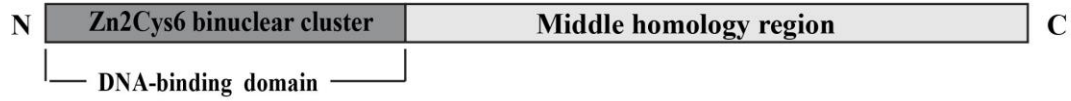
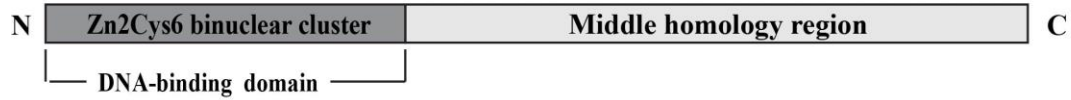


A

A. flavus FarA



A. flavus FarB



A. flavus FarC



B

AFLA_012010_FarB	1	-----MTNLTASPSSSNMARENAKGRKASTAGLPANARPVKRFASKACCCARKVR
AFL2G_05109_FarA	1	MSTTGENHTDSTSRPSPAPSATGSGTSGITVVRAGSNCOMSFRRQRASRACETCHARKVR
AFLA_082910_FarC	1	-----
AFLA_012010_FarB	54	CDVVENGSPTNCRLDQVDCIWTESKRRKRVHAENMIRLPHSSQNRGLTSSALLCHFPGN
AFL2G_05109_FarA	61	CDAASLGVPTNCVAFSLECKIPTPKRKKNQTKAKESGSE-----
AFLA_082910_FarC	1	-----
AFLA_012010_FarB	114	HVLRLTPTTSSLNRPRRLPKTEVDFYDSDVNATG-----RMIFQRRLPSPVIWTRGN
AFL2G_05109_FarA	102	-----ENPKETPKDDQSTTDGKDAFGSSNRMAVDGMEVTSLETESQA-----
AFLA_082910_FarC	1	-----
AFLA_012010_FarB	167	ICHISSVRISLRPGMRLIECKLYTFIISTIDQSQVSRIGAGPERYRRRMAPNPVAVPAT
AFL2G_05109_FarA	145	-A-----Q-----QATQNGAYAQFVKPKAR-APTK--EAGRVAVLG-----
AFLA_082910_FarC	1	-----
AFLA_012010_FarB	227	MPLHHVTSQIQQLDPSFANARSGGII LPDYI---RGLPPELQKEIDIDYLAMKGA LTPD
AFL2G_05109_FarA	178	-----ESSNLSLLVQDRHGCTDVVHYFLPPNIRGSRARLADLDNLELDILHORGAFLLPP
AFLA_082910_FarC	1	-----MAEYHSTCHPDELEPLELEILLHRRDAERLPP
AFLA_012010_FarB	284	VGLRNELLKAYIHYVHTYMP LIDLEDFLQITIAQN GIRMSLLLFQAVMFA GAFVLDLKH
AFL2G_05109_FarA	233	RFLCDELVDAYFKWVAPVVPVNNRSRFRHYRDPK--NPPSLLLLQATLLAGSRVCTNPQ
AFLA_082910_FarC	32	KAVQDILVEVDFKQVAPLLPVDRDAFLRQYESAE--DSPSLLLQAMLMVSRCS TSEQ
AFLA_012010_FarB	344	LQAAGYSRKAARKSEFFQRAILLYDFDYVDRI SLVQSL LLMTYWYETPDDQK--DTWHW
AFL2G_05109_FarA	291	LMDA-NGSTTPAAMTFYKRAKALYDANYEDDRWTVQALVLLGWYWEGPE DWTKNV FYW
AFLA_082910_FarC	90	RS----KEYTVSPRTFYKRAKALYDAGYETNLITVQAVVLLGAYWEGPDDLETESGIF YW
AFLA_012010_FarB	402	MGVSLSLAHTGLHRDPGNSRM DVRRQRWVKRIWWTYTRDLIALGMRRP MRVKDDDCD

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AFL2G_05109_FarA 349 TRVAMVVAQSGMHRSEVESQLSKPKRLWKRIWWTLETRDRSVAALGRPTGINDDSD
AFLA_082910_FarC 146 SRLGLALAOEGLHDSERYICLQPSERGLRKRIWWTLYTRDRSVAAAFGRPLHINPNYCT

AFLA_012010_FarB 462 VEMLTEDDFEFHPFSPFIVSMVGNSEVLQNVSHQKELALMTEKAKLCLCWSHVLSAQYS
AFL2G_05109_FarA 409 VGMLTEDDFLEDEIDIA-----AEYFPDPVHVQFFIQQYVKLCEIMGLVLAQQYS
AFLA_082910_FarC 206 VEPLTESDFEYDGN-----PSEPTGEVQAREFVEYVKLCQIMDLGLCLNLS

AFLA_012010_FarB 522 VLSHKFGGTMETMMLVPPKSAAEFEVVRCDQELDLDLAHLPSERQYAPMAPAKLTEAQ
AFL2G_05109_FarA 458 VASKS-----RRMNAMDLTHSDMALADWLQNCPEKWCWQRQNH-----
AFLA_082910_FarC 254 ARSTQ-----DARAGAAQCGLCLNEWLVACPPELHWRQTRH-----

AFLA_012010_FarB 582 EVLHSHRALLFMVYLTTSSALHRPQILPAMPFPSIDA--EIQDISRNKVRFAAVEITNIA
AFL2G_05109_FarA 496 ---HFWAALLANYTTLCLLHRAHPPASSAPNRYRVEEMAYPSRTIAFQAAGMITISIV
AFLA_082910_FarC 291 ---TELSAALLFSTF-----

AFLA_012010_FarB 640 QDLHALDLTRYEPPTTCVTVLLPAVITLHLLDKSSDENVRMVSLQRFYQCMRILQRVREIY
AFL2G_05109_FarA 553 ENLQTHQEIRYTPAFIVYSLFSALILHVVYQMRSSVETVVATCQERINICMQALKDYSKVV
AFLA_082910_FarC -----

AFLA_012010_FarB 700 ASADFATSFLEAAIRKAGIQLTVAP---QDVQ-----SRNNECTFDSVRLN
AFL2G_05109_FarA 613 LVAKMVRITLFSIILGNKVIIEERLQKAAGKRHRQIRHDTAQHQPPRPDPKPKKFDVMDLG
AFLA_082910_FarC -----

AFLA_012010_FarB 742 TLT---PPDLSLAQKIEDLTYEKTSGLRLAGEAAEASGFASSTPPESDGENGSTNNINPH
AFL2G_05109_FarA 673 LPNGGPTPPVSYERSRFQ--TEAVIPSRREMCQPLNVPOSSPTGEPAGNSRGNTRPTTF
AFLA_082910_FarC -----

AFLA_012010_FarB 799 YHODAFATPNLSDLSISELMDLANDAEVTQNDFDALINFDITGAEIF-----AAD
AFL2G_05109_FarA 731 --NAQHSIPATPPDLFIVTRTSPNLS-PSLWENFQPDQLEFD-GTAFPELTSPQQTAVD
AFLA_082910_FarC -----

AFLA_012010_FarB 850 DGLDINGNPKGQGYGF-----NIGTMDNVFDLFGTESKGVGLITGLNGQVHEDR
AFL2G_05109_FarA 787 PQLQSSQLQTQGMQRHMMPHQMSRGLPGTQGSPEMISNIPPGLGMOQQPPQVFGME
AFLA_082910_FarC -----

AFLA_012010_FarB 899 TSTT-----LCA-----NEAPRATELDGTADLEAELGNL-----
AFL2G_05109_FarA 847 NQQPWPAGLEAALHTGVEAASQDDTWSNSRSRSCPTAPPTLNVEDWFQFFGNGSGDLS
AFLA_082910_FarC -----

AFLA_012010_FarB ---
AFL2G_05109_FarA 907 TSA
AFLA_082910_FarC ---

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Figure S2 Functional domains and multiple sequence alignment of Far proteins in *A. flavus*. (A) These regions contribute to protein-DNA and protein-protein interactions. MHR, fungal-specific middle homology region. (B) Multiple sequence alignment (using Clustal) showing three *A. flavus* Far protein alignment and FarC lacking Zn2Cys6 DNA binding domain.