetic stock center
- Bastos RW, Rossato L, Valero C, Lagrou K, Colombo AL and Goldman GH (2019) Potential of Gallium as an Antifungal Agent. *Front. Cell. Infect. Microbiol.* 9:414. doi: 10.3389/fcimb.2019.00414

Supplementary Table S5 – Primers used in this work

Primer	Sequences	Gene	ID
chsA FW	5'-CTGGAGTGTGGCTGGTCTCT-3'	<i>chsA</i>	AFUB_018960
cshA REV	5'-GCGTGTGAAAGCAGTATGGA-3'	<i>chsA</i>	AFUB_018960
chsB FW	5'-GCTCTCCACTGTCGGTCTCT-3'	<i>chsB</i>	AFUB_098840
chsB REV	5'-GGTCGTTGTTGATGGTGTTG-3'	<i>chsB</i>	AFUB_098840
chsC FW	5'-TTGCTGCGAGTTGTATTCC-3'	<i>chsC</i>	AFUB_049230
chsC REV	5'-GCCAGTAGGATGCCAAAGAG-3'	<i>chsC</i>	AFUB_049230
chsD FW	5'-CAGAACACGATCCGAACAAC-3'	<i>chsD</i>	AFUB_012070
chsD REV	5'-GCTTCGCACCCAAGTAGAAC-3'	<i>chsD</i>	AFUB_012070
chsE FW	5'-TGGTGTTCGTTGACTTGCTC-3'	<i>chsE</i>	AFUB_029080
chsE REV	5'-TCATCCATCCAACCATTCC-3'	<i>chsE</i>	AFUB_029080
chsF FW	5'-AACCTGCTTCTTCTGGGTGA-3'	<i>chsF</i>	AFUB_081920
chsF REV	5'-GAGCACGAGTTCCATGAGGT-3'	<i>chsF</i>	AFUB_081920
chsG FW	5'-AGGATGAGGGCAAAGAGGTT-3'	<i>chsG</i>	AFUB_034810
chsG REV	5'-AAGGC GTTGCTAAAGATCCA-3'	<i>chsG</i>	AFUB_034810
csmB FW	5'-ACAATACGCGGCGAATCC-3'	<i>csmB</i>	AFUB_029070
csmB REV	5'-GTTATCCCGACTGCCAAAA-3'	<i>csmB</i>	AFUB_029070