Supplementary Table 1 The *A. fumigatus* orthologs of *C. albicans* biofilms formation transcriptional regulators

Biofilm regulators in *C.albicans*	Orthologs in *A. fumigatus*	Function in *A. fumigatus*	Identities	References
flo8	Afu7g02260 (*somA*)	Regulator of adherence, biofilm formation, development, virulence and cell wall homeostasis	23%	1-3
efg1	Afu2g07900 (*stuA*)	APSES domain transcription factor involved in regulation of conidiophore development, biofilm formation and secondary metabolism	73%	2,4-6
bcr1	Afu3g09820 (*dvrA*)	Regulator of virulence and host cell interactions	71%	7
brg1	Afu3g13870 (*nsdD*)	Regulator of asexual development, mating and putative regulator of cell wall synthesis	68%	8-10
tec1	Afu1g04830 (*abaA*)	Transcriptional activator involved in regulation of conidiation, cell death, autolysis and biogenesis of gliotoxin	48%	11,12
leu3	Afu2g03460 (*leuB*)	The Zn2Cys6-type transcription factor LeuB cross-links regulation of leucine biosynthesis and iron acquisition	43%	13
tup1	Afu6g05150 (*rocA*)	Transcriptional repressor	59%	14
zap1	Afu1g10080 (*zafA*)	The zinc-responsive transcription factor that controls the adaptive response to zinc starvation and virulence	39%	15,16
cas5	Afu1g16590 (*brlA*)	A key activator for developmental initiation and transcription factor of response to nitrogen depletion	48%	6,17,18
rim101	Afu3g11970 (*pacC*)	The pH-responsive PacC transcription factor governs epithelial entry and tissue invasion during pulmonary aspergillosis	67%	19,20

bpr1	Afu1g03210 (*flbD*)	Transcription activator governs conidium formation and development	61%	17
ada2	Afu2g10640 (*adaB*)	A subunit of the SAGA complex, involved in regulation of conidiophore development, biofilm formation and drug resistance	43%	21,22
ace2	Afu3g11250 (*ace2*)	Transcription factor governs pigment production, conidiation and virulence	45%	23
gcn4	Afu4g12470 (*cpcA*)	Regulator of amino acid biosynthesis and virulence	39%	24,25
fcr3	Afu2g02540 (*rmsA*)	Transcription factor governs gliotoxin cluster metabolites	28%	26
gzf3	Afu2g13380 (*areB*)	Regulator involved in nitrogen and carbon metabolism in *Aspergillus nidulans*	89%	27,28
snf5	Afu2g16840	Unknown function	32%	—
try2	Afu3g02380	Unknown function	42%	—
sfp1	Afu1g14750	Unknown function	66%	—
taf14	Afu5g12190	Unknown function	38%	—
war1	Afu7g01640	Unknown function	45%	—
try5	Afu2g16230	Unknown function	73%	—
gal4	Afu3g06740	Unknown function	38%	—
suc1	Afu1g17150	Unknown function	28%	—
rfg1	Afu4g10820	Unknown function	49%	—
zcf28	Afu1g01650	Unknown function	38%	—
zcf32	Afu1g01850	Unknown function	56%	—
zcf34	Afu5g01700	Unknown function	37%	—
ahr1	Afu5g11070	Unknown function	35%	—
dal81	Afu3g08050	Unknown function	32%	—

fgr27	Afu8g04540	Unknown function	29%	—
ndt80	ND	—	—	—
rob1	ND	—	—	—
rfx2	ND	—	—	—
nrg1	ND	—	—	—
try4	ND	—	—	—
try6	ND	—	—	—
als1	ND	—	—	—
als2	ND	—	—	—
als3	ND	—	—	—
hwp1	ND	—	—	—
ugm6	ND	—	—	—
tye7	ND	—	—	—
mss11	ND	—	—	—
czf1	ND	—	—	—
try3	ND	—	—	—
uga33	ND	—	—	—
zcf31	ND	—	—	—
zcf39	ND	—	—	—
zfu2	ND	—	—	—
znc1	ND	—	—	—
meT4	ND	—	—	—
not3	ND	—	—	—
sap6	ND	—	—	—

To detect the orthologs, a method called reciprocal Best Hits (RBH) was used. Orthologs are assumed if two genes each in a different genome find each other as the best hit in the other genome[29].

The descriptions of the orthologs in *A. fumigatus* are based on FungiDB database (http://fungidb.org/fungidb/) release 56, 15 Feb 2022 and NCBI-Pubmed (https://www.ncbi.nlm.nih.gov).

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