

Fig. S1. Structures of A) FR901512, B) lovastatin, and C) ML-236B (compactin), drawn in active (beta-hydroxy acid) forms.

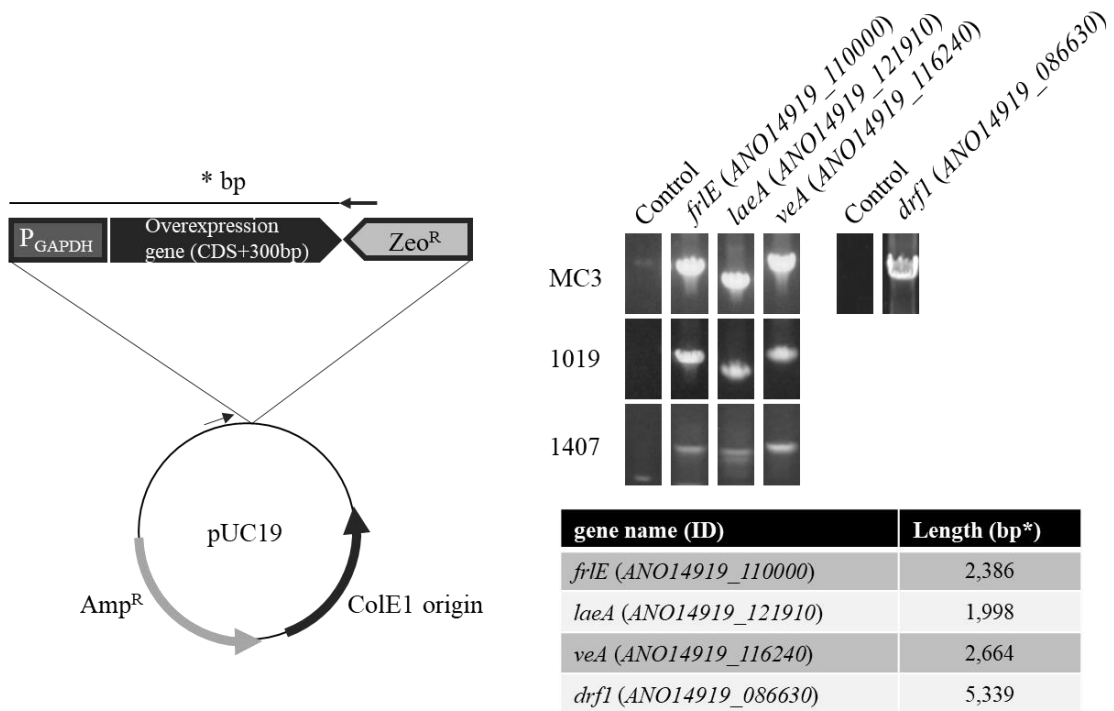


Fig. S2. Plasmid preparation for construction of overexpression mutants and direct PCR results that confirmed the construction. Primers used for confirmation were shown as arrows. Amplification length of each gene is listed in a table.

Fr1E	1	MDAGE---NSLQSLGDETQSAIGTNSAQAVRKSCDRCYVQKIKC SR TRS--PTQCQRC
LovE	1	MAADQGIFTNSVTLSPVEGSRGTGGLP RR AFRRSCDRCHAQKIKCTGNKEVTGRA PC QRC
MlcR	1	MSLPH-----AT I PTNLR RR AFRRSCDRCHAQKIKCTGSNANLVRAQCQRC
consensus	1	* * * * * * *
		←-----
		GAL4-like Zn₂Cys₆ DNA-binding domain
Fr1E	55	ERAGLKCVFGRNPRQAARTKASVPTT PS IPSSQD-----EVNOPYQ----
LovE	61	QQAGLRVCYSERCPKRKLRSRAA-----DLVSAD PDF CLHMSS
MlcR	47	QQAGLRVCYSERL PK RNLHKEAAAGTTRATE T SQPMTATSS TV FSSIAETPPPYC----S
consensus	61	..****.*... *...
		-----→
Fr1E	97	-PMMEPI I GTRGSSSSSGASSIDWLG---SFDGSEVGE L PPWSW-----RDFSGSS-NG
LovE	100	PPVPSQSI PL DVSESHSSNTSRQF-----LD PP DSYD---WSWTSIGT--DEAIDTDCW
MlcR	103	PPTHIGT S ALKETLSEPSAATLQFYDTSIN F DDPES EP ---GGWQPNTFRDDANSNESS
consensus	121	.* * * * * *
Fr1E	146	GFPDVS---DQPT-CSPPVSS T PLAA EE EPDA-----SISGYQSAFERLCMISTT
LovE	149	GISQCDGG F SCQLE PT LDL SP PFEST VE KAPLPPVSSDIARAASAQRELF DD LSAVSQE
MlcR	160	GIFD L GYDFE G PLDATAPVSPS L EDLEVEGNS---SSGQSN I SN T QRDLFESLSDVSQD
consensus	181	* * * * * *
Fr1E	192	LED CV KS I TSQQNREN VQ NT-----PIGKVI
LovE	209	LEEI LL AVTVEWPKQE I W TR ASPHSPTASRERIAQR RQ NVWAWLTDLHM F SLDPIGMFF
MlcR	216	LEV I LHGVTVEWPKQK IL SY-----PIGDFL
consensus	241	** * * * * *
Fr1E	218	GTQ EF LG IL RIQ TP GG-KLSML EG C Q TK TL LASHCYMVCLKIMEALADSF CRE M PV H
LovE	269	NASRRLL TV L RQ QAQAD CH QGTL DE CL R T K NL F TA VH CY IL NV RI LTAISELL SQ --IR
MlcR	242	NA FGR LL LH Q ERV ITSSNS S ML DG CL Q T K NL F MA VH CY ML SVKIM TS L S QL LL SE--VM
consensus	301* . * * * * * *
Fr1E	277	RRQ---SGTW H PPAA DV SG NG SKTD-----LLVSE SF SQ LY PLASY
LovE	327	RTQ---NSH M SP LE GSR SQ SPSRD DT SS SS G H SSV DT IP PF SEN LPI GEL FS Y VD PL TH A
MlcR	300	KAQ PC GQKQ STR MD WY WS GS T TR ND NG RA-----EAL PS F H SN LH IGEL I SH LDP FMHA
consensus	361	. * * * * * *
Fr1E	315	I MS ACTT LQ V GAS I L SE IE VE FG V PQ SG IA AT-N--T ST AP---MAV G GD MT PLE S DKM
LovE	384	L FS ACTT LH V GV QL L RE NE I T L GV HSAQ GIA ASIS--M S G EP GED I ART GAT NSAR CEE -
MlcR	354	L SS ACTT LR V S LR L LSE IE TAL G IAQ EH GAA AS I R LV LS D MP ST SW Q IL GAEN-----
consensus	421	* ***** . * . . * . * . . . * . . . * . . . * . . * . . . *
Fr1E	369	DQ K GF S RV FRL LEAM ME G KG G SE V S T-----TL ON FORD HAK I V RL T K Q T S SS IL ---
LovE	441	--Q PT TPAAR V LF M F LS DE GA FQ EAK S AG SR GRT IAAL RRC YED IF SLAR KHK H K GM LR DL
MlcR	407	--K TIT PAS RL L S V LS W DE AG DE E PK SK AS G KT I N V LR RCY KE I F ALAK KH N-----
consensus	481 * . * * * * * *
Fr1E	420	--A PS
LovE	499	NNI EP
MlcR	458	---I A
consensus	541	.

Fig. S3. Amino acid sequence comparison of transcription factor Fr1E, LovE and MlcR proteins showing conserved protein GAL4-like Zn₂Cys₆ DNA-binding domain.

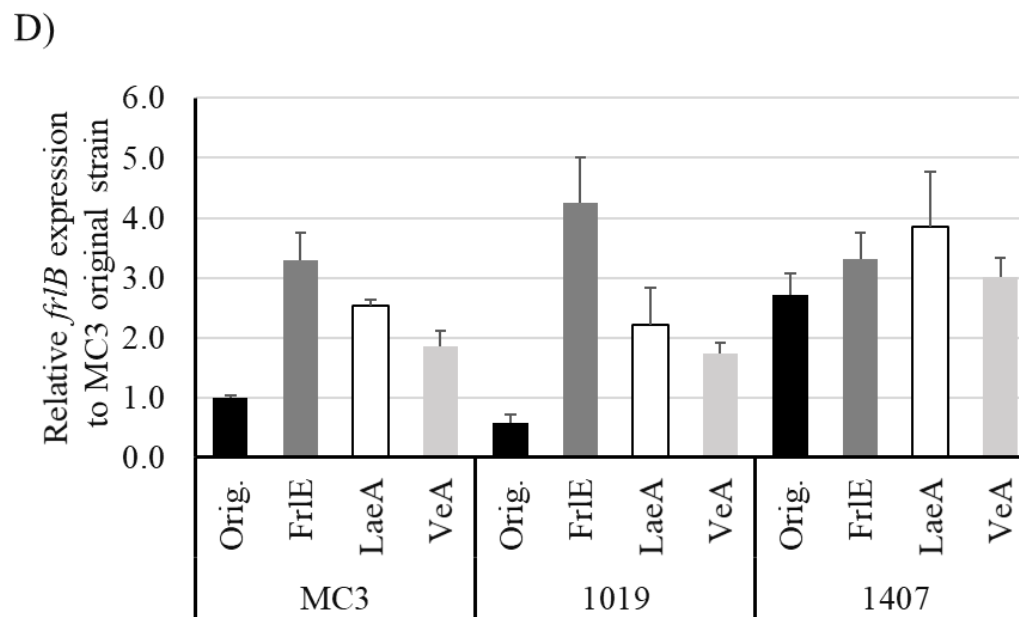
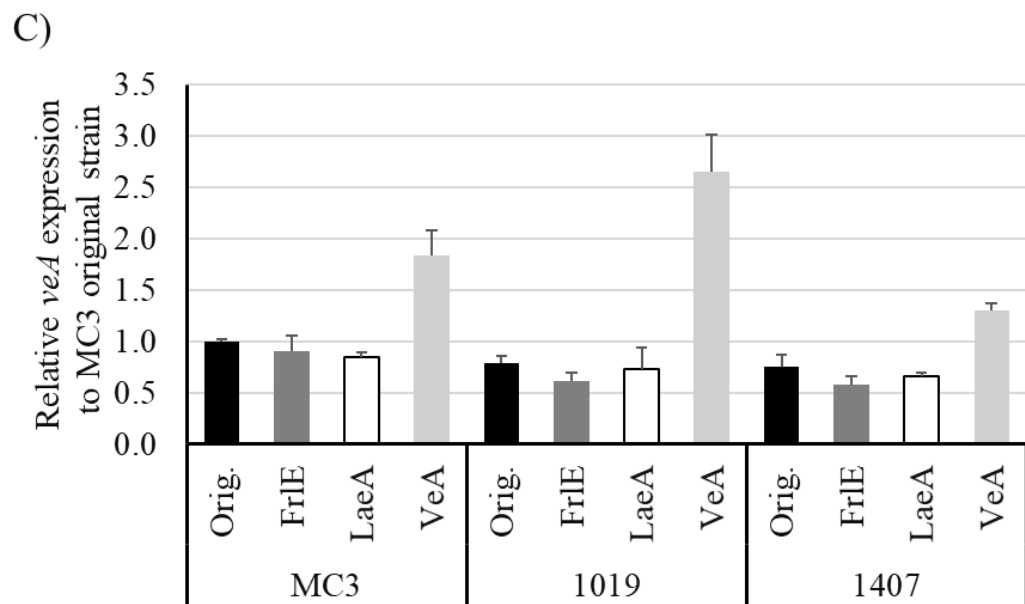
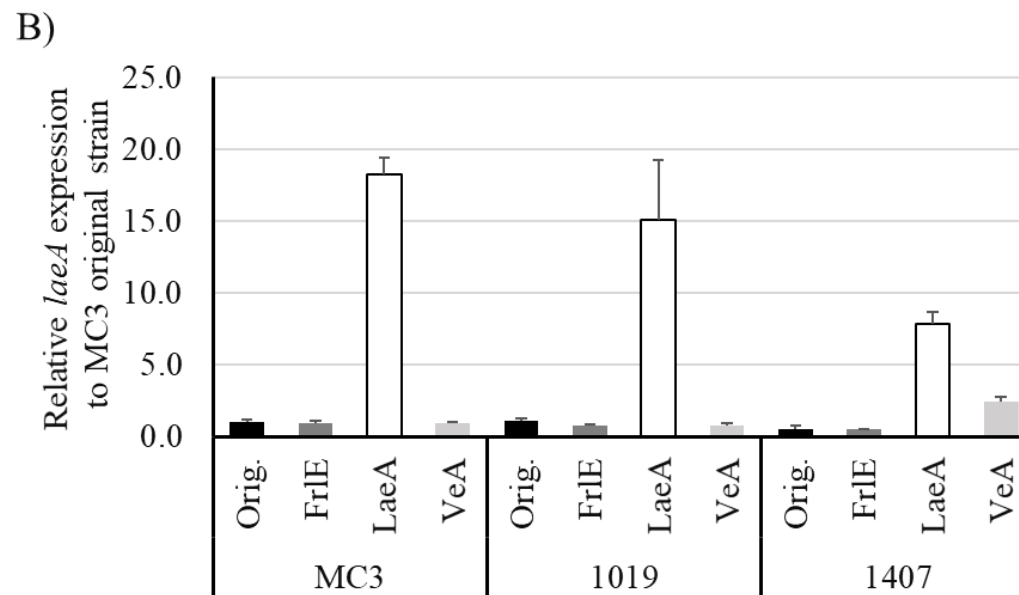
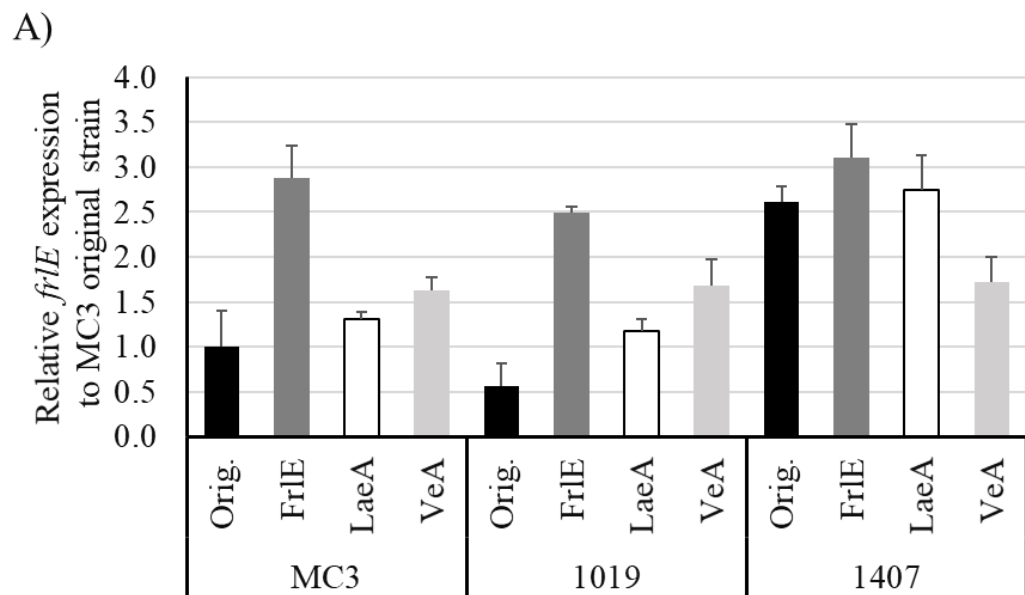


Fig. S4. Another version of Fig. 2 in different description. The relative expression levels of respective genes in each mutant to "Orig." of the MC3 strain are shown.

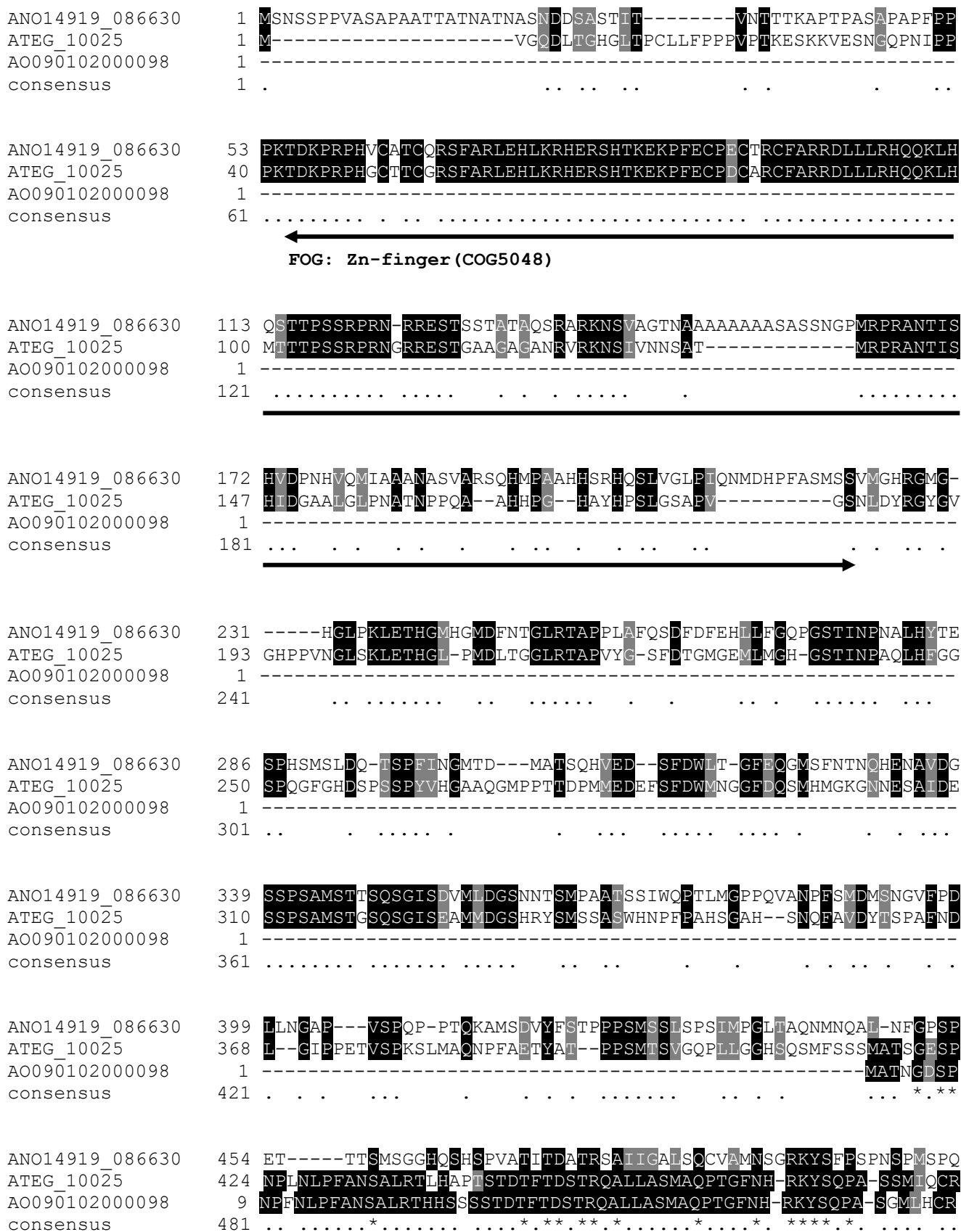



Fig. S5. Amino acid sequence comparison of Drf1 and its homologous proteins. The conserved Zn-finger domain and fungal specific transcription factor domain was displayed.

ANO14919_086630	509	IQPSQDSLPEIAKNLPSTQDLQRYVRSYLQYCHPHLPFLHIPTLSFDLPPTTS-----
ATEG_10025	482	DLFSRASFSFGSSGQLPSTPDMQRYISAYITYFHPPHMPFLHIPTLDFQAPEYTNNLRTPSG
AO090102000098	67	DLFLRSSSFNSSFPLPSTSDMQRYISAYITYFHPPHMPFLHIPTLDFQAPEYTNNLRTPSG
consensus	541* ..***** *.....*.....*.....*.....*.....*



Fungal specific transcription factor domain (pfam04082)

ANO14919_086630	562	----GRISTVGGSGCLILSMAAIGALYELERPOSRLEFEMAKKMIQLYLEERRKADMRLKA
ATEG_10025	542	HLNLSSTGVAGGGGCLILSMAAIGALYELDTASSKDLFEAAKKMIQLYLEERRKADMSSA
AO090102000098	127	HLNLSSTGVAGGGGCLILSMAAIGALYEDTAASKDLFEAAKKMIQLYLEERRKADMSSAA
consensus	601**.....*.....*.....*.....*.....*

ANO14919_086630	618	DFRRTPASDQGTQGCDPSVH--TPLWLWQAMLLNVVYGHNCGDKIANDIASTHSAAALVSLA
ATEG_10025	602	ISRSNPTRDN-----SVHNTPLWLWQAMLLNVIYGHTCGDKTSADIASTHCAALVSLA
AO090102000098	187	FSRANSARDN-----SVHNTPLWLWQAMLLNVIYGHTCGDKTSADIASTHCAALVSLA
consensus	661	. ** ..*****.....*.....*.....*.....*

ANO14919_086630	677	KAAGLLRPLQLDSTEQDIQVNDAEGN-----WNGGVKSENEEQAEWLRWKT
ATEG_10025	655	RAAGLNH--HLDAKDLPQDYLNLTGLST-----GADLEGWNSN-PGQOKERRDWDLDWKI
AO090102000098	240	RAAELTH--HLDARDLPQDYLKAGLGSRDSSQDASDPETWASS-MGPPRERKDWLDWKI
consensus	721	. ** * . *** ..*****.....*.....*.....*

ANO14919_086630	724	VEERKRTLYIIFILSSLLVTIAYNHAPALTNSEIILLDLPCDEEFFAAESAAGAFQLKGGARA
ATEG_10025	705	VEERKRTLYAIFCLSCFLVSAYNHAPALTNSEIRLDLPCQEDLWAAESPOAWKLLGGTEA
AO090102000098	297	VEERKRTLYAIFTLSCFLVSAYNHAPALTNSEIRLDLPCQEDLWAAESPOAWRKKGGPLA
consensus	781	***** ** ** * ..*****.....*.....*.....*.....*



ANO14919_086630	784	ANHNRMTFHEALGELLTNEKQOKLAFNNNHQTFGPTVN---IHDIPKSELKLPSTLGGCLV
ATEG_10025	765	S-RNGSSFSALTLLTASQREQE-----SMSGNASGGDLQFPSTFGCLV
AO090102000098	357	S-QKGLSFPALTLLTASQREQS-----QSQTPTSNNITSEDSNNNDLKPSTFGCLV
consensus	841* ..*****.....*.....*.....*

ANO14919_086630	841	LINALHNYIWETRQRHHSKVWTNEETEKMHRHIEPALKAWQSAWASNPVHSLERPFPGM
ATEG_10025	808	LIYALHNYIWETRQRHMGRQWTSRETDAMQAHIEPALRAWQTAWASNPVHSLERPYPGA
AO090102000098	409	LIYALHNYIWETRQRHMGRQWTAARETDAMQAHIEPALRAWQAAWASNPVHSLERPFPFGA
consensus	901	**.....*.....*.....*.....*.....*.....*

ANO14919_086630	901	GPLSADAIPLLDLAYVRLFVNMAKTKEMFWRDWEGLAEELSARGAETIQHAEHSPGSNAE
ATEG_10025	868	GPLSADSIPLLDLAYVRLFVNLGRCKEAFWQDWNAMSDELARGTDIVHPTDDVPA----
AO090102000098	469	GPLSADSIPLLDLAYVRLFVNLGRCKEAFWQDWNAMSDELARGTDIVNHVVEIIPP----
consensus	961	*****.....*.....*.....*.....*.....*.....*

ANO14919_086630	961	SITDPS---DASASSVVFVDSPTQSSSPEFSATKFPSS---LSTQPQSQSPGSSRVVSR
ATEG_10025	924	DVLDPSIIGEGNQATHLRDSDVADLGVSELAISKPTPTQENPMQTLTLPQRSQGQ----SK
AO090102000098	525	DVLDPSIT-ESVFHMDNRRDSDVADLGVADLAISKPTPTQEHMPTLMGVHRPGQ----SK
consensus	1021* ..*****.....*.....*.....*.....*.....*

Fig. S5 (continued). Amino acid sequence comparison of Drfl and its homologous proteins. The conserved Zn-finger domain and fungal specific transcription factor domain was displayed.

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ANO14919_086630 1015 REKHLRKAAFYAADSLMSDKLGVTFAEFSSRELVPQSAMCSFDCAQVLAEWISTLQDRV
ATEG_10025      979 RERHLRKAAFYAADSI SMSNQLGNTFAEFTCRDLPIQSAMCAFDCAQVLAEWVMTVQERV
AO090102000098 579 RERHLRKAAFYAADSI SMSDR LGNTFAEFTCRDLPIQCAMCTFDCAQVLAEWITTVQERV
consensus      1081 ** .*****.***.***.***.***.***.***.***.***.***.***.***.***.***.***

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ANO14919_086630 1075 GRYLGILGKDDVDLTAIPAVMLLEEDMKLI IKIQEILLSSAEMKMGIDIVNGTINGGFDP
ATEG_10025      1039 GPYLGLLGRDDIDLEQASNSMLLDEKDKLLDKVKEILTTIEGKMQKEVQSGASAAALSV
AO090102000098 639 GPYLGLLGRDFVDLVQASRVMLLEEDCKLLEKIKEILASVETKMQAQEVQTSATVSTLSV
consensus      1141 * .***.***.***.***.***.***.***.***.***.***.***.***.***.***.***.***

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ANO14919_086630 1135 QLQLDAM--GGYAAKILRV TACMLDKSAVWPVLNLMARCLETHAAIARTRAEKSVLATE
ATEG_10025      1099 LQRLPSVVEGGYGCKILVATASLLDRAAVVPVTKLMARSLEAQAMRLKERAESAIAESN
AO090102000098 699 LQRLPSVVEGGYGCKILVATASLLDRAAVVPVTKLMARSLEAQAMRLKERAENSAMRTD
consensus      1201 ...*.....***.***.***.***.***.***.***.***.***.***.***.***.***.***

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Fig. S5 (continued). Amino acid sequence comparison of Drf1 and its homologous proteins. The conserved Zn-finger domain and fungal specific transcription factor domain was displayed.

ANO14919_121910 1 ---MAYNG-----
LaeA2 1 MSYRETPGSFPAPDRTS LPKMFTNGDSRMRHLP--PINSPPPPKRYKSESTPASDAGHSR
LaeA1 1 MSYRESFGSFPAPDRTS LPKMFTNGDSRMRHLP--PINSPPPPKRYKSESTPASDAGHSR
LaeA-alpha 1 -----MFGNG-----HGFGQPVTMTTP-----SYNK
LaeA-beta 1 -----
consensus 1

ANO14919_121910 6 -----MNGS-----S
LaeA2 59 YYSQSVASDRVRSRQPSSAMDLYTLIDRDPVDDKPRRNARFTSNGSVATQASHTSNMSQI
LaeA1 59 YYSHSIASDRVRSRQPSSAMDLYTLIDRDPVDDKPRRNARFTSNGSVATQASHTSNMSQV
LaeA-alpha 22 FGSQSSASG--RSRTNSDAMDIVHVTITDR--DLDAREHNPGYSNWT-----
LaeA-beta 1 -----
consensus 61

ANO14919_121910 11 TTTIDPLDDRDPDW--HKWYTLRWGRHYGTFKQGRYLLPCDDIECDRLDIMHKFFLV
LaeA2 119 SRSSPIIISDRKIPEKYPNHK----ENGRMYHG YRKG VYPLPCDEEEQDRLDIFHKLFV
LaeA1 119 SRSSPIIISDRKIPEKYPNHK----ENGRMYHG YRKG IYPLPCDEEEQDRLDIFHKLFV
LaeA-alpha 63 NNGSPS IYIT--KSPEK-QYYE----ENGRLYHAYRKG VYMLPCDDEEQDRLDIFHKLFTE
LaeA-beta 1 -----MLPCDDEEQDRLDIFHKLFTE
consensus 121

ANO14919_121910 69 VREYEITAFRGLYTHRLPDRPRRILDLGCGTGIWAIDAADRLGGQGNHYHIEGWDLNLTQPE
LaeA2 175 AR----AEDGLIYAPHPGSRILDLGCGTGIW SIEVANKF--PNSFVVGVDLAPIQPA
LaeA1 175 AR----AEDGLIYAPHPGSRILDLGCGTGIW SIEVANKF--PNSFVVGVDLAPIQPA
LaeA-alpha 116 AR----VSDGLIYAPHPRNGRFLDLGCGTGIWAIDVANKY--PDAFVVGVDLAPIQPP
LaeA-beta 22 AR----VSDGLIYAPHPRNGRFLDLGCGTGIWAIDVANKY--PDAFVVGVDLAPIQPP
consensus 181 . *

Methyltransferase domain

ANO14919_121910 129 AIPPSLYFYRR-DIEEPWERVDVNSFDLIHMRTLNGSIEDWPRIYFQAFRHLKPGSGLLE
LaeA2 227 NFPKNCDFYAPFDPEAPWT-LGEDSWDI IHMQMCGGSVASWPSLYRRVFQHLRPGA-WFE
LaeA1 227 NFPKNCDFYAPFDPEAPWT-LGEDSWDI IHMQMCGGSVASWPSLYRRVFQHLRPGA-WFE
LaeA-alpha 168 NHPKNCFYAPFDYESPWA-MGEDSWDLIH LQMCGSVLGWPNLYRRIFAHLRPGA-WFE
LaeA-beta 74 NHPKNCFYAPFDYESPWA-MGEDSWDLIH LQMCGSVLGWPNLYRRIFAHLRPGA-WFE
consensus 241 . *

ANO14919_121910 188 QVEIDWRPHSDGDP RPLA-NSKLAEWSQKVHQGFARAGRKLEMDPN-TKAILEDIGFVDV
LaeA2 285 QVEIDFRPRV--EDKDGE PGRAMASWYSTLKHATEATMRPLAHS SNETIRNLQEAGFTEI
LaeA1 285 QVEIDFRPRV--EDKDGE PGRAMASWYSTLKHATEATMRPLAHS SNETIRNLQEAGFTEI
LaeA-alpha 226 QVEIDFEPRC--DDRS LD-GLALREWYQYLKRATQETMRPIAHNSRET IKDLQDAGFTEI
LaeA-beta 132 QVEIDFEPRC--DDRS LD-GLALREWYQYLKRATQETMRPIAHNSRET IKDLQDAGFTEI
consensus 301 *****

ANO14919_121910 246 EHKKIPIAFNPWPEDEHKKETARWFNLGLTQGLDALTFESVIHWLNYPEHEVREILDRVK
LaeA2 343 DHQIVGLPMNPWHPSHEQKVARWYNLAISESVQPLCLAPFSRVL SWSREQIDRIAEDVK
LaeA1 343 DHQIVGLPMNPWHPSHEQKVARWYNLAISESVQPLCLAPFSRVL SWSREQIDRIAEDVK
LaeA-alpha 283 DHQMVGLPLNPWHQDEHEKMVARWYHLAITES IETLSLAPFSRVFGWDREKIRRIASEVR
LaeA-beta 189 DHQMVGLPLNPWHQDEHEKMVARWYHLAITES IETLSLAPFSRVFGWDREKIRRIASEVR
consensus 361 . *

ANO14919_121910 306 EDICKREWRTYCTLHIYVARKPPLPGRRV
LaeA2 403 QEAFD K K I K T Y N I L H I Y Q A R K P L E E ----
LaeA1 403 QEAFD K K I K T -----
LaeA-alpha 343 SEAFNKDIHAYNILHIYQARKPPVN----
LaeA-beta 249 SEAFNKDIHAYNILHIYQARKPPVN----
consensus 421

Fig. S6. Amino acid sequence comparison of LaeA proteins showing conserved protein methyltransferase SAM binding sites. The sites are described as outline asterisks on black background. LaeA2 (BAL61197.1) and LaeA1 (BAL61196.1) of *P. citrinum*, LaeA-alpha (ARB51348.1) and LaeA-beta (ARB51350.1) of *A. terreus* were used as a reference.

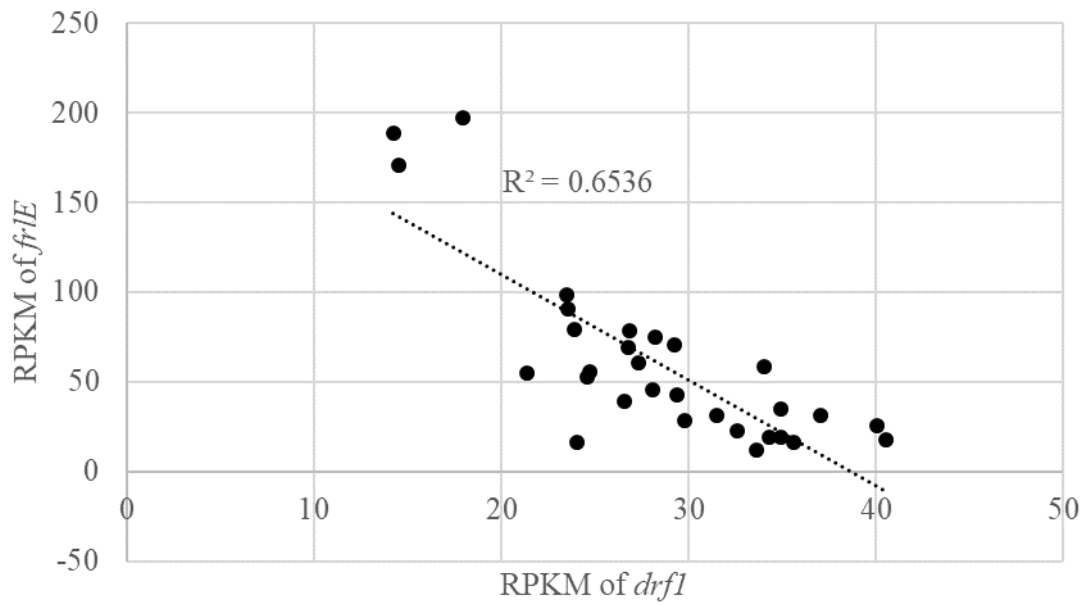


Fig. S7. Plot of RPKM values of *drf1* and *frlE*. These RPKM values in MC3 and Nos. 425, 1019, 1225 and 1407 strains at culture days 3 and 5 were plotted. The reverse correlation was confirmed at -0.81 of the correlation coefficient (R).

Table S1 (1/2)

Primers used in this study.

Purpose	Name	Sequence
Construction of overexpression plasmid	GAP_Pro_pUC_F	cggtaccgggggGATGCCATGTACCTCACAAAGTACC
	GAP_Pro_R	AATGGTGCTTTAGGTCTAGAAGGAAGAGG
	ble_F	aggagccatggcgggGGGTGGTGACGAAAATCTGCAA
	ble_pUC_R	cgactctagaggatcACTCCAACATGGAGGGGTACAGG
	frlE_oe_F	acctaagcaccattATGGATGCGGGCGAAAATCTCGC
	frlE_oe_R	cccgccatggctcctTCACGACGGGGCCAAGAGCGAA
	laeA_oe_F	acctaagcaccattATGCACAAGTTTTTCTTGGTGG
	laeA_oe_R	cccgccatggctcctTCACAGAGTACAATATGTCCGCC
	veA_oe_F	acctaagcaccattATGTTAACAATCGCTCTATCATCACAG
	veA_oe_R	cccgccatggctcctCTATGGTAACCAAAGGTGTTGTGG
	drfl_oe_F	acctaagcaccattATGTCCAATTCGTCACCGCC
	drfl_oe_R	cccgccatggctcctGGCTGTCCCTCACATAAGATCG
Sequence analysis of overexpression plasmid	GAP_P_SQ_F	CAACAGGCGTTCGGTCTACC
	M13-F	GACGGCCAGTGAATTCGAGCTC
	M13-R	TCACACAGGAAACAGCTATGAC
	frlE_SQ	GAAGTCTCTAACCAGCCAGC
	laeA_SQ	CCTCATTCTGATGGCGACCC
	veA_SQ_1	CTGCTATCTCGACCGACCTG
	veA_SQ_2	CCAAGCGAACAAGTCTTCAG
	drfl_SQ_1	GGAGCATAACGGCAGGGATC
	drfl_SQ_2	CAGCATGCTGGATGATTCA
	drfl_SQ_3	CCAATGCTTCATGGAAGGTC
	drfl_SQ_4	GTAGCATAGCCTGGACGAGC
	drfl_SQ_5	CGCTGTTTCATAGCCACACAC
	drfl_SQ_6	GCTAGTTGTGCTCATTGCAG
drfl_SQ_7	GCCAACAAGGCTTTGATGAC	
drfl_SQ_8	GTAGCGCAGACATGAGGACG	
Direct PCR for clone check	M13-F	GACGGCCAGTGAATTCGAGCTC
	ble-R	ATTGCAGATTTTCGTCACCAACC

Overlapping sequences used for In-Fusion HD cloning were expressed in lower case.

Table S1 (2/2)

Primers used in this study.

Purpose	Name	Sequence
qRT-PCR analysis of overexpressed strain	Actin_qF	GGACCGTATGCAGAAGGAGATC
	Actin_qR	ACTTGCGGTGAACGATCGAAG
	frlE_qF	GACATGACGCCCCCTTGAATCG
	frlE_qR	GACGAACGATCTTTGCGTGATCC
	laeA_qF	CATTGGCTTTGTTGATGTCGAGC
	laeA_qR	CTCGTGCTCTGGATAGTTCAGCC
	veA_qF	CCGTCTGCTCTCATGTAACCTCG
	veA_qR	GTAGGCAGGTTAAACGGTCAGC
	frlB_qF	GCTCATCACGTTCAAGCTGAAGG
	frlB_qR	CTGTCTGGTCCAGACGTCCTTC

Overlapping sequences used for In-Fusion HD cloning were expressed in lower case.

Table S2. Search result of *drf1* homologue gene in filamentous fungi.

Gene ID (Accession No.)	organism	Description	Max score	Total score	Query cover	E value	Ident
ATEG_10025 (XP_001209327.1)	<i>Aspergillus terreus</i> NIH2624 (taxid:341663)	hypothetical protein ATEG_10025 [<i>Aspergillus terreus</i> NIH2624]	974	974	95%	0	49%
-	<i>Penicillium citrianum</i> (taxid:5077)	-	-	-	-	-	-
AO090102000098 (XP_001822339.3)	<i>Aspergillus oryzae</i> RIB40 (taxid:510516)	unnamed protein product [<i>Aspergillus oryzae</i> RIB40]	699	699	61%	0	51%

Table S3. List of genes whose expression was affected by *drf1*.

Gene ID	KEGG ID	Description	Max score	Total score	Query cover	E value	Ident	Accession No.	log2 (drf1/MC3)		log2 (1407/MC3)		log2 (1407/1225)	
									day3	day5	day3	day5	day3	day5
<i>ANO14919_003870</i>	-	Epigen	30.8	30.8	15%	6.6E+00	29%	Q924X1.1	-1.34	-0.68	1.71	0.42	0.47	0.88
<i>ANO14919_010330</i>	-	Putative nudix hydrolase 7	63.9	63.9	58%	3.0E-10	26%	P91148.2	-1.60	-1.04	0.45	0.29	1.15	0.62
<i>ANO14919_010760</i>	-	Nitrogen assimilation transcription factor nirA	96.3	96.3	45%	5.0E-19	24%	P28348.1	-1.01	-0.84	1.35	1.01	0.98	1.27
<i>ANO14919_011490</i>	-	No significant similarity found.							-3.90	-3.20	0.75	0.38	1.19	1.36
<i>ANO14919_013460</i>	K19366	Satratoxin biosynthesis SC1 cluster protein 4	37.0	37.0	40%	4.7E-02	27%	A0A084B9Z2.1	*	-1.52	1.42	0.72	1.49	0.30
<i>ANO14919_017610</i>	-	Uncharacterized protein C3H1.02c	535.0	535.0	91%	2.0E-171	31%	Q10068.1	-0.39	-0.66	1.09	0.76	0.58	0.49
<i>ANO14919_022420</i>	-	Efflux pump FUS6	221.0	221.0	95%	5.0E-67	43%	W7MLD3.1	-2.09	-0.85	1.49	0.61	2.02	0.66
<i>ANO14919_023990</i>	-	Non-reducing end beta-L-arabinofuranosidase	284.0	284.0	89%	3.0E-85	33%	E8MGH8.1	-2.56	-1.34	1.01	1.12	0.83	0.76
<i>ANO14919_024000</i>	K12580	Zinc finger protein MSN2	68.2	105.0	17%	6.0E-11	55%	P33748.1	-1.07	-0.56	1.59	0.75	1.22	0.52

Table S3. (continued) List of genes whose expression was affected by *drf1*.

Gene ID	KEGG ID	Description	Max score	Total score	Query cover	E value	Ident	Accession No.	log2 (drf1/MC3)		log2 (1407/MC3)		log2 (1407/1225)	
									day3	day5	day3	day5	day3	day5
<i>ANO14919_025830</i>	-	Mitotic-spindle organizing protein 1	100.0	100.0	72%	1.0E-28	79%	A4QYG1.1	-0.46	-0.82	0.30	0.57	1.35	0.75
<i>ANO14919_028640</i>	-	Forkhead protein sep1	33.1	33.1	10%	5.9E+00	32%	O43058.1	-4.63	-3.99	2.10	0.50	0.56	0.43
<i>ANO14919_030430</i>	-	Putative NADP-dependent oxidoreductase YfmJ	266.0	266.0	99%	4.0E-86	44%	O34812.1	-0.93	-0.36	1.65	2.39	1.51	1.51
<i>ANO14919_038080</i>	K11483	Uncharacterized N-acetyltransferase YsnE	32.0	32.0	18%	2.5E+00	31%	P94562.1	-0.94	-0.55	1.34	1.11	0.63	0.60
<i>ANO14919_040320</i>	-	Ankyrin repeat and SOCS box protein 3	55.5	55.5	31%	7.0E-07	30%	Q9Y575.1	-2.42	-1.30	1.36	1.39	0.84	1.30
<i>ANO14919_041010</i>	-	Efflux pump patC	399.0	399.0	96%	3.0E-132	40%	A1CFL0.1	-0.45	-0.89	1.98	0.29	2.45	0.67
<i>ANO14919_046120</i>	-	No significant similarity found.							-1.04	-1.04	1.03	0.39	0.69	0.81
<i>ANO14919_051740</i>	-	No significant similarity found.							-2.90	*	3.57	1.66	2.23	1.70
<i>ANO14919_053640</i>	-	Transcriptional repressor NrdR	27.3	27.3	33%	5.2E+00	56%	Q983B3.1	-2.58	*	0.70	2.26	0.90	4.39

Table S3. (continued) List of genes whose expression was affected by *drf1*.

Gene ID	KEGG ID	Description	Max score	Total score	Query cover	E value	Ident	Accession No.	log2		log2		log2	
									(drf1/MC3)		(1407/MC3)		(1407/1225)	
									day3	day5	day3	day5	day3	day5
<i>ANO14919_059150</i>	-	No significant similarity found.							-1.25	-2.50	3.17	1.63	2.04	0.47
<i>ANO14919_059330</i>	-	Uncharacterized MFS-type transporter C1683.03c	264.0	264.0	87%	1.0E-80	34%	Q9P6J7.1	-3.65	-7.24	6.11	2.52	2.09	1.06
<i>ANO14919_059340</i>	-	No significant similarity found.							-2.70	-6.25	5.94	2.36	2.73	0.44
<i>ANO14919_059720</i>	-	Berberine bridge enzyme-like 26	78.2	78.2	33%	4.0E-14	29%	Q9FKU8.1	-1.70	-1.88	5.50	2.87	2.03	0.73
<i>ANO14919_061820</i>	-	NACHT, LRR and PYD domains-containing protein 4B	31.6	31.6	13%	9.8E+00	38%	Q8C6J9.1	-0.41	-0.53	1.91	1.84	0.84	0.44
<i>ANO14919_062740</i>	K00750	Lon protease homolog 2, peroxisomal	31.2	31.2	13%	4.1E+00	45%	Q2V573.1	-1.32	-0.62	0.30	0.90	2.21	0.30
<i>ANO14919_063230</i>	-	FAD-dependent monooxygenase BOA8	145.0	145.0	99%	1.0E-37	31%	G0LET6.1	-2.38	-1.18	1.16	0.98	1.18	1.89
<i>ANO14919_063240</i>	-	Homoserine O-acetyltransferase	28.1	28.1	45%	6.8E+00	35%	B8IZQ7.1	-4.51	-1.51	1.65	0.64	1.63	1.68
<i>ANO14919_063250</i>	-	Probable feruloyl esterase B-2	145.0	145.0	79%	1.0E-40	59%	B8NPT0.1	-1.70	-2.14	0.98	0.44	0.91	0.96

Table S3. (continued) List of genes whose expression was affected by *drf1*.

Gene ID	KEGG ID	Description	Max score	Total score	Query cover	E value	Ident	Accession No.	log2 (drf1/MC3)		log2 (1407/MC3)		log2 (1407/1225)	
									day3	day5	day3	day5	day3	day5
<i>ANO14919_063260</i>	-	Replication-associated protein	28.5	28.5	76%	7.4E+00	27%	Q80GM6.2	-0.91	-1.62	1.02	0.95	0.98	1.18
<i>ANO14919_069190</i>	-	Periplasmic beta-glucosidase	282.0	282.0	97%	1.0E-82	31%	P33363.2	-1.32	-1.07	0.86	1.12	0.67	0.79
<i>ANO14919_070800</i>	-	No significant similarity found.							-1.16	-0.75	1.96	1.23	1.42	0.71
<i>ANO14919_075280</i>	K08192	Acyl-CoA synthetase short-chain family member 3, mitochondrial	496.0	496.0	95%	4.0E-166	41%	Q9H6R3.1	-0.70	-1.44	0.97	0.28	0.74	0.51
<i>ANO14919_076630</i>	-	Uncharacterized transcriptional regulatory protein C1773.12	37.4	37.4	75%	1.4E-01	23%	O94569.1	-1.38	-0.71	1.35	0.99	1.10	0.37
<i>ANO14919_079220</i>	-	Probable cytosol aminopeptidase	33.9	33.9	9%	3.2E+00	36%	O32956.1	-2.48	-1.23	2.32	1.11	1.30	2.27
<i>ANO14919_079750</i>	-	No significant similarity found.							-2.99	-0.59	2.13	3.07	0.56	1.45
<i>ANO14919_082030</i>	-	No significant similarity found.							-1.30	-2.41	3.61	2.05	1.05	1.07

Table S3. (continued) List of genes whose expression was affected by *drf1*.

Gene ID	KEGG ID	Description	Max score	Total score	Query cover	E value	Ident	Accession No.	log2 (drf1/MC3)		log2 (1407/MC3)		log2 (1407/1225)	
									day3	day5	day3	day5	day3	day5
<i>ANO14919_083960</i>	-	Halotolerance protein 9	44.3	44.3	7%	3.0E-03	40%	Q12180.1	-1.29	-0.48	0.94	1.59	1.00	0.73
<i>ANO14919_086180</i>	-	Regulatory protein cys-3	45.4	45.4	27%	5.0E-04	29%	P22697.1	-1.09	-1.10	1.12	1.70	0.99	0.40
<i>ANO14919_088480</i>	-	No significant similarity found.							-1.23	*	0.41	2.18	1.22	1.88
<i>ANO14919_089660</i>	-	Alkaline phosphatase H	92.0	92.0	51%	4.0E-19	35%	P35483.2	-1.38	-0.43	0.89	1.96	0.63	0.43
<i>ANO14919_092390</i>	-	Vacuolar basic amino acid transporter 1	126.0	126.0	55%	1.0E-29	30%	Q04301.1	-0.59	-0.53	0.58	0.52	0.41	0.38
<i>ANO14919_095610</i>	-	No significant similarity found.							-2.12	-1.01	0.66	1.81	1.56	1.39
<i>ANO14919_097970</i>	-	2,4-dichlorophenol 6-monooxygenase	419.0	419.0	99%	5.0E-139	39%	Q8KN28.3	-2.10	-0.45	1.60	1.02	1.44	0.84
<i>ANO14919_101040</i>	K17807	Enolase	34.3	34.3	7%	3.5E+00	36%	C4Z1M9.1	-1.01	-1.70	1.43	0.39	1.29	0.28
<i>ANO14919_102660</i>	-	SEC14 cytosolic factor	118.0	118.0	71%	5.0E-29	28%	Q75DK1.2	-0.88	-0.76	0.98	1.07	0.38	0.41

Table S3. (continued) List of genes whose expression was affected by *drf1*.

Gene ID	KEGG ID	Description	Max score	Total score	Query cover	E value	Ident	Accession No.	log2 (drf1/MC3)		log2 (1407/MC3)		log2 (1407/1225)	
									day3	day5	day3	day5	day3	day5
<i>ANO14919_103830</i>	-	Protein CfxQ	134.0	301.0	58%	2.0E-33	36%	P23013.1	-0.62	-1.09	2.17	2.61	0.72	1.58
<i>ANO14919_106840</i>	K00108	MICAL-like protein 2	35.0	35.0	26%	7.2E-01	32%	D3ZEN0.2	-1.56	-0.67	2.03	1.34	0.46	0.64
<i>ANO14919_107950</i>	K15877	Uncharacterized transporter YIL166C	406.0	406.0	84%	1.0E-134	42%	P40445.1	-0.69	*	4.52	2.12	3.83	2.55
<i>ANO14919_109940 (frID)</i>	-	Transesterase (FR901512 biosynthetic gene)	-	-	-	-	-	-	-1.75	-1.63	3.69	1.90	3.12	2.17
<i>ANO14919_109950 (frIG)</i>	-	Thioesterase (FR901512 biosynthetic gene)	-	-	-	-	-	-	-1.04	-0.69	3.08	2.08	2.45	1.94
<i>ANO14919_109960 (frIC)</i>	-	Enoyl reductase (FR901512 biosynthetic gene)	-	-	-	-	-	-	-1.52	-1.24	3.54	2.17	2.99	2.13
<i>ANO14919_109970 (frIA)</i>	-	P450 monooxygenase (FR901512 biosynthetic gene)	-	-	-	-	-	-	-1.69	-2.55	2.91	1.22	2.81	1.64

Table S3. (continued) List of genes whose expression was affected by *drf1*.

Gene ID	KEGG ID	Description	Max score	Total score	Query cover	E value	Ident	Accession No.	log2		log2		log2	
									(drf1/MC3)	day3	day5	(1407/MC3)	day3	day5
<i>ANO14919_109980</i>	-	Polyketide Synthase (FR901512 biosynthetic gene)	-	-	-	-	-	-	-2.07	-2.43	3.13	1.50	2.92	1.81
<i>ANO14919_114840</i>	-	Hydroxymethylglutaryl-CoA synthase	590.0	590.0	99%	0.0E+00	62%	P54874.1	-1.11	-0.97	0.87	0.38	1.05	0.34
<i>ANO14919_118640</i>	-	Probable 1-alkyl-2-acetylgllycerophosphocholine esterase	142.0	142.0	97%	1.0E-37	30%	D4AZY1.1	-3.95	-3.01	1.09	1.95	0.91	1.16
<i>ANO14919_119550</i>	-	Beta-glucosidase	32.7	32.7	13%	2.0E+00	48%	P07337.1	-1.82	*	0.84	1.48	0.92	0.84
<i>ANO14919_124110</i>	K13093	B3 domain-containing transcription repressor VAL1	33.5	33.5	26%	2.6E+00	34%	Q8W4L5.1	-1.31	-1.58	2.26	2.73	0.55	1.34
<i>ANO14919_125450</i>	-	Pantothenate transporter liz1	386.0	386.0	99%	9.0E-129	41%	O43000.2	-2.13	-2.42	0.60	0.97	0.68	1.39
<i>ANO14919_125800</i>	-	No significant similarity found.							-1.75	-0.43	0.37	0.97	1.23	1.21
<i>ANO14919_127530</i>	-	(+)-eremophilene synthase	100.0	100.0	48%	2.0E-24	55%	S0DX56.1	-0.37	-4.30	2.45	0.85	2.88	1.41

Table S3. (continued) List of genes whose expression was affected by *drf1*.

Gene ID	KEGG ID	Description	Max score	Total score	Query cover	E value	Ident	Accession No.	log2 (drf1/MC3)		log2 (1407/MC3)		log2 (1407/1225)	
									day3	day5	day3	day5	day3	day5
<i>ANO14919_129040</i>	-	No significant similarity found.							*	-3.94	3.83	3.03	0.35	0.96
<i>ANO14919_131620</i>	-	Isoaspartyl peptidase	160.0	160.0	29%	4.0E-42	36%	Q7CQV5.1	*	-0.55	0.75	0.40	2.21	0.95
<i>ANO14919_142050</i>	-	Heterokaryon incompatibility protein S	110.0	110.0	100%	5.0E-28	27%	B2ACC7.1	-1.83	-1.59	1.24	0.39	0.84	1.08
<i>ANO14919_144960</i>	-	Drug resistance protein YOR378W	187.0	187.0	70%	1.0E-51	33%	Q08902.1	-3.03	-2.00	2.01	1.74	1.01	1.57

The Blast search result of each gene and the fold change value of expression are described. The case, in which the expression level after affected by *drf1* is 0, is indicated by *.

Table S4. The fold change value of secondary metabolite genes in fungal sp. No. 14919.

Gene ID	Gene cluster type	log2(<i>drf1</i> /MC3)		log2(1407/MC3)	
		day3	day5	day3	day5
<i>ANO14919_017950</i>	T1PKS	-1.91	-1.62	-0.34	-0.71
<i>ANO14919_026880</i>	Terpene	-1.78	0.28	-1.15	1.68
<i>ANO14919_029360</i>	NRPS	2.14	1.73	0.00	-3.70
<i>ANO14919_033500</i>	Other	-0.75	-0.45	0.31	1.04
<i>ANO14919_041050</i>	NRPS	2.54	0.69	3.20	-0.10
<i>ANO14919_043060</i>	T1PKS	0.27	-1.45	-2.27	-3.70
<i>ANO14919_043340</i>	T1PKS	-2.59	-1.26	0.28	-1.54
<i>ANO14919_046260</i>	Other	-0.93	-0.73	-0.12	-0.69
<i>ANO14919_051690</i>	Terpene	-0.18	0.08	-1.98	-2.45
<i>ANO14919_053210</i>	T1PKS	1.17	1.21	-0.58	-0.61
<i>ANO14919_053300</i>	T1PKS	2.06	-0.70	1.76	-2.38
<i>ANO14919_053420</i>	T1PKS	0.96	0.85	-2.46	0.94
<i>ANO14919_054390</i>	T1PKS	0.46	1.91	*	0.00
<i>ANO14919_055580</i>	T1PKS	-0.26	0.45	-3.60	-0.26
<i>ANO14919_056580</i>	T1PKS	-1.16	-1.32	-0.88	-1.44
<i>ANO14919_060780</i>	T1PKS	1.87	-1.65	9.98	-1.06
<i>ANO14919_063150</i>	T1PKS	-0.09	0.95	-2.19	-1.30
<i>ANO14919_064510</i>	T1PKS	0.06	0.11	-0.60	-1.23
<i>ANO14919_066200</i>	T1PKS	-0.49	0.32	-0.41	-1.47
<i>ANO14919_066680</i>	T1PKS	-2.04	-0.49	-2.16	0.43
<i>ANO14919_069210</i>	Terpene	**	-0.19	**	0.70
<i>ANO14919_069500</i>	Other	1.99	-0.11	-0.41	-1.00
<i>ANO14919_069660</i>	T1PKS	0.92	-0.42	0.47	-0.44
<i>ANO14919_070760</i>	T1PKS	4.59	4.29	-1.38	-0.48
<i>ANO14919_073600</i>	Other	-0.76	-1.82	-0.94	-1.24
<i>ANO14919_074860</i>	T1PKS-NRPS	-0.38	0.93	0.94	-1.87
<i>ANO14919_075550</i>	T1PKS	1.51	-2.07	0.51	-3.39
<i>ANO14919_075570</i>	NRPS	-1.60	-1.37	-0.81	-3.61
<i>ANO14919_079710</i>	T1PKS	**	*	**	2.70
<i>ANO14919_082590</i>	T1PKS-NRPS	**	0.00	**	1.32
<i>ANO14919_085260</i>	T1PKS	-0.47	-0.34	-1.75	-1.25

Table S4. (continued) The fold change value of secondary metabolite genes in fungal sp. No. 14919.

Gene ID	Gene cluster type	log2(<i>drf1</i> /MC3)		log2(1407/MC3)	
		day3	day5	day3	day5
<i>ANO14919_087960</i>	NRPS	-5.17	**	*	**
<i>ANO14919_089730</i>	Other	-0.59	0.18	0.49	1.76
<i>ANO14919_090610</i>	Other	**	**	**	**
<i>ANO14919_091750</i>	Terpene	0.89	0.19	-4.11	-3.93
<i>ANO14919_092940</i>	T1PKS	-0.60	0.12	0.11	-0.05
<i>ANO14919_093480</i>	T1PKS	0.45	0.69	-0.22	-0.82
<i>ANO14919_096270</i>	T1PKS	-2.44	-2.18	-3.24	-1.40
<i>ANO14919_097410</i>	T1PKS	1.67	1.68	1.34	4.03
<i>ANO14919_103570</i>	T1PKS	**	**	**	**
<i>ANO14919_104050</i>	NRPS	0.04	0.02	-1.15	-1.07
<i>ANO14919_105450</i>	Terpene	0.40	0.87	-0.53	0.11
<i>ANO14919_107290</i>	Terpene	-0.34	-0.19	0.90	0.71
<u><i>ANO14919_109980</i></u>	<u>T1PKS</u>	<u>-2.07</u>	<u>-2.43</u>	<u>3.13</u>	<u>1.50</u>
<i>ANO14919_110090</i>	T1PKS	0.75	-2.09	1.98	0.36
<i>ANO14919_110610</i>	T1PKS	-1.00	3.75	-0.12	2.81
<i>ANO14919_113090</i>	Other	-0.25	-0.14	-3.33	-0.03
<i>ANO14919_115540</i>	Other	1.00	0.97	4.25	2.38
<i>ANO14919_116520</i>	Other	**	**	**	**
<i>ANO14919_116660</i>	NRPS	-0.85	-0.66	-0.76	-1.23
<i>ANO14919_116900</i>	T1PKS	0.97	0.22	-0.40	-1.61
<i>ANO14919_117890</i>	T1PKS	-0.61	1.23	-1.30	-2.77
<i>ANO14919_126310</i>	Terpene	-2.32	-4.32	-0.11	-1.44
<i>ANO14919_138060</i>	NRPS	-2.34	0.19	-1.81	-0.40
<i>ANO14919_139500</i>	T3PKS	-1.86	-4.23	1.27	-6.51
<i>ANO14919_141970</i>	Other	-1.00	**	*	**
<i>ANO14919_142930</i>	T1PKS	-2.07	-2.00	0.36	-0.13
<i>ANO14919_143200</i>	Other	-1.78	-0.67	-5.90	0.13

The fold change values of *drf1* overexpression strain and 1407 strain from MC3 are shown. The case, in which the expression level of comparative strain is 0, is indicated by * and in which the expression level of MC3 is 0, is indicated by **. *ANO14919_109980* encoding FR901512 biosynthetic PKS is underlined. The words “T1 (or T3) PKS (T3PKS)” and “NRPS” mean “Type 1 (or Type 3) polyketide synthase” and “Non-ribosomal peptide synthetase”.