

Table S1 Quantification of conidiation

Medium	CM	
Strains	Wild type	<i>actA(p)-agnB</i>
Conidiation	100% ± 9.7%	94.7% ± 5.9%

10⁵ conidia were grown on 1.5mL medium in 24-well plate at 30 °C for 4 d. 1 mL ultra-pure H₂O was used to collect conidia from each well. Conidia were quantified by hemocytometer. Results represent the average of three independent quantification tests with triplicates each time ± standard deviation.

Table S2 Expression of *agsB* in *amyD*Δ and *actA(p)-amyD* strains

	A1149	<i>amyD</i> Δ	<i>actA(p)-amyD</i>
<i>agsB</i>	1	1.12± 0.27	1.08± 0.15

A large number of conidia (2 × 10⁷) were inoculated in liquid CM and incubated at 30 °C for 14 h. The expression of *agsB* in A1149 strain was defined as 1. Results present the mean of three independent qPCR tests with triplicates each time ± standard deviation.

Table S3 *Aspergillus nidulans* strains in this study

Strains	alias	Genotype	Origin
A1149	A1149	<i>pyrG89; pyroA4; nkuA::argB</i>	FGSC*
<i>actA(p)-amyD</i>	AXH38	<i>amyDp:: AfpyroA:actAp:amyD; pyrG89; pyroA4; nkuA::argB</i>	He et al. [10]
<i>actA(p)-amyC</i>	AXH52	<i>amyCp:: AfpyroA:actAp:amyC; pyrG89; pyroA4; nkuA::argB</i>	this study
<i>actA(p)-amyE</i>	AXH53	<i>amyE:: AfpyroA:actAp:amyE; pyrG89; pyroA4; nkuA::argB</i>	this study
<i>agnB</i> Δ	AXH78	AN3790:: <i>AfpyroA; pyrG89; pyroA4; nkuA::argB</i>	this study
<i>agnE</i> Δ	AXH42	AN1604:: <i>AfpyroA; pyrG89; pyroA4; nkuA::argB</i>	this study
<i>mutA</i> Δ	AXH79	AN7349:: <i>AfpyrG; pyrG89; pyroA4; nkuA::argB</i>	this study
<i>agnB</i> Δ, <i>mutA</i> Δ	AXH80	AN3790:: <i>AfpyroA; AN7349::AfpyrG; pyrG89; pyroA4; nkuA::argB</i>	this study
<i>actA(p)-agnB</i>	AXH50	<i>agnBp:: AfpyroA:actAp:agnB; pyrG89; pyroA4; nkuA::argB</i>	this study
<i>actA(p)-agnE</i>	AXH47	<i>agnEp:: AfpyroA:actAp:agnE; pyrG89; pyroA4; nkuA::argB</i>	this study
<i>actA(p)-mutA</i>	AXH51	<i>mutAp:: AfpyroA:actAp:mutA; pyrG89; pyroA4; nkuA::argB</i>	this study
<i>actA(p)-agnB, amyD</i> Δ	AXH55	<i>agnBp:: AfpyroA:actAp:agnB; AN3308::AfpyrG; pyrG89; pyroA4; nkuA::argB</i>	this study
<i>actA(p)-mutA, amyD</i> Δ	AXH56	<i>mutAp:: AfpyroA:actAp:mutA; AN3308::AfpyrG; pyrG89; pyroA4; nkuA::argB</i>	this study
<i>amyD-gfp</i>	AXH86	<i>amyD:: AfpyroA:actAp:gfp; pyrG89; pyroA4; nkuA::argB</i>	this study

* Fungal Genetics Stock Center

Table S4 Primers and plasmids in this study

Primers	Sequence 5' to 3'	Description
Selective marker and strain confirmation		
AME1	ATGTCGTCCAAGTCGCAATT	<i>AfpyrG</i> *
AME2	TCATGACTATGCCGATACTAC	<i>AfpyrG</i> *
SE231	GGACATCAGATGCTGGACTAAAG	<i>AfpyrA</i> with native promoter
SE232	TTACCATCCTCTCTGGCCA	<i>AfpyrA</i> with native promoter
AME7	CAATACCGTCCAGAAGCAATAC	<i>AfpyrG</i> confirmation*
AME8	CACATCCGACTAGCACTATCC	<i>AfpyrG</i> confirmation*
AME15	ATTCTGTTCATGGCCAAAG	<i>AfpyrA</i> confirmation*
AME16	TCAACAACATCTCCGGTACC	<i>AfpyrA</i> confirmation*
Gene deletion		
SE103	CGGCCATTGACCATGAAC	<i>amyD</i> upstream F
SE104	AATTGCGACTATGGACGACATTGTGACGATGTCTGGACCG	<i>amyD</i> upstream R (pyrG tail)
SE105	GAGTATGCGCAAGTCATGATTTGATCTGTTTTTCATCTTTTTGC	<i>amyD</i> downstream F (pyrG tail)
SE106	GTCATAGATGTCATACCCGTTTC	<i>amyD</i> downstream R
SE107	GTCTTCATCCGGTCCACTATC	<i>amyD</i> Fusion F
SE108	GAAGATGAGGGTGTGTCG	<i>amyD</i> Fusion R
SE343	GGGGAGTCGAGTTTACACCA	<i>agnB</i> upstream F
SE344	CTTAGTAATCCAGCATCTGATGTCCGATCTGGACCGTCAGTTTCG	<i>agnB</i> upstream R (pyroA tail)
SE408	TGGCCAAGAGAGGATGGTAATTAGCGCATTGTTTCTGCAG	<i>agnB</i> downstream F (pyroA tail)
SE409	GTAGAGACCGCGCTCTGTCT	<i>agnB</i> downstream R
SE347	TTCTCAGTAACCCCAAGACG	<i>agnBA</i> Fusion F
SE410	CGAAGACTGACTTTGGTACCG	<i>agnBA</i> Fusion R
SE320	ATGCCATTGAGCTGGACATT	<i>agnE</i> F
SE321	TCATATCAGGCAAGAGAGCAGG	<i>agnE</i> R
SE322	CTGGCGAGAGATTCTGGAAC	<i>agnE</i> upstream F
SE323	TCCATTACCCATTTCAAGC	<i>agnE</i> upstream R (pyroA tail)
SE324	TGGCCAAGAGAGGATGGTAACACCTAATACCAGGCCAGTTTT	<i>agnE</i> downstream F (pyroA tail)
SE325	CCTCATATAGAGACCGCGCA	<i>agnE</i> downstream R
SE326	CTAGCCTAGCATCTTTACCGACTG	<i>agnEΔ</i> Fusion F
SE327	GTAGAGTTGGGACTTAAGCTAGTCG	<i>agnEΔ</i> Fusion R
SE349	AGTAATTTGCGCGATACCC	<i>mutA</i> upstream F
SE411	GGGCGAGCCTTTAACGTACAGTTGCTTGCTTGAGGCT	<i>mutA</i> upstream R (pyrG tail)
SE190	AATTGCGACTTGGACGACATGGTGTGTTAGGGGTG	<i>actAp</i> R (pyrG tail)
SE191	TACGTTAAAGGCTCGCCC	<i>actAp</i> F
SE412	GAGTATGCGCAAGTCATGATGCTAGAAGGATCGAGCCA	<i>mutA</i> downstream F (pyrG tail)
SE413	GTTTTCTCTGACCCAGTCG	<i>mutA</i> downstream R
SE353	GTTTCGAGTTGGTTGCGAGTC	<i>mutAΔ</i> Fusion F
SE414	CCAAGTTGAGTCTTACGCCG	<i>mutAΔ</i> Fusion R
Promoter exchange		
SE234	TGGCCAAGAGAGGATGGTAATACGTTAAAGGCTCGCCC	<i>actA(p)</i> F (pyroA tail)
SE208	GGTGTGTTAGGGGTGGATTAGAA	<i>actA(p)</i> R
SE355	AGAGCTCATCGTGAAGGATGA	<i>amyC</i> upstream F
SE356	CTTAGTAATCCAGCATCTGATGTCCGTTTGATAGACGGATCTGTCTT	<i>amyC</i> upstream R (pyroA tail)
SE357	TTCTAATCCACCCCTAAACACCATGACTGACAGATTCGCCC	<i>amyC</i> F (<i>actA(p)</i> tail)
SE358	CGTGTGTAAAGTGGGGAGG	<i>amyC</i> _1100 R
SE359	CCTGGAAGTACCTAGGAAACTGG	<i>actA(p)-amyC</i> Fusion F
SE360	AAATTATTGAGTCTAATGGGCGAC	<i>actA(p)-amyC</i> Fusion R

SE361	GGCGCTCCAGTTATACCG	<i>amyE</i> upstream F
SE362	CTTAGTAATCCAGCATCTGATGTCCCCTTAGAAAGGTAGGTTGCTGTG	<i>amyE</i> upstream R (pyroA tail)
SE363	TTCTAATCCACCCCTAAACACCATGCGGCGCCTCACATGT	<i>amyE</i> F (<i>actA</i> (p) tail)
SE364	GTCAGTAGAAGTATGCAGCAGGTTCT	<i>amyE</i> _1100 R
SE365	AAATACCGTTCACCTTGGACG	<i>actA</i> (p)- <i>amyE</i> Fusion F
SE366	CATGGGGTAATTCAGGAGACC	<i>actA</i> (p)- <i>amyE</i> Fusion R
SE343	GGGGAGTCGAGTTTACACCA	<i>agnB</i> upstream F
SE344	CTTAGTAATCCAGCATCTGATGTCCGATCTGGACCGTCAGTTTCG	<i>agnB</i> upstream R (pyroA tail)
SE345	TTCTAATCCACCCCTAAACACCATGTATCTGAAAACGCTCTTTTTG	<i>agnB</i> F (<i>actA</i> (p) tail)
SE346	TTCTCGTCTTGAATGTACTGGTC	<i>agnB</i> _1140 R
SE347	TTCTCAGTAACCCCAAGACG	<i>actA</i> (p)- <i>agnB</i> Fusion F
SE348	GAATGCTGCTCACATGTCCA	<i>actA</i> (p)- <i>agnB</i> Fusion R
SE322	CCGACTGACCATTTCATC	<i>agnE</i> upstream F
SE323	CTTAGTAATCCAGCATCTGATGTCCTTTGCTTCAGGTTTCGCTTC	<i>agnE</i> upstream R (pyroA tail)
SE340	TTCTAATCCACCCCTAAACACCATGCCATTGAGCTGGACATT	<i>agnE</i> F (<i>actA</i> (p) tail)
SE341	ACAGCTTGATGAGAGCTCTTGC	<i>agnE</i> _1100 R
SE326	CTAGCCTAGCATCTTTACCGACTG	<i>actA</i> (p)- <i>agnE</i> Fusion F
SE342	TCACAGGGCCGATATAATGG	<i>actA</i> (p)- <i>agnE</i> Fusion R
SE349	AGTAATTTGCGCGATACCC	<i>mutA</i> upstream F
SE350	CTTAGTAATCCAGCATCTGATGTCCCAGTTGCTTGCTTGAGGCT	<i>mutA</i> upstream R (pyroA tail)
SE351	TTCTAATCCACCCCTAAACACCATGAAGATCTCCACCGCTG	<i>mutA</i> F (<i>actA</i> (p) tail)
SE352	CTAGGCGCTAAAAGAGCCAA	<i>mutA</i> _1100 R
SE353	GTTGAGTTGGTTGCGAGTC	<i>actA</i> (p)- <i>mutA</i> Fusion F
SE354	TACGTCAACCGAAAACCTCCAG	<i>actA</i> (p)- <i>mutA</i> Fusion R
SE429	CCAGTGAAAAGTTCTTCTCCTTTACTGCAGTATAGACCAGCGGTCG	<i>amyD</i> _186R gfp tail
SE427	CATGGCATGGATGAAGTATACAAAGCTGGGGGAACGTTAGT	<i>amyD</i> _1633F gfp tail
SE328	AGTAAAGGAGAAGAAGCTTTTCACTGG	gfp F no start codon
SE315	TTGTATAGTTCATCCATGCCATG	gfp R no stop codon
qPCR		
SE244	CACCCGGACACTAGGTATCTC	Histone qPCR F#
SE245	GAATACTATCGTAACGGCCTTGG	Histone qPCR R#
SE153	GGATGGAGATGACCCTGCTA	<i>amyD</i> qPCR F
SE154	TGCGCATCATGGTAGTCATT	<i>amyD</i> qPCR R
SE334	GGATTCCAGCCAAGTGTGT	<i>amyC</i> qPCR F
SE335	AAAGCCCACTCCCTCTCATT	<i>amyC</i> qPCR R
SE336	TCTGGGTAAAGGGACTGGTG	<i>amyE</i> qPCR F
SE337	GTAGACTTCCCCCATCGTGA	<i>amyE</i> qPCR R
SE332	CTGGCGAGAGATTCTGGAAC	<i>agnB</i> qPCR F
SE333	TCCATTACCCATTTTGAAGC	<i>agnB</i> qPCR R
SE330	CATGATGGGTGGAGGAGTCT	<i>agnE</i> qPCR F
SE331	CAGGAGAGAGCCGATACCAG	<i>agnE</i> qPCR R
SE338	CCAAATGGAATCAACCTGCT	<i>mutA</i> qPCR F
SE339	ATGGGGAAGCTGTTTGTAC	<i>mutA</i> qPCR R

#, Fujioka et al. (2007); *, Alam et al. (2012)

A Percent Identity Matrix - created by Clustal2.1

1: AN4507|amyC 100.00 58.97
 2: AN3308|amyD 58.97 100.00

CLUSTAL O(1.2.4) multiple sequence alignment

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AN4507|amyC -----MTRFARTDGSSTHSCNLTGL
AN3308|amyD MKILPSRLAYIMTVLSVLNISNAATTAEWKARSIQVTMDRFRARTDGSSTHACNTAGL
                * * * * *

AN4507|amyC YCGGTWRGTIDHLDVIQGMGFDAVLISPIIKNVEKAKKGEAYHCHWAQDMYSLNPHFGT
AN3308|amyD YCGGTWRGTINHLDIQGMGFDAVMISPIIENIGGRVSYGEAYHGWPLDLYSLNDHFGT
                * * * * *

AN4507|amyC HEDLLDLSQALHNRGMFIMMDTVINNMAYTMNGGNPATDVNYSINLNFNEKSFYHPYCKI
AN3308|amyD HQDLLDLSAALHERGMVLMMDTVINNMAYMTDGGDFARNIDYALFPFNKSEYHPYCKI
                * * * * *

AN4507|amyC DWNDYFQSQYCWTDGNIVALFDLNTEDERVQTIEMMIQEMIATYSIDGLRIDAAKHVT
AN3308|amyD KDWNDYHDAQWCQTGDNKVALFDLYTERKDVQDTLISWARGIVKTYSIDGLRIDAAKHVN
                * * * * *

AN4507|amyC PDFIGFKAADVFMEGVYERSVDIICGYQSNIMPSVTNYPIVFALLDAFTIGDTESLP
AN3308|amyD TGFLKTFSDSDVMYVTGEVLQREVDIICNYTENYIDSVENYPIYVSMLDAPGQNTTSLY
                * * * * *

AN4507|amyC NQVESMKSKCPSVTLIIFSENHDLPRFASLKDIDINLAKNITFTLLFDGLPIIYQGOEQ
AN3308|amyD HQVENMKKSCRDUVTIWSFSENHDVARUPSFNDMDLAKNIIITFTLLFDGIPMIYQGOEQ
                * * * * *

AN4507|amyC HFSGSDPHNREALMPSAYDTSSELYNTIHTLNTIRKHAIQIDPDYIYNYTVFVYRGS
AN3308|amyD HLSGSDTFNRQAWLSAYNTDSELYKLIATLAKIRKHVISLGSQY-LDEQTVLRYRGS
                * * * * *

AN4507|amyC EMAFRKGREGRQIIMVLSTQGSNGAYTIRMNGFQPSVVARDFVSCRITWVNV---DMG
AN3308|amyD ELAFSKVGEGRQIIMLLSGQSGKDPYTLTLFVSYNAGTIVDVLHCVNYTSVSGGERAG
                * * * * *

AN4507|amyC ELRLMDRGEFRVLFPEALMRGSLCCHAREKVTYMDFNKTYSPESGDDKSGGGVSS
AN3308|amyD ELDFMKSKEFRVFFADLMESGSLCCHAGNVSIAKLETG-----KDRV---VSGG
                * * * * *

AN4507|amyC VVVGGTGVALVNV---ALLGLISFAMC*
AN3308|amyD RIVGEANATLVIMSVLAGVLLLA*--
                * * * * *
    
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B Percent Identity Matrix - created by Clustal2.1

1: AN6324|amyE 100.00 45.10
 2: AN3308|amyD 45.10 100.00

CLUSTAL O(1.2.4) multiple sequence alignment

```

AN6324|amyE MRLTCLSAFFLA---SASVAVASPSAEQWARSIVQVMTDRFARFAPGSPGDK-PCDFYR
AN3308|amyD MKILPSRLAYIMTVLSVLNISNAATTAEWKARSIQVTMDRFRARTDGSSTHACNTAGL
                * * * * *

AN6324|amyE YCGGSWTQVIDKLDYIQDLGPTAVQISFPVENIPDMTVYGEAYHGYWPCNMHALNEHFGT
AN3308|amyD YCGGTWRGTINHLDIQGMGFDAVMISPIIENIGGRVSYGEAYHGWPLDLYSLNDHFGT
                * * * * *

AN6324|amyE ADELKRLSELKHKRGMVLMVDVINDMAQAVNSLDGSGNINNSRLIFPNDKYYHFCR
AN3308|amyD HQDLLDLSAALHERGMVLMMDTVINNMAYMTDGGDFARNIDYALFPFNKSEYHPYCKI
                * * * * *

AN6324|amyE IEDWNNPDESKNCWFSTEVVAFDLKTEDESUVSMIEIHWKGLVGNYSIDGLRVDATRHM
AN3308|amyD IKDNDYHDAQWCQTGDNKVALFDLYTERKDVQDTLISWARGIVKTYSIDGLRIDAAKHVN
                * * * * *

AN6324|amyE DEAYLTSPEAAGVTFMGEVYTEDDRAVCKYEEV-LSGLLNYPMYRPMVQARTAGMPLG
AN3308|amyD NTGFLKTFSDSDVMYVTGEVLQREVDIICNYTENYIDSVENYPIYVSMLDAPGQNTTSL
                * * * * *

AN6324|amyE AENVRAVNSKCKDFTRLATFTENHDTFRFASLINDITLARNAMAFNLLSDGIPVYVQGOE
AN3308|amyD YHQVENMKKSCRDUVTIWSFSENHDVARUPSFNDMDLAKNIIITFTLLFDGIPMIYQGOEQ
                * * * * *

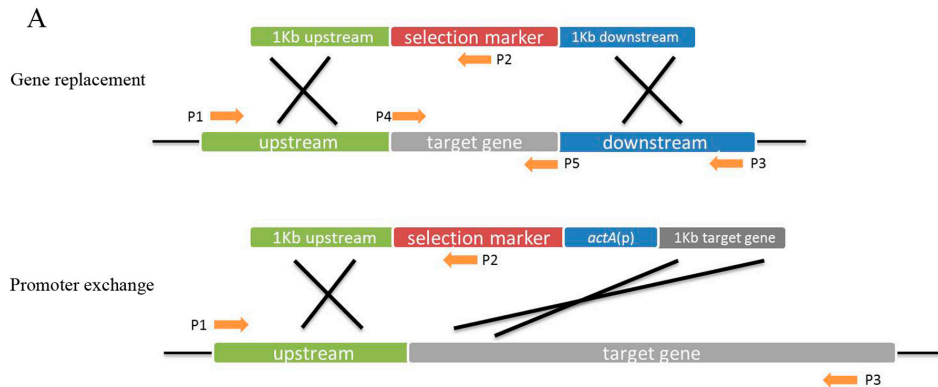
AN6324|amyE QHMKGFPAPYHREPLMKTSYNTNGSLKHTSTLAKLNHAILOKHVVSSELELLDGS
AN3308|amyD HLSGSDTFNRQAWLSAYNTDSELYKLIATLAKIRKHVISLGSQY-LDEQTVLRYRGS
                * * * * *

AN6324|amyE TVYTRKSGEGSQIVSVFNSQSGGQFPYLRIRPRAYKFGTEVIEVLSCKRVAD---NEG
AN3308|amyD ELAFSKVGEGRQIIMLLSGQSGKDPYTLTLFVSYNAGTIVDVLHCVNYTSVSGGERAG
                * * * * *

AN6324|amyE QLVARMKRGEPKAFPFVVKRMNGSGLCGFKGRRRGKAICSSAGKGNTRKNDTVNEGTV
AN3308|amyD ELDFMKSKEFRVFFADLMESGSLCCHAGNVSIAKLETG-----KDRV---VSGG
                * * * * *

AN6324|amyE QTSAGNGASVTIPMVLISICVGLAGLEF*--
AN3308|amyD G---E-ANATL---VMIMSVLAGVLLLA*
                * * * * *
    
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Figure S1 Amino acid sequence alignment of AmyD with AmyC and AmyE using Clustal Omega online server



B

actA(p)-amyC: 1Kb amyC upstream + AfpyroA + actAp+ 1Kb amyC (SE355+SE356) (SE231+SE232) (SE234+SE208) (SE357+SE358)	Fusion PCR: SE359+SE360
actA(p)-amyE: 1Kb amyE upstream + AfpyroA + actAp+ 1Kb amyE (SE361+SE362) (SE231+SE232) (SE234+SE208) (SE363+SE364)	Fusion PCR: SE365+SE366
agnBΔ: 1 Kb agnB upstream + AfpyroA + 1Kb agnB downstream (SE343+SE344) (SE231+SE232) (SE408+SE409)	Fusion PCR: SE347+SE410
agnEΔ: 1 Kb agnE upstream + AfpyroA + 1Kb agnE downstream (SE322+SE323) (SE231+SE232) (SE324+SE325)	Fusion PCR: SE326+SE327
mutAΔ: 1Kb mutA upstream + actAp+ AfpyrG + 1Kb mutA downstream (SE349+SE411) (SE190+SE191) (AME1+AME2) (SE412+SE413)	Fusion PCR: SE353+SE414
agnBΔ, mutAΔ: 1 Kb agnE upstream + AfpyroA + 1Kb agnE downstream (SE322+SE323) (SE231+SE232) (SE324+SE325)	Fusion PCR: SE326+SE327
1Kb mutA upstream + actAp+ AfpyrG + 1Kb mutA downstream (SE349+SE411) (SE190+SE191) (AME1+AME2) (SE412+SE413)	Fusion PCR: SE353+SE414
actA(p)-agnB: 1Kb agnB upstream + AfpyroA + actAp+ 1Kb agnB (SE343+SE344) (SE231+SE232) (SE234+SE208) (SE345+SE346)	Fusion PCR: SE347+SE348
actA(p)-agnE: 1Kb agnE upstream + AfpyroA + actAp+ 1Kb agnE (SE322+SE323) (SE231+SE232) (SE234+SE208) (SE340+SE341)	Fusion PCR: SE326+SE342
actA(p)-mutA: 1Kb mutA upstream + AfpyroA + actAp+ 1Kb mutA (SE349+SE350) (SE231+SE232) (SE234+SE208) (SE351+SE352)	Fusion PCR: SE353+SE354
actA(p)-agnB, amyDΔ: 1Kb agnB upstream + AfpyroA + actAp+ 1Kb agnB (SE343+SE344) (SE231+SE232) (SE234+SE208) (SE345+SE346)	Fusion PCR: SE347+SE348
1 Kb amyD upstream + AfpyrG + 1Kb amyD downstream (SE103+SE104) (AME1+AME2) (SE105+SE106)	Fusion PCR: SE107+SE108
actA(p)-mutA, amyDΔ: 1Kb mutA upstream + AfpyroA + actAp+ 1Kb mutA (SE349+SE350) (SE231+SE232) (SE234+SE208) (SE351+SE352)	Fusion PCR: SE353+SE354
1 Kb amyD upstream + AfpyrG + 1Kb amyD downstream (SE103+SE104) (AME1+AME2) (SE105+SE106)	Fusion PCR: SE107+SE108

Figure S2 Gene replacement and promoter exchange schema and PCR constructs of each strain. (A) Design of construct was shown in the figure. Positions of verification PCR primers were also listed. Generally, P1+P2 were used to confirm the construct insertion into the genome. Wildtype strain results no band and the constructed strains usually result a 2Kb band. P1+P3 were used to detect whether ectopic insertion was occurred in the same genome. Because the sequence length of the selection marker (or plus *actA* promoter) is mostly different from that of the target sequence, this pair of primer should result different bands in different strains. In addition, if ectopic insertion happened, the result of the constructed strain should also show a band as that of wildtype. Occasionally, P4+P5 were used to confirm the absence of the target gene, which was only used in gene replacement construct. (B) Details of primers used for construct generation were listed.

>AN6542 upstream COORDS:ChrI_A_nidulans_FGSC_A4
TACGTTAAAGGCTCGCCCCAACCTCGAAAAGGCGGTAAAATACTAAAAACGGTCCTTAGA
AGGCCTTTTCGACAACGATTTAGAAGGGCTGAGTACAAAAGGAGATCAACCACAGATAGT
ATCGAGCGTGGTTATAGAGAACTAGTTCAGCACATGCCTTATTCCTTTTTTTTCTTCCCATT
TTTTTTTCTTTCTTAAAGGACAGATATAAAAATCTGGAAGCCTGGAGTAGGATCCCCTTAG
GCATTGTTGAACTTCAGGAAAAAGTGAGTCGTCATCGTGCTTACAAGCAGAGAGCGATAA
TAATAGAACGAATGAGAGGACAGACCCTGTTCTTTGAAAACCTGGACACGCTGGGCTGAA
CCATCATTACGGCCTTGGTCGTCGGTCTCTGCCCCACGAGGATTCATCATCTCGCGAGGCC
ACCTCAGCGCGCAATCATTCTGCCTGAGAGGCAACACTTGGTCGCCAGTATAAAAGAACC
AATTGAACAAGAGACACCTATCTCGTAGCAGTCTTTGTGTAGTCTGTACTTTATTCGTTTTA
CCCTCTGAGGAAACGCGGTGGCGGTGACCATTGACTAGACGAGACTAAGCCCCTTTGG
CGCCTGAACCTCCAGCCCCTTTCCAGTCCTTCTGTTTCAGTTCGAGCGGCTGTCGAGCTGCT
GCTGACTACTCCGCCTACCGCTACAACCTCCACCACCACCGACCACCAACAACCCTCGAC
TCTCTCCCCTTCTCTCCTCCACTTCTCAACATCCAACCTCCCATTCTCGCTCTGTTCATCATCT
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TTCTAATCCACCCCTAAACACC

Figure S3 Sequence of *actA* upstream

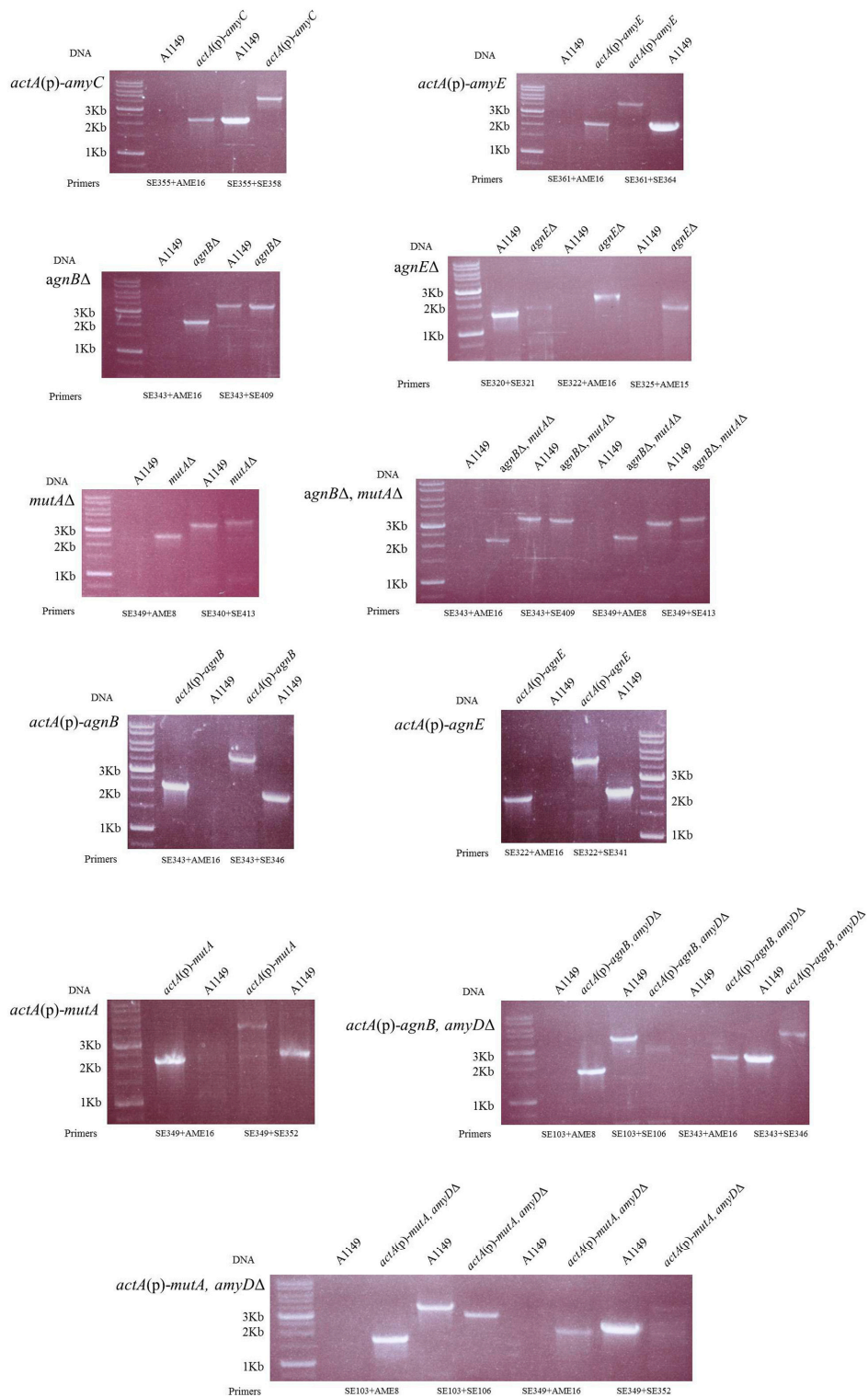


Figure S4 PCR confirmation of all constructed strains. Strains labeled at right of each gel picture. Primers are indicated at the bottom and DNA templates are on the top.