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Transcription Factors Encoded on Core and Accessory Chromosomes of *Fusarium oxysporum* Induce Expression of Effector Genes

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DOI

[10.1371/journal.pgen.1006401](https://doi.org/10.1371/journal.pgen.1006401)

Publication date

2016

Document Version

Other version

Published in

PLOS Genetics

[Link to publication](#)

Citation for published version (APA):

van der Does, H. C., Fokkens, L., Yang, A., Schmidt, S. M., Langereis, L., Lukasiwicz, J. M., Hughes, T. R., & Rep, M. (2016). Transcription Factors Encoded on Core and Accessory Chromosomes of *Fusarium oxysporum* Induce Expression of Effector Genes. *PLOS Genetics*, 12(11), [e1006401]. <https://doi.org/10.1371/journal.pgen.1006401>

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TF2: Forkhead domain (Pfam: Forkhead)

PK Y LI AI P T

FOXG_17260T0 123 NMKFW-QEFPPTGEPPEYQANSRVKSEPLELKS-TAVLPAKAKPEYAKLYRALMSAPDQAMT
 FOWG_16911T0 123 NMKFW-QEFPPTGEPPEYQANSRVKSEPLELKS-TAVLPAKAKPEYAKLYRALMSAPDQAMT
 Necha2_75425 239 YMTTQKEEHPAVBPENRASPQKQPEPSESQSSSAVGGAKPEPYAQLLYRALMGAPGHAMT
 FVEG_00384T0 233 LMKAR-HKSPAGVPEYRASSEVVQEGKDLQATAAGGAKTDEPYAKLLYRALMSVPHAMT
 FOPG_04623T0 233 LMKAR-HKSPAGVPEYRANSEVVQEGKDLQAAAAGGAKTDEPYAKLLYRALMSVPHAMT
 FOXB_06599T0 233 LMKAR-HKSPAGVPEYRANSEVVQEGKDLQAAAAGGAKTDEPYAKLLYRALMSVPHAMT
 FOTG_04534T0 233 LMKAR-HKSPAGVPEYRANSEVVQEGKDLQAAAAGGAKTDEPYAKLLYRALMSVPHAMT
 FOQG_03457T0 234 LMKAR-HKSPAGVPEYRANSEVVQEGKDLQAAAAGGAKTDEPYAKLLYRALMSVPHAMT
 FOVG_00276T0 233 LMKAR-HKSPAGVPEYRANSEVVQEGKDLQAAAAGGAKTDEPYAKLLYRALMSVPHAMT
 FOIG_13226T0 233 LMKAR-HKSPAGVPEYRANSEVVQEGKDLQAAAAGGAKTDEPYAKLLYRALMSVPHAMT
 FOYG_06154T0 233 LMKAR-HKSPAGVPEYRANSEVVQEGKDLQAAAAGGAKTDEPYAKLLYRALMSVPHAMT
 FOCG_14298T0 233 LMKAR-HKSPAGVPEYRANSEVVQEGKDLQAAAAGGAKTDEPYAKLLYRALMSVPHAMT
 FOZG_01910T0 233 LMKAR-HKSPAGVPEYRANSEVVQEGKDLQAAAAGGAKTDEPYAKLLYRALMSVPHAMT
 FOWG_10385T0 233 LMKAR-HKSPAGVPEYRANSEVVQEGKDLQAAAAGGAKTDEPYAKLLYRALMSVPHAMT
 FOXG_01132T0 233 LMKAR-HKSPAGVPEYRANSEVVQEGKDLQAAAAGGAKTDEPYAKLLYRALMSVPHAMT
 FOMG_01923T0 233 LMKAR-HKSPAGVPEYRANSEVVQEGKDLQAAAAGGAKTDEPYAKLLYRALMSVPHAMT

L WONSIRHNL N F K

FOXG_17260T0 181 LHEIYQWFRNTDKHIKKDSRRPRPGKNDNGWQNSIRHNLMSNDAFVKREYKQLSDPASN
 FOWG_16911T0 181 LHEIYQWFRNTDKHIKKDSRRPRPGKNDNGWQNSIRHNLMSNDAFVKREYKQLSDPASN
 Necha2_75425 299 LQEIYQWFRNTDKHSKNNENLCKKSGKNAEGWQNSIRHNLMSNDAFTKDPKKEPGSGPS
 FVEG_00384T0 292 LQEIYQWFRNTDKDIKKDKSEKRPKNAEGWQNSIRHNLMSNDAFVKREHKLSDSASR
 FOPG_04623T0 292 LQEIYQWFRENTDKDIKKDKSEKRPKNAEGWQNSIRHNLMSNDAFVKREHKLSDSASR
 FOXB_06599T0 292 LQEIYQWFRNTDKDIKKDKSEKRPKNAEGWQNSIRHNLMSNDAFVKREHKLSDSASR
 FOTG_04534T0 292 LQEIYQWFRENTDKDIKKDKSEKRPKNAEGWQNSIRHNLMSNDAFVKREHKLSDSASR
 FOQG_03457T0 293 LQEIYQWFRENTDKDIKKDKSEKRPKNAEGWQNSIRHNLMSNDAFVKREHKLSDSASR
 FOVG_00276T0 292 LQEIYQWFRENTDKDIKKDKSEKRPKNAEGWQNSIRHNLMSNDAFVKREHKLSDSASR
 FOIG_13226T0 292 LQEIYQWFRENTDKDIKKDKSEKRPKNAEGWQNSIRHNLMSNDAFVKREHKLSDSASR
 FOYG_06154T0 292 LQEIYQWFRENTDKDIKKDKSEKRPKNAEGWQNSIRHNLMSNDAFVKREHKLSDSASR
 FOCG_14298T0 292 LQEIYQWFRENTDKDIKKDKSEKRPKNAEGWQNSIRHNLMSNDAFVKREHKLSDSASR
 FOZG_01910T0 292 LQEIYQWFRENTDKDIKKDKSEKRPKNAEGWQNSIRHNLMSNDAFVKREHKLSDSASR
 FOWG_10385T0 292 LQEIYQWFRENTDKDIKKDKSEKRPKNAEGWQNSIRHNLMSNDAFVKREHKLSDSASR
 FOXG_01132T0 292 LQEIYQWFRENTDKDIKKDKSEKRPKNAEGWQNSIRHNLMSNDAFVKREHKLSDSASR
 FOMG_01923T0 292 LQEIYQWFRENTDKDIKKDKSEKRPKNAEGWQNSIRHNLMSNDAFVKREHKLSDSASR

FOXG_17260T0 241 GG--DHGSTKDDSSKKPTKWTLESWAVQDGVKSTRFYRHNKYGVLR-----
 FOWG_16911T0 241 GG--DHGSTKDDSSKKPTKWTLESWAVQDGVKSTRFYRHNKYGVLR-----
 Necha2_75425 359 MT---ESTAGGLEKSTEWRLVDWARLDGVQSTTYRPGNSARRALGKTKVQHHPYNHHG
 FVEG_00384T0 352 ATEQSGSTKTGEAKKATEWVLEDWAVLNGVESTTKYRGKNTSRRGMGRKYHHHPYDY--
 FOPG_04623T0 352 ATEQSGSTKTGEAKKATEWVLEDWAVLNGVESTTKYRGKNTSRRGMGRKYHHHPYDY--
 FOXB_06599T0 352 ATEQSGSTKTGEAKKATEWVLEDWAVLNGVESTTKYRGKNTSRRGMGRKYHHHPYDY--
 FOTG_04534T0 352 ATEQSGSTKTGEAKKATEWVLEDWAVLNGVESTTKYRGKNTSRRGMGRKYHHHPYDY--
 FOQG_03457T0 353 ATEQSGSTKTGEAKKATEWVLEDWAVLNGVESTTKYRGKNTSRRGMGRKYHHHPYDY--
 FOVG_00276T0 352 ATEQSGSTKTGEAKKATEWVLEDWAVLNGVESTTKYRGKNTSRRGMGRKYHHHPYDY--
 FOIG_13226T0 352 ATEQSGSTKTGEAKKATEWVLEDWAVLNGVESTTKYRGKNTSRRGMGRKYHHHPYDY--
 FOYG_06154T0 352 ATEQSGSTKTGEAKKATEWVLEDWAVLNGVESTTKYRGKNTSRRGMGRKYHHHPYDY--
 FOCG_14298T0 352 ATEQSGSTKTGEAKKATEWVLEDWAVLNGVESTTKYRGKNTSRRGMGRKYHHHPYDY--
 FOZG_01910T0 352 ATEQSGSTKTGEAKKATEWVLEDWAVLNGVESTTKYRGKNTSRRGMGRKYHHHPYDY--
 FOWG_10385T0 352 ATEQSGSTKTGEAKKATEWVLEDWAVLNGVESTTKYRGKNTSRRGMGRKYHHHPYDY--
 FOXG_01132T0 352 ATEQSGSTKTGEAKKATEWVLEDWAVLNGVESTTKYRGKNTSRRGMGRKYHHHPYDY--
 FOMG_01923T0 352 ATEQSGSTKTGEAKKATEWVLEDWAVLNGVESTTKYRGKNTSRRGMGRKYHHHPYDY--

TF3: Cys2His2 domain (Pfam: zf-C2H2)

C C F L H H

FOXG_17266T0 181 YKCEWPGCEKTFQKKS LRVHAKTRCFQFPIFVPSDTISGLGVEGWHD SATGRDEVPSPA
 FOWG_16923T0 95 YKCEWPGCEKTFQKKS LRVHAKTRCFQFPIFVPSDTISGLGVEGWHD SATGRDEVPSPA
 FOXB_02292T0 181 YKCRWPDCEKTFQKKS LRVHAKTRCFQFPIFVPSDTISGLGAEVWHD SATGRDGVPSPA

C C F L H H

FOXG_17266T0 481 CPLEAKKEAQYKTHLRHTGERPFKCRREGCGKSFARPD SLKRHKKTCRHRKQEVLSLPQ
 FOWG_16923T0 395 CPLEAKKEAQYKTHLRHTGERPFKCRREGCGKSFARPD SLKRHKKTCRHRKQEVLSLPQ
 FOXB_02292T0 481 CSLEAK-----TFARQDSLKRHEKTCRHR-----

TF4: Cys2His2 domain (Pfam: zf-C2H2_4)

				C C		H H	
FOMG_17760T0	357	K	P	G	R	T	K
FOQG_19500T0	343	K	P	G	G	T	V
FOQG_18201T0	388	K	P	G	G	T	V
FOYG_17532T0	388	K	P	G	G	T	V
FOPG_18318T0	383	K	P	G	G	T	V
FOX_B_21280T0	383	K	P	G	G	T	V
FOCG_17777T0	388	K	P	G	G	T	V
FOXG_14201T0	388	K	P	G	G	T	V
FOWG_17617T0	388	K	P	G	G	T	V
FOCG_17847T0	388	K	P	G	G	T	V
FOYG_17398T0	388	K	P	G	G	T	V
FOMG_17942T0	388	K	P	G	G	T	V
FOTG_16282T0	388	K	P	G	G	T	V
FVEG_03239T0	436	K	P	G	G	T	V
FOMG_06221T0	436	K	P	G	G	T	V
FOIG_09417T0	436	K	P	G	G	T	V
FOPG_09778T0	436	K	P	G	G	T	V
FOX_B_14509T0	436	K	P	G	G	T	V
FOTG_12319T0	436	K	P	G	G	T	V
FOWG_08287T0	436	K	P	G	G	T	V
FOCG_03799T0	436	K	P	G	G	T	V
FOZG_10619T0	436	K	P	G	G	T	V
FOXG_04904T0	436	K	P	G	G	T	V
FOYG_07670T0	436	K	P	G	G	T	V
FOQG_08017T0	436	K	P	G	G	T	V
FOVG_05700T0	436	K	P	G	G	T	V

TF5: Basic Leucine Zipper domain (Pfam: bZIP_1, bZIP_2 and bZIP_Maf)

				R NR AA		RK		L		L	
FOXG_14230T0	108	K	R	A	K	T	E	D	E	K	E
Necha2_99800	97	H	G	P	H	T	A	S	R	K	R
FGSG_11623T0	117	E	S	D	T	L	N	R	K	R	A
FOWG_17414T0	108	K	R	A	K	T	E	D	E	K	E
FOX_B_02757T0	108	K	R	A	K	T	E	D	E	K	E
FVEG_13087T0	105	K	R	A	K	T	E	D	E	K	E
FOCG_08851T0	104	K	R	A	K	T	E	D	E	K	E
FOWG_12843T0	104	K	R	A	K	T	E	D	E	K	E
FOZG_08258T0	104	K	R	A	K	T	E	D	E	K	E
FOYG_10272T0	104	K	R	A	K	T	E	D	E	K	E
FOMG_15447T0	104	K	R	A	K	T	E	D	E	K	E
FOTG_11072T0	104	K	R	A	K	T	E	D	E	K	E
FOPG_10256T0	104	K	R	A	K	T	E	D	E	K	E
FOQG_14359T0	104	K	R	A	K	T	E	D	E	K	E
FOX_B_03192T0	104	K	R	A	K	T	E	D	E	K	E
FOVG_08874T0	104	K	R	A	K	T	E	D	E	K	E
FOIG_12632T0	104	K	R	A	K	T	E	D	E	K	E
FOXG_15625T0	104	K	R	A	K	T	E	D	E	K	E
FOXG_14230T0	160	Q	E	A	N	A	R	L	M	E	L
Necha2_99800	157	Q	R	T	N	M	L	L	A	N	E
FGSG_11623T0	177	Q	E	A	N	A	R	L	M	E	L
FOWG_17414T0	160	Q	E	A	N	A	R	L	M	E	L
FOX_B_02757T0	160	Q	E	A	N	A	R	L	M	E	L
FVEG_13087T0	157	Q	E	A	N	A	R	L	M	E	L
FOCG_08851T0	156	E	Q	M	N	A	R	L	M	D	E
FOWG_12843T0	156	E	Q	M	N	A	R	L	M	D	E
FOZG_08258T0	156	E	Q	M	N	A	R	L	M	D	E
FOYG_10272T0	156	E	Q	M	N	A	R	L	M	D	E
FOMG_15447T0	156	E	Q	M	N	A	R	L	M	D	E
FOTG_11072T0	156	E	Q	M	N	A	R	L	M	D	E
FOPG_10256T0	156	E	Q	M	N	A	R	L	M	D	E
FOQG_14359T0	156	E	Q	M	N	A	R	L	M	D	E
FOX_B_03192T0	156	E	Q	M	N	A	R	L	M	D	E
FOVG_08874T0	156	E	Q	M	N	A	R	L	M	D	E
FOIG_12632T0	156	E	Q	M	N	A	R	L	M	D	E
FOXG_15625T0	156	E	Q	M	N	A	R	L	M	D	E

TF7: Cys2His2 domain (Pfam: zf-C2H2)

			C	C	F	L	H	H		
FOQG_18533T0	266	GI	-----A--	GSYTCTVHG	CNAAPFQ	TYLLNSHM	NVHSSIR	PHYCPVKGC	PRSEGGKG	
FOXG_19464T0	266	GI	-----A--	GSYTCTVHG	CNAAPFQ	TYLLNSHM	NVHSSIR	PHYCPVKGC	PRSEGGKG	
FOXG_22293T0	266	GI	-----A--	GSYTCTVHG	CNAAPFQ	TYLLNSHM	NVHSSIR	PHYCPVKGC	PRSEGGKG	
FOXG_22413T0	266	GI	-----A--	GSYTCTVHG	CNAAPFQ	TYLLNSHM	NVHSSIR	PHYCPVKGC	PRSEGGKG	
FOXB_08620T0	266	GI	-----A--	GSYTCTVHG	CNAAPFQ	TYLLNSHM	NVHSSIR	PHYCPVKGC	PRSEGGKG	
FOPG_18275T0	266	GI	-----A--	GSYTCTVHG	CNAAPFQ	TYLLNSHM	NVHSSIR	PHYCPVKGC	PRSEGGKG	
FOXG_14275T0	287	GM	THPQP	IT	--GLYTCTV	QGCHVEPF	QTYLLNSHM	NVHSSIR	PHYCPVKGC	PRSEGGKG
FOWG_17588T1	287	GM	THPQP	IA	--GLYTCTF	QGCRRVDP	FQTKYLLNSHM	NVHSSIR	PHYCPVKGC	PRSEGGKG
FOXG_21311T0	287	GM	THPQP	IA	--GLYTCTF	QGCRRVDP	FQTKYLLNSHM	NVHSSIR	PHYCPVKGC	PRSEGGKG
FOXG_22662T0	287	GM	THPQP	IA	--GLYTCTF	QGCRRVDP	FQTKYLLNSHM	NVHSSIR	PHYCPVKGC	PRSEGGKG
FOXG_21046T0	287	GM	THPQP	IA	--GLYTCTF	QGCRRVDP	FQTKYLLNSHM	NVHSSIR	PHYCPVKGC	PRSEGGKG
FOXG_21006T0	287	GM	THPQP	IA	--GLYTCTF	QGCRRVDP	FQTKYLLNSHM	NVHSSIR	PHYCPVKGC	PRSEGGKG
FOMG_18197T0	287	GM	THPQP	IT	--GLYTCTV	QGCHVEPF	QTYLLNSHM	NVHSSIR	PHYCPVKGC	PRSEGGKG
FOVG_18828T0	287	GM	THPQP	IT	--GLYTCTV	QGCHVEPF	QTYLLNSHM	NVHSSIR	PHYCPVKGC	PRSEGGKG
FOQG_16628T0	287	GM	THPPA	IT	----ICQLNQ	S-ITPLK	SIKSSNS	SF---Q	SNQITHC	-----
FOQG_19377T0	346	GITHPQP	IP	--GSYTCTA	NGCNAAP	FRTOYLLNSH	MDVHSSIR	PHYCPVKE	CPRSGGGKG	
FOTG_18879T0	346	GITHPQP	IL	--GSYTCTA	NGCNAAP	FRTOYLLNSH	MDVHSSIR	PHYCPVKE	CPRSEGGKG	
FOXB_03115T0	346	GITHPQP	IL	--GSYTCTA	NGCNAAP	FRTOYLLNSH	MDVHSSIR	PHYCPVKE	CPRSEGGKG	
FOQG_19073T0	346	GITHPQP	IP	--GSYTCTA	NGCNAAP	FRTOYLLNSH	MDVHSSIR	PHYCPVKE	CPRSEGGKG	
Necha2_47170	340	GITHPQP	AT	GTGAV	VCNFAGC	TALPF	QTYLLNSH	ANVHSSIR	PHYCPVKGC	PRSEGGKG
FGSG_05381T0	228	GITHPQH	MT	--GSYTCTV	PGCNAAP	FQTYLLNSHM	NVHSSIR	PHYCPVKGC	PRSEGGKG	
FVEG_07153T0	357	GITHPQP	LS	--GSYTCTV	TGCNAAP	FQTYLLNSHM	NVHSSIR	PHYCPVKGC	PRSEGGKG	
FOXG_20064T0	262	GITHPQP	LS	--GSYTCTV	TGCNAAP	FQTYLLNSHM	NVHSSIR	PHYCPVKGC	PRSEGGKG	
FOIG_07901T1	357	GITHPQP	LS	--GSYTCTV	TGCNAAP	FQTYLLNSHM	NVHSSIR	PHYCPVKGC	PRSEGGKG	
FOQG_03601T0	357	GITHPQP	LS	--GSYTCTV	TGCNAAP	FQTYLLNSHM	NVHSSIR	PHYCPVKGC	PRSEGGKG	
FOWG_04951T1	357	GITHPQP	LS	--GSYTCTV	TGCNAAP	FQTYLLNSHM	NVHSSIR	PHYCPVKGC	PRSEGGKG	
FOZG_12836T0	357	GITHPQP	LS	--GSYTCTV	TGCNAAP	FQTYLLNSHM	NVHSSIR	PHYCPVKGC	PRSEGGKG	
FOTG_03788T1	357	GITHPQP	LS	--GSYTCTV	TGCNAAP	FQTYLLNSHM	NVHSSIR	PHYCPVKGC	PRSEGGKG	
FOVG_10762T1	357	GITHPQP	LS	--GSYTCTV	TGCNAAP	FQTYLLNSHM	NVHSSIR	PHYCPVKGC	PRSEGGKG	
FOPG_01942T1	357	GITHPQP	LS	--GSYTCTV	TGCNAAP	FQTYLLNSHM	NVHSSIR	PHYCPVKGC	PRSEGGKG	
FOXB_19015T1	357	GITHPQP	LS	--GSYTCTV	TGCNAAP	FQTYLLNSHM	NVHSSIR	PHYCPVKGC	PRSEGGKG	
FOCG_11063T0	357	GITHPQP	LS	--GSYTCTV	TGCNAAP	FQTYLLNSHM	NVHSSIR	PHYCPVKGC	PRSEGGKG	
FOYG_11053T0	357	GITHPQP	LS	--GSYTCTV	TGCNAAP	FQTYLLNSHM	NVHSSIR	PHYCPVKGC	PRSEGGKG	
FOMG_08371T0	357	GITHPQP	LS	--GSYTCTV	TGCNAAP	FQTYLLNSHM	NVHSSIR	PHYCPVKGC	PRSEGGKG	