

Supplementary Information

The Fungal Effector Avr-Pita Suppresses Innate Immunity by Increasing COX Activity in Rice Mitochondria

Jingluan Han^{1, 2, 3 #}, Xiaoyu Wang^{1, 3 #}, Fengpin Wang^{1, 3 #}, Zhe Zhao^{1, 2, 3}, Gousi Li^{1, 3}, Xiaoyuan Zhu⁴, Jing Su^{4 *}, and Letian Chen^{1, 2, 3 *}

Supplementary Figures

Fig. S1 Ectopic expression of *Avr-Pita* in rice.

Fig. S2 Avr-Pita specifically binds to the conserved domains of OsCOX11.

Fig. S3 Avr-Pita and OsCOX11 co-localize to the mitochondria in onion epidermal cells.

Fig. S4 Characterization of *OsCOX11* transgenic plants and pathogen resistance of *OsCOX11-RNAi* plants.

Fig. S5 *OsCOX11* expression in response to chitin and *M. oryzae* treatment.

Supplementary Tables

Table. S1 Candidates of Avr-Pita interacting protein screened by Y2H.

Table. S2 Primers used in this study.

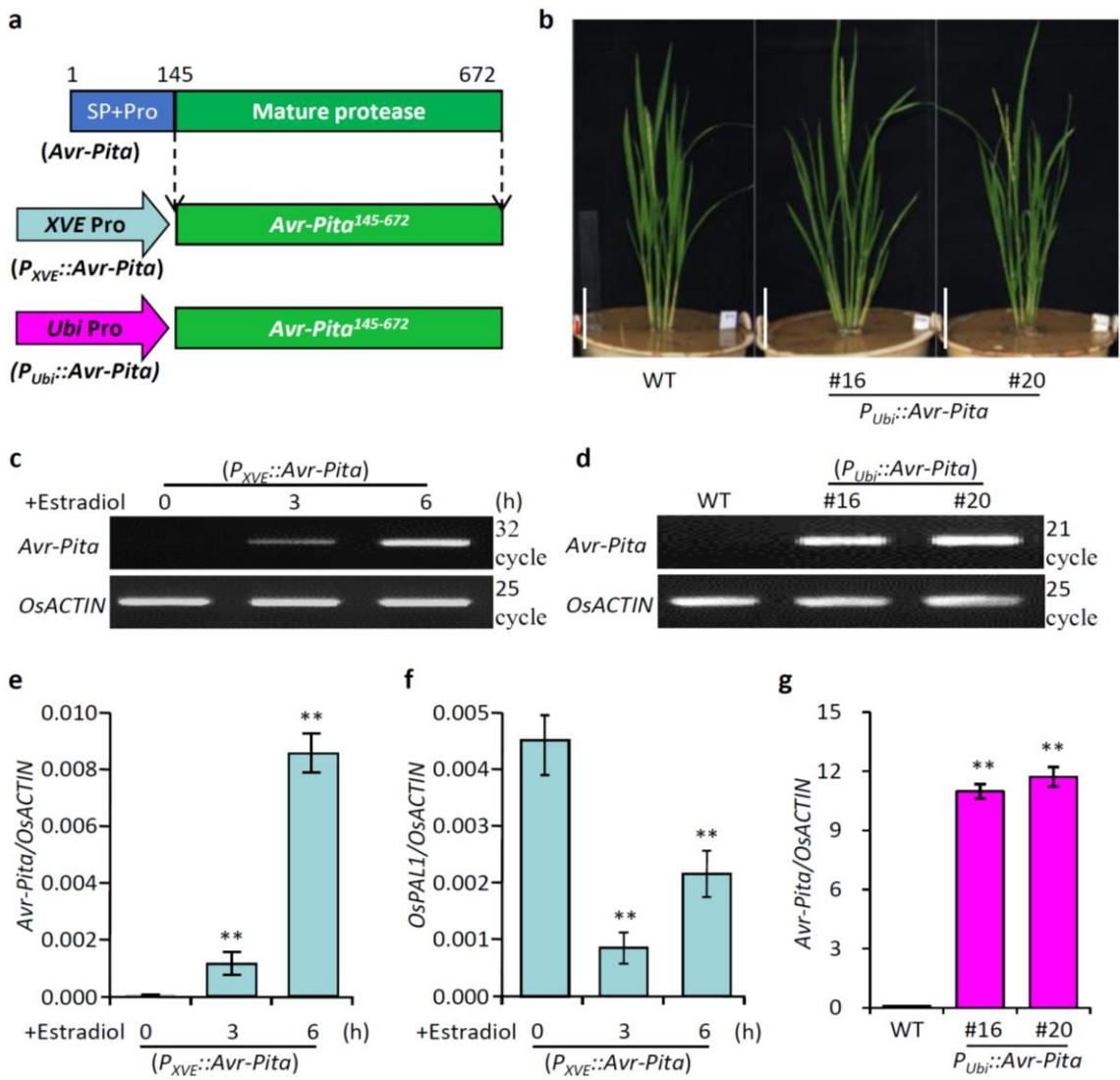


Fig. S1 Ectopic expression of *Avr-Pita* in rice.

(a) Diagram of the $P_{XVE}::\text{Avr-Pita}$ and $P_{Ubi}::\text{Avr-Pita}$ constructs. In these constructs, a truncated $\text{Avr-Pita}^{145-672}$ fragment encoding mature protease is driven by the estradiol-inducible promoter *XVE* or the maize *Ubiquitin* (*Ubi*) promoter. SP: signal peptide; Pro: predicted prosequence. **(b)** The growth and developmental morphology of $P_{Ubi}::\text{Avr-Pita}$ plants were not obviously affected in these lines. Scale bars: 10 cm. **(c)** Transcript levels of *Avr-Pita* was measured by RT-PCR in $P_{XVE}::\text{Avr-Pita}$ transgenic suspension cell lines after estradiol treatment. **(d)** Transcript levels of *Avr-Pita* was measured by RT-PCR in $P_{Ubi}::\text{Avr-Pita}$ transgenic lines. **(e)** The expression of *Avr-Pita* in $P_{XVE}::\text{Avr-Pita}$ transgenic suspension cell lines after estradiol treatment using qRT-PCR. **(f)** The expression of defense-response gene *OsPAL1* in $P_{XVE}::\text{Avr-Pita}$ suspension cell lines after estradiol treatment using qRT-PCR. **(g)** Overexpression of *Avr-Pita* in $P_{Ubi}::\text{Avr-Pita}$ transgenic lines using qRT-PCR. *OsACTIN* served as a control to normalize the expression levels of target genes. Data are shown as mean \pm SD (** $P < 0.01$, $n = 3$).

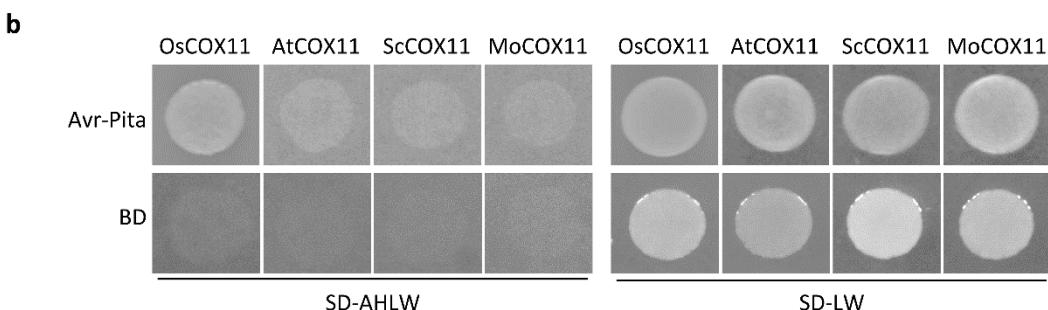
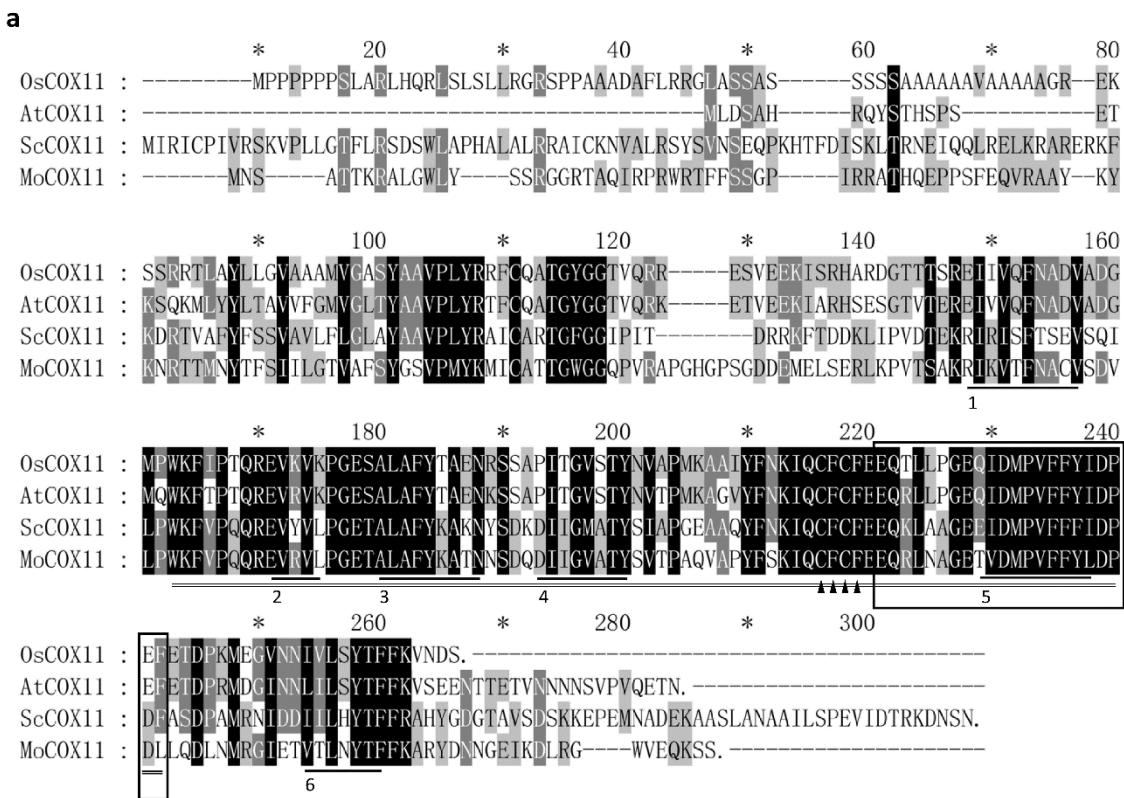


Fig. S2 Avr-Pita specifically binds to the conserved domains of OsCOX11.

(a) Amino acid sequence alignment of COX11 orthologs OsCOX11 (*O. sativa*, XP_006650503.1), AtCOX11 (*A. thaliana*, AAG00893), ScCOX11 (*S. cerevisiae*, NP_015193), and MoCOX11 (*M. oryzae*, XP_003717808). Six β sheets (indicated by a single underline and numbered 1–6) and Cu-binding core region CFCF (indicated by four triangles \blacktriangle) are present in the conserved region of COX11. Residues 140–220 of OsCOX11, which are responsible for the interaction with Avr-Pita, are double underlined. The critical region OsCOX11^{199–220} is labelled with boxes. **(b)** Avr-Pita specifically interacts with rice OsCOX11 in a Y2H assay. Yeast cells were cultured on selective medium SD-LW or SD-AHLW; cell growth on SD-AHLW indicates a positive interaction.

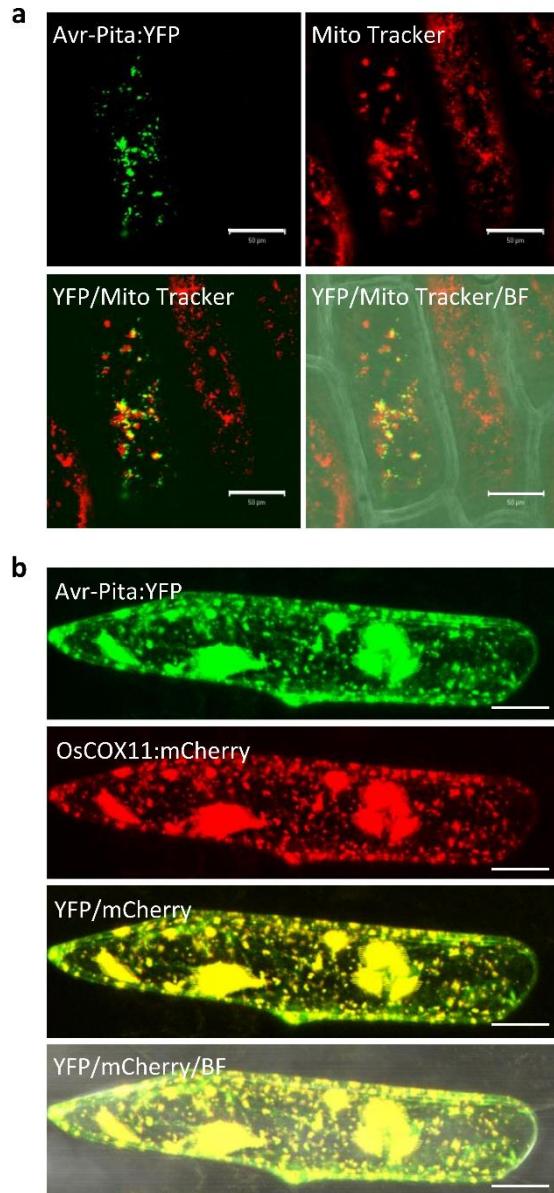


Fig. S3 Avr-Pita and OsCOX11 co-localize to the mitochondria in onion epidermal cells.

(a) *Avr-Pita:YFP* was introduced into onion epidermal cells by particle bombardment and stained with the mitochondrial dye MitoTracker. **(b)** *Avr-Pita:YFP* and *OsCOX11:mCherry* were transiently introduced into onion epidermal cells by particle bombardment. Scale bar = 50 μ m.

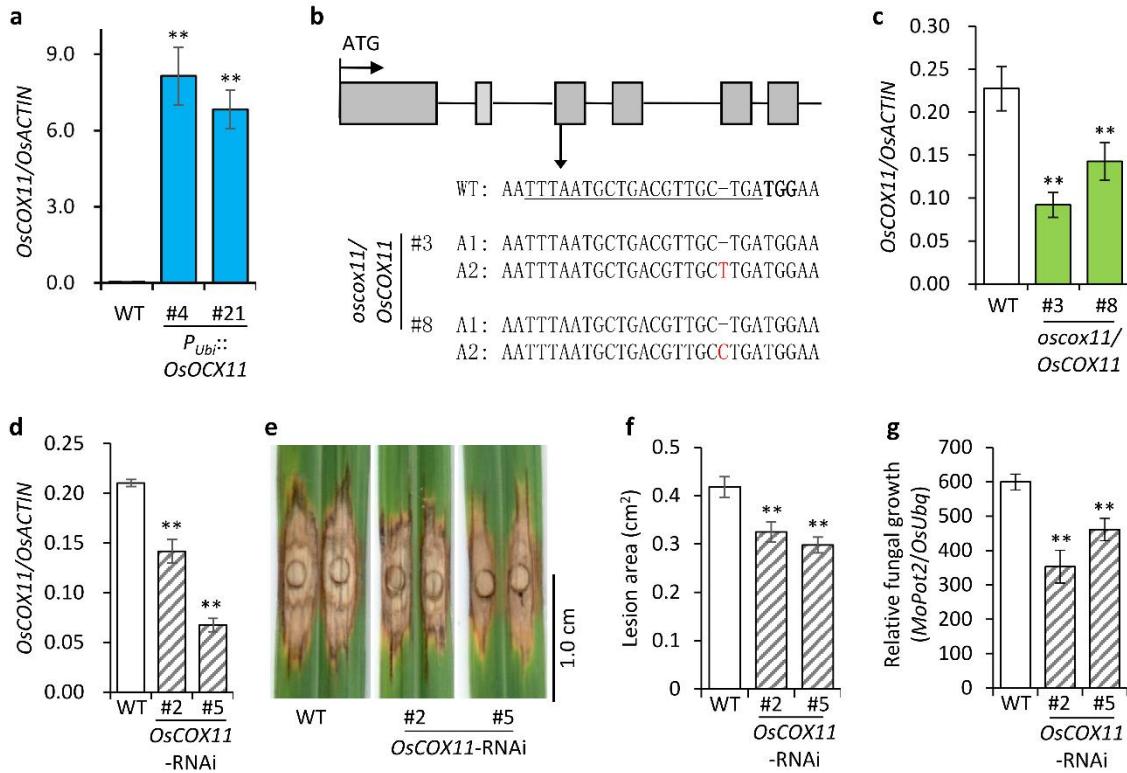


Fig. S4 Characterization of *OsCOXII* transgenic plants and pathogen resistance of *OsCOXII*-RNAi plants.

(a) Expression levels of *OsCOXII* in *P_{Ubi}::OsCOXII* lines; *OsACTIN* served as an internal control. Data are shown as mean \pm SD (** $P < 0.01$, $n = 3$). **(b)** Genotypes of heterozygous *oscox11/OsCOXII* lines carrying a “T” or “C” base insertion. **(c)** Expression levels of *OsCOXII* in *oscox11/OsCOXII* plants. *OsACTIN* served as an internal control. Data are shown as mean \pm SD (** $P < 0.01$, $n = 3$). **(d)** Expression levels of *OsCOXII* in *OsCOXII*-RNAi plants. *OsACTIN* served as an internal control. Data are shown as mean \pm SD (** $P < 0.01$, $n = 3$). **(e)** Disease symptoms of *OsCOXII*-RNAi transgenic plants at 12 dpi inoculated with *M. oryzae* isolate 13-219. **(f)** Lesion area in *OsCOXII*-RNAi transgenic plants at 12 dpi inoculated with *M. oryzae* isolate 13-219. Data are shown as mean \pm SD (** $P < 0.01$, $n > 12$). **(g)** Relative fungal biomass on inoculated leaves at 12 dpi, as determined by qPCR. Data are shown as mean \pm SD (** $P < 0.01$, $n = 3$).

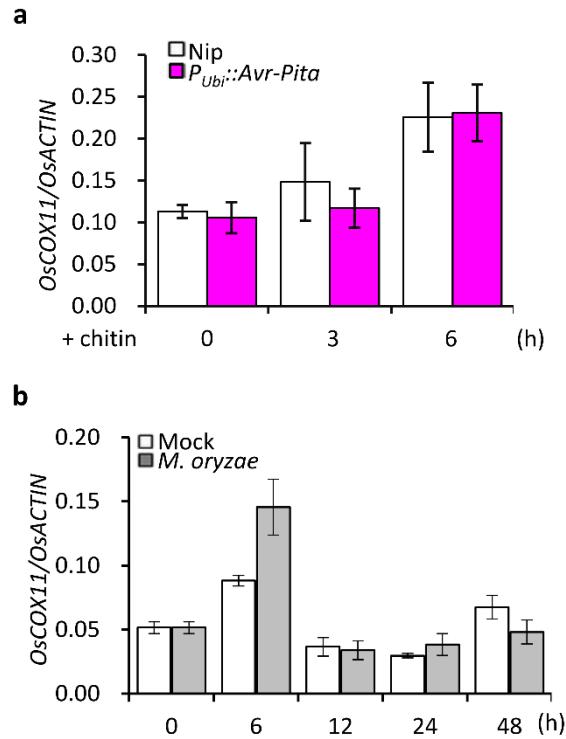


Fig. S5 *OsCOXII* expression in response to chitin and *M. oryzae* treatment.

(a) The expression levels of *OsCOXII* in *P_{Ubi}::Avr-Pita* and WT plants after chitin treatment. **(b)** The expression levels of *OsCOXII* in rice seedlings in response to *M. oryzae* compatible strain 08-T13 inoculation at the indicated time points. *OsACTIN* served as an internal control. Data are shown as mean \pm SD (** $P < 0.01$, $n = 3$).

Table. S1 Candidates of Avr-Pita interacting protein screened by Y2H.

Gene ID	Predicted Function
Os01g0127500	Dihydroflavonol-4-reductase
Os01g0531500	Dienelactone hydrolase family protein
Os03g0718600	Cytochrome c oxidase assembly protein COX11
Os08g0532900	Emp24/gp25L/p24 family protein
Os06g0149900	Cysteine synthase
Os11g0171300	Fructose-bisphosphate aldolase isozyme

Table. S2 Primers used in this study.

Primer Name	Sequence (5' — 3')
Genetic modification	
P _{XVE} -Avr-Pita-F	TCGACCTGCAGATGCGCTATTCCAATGTTCA
P _{XVE} -Avr-Pita-R	CATGCCTGCAGTTAACAAATTATAACGTGC
P _{ubi} -Avr-Pita-F	TCGACCTGCAGATGGAACGCTATTCCAATGTTCA
P _{ubi} -Avr-Pita-R	TCAGGATCCTTAACAAATTATAACGTGC
P _{ubi} -OsCOX11-F	ACTTGGATCCATGCCGCCGCCGCCCTCGTT
P _{ubi} -OsCOX11-R	TCAGGATCCTTAACGTGCGTTACCTTAAAGA
OsCOX11-U6b	TCAGCAACGTCAGCATTAAACAAACACAAGCGGCAGC
OsCOX11-gRNA	TTAACGCTGACGTTGCTGAGTTTAGAGCTAGAAAT
OsCOX11-Ri-1F	TTACGGTACCATGGATGCTAGCGAACTAGTC
OsCOX11-Ri-1R	CATGGTACCGTACACTCACTGCCTTAAAG
OsCOX11-Ri-2F	CATGGTACCGCTGAGGGTAAATTCTAGT
OsCOX11-Ri-2R	TTGCGGATCCTCAGCTGAGACATCACT
Genotyping	
OsCOX11-In2Ex4-F	TGGAATAGCCATACAGCC
OsCOX11-In2Ex4-R	CCTTCATAGGAGCTACGTTATATGTG
OsCOX11-seq-F	GCAAATTGCTGTAATCATGGGCTAA
qPCR	
Avr-Pita-qF	CCTCCTTCTTCAACAAACCC
Avr-Pita-qR	CCATCCCATTGTAACCA
OsCOX11-qF	CAACACAGAGAGAAGTGAAGGT
OsCOX11-qR	GTGGATACACCAGTTATTGGAG
OsPAL1-qF	CCTGCCAATCTGCTGAACCTA
OsPAL1-qR	TTTGAAACCTGCCACTCGTA
OsPBZ1-qF	CCGAATACGCCCTAACAGATGAA
OsPBZ1-qR	TCTCACGGACTCAAACGC
OsPR10-qF	AGGACTACCTCGTCGCTCA
OsPR10-qR	TTGGATTGTCGTGGCTC
OsActin-qF	GCATCTCTCAGCACATTCCA
OsActin-qR	ACCACAGGTAGCAATAGGTA
OsUbi-qF	TTCTGGTCCTCCACTTCAG

OsUbi-qR	ACGATTGATTAAACCAGTCCATGA
MoPot2-qF	ACGACCCGTCTTACTTATTGG
MoPot2-qR	AAGTAGCGTTGGTTTGTGGAT
Protein subcellular localization	
Avr-Pita-YFP-F	TACTAAGCTTATGGAACGCTATTCCAATG
Avr-Pita-YFP-R	TCAGGATCCCACAATATTATAACGTGC
OsCOX11-mCh-F	CATGAAGCTTATGCCGCCGCCGCCGC
OsCOX11-mCh-R	TCAGGATCCACTGTCGTTACCTTAAAGA
Yeast two-hybrid	
BD-Avr-Pita-F	TACCATATGGAACGCTATTCCAATGTTAGA
BD-Avr-Pita-R	TCAGGATCCTAACAAATATTATAACGTGC
AD-OsCOX11-F	ACTTCATATGATGCCGCCGCCGCCGC
AD-OsCOX11-R	TCAGGATCCTAACTGTCGTTACCTTAAAGA
AD-AtCOX11-F	GTACTGGAATTCATGTTAGATAGTCCCCATGCC
AD-AtCOX11-R	CTGAGTCTCGAGTTAATTGGTTCTGAACGGAA
AD-ScCOX11-F	CGACGGATCCGTATGATAAGAATATGTCCCATTGTTAG
AD-SsCOX11-R	CTATGGATCCTAACATTGAGTTGTCTTCCTGTGTC
AD-MoCOX11-F	ACGTTGGAATTCATGAACCTCAGCAACGACGAAGC
AD-MoCOX11-R	GGATCTCTCGAGCTATGAGCTCTGCTCCACC
AD-OsCOX11 ¹⁻¹⁹⁸ -F	ATGTTTGCTTGAGGATCCATCGAGCTCGAGCTGCAGAT
AD-OsCOX11 ¹⁻¹⁹⁸ -R	TCGAGCTCGATGGATCCTCAAAGCAAAACATTGTATCTTA
AD-OsCOX11 ⁸⁰⁻²²⁰ -F	CATCGATCCTGAGTTGGATCCATCGAGCTCGAGCTGCAGA
AD-OsCOX11 ⁸⁰⁻²²⁰ -R	CGAGCTCGATGGATCCAAACTCAGGATCGATGTAGAAGAAC
AD-OsCOX11 ¹¹⁰⁻²²⁰ -F	AGATTACGCTCATATGGAGGAGAAGATCTCACGACATGCTC
AD-OsCOX11 ¹¹⁰⁻²²⁰ -R	GTGAGATCTCTCCTCCATATGAGCGTAATCTGGTACGTCG
AD-OsCOX11 ¹⁴⁰⁻²⁴⁴ -F	AGATTACGCTCATATGCCGTGAAATTCAACACAGA
AD-OsCOX11 ¹⁴⁰⁻²⁴⁴ -R	GAATGAATTCCACGGCATATGAGCGTAATCTGGTACGTCG
Pull-down	
GST-Avr-Pita-F	CTGGTTCCCGGTGGATCCCCAGGAGAACGCTATTCCAATGTTCA
GST-Avr-Pita-R	TCACGATGCGGCCGCTCGAGTCGATTAACAATATTATAACGTGC
His-OsCOX11-F	ATGGCTGATATCGGATCCGAATTCCGCCGCCGCCGC
His-OsCOX11-R	TCGAGTGCAGCGCAAGCTGTCGTTAAGCTGTCGTTACCTTAAAGA
