

IMP4	LLTTSRNPSAPLIRFTKELKFVFP—NSQR—INRGSQVISEI IETARSHDFTDVIIVHEHRGVPDGLI I SHLPFGPTAYFGLLNVVTRHDI SDK	91
RPF1	LLTTCRFNSTRGPALISELLSVIP—NSHY—QKRGTYDLKKIVEYATKDFTS LI VVHTNRREPDALL I IGLPNGPTAHFKLSNLVLRKDIKN—	90
BRX1-1	LVTCSRRI NFRYRHLMLNMVSLLP—HCKKDSKVEAKSSRGATLNEL I ELKGSSSCLFFECRKHKDLYMMWVKSPGGPSVKFLVNAVHTMEELKLT	94
BRX1-2	LVTCSRRI SFYRSLMLNIVSLLP—HCKKDSKVEAKSSKGATLNEL I ELKNSNSCLFFECRKHKDLYMMWVKSPNGPSVKFLVKAVHAMEEMKLT	94
SNAIL1	FVFSRMKLAGPVKQLQMDLRKLM—PYTALS LKEKKRNTLRDFLNVSGPMGVTHFLMLS KTAS—SLSLRVARTPQGPTLTFK I HQYSLASDIAQS	93
ARPF2	LILHGTKTSATLSSVMTELYRLKGGGAI RYSRRNENIRPFESGGETSLEFFSQKTDGSI FVYGSHTKKRPDNLVLGRMYDHQVYDL I EVG I ENFKSLRAF	100
IMP4	KSIGKMPE—QYPHLIFN—NFTTQMQRVGNILKHIFP—APKLDAGR—IVTFSNQSD—YISFRNHVY—	152
RPF1	—HGNPTS—HQPELVLN—NFTTRLGNRVGRFFQSLFPPDPNFRGRR—VVTFHNRD—FIFFRHHRYIFETKESK—	158
BRX1-1	GNHLKGSR—PLLTSSN—FENDAHWKLKEMLTQIFGIPEGHRKSKPYHDHVFVFSIVDD—HIWFRNYQISVPHNES—	168
BRX1-2	GNHLKGSR—PLLTSSN—FDKAHWKLKEMLTQVFGIPKEHRKSKPYHDHVFVFSIVDE—HIWFRNYQISVPHNES—	168
SNAIL1	QLRPRCPQDLFKSPPLIVLSGF—GSQELHLKLATIMFQNI FPAIDINTVKLSTCQRLVLLNYNKDTKLIDFRHYSIRLQPVGVSRRI RKFVQNHQVPDLR	192
ARPF2	SYDKKFAPHEG—TKPFI CF I GEGFENVSELKHLKEVLTDLFRGEVVDNLNLTGLDRAYVCSAISP—TKVFLTHCALK—	177
IMP4	—DKGEGGPK—SIELKEIGPRFELRLYQV	178
RPF1	—SDKGKEETI—KPRLQECGPRFTLKLVTL	185
BRX1-1	—DKIARGDLD—KMTLIEVGPRFCLNPIKI	195
BRX1-2	—DKIAGGLD—KMTLIEVGPRFCLNPIKI	195
SNAIL1	NLQDVSDVFTKAGYGSESEGDDEEAATVTLSSDLGRVNGGATKSAVKLQEI GPRMTMQLVKV	253
ARPF2	—KSGSIVPRMELVEVGPSMDLVI RRN	202

Figure S1 Alignment of amino acid sequences of Brix domains from *Arabidopsis thaliana*. The sequence alignment was produced with the ClustalW program (<http://www.genome.jp/tools/clustalw/>). Amino acid residues conserved in all amino acid sequences are shaded in gray.

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ARPF2 MMEIRTPKTKGAKRVLESRAPKLVETGKKTLLHGTKTSATLSSVMTELYRLKKGGAIRY 60
Rpf2 MIRTVKPKNARAKRALVKREAKLVENVKQALFIPGQSCNKLHDIMVDLSALKKPKDMKRF 60
ARPF2 SRRNENIRPFESGGETSLEFFSQKTDCSIFVYGSHTKKRPDNLVLGRMYDHQVYDLIEVG 120
Rpf2 NRKND-IHPFED--MSPLEFFSEKNDCSLMVLMTSSKKRKNMFIIRTFGYKIYDMIELM 117
ARPF2 IENFKSLRAFSYDKKFAPHEGTPKPFICFIGEGFENVSELKHLKEVLTDLFRGEVVDNLNL 180
Rpf2 VADN--FKLLSDFKKLTFVGLKPMFTFQGAADFTHPVYKQIKSLFLDFFRGESTDLQDV 175
ARPF2 TGLDRAYVCSAISPT-----KVFLTHCALKLKKS---GSI VPRMELVEVGPSMDLVIIR 230
Rpf2 AGLQHVISMTIQGDFQDGEPLPNVLFVYKLSYKSDQGGKRLPRIELVEIGPRLDFKIG 235
ARPF2 RNRLPNDSLMKEAMRTSKDKPKKKEKNVDQDAVLGKTGKIYMPDQ-----KLKEMKLFDK 285
Rpf2 RIHTPSPDMVTEAHKKPKQLEMKTKKNVELDIMGDKLGRIMGKQDLGKLQTRKMKGLKS 295
ARPF2 SKGSKRERKDAKLKHKEETVAKMKVSS----- 314
Rpf2 KFDQGTEEGDGEVDEDYEDEASYSDDGQEEYEEEFVSATDIEPSAKRQKK 344

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Figure S2 Alignment of amino acid sequences of ARPF2 and Rpf2. The sequence alignment of ARPF2 (At3g23620.1) and *Saccharomyces cerevisiae* Rpf2 (NP_013007.1) was produced with the ClustalW program (<http://www.genome.jp/tools/clustalw/>). Similar and identical amino acid residues in the two amino acid sequences are shaded in light and dark gray, respectively. The sequences of the Brix domain are indicated by red line.

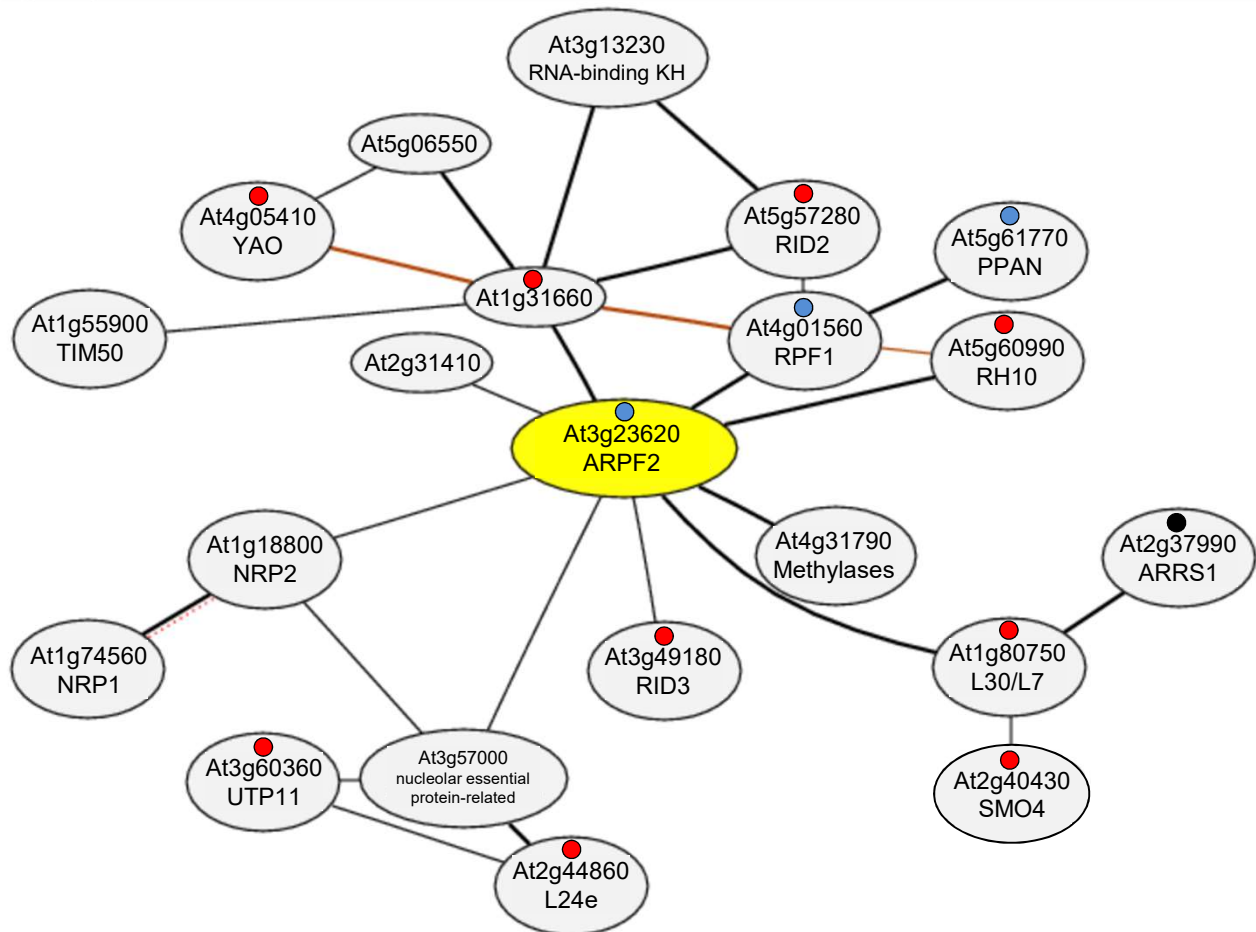


Figure S3 Co-expression network including *ARPF2*. A co-expression network of *ARPF2* was obtained using the ATTEDII program (<http://atted.jp/>) with the parameter “Coexpression data; All”. Genes reported as “ribosome-related gene” are indicated by red dots; *At1g31660*, Missbach et al. (2013); *RID2* (*At5g57280*) and *RID3* (*At3g49180*), Shinohara et al. (2014); *YAO* (*At4g05410*), Li et al. (2010); *L24e* (*At2g44860*) and *L30/L7* (*At1g80750*), Carroll et al. (2008); *RH10* (*At5g60990*), Matsumura et al. (2016); *SMO4* (*At2g40430*), Zhang et al. (2015). Genes encoding Brix domain-containing proteins are indicated by blue dots. *ARRS1* is indicated by black dot.

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ARRS1 -----MDTEMETEQIYQVDVGNLLAFNP-----NHRFPSAPSSRGELVKEILTEGTKL 48
Rrs1  MSAEDYKNLPVTVEKPIPVVYDLGNLAAFDSNVLDKNDLDSSNARREEKIKSLTRDNVQL 60

ARRS1  VQEIANLKFNFSTETNDGP-----IVQLPPPTTKLPREKHIPRPKPPTKWEFALK 100
Rrs1  LINQLLSLPMKTTTESVGGTGGQSSVMTLLQLPDPTDLPREKPLPKAKAMTKWEKFAAK 120

ARRS1  KGIQKRKKE-KVVWDEQTNQFKRRHGYDRVNDNDVPIIEAKESDEPG-----VDPFAKR 154
Rrs1  KGIKPKERAGKMIYDEASGEWVPKWGYKGANKKLDQWLVEVDDKVKGTDNELIDPRTLN 180

ARRS1  LDDKKKRVGKQEKRLQNLKAAEKAGALPSHVQLAATSLPISGTKAQPCKIGKDELGDVA 214
Rrs1  RAERKRLVKKNEKQRRNMKNAL----- 203

ARRS1  GLAATSTASGGKFDKLPGEKPPKKQGHKHYLPVVSGRGDVNAEKEQTNNVLSKIFSKH 274
Rrs1  -----

ARRS1  SHEILNVGKAINMYNVKKEKKKSGRSDKLPKPKDITKPKANKAK 318
Rrs1  -----

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Figure S4 Alignment of amino acid sequences of ARRS1 and Rrs1. Sequence alignment of ARRS1 (At2g37990.1) and *Saccharomyces cerevisiae* Rrs1 (NP_014937.1) was produced with the ClustalW program (<http://www.genome.jp/tools/clustalw/>). Similar and identical amino acid residues in the two amino acid sequences are shaded in light and dark gray, respectively.

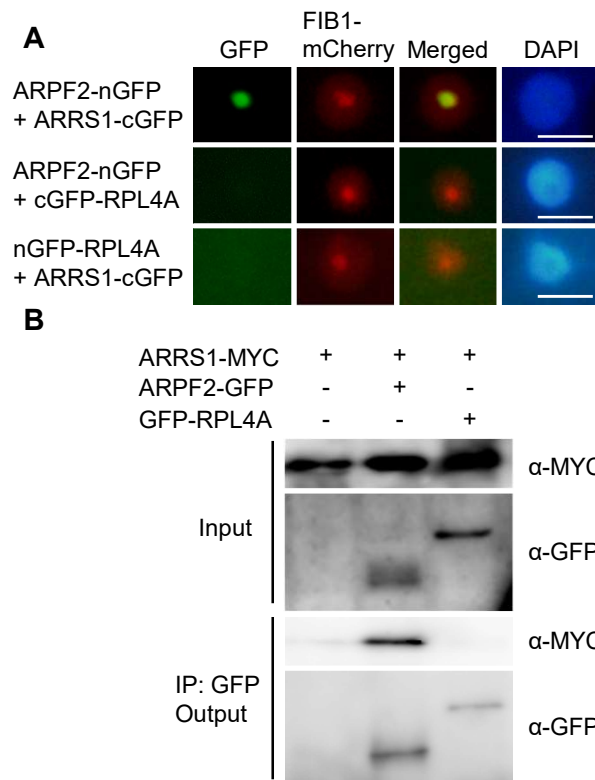


Figure S5 Specificity of the ARPF2- ARRS1 interaction. (A) BiFC assays. ARPF2 fused to nGFP (ARPF2-nGFP) was co-expressed with cGFP-fused ARRS1 (ARRS1-cGFP) or RPL4A (cGFP-RPL4A) and FIB1-mCherry in *N. benthamiana* leaves. ARRS1-cGFP was also co-expressed with GFP-fused RPL4A (nGFP-RPL4A) and FIB1-mCherry. Scale bars: 10 μ m. (B) Co-immunoprecipitation assays. ARRS1-MYC was transiently expressed alone or with ARPF2-GFP or GFP-RPL4A in *N. benthamiana* leaves. The ARPF2-GFP or GFP-RPL4A proteins in the crude cell extracts (Input) were immunoprecipitated with an anti-GFP antibody, and the obtained precipitates (Output) were analyzed with anti-GFP and anti-MYC antibodies.

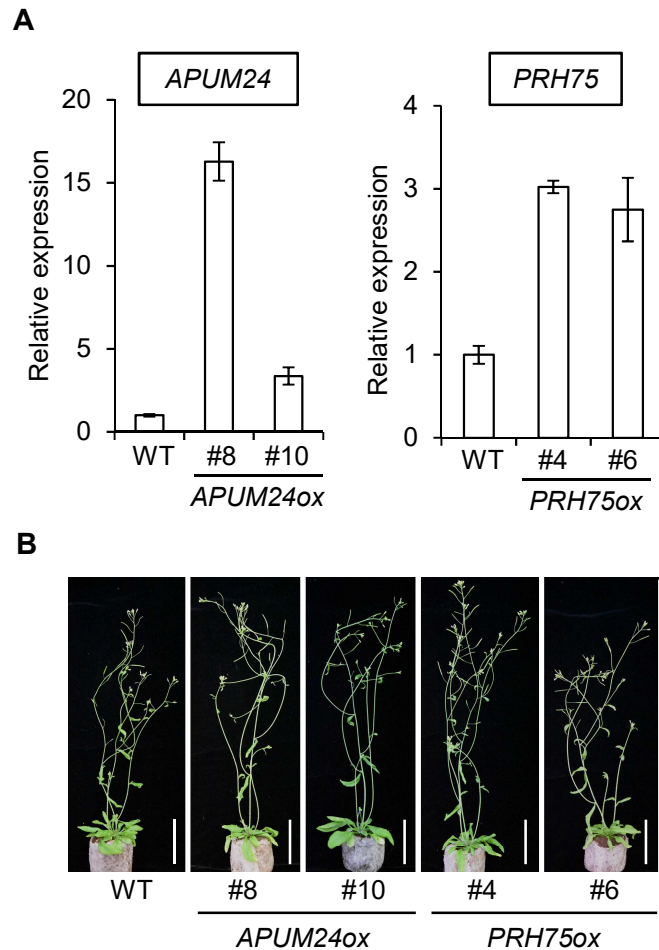


Figure S6 Phenotypic analysis of transgenic *Arabidopsis* overexpressing *APUM24* or *PRH75*. **(A)** Levels of *APUM24* and *PRH75* transcripts in the wild type and *APUM24* or *PRH75* overexpressing plants. RNA was extracted from 10-day-old seedlings and technical triplicates were used for quantification. *UBQ10* was used as an internal control. The expression levels are relative to that in the wild type, and the values obtained with the wild type were set to 1. Error bars represent SD. **(B)** Photographs of the plants grown for 5 weeks. Scale bars: 5 cm.

Supplemental Table S1. List of the Primer Sequences.

Primer name	Sequence (5'-3')
Vector construction	
pRPF2 5'entry	CACCACCTATAGAGACGACAATGTC
pRPF2 3'entry	GACTCTGTTAAATCGCCGAAAG
RPF2 5'entry	CACCATGATGGAATACGAACTCC
RPF2 3'entry	CTCAGAAGAGACCTTCATCTTTTTG
RRS1 5'entry	CACCATGGACACGGAGATGG
RRS1 3'entry	CTTGGCTTTGTTGGCAGGCTTC
APUM24 5'entry	CACCATGTCTTCCAAAGG
APUM24 3'entry	TTCAGTTTCTTGTTGCTGAGATC
PRH75 5'entry	CACCATGCCTTCCCTAATGTTATCTG
PRH75 3'entry	TCAATATCTCTGGCCTCTACCACCAC
RPL4A 5'entry	CACCATGGCCGCCGCCGCT
RPL4A 3'entry	TTACTGGCTAGCACCCGAGCCATTTG
Genotype check	
Primer "A"	TGGTTCACGTAGTGGGCCATCG
Primer "B"	TTCATAACCAATCTCGATACAC
Primer "F"	GTCACTATAGTTGTTGCTTACCTCATG
Primer "R"	GTCGTTTCTTCGTGTGAGAACC
RT-qPCR	
RPF2 F	CATCCAAGGATAAGCCTAAGAAGAAG
RPF2 R	CTCAGAAGACACCTTCATCTTTTTG
RRS1 F	TGGGGATGTTAACGCAGAAAAAGAAC
RRS1 R	CTTGGCTTTGTTGGCAGGCTTC
APUM24 F	CTTGTCACACAGTGGCCTTG
APUM24 R	TCACACAGCTTCTCGCTCAG
PRH75 F	GAGGATTCTACTAAAGTCCAGAC
PRH75 R	ATAATATCAGGAATCAACCGAGCC
UBQ10 F	GATCTTTGCCGAAAAACAATTGGAGGATGGT
UBQ10 R	CGACTTGTCCATTAGAAAAGAAAGATAACAGG
Forward primer of "1" in Fig. 5	TTCGGCGTATGAGTGGTG
Reverse primer of "1" in Fig. 5	CATTCATCGATCACGGCAATTCC
Forward primer of "2" in Fig. 5	AACGACCCGCGAACCAAAGATCAC
Reverse primer of "2" in Fig. 5	ACACTTTTCGTGCCGGGTTTTGTG
Forward primer of "3" in Fig. 5	CGACTCTCGGCAACGGATAT
Reverse primer of "3" in Fig. 5	TTGTGACACCCAGGCAGACG
Forward primer of "4" in Fig. 5	ATCGTCGTCCCTCACCATCCTTTGCTGATG
Reverse primer of "4" in Fig. 5	GCATGTCCGTACGCTCCA
Forward primer of "5" in Fig. 5	TGATCCATTACATTTTATCGGTCCG
Reverse primer of "5" in Fig. 5	CTTAAACTCAGCGGGTAATCC
Forward primer of "6" in Fig. 5	CACGTCTGCCTGGGTGTCAC
Reverse primer of "6" in Fig. 5	Same as reverse primer of "5" in Fig. 5
Forward primer of "7" in Fig. 5	AATCCGGGCTAGAAGCGACG
Reverse primer of "7" in Fig. 5	AATTCAAGGCGGTCCGAACGAC
Forward primer of "8" in Fig. 5	GCCCTTTGTCGCTAAGATTCCA
Reverse primer of "8" in Fig. 5	GTTTTGGACAAGTCTGTCTCTTCAC
Forward primer of "9" in Fig. 5	GATGCGATCATACCAGCACTAATGC
Reverse primer of "9" in Fig. 5	AGGGATGCAACACGAGGACTTC