

Supplemental Material:

Contribution of Peroxisomes to Secondary Metabolism and Pathogenicity in the Fungal Plant Pathogen *Alternaria alternata*

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TABLE S1. Oligonucleotide primers used in this study

Primer	Sequence (5' to 3') ^a
AKT1-f	ATCCT <u>GATCA</u> TGG TTTTCGCAGCTCCCTG
AKT1-r	TGCCT <u>GATCA</u> CTA TATCTTGCTCGACAGCC
AKT2-f	TTAAG <u>GATCCT</u> GAT G CAGCAGCCCATCATTGG
AKT2-r	GCCCGA <u>ATTCT</u> T AGAGTTTCGACTGCAGAT
AKT3-f	GCCCT <u>TGATCA</u> TG CTTAACCGGATTCTCTTA
AKT3-r	TGCCGA <u>ATTCT</u> C AGAGCTTTGGCTTGGAAG
AKT1-r2	TCCT <u>GATCA</u> CTA CGACAGCCTGCCATTGACTT
AKT2-r2	GCCGA <u>ATTCT</u> T ACTGCAGATATTTTCATCCAAG
AKT3-r2	AACGA <u>ATTCT</u> C ACTTGGAAGCCAGGCCAACTA
PEX6-f	GCCAAGGGGCATGAAGAAGCG
PEX6-r	AGGTACAGCATCTTGTCGAA
PEX6-6	GTCTTGACCTGCCCTCCTAT
PEX6-9	TCTGTAGCGAAATGGTCG
AaPEX6-f	<i>GAAGTTATCAGTCGAAGAAGCGTCTGTACGTGAGT</i>
AaPEX6-r	<i>ATGGTCTAGAAAGCTAGACTTGAGCGCGATATCAC</i>

^a The initiation and termination codons are indicated as bold letters. Restriction enzyme sites added are underlined: TGATCA, *Bcl*I; GGATCC, *Bam*HI; GAATTC, *Eco*RI; CTGCAG, *Pst*I; CTCGAG, *Xba*I. AaPEX6-f and AaPEX6-r have 15 bases (italicized) identical to sequences at the ends of the linearized plasmid pDNR-CMV. The linearized plasmid and the 6.5-kb AaPEX6 fragment were subjected to the In-Fusion cloning reaction.

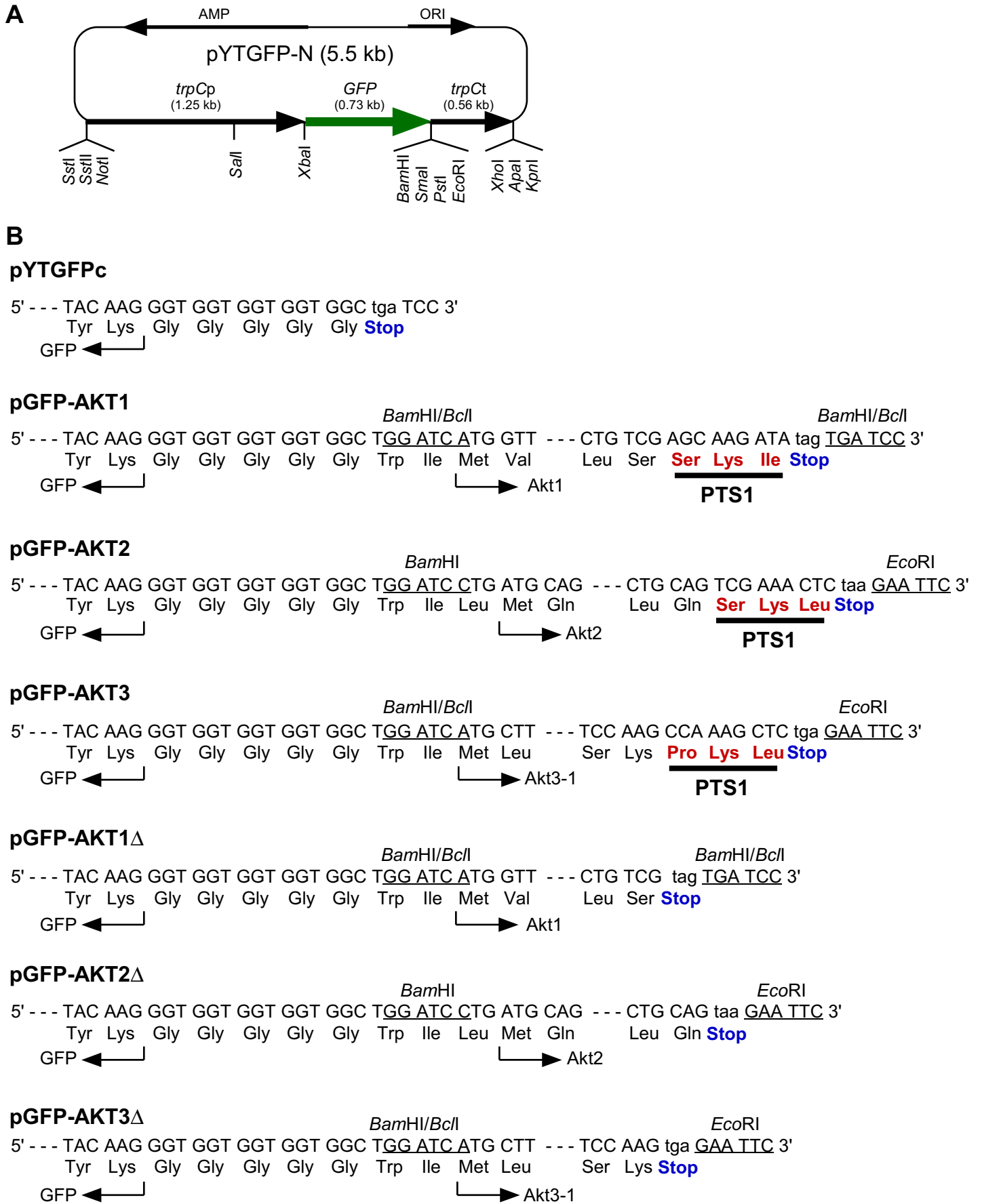


FIG. S1. GFP-fusion protein expression vectors used in this study. (A) The plasmid pYTGF-N used for construction of GFP-fusion protein expression vectors. (B) GFP-fusion protein expression vectors. The pGFP-AKT-series vectors were constructed by inserting the *AKT1*, *AKT2*, and *AKT3-1* cDNAs downstream of *GFP* in pYTGF-N. The pGFP-AKTΔ-series vectors contain the mutated *AKT1*, *AKT2*, and *AKT3-1* cDNAs, of which nine nucleotides encoding peroxisomal targeting signal type 1 (PTS1) sequences were eliminated.

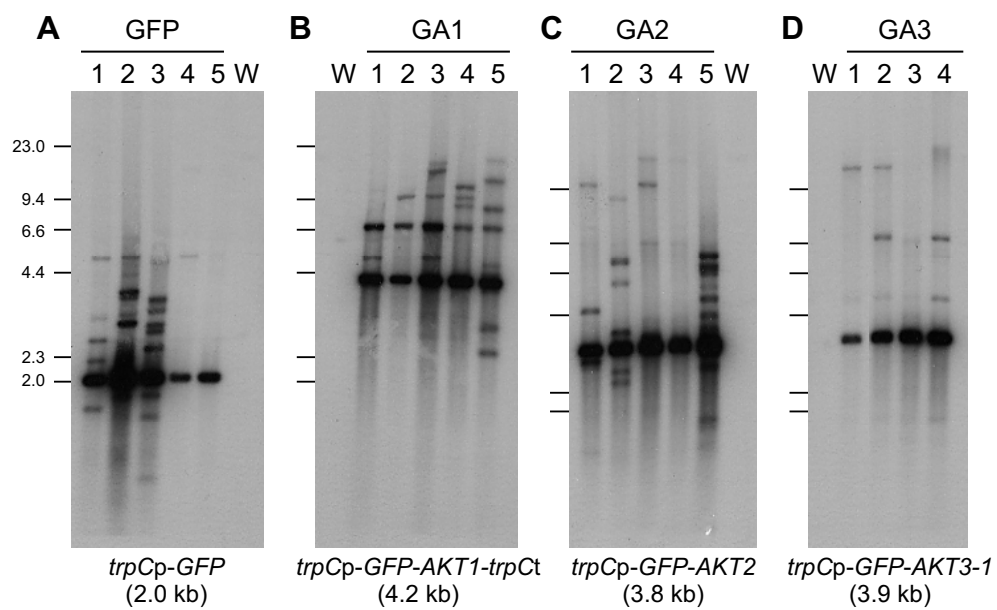


FIG. S2. DNA gel blot analysis of transformants. Total DNA was digested with *NotI-EcoRI* (A, C and D) or *NotI-KpnI* (B) and fractionated in 0.8% agarose gels. The blots were probed with the *GFP* sequence. Sizes (in kilobases) of marker DNA fragments (*HindIII*-digested λ DNA) are indicated on the left. W, wild-type strain 15A; GFP, pYTEGFPc transformants; GA1, pGFP-AKT1 transformants; GA2, pGFP-AKT2 transformants; GA3, pGFP-AKT3 transformants.

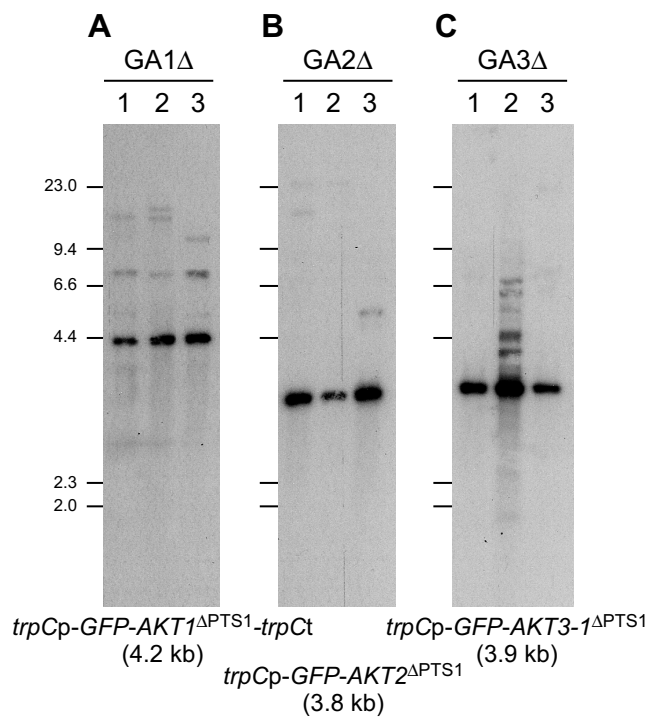


FIG. S3. DNA gel blot analysis of transformants. Total DNA was digested with *NotI-KpnI* (A) or *NotI-EcoRI* (B and C) and fractionated in 0.8% agarose gels. The blots were probed with the *GFP* sequence. Sizes (in kilobases) of marker DNA fragments (*HindIII*-digested λ DNA) are indicated on the left. GA1 Δ , pGFP-AKT1 Δ transformants; GA2 Δ , pGFP-AKT2 Δ transformants; GA3 Δ , pGFP-AKT3 Δ transformants.

AaPex6	-----MDA[NGVVAHAKRRRRRDRPPI SARL LDDDRK]G--VGVLSDELFDLDFPFCSESRSAANGTTPD[SHRQVHAI]PMLPSSIVASQNP[PTTL]PVRADKTKMGTARPHSS	: 112
MoPex6	-----MDPACTRRRRRRRQDRPI SARL LDDHVR--DVGLSDELFDLDFPHLS-----PVEVHEDD[VYVAI]SPMIPG--ATPESID[ITIVAVTR]SIALSHSTVQVQSPS	: 99
CoPex6	---MTTSELVPP[PAARS]P[TRRRR]ODK[AL SARL]WDDHE[NGOV]GLSDELFDLDFPHL[EN]---VPSRED[CE]D[THVVAI]APMPS--PSPITE[TAIVYV]VPLKSSALKPSTVQVQSPS	: 111
PcPex6	MDFEYQYQSS[QQR]R[RRRR]RAGK[RRL]M[KTP]AARLALD[PLRG--KVG]LSELD[AMD]L[QQ]QALQ----DVITSD[GWLYVAI]APHTPT--YTSV[EDQ]A[ITL]PVRIQPTERSPVAMSHST	: 113
ScPex6	-----MKASLTFSLSGI[VAPCS]ISRD[VLEY]GDKKAC[LYGT]IRLP[VYGP]-----GCTPGKIV[CVLDD]S[L]PFC[SI]VVP[S]KLF[GM]TQ[Q]TMD	: 83
AaPex6	LQIPASSLALQSFHLLQNIAPMKTQRDR--TFIEVRIYD[VVPV]GLD[VTV]VMD[TEA]RKLDE[HAH]KFGGGITQMMCASR[ASR]LEANGTKGKAVD[LAAQ]E[VWRQ]AVREALQ[LV]TLVH	: 231
MoPex6	ASA-----LALQIPATSLQ[PVAP]SKLSSHRS[GD]LLVLDLALSLD[VV]SLD[GL]ELARL[DH]GEGV[DH]RHP--IGKGSATP-----SPEOKLAAAVRAALG[TV]RVVH	: 197
CoPex6	S-----LSLQSFATLQ[VAP]SKLSSHRS[GD]E[VQ]ILD[VVAL]SLD[VV]SLE[SEL]L[ARL]D[Q]GEGIT[FRD]R[PK]GK[GA]PAQD-----TPEDRLISALRVALG[SL]KVLH	: 210
PcPex6	VLFPE[AD]SLQ[PL]LQALG[KWD]SR[SR]SLQ[AHRS]VET[EL]LDVAP[IL]DLT[FTV]T[ER]HL[RN]HD[VQ]TKF[GGG]TNA[QGN]LW[GR]TKGSVEAK[KY]SKRAA[DAE]QRL[AAV]REALG[AG]RIVH	: 233
ScPex6	-----FCYFEP[ILL]M[VV]P[LDS]V[TF]L[NE]Q[LY]SKL[MD]LP-----QEQMQI[Q]FLHY	: 128
AaPex6	TGDLPLK[LA]HPI[TE]VPP[PAKI]SASE[PVS]QGLL[LPS]TRIVYLQ[SHRS]SSKQAVLL[PV]KQ[PAT]TNGFGDD[ET]D[TS]M[IT]FYSAAE[DN]SRNAS[PP]DE[ES]D[MF]E[SEL]SE[SD]AGL[LS]DE	: 351
MoPex6	SGDLFPLP[PH]P[IT]HVP[PM]K[GV]LCE[PVA]Q[GL]S[PM]TK[IV]S[SGR]---SPLKGM[DR]G[S]R[Q]S[RM]D[GV]EA[ED]E--TAND[AF]SAAE[RY]KTE[ASE]T[ADE]SAA[TS]ASE[TEL]S[GD]ID[DL]	: 314
CoPex6	SGDLFSLP[PH]P[IT]HVP[PM]K[GV]LCE[PVS]REYL[SDD]TKI[VM]RGR--VHAKRG[SAPAI]P[MR]SLM[GV]E[DE]D[ED]TAND[QY]SAAE[RY]KTE[DAAT]E[MT]VTE[TE]S[DL]S[GV]D[HD]DL	: 328
PcPex6	TGDVLP[PL]P[SH]P[IT]YAP[PP]ARI[SCE]P[VS]QGLL[MS]TKI[V]L[Q]AR---PQ[IRA]Q[OT]M[PS]R[SA]L[KQ]VAE[DA]D[TS]M[E]Q[YS]AAE[DP]G[S]G[TE]M[VT]SAAE[SE]--TE[S]AG[S]M[S]D[S]	: 349
ScPex6	KYNINSMET[VV]H[SR]D[IL]T[SGL]C[QL]M[C]S[P]F[Q]G[L]V[D]F[ET]Q[LL]VMD-----TQ[KL]SALKY[ME]DEE[VAL]PK[IG]T[MS]AI	: 203
AaPex6	S---[DD]I[SL]M[AP]M[PP]Q[SS]G[VL]S[FT]S[AT]P[PP]C[M]R--TNGIAT[PG]S[V]S[FT]ATT[ARG]P[TS]K[S]K[V]FKAQGL[Q]S[V]D[DL]V[HP]K[GS]E[DE]E[AR]V[FD]INT[LV]K[GC]F[SG]D[V]K[LG]E	: 466
MoPex6	SDDSLDDMISLQ[PH]L[PS]M[AS]C[HT]A[Q]C[PT]M[IT]G[R]K[TV]G[AT]P[GS]W[FS]S[FT]ATT[AR]P[DR]P[GR]L[FKA]QGL[V]K[P]I[PE]L[LHP]K[PS]A[ED]D[EA]H[IV]D[V]S[HL]S[RI]G[CF]S[GD]V[VR]E[AS]A	: 434
CoPex6	SDD[FM]D[M]S[LQ]A[PI]L[IT]A[SG]V[S]M[Q]P[IT]M[IT]G[R]K[TV]G[AT]P[AS]V[S]M[FT]ATT[AR]P[DR]P[GR]L[FKA]QGL[V]K[P]I[PE]L[LHP]K[PS]A[ED]E[AR]I[V]D[V]A[S]L[SK]I[GC]F[SG]D[V]V[RE]A[E]	: 448
PcPex6	SDD[SL]E[M]S[L]S[A]P[E]L[Q]P[PP]G[MS]S[LT]S[AT]P[RA]G[GR]--SD[GH]T[PG]S[W]A[S]M[FT]S[AT]M[RP]G[GG]K[IT]K[V]E[GL]Q[V]E[V]L[H]R[PR]D[ED]V[S]F[V]D[IST]LAK[IG]C[F]S[GD]V[VR]E[A]E	: 468
ScPex6	S-----[DL]E[SL]P[CT]I[SR]D[L]R[RA]P[HI]M[D]N[S]IYA[TD]A[E]T[L]R[L]D[V]T[S]G[S]F[IT]V[S]M[G]	: 257
AaPex6	APSSHP[LW]L[CA]F[GRAD]--EENTN[MR]P[V]R[V]F[GL]P[EM]M[S]K[V]A[R]Y[P]VQ[KT]S[D]L[R]R[S]S[FG]S[Q]P[AS]L[HAY]L[S]P[ILL]A[N]D[G]S[P]S[HL]R[IT]P[L]T[PS]Q[S]--S[HL]P[RA]I[Q]P[R]L[N]S[S]L[P]P[S]A[R]	: 584
MoPex6	APPANGF[PA]L[GS]F[EP]D[A]Q[P]V[OR]P[AR]V[FL]P[EG]Y[S]M[R]P[S]R[IP]S[K]H[R]E[S]L[S]F[FE]S[Q]V[OR]K[S]G[LAY]A[S]P[ILL]A[N]D[L]P[SH]L[R]L[P]K[R]T[IE]--H[HG]M[G]P[Q]S[Q]---A[T]A[V]O[P]P[PY]A[R]	: 550
CoPex6	EPPANGF[PA]F[GL]S[FT]S[LE]P[TE]S[M]R[P]V[R]V[GL]P[EG]Y[S]O[R]P[V]R[IP]S[A]K[H]E[R]R[M]S[F]F[E]S[Q]L[Q]P[TS]P[AY]I[S]P[VL]L[A]N[E]S[PS]Y[L]R[S]I[K]R[CT]--Y[Q]K[G]T[L]P[K]---F[TS]A[S]R[P]P[PY]A[R]	: 563
PcPex6	EPQLM[MA]S[LK]F[S]E[ND]S[PE]D[S]G[D]M[P]F[K]I[F]L[S]G[L]P[S]K[R]Y[A]L[N]---H[S]G[E]R[P]S[IS]Q[R]P[TR]L[T]S[V]F[V]P[L]L[G]M[E]M[E]R[Y]L[R]S[M]T[F]A[T]E[N]G[S]K[P]G[L]H[M]K[N]T[A]A[K]N[P]L[A]K	: 585
ScPex6	-----C[V]L[W]K[L]F[V]L[L]P[N]G-----F[K]K[R]I[Y]A[P]K[I]A[S]F[D]C[S]V[IT]I[S]K[S]N[IC]H[T]-----D[TR]I[A]M	: 310
AaPex6	EVILLK[V]S[T]P[L]S[D]R[L]Q[P]S[L]F[A]L[K]D[H]E[Q]K[R]I[V]K[S]G[D]L[G]V[S]I[D]E[S]L[G]R[A]V[F]Q[IT]I[E]D[V]G[M]E[L]L[A]R[P]T[A]S[D]E[S]T[S]V[S]R[N]P[K]V[S]U[F]R[I]C[V]W[S]P[IT]H[T]S[H]D[G]E[V]D[L]G[G]A[V]T	: 704
MoPex6	GVVYQ[V]R[P]L[T]S[K]D[V]E[V]A[V]L[A]G[L]K[H]F[E]K[L]E[V]I[K]A[G]D[L]A[V]P[D]T[Q]L[G]T[M]R[E]T[S]N[G]E[S]A[D]N[L]S[L]A[E]S[S]M[G]T[A]A[S]R[R]K[L]Y[D]B[V]A[U]F[V]K[V]S[H]V[Q]T[R]Q[D]A[D]--D[ED]L[W]C[S]A[A]C	: 669
CoPex6	DITIQ[H]R[S]P[V]T[A]E[R]A[Y]O[S]A[V]L[G]K[R]Y[F]A[Q]I[R]L[W]R[IG]D[L]A[V]P[D]T[Q]L[G]K[A]L[Q]E[P]S[A]N[G]S[E]V[D]V[M]A[L]K[E]S-----C[R]F[D]V[A]U[F]K[V]G[H]I[Q]T[K]D[A]H[D]Q[ED]L[W]G[G]V[A]C	: 674
PcPex6	EVILLK[V]S[T]P[L]S[D]R[L]Q[P]S[L]F[A]L[K]D[H]E[Q]K[R]I[V]K[S]G[D]L[G]V[S]I[D]E[S]L[G]R[A]V[F]S[G]--T[S]E[S]D[S]A[S]Q[E]E[D]I[T]R[L]G[O]G[A]M[A]T[A]G[A]P[K]I[G]V[A]U[F]R[V]G[W]A[P]T[V]E[E]L[E]E[T]G[E]D[Q]G[G]V[A]V	: 704
ScPex6	QVFLSRW[G]G[L]Q[S]Q[K]C[F]Q[N]I[L]T[L]K[F]F[S]E[S]K[R]L[C]Q[N]D[L]P[A]I[F]D[S]M[A]D[L]N[A]E[EN]D[S]D[E]D[E]L[G]Q[Y]K[R]D[S]-----L[V]U[F]F[T]S[A]E[L]D[C]F[S]K[D]N[S]H[F]I[D]P[N]R[T]K[L]	: 416
AaPex6	VDAASTR[ME]M[G]S[E]Q[G]K[T]P[A]P[S]M[A]Q[Y]L[G]A[K]R[A]P[V]S[S]--Q[K]M[A]L[D]E[L]P[K]T--Y[IS]S[L]R[R]R[L]R[E]L[M]S[V]A[T]S[P]R[A]I[H]L[G]L[P]I[A]V[L]I[T]S[T]O[R]G[I]G[K]S[V]A[T]R[A]C[E]D[L]G[L]H[T]F[S]I[D]A[F]D[I]	: 821
MoPex6	VEITMAH[F]S[S]G[V]N[G]R[V]P[G]V[D]S[M]P[Y]L[G]L[V]P[PN]P[G]S[L]P[V]A[I]C[P]A[K]K--H[IS]A[L]R[R]R[M]S[L]L[A]A[T]S[P]R[A]I[H]L[K]A[P]A[V]A[I]L[V]S[T]Q[R]N[I]G[K]A[T]A[D]T[D]C[R]D[I]G[L]H[T]F[T]I[D]A[Y]D[I]	: 787
CoPex6	IDSSVAM[H]G[S]G[F]A[T]S[R]P[A]D[A]S[A]T[P]Y[L]G[V]K[K]M[P]K[S]E[N]G[A]S[A]L[M]V[P]E[Q]O[R]--F[V]S[PL]R[R]R[L]E[L]A[A]A[T]S[P]R[A]I[H]L[K]M[P]V[A]I[L]L[T]S[T]R[M]N[I]G[K]A[T]A[S]A[C]S[D]I[G]H[T]Y[A]I[D]A[Y]D[I]	: 792
PcPex6	LDPAT[RM]V[A]G[S]D[V]S[V]R[V]G[V]L[G]M[G]E[V]O[L]G[V]K[T]I[P]K[T]V[D]A[P]T[P]H[G]I[V]A[D]P[Q]S[V]I[P]E[L]Q[R]T[R]D[L]M[S]A[A]T[S]P[R]A[T]Q[L]G[M]P[V]F[L]L[R]S[Q]R[H]I[G]K[A]T[V]A[T]R[A]C[S]D[I]C[H]T[P]I[D]A[Y]D[I]	: 824
ScPex6	LITNI[MR]R[PL]P[LS]R[S]M[L]Q[Y]Y[G]F[A]C[T]F[Y]D[L]H[I]F[V]Y[R]Q[V]L[M]I[E]T[S]F[N]C[S]Q-----R[G]I[L]M[A]S---V[L]L[H]E[T]M[V]G[K]A[M]V[R]P[A]S[K]Y[L]G[H]L[L]E[I]D[C]L[S]L	: 512
AaPex6	VTEGGAGG[V]D[V]R[E]G[L]K[A]R[A]E[R]A[L]C[CA]E[F]T[L]W[K]H[V]D[A]L[M]A[D]R[M]M[T]A[K]E[I]L[A]D[S]R-----V[L]I[A]T[T]D[E]D[V]K[V]P[G]I[R]G[L]F[T]H[E]L[E]M[T]A[P]D[E]G[E]R[E]G[L]L[R]S[I]	: 921
MoPex6	LMEGGG[V]G[S]D[V]K[D]G[L]K[A]R[A]E[R]A[L]S[C]G[P]E[F]C[L]L[R]H[E]A[L]T[A]D[R]M[Y]S[T]R[S]I[L]S[A]R-----V[L]I[A]T[T]D[E]P[D]K[I]P[D]G[V]R[G]L[F]T[H[E]L[E]M[T]A[P]D[E]G[E]R[E]G[L]L[R]S[I]	: 887
CoPex6	LSEAGT[S]G[D]V[R]T[E]G[L]R[T]S[R]A[M]S[C]G[P]D[T]A[L]L[K]H[E]A[L]T[A]D[R]M[Y]S[T]M[E]I[L]O[D]R-----V[L]W[A]T[S]D[V]D[V]K[V]P[G]I[R]G[L]F[S]H[E]L[E]V[G]A[P]D[E]A[E]R[E]G[L]L[R]I[L]	: 892
PcPex6	LTEGGAGG[V]D[V]K[T]E[A]Y[L]K[A]R[A]E[R]A[F]H[C]G[A]N[C]T[A]L[L]R[H]E[V]I[L]T[A]D[R]I[V]T[A]M[S]D[L]M[A]R-----V[V]I[A]T[T]D[W]E[T]I[P]E[G]I[S]L[I]T[H[E]P[E]M[G]A[P]E[E]R[E]G[L]L[Q]N[A]	: 924
ScPex6	TMSNRQ[L]D[S]T[S]R[I]G[Y]R[A]K[E]N[V]L[P]Y--A[S]P[A]V[I]F[L]A[G]L[S]L[L]D[V]W[A]N[Q]D[P]E[A]I[K]L[K]S[I]N[F]E[M]S[K]L[L]D[F]T[F]K[P]G[T]T[F]V[G]S[V]N[M]D[V]W[P]S[S]F[R]S[H]M[F]E[L]V[P]W[P]S[A]Q[L]L[R]I[F]Q[Y]	: 631
AaPex6	VDDAGI[R]L[S]P[E]V[D]L[A]N[V]A[K]T[A]A[V]A[G]D[L]V[D]V[D]R[A]L[V]A[K]O[R]L[E]A[L]A[S]A[S]K[S]LTP--P[D]T[I]T[D]R[D]I[E]L[A]G[H]F[S]N[S]L[K]A[D]L[T]A[V]D[A]A[R]K[F]A[D]A[G]A[P]K[I]P[N]V[G]S[D]V[G]G[L]T[W]K[D]A	: 1040
MoPex6	VDRQINL[D]P[E]V[D]L[G]V[A]L[K]T[A]A[V]A[G]D[L]V[D]D[R]A[T]V[A]O[S]R[L]E[S]L[A]E[K]A[S]Q[R]G[N]Q[P]A[V]L[T]D[V]Q[V]A[G]G[T]A[V]R[G]L[T]K[D]L[T]A[V]E[A]A[R]K[F]A[D]A[G]A[P]K[I]P[N]V[T]D[V]D[V]G[L]G[V]K[D]A	: 1007
CoPex6	VEDRGINL[D]P[E]V[D]L[G]A[L]K[T]A[A]V]A[G]D[L]V[D]V[D]R[A]L[V]A[K]O[R]L[E]I[S]S[K]T[G]-----Q[A]V[Y]R[D]L[Q]V[A]G[G]A[M]A[R]C[V]T[K]G[D]E[V]A[V]E[A]A[R]K[F]A[D]A[G]A[P]K[I]P[N]V[T]D[V]D[V]G[L]G[V]K[D]A	: 1005
PcPex6	VTEBGR[L]S[A]D[V]L[G]S[A]L[K]T[A]A[V]A[G]D[L]V[D]V[V]E[R]A[A]G[A]R[T]A[R]L[E]S[L]A[E]A[S]K[S]I[S]G[S]---E[V]F[V]R[D]L[L]A[G]G[D]G[A]R[G]V[T]K[A]D[A]A[V]E[A]A[R]K[F]A[D]A[G]A[P]K[I]P[N]V[G]D[V]D[V]G[L]T[V]K[D]A	: 1041
ScPex6	LSSH[L]M[R]D[V]Q[V]K[V]P[V]S[Y]M[D]N[S]I[S]F[S]L[S]S[Y]S[A]G[L]P[L]D[E]S[V]E[T]A[R]M[T]A[T]A[R]F[Y]Q[-----SKK]G[L]P[S]I[L]I[Q]E[D]L[S]K[A]T[S]K[A]R[M]E[S]V[S]I[G]A[P]I[P]N[V]T[D]D[V]G[D]F[V]K[E]	: 743
	Walker A Walker B	
AaPex6	VMETIQLP[L]RPELFAKGMKRSGLFYGP[PG]T[GT]L[LAKA]TATEFSLNFFSVKGP[EL]LMNYIGE[SE]ANVRRV[Q]RARDARPC[V]VFFDELD[SV]APKRG[N]Q[G]S[G]G[V]M[D]R[V]S[Q]L[L]A[E]L[D]G	: 1160
MoPex6	VMETIQLP[L]RPELFAKGMKRSGLFYGP[PG]T[GT]L[LAKA]TATEFSLNFFSVKGP[EL]LMNYIGE[SE]ANVRRV[Q]RARDARPC[V]VFFDELD[SV]APKRG[N]Q[G]S[G]G[V]M[D]R[V]S[Q]L[L]A[E]L[D]G	: 1127
CoPex6	VMETIQLP[L]RPELFAKGMKRSGLFYGP[PG]T[GT]L[LAKA]TATEFSLNFFSVKGP[EL]LMNYIGE[SE]ANVRRV[Q]RARDARPC[V]VFFDELD[SV]APKRG[N]Q[G]S[G]G[V]M[D]R[V]S[Q]L[L]A[E]L[D]G	: 1125
PcPex6	VMETIQLP[L]RPELFAKGMKRSGLFYGP[PG]T[GT]L[LAKA]TATEFSLNFFSVKGP[EL]LMNYIGE[SE]ANVRRV[Q]RARDARPC[V]VFFDELD[SV]APKRG[N]Q[G]S[G]G[V]M[D]R[V]S[Q]L[L]A[E]L[D]G	: 1161
ScPex6	ILDITDMP[L]KPEL[F]T[S]G[M]K[R]S[G]L[F]Y[G]P[PG]T[GT]L[LAKA]TATEFSLNFFSVKGP[EL]LMNYIGE[SE]ANVRRV[Q]RARDARPC[V]VFFDELD[SV]APKRG[N]Q[G]S[G]G[V]M[D]R[V]S[Q]L[L]A[E]L[D]G	: 863
	AAA-protein signature	
AaPex6	MSD[Q]---G[E]GVFVIGATNRPD[L]LQALLRPGRFDK[L]YLGVS[DT]HEK[Q]TILEALTRKFTLHP[SV]S[L]A[V]S[Q]L[P]FTYTGAD[V]A[L]C[S]D[A]M[L]K[A]I[T]R[S]A[S]V[D]E[K]V[A]A[V]M[S]T---H[N]P[P]I	: 1274
MoPex6	MSGDD[SG]G[V]FVIGATNRPD[L]LQALLRPGRFDK[L]YLGVS[DT]HEK[Q]TILEALTRKFTLHP[SV]S[L]A[V]A[E]K[L]PFTYTGAD[V]A[L]C[S]D[A]M[L]K[A]I[T]R[S]A[S]V[D]E[K]V[A]A[V]M[S]A[E]---R[Q]Q[E]I	: 1244
CoPex6	MSGDD[SG]G[V]FVIGATNRPD[L]LQALLRPGRFDK[L]YLGVS[DT]HEK[Q]TILEALTRKFTLHP[SV]S[L]H[S]V[A]Q[L]PFTYTGAD[V]A[L]C[S]D[A]M[L]K[A]I[T]R[S]A[S]V[D]E[K]V[A]A[V]M[S]A[E]P[R]S[R]T[G]P[I]	: 1245
PcPex6	MNGEENS[GV]FVIGATNRPD[L]LQALLRPGRFDK[L]YLGVS[DT]HEK[Q]TILEALTRKFTLHP[SV]S[L]D[R]V[A]E[Q]LPLFTYTGAD[V]A[L]C[S]D[A]M[L]K[A]I[T]R[S]A[S]V[D]E[K]V[A]A[V]M[S]P[N]G-----P[V]	: 1275
ScPex6	MSD[Q]---A[D]GVFVIGATNRPD[L]LQALLRPGRFDK[L]YLGIP[DT]TKQ[L]MILEALTRKFTLHP[SV]D[N]D[W]K[L]E[L]A[K]L[P]E[M]YTGAD[V]A[L]C[S]D[A]M[L]M[A]M[S]I[A]R[M]W[K]E[V]S[Q]H[E]L[T]G---E[M]I	: 977
AaPex6	TIAYFFDHFAT[ED]I[V]M[V]T[E]D[F]M[A]H[R]E[L]V[PS]Y[S]A[D]E[L]H[Y]D[R]V[R]K[F]E[G]A[K]K[E]G[A]E[T]K[N]G[A]A[A]P[L]A[T]E[Q]A[F]S[A]T[T]A[K]K[A]K[A]P[V]H[E]D[E]T[E]M[V]I[R]T[Q]N[V]Q[L]N[G]A[G]S[G]N[G]L[A]G[G]	: 1394
MoPex6	TIAYFFDHFAT[ED]I[V]M[V]T[E]D[L]A[A]H[E]M[P]S[V]S[A]G[E]L[A]H[Y]E[R]V[R]A[T]F[E]G[---R]K[Q]Q[Q]Q[Q]Q[R]K[L]G[A]R[T]V[S]G[A]S[S]W[K]-----G[K]	: 1325
CoPex6	STAYFFDHFAT[ED]I[V]M[V]T[E]D[F]L[A]A[N]R[L]V[PS]Y[S]A[G]E[L]S[H]Y[E]Q[V]R[A]M[F]E[G]P[P]E[K]D[R]Q[Q]Q[Q]Q[Q]R[P]S[G]D[R]A[V]S[G]S[V]S[K]K[K]A-----I[A]G[G]S[G]K	: 1339
PcPex6	STAYFFDHFAT[ED]I[V]M[V]T[E]D[F]L[S]A[Q]G[E]L[V]P[S]Y[S]A[K]E[L]E[H]F[E]R[I]Q[T]E[A]V[D]K[S]K[D]P[A]A[A]P[Q]T[A]E[M]A[F]S[L]G[G]S[A]I[P]E[E]A[P]T[I]N[G]D[S]LTP[G]G[H]G[R]I[K]G[L]N[R]W[P]G[N]P[V]R[S]T[S]G[Q]	: 1395
ScPex6	STRR[F]D[K]I[A]T[K]E[D]F[W]W[K]M[D]F[L]K[A]Q[Q]L[P]S[V]S[R]A[E]L[M]H[Y]E[A]W[R]A[F]E[G]A-----	: 1030
AaPex6	VDISG[S]A[A]S[S]G[E]S[S]G[K]G[K]A[P]W[H]S[Q]G[S]S[V]D[I]A[E]G[G]F[D]A[T]Q[D]D[L]Y[S]-----	: 1444
MoPex6	GKGGK[A]I[A]S[S]G[E]E[E]D[Q]D[G]V[N]G[K]M[K]K[K]A[V]A[S]E[V]G[S]G[G]D[E]G[L]Y[D]-----	: 1375 (53%)
CoPex6	GKGA[V]A[T]G[S]D[E]Y[S]E[G]E[V]A[V]W[N]G[K]G[K]G[K]A[V]A[G]F[D]G[E]S[D]D[E]G[L]Y[D]-----	: 1388 (52%)
PcPex6	SIT[S]S[K]G[K]S[V]S[K]K[G]S[IT]G[A]E[S]D[G]S[V]D[ED]E[M]A[D]N[S]K[E]D[E]D[E]D[V]V[R]T[D]H[L]R[M]P[E]E[V]E	: 1459 (50%)
ScPex6	-----	: (30%)

FIG. S4. Similarity of AaPex6 to Pex6 proteins from other fungi. The amino acid sequence of AaPex6 of *Alternaria alternata* was aligned with those of Pex6 proteins from *Magnaporthe oryzae* (MoPex6; accession no. ABG79929), *Colletotrichum orbiculare* (CoPex6; accession no. AAK16738), *Penicillium chrysogenum* (PcPex6; accession no. AAG09749), and *Saccharomyces cerevisiae* (ScPex6; accession no. P33760-1). Amino acids that are conserved between any two proteins are indicated as white letters on a black background. These proteins contain Walker A and Walker B motifs and AAA-protein family signature motif.

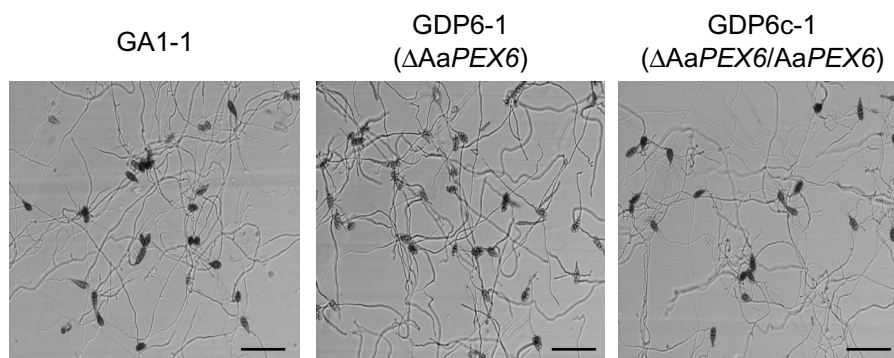


FIG. S5. Conidial germination of $\Delta AaPEX6$ strain. Conidial suspension of each strain was incubated on glass for 24 h. GA1-1, *GFP-AKT1* expressing strain made from the wild-type strain 15A; GDP6-1, *AaPEX6*-disrupted transformant made from GA1-1; GDP6c-1, *AaPEX6*-complemented transformant made from GDP6-1. Bar=100 μm .