

Table S1 The gene-specific primers for RT-qPCR used in this study

Gene name	Forward Primer(5' to 3')	Reverse Primer(5' to 3')
<i>PyunARF33</i>	GATGCAGCAGAGGCTAGATCC	AGCTGCAACAGTGGATTGGG
<i>PyunARF5</i>	TGCAGCAGCGCATTTCAGTAT	CGCCTGCAAAGATGGAGAGT
<i>PyunARF27</i>	GGGAACCTCGTGACAAGCC	CAGCTGCTCTACTTGGCCC
<i>PyunARF35</i>	TTGTCAGAAATGGCTGGTCAC	AGCTAAAGAGTGTACACGGCA
<i>PyunARF18</i>	CCAGCAGCAGCAGAATCAAC	CTGTCCAAGTTGACCAGCCT
<i>PyunARF21</i>	GGAGTCCGCAGATACATGGG	CCTGGCTGCTTAGGGAACCTT
<i>PyunARF3</i>	GAGCTCCTCAATGCATGGTG	GTTGATCAGTGCCACCATCC
<i>PyunARF4</i>	TGCAACCACCATCTCAGGAGC	GCCTCACACCCACCATCAAG T
<i>PyunARF16</i>	TCGAGGACAACCCAAGAGG	AGGCATGAAAGTTTGAAGAC G
<i>PyunARF13</i>	TTCTCTGTTCTCGTCGTGC	ACAAACACACTCCAACCCGT
<i>PyunARF17</i>	CAATGCAACCGCCAACTCAG	GCCTCACACCCACCATTAAC T
<i>PyunARF34</i>	TATGGTGGTACCGCACAAGA	TGATTCTGGTTGGTCCAGGC
<i>HIS</i>	TTTAAGACTGATCTGCGTTTCC	GAACAGCCCAACAAGGTATG

Table S2 The proportion of Gln(Q),Ser(S),Leu(L),Pro(P) and Thr(T) in MR domain of *PyuARFs* gene. The proportion of Gln (Q), Ser (S), Leu (L), Pro (P), Thr (T) determines whether the MR Domain of ARFs has transcriptional activation or inhibition.**>PyuARF17/207-279**

NR SPFT I FY N PRAD FV I P LI K FR KA VFGQV SVGMR F G M M FETE E
S GKRRY M GTI V G IS DDP L RWPGS K WR N LQ

Gln (Q) 2 2.7%

Ser (S) 5 6.8%

Leu (L) 3 4.1%

Pro (P) 5 6.8%

Thr (T) 3 4.1%

>PyuARF4/207-279

NRSSFTIFYNPRADFVIPLIKFRKTVFGQVSVGMRFGMMFETEESAK RRY
M GTI V G NS DDP L RWPGS K WR N LQ

Gln (Q) 2 2.7%

Ser (S) 6 8.2%

Leu (L) 3 4.1%

Pro (P) 4 5.5%

Thr (T) 4 5.5%

>PyuARF21/207-279

NNSPFTIFYNPRAEFVIPFSKYNKALYTQVSLGMRFRMMFETEESGV RRY
M GTI T G IS DDPVRW KN S Q WR N LQ

Gln (Q) 3 4.1%

Ser (S) 6 8.2%

Leu (L) 3 4.1%

Pro (P) 4 5.5%

Thr (T) 5 6.8%

>PyuARF34/207-279

NN SPFT I FY N PSA EFV I P FS K YN KAM YTQG S L GMRF R M M F T TE
E S G V R R Y M G T I T G I S D D P V R W K N S Q W R N L Q

Gln (Q) 3 4.1%

Ser (S) 7 9.6%

Leu (L) 2 2.7%

Pro (P) 4 5.5%

Thr (T) 6 8.2%

>PyuARF18/207-279

NN SPFT V F Y N P R A E F V I P L A K Y Y K A V Y S Q I S L G M R F R M M F E T E E
S G T R R Y M G T I T G I S D D P A R W K N S Q W R N L Q

Gln (Q) 3 4.1%

Ser (S) 6 8.2%

Leu (L) 3 4.1%

Pro (P) 4 5.5%

Thr (T) 5 6.8%

>PyuARF35/207-279

N N S P F T V Y Y N P R A E F V I P L A K Y Y K A V Y S Q I S L G M R F R M M F E T E E S G T R R
H M G T I T G I S D D A V R W K N S Q W R N L Q

Gln (Q) 3 4.1%

Ser (S) 6 8.2%

Leu (L) 3 4.1%

Pro (P) 3 4.1%

Thr (T) 5 6.8%

>PyuARF13/165-235

P A Q E L I A R D L H D V E W K F R H I F R G Q P K R H L L T T G W S V F V S A K R L V A G D S V
L F I W N E K N Q L L L G I R R A T R P Q T

Gln (Q) 4 5.6%

Ser (S) 3 4.2%

Leu (L) 9 12.7%

Pro (P) 3 4.2%

Thr (T) 4 5.6%

>PyuARF33/207-279

T N S C F T V F Y N P R A E F V I P L S K Y V K A V F H R I S V G M R F R M L F E T E E
S S V R R Y M G T I T G T S D D P V R W P N S H W R S V K

Gln (Q) 0 0.0%

Ser (S) 8 11.0%

Leu (L) 2 2.7%

Pro (P) 4 5.5%

Thr (T) 6 8.2%
>PyuARF3/207-279
T N S R F T I F Y N P R A E F V I P L A K Y L K A V Y Y R V S V G M R F R M M F E T E
E S S V R R Y M G T I T G I S D D V V R W P N S Q W R S V K
Gln (Q) 1 1.4%
Ser (S) 7 9.6%
Leu (L) 2 2.7%
Pro (P) 3 4.1%
Thr (T) 5 6.8%
>PyuARF27/207-279
T N S R F T I F Y N P R A E F V I P L A K Y L K A V Y Y R V S V G M R F R M L F E T E E
S S V R R Y M G T I T G I S D D V A R W P N S L W R S V K
Gln (Q) 0 0.0%
Ser (S) 7 9.6%
Leu (L) 4 5.5%
Pro (P) 3 4.1%
Thr (T) 5 6.8%
>PyuARF16/207-279
T N S R F T I F Y N P R A E F V I P L V K Y I K A V Y H R V S V G M R F R M L F E T E E
S S V R R Y M G T I T G I S D D P V R W P N S H W R S V K
Gln (Q) 0 0.0%
Ser (S) 7 9.6%
Leu (L) 2 2.7%
Pro (P) 4 5.5%
Thr (T) 5 6.8%
>PyuARF5/207-279
T N S R F T I F Y N P R T E F V I P L V K Y I K A V Y H R V S V G M R F R M L F E T E E
S S V R R Y M G T I T G I S D D P A R W P N S H W R S V K
Gln (Q) 0 0.0%
Ser (S) 7 9.6%
Leu (L) 2 2.7%
Pro (P) 4 5.5%
Thr (T) 6 8.2%

Figure S1 Sequence alignment and corresponding domain of *PyuARFs*. ARFs has three main domains: B3, MR And AUX/IAA

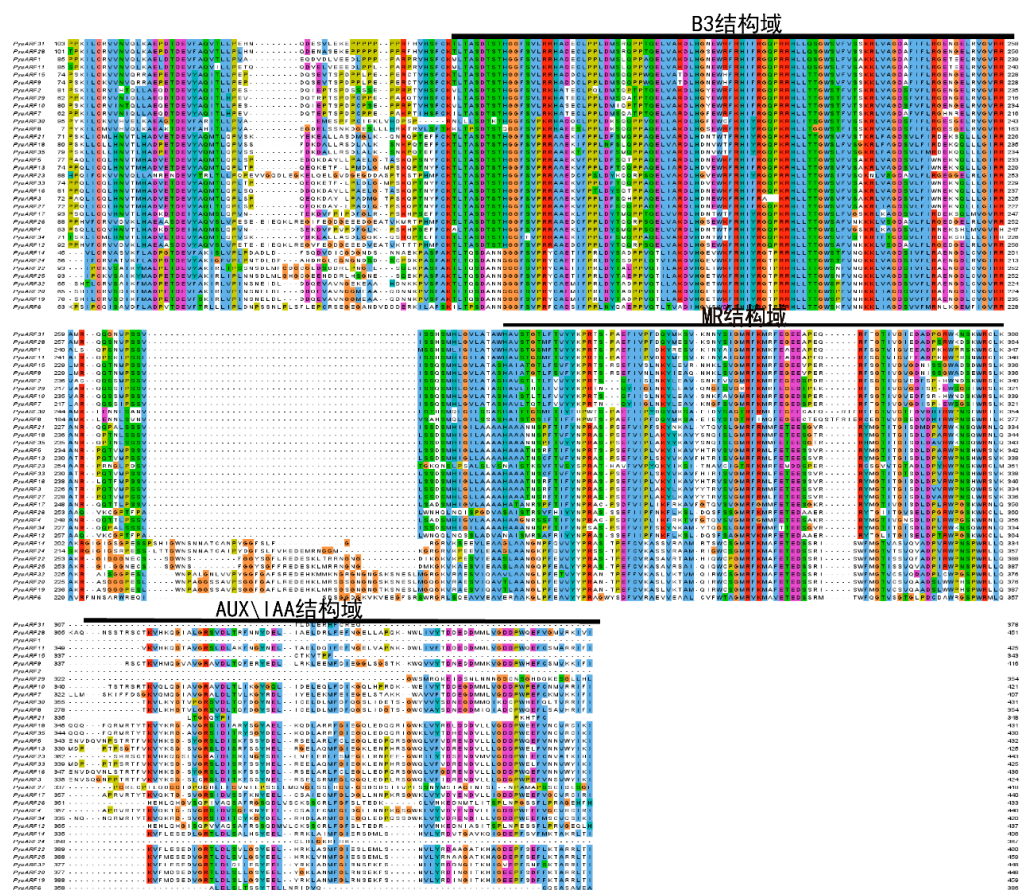


Figure S2 The number and types of Motifs of *PyuARFs*.

