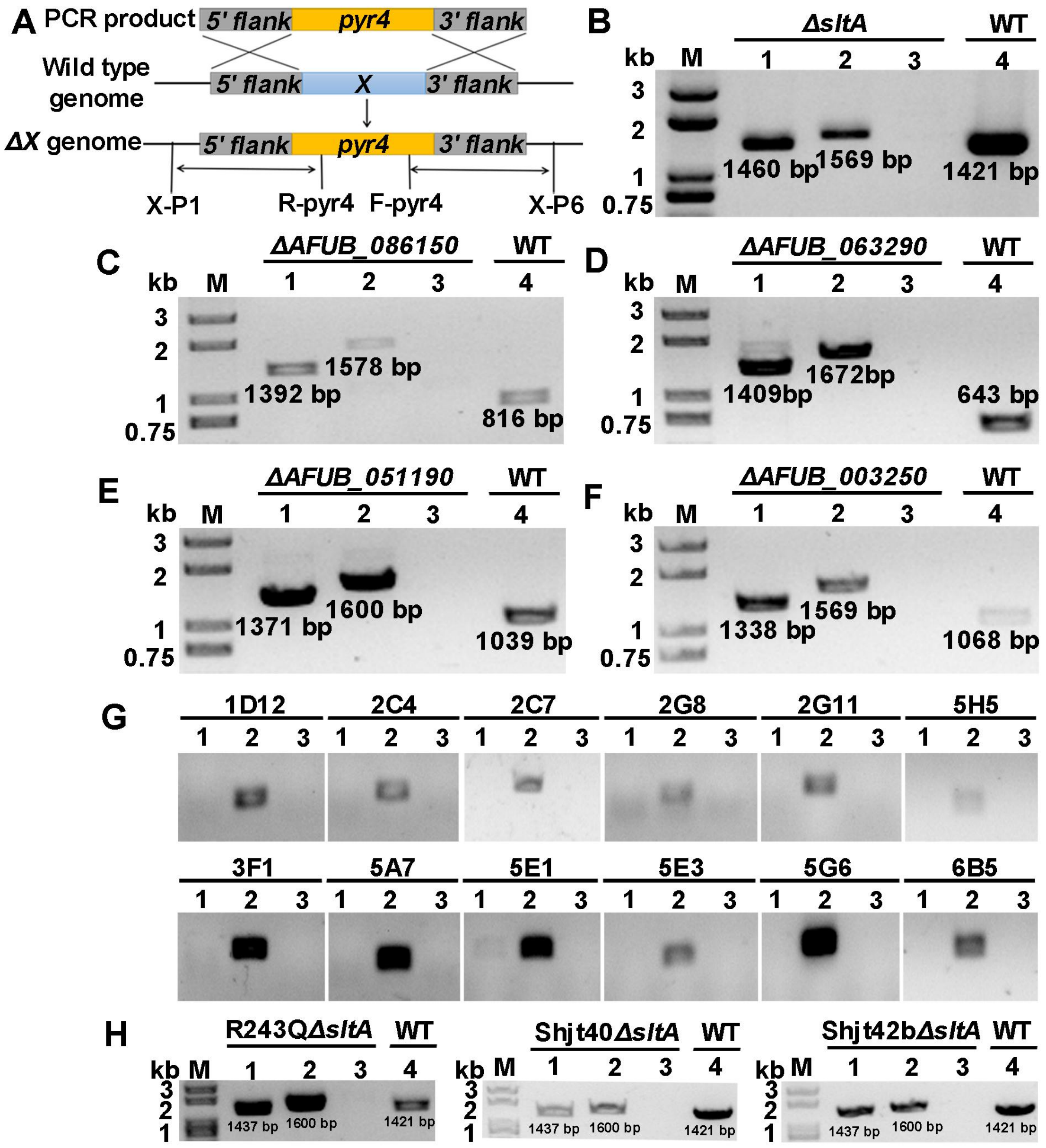
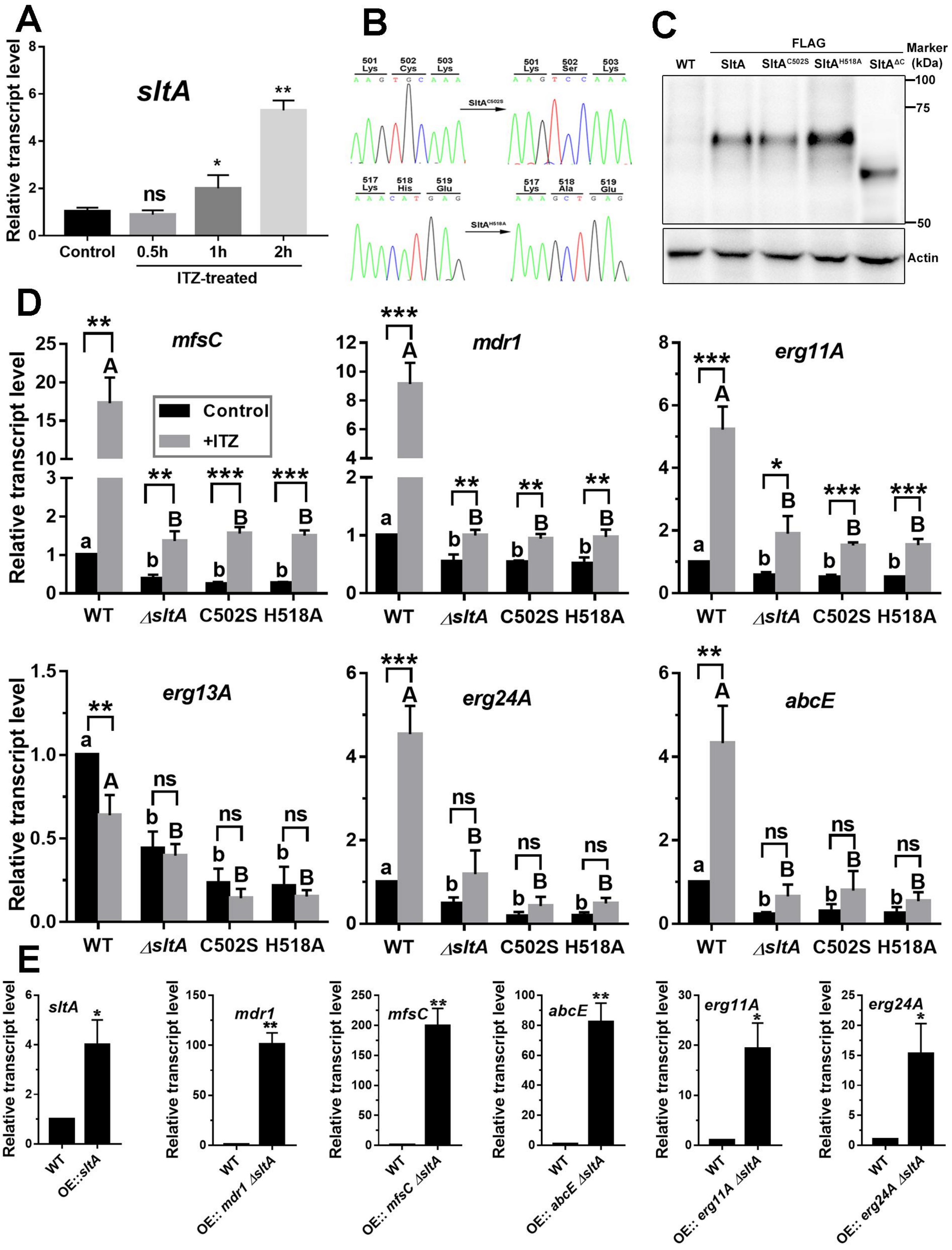
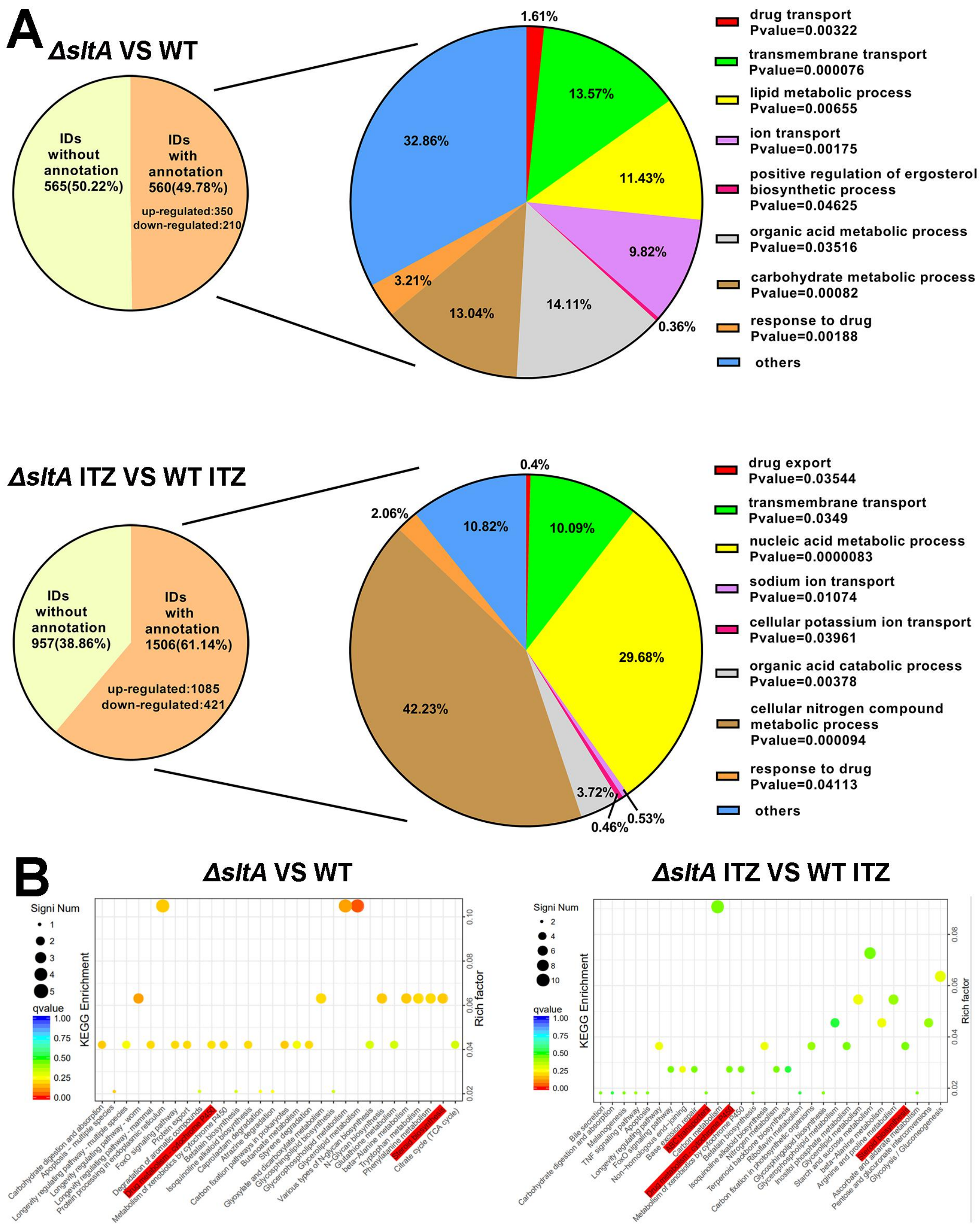


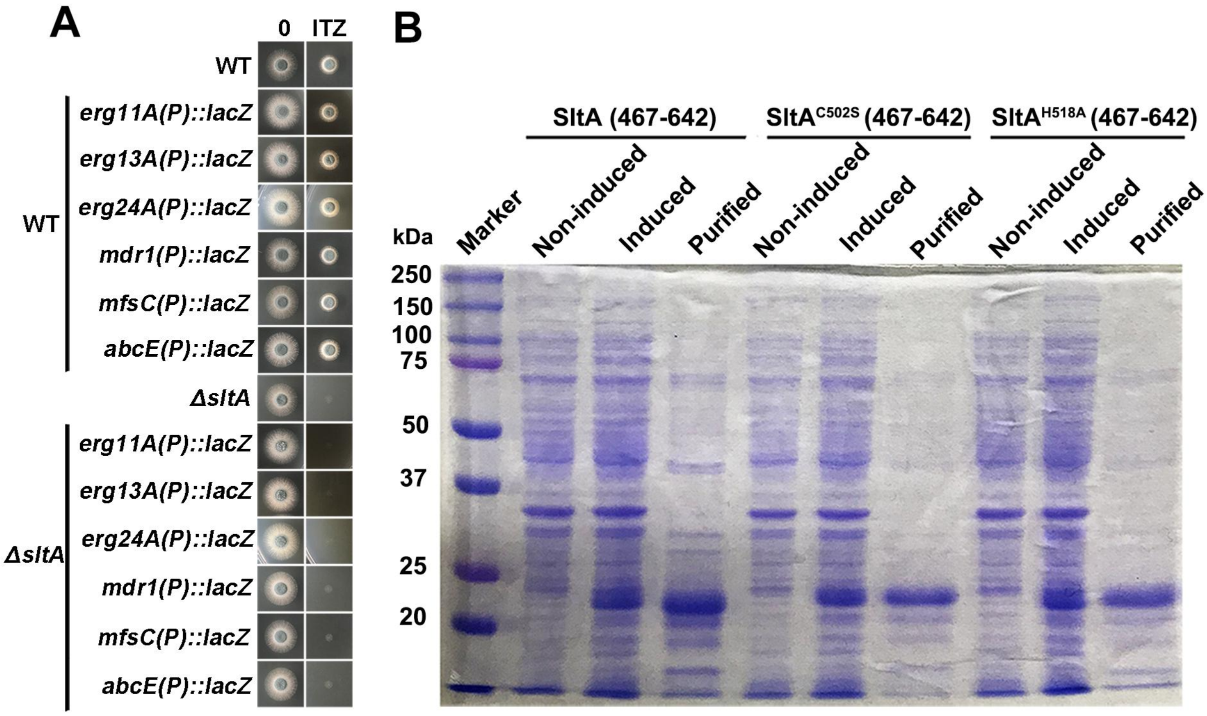
Supplementary Figure S1 – Diagnostic PCR analyses of indicated deletion mutants. (A) Schematic view of gene knock-out using homologous recombination strategy. (B to F) The indicated mutations were confirmed by diagnostic PCR. The corresponding mutant genomic DNA was used for PCR with primer pairs x-P1/R-Pyr4 (line 1), x-P6/F-Pyr4 for (line 2), x ORF own primer pair x-S/x-A showing no detectable products, suggesting deletion of *x* (line 3). In line 4, WT strain showed the predicted size with primer pair x-S/x-A. (G) The indicated mutations from the transcription factors knock-out library were confirmed by diagnostic PCR. Line 1, line 2 and line 3 PCR products were amplified from corresponding mutant genomic DNA, the parental wild-type genomic DNA and double distilled water, respectively, using corresponding own primer pair. (H) The corresponding mutant genomic DNA was used for PCR with primer pairs sltA-P1/R-Hph (line 1), sltA-P6/F-Hph for (line 2), *sltA* ORF own primer pair sltA-S/sltA-A showing no detectable products, suggesting deletion of *sltA* (line 3). In line 4, WT strain showed the predicted size with primer pair sltA-S/sltA-A.



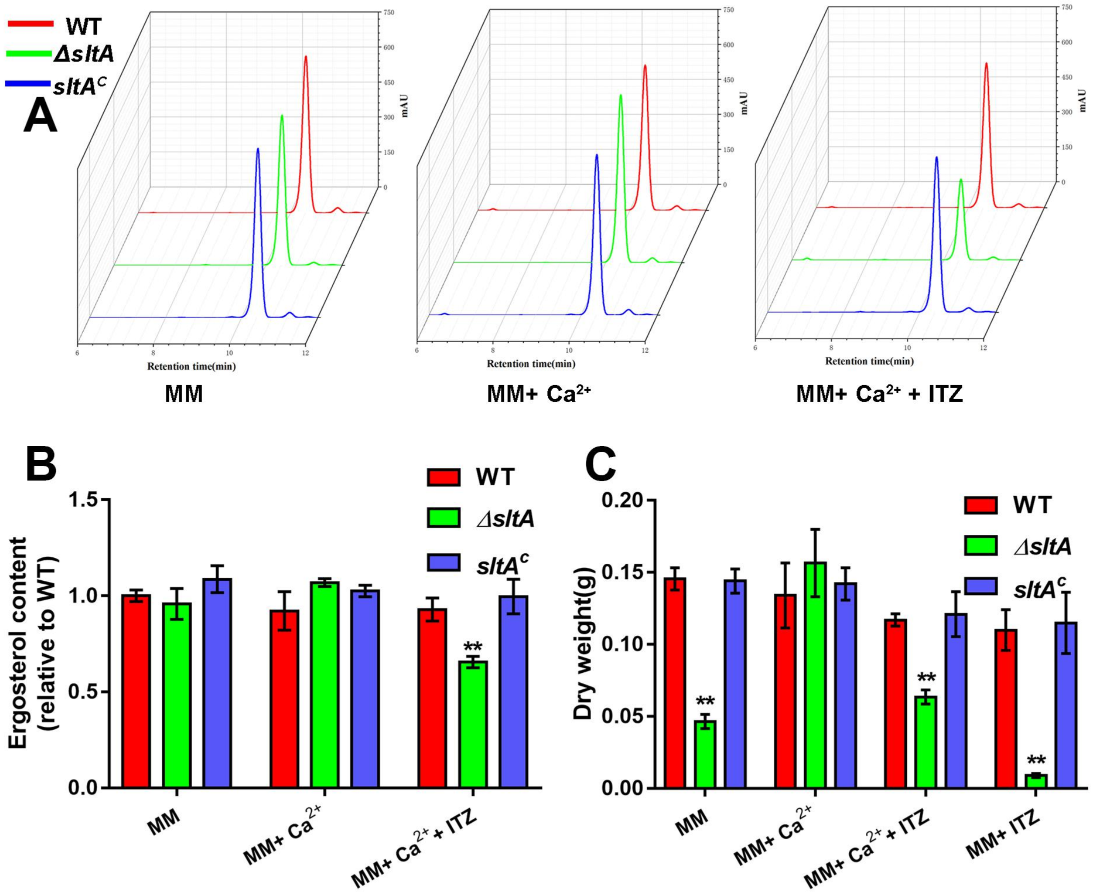
Supplementary Figure S2 – The analysis of qRT-PCR in the indicated mutants. (A) qRT-PCR analysis was performed after growth of cultures in MM for 18 h at 37°C and subsequently for 0.5 h, 1 h or 2h of 0.5 µg ml^{-1} itraconazole treatment. The *tubA* gene was used as an internal control. Samples were assessed in biological triplicates. P-values were calculated using one-way ANOVA: $^{*}P < 0.05$; $^{**}P < 0.01$; ns, $P > 0.05$. (B) The mutated amino acid was determined by sequence alignment between the parental wild-type and mutant strains. The numbers indicate the position of amino acid. (C) Western blot analysis for the indicated strains cultured in MM at 37°C for 24 h. (D) qRT-PCR analysis was performed after growth of cultures in MM for 18 h at 37°C indicated as control and subsequently 2 h 0.05 μg ml^{-1} itraconazole induction indicated as + ITZ. The *tubA* gene was used as an internal control. *P* values were calculated using unpaired t-test between treatments: $^{*}P < 0.05$; $^{**}P < 0.01$; $^{***}P < 0.001$; ns, $P > 0.05$. Different letters (lowercase for the control; uppercase for the + ITZ) indicated significant differences among treatments ($P < 0.05$, Duncan's test). C502S, SltA^{C502S}; H518A, SltA^{H518A}. (E) qRT-PCR analysis was performed after growth of cultures in MM for 18 h at 37°C. The *tubA* gene was used as an internal control. P-values were calculated using unpaired t-test: $^{*}P < 0.05$; $^{**}P < 0.01$.



Supplementary Figure S3 – The analysis of RNA-seq data in *sltA* mutants and the wild-type strain. (A) The genome-wide genes that were significantly changed in the Δ*sltA* mutant versus its parental wild-type strain with or without itraconazole were categorized using the FungiFun suite. Both the parental wild-type strain and Δ*sltA* grew in liquid MM for 18 h at 37℃ and subsequently for 2 h with or without 0.5 μg ml-1 itraconazole. (B) KEGG analysis of down-regulated genes in *sltA* mutant versus wild type strain without or with itraconazole treatment. ABC transporters, drug metabolism and steroid biosynthesis which may contribute to *sltA*-mediated itraconazole resistance were highlighted with red.



Supplementary Figure S4 – Colony morphology of the indicated strains and prokaryotic expression of DNA binding domain of SltA, SltA^{C502S} and SltA^{H518A}. (A) Colony morphology of the indicated strains grown on YAG medium with or without 0.05 μg ml^{-1} itraconazole at 37°C for 48 h and 36h, respectively. (B) Prokaryotic expression of DNA binding domain of SltA, SltA^{C502S} and SltA^{H518A}. The protein bands were stained by coomassie brilliant blue.



Supplementary Figure S5 – The measurement of ergosterol contents for *sltA*-related strains. (A) The chromatogram showing the ergosterol content of indicated strains. The parental wild-type, Δ*sltA* and *sltA*^{C} strains in MM medium with or without 0.5 mM calcium or 0.5 mM calcium and 0.015 µg ml^{-1} itraconazole incubated for 24 h. (B) Ergosterol content of each mutant was normalized to that of the parental wild-type strain, and shown as a relative fold change. Samples were assessed in biological triplicates. $^{**}P < 0.01$ according to Student's t-test. (C) The indicated strains grown in MM with or without 0.5 mM calcium or 0.5 mM calcium and 0.015 µg ml^{-1} itraconazole for 24 h. We weighed harvested mycelia after dried them. $^{**}P < 0.01$ according to Student's t-test.

Supplementary Table S1. MEME analysis for the promoters of *mdr1* and *erg11A*

Aspergillus	**Start**	***p*-value**	**Sites**		
			***mdr1* promoters**		
A. japonicus	-136	7.63e-4	**AAAGCTCTTT**	**AGGCA**	**CCGATGCTGG**
A. tubingensis	-514	7.63e-4	**GAAGATTGGA**	**AGGCA**	**AAGATGGGGA**
A. eucalypticola	-517	7.63e-4	**GAAGATTGGA**	**AGGCA**	**AAGATGGGGA**
A. vadensis	-514	7.63e-4	**GAAGATTGGA**	**AGGCA**	**AAGATGGGGA**
A. clavatus	-136	7.63e-4	**CTACTGCATC**	**AGGCA**	**TGATCATGAA**
A. lentulus	-893	7.63e-4	**GTCCACTATT**	**AGGCA**	**TGCTAAGCTA**
A. fischeri	-692	7.63e-4	**GTTGTTCTCT**	**AGGCA**	**ACACAGTGCG**
A. fumigatus	-670	7.63e-4	**CATGTTCTCT**	**AGGCA**	**ACACAGTGTG**
			***erg11A* promoters**		
A. pseudonomius	-1410	8.12e-4	**GAAGTAGAGA**	**AGGCA**	**CTCAAACGCA**
A. oryzae	-126	8.12e-4	**CATCCAGATT**	**AGGCA**	**TACACATTGT**
A. flavus	-108	8.12e-4	**CATCCAGATT**	**AGGCA**	**TACACATTGT**
A. bombycis	-863	8.12e-4	**CTATAGGCAA**	**AGGCA**	**TCGTAGTTCA**
A. terreus	-445	8.12e-4	**ATGGACTTGC**	**AGGCA**	**AGATAAGATT**
A. clavatus	-1641	8.12e-4	**GTAGGTAGGC**	**AGGCA**	**AAACCAGAAT**
A. lentulus	-985	8.12e-4	**TTCAATGCTC**	**AGGCA**	**TGGCGGGGGC**
A. fumigatus	-958	8.12e-4	**TTCAATGCTC**	**AGGCA**	**TGGCGGTGCT**

Supplementary Table S2. *A. fumigatus* strains used in this study

Strain	Genotype	Reference or source
A1160	*Δaku80*; *pyrG1*	FGSC
WT (A1160C')	*Δaku80*; *pyrG1*; *pyrG*	(1)
DWA01	*Δaku80*; *pyrG1; ΔsltA*::*pyr4*	This study
DWA02	*Δaku80; pyrG1; ΔsltA::pyr4; sltA (p)::sltA::hph*	This study
DWA03	*Δaku80; pyrG1; ΔsltA::pyr4; AfsltA (p)::AnsltA::hph*	This study
DWA04	*Δaku80; pyrG1; ΔsltA::pyr4; AfsltA (p)::AflsltA::hph*	This study
DWA05	*Δaku80*; *pyrG1*; *pyrG; gpd (p)::sltA::hph*	This study
DWA06	*Δaku80; pyrG1; ΔsltA::pyr4; sltA (p)::sltA*^{C502S}*::hph*	This study
DWA07	*Δaku80; pyrG1; ΔsltA::pyr4; sltA (p)::sltA*^{H518A}*::hph*	This study
DWA08	*Δaku80; pyrG1; ΔsltA::pyr4; sltA (p)::sltA*$^{\Delta N}$*::hph*	This study
DWA09	*Δaku80; pyrG1; ΔsltA::pyr4; sltA (p)::sltA*$^{\Delta C}$*::hph*	This study
DWA10	*Δaku80; pyrG1; ΔsltA::pyr4; tet (p)::sltA*$^{\Delta N}$*::hph*	This study
DWA11	*Δaku80*; *pyrG1; ΔsltA*::*pyr4; gpd (p)::mdr1::hph*	This study
DWA12	*Δaku80*; *pyrG1; ΔsltA*::*pyr4; gpd (p)::mfsC::hph*	This study
DWA13	*Δaku80*; *pyrG1; ΔsltA*::*pyr4; gpd (p)::abcE::hph*	This study
DWA14	*Δaku80*; *pyrG1; ΔsltA*::*pyr4; gpd (p)::erg11A::hph*	This study
DWA15	*Δaku80*; *pyrG1; ΔsltA*::*pyr4; gpd (p)::erg24A::hph*	This study
DWA16	*Δaku80*; *pyrG1*; *pyrG; mdr1(p)::lacZ::hph*	This study
DWA17	*Δaku80*; *pyrG1*; *pyrG; mfsC(p)::lacZ::hph*	This study
DWA18	*Δaku80*; *pyrG1*; *pyrG; abcE(p)::lacZ::hph*	This study
DWA19	*Δaku80*; *pyrG1; ΔsltA*::*pyr4; mdr1(p)::lacZ::hph*	This study
DWA20	*Δaku80*; *pyrG1; ΔsltA*::*pyr4; mfsC(p)::lacZ::hph*	This study
DWA21	*Δaku80*; *pyrG1; ΔsltA*::*pyr4; abcE(p)::lacZ::hph*	This study
DWA22	*Δaku80*; *pyrG1*; *pyrG; erg11A(p)::lacZ::hph*	This study
DWA23	*Δaku80*; *pyrG1*; *pyrG; erg13A(p)::lacZ::hph*	This study
DWA24	*Δaku80*; *pyrG1*; *pyrG; erg24A(p)::lacZ::hph*	This study
DWA25	*Δaku80*; *pyrG1; ΔsltA*::*pyr4; erg11A(p)::lacZ::hph*	This study
DWA26	*Δaku80*; *pyrG1; ΔsltA*::*pyr4; erg13A(p)::lacZ::hph*	This study
DWA27	*Δaku80*; *pyrG1; ΔsltA*::*pyr4; erg24A(p)::lacZ::hph*	This study
DWA28	*Δaku80*; *pyrG1*; *pyrG; Erg11A::GFP::hph*	This study
DWA29	*Δaku80*; *pyrG1; ΔsltA*::*pyr4; Erg11A::GFP::hph*	This study
DWA30	*Δaku80*; *pyrG1*; *pyrG; Erg11B::GFP::hph*	This study
DWA31	*Δaku80*; *pyrG1; ΔsltA*::*pyr4; Erg11B::GFP::hph*	This study
Shjt40	TR34/L98H	(2)
Shjt42b	TR34/L98H/S297T/F495I	(2)
Cox10^{R243Q}	*Δku80; pyrG1; cox10(p)::cox10*^{R243Q}*::pyr4*	(3)
DWA32	Shjt40; *ΔsltA*::*hph*	This study
DWA33	Shjt42b; *ΔsltA*::*hph*	This study
DWA34	*Δku80; pyrG1; cox10(p)::cox10*^{R243Q}*::pyr4; ΔsltA*::*hph*	This study

DWA35	*Δaku80*; *pyrG1; ΔAFUB_063290*::*pyr4*	This study
DWA36	*Δaku80*; *pyrG1; ΔAFUB_051190*::*pyr4*	This study
DWA37	*Δaku80*; *pyrG1; ΔAFUB_003250*::*pyr4*	This study
DWA38	*Δaku80*; *pyrG1; ΔAFUB_086150*::*pyr4*	This study
DWA39	*Δaku80*; *pyrG1*; *pyrG; sltA(p)::lacZ::hph*	This study
DWA40	*Δaku80*; *pyrG1*; *ΔsltA*::*pyr4*; *sltA(p)::lacZ::hph*	This study
DWA41	*Δaku80*; *pyrG1*; *SltA::FLAG::pyr4*	This study
DWA42	*Δaku80*; *pyrG1*; *ΔsltA*::*pyr4*; *SltA*^{C502S}*::FLAG::hph*	This study
DWA43	*Δaku80*; *pyrG1*; *ΔsltA*::*pyr4*; *SltA*^{H518A}*::FLAG::hph*	This study
DWA44	*Δaku80; pyrG1; ΔsltA::pyr4; SltA*$^{\Delta C}$*::FLAG::hph*	This study

1. Jiang H, Shen Y, Liu W, Lu L. 2014. Deletion of the putative stretch-activated ion channel Mid1 is hypervirulent in *Aspergillus fumigatus*. Fungal Genet Biol 62:62-70.
2. Liu MS, Zeng R, Zhang LL, Li DM, Lv GX, Shen YN, Zheng HL, Zhang QQ, Zhao JJ, Zheng N, Liu WD. 2015. Multiple *cyp51A*-Based Mechanisms Identified in Azole-Resistant Isolates of *Aspergillus fumigatus* from China. Antimicrobial Agents And Chemotherapy 59:4321-4325.
3. Wei XL, Chen PY, Gao RS, Li YQ, Zhang AX, Liu FF, Lu L. 2017. Screening and Characterization of a Non-*cyp51A* Mutation in an *Aspergillus fumigatus* cox10 Strain Conferring Azole Resistance. Antimicrobial Agents And Chemotherapy 61:e02101-16.

Supplementary Table S3. Primers used in this study

Primer/Purpose	Sequence (5’ - 3’ direction)
***sltA* and other TFs deletion and complementation**	
sltA-P1	ACCTGAATCAAACGACCCC
sltA-P2	TTTCGACCCGTAATACAGCG
sltA-P3	ACACCCGCCAACACCCGGCTGAAAAGGCAAGCACGA
sltA-P4	CGCCATTCGCCATTCATTTCACCGGTCATACTGGA
sltA-P5	GGAAGAAATCCGTCTGCCTA
sltA-P6	AGACCATTCACCTCGCAAA
sltA-P3hph	CGTCCGTCTCTCCGCATGCGGCTGAAAAGGCAAGCACGA
sltA-P4hph	GCTCCTCTTCTTTACTCTGATTTCACCGGTCATACTGGA
sltA-S	ATGTCGACCTCTCAGGCTGA
sltA-A	CTGAGAGAACGCTTCATCG
Com-sltA-F	ACCTGCAGGCATGCAAGCTTCCGTGGTGCCTCCTTGTCTT
Com-sltA-R	CGACGGCCAGTGCCAAGCTTGCGTCTACCAAGGGTCTGA
F-Pyr4	GCTGCGTTTCCTGACTTGTC
R-Pyr4	GGGCGATAATAGATGCTTGG
Pyr4-F	GGGTGTTGGCGGGTGT
Pyr4-R	TGAATGGCGAATGGCG
Hph-F	GCATGCGGAGAGACGGACG
Hph-R	TCAGAGTAAAGAAGAGGAGC
F-Hph	AGGGCAAAGGAATAGAGT
R-Hph	CATTCTCCTTCGCTTACTGC
3250-p1	CCACGCACGACTTGGCTACT
3250-p2	TTTGCTCCCTGCGAAGTAC
3250-p3	ACACCCGCCAACACCCGGAGGCGGGCTTTGAAGG
3250-p4	CGCCATTCGCCATTCAGCCAAGATGACCCCCGTTG
3250-p5	GCATTTATGGCGGGTCTGG
3250-p6	GGACTGCGGGAGGGTATTT
3250-F	ATGACCGACGCATACGAAC
RT-3250-R	ATCAGTGGGAGTGGGATAGTT
1190-P1	AGCCTCATAGCCATACCCC
1190-P2	CAATGCTTTTACTCCGACCA
1190-P3	ACACCCGCCAACACCCCGCTGCTGATAATGGCCTT
1190-P4	CGCCATTCGCCATTCAGTCATATATTCCAACTTAAAG
1190-P5	GCAATGCCAATGCACTACG
1190-P6	GGAGCTTCGGCATCATCCA
1190-F	GCATTCACAGACTACAAAGG
RT-1190-R	CTGTGAAGGATGTAGCGGAC
3290-P1	TTGTCATCGGGGCTTCTTC
3290-P2	CGAAAAGGAGCAAAATCACC
3290-P3	ACACCCGCCAACACCCCTTGTGCAGGAAAAGGAAG
3290-P4	CGCCATTCGCCATTCATTGAGCTGTTGTCGTTTATT
3290-P5	GCAGAGCCCCACTGAGAATC

3290-P6	GTCGCTTGATTCCCCTTGC
3290-F	ATGCATCGCTCTTCGAACA
RT-3290-R	GCACTGGGTTTCCATATTCC
86150-P1	TGGACAACGCAGTGAGTGA
86150-P2	GCTGGAGGGGCAATAACAC
86150-P3	ACACCCGCCAACACCCTGTGTGAACGCTTCTTCAG
86150-P4	CGCCATTCGCCATTCATATGCAATCCTGCAGCCCC
86150-P5	TACCGATGTCCCGATTCTC
86150-P6	TCAGGGATCTTCGATGCTAA
86150-F	ATGGACGTCAATCGTAAGC
RT-86150-R	CTCAGATGCGACGGTGCTT
***sltA* mutation and homolog complementation experiments**	
Com-sltA-F	ACCTGCAGGCATGCAAGCTTCCGTGGTGCCTCCTTGTCTT
Com-sltA-R	CGACGGCCAGTGCCAAGCTTGCGTCTACCAAGGGTCTGA
C502S-F	GATATTAACCAGAAGTCCAAAGACTGCGACAAG
C502S-R	CTTGTCGCAGTCTTTGGACTTCTGGTTAATATC
H518A-F	GACCGGTTCTAGGAAAGCTGAGAAGACGCACTCTC
H518A-R	GAGAGTGCGTCTTCTCAGCTTTCCTAGAACCGGTC
sltA-P3free	GGCTGAAAAGGCAAGCACGA
ΔN-F	TCGTGCTTGCCTTTTCAGCCATGGCTCGCCGCAAGAAGAA
ΔC-R	TCCAGTATGACCGGTGAAAGCCATTATGTTTTGAGCG
sltA-P4free	TTTCACCGGTCATACTGGA
Tet-F HindIII	ACCTGCAGGCATGCAAGCTTGTTTCAAGTTGCAATGACT
Tet-R	GGTGATGTCTGCTCAAGCGG
Tet-ΔNsltAF	CCGCTTGAGCAGACATCACCATGGCTCGCCGCAAGAAGAA
ComAnsltA-F	TCGTGCTTGCCTTTTCAGCCATGAGTCCAGCACAAGACTC
ComAnsltA-R	TCCAGTATGACCGGTGAAATTAGAGACCACCAGGGCC
ComAflsltA-F	TCGTGCTTGCCTTTTCAGCCATGTCTTCCGCTCAGCCTG
ComAflsltA-R	TCCAGTATGACCGGTGAAATTACATGGAAGATTGGTCGG
Over-expression	
OE::sltA-F	CTTTAATCAAGCTTATCGATATGTCGACCTCTCAGGCTGA
OE::sltA-R	TCGAGGTCGACGGTATCGATTTAGAAATGTTCCATCTCCATA
OE::mdr1-F	CTTTAATCAAGCTTATCGATATGCCTGCGCCTGAAACC
OE::mdr1-R	TCGAGGTCGACGGTATCGATTCAATGAGTCTTTCCGAGAC
OE::mfsC-F	CTTTAATCAAGCTTATCGATATGACGTCCAACAAAAAATC
OE::mfsC-R	TCGAGGTCGACGGTATCGATTCACAGCCTTGTGTCTGCGA
OE::abcE-F	CTTTAATCAAGCTTATCGATATGGCCCTGCAGCAAGTG
OE::abcE-R	TCGAGGTCGACGGTATCGATTTATGTCAAAAATCGAGGG
OE::erg11A-F	CTTTAATCAAGCTTATCGATATGGTGCCGATGCTATGGC
OE::erg11A-R	TCGAGGTCGACGGTATCGATTCACTTGGATGTGTTTTTCG
OE::erg24A-F	CTTTAATCAAGCTTATCGATATGGCACCAAGAAAGGAT
OE::erg24A-R	TCGAGGTCGACGGTATCGATCTAGTAAATACCAGGAATAATG
β-galactosidase activity experiments	
LacZ-S	ATGACCATGATTACGGATTC
LacZ-TrpC-A	CGACGGCCAGTGCCAAGCTTTCAGAGTAAAGAAGAGGAGC
Pmdr1-F	ACCTGCAGGCATGCAAGCTTCCTATACTAGCCTATACC

Pmdr1-R-lacZ	GAATCCGTAATCATGGTCATGTTGCGGTTGAGGGTATGC
PmfsC-F	ACCTGCAGGCATGCAAGCTTGAGCTTTTTCCCTGAGCTC
PmfsC-R-lacZ	GAATCCGTAATCATGGTCATCCTAGCCACCTCCTGAACAG
PabcE-F	ACCTGCAGGCATGCAAGCTTCGAACGAGACACATCTAGGG
PabcE-R-lacZ	GAATCCGTAATCATGGTCATCTTCAGATCTACCCATTTTG
Perg11A-F	ACCTGCAGGCATGCAAGCTTGACCGAGAGGCGATTTCGG
Perg11A-R-lacZ	GAATCCGTAATCATGGTCATTTCGAGGAGACACAGGGAGG
Perg13A-F	ACCTGCAGGCATGCAAGCTTGGATTTGAGCGATTGAATG
Perg13A-R-lacZ	GAATCCGTAATCATGGTCATGGTTGGTCGAAAGAATGCCA
Perg24A-F	ACCTGCAGGCATGCAAGCTTCGGTGTATCTGCCTGAAGG
Perg24A-R-lacZ	GAATCCGTAATCATGGTCATGTTCGCCCGAGATCGGGTG
PsltA-F	ACCTGCAGGCATGCAAGCTTCCGTGGTGCCTCCTTGTCTT
PsltA-R-lacZ	GAATCCGTAATCATGGTCATGGCTGAAAAGGCAAGCACGA
Construction of FLAG labeled strains	
SltA-FLAG-P1	GGCTCGCCGCAAGAAGAAT
SltA-FLAG-P2	GAATCTGCTTTGCTCCGTAA
SltA-FLAG-P3	CATTCCCGGGGATCCCTCGAGGAAATGTTCCATCTCCATATCC
SltA-FLAG-P4	CGCCATTCGCCATTCATAATTTCACCGGTCATACTG
SltA-FLAG-P5	GGAAGAAATCCGTCTGCCTA
SltA-FLAG-P6	AGACCATTCACCTCGCAAA
FLAG-F	CTCGAGGGATCCCCGGGAATG
Pyr4-R	TGAATGGCGAATGGCG
Com-sltA-F	ACCTGCAGGCATGCAAGCTTCCGTGGTGCCTCCTTGTCTT
C502S-R	CTTGTCGCAGTCTTTGGACTTCTGGTTAATATC
C502S-F	GATATTAACCAGAAGTCCAAAGACTGCGACAAG
FLAG-R-PAN7-1	CGACGGCCAGTGCCAAGCTTGACATTCCTTTTACCCGGGCT
H518A-F	GACCGGTTCTAGGAAAGCTGAGAAGACGCACTCTC
H518A-R	GAGAGTGCGTCTTCTCAGCTTTCCTAGAACCGGTC
ΔC-R-FLAG	CATTCCCGGGGATCCCTCGAGGCCATTATGTTTTGAGCG
Hph-R	TCAGAGTAAAGAAGAGGAGC
EMSA	
EX-sltA-P1NdeI	AAGAAGGAGATATACATATGCCTGCGATGAAGCGTTCTCT
EX-sltA-P2	GTGAGATCACAAGGTCTTT
EX-sltA-P3	AAAGACCTTGTGATCTCACGAAACATGAGAAGACGCAC
EX-sltA-P4EcoRI	GTCGACGGAGCTCGAATTCGTAGGCAGTGACGGGTTCG
C502S-F	GATATTAACCAGAAGTCCAAAGACTGCGACAAG
C502S-R	CTTGTCGCAGTCTTTGGACTTCTGGTTAATATC
H518A-F	GACCGGTTCTAGGAAAGCTGAGAAGACGCACTCTC
H518A-R	GAGAGTGCGTCTTCTCAGCTTTCCTAGAACCGGTC
Cy5	AGCACGTGGTCGAAAG
EMSA-erg11A-F	AGCACGTGGTCGAAAGGGGTGTCCAAAGCAGTGTTG
EMSA-erg11A-R	AGCACGTGGTCGAAAGGCATCCAGAGAAATTCATAC
EMSA-erg24A-F	AGCACGTGGTCGAAAGCCTGGAGGGCAAGATGTTGA
EMSA-erg24A-R	AGCACGTGGTCGAAAGGTAGTAATACTAATCACCGG
EMSA-mdr1-F	AGCACGTGGTCGAAAGCGCCTTTATTCAGCAAATC
EMSA-mdr1-R	AGCACGTGGTCGAAAGGTTAAGTTAATGGGGACCAC

EMSA-mfsC-F	AGCACGTGGTCGAAAGTGCAAGGAGTAGAGATCAG
EMSA-mfsC-R	AGCACGTGGTCGAAAGCATCTGACGGGGACTAGG
EMSA-abcE-F	AGCACGTGGTCGAAAGAGACGTAGTCAGAATCACA
EMSA-abcE-R	AGCACGTGGTCGAAAGTGGAAGTCCGGGCACCTGA
EMSA-sltB-F	AGCACGTGGTCGAAAGCCTGCCACGTGATCTGCCA
EMSA-sltB-R	AGCACGTGGTCGAAAGGATGATCTGAAAAGACCAC
EMSA-sltA-F	AGCACGTGGTCGAAAGATCCAACCAGCGCTCTGAT
EMSA-sltA-R	AGCACGTGGTCGAAAGGGGAAGACGATAGCCTATG
EMSA-erg13A-F	AGCACGTGGTCGAAAGCGGTCATATAGCGCAAATC
EMSA-erg13A-R	AGCACGTGGTCGAAAGCATGATGACCATATGAATC
EMSA-MUerg11A-F	CACCACTTCTTCAATGCTCCAAACTGGCGGTGCTCGGG
EMSA-MUerg11A-R	CCCGAGCACCGCCAGTTTGGAGCATTGAAGAAGTGGTG
EMSA-MUmdr1-F	CGAACTTAACATGTTCTCTCAAACACACAGTGTGGCGTAC
EMSA-MUmdr1-R	GTACGCCACACTGTGTGTTTGAGAGAACATGTTAAGTTCG
EMSA-MUsltB-F	CGCCACTCCCTATTGGTTCAAACACAGGATTCCTGCCCACC
EMSA-MUsltB-R	GGTGGGCAGGAATCCTGTGTTTGAACCAATAGGGAGTGGCG
qRT-PCR	
RT-tub-F	TTCCGTCCCGACAACTTCGT
RT-tub-R	TCACAGCCTTCAGCCTCACG
RT-sltA-F	AGGCTCAGGGCATTACAACA
RT-sltA-R	AGTGAAAAGAGGGAAGTCGC
RT-mdr1-F	ATCTTCCGCTTCTTCGTCTG
RT-mdr1-R	AATGGTTGGCTTGCTGTCG
RT-mfsC-F	GGGTACTTGAACGCCTTTTG
RT-mfsC-R	CGCAGTTGCATCTTTGCTC
RT-abcE-F	GCCACCGATCCAAAGCAGGT
RT-abcE-R	TGTGCATGGTAAGGCGGCAA
RT-erg11A-F	CCTATCTTCCGTTTGGTGC
RT-erg11A-R	TTTCAGGGACTCCTTTCTTTC
RT-erg24A-F	ATTATGGACGGATTCGGTTAC
RT-erg24A-R	CAGAAGGATTTCCCTCAAGC
RT-erg13A-F	CGACGAACTGCGGCAACAT
RT-erg13A-R	ATCCCGATGCGCTTGTCCT
RT-abcB-F	GCAGCATCAGACGCAACAT
RT-abcB-R	CGGTGTCTAGTCCGCCTTTC
RT-erg2-F	TCAAGCAATACAAGATGGAGC
RT-erg2-R	ACAGGGTAGGGAAGTCAAGG
RT-erg25A-F	TGCAGCCAGTAGTGGTATGT
RT-erg25A-R	CCACTTTGTCGTCGAACTCC
RT-3250-F	CAATCGCAGTGGAGGCATA
RT-3250-R	ATCAGTGGGAGTGGGATAGTT
RT-4490-F	GACAGAGGTCCACTCAAACGA
RT-4490-R	AACGACGACGGTCTATACATG
RT-15800-F	AATGATTCTCCTGTCGGTGTC
RT-15800-R	TTTTCAGATCGGATGGTGC
RT-18270-F	CTCGCACTTTCCGCTAACC

RT-18270-R	CCACATCCAGATCGTCCAG
RT-40000-F	CGGTTCAAGAATCGGACTATG
RT-40000-R	TGAGACGCAATGGGAGTGA
RT-1190-F	GATGCCACTGCCTAAGACC
RT-1190-R	CTGTGAAGGATGTAGCGGAC
RT-53880-F	TCGTCTACGCCGTCCTAAC
RT-53880-R	CTGCTGATTCTGCCTGTGAG
RT-55060-F	TCCTGATTCGCTGTTTCGC
RT-55060-R	TTTCGTCCCCAGACACCAC
RT-3290-F	CAGGCAACTGTCAGCGTCA
RT-3290-R	GCACTGGGTTTCCATATTCC
RT-70520-F	AATACATACCTCGCTGCCACA
RT-70520-R	CCTCAACGGACTCGAAAATC
RT-80380-F	CATTGACCCTTCTCCTTCCC
RT-80380-R	CATACTGACATCGCCATCGT
RT-86150-F	CCGACTTGAATATGGGGATG
RT-86150-R	CTCAGATGCGACGGTGCTT
RT-89440-F	CGAGCGAATGGATGAAGAG
RT-89440-R	AGCTGCTGCCAGAATGAGA
RT-94860-F	TCGCCCTACTCCGACTATCC
RT-94860-R	CCACATTTCACGGGGTTTG
RT-96380-F	GACGCCCATCAATCCTCAA
RT-96380-R	CCGTTCATATCATGCCATCC