Applied Microbiology and Biotechnology

Supplementary Material

FvatfA regulates growth, stress tolerance as well as mycotoxin and pigment productions in *Fusarium verticillioides*

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Supplementary Tables

Supplementary Table S1. Homologies between FvAtfA orthologous proteins identified in various fungal species.

Species	**Expect value (blastp to FVEG_02866)**	**Name**	**NCBI Accession number**
Fusarium verticillioides	0.0	FVEG_02866 hypothetical protein (FvAtfA)	XP_018746682.1
Fusarium oxysporum f. sp. cubense	0.0	FoAtf1 (Qi et al. 2013)	TVY66251.1
Fusarium graminearum	0.0	FgAtf1 (Nguyen et al. 2013; Jiang et al. 2015)	XP_011319081.1
Aspergillus nidulans	3e-96	AtfA (Hagiwara et al. 2009; Balázs et al. 2010)	ACJ61780.1
Aspergillus oryzae	3e-96	AtfA (Sakamoto et al. 2009)	XP_001819834.1
Aspergillus fumigatus	2e-102	AtfA (Hagiwara et al. 2014)	XP_754486.2
Schizosaccharomyces pombe	1e-33	Atf1 (Takeda et al. 1995)	BAA12194.1
Homo sapiens	4e-21	ATF-2 (Venter et al. 2001)	EAX11109.1
Claviceps purpurea	4e-149	CPTF1 (Nathues et al. 2004)	CCE33955.1
Magnaporthe oryzae	8e-122	Moatf1 (Guo et al. 2010)	XP_003715195.1
Botrytis cinerea	6e-32	BcAtf1 (Temme et al. 2012)	CCD34747.1
Penicillium marneffei	6e-87	AtfA (Nimmanee et al. 2014)	XP_002143956.1
Neurospora crassa	9e-147	ATF-1 (Colot et al. 2006)	XP_011394512.1

Supplementary Table S2. Oligonucleotides used in this study

Name	Sequence (5’-3’)	Purpose
Primers used to generate the gene deletion and complemented strains		
FvatfAupfwd	TTCATTCTGGGTTCCTTCTATGGC	5’-flanking region of *FvatfA*
FvatfAdownrev	TCCTCCTTGTCGATGTTCTTTTAG	3’-flanking region of *FvatfA*
FvatfAupkimrev	TCACTGGCCGTCGTTTTACAAAGATCCGCCGGCCTGAACCGCGAA	5’ *FvatfA* with *hph* tail
FvatfAdownkimfwd	CATGGTCATAGCTGTTTCCTGACTTCATTTCGCGTTTGAGCTGTA	3’ *FvatfA* with *hph* tail
FvatfAnestedfwd	ACAGTGCCTACAGTGTGAAGCAGG	5’ nested of *FvatfA*
FvatfAnestedrev	GGTTCCATTTGTTGTCGGTGCCTT	3’ nested of *FvatfA*
M13F	TTGTAAAACGACGGCCAGTGA	5’ *hph*/*gen* marker gener
M13R	CAGGAAACAGCTATGACCATG	3’ *hph*/*gen* marker gene
FvatfAcompkimfwd	CATGGTCATAGCTGTTTCCTGACAGTGCCTACAGTGTGAAGCAGG	5’ *FvatfA* with *gen* tail
FvatfAcomprev	TCTCAATCGCAGCTTGTGTTGCTT	3’ *FvatfA* flaking region outside the terminator region
Primers used in copy number determinations		
FVEG2866shortfwd	CTTGAGGACGGGTTTGACAC	forward primer of the *FvatfA* gene
FVEG2866shortrev	CGCTTCGGACTTATTGGTTG	reverse primer of the *FvatfA* gene
FVEG11192shortfwd	CAAGCACCACCAGACCTATGT	forward primer of the *FvmnSOD* gene
FVEG11192shortrev	CTCCCAAGCGTCAATACCG	reverse primer of the *FvmnSOD* gene
Primers used in qRT-PCR experiments		
carRAF	AGCAAACCGACCTTTCAC	forward primer of the *carRA* gene
carRAR	CCATCCCACAAGACAATG	reverse primer of the *carRA* gene
carBF	CTTCTCCTCCCTCGCTTCTTC	forward primer of the *carB* gene
carBR	CTCGCCAGACTCAAAATGCTAG	reverse primer of the *carB* gene
carTF	ATGAGTGGATTGCTGATGTG	forward primer of the *carT* gene
carTR	GGGGTTGAAGAGTTGAAGG	reverse primer of the *carT* gene
fum1F	ACAGCCCAAGCAGTAAGC	forward primer of the *fum1* gene
fum1R	CACCCGACACACGATATG	reverse primer of the *fum1* gene
fum8F	AGCATCCAACAGAAATACGC	forward primer of the *fum8* gene
fum8R	GCCTCTCTCATTGAAACGAC	reverse primer of the *fum8* gene
fum21F	CCATTACAAGCCATTCCAC	forward primer of the *fum21* gene
fum21R	ACAAGCCACGATTTAGACG	reverse primer of the *fum21* gene
bik1F	GAGCACACACCAACCATTC	forward primer of the *bik1* gene
bik1R	GACTGAGCCGAGATACAAGC	reverse primer of the *bik1* gene
tef1F	GAGCGTGAGCGTGGTATC	forward primer of the *tef1* reference gene
tef1R	CGAGGGTGTAGGCAAGAAG	reverse primer of the *tef1* reference gene
tub2F	CGGTCAGTGCGGTAACCAA	forward primer of the *tub2* reference gene
tub2R	GGCTCGGGGAACATACTTGT	reverse primer of the *tub2* reference gene
cyp2F	CTACCCCGCCATAACTGCTT	forward primer of the *cyp2* reference gene
cyp2R	AGAGCACGGAAGTTCTCAGC	reverse primer of the *cyp2* reference gene

Supplementary Table S3. Names and functions of *Fusarium verticillioides* genes used in qRT-PCR experiments

Name	**Accession number**	**Function**	**Reference**
fum1	FVEG_00316	polyketide synthase essential for fumonisin production	Butchko et al. 2012
fum8	FVEG_14635	α-oxoamine synthase	Lazzaro et al. 2012
fum21	FVEG_14633	transcription factor with Zn(II)2Cys6 DNA-binding domain	Butchko et al. 2012
carRA	FVEG_10718	bifunctional enzyme with phytoene synthase and carotene cyclase activities	Ádám et al. 2011
carB	FVEG_10717	carotene desaturase	Ádám et al. 2011
carT	FVEG_09251	carotene-cleaving oxygenase	Ádám et al. 2011
bik1	FVEG_03379	polyketide synthase essential for bikaverin production	Lazzaro et al. 2012
tef1	FVEG_02381	translation elongation factor 1-α	Brown et al. 2007
tub2	FVEG_04081	β-tubulin	Lazzaro et al. 2012
cyp2	FVEG_00403	putative cyclophilin	Johnson et al. 2018

Supplementary Table S4. Results of the *in silico* promoter analyses for putative ATF/CREB transcription factor binding motifs

Transcription factor	ID	Species
ATF	[T00049]	*Saccharomyces cerevisiae*
ATF	[T00051]	*Homo sapiens*
ATF-1	[T00968]	*Homo sapiens*
ATF-2	[T00167]	*Homo sapiens*
ATF3	[T01313]	*Homo sapiens*
CREB	[T00163]	*Homo sapiens*
CREB	[T00164]	*Rattus norvegicus*
CREB	[T00989]	*Mus musculus*
CRE-BP2	[T01017]	*Mus musculus*

Gene	Transcription factor	ID	Sequence	Position	Dissimilarity (%)
fum1	ATF3	[T01313]	TGACTCAA	- 464 - -457	7.45
			TGACATCT	-360 - -353	7.45
fum8	ATF3	[T01313]	TGACTTGT	-162 - -155	4.93
			TGACTACC	107-114	12.39
			TGACATCC	125-132	8.66
			ATCCGTCA	209-216	7.45
			CCTAGTCA	359-369	13.59
			TGACTCGA	384-391	8.66
			GAAAGTCA	452-459	6.14
			TTGTGTCA	486-493	11.18
fum21	ATF3	[T01313]	ATTAGTCA	63-70	11.18
			TATCGTCA	205-212	8.66
			TGACAGAT	591-598	14.91
			TGACTACT	742-749	11.18
			CCAAGTCA	780-787	6.14
			TCCCGTCA	791-798	8.66
			CATAGTCA	807-814	13.59
			TGACGCCT	949-956	3.73
			TGACTGTA	1064-1071	12.39

Gene	Transcription factor	ID	Sequence	Position	Dissimilarity (%)
carRA	ATF	[T00049]	CGTGACGTCA	254-263	0.48
			TGACGTCAAC	256-265	0.24
	ATF	[T00051]	GTGACGTCA	255-263	0.31
			TGACGTCAA	256-264	0.54
	ATF-2	[T00167]	GTGACGTCA	255-263	0.00
			TGACGTCAA	256-264	0.05
	ATF-1	[T00968]	CGTGACGTCAA	254-264	4.58
			GTGACGTCAAC	255-265	2.83
	ATF3	[T01313]	GTATGTCA	-76 - -83	8.66
			ATTTGTCA	114-121	14.91
			ACGCGTCA	121-128	4.93
			CAATGTCA	160-167	9.86
			TGACGTCA	256-263	0.00
			TGACAGAA	285-292	14.91
			TGACTCTG	477-484	9.86
	CREB	[T00163]	GTGACGTCA	255-263	0.02
			TGACGTCAA	256-264	0.02
	CREB	[T00164]	GTGACGTCA	255-263	0.00
			TGACGTCAA	256-264	0.02
	CRE-BP2	[T01017]	GTGACGTCA	255-263	0.00
			TGACGTCAA	256-264	0.47
			ATGCCGTCA	508-516	13.99
			TGCCGTCAC	509-517	13.52
	CREB	[T00989]	CGTGACGTCA	254-263	0.00
			TGACGTCAAC	256-265	0.48
			TGCCGTCACG	509-518	14.72
carB	ATF	[T00049]	GAAGACGTCA	204-213	2.28
	ATF	[T00051]	AAGACGTCA	205-213	1.29
	ATF-1	[T00968]	GAAGACGTCAT	204-214	3.49
	ATF-2	[T00167]	AAGACGTCA	205-213	1.85
	ATF3	[T01313]	ACCCGTCA	23-30	8.66
			GATCGTCA	33-40	9.86
			AGACGTCA	206-213	0.00
			TGACTCTA	215-222	8.66
			TGACTGAG	267-274	12.39
	CREB	[T00989]	GAAGACGTCA	204-213	6.12
	CREB	[T00163]	AAGACGTCA	205-213	0.86
	CREB	[T00164]	AAGACGTCA	205-213	3.17
	CRE-BP2	[T01017]	AAGACGTCA	205-213	13.99
			AGACGTCAT	206-214	13.99

Gene	Transcription factor	ID	Sequence	Position	Dissimilarity (%)
carT	ATF3	[T01313]	TTCCGTCA	-56 - -63	7.45
			TCGAGTCA	22-29	8.66
			ACTCGTCA	180-187	8.66
			TAGGGTCA	212-219	12.39
			AAGAGTCA	395-402	8.66
			AGTCGTCA	418-425	7.45
			TCTCGTCA	482-489	8.66
			TGTCGTCA	580-587	7.45
			TAGCGTCA	814-821	4.93
			TGACTTTA	823-830	4.93
			TGACGACA	959-966	7.45
	CRE-BP2	[T01017]	TTGTCGTCA	579-587	13.99
			TGTCGTCAG	580-588	13.99
			ATGACGACA	958-966	13.99
			TGACGACAG	959-967	13.99
bik1	ATF3	[T01313]	TGACTCGA	-67 - -60	8.66
			TGACCCTG	71-78	13.59
			AAGGGTCA	158-165	12.39
	CREB	[T00164]	CAAGGAGAG	-172 - -164	10.36
			CTGACCCTG	70-78	14.90

* - Positions are counted starting from the TSS of the DNA sequence of genes selected for promoter analyses (Supplementary Figure S6).

Supplementary Table S5. Results of One-Way ANOVA analysis.

Studied property		**Strains**				**One-Way ANOVA**	**Tukey post hoc test**			**Number of biological replicates with each strain**
		FGSC 7600 (A)	***ΔFvatfA* (B)**	***FvatfA* 'C (H7) (C)**	***FvatfA* 'C (H9) (D)**	**p - value (p <)**	**adj. p-value**			
							B vs. A	**B vs. C**	**B vs. D**	
Vegetative growth (colony diameter. mm)	**Czapek-Dox agar plates**	79.50±0.60	70.13±1.15	77.75±1.39	77.92±1.51	2.20E-16	0.00E+00	0.00E+00	0.00E+00	3
	Potato Dextrose agar plates	81.83±0.39	63.71±1.12	82.00±0.43	82.08±0.29	2.20E-16	0.00E+00	0.00E+00	0.00E+00	3
Invasive growth (colony diameter. mm)	**72 h tomato**	7.92±2.07	2.25±0.87	6.58±1.38	7.42±1.98	1.19E-10	0.00E+00	4.00E-07	0.00E+00	3
	72 h Czapek-Dox agar plate	36.67±0.58	30.33±1.15	37.33±0.58	38.67±1.53	4.42E-05	3.32E-04	1.63E-04	4.57E-05	3
	96 h tomato	12.75±4.16	3.08±0.79	10.33±3.73	11.50±3.80	3.42E-08	1.00E-07	2.68E-05	1.60E-06	3
	96 h Czapek-Dox agar plate	53.33±1.53	43.67±0.58	52.00±2.65	51.67±0.58	2.68E-04	3.22E-04	8.94E-04	1.17E-03	3
Spore production (x × 10^7/cm^2)		6.21±0.29	3.98±0.36	5.97±0.14	6.24±0.41	5.85E-05	1.18E-04	2.65E-04	1.08E-04	3
Spore size (µm)	**Arc lenght**	10.43±0.23	8.07±0.13	8.95±0.41	9.02±0.90	3.25E-03	2.07E-03	2.22E-01	1.78E-01	3
	Spore diameter	4.85±0.66	4.94±0.18	3.93±0.51	4.19±0.51	9.64E-02	9.96E-01	1.36E-01	3.16E-01	3
Spore viability (number of colonies)	**25 °C**	86.67±10.67	81.67±7.42	71.78±11.72	87.44±11.63	1.25E-02	7.45E-01	2.10E-01	6.52E-01	3
	42 °C	74.67±11.62	71.44±11.96	68.33±7.38	71.33±8.36	6.16E-01	9.02E-01	9.11E-01	1.00E+00	3
	45 °C	46.67±6.63	39.89±5.75	45.56±7.38	49.33±5.00	2.30E-02	1.20E-01	2.40E-01	1.55E-02	3
	4 °C	25.00±8.83	24.11±6.60	32.00±4.61	30.11±6.11	4.70E-02	9.92E-01	8.02E-02	2.50E-01	3
Abiotic stress tolerance (relative growth)	**H_2O_2**	74.59±1.23	40.04±0.94	68.23±5.96	66.87±7.34	9.84E-05	9.88E-05	4.21E-04	5.93E-04	3
	***t*BOOH**	54.58±0.69	47.83±1.75	50.55±2.83	50.67±2.55	2.87E-02	1.93E-02	4.46E-01	4.13E-01	3
	MSB	6.39±2.70	39.76±7.22	59.14±4.02	58.57±3.45	1.80E-03	2.87E-03	4.22E-03	5.07E-03	3
	CR	52.91±2.90	40.22±2.27	48.51±3.27	49.60±2.57	3.02E-03	2.31E-03	2.69E-02	1.40E-02	3
Fumonisin production (µg/g DCM)	**FB1**	37.27±4.89	0.00±0.00	37.34±11.17	28.44±8.81	4.83E-06	4.00E-06	1.60E-04	1.04E-04	5
	FB2	8.78±1.92	0.00±0.00	5.62±1.86	6.32±1.01	3.58E-07	2.00E-07	6.37E-05	1.65E-05	5
Carotenoid production (µg/g DCM)		19.44±2.68	0.47±0.03	24.46±8.69	27.05±4.87	9.08E-04	8.60E-03	2.02E-03	1.04E-03	3
Bikaverin production (mg/g DCM)	**day 5**	4.26±1.12	41.37±13.32	9.57±4.06	9.50±4.24	4.87E-12	0.00E+00	0.00E+00	0.00E+00	3
	day 7	7.18±5.36	52.50±17.45	14.31±5.90	14.44±7.24	2.13E-10	0.00E+00	0.00E+00	0.00E+00	3
	day 9	9.79±2.56	54.50±5.67	15.60±7.03	11.53±6.09	2.20E-16	0.00E+00	0.00E+00	0.00E+00	3

Gene expression (-ΔC_T)	***fum1***	8.10±0.88	12.10±0.31	8.50±0.26	8.86±0.05	2.93E-05	3.81E-05	8.31E-05	1.76E-04	3
	fum8	5.19±0.30	8.78±0.16	4.08±0.50	4.84±0.20	4.13E-07	3.60E-06	4.00E-07	1.70E-06	3
	fum21	6.25±0.52	6.57±0.52	4.95±0.54	5.54±0.45	1.84E-02	8.64E-01	1.93E-02	1.36E-01	3
	***bik1* (day 3)**	6.93±2.93	11.46±0.69	7.85±0.48	8.15±0.83	3.55E-02	3.23E-02	8.85E-02	1.23E-01	3
	***bik1* (day 5)**	10.65±0.80	12.94±2.59	8.51±2.28	10.00±2.98	2.07E-01	6.36E-01	1.66E-01	4.51E-01	3
	carRA	7.19±1.22	17.12±1.29	6.33±0.94	5.50±1.73	1.54E-05	7.46E-05	4.06E-05	2.32E-05	3
	carB	4.68±2.00	13.94±0.83	4.56±1.08	3.22±1.90	9.35E-05	3.54E-04	3.23E-04	1.25E-04	3
	carT	9.79±0.99	10.67±1.54	10.40±1.40	9.93±1.26	8.31E-01	8.43E-01	9.94E-01	8.97E-01	3

Supplementary Table S6. Two-Way ANOVA analysis of abiotic stress tolerance

Studied property		**Strains**								**Two-Way ANOVA**		
		FGSC 7600 (A)		***ΔFvatfA* (B)**		***FvatfA* 'C (H7) (C)**		***FvatfA* 'C (H9) (D)**		**p-value (strain)**	**p-value (treatment)**	**p-value (interaction between strain and treatment)**
		untreated	**treated**	**untreated**	**treated**	**untreated**	**treated**	**untreated**	**treated**			
Abiotic stress tolerance (colony diameter. mm)	H_2O_2	79.21±0.52	59.08±1.01	70.04±1.45	28.04±1.64	78.17±1.94	53.29±4.08	78.17±1.94	52.25±5.52	2.20E-16	2.20E-16	2.20E-16
	*t*BOOH	79.46±1.13	43.38±1.09	69.75±1.44	33.38±1.89	78.17±1.94	39.54±3.07	78.17±1.94	39.63±2.70	2.00E-16	2.00E-16	8.87E-02
	MSB	78.33±1.50	47.29±1.91	70.92±1.54	28.17±4.82	77.46±1.66	45.79±2.77	77.71±1.55	45.50±2.38	2.20E-16	2.20E-16	4.10E-15
	CR	79.38±1.00	42.00±2.46	69.88±1.23	28.13±2.07	78.17±1.94	37.88±1.69	78.17±1.94	38.79±2.77	2.20E-16	2.20E-16	1.20E-03

Studied property		**Tukey post hoc test (adj. p-value)**					
		B vs. A (untreated)	**B vs. C (untreated)**	**B vs. D (untreated)**	**B vs. A (treated)**	**B vs. C (treated)**	**B vs. D (treated)**
Abiotic stress tolerance (colony diameter. mm)	H_2O_2	2.00E-07	5.30E-06	5.30E-06	0.00E+00	0.00E+00	0.00E+00
	*t*BOOH	0.00E+00	0.00E+00	0.00E+00	0.00E+00	0.00E+00	0.00E+00
	MSB	0.00E+00	0.00E+00	0.00E+00	0.00E+00	0.00E+00	0.00E+00
	CR	0.00E+00	0.00E+00	0.00E+00	0.00E+00	0.00E+00	0.00E+00

Supplementary Table S7. Distribution of fumonisins FB1 and FB2 between culture supernatants and mycelia in *Fusarium verticillioides* static liquid cultures

	FB1		**FB2**	
Strains	**In supernatant (µg/g DCM)**	**In mycelium (µg/g DCM)**	**In supernatant (µg/g DCM)**	**In mycelium (µg/g DCM)**
FGSC 7600	31.02±4.71 (80.44±2.44%)	7.68±2.36 (19.56±2.44%)	5.26±0.95 (83.78±2.04%)	1.03±0.31 (16.22±2.04%)
ΔFvatfA	0.00±0.00 (0.00±0.00%)	0.00±0.00 (0.00±0.00%)	0.00±0.00 (0.00±0.00%)	0.00±0.00 (0.00±0.00%)
FvatfA ’C (H7)	26.17±5.76 (83.98±6.25%)	4.85±1.62 (16.02±6.25%)	3.63±1.76 (80.06±10.09%)	0.79±0.20 (19.94±10.09%)
FvatfA ’C (H9)	37.16±11.75 (90.78±3.62%)	3.56±1.28 (9.22±3.62%)	3.94±0.24 (84.54±3.78%)	0.72±0.18 (15.46±3.78%)

Supplementary Table S8. Results of the PCA analysis

Coordinates of the strains:

	Coordinates			
Strain	**PC1**	**PC2**	**PC3**	**PC4**
FGSC 7600	-2.96274	-3.23396	-0.40362	3.00E-16
ΔFvatfA	7.161313	-0.30343	-0.03184	1.84E-15
***FvatfA* 'C (H9)**	-2.08427	2.352623	-1.5677	-1.34E-14
***FvatfA* 'C (H9)**	-2.11431	1.184762	2.003158	1.90E-14

Importance of components:

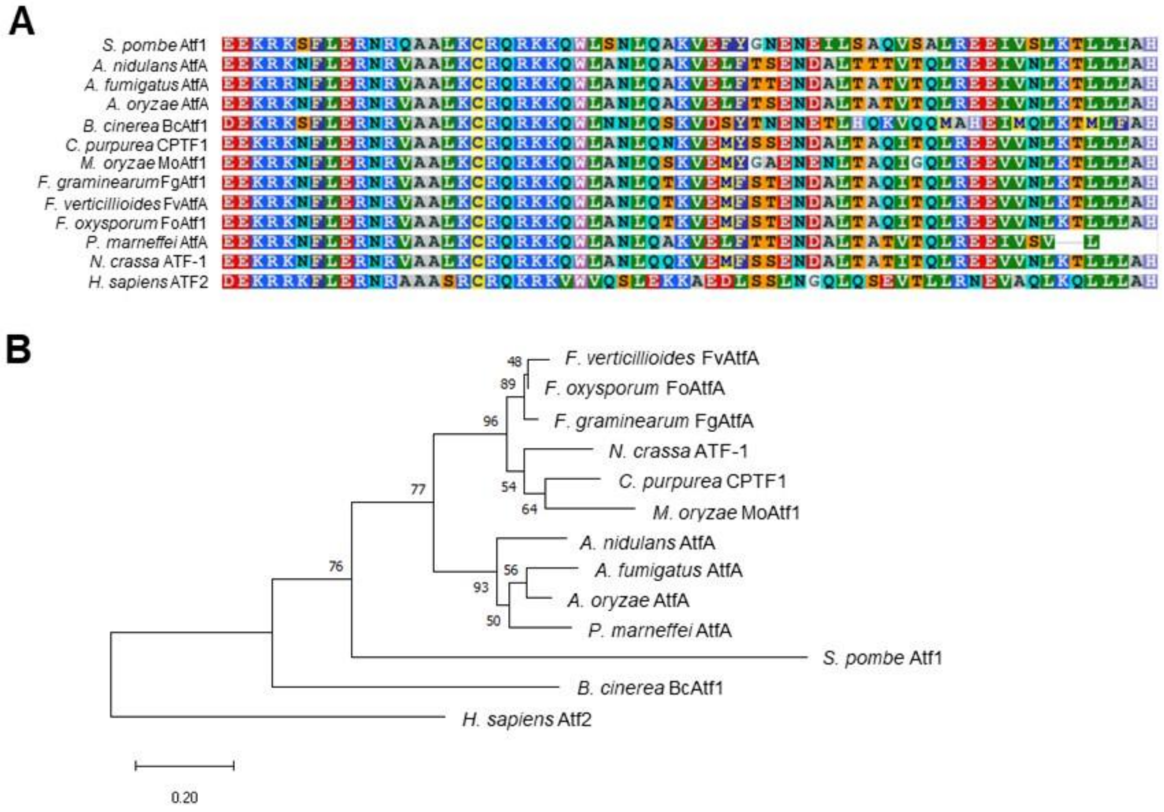
	PC1	**PC2**	**PC3**	**PC4**
Standard deviation	4.7915	2.4145	1.48708	2.335E-15
Proportion of Variance	0.7406	0.1880	0.07134	0
Cumulative Proportion	0.7406	0.9287	1	1

Studied property		**PC1**[1]	**PC2**[1]	**PC3**	**PC4**
Vegetative growth (colony diameter. mm)	**Czapek-Dox agar plates**	-0.20758	-0.04279	-0.00465	0.434012
	Potato Dextrose agar plates	-0.20774	0.038742	0.013478	0.055648
Invasive growth (colony diameter. mm)	**72 h tomato**	-0.20622	-0.04442	0.073948	-0.09748
	72 h Czapek-Dox agar plate	-0.20608	-0.05582	0.055358	-0.04607
	96 h tomato	-0.19971	0.090416	0.128655	-0.14456
	96 h Czapek-Dox agar plate	-0.20797	-0.02835	-0.03227	0.328134
Spore size (µm)	**Arc lenght**	-0.16154	-0.259	-0.06652	0.13909
	Spore diameter	0.116462	-0.34304	0.034062	0.222351
Spore viability (number of colonies)	**25 °C**	-0.01292	-0.25843	0.523838	-0.41231
	42 °C	-0.01587	-0.39504	0.19545	0.023971
	45 °C	-0.18929	0.037402	0.27661	0.223427
	4 °C	-0.11983	0.338667	-0.0277	0.217727
Spore production (x × 10^7/cm^2)		-0.20756	0.007685	0.069213	-0.03962
Abiotic stress tolerance (relative growth)	**H_2O_2**	-0.09997	-0.30782	-0.31408	-0.06236
	***t*BOOH**	0.207575	-0.04091	0.021349	-0.14876
	MSB	-0.10626	-0.24973	-0.413	-0.31792
	CR	-0.11249	-0.2497	-0.39555	-0.0449
Fumonisin production (µg/g DCM)	**FB1**	-0.20478	-0.07977	-0.0087	0.01921
	FB2	-0.19993	-0.11855	0.012671	-0.04186
Bikaverin production (mg/g DCM)	**day 5**	0.2083	0.025066	0.00881	0.009269
	day 7	0.208015	0.032401	0.014124	0.090683
	day 9	0.208101	0.005846	-0.05006	0.03274
Carotenoid production (µg/g DCM)		-0.19628	0.126594	0.099979	-0.10448
Gene expression ($-\Delta C_T$)	***fum1***	-0.20757	-0.01958	-0.06238	0.021576
	fum8	-0.19977	0.112684	-0.06622	-0.00509
	fum21	-0.13033	0.314506	-0.12283	-0.4052
	***bik1* (day 3)**	-0.20512	-0.06493	-0.06522	-0.03442
	***bik1* (day 5)**	-0.17524	0.201537	-0.16213	-0.057
	carRA	-0.20433	0.073964	0.065656	-0.06968
	carB	-0.2048	0.055817	0.092464	-0.06653
	carT	-0.16848	-0.18475	0.259818	-0.01311

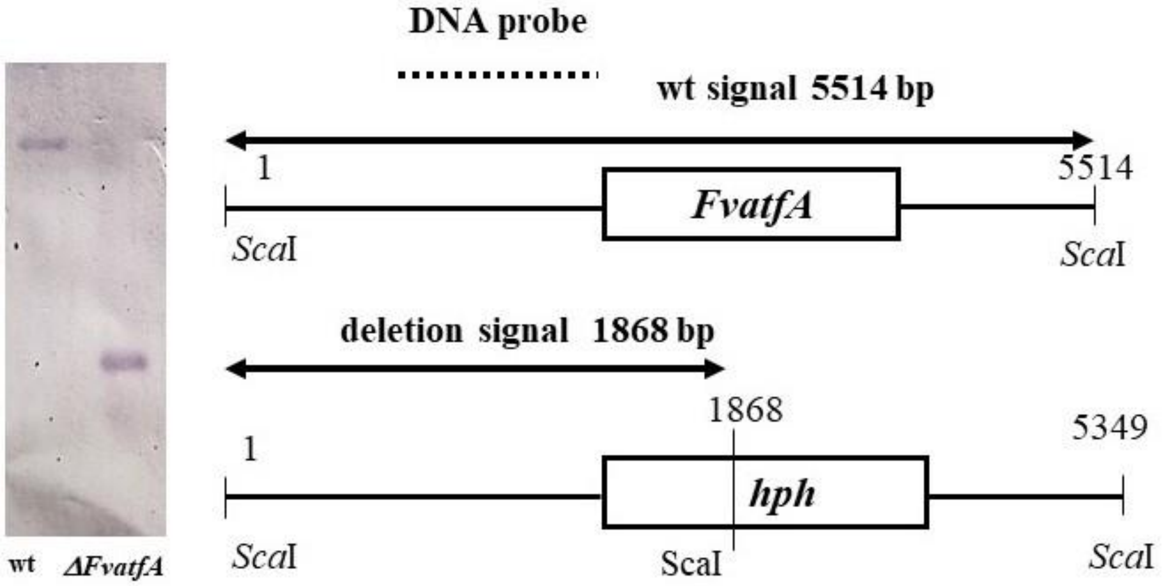
[1] - Properties highlighted with blue, red and green are important component of PC1, PC2 or both, respectively. The PC1 (*i.e.* the difference between the mutant and the other strains) highly depended on: growth, invasive growth, stress tolerance, spore morphology, spore production and secondary

metabolite production. The PC2 (*i.e.* the difference between the reference and the complemented strains) highly depended on: spore viability at 4, 25 and 42 °C, spore morphology, stress tolerance (excluding *t*BOOH and 45 °C heat stress) as well as on the expression of *bik1* (day 5) and *fum21* genes.

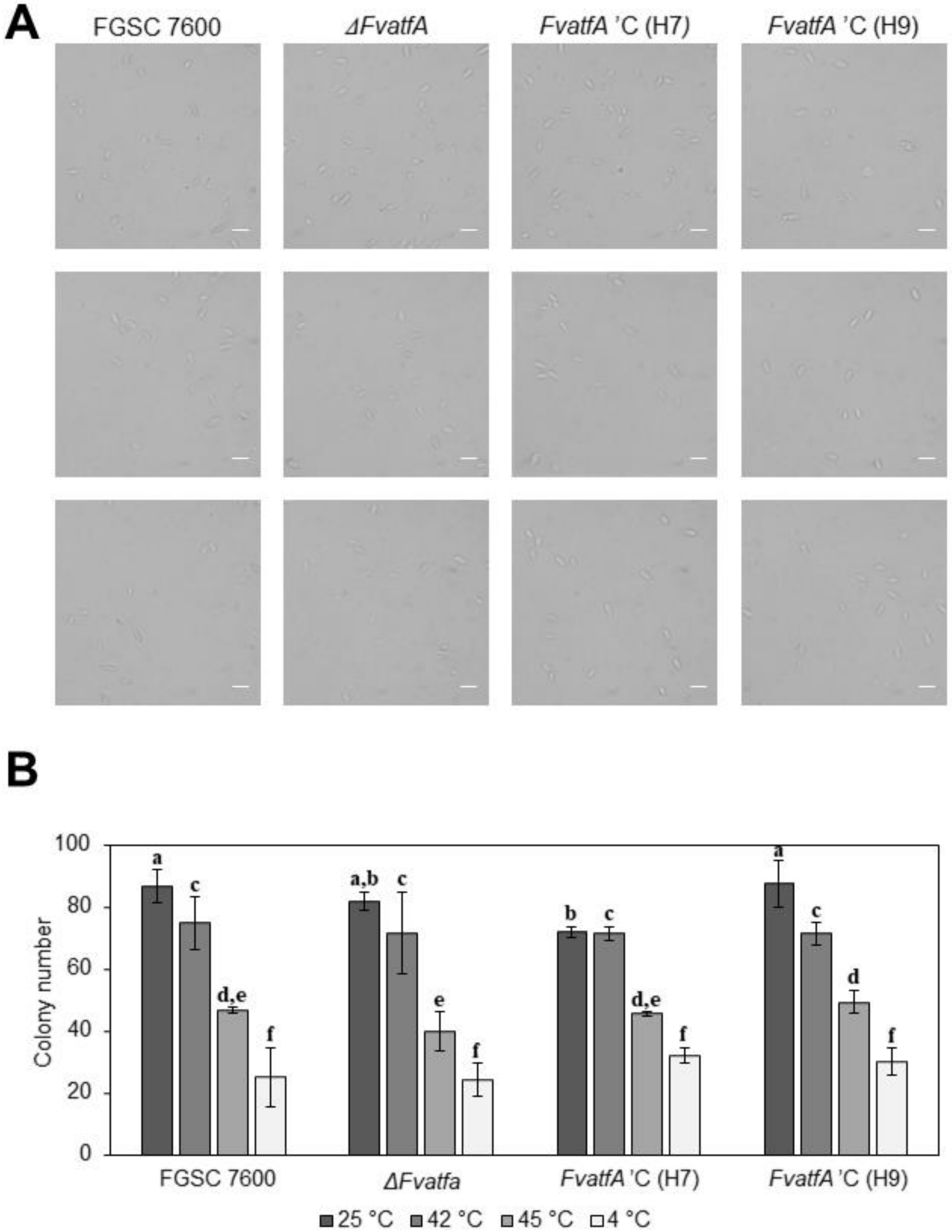
Supplementary Figures



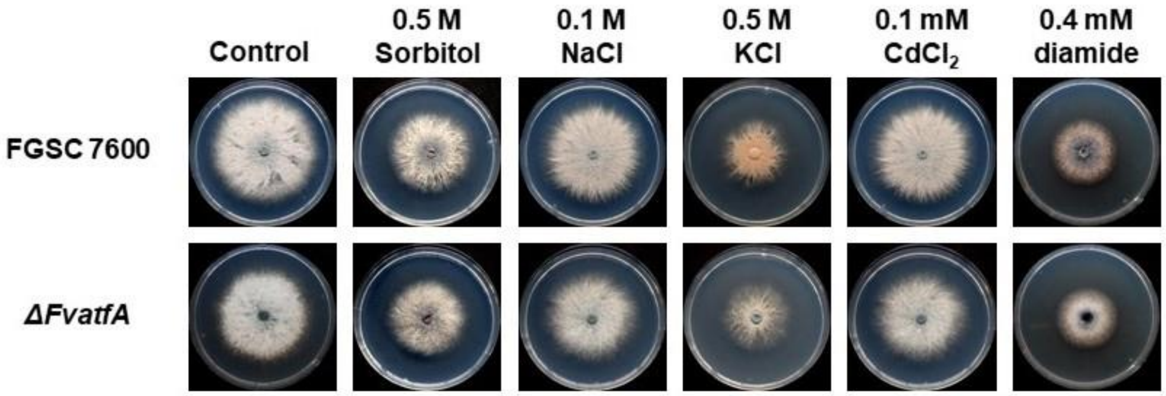
Supplementary Figure S1. Multiple sequence alignment and phylogenetic tree construction. In Part A, alignment of bZIP domains of the Atf1/AtfA ortholog transcription factors is presented. In Part B, the phylogenetic tree constructed by the Maximum Likelihood method and JTT matrix-based model is shown. Homology E expect values in comparison to *F. verticillioides* to FVEG_02866 (putatively encoding FvAtfA; NCBI blastp analysis) are summarized in Supplementary Table S1.



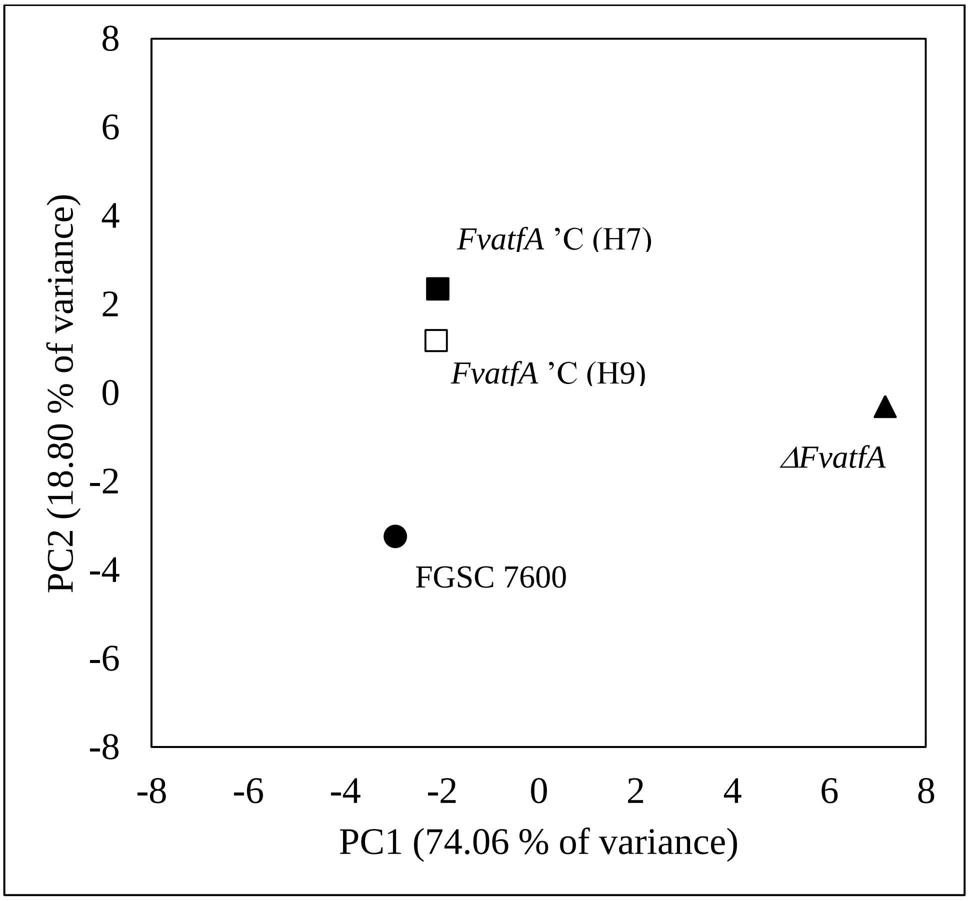
Supplementary Figure S2. Confirmation of the *F. verticillioides atfA* gene deletion on Southern blot. The *Sca*I restriction sites inside an approximately 5.5 kb long genomic region surrounding the *FvatfA* gene are presented in the wild type FGSC 7600 strain and in the *ΔFvatfA* deletion mutant. The upstream noncoding region of the *FvatfA* gene (indicated by a broken line) was amplified by PCR, labelled, and was used as a probe in Southern blotting. The probe hybridized to a 5514 bp restriction fragment in the parental FGSC 7600 strain while in the *ΔFvatfA* mutant it labelled a 1868 bp fragment (see arrows), as expected.



Supplementary Figure S3. Variations in the morphology as well as in the heat and cold tolerances of the conidiospores the *F. verticillioides* FGSC 7600 control, the *ΔFvatfA* mutant and the *ΔFvatfA* 'C H7 and H9 complemented strains. In Part A, a typical set of microscopic photos taken on spore suspensions of the strains are presented. White bars indicate 10 μm. For statistical evaluation of spore yields and sizes, you can consult Figure 3. As shown in Part B, no significant differences were found in the heat and cold tolerances of the conidiospores. In these experiments, freshly grown conidia were kept at 25, 42 or 45 ^{o}C for 60 min or stored at 4 ^{o}C for a week. Following that, spore suspensions were spread on Czapek-Dox Agar medium and the colonies were counted after 2 d incubation at 25 ^{o}C. Different letters indicate significant differences between the tested strains (one-way ANOVA fallowed by Tukey post-hoc test; adj. $p < 0.05$). For further details of the ANOVA see also Supplementary Table S5.



Supplementary Figure S4. Testing and comparing the high-osmolarity, heavy metal and diamide tolerances of the *F. verticillioides* control and *ΔFvatfA* gene deletion mutant strains. A typical set of photos taken on the Czapek-Dox stress agar plates after 6 d incubations at 25 °C are presented. Please note that all differences observed between the colony diameters of the tested *F. verticillioides* strains in stress agar cultures could be attributed to the slow growth phenotype of the *ΔFvatfA* strain (Figure 1).



Supplementary Figure S5. Principal component analysis of the studied strains. The separation of the strains in the score plot of PC1 and PC2 can be interpreted as follow: (i) the deletion mutant clearly separated from the other three strains, (ii) the wild-type FGSC 7600 separated from the other three strains, (iii) the complemented strains created a group separating from the wild-type and deletion mutant strains too. PCA was applied on mean values presented in Supplementary Table S5. For more information of the results of the PCA analysis see also Supplementary Table S8.

FVEG_00316 *fum1*

CCACCTCTATGCCAGCCCTGACTCAATGGCACAGCACGCACACCATCACTAACGGTAAACTCAAAACGACAGC
CGCTTGCATTGAGGCTAAAGCACGGTTCCGGCTTATACGAACAGAAGTCTGACATCTTTCATGATAAGAAGAA
GAAGAAGAAGCTGTCGGAATGATACAGACCCAAATCAGATATCCGACCGGCTCCTGGTCCCATTCCATTATGA
GCCAATGGGGCAATTGCCCCCTTTCCCTACCCGAGTGTTTTCGGACGTTACTGTCCCTCACCCGGGAACTCTAG
CAAACTATTGGGATGTAGGATAATAATAGTAACCTTCCTACTGGTTGCCGAATTTCCGGGTCTCTTACTCGTCTT
TGAGGATACTGACAATTGCGCTTCGGAGTATTGCGTGTCCTCTCGGATGGGAGACTAAATCGTATACAACAAC
CGGAATTTCGATGCTGATTGCAATGATAGAGACGAGACAGA**TATATAACCATGAAATACAGTGTTATTGGAG**
ACTCTGTATTTGATCCATCGCAACCTTATTATCGTTTTAAACGCTACTGATATCATCAACGTTCGACATG

FVEG_14635 *fum8*

AATTAACAGTTTTAAAACTTGAAATCAAGATAAACACTTACCAAGCTAGCACTTGACTTGTTGTGTGAAAGTGA
ATTACTCTGTAAACCGAGAAATCCAATATCATGCATTGGCGTTGGCAAAAACAATCCTCTGCTTTTTTGCATGA
ACAATATAACGGAATCTAAATACTCGATGGACCACACGAGTACGTAAAGGTAGCAGCAAATGAAGGC**TATAT**
AATGAACAAGACGCTCAACTCAATGTATCTCTACTCTCCAAGGAACAGATCTCAAAATGGCTTCCTTCTC
CTGTGCCAAGCTGGGCTGGTACGAGGAATGTTGACTACCTTACCGAATGTGACATCCAGAAAACTGTTG
TATGTACAACTTTCAATTATATGCTACAGGTTGAGCTGAGCTACTAGGTAGGTAGCAATGATTTATCCGT
CACTCACAGAAACAGTGCCCGGAAGCATCTTTTCAAACATCCGACAGATGCCACACGGGGTATCCGAAC
TTCCGAATAACCCCCAGTACAACGTTGGCCTTTTGGATTCTTGGTAGCAGAGTCTACCGATCAGCTACCT
TACCTAGTCAGTCCATCAGTTTCCAGTCGTTGACTCGAAATGAGGAACAGATACAAAATCATCCCGGGTT
ACATTTAAAACTGAGGTTTTCATACAGTGAAAGTCATAACTCTGAACAACTTCATTTTTACCTTGTGTCA
GCCCTTGCATTGCCCATCATG

FVEG_14633 *fum21*

AAAAAATATAGAAGAATAATAGATCAAATATGCCTAAAAGAAATGCTCCCAGACACGATCCTAGGCAA**GCAT**
AAAAGCTCATATAACTCCATCCACAAGCTCCTCACCAGTGAACGCTGAATACTGTCCTATTAGTCAATTG
GCTCCAGAAACCACGCCCTTTCTTCCAAGTAAAGTGCCCATAACCACTGGATAAGCAAGCAGATGGAAA
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FVEG_10718 *carRA*

GTATGTCAAAGCATACGATACTCCATGAAGCTATACATACAGGATACACCCATCCACAGCCAGCAGACCACCA
GTAACTTAAC**TATATAGCCAAACCCTCATCAGATCGAGATGATCAGGAAGGACGTAGGTCGCATCAATCG**
CTGGATAACACGGCACGCGATGGGAATATCCATCCATCAAAACCACTAGCACAATTTGTCACGCGTCAT
AATCAAGACCCATCTCCATCACGGTAACGGCAATGTCAAAAAGACCGAGTAACCCGAAAAAAAAGGGTC
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TTGACTCTGGCTTTATTTGAAGCCCATATCGTATGCCGTCACGATCTGCTTTTTGTTGTTGTTCACGTAC
ACGAAATAAATAAACCTCTGTCAAAATG

FVEG_10717 *carB*

CATAAACCCACCAACCAATCATTCAACACGCATCACACCGCCAAGTCC**ACTTAAAGACCCTCCAAACCAAAC**
CCGTCAATGATCGTCAACGCATCAACGACTTCAATTCTCCTGTAATCTTCAATGAATCACTAAAATCCCT
CAAAAAACAAACTGCGCCTCGCTAAGCACAGGGTAATCTGGCCTTTCACATGTACGCCAAGTGGTCTCAT
TAGACGAGTGCGAAGGAAAAAGTGGATCAAAACAAAATGGAAGACGTCATTGACTCTATTGCTTTGGCT
ATCAAAACCGTTGGCTTCGGGTGAGTCGGTTACTGACTGAGCATCTTCACTTTTTACAGCAAAAATG

FVEG_09251 *carT*

TAGCTTGATGTTCCGTCAGATGTTTTCATGGAAGCAATTAATGAAACCATGAAAGTAACTATTGTTGCCAAGA**C**
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TCGCAAATAAACTTTACTATG

FVEG_03379 *bik1*

ACTAAAGCCAACTGTCAAGGAGAGTCTATTCAAGTGCCGAGATTCGAATCACCATCCAGGGACAGAGCCTCAC
GTAGTTGGTATTCACACATTAGCGCATCGCGTCCGTGGCTCTTCTCTTGACTCGATTCGTCCTCGGTTCACGGCA
CATACTACGCCACCCTGCCCGTTTCAGCTTCCCCTGCAA**GATAAGAATTCGGACCTCTTCGGAGCTTCATCT**
CTGATCTGATCCTGCGTGGCGTAACTAGCCGCTATACTGACCCTGGCCCACCCATGCAAGCCACTACGG
ACATTTTCGCAAAAGCGCGGAACCAACACTAGCCAGACCCTTACGAATTACCAAAAAGGGTCACGTATG
TTTGAACCTCTACAGTATAAGCCAGATACATCTTGGCGAGAAAATAGCCAAGACAAACGAATATTGCACC
TTTGTTACAGCTTTCAACAGCGATTCTTTTTGCCATCTTACATTTTCAAGATG

Overlapping genes with the tested gene promoters:

Gene	Chain	Overlapping gene	Function	Chain
carRA	-	*carX* (FVEG_10719)	carotenoid oxygenase	+
carB	-	*carRA* (FVEG_10718)	carotene cyclase	-
carT	+	FVEG_09250	NA	-
fum1	+	*fum21* (FVEG_14633)	Zn(II)2Cys6 transcription factor	+
fum8	-	*fum3* (FVEG_00320)	dioxygenase	-
fum21	+	*zbd1* (FVEG_00314)	zinc binding dehydrogenase	+
bik1	-	*bik2* (FVEG_03380)	monooygenase	-

Supplementary Figure S6. Putative ATF/CREB transcription factor binding sites on the promoter regions of the genes involved in secondary metabolite production. Colour code: **ACGT** – 5' untranslated region between TSS and ATG, 🟫 – first base of the transcription start site (TSS), 🟦 – poly-A tail (PolA), **ATG** – translation start codon, GTAT – TSS region of the *carX* gene up-stream of *carRA*, 🟦 – binding sites between -150 - +50 bp with respect to (w.r.t.) TSS, 🟪 – binding sites up-stream of position -150 bp w.r.t. TSS, 🟩 – binding sites down-stream of position +50 bp w.r.t. TSS.

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