Supplementary Materials: The Stress Response Regulator AflSkn7 Influences Morphological Development, Stress Response, and Pathogenicity in the Fungus *Aspergillus flavus*

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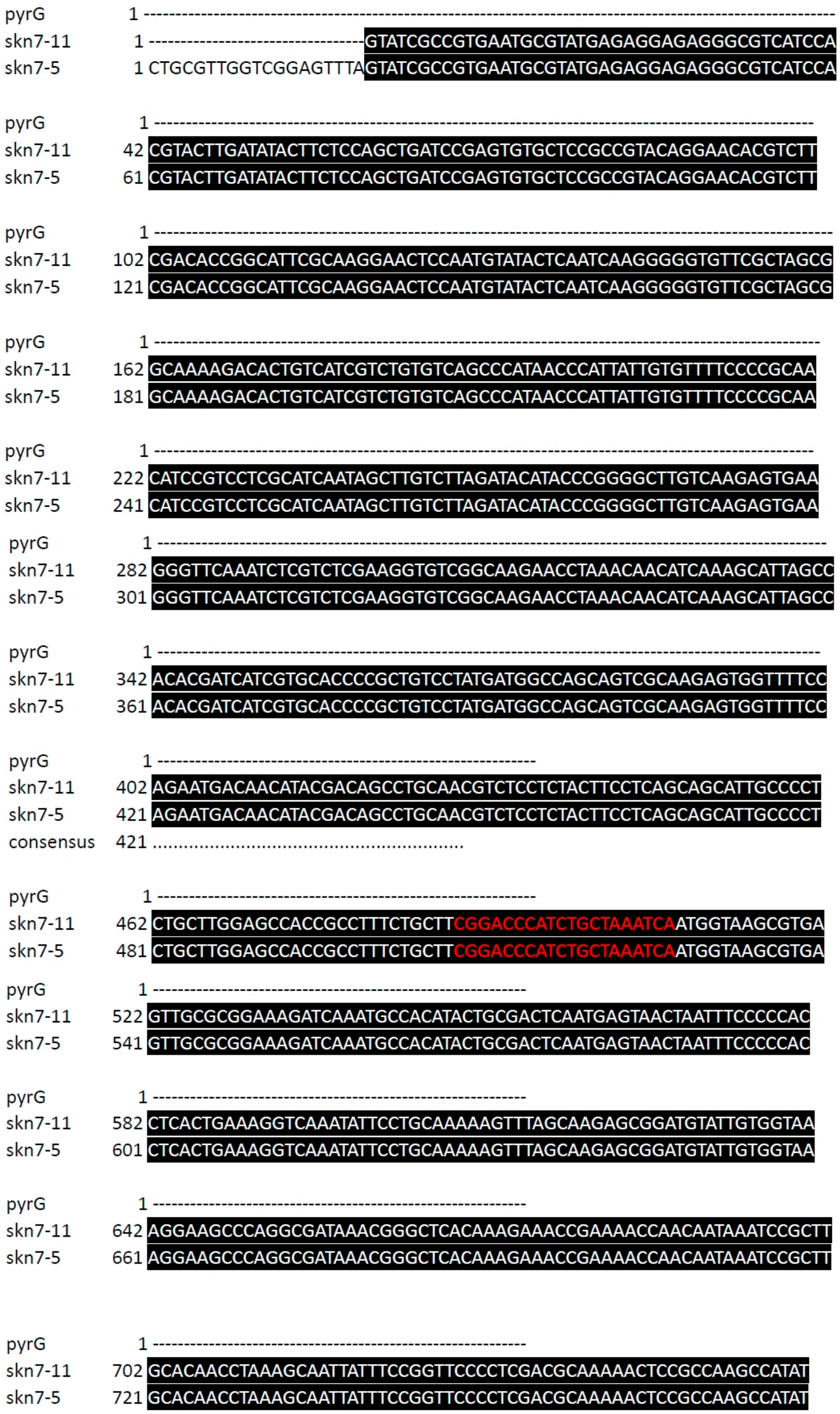
Table S1. Primers used in this study.

Primers	Sequences (5′-3′)
AflSkn7UF	CAGCAGCCTATCTCCATCTT
AflSkn7UR	GGGTGAAGAGCATTGTTTGAGGCCGAACAAGCAACAGGCTCAA
AflSkn7DF	GCATCAGTGCCTCCTCTCAGACACACGCAACCATTCACCTAC
AflSkn7DR	AACATCCGTCCTCGCATCAA
AflSkn7UUF	ATCAGTATGTGCCTTCCGAGTG
AflSkn7DDR	CGACGATAGCGATCTCCATT
pyrGF	GCCTCAAACAATGCTCTTCACCC
pyrGR	GTCTGAGAGGAGGCACTGATGC
AflSkn7F	TGTCGTCTTGGAGGTAATGC
AflSkn7R	ATTGTCTGCGAACTGTCTCC
AflSkn7RTF	CGGGCGAACAGCAAAGAATC
AflSkn7RTR	TCAAACTGCCGAATGAGGTG
AflJ/qF	CGTCTACACCTCTTGTCTTCTG
AflJ/qR	TCATCAACCTGGCATCATCTC
AflQ/qF	GTCGCATATGCCCCGGTCGG
AflQ/qR	GGCAACCAGTCGGGTTCCGG
NsdC/qF	CTTCATCGCGCTCACTCTCC
NsdC/qR	GGTTGCTAGAATGGCTGTGG
NsdD/qF	CGGAACCAGGATGCCTTACTAC
NsdD/qR	CTGCTTTGCCTCGTCGCTTC
gtr/qF	ACATTCTCGGACTCGGCGT
gtr/qR	AGCACTGGTAGGGTGGATCG
sod/qF	TGAGCGTGCCTTCCATGTC
sod/qR	CGTGGCGGTTCTCATCCTC
fsk1/qF	CAACATCGCCTGGTGGACT
fsk1/qR	CTTGCGGAGCTTAGACTGC
och1/qF	CACGGAGGAAACACTACGGATGAAGAAGG
och1/qR	CAGGGCTGAAGCTCGTAATGGGTAGAACT
Actin/qF	ACGGTGTCGTCACAAACTGG
Actin/qR	CGGTTGGACTTAGGGTTGATAG



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pyrG          1 ------------------------------------------------------------
skn7-11       1 -------------------GTATCGCCGTGAATGCGTATGAGAGGAGAGGGCGTCATCCA
skn7-5        1 CTGCGTTGGTCGGAGTTTAGTATCGCCGTGAATGCGTATGAGAGGAGAGGGCGTCATCCA

pyrG          1 ------------------------------------------------------------
skn7-11      42 CGTACTTGATATACTTCTCCAGCTGATCCGAGTGTGCTCCGCCGTACAGGAACACGTCTT
skn7-5       61 CGTACTTGATATACTTCTCCAGCTGATCCGAGTGTGCTCCGCCGTACAGGAACACGTCTT

pyrG          1 ------------------------------------------------------------
skn7-11     102 CGACACCGGCATTCGCAAGGAACTCCAATGTATACTCAATCAAGGGGGTGTTCGCTAGCG
skn7-5      121 CGACACCGGCATTCGCAAGGAACTCCAATGTATACTCAATCAAGGGGGTGTTCGCTAGCG

pyrG          1 ------------------------------------------------------------
skn7-11     162 GCAAAAGACACTGTCATCGTCTGTGTCAGCCCATAACCCATTATTGTGTTTTCCCCGCAA
skn7-5      181 GCAAAAGACACTGTCATCGTCTGTGTCAGCCCATAACCCATTATTGTGTTTTCCCCGCAA

pyrG          1 ------------------------------------------------------------
skn7-11     222 CATCCGTCCTCGCATCAATAGCTTGTCTTAGATACATACCCGGGGCTTGTCAAGAGTGAA
skn7-5      241 CATCCGTCCTCGCATCAATAGCTTGTCTTAGATACATACCCGGGGCTTGTCAAGAGTGAA
pyrG          1 ------------------------------------------------------------
skn7-11     282 GGGTTCAAATCTCGTCTCGAAGGTGTCGGCAAGAACCTAAACAACATCAAAGCATTAGCC
skn7-5      301 GGGTTCAAATCTCGTCTCGAAGGTGTCGGCAAGAACCTAAACAACATCAAAGCATTAGCC

pyrG          1 ------------------------------------------------------------
skn7-11     342 ACACGATCATCGTGCACCCCGCTGTCCTATGATGGCCAGCAGTCGCAAGAGTGGTTTTCC
skn7-5      361 ACACGATCATCGTGCACCCCGCTGTCCTATGATGGCCAGCAGTCGCAAGAGTGGTTTTCC

pyrG          1 ------------------------------------------
skn7-11     402 AGAATGACAACATACGACAGCCTGCAACGTCTCCTCTACTTCCTCAGCAGCATTGCCCCT
skn7-5      421 AGAATGACAACATACGACAGCCTGCAACGTCTCCTCTACTTCCTCAGCAGCATTGCCCCT
consensus   421 ..................................................

pyrG          1 ------------------------------------------
skn7-11     462 CTGCTTGGAGCCACCGCCTTTCTGCTTCGGACCCATCTGCTAAATCAATGGTAAGCGTGA
skn7-5      481 CTGCTTGGAGCCACCGCCTTTCTGCTTCGGACCCATCTGCTAAATCAATGGTAAGCGTGA
pyrG          1 ------------------------------------------
skn7-11     522 GTTGCGCGGAAAGATCAAATGCCACATACTGCGACTCAATGAGTAACTAATTTCCCCCAC
skn7-5      541 GTTGCGCGGAAAGATCAAATGCCACATACTGCGACTCAATGAGTAACTAATTTCCCCCAC

pyrG          1 ------------------------------------------
skn7-11     582 CTCACTGAAAGGTCAAATATTCCTGCAAAAAGTTTAGCAAGAGCGGATGTATTGTGGTAA
skn7-5      601 CTCACTGAAAGGTCAAATATTCCTGCAAAAAGTTTAGCAAGAGCGGATGTATTGTGGTAA

pyrG          1 ------------------------------------------
skn7-11     642 AGGAAGCCCAGGCGATAAACGGGCTCACAAAGAAACCGAAAACCAACAATAAATCCGCTT
skn7-5      661 AGGAAGCCCAGGCGATAAACGGGCTCACAAAGAAACCGAAAACCAACAATAAATCCGCTT


pyrG          1 ------------------------------------------
skn7-11     702 GCACAACCTAAAGCAATTATTTCCGGTTCCCCTCGACGCAAAAACTCCGCCAAGCCATAT
skn7-5      721 GCACAACCTAAAGCAATTATTTCCGGTTCCCCTCGACGCAAAAACTCCGCCAAGCCATAT
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pyrG         1 ------------------------------------------------------------
skn7-11    762 TGAATGATTCATCCCACTCCCGTCCTTTTGTTTGCATGTTTGATCTGTTTGCGAGGTTTG
skn7-5     781 TGAATGATTCATCCCACTCCCGTCCTTTTGTTTGCATGTTTGATCTGTTTGCGAGGTTTG

pyrG         1 ------------------------------------------------------------
skn7-11    822 CCGCCCAAGTTCTGTTCCTTTCACGTGACCCACGTGACTGGGAGCATTAGCCACACACAA
skn7-5     841 CCGCCCAAGTTCTGTTCCTTTCACGTGACCCACGTGACTGGGAGCATTAGCCACACACAA

pyrG         1 ------------------------------------------------------------
skn7-11    882 CCTGAAGGACCAGCTTCAGCCCCAAAGAGTCCAGAACACCATCCAAGGCCCAGGCCCTCC
skn7-5     901 CCTGAAGGACCAGCTTCAGCCCCAAAGAGTCCAGAACACCATCCAAGGCCCAGGCCCTCC

pyrG         1 ------------------------------------------------------------
skn7-11    942 TGGACTGCTGGTAGTATCCCTTGTTCAGGAACCAAAGGTCTAGAACCTTAATATGCATCT
skn7-5     961 TGGACTGCTGGTAGTATCCCTTGTTCAGGAACCAAAGGTCTAGAACCTTAATATGCATCT

pyrG         1 ------------------------------------------------------------
skn7-11   1002 CTATTGTACGTCAAATTAAATAGGAGTTCCGGTCAGACGATATCTTCCCCCCGAGTCGAA
skn7-5    1021 CTATTGTACGTCAAATTAAATAGGAGTTCCGGTCAGACGATATCTTCCCCCCGAGTCGAA
pyrG         1 ------------------------------------------------------------
skn7-11   1062 GGGCAATCGGAAGCTCCCAAGCTCCTGTGGATTACCCGGTCCGTCTGGGGCTGGGGTAGT
skn7-5    1081 GGGCAATCGGAAGCTCCCAAGCTCCTGTGGATTACCCGGTCCGTCTGGGGCTGGGGTAGT

pyrG         1 ------------------------------------------------------------
skn7-11   1122 GCAAAGAGTGTGGAATGATATGTGTTCCGGACGAAGCATACCCACTTGTGTACGTGTGCG
skn7-5    1141 GCAAAGAGTGTGGAATGATATGTGTTCCGGACGAAGCATACCCACTTGTGTACGTGTGCG

pyrG         1 ------------------------------------------------------------
skn7-11   1182 CACAGTGTAGGAAGGGCTTCTGAGTGGAGGATATATTGCAGGATGACTGATCTGAAGAAT
skn7-5    1201 CACAGTGTAGGAAGGGCTTCTGAGTGGAGGATATATTGCAGGATGACTGATCTGAAGAAT

pyrG         1 ---------------------GTCTGAGAGGAGGCACTGATGCGTGATGCCAAGCTGTTA
skn7-11   1242 GGTAGGTGAATGGTTGCGTGTGTCTGAGAGGAGGCACTGATGCGTGATGCCAAGCTGTTA
skn7-5    1261 GGTAGGTGAATGGTTGCGTGTGTCTGAGAGGAGGCACTGATGCGTGATGCCAAGCTGTTA

pyrG        40TCTCTTCTGCACAGGTCGACTTGTCCTGAGGGACCTTCCATATTAAGCTATCAGTCCACT
skn7-11   1302 TCTCTTCTGCACAGGTCGACTTGTCCTGAGGGACCTTCCATATTAAGCTATCAGTCCACT
skn7-5    1321 TCTCTTCTGCACAGGTCGACTTGTCCTGAGGGACCTTCCATATTAAGCTATCAGTCCACT
pyrG       100TTGCTTATCGACTACATAGATAAAGCCTTGGCGTTTCTGGCAAAGCTTACCTCACTTGCT
skn7-11   1362 TTGCTTATCGACTACATAGATAAAGCCTTGGCGTTTCTGGCAAAGCTTACCTCACTTGCT
skn7-5    1381 TTGCTTATCGACTACATAGATAAAGCCTTGGCGTTTCTGGCAAAGCTTACCTCACTTGCT


pyrG       160AGATGACTGGTAGGAATCTAACAAAGGGAAAACCTTGACGATTGGGGGCGGAAAACATGG
skn7-11   1422 AGATGACTGGTAGGAATCTAACAAAGGGAAAACCTTGACGATTGGGGGCGGAAAACATGG
skn7-5    1441 AGATGACTGGTAGGAATCTAACAAAGGGAAAACCTTGACGATTGGGGGCGGAAAACATGG

pyrG       220CATTACAGGGGCCAATACGGACGAGCTCATCGTTTAATGACAGGCACAATGTATGCAGCC
skn7-11   1482 CATTACAGGGGCCAATACGGACGAGCTCATCGTTTAATGACAGGCACAATGTATGCAGCC
skn7-5    1501 CATTACAGGGGCCAATACGGACGAGCTCATCGTTTAATGACAGGCACAATGTATGCAGCC

pyrG       280 TTCCTCCACAACACTCGTACTGGCACTACACTTTTGCTCCAAGAGGAAATCATGACTTGC
skn7-11   1542TTCCTCCACAACACTCGTACTGGCACTACACTTTTGCTCCAAGAGGAAATCATGACTTGC
skn7-5    1561TTCCTCCACAACACTCGTACTGGCACTACACTTTTGCTCCAAGAGGAAATCATGACTTGC
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pyrG       340 CGCATACTCTGGCCATATAAGCTTCCCAGCCTTCTTTCTGGTACCGCTGTGCAGCTTCAA
skn7-11   1602CGCATACTCTGGCCATATAAGCTTCCCAGCCTTCTTTCTGGTACCGCTGTGCAGCTTCAA
skn7-5    1621CGCATACTCTGGCCATATAAGCTTCCCAGCCTTCTTTCTGGTACCGCTGTGCAGCTTCAA


pyrG       400CCGGGTCGGGAGCAGCGTAGATGCCTCGACCGGCGATGATAAAGTCGGCACCGCGTCCAA
skn7-11   1662 CCGGGTCGGGAGCAGCGTAGATGCCTCGACCGGCGATGATAAAGTCGGCACCGCGTCCAA
skn7-5    1681 CCGGGTCGGGAGCAGCGTAGATGCCTCGACCGGCGATGATAAAGTCGGCACCGCGTCCAA

pyrG       460TAGCCGATGCAGGAGTCTGGTATTGCTGTCCAAGCTTATCTCCTTTGGAAGAGAGGTTCA
skn7-11   1722 TAGCCGATGCAGGAGTCTGGTATTGCTGTCCAAGCTTATCTCCTTTGGAAGAGAGGTTCA
skn7-5    1741 TAGCCGATGCAGGAGTCTGGTATTGCTGTCCAAGCTTATCTCCTTTGGAAGAGAGGTTC
pyrG       520CACCCGTCGTGAAGACCACGAAATCTTCATCCTCCGAGGCTGAAGACACATCCGACTGCA
skn7-11   1782 CACCCGTCGTGAAGACCACGAAATCTTCATCCTCCGAGGCTGAAGACACATCCGACTGCA
skn7-5    1801 CACCCGTCGTGAAGACCACGAAATCTTCATCCTCCGAGGCTGAAGACACATCCGACTGCA

pyrG       580CTTCCGTCAGGGCCCGCGTCGACACGAAACCCATAACGAAGTTCTTGTATTTGCGAGCGT
skn7-11   1842 CTTCCGTCAGGGCCCGCGTCGACACGAAACCCATAACGAAGTTCTTGTATTTGCGAGCGT
skn7-5    1861 CTTCCGTCAGGGCCCGCGTCGACACGAAACCCATAACGAAGTTCTTGTATTTGCGAGCGT
pyrG       640AGTCAACCGATGCCTTGGTATACTCGCCCGTAGCCAGCGATCCTTTGGAGGTCATCTCTG
skn7-11   1902 AGTCAACCGATGCCTTGGTATACTCGCCCGTAGCCAGCGATCCTTTGGAGGTCATCTCTG
skn7-5    1921 AGTCAACCGATGCCTTGGTATACTCGCCCGTAGCCAGCGATCCTTTGGAGGTCATCTCTG

pyrG       700CCAGGACCAACAGTCCTCTCTCAGGACCATAGGGGAAGTCTTGCGCAGATGCGGTCTGGG
skn7-11   1962 CCAGGACCAACAGTCCTCTCTCAGGACCATAGGGGAAGTCTTGCGCAGATGCGGTCTGGG
skn7-5    1981 CCAGGACCAACAGTCCTCTCTCAGGACCATAGGGGAAGTCTTGCGCAGATGCGGTCTGGG

pyrG       760CCAGAGCCTCGACGATGCCCTCGCCAGGGAGAACGCTGCAGTTGATAATGTGGGCCCATT
skn7-11   2022 CCAGAGCCTCGACGATGCCCTCGCCAGGGAGAACGCTGCAGTTGATAATGTGGGCCCATT
skn7-5    2041 CCAGAGCCTCGACGATGCCCTCGCCAGGGAGAACGCTGCAGTTGATAATGTGGGCCCATT

pyrG       820 CGGAGATCCTCAGAGCACCGCCGTGGTATTGCTTCTGGACGGTATTGCCGATGTCGATGA
skn7-11   2082 CGGAGATCCTCAGAGCACCGCCGTGGTATTGCTTCTGGACGGTATTGCCGATGTCGATGA
skn7-5    2101 CGGAGATCCTCAGAGCACCGCCGTGGTATTGCTTCTGGACGGTATTGCCGATGTCGATGA


pyrG       880 ATTTGCGGTCCTCGAAGATCAAAAAGTTGTGCTTTTGAGCCAGCACATTCAGGCCATTGA
skn7-11   2142 ATTTGCGGTCCTCGAAGATCAAAAAGTTGTGCTTTTGAGCCAGCACATTCAGGCCATTGA
skn7-5    2161 ATTTGCGGTCCTCGAAGATCAAAAAGTTGTGCTTTTGAGCCAGCACATTCAGGCCATTGA
pyrG       940TAGTGTCGACGCTGAAATCGGTGAGGATGTCGATGTGTGTCTTGATGACGGCGATGTAGG
skn7-11   2202 TAGTGTCGACGCTGAAATCGGTGAGGATGTCGATGTGTGTCTTGATGACGGCGATGTAGG
skn7-5    2221 TAGTGTCGACGCTGAAATCGGTGAGGATGTCGATGTGTGTCTTGATGACGGCGATGTAGG

pyrG      1000GACCGAGACCTGTATCATCAAAAGTTGATTAGTCCATTGCTAGACGGCATATGTATTGGA
skn7-11   2262 GACCGAGACCTGTATCATCAAAAGTTGATTAGTCCATTGCTAGACGGCATATGTATTGGA
skn7-5    2281 GACCGAGACCTGTATCATCAAAAGTTGATTAGTCCATTGCTAGACGGCATATGTATTGGA

pyrG      1060TCCAACAGCTTCCGTACGGTCAGCGAGGTCCAGGAGTTCTCGGGTTGTCGTCACATCAGC
skn7-11   2322 TCCAACAGCTTCCGTACGGTCAGCGAGGTCCAGGAGTTCTCGGGTTGTCGTCACATCAGC
skn7-5    2341 TCCAACAGCTTCCGTACGGTCAGCGAGGTCCAGGAGTTCTCGGGTTGTCGTCACATCAGC

pyrG      1120AGAGACGGTAACGTTTGTCTTCTTTGCTTCGGCAATCTCAAAAAGTCTCTTTGCCAGAGG
skn7-11   2382 AGAGACGGTAACGTTTGTCTTCTTTGCTTCGGCAATCTCAAAAAGTCTCTTTGCCAGAGG
skn7-5    2401 AGAGACGGTAACGTTTGTCTTCTTTGCTTCGGCAATCTCAAAAAGTCTCTTTGCCAGAGG
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pyrG       1180 ATTGGGGTGCTTGCTGGCTCGAGCACCGTAAGTCAATTGCGACTTGGACGACATCGTGGG
skn7-11    2442 ATTGGGGTGCTTGCTGGCTCGAGCACCGTAAGTCAATTGCGACTTGGACGACATCGTGGG
skn7-5     2461 ATTGGGGTGCTTGCTGGCTCGAGCACCGTAAGTCAATTGCGACTTGGACGACATCGTGGG

pyrG       1240 AATGGAGGGTTATATGCGGGGTATGACGGTGATTGATGAGTTGAAGTAGCCGAGCAATGA
skn7-11    2502 AATGGAGGGTTATATGCGGGGTATGACGGTGATTGATGAGTTGAAGTAGCCGAGCAATGA
skn7-5     2521 AATGGAGGGTTATATGCGGGGTATGACGGTGATTGATGAGTTGAAGTAGCCGAGCAATGA

pyrG       1300 GGTATATTATCCAATTGAGGGTGACCCAACCAAATCAATTGCTTGAGAATCAAATCTCAA
skn7-11    2562 GGTATATTATCCAATTGAGGGTGACCCAACCAAATCAATTGCTTGAGAATCAAATCTCAA
skn7-5     2581 GGTATATTATCCAATTGAGGGTGACCCAACCAAATCAATTGCTTGAGAATCAAATCTCAA

pyrG       1360 ATATTCTAAAATAGAAGCCGCCGGGGACTAAATTTAAAGTCGTACTCTATCTCGATCTTT
skn7-11    2622 ATATTCTAAAATAGAAGCCGCCGGGGACTAAATTTAAAGTCGTACTCTATCTCGATCTTT
skn7-5     2641 ATATTCTAAAATAGAAGCCGCCGGGGACTAAATTTAAAGTCGTACTCTATCTCGATCTTT

pyrG       1420 TCCGCGTGTAAAAATTGCGTGCCAATCTGGATGGAGACAGGCCACATCGGTGCTGTATTC
skn7-11    2682 TCCGCGTGTAAAAATTGCGTGCCAATCTGGATGGAGACAGGCCACATCGGTGCTGTATTC
skn7-5     2701 TCCGCGTGTAAAAATTGCGTGCCAATCTGGATGGAGACAGGCCACATCGGTGCTGTATTC

pyrG       1480 CTCCGCCTCCGACTGTGGGGTCAACCACAATTAAACTATTCTGTAGTCAGGTACAGCTAG
skn7-11    2742 CTCCGCCTCCGACTGTGGGGTCAACCACAATTAAACTATTCTGTAGTCAGGTACAGCTAG
skn7-5     2761 CTCCGCCTCCGACTGTGGGGTCAACCACAATTAAACTATTCTGTAGTCAGGTACAGCTAG

pyrG       1540 AATGGGGTAGACAGGCAGAACTGTAGAAGATAAAACATTGGTCAATCACTGGTAACTCCA
skn7-11    2802 AATGGGGTAGACAGGCAGAACTGTAGAAGATAAAACATTGGTCAATCACTGGTAACTCCA
skn7-5     2821 AATGGGGTAGACAGGCAGAACTGTAGAAGATAAAACATTGGTCAATCACTGGTAACTCCA


pyrG       1600 CGGAACTTTTAACGTACATATATATATATACACAACATATTTCGTCAGACACAGAATAAC
skn7-11    2862 CGGAACTTTTAACGTACATATATATATATACACAACATATTTCGTCAGACACAGAATAAC
skn7-5     2881 CGGAACTTTTAACGTACATATATATATATACACAACATATTTCGTCAGACACAGAATAAC

pyrG       1660 TCTCAGTAAGAGATCATGTCTTTGGCAACACCAAACACACTCAGAGCCCACAGAGCGCCT
skn7-11    2922 TCTCAGTAAGAGATCATGTCTTTGGCAACACCAAACACACTCAGAGCCCACAGAGCGCCT
skn7-5     2941 TCTCAGTAAGAGATCATGTCTTTGGCAACACCAAACACACTCAGAGCCCACAGAGCGCCT
pyrG       1720 TGAGAAAACCAGAAGAAACCTCCCAGCAATCTGCCCTTGCCTTGTGGCTTACCCGAGTAC
skn7-11    2982 TGAGAAAACCAGAAGAAACCTCCCAGCAATCTGCCCTTGCCTTGTGGCTTACCCGAGTAC
skn7-5     3001 TGAGAAAACCAGAAGAAACCTCCCAGCAATCTGCCCTTGCCTTGTGGCTTACCCGAGTAC

pyrG       1780 ACATAGCCGTACAAGTAGAGAGATCGGAAAAACAGCCATGAAGCGCCAATTGCTGTTGCC
skn7-11    3042 ACATAGCCGTACAAGTAGAGAGATCGGAAAAACAGCCATGAAGCGCCAATTGCTGTTGCC
skn7-5     3061 ACATAGCCGTACAAGTAGAGAGATCGGAAAAACAGCCATGAAGCGCCAATTGCTGTTGCC

pyrG       1840 AGGTGAGGGTATTTCAGACCCGCGAAGAGGGTGAAGAGCATTGTTTGAGGC---------------
skn7-11    3102 AGGTGAGGGTATTTCAGACCCGCGAAGAGGGTGAAGAGCATTGTTTGAGGCCGAACAAGC
skn7-5     3121 AGGTGAGGGTATTTCAGACCCGCGAAGAGGGTGAAGAGCATTGTTTGAGGCCGAACAAGC

pyrG            ----------------------------------------------------------------------------------------------------
skn7-11    3162 AACAGGCTCAAGCACGTCGCAGAACCTCAAGAACAACGGCTGCGGGAGAGTATGAAAAGA
skn7-5     3181 AACAGGCTCAAGCACGTCGCAGAACCTCAAGAACAACGGCTGCGGGAGAGTATGAAAAGA

pyrG            ---------------------------------------------------------------------------------------------------
skn7-11    3222 ACAAGAAAATGAACATCCAAGTCGGTGGTCAATTACGCACCGGGATCGAGAAGGAGGAAT
skn7-5     3241 ACAAGAAAATGAACATCCAAGTCGGTGGTCAATTACGCACCGGGATCGAGAAGGAGGAAT
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pyrG          ------------------------------------------------------------
skn7-11  3282 TTCCGGGAGAAAGGATAAGTAAGAATAACGGTGAAGAAGAGAAAGAGAAAAGAAAAAAAG
skn7-5   3301 TTCCGGGAGAAAGGATAAGTAAGAATAACGGTGAAGAAGAGAAAGAGAAAAGAAAAAAAG

pyrG          ------------------------------------------------------------
skn7-11  3342 AAGGGAAAAAAATGACGGTCTAACCTGGACGGCGTTTGGTTGGGAGAGGTCAAGAGAAAG
skn7-5   3361 AAGGGAAAAAAATGACGGTCTAACCTGGACGGCGTTTGGTTGGGAGAGGTCAAGAGAAAG

pyrG          ------------------------------------------------------------
skn7-11  3402 AGTAGGGAAAGAGATGGTGGCAGTTCCCTTCAGTTAAGTTTTGGGTAATTTACTACTTCT
skn7-5   3421 AGTAGGGAAAGAGATGGTGGCAGTTCCCTTCAGTTAAGTTTTGGGTAATTTACTACTTCT

pyrG          ------------------------------------------------------------
skn7-11  3462 TGCGAAAAGTGGGACTTTTGATGGGGGGTCACTGACTTGGTATCTGCACCCGCCATTGGC
skn7-5   3481 TGCGAAAAGTGGGACTTTTGATGGGGGGTCACTGACTTGGTATCTGCACCCGCCATTGGC

pyrG          ------------------------------------------------------------
skn7-11  3522 CTTTCCTGTGCTGTCCGAACCACCGGTCACCGTTCACTAGCCACAACTTGCCATTTTTCC
skn7-5   3541 CTTTCCTGTGCTGTCCGAACCACCGGTCACCGTTCACTAGCCACAACTTGCCATTTTTCC
pyrG          ------------------------------------------------------------
skn7-11  3582 TCTGCTTTTTTTTACTTTTCAAATTCCTTTCATTGCTTTTTCTTTTTTTTTTTTGGTCCT
skn7-5   3601 TCTGCTTTTTTTTACTTTTCAAATTCCTTTCATTGCTTTTTCTTTTTTTTTTTTGGTCCT

pyrG          ------------------------------------------------------------
skn7-11  3642 CCCCTTCTGAAATTCTTTGGTACACATTATGGCAATGTTAAACAGCTTTACCTCCGATAA
skn7-5   3661 CCCCTTCTGAAATTCTTTGGTACACATTATGGCAATGTTAAACAGCTTTACCTCCGATAA

pyrG          ------------------------------------------------------------
skn7-11  3702 TGCAAGGAGCTAAAAAGGGGAAGGGCAGAAGGCCAGGAGCTCCTCTCTGACACACTGACC
skn7-5   3721 TGCAAGGAGCTAAAAAGGGGAAGGGCAGAAGGCCAGGAGCTCCTCTCTGACACACTGACC

pyrG          ------------------------------------------------------------
skn7-11  3762 GTAAACAACAGCCGACAAGACATCTACTAAGTGCAATCACCTCGGAGGGGAAATGTCGAT
skn7-5   3781 GTAAACAACAGCCGACAAGACATCTACTAAGTGCAATCACCTCGGAGGGGAAATGTCGAT

pyrG          ------------------------------------------------------------
skn7-11  3822 GTGGAGACAACAATCCACTTCTCGTACTCTCTGCCTTAATGCCTTAAGAGTAAAGAACAT
skn7-5   3841 GTGGAGACAACAATCCACTTCTCGTACTCTCTGCCTTAATGCCTTAAGAGTAAAGAACAT
pyrG          ------------------------------------------------------------
skn7-11  3882 GGTTTGATCATTACGAGTAGATTTGTCGCCAGTCATGAAGGGACAGCTAATTACATCCGA
skn7-5   3901 GGTTTGATCATTACGAGTAGATTTGTCGCCAGTCATGAAGGGACAGCTAATTACATCCGA

pyrG          ------------------------------------------------------------
skn7-11  3942 GTTATTCTCTCTTTGCCTTTCGTCGTGTTCTGGCGTCCAAGGAGTGAACGTTGCAAAGAA
skn7-5   3961 GTTATTCTCTCTTTGCCTTTCGTCGTGTTCTGGCGTCCAAGGAGTGAACGTTGCAAAGAA

pyrG          ------------------------------------------------------------
skn7-11  4002 AGGTCAATGCGTTCATGATGCAGATAACGTGCGAGGAAAGGATGGAGGGGAAAAGATGGA
skn7-5   4021 AGGTCAATGCGTTCATGATGCAGATAACGTGCGAGGAAAGGATGGAGGGGAAAAGATGGA

pyrG          ------------------------------------------------------------
skn7-11  4062 GATAGGCTGCTGGAGATGCAAGAGGAGGGGCAAATCAACCTGCAGCGATCGTCGAACAAA
skn7-5   4081 GATAGGCTGCTGGAGATGCAAGAGGAGGGGCAAATCAACCTGCAGCGATCGTCGAACAAA
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pyrG            ------------------------------------------------------------
skn7-11    4122 AAAAGAGGAGAGAATGAGCGGAGACTCTGTATTCTCATCGACATACTAGACAATCATGAC
skn7-5     4141 AAAAGAGGAGAGAATGAGCGGAGACTCTGTATTCTCATCGACATACTAGACAATCATGAC

pyrG            ------------------------------------------------------------
skn7-11    4182 ATTGACCCTTTTTTTTAATCCAATCATTCAACCATCCGAATTTTGAGGGCACTAGTCAAA
skn7-5     4201 ATTGACCCTTTTTTTTAATCCAATCATTCAACCATCCGAATTTTGAGGGCACTAGTCAAA

pyrG            ------------------------------------------------------------
skn7-11    4242 AAGGTGACCTTGAATCATTCCTTTTTAGGATGCATTCTAGTCAGGTGTACATATTACATA
skn7-5     4261 AAGGTGACCTTGAATCATTCCTTTTTAGGATGCATTCTAGTCAGGTGTACATATTACATA


pyrG            ------------------------------------------------------------
skn7-11    4302 ACATTAATTATGTACACACGGTGGTATGTACTAGTATGTACTATGTAGTACTCCTTTGCA
skn7-5     4321 ACATTAATTATGTACACACGGTGGTATGTACTAGTATGTACTATGTAGTACTCCTTTGCA
pyrG            ------------------------------------------------------------
skn7-11    4362 TGGATCCATACTTCACACTACTTATGTAGTAGGGTAGTATTGACTGAGAGAATTTTTATT
skn7-5     4381 TGGATCCATACTTCACACTACTTATGTAGTAGGGTAGTATTGACTGAGAGAATTTTTATT


pyrG            ------------------------------------------------------------
skn7-11    4422 TATTCATTTTCCCCCCTTGAAGATAGGAGACAAATAAAGATATCATTGACTTTCTTTGTC
skn7-5     4441 TATTCATTTTCCCCCCTTGAAGATAGGAGACAAATAAAGATATCATTGACTTTCTTTGTC

pyrG            ------------------------------------------------------------
skn7-11    4482 CTTCACGTTTCAGTTGTACAGTTGTTTAGTTTTAAATCCTCAACGGTGGAGACTA-----
skn7-5     4501 CTTCACGTTTCAGTTGTACAGTTGTTTAGTTTTAAATCCTCAACGGTGGAGACTACCCCA

pyrG            ----------------
skn7-11        ----------------
skn7-5     4561 ATTGTGTTTTGGTTCA
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Figure S1. The alignment between the sequenced products and the expected sequences. The *skn7-5* and *skn7-11* indicated the sequenced products, while the *pyrG* indicated the expected sequences. Sequences marked with red and yellow letters were two primer pairs (i.e., Afl*Skn7*DR and Afl*Skn7*UF, respectively), which were used for amplifying fusion fragments.

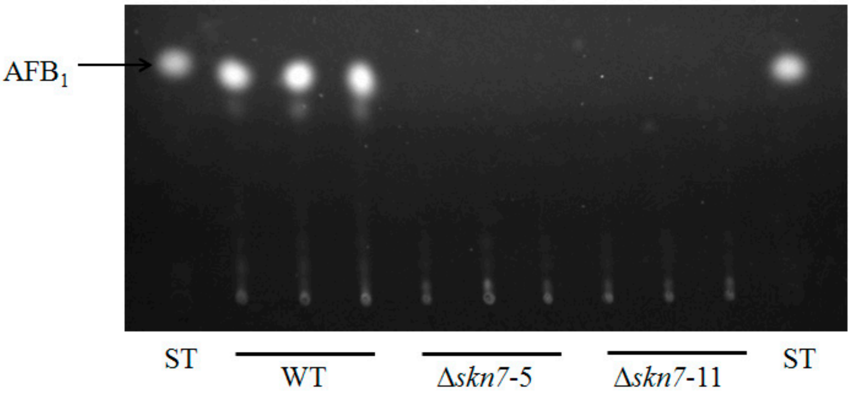

Figure S2. Thin-layer chromatography analysis for aflatoxin production in the indicated strains. Each strain was inoculated into 25 mL of potato dextrose broth (PDB) (supplemented with Zinc and Molybdenum ions) in a 100 mL flask and incubated with shaking at 180 r/m at 28 °C. After six days, the aflatoxin was extracted using a chloroform method. ST, aflatoxin B1; WT, the wild type; Δ*Skn7-5* and Δ*Skn7-11*, two *AflSkn7* deletion mutants.