```
                                 β1          α2                                        β2                 β3
         .................................. .   ..........................................   ......      ....... .
ARF5.....CLPQVGSLVYYFSQGHSEQVAVSTRRS.......ATTQVPNYPNLPSQLMCQVHNVTLHADKDSDEIYAQMSLQPV
ARF6.....SLPPVGSRVVYFPQGHSEQVAASTNKE.......VDAHIPNYPSLHPQLICQLHNVTMHADVETDEVYAQMTLQPL
ARF7.....SLPPAGSLVVYFPQGHSEQVAASMQKQ.......TDFIPSYPNLPSKLICMLHNVTLNADPETDEVYAQMTLQPV
ARF1.....TLPREGERVYYFPEGHMEQLEASMHQG.......LEQQMPSF.NLPSKILCKVINIQRRAEPETDEVYAQITLLPE
ARF9.....DVPQAQERVYYFPQGHMEQLEASTQQV......DLNTMKPLF.VLPPKILCNVMNVSLQAEKDTDEVYAQITLIPV
ARF3.....SLPKRGSLVLYFPQGHLEQAPDFSAAI.............Y.GLPHVFCRILDVKLHAETTTDEVYAQVSLLPE
ARF10....QIPSLNSTVFYFAQGHTEHAHAPPDFH.........APRVPPLILCRVVSVKFLADAETDEVFAKITLLPL
PpARF1...QLPQVGAKVIYFPQGHGEQAATTPDFS.......ASMGPSGTIPCRVVSVNFLADTETDEVFARMRLQPE
PpARF2...QLPHVGAKVVYFPQGHGEQAASTPEFP.......RTLVPNGSVPCRVVSVNFLADTETDEVFARICLQPE
SmARF1...QLPPVGAKVIYFPQGHGEQAAAIPDFP.......RSGGTILCRVISVDFLADAETDEVYAKMKLQPE
SmARF2...QLPTVGSKIIYFPQGHAEQAASSPDFP.......RALGPAGTVPCRVLSVKFLADKETDEVFASLRLHPE
PpBRWD...YSPQFGDEVAYLHQGHREYLEASKVKE.......KGPWKKHE.LRAVEFCRITNLEYHIEPGGGT.SCKLELEFL
DfBRWD...YIPQIGDNVIYFHQGHKKYLDMYPDEVV......QDVGLSLLWLSTAEECIIKELKYIITSPQSSNPGLHQAQIT
PopBRWD..YSPQIGDSVIYFHQGHKKYIETFPDETE.........QVEQSQLSTAEECNIINIKYIIASPKSVNPGLHQAEIT
AcBRWD...YIPQVNDEVVYFRQGHSIHIEKFAKVQ......HPTPPWETFPRLRAQEVCRVVQIEYRPSPYGIQTLLTLELLDT
AiBRWD...LIPQVGDTLMYCPQGHEVFLRSFPSKF........QAAYKSLPKPFAVLQCHVLDIQYTFPPVDLYPQQNRIVMEL
CcBRWD...SSPQLGDDVMYFPEGHASAM.AISRET......GVEPVAGLAALKKAGKELDGSSFPADASPVRFQIVQKPRSASS
MmPHIP...FVPQMGDEVYYFRQGHEAYVEMARKNKIYSINPKKQPWH..KMELREQELMKIVGIKYEVGLPTL..CC.LKLAFL
HsWDR9...FVPQMGDEVIYFRQGHEAYIEAVRRNNIYELNPNKEPWR..KMDLRDQELVKIVGIRYEVGPPTT..SCKLELEFL
DmWDR9...YYPQMGDEVVYFRQGHAKYLDAVRLKKVYKLSHSSEPWN..FHTLRDHELVRVIGIKYEIRPPRL..CC.LKLAII
GmBRWD...YIPQLGDEVVYFRQGHQEYIESYSLSE........SGPWRLFVGLGASEICKVEELEYAELPGSGDSCCKLKLRFV
AtBRWD...YIPQMGDEVAYLRQGHQEYLNFSSLRE......VAPWTSIKGGNIKAVEICKVESLEYATLPGSGDSCCKMILKVI
TgCRM....QLPEVGSRLFYFRKGHEQMMKSMQQE-------------------------------------------------


ARF5............HSERDVFPVPDFGMLRGSK*HQQTAL.............................................
ARF6............NAQEQKDPYLPAELGVPSR*QRPQTVM.............................................
ARF7............NKYDRDALLASDMGLKLNR*QANRQTPTL..........................................
ARF1................LPTSPDAPVQEPEK*RQQTNI...............................................
ARF9............GTEVDEPMSPDPSPPELQR*LQQSSM..............................................
ARF3...SEDIERKVREGIIDVDGGEEDYEVLKRSN*QIEGTA.............................................
ARF10..PGNDLDLENDAVLGLTPPSSDGNGNGKEK*RGGLGSNAGSDNPYPGFSGFLRDDESTTTTSKLMMMKRNGNN.........
PpARF1..........GLHGLNDMTEEAPSSPPPEK*RGAMGDNGHGGS.SNGVSRSGSQGASTT.........................
PpARF2..........IGSSAQDLTDDSLASPPLEK*RGVSNGESSS..WHSSISNASTIRPSRWEVKGTESFSDFLGG.VGDNGYALNT.
SmARF1....VAPAPLFGTRMGDDEELVSSPTVVEK*RGPGNGDSG.ISWHSSPGQSGYSELLSGNGSGTSG..................
SmARF2...........SGSDEDNDRAAALSPSPEK*RGGGSGNADALLWHSASSRSS....SRWELRPPMDTGLSDGTLMGENGSSRSAG
PpBRWD..DMESSASG..................................................................
DfBRWD..LKPVSSPDEE.................................................................
PpBRWD..LSVLSTG....................................................................
AcBRWD..LVPPSPSMLGEDESYEPEESLNAN...................................................
AiBRWD..IMDVVGLPSVYFRNEDDQPSVDVLDFGSFVPVNNLFVRDESEARRK.............................
CcBRWD..RPKASRGSHVHNRVTAKTTLVLTLRLVSGLPSRTDGA......................................
MmPHIP..DPDTGKLTG..................................................................
HsWDR9..DMESSASG...................................................................
DmWDR9..DEEEGNMTG..................................................................
GmBRWD..DPSSCVHG...................................................................
AtBRWD..DPNSEVFN...................................................................
TgCTM...----------------------------------------------------------------------------
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Supplemental Figure 1. Guilfoyle. (2014) Plant Cell. 10.1105/tcp.114.132753.

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                                    [α6]           [β11]      [β12]   [α7]              [β13]
ARF5.............PSSVLSADSMHIGVLAAAAHATANRTPFLIFYNPRACPAEFVIPLAKYRKAICGSQLSVGMRFGMMFET.....
ARF6.............PSSVLSSDSMHLGLLAAAAHAAATNSRFTIFYNPRASPSEFVIPLAKYVKAVYHTRVSVGMRFRMLFET.....
ARF7.............SSSVISSDSMHIGILAAAAHANANSSPFTIFFNPRASPSEFVVPLAKYNKALYA.QVSLGMRFRMMFET.....
ARF1.............PSSVISSHSMHIGVLATAAHAITTGTIFSVFYKPRTSRSEFIVSVNRYLEAKTQ.KLSVGMRFKMRFEG.....
ARF9.............PSSVISSHSMHLGVLATARHATQKTMFIVYYKPRT..SQFIISLNKYLEAMSN.KFSVGMRFKMRFEG.....
ARF3.............ALSAQYNQNMHNNFSEVAHAISTHSVFSISYNPKASWSNFIIPAPKFLKVVDY.PFCIGMRFKARVES.....
ARF10..........DGNAAATGRVRVEAVAEAVARAACGQAFEVVYYPRASTPEFCVKAADVRSAMRI.RWCSGMRFKMAFET.....
PpARF1........SSFARNRARVTAKSVLDAAALAVAGK.PFEVVYYPRASTAEFCVKAGLVKQALDH.TWYAGMRFKMAFET.....
PpARF2........SSFARDRARVTAKSVLEAAALAVSGE.RFEVVYYPRASTAEFCVKAGLVKRALEQ.SWYAGMRFKMAFET.....
SmARF1........ASFARNRARVTSKSVLEAASLAAAGQ.AFEVVYYPRASTAEFCVRASVVKASLEH.SWYPGMRFKMAFET.....
SmARF2...GGGGNGGGSFTRAKVTAKSVLDAATLAASGK.AFEVVYYPRASTAEFCVRAQTVRAALSH.GWYAGMRFKMAFET.....
PpBRWD......................YKFQLTWPELTDYPDFLVEKSRFDASMAK.GWVARDHCKVWWASEKG..
DfBRWD......................DEIKVFYH.VSDIPDYLVLASKVKRSLET.RWAPGMKFKMYYPD.....
PopBRWD.....................HTISVLYH.VSDIPDYLVLASRVRKSLES.HWASDDQFKMFYID.....
AcBRWD......................RRFMLSYHPTTRTVDFLVLRSRYESSLEA..CHVGRRVTVLFFSGKE.
AiBRWD......................WRFRLQHQPSEC.AEFLLLEQKYLSGFQAPRWKVGATVQMAYHTMDDHG
CcBRWD......................TRFVLCYYPVDAP.EYLVLTNRVEAALN.RAWTASDRFRILFLN.....
MmPHIP......................GSFTMKYHDMPDVIDFLVLRQQFDDAKYR.RWNIGDRFRSVIDD.....
HsWDR9......................KSFSIRYHDMPDVIDFLVLRQFYDEARQR.NWQSCDRFRSIIDD.....
DmWDR9......................TTFKIKYHDMPDVLDFLVLRQTFDLAVQR.NWSIGDRFRCMIVD.....
GmBRWD......................KSFKLTLPELINFTDFVIEKTWYDTAMKR.NWSSRDKCMVWWRN.....
AtBRWD......................KAFKLTLPEVVTFPDFLVERSRYEAAIQR.NWTCRDKCKVWWRD.....
TgCRM....----------------394aa--------------------VEFVVRREKVFHALNL.NWNPGMRFRMVFHT-----
Tudor...........................................FQINEQVLACW.......


                                 [β14]              [β15]           [β16-η1-β17]
ARF5...............EDSG.KRRYMGTIVGISDLDPLRWPGSKWRNLQVEWDEPGC....NDKPTRVSPWDIETPE
ARF6...............EESS.VRRYMGTITGICDLDPTRWANSHWRSVKVGWDESTA....GERQPRVSLWEIEPLT
ARF7...............EECG.VRRYMGTVTGISDLDPVRWKNSQWRNLQIGWDESAA....GDRPSRVSVWDIEPVL
ARF1...............EEAP.EKRFSGTIVGVQENKSSVWHDSEWRSLKVQWDEPSS....VFRPERVSPWELEPLV
ARF9 ..............EDSP.ERRYSGTVIGVKDCSPH.WKDSKWRCLEVHWDEPAS....ISRPNKVSPWEIEPFV
ARF3...............EDAS.ERRSPGIISGISDLDPIRWPGSKWRCLLVRWDDIVA....NGHQQRVSPWEIEPSG
ARF10..............EDSSRISWFMGTVSAVQVADPIRWPNSPWRLLQVAWDEPDL....VQNVKRVSPWLVELVS
PpARF1.............EDSSRISWFMGTIAAVKPADPLLWPNSPWR...VTWDEPDL....LQGVSRVSPWQVELVA
PpARF2.............EDSSRISWFMGTIAAVQAADPVLWPSSPWRVLQVTWDEPDL....LQGVNRVSPWQLELVA
SmARF1.............EDSSRISWFMGTISAVQPADPIRWPSSPWRILQVSWDEPDL....LQGVNRVSPWQVELVS
SmARF2.............EDSSRISWFMGTISAVQAADPILWPSSPWRVLQVAWDEPDL....LQGVSRVSPWQVELVS
PpBRWD..................ADEKGQWWDGRIKTIKAKSDD.FPDSPWEKYIVTYRESA.......EPQAHSPWELFDRN
DfBRWD.....................EEKWYNGRIKSIAPSDPN.YPDSLWERILVCWSQDGN......DDRVSPWEIELLT
PopBRWD....................ENQWFTGVITEVSPSDPT.YPDSLWERIVVRWDQDGG......EGRVSPWEIELVH
AcBRWD....DGVSSRKSTTITDSVRQAAWYSGTVLSVSPLSPDTFPDSKWDCLEVAWDDEPGEPAGTGGVTRVSPWESKEYH
AiBRWD.....................MIQNTQMDTGKILELSPLDP..AMTSPWECIVVQWENED.......TPCRVSPWELESDQ
CcBRWD.....................ESAWQYGTI...RSVRP.TIRSVMWNSVEVVYDNEGE..KEKTTCELVSPWELESFH
MmPHIP.....................AWWFGTIESQEPLQP.EYPDSLFQCYNVCWDN........GDTEKMSPWDMELIP
HsWDR9.....................AWWFGTVLSQEPYQPQ.YPDSHFQCYIVRWDN........IEKLSPWDMEPIP
DmWDR9.....................GWWMGQIESRHALSAD.FPDSSFMCFRVRWDN..........YEFMSPWDMEPID
GmBRWD.................EDGKGGSWWDGRIIQVQAKSDD.FPNSPWERYRVQYKTDP......SENHLHSPWELYDPE
AtBRWD.................EGEEDGSWWEGRILAVKPKSPD.FPDSPWERYTVKYKSDP......AETHLHSPWELFDAD
TgCRM....------80aa---------TRYTGTIRRVNLL....HPD.FWENVVVEWEDR---41aa---ENVSLWELEPLK
Tudor...................SDCRFYPAKVTAVNKDG..........TYTVKFYDGVV.......QTVKHIHVKAF
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Supplemental Figure 1. Amino acid sequence alignments for the BRWD-like fragment in selected Arabidopsis ARFs and BRWD proteins.

Identical amino acids are boxed in yellow and similar amino acids are boxed in grey. Secondary structures for ARFs (Boer et al., 2014) and predicted for BRWD proteins (Phyre2) are shown at approximate positions above the alignments. The Tudor domain (Boer et al., 2014) and another Auxin_resp domain protein (TgCRM) are shown for comparison. Sequences for ARF5 (At1g19850), ARF6 (At1g30330), ARF7 (At5g20730), ARF1 (At1g59750), ARF9 (At4g23980), and ARF3 (At2g33860), PpARF1 and PpARF2: *Physcomitrella patens* (XP_001782750 and DAA06632), SmARF1 and SmARF2: *Selaginella moellendorffii* (XP_002969449 and XP_002976921), PpBRWD: *Physcomitrella patens* (XP_001755663), DfBRWD: *Dictyostelium fasiculatum* (XP_004357233), PopBRWD: *Polysphondelium pallidum* (ADBJ01000037), AcBRWD: *Acanthamoeba castellani* (XP_004337512), AiBRWD: *Aphanomyces invadans* (gb ETW016454), CcBRWD: *Chondrus crispus* (XP_005719095), MmPHIP: *Mus musculus* (gb EDL26451), HmWDR9: *Homo sapiens* (AB080587), DmWDR9: *Drosophila melanogaster* (AY094828), GmBRWD: *Glycine max* (XM_006588511), AtBRWD: *Arabidopsis thaliana* (At5g49430), TgCRM: *Toxoplasma gondii* (XP_002366434) chloroquine resistance marker protein, and Tudor: Tudor domain from *Homo sapiens* PHD-finger protein 20 (NP_057520.2) are aligned. Asterisk is the position of the B3 domain in ARFs that has been excised from the alignment. The dashed lines in TgCRM show the number of amino acid residues between the conserved motifs that are found in ARFs or BRWD proteins. The FD_1- related sequences are located within residues 3324-3359, and FD_2-related sequences are located within residues 3744-3773, 3854-3881, and 3921-3934 of the TgCRM protein.