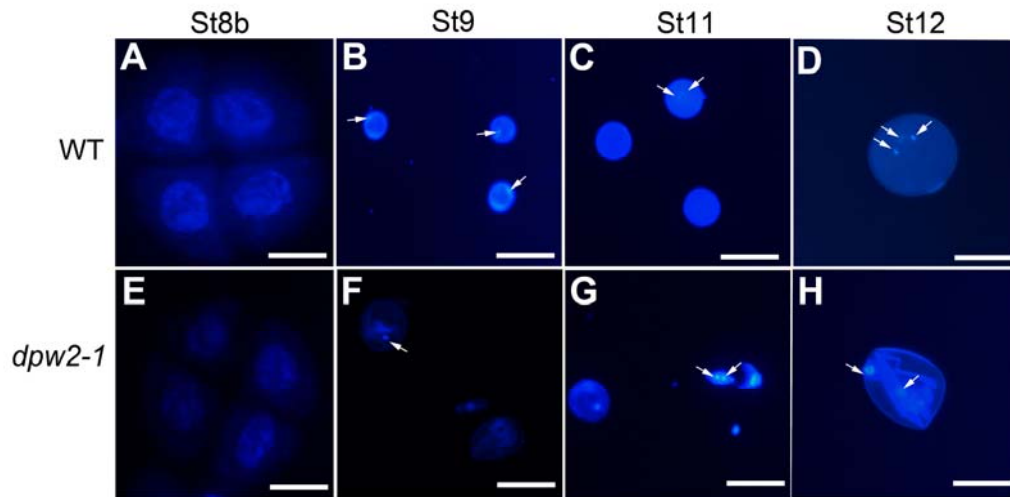


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1 **Supplemental materials**

2 **Supplemental Figures**



3  
4 **Supplemental Figure 1.** DAPI staining of *dpw2-1* microspores.

5 (A) to (D) wild-type microspores.

6 (E) to (H) *dpw2-1* mutant mrospores.

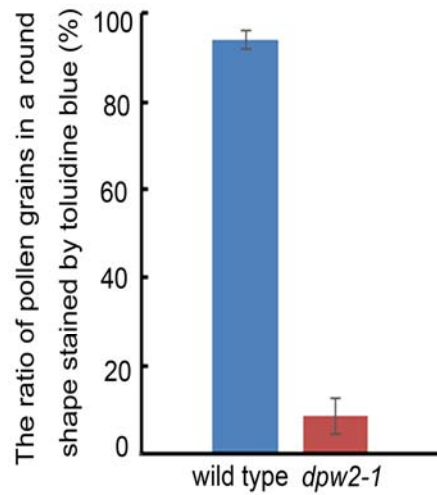
7 Arrows indicate the nucleus. There is one nucleus at stage 9 (B), two nuclei at  
8 stage 11 (C), and three nuclei at stage 12 (D) in the wild-type. In contrast,  
9 *dpw2-1* does not form microspores with three obvious nuclei (H). Bars = 10  
10  $\mu\text{m}$ .

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16 **Supplemental Figure 2.** The ratio of pollen grains in a normal round shape in  
17 the semi-thin section of WT and *dpw2-1* mutant at heading stage.

18 Error bars indicate SD of the ratio of stained pollen grains from five  
19 independent sections.

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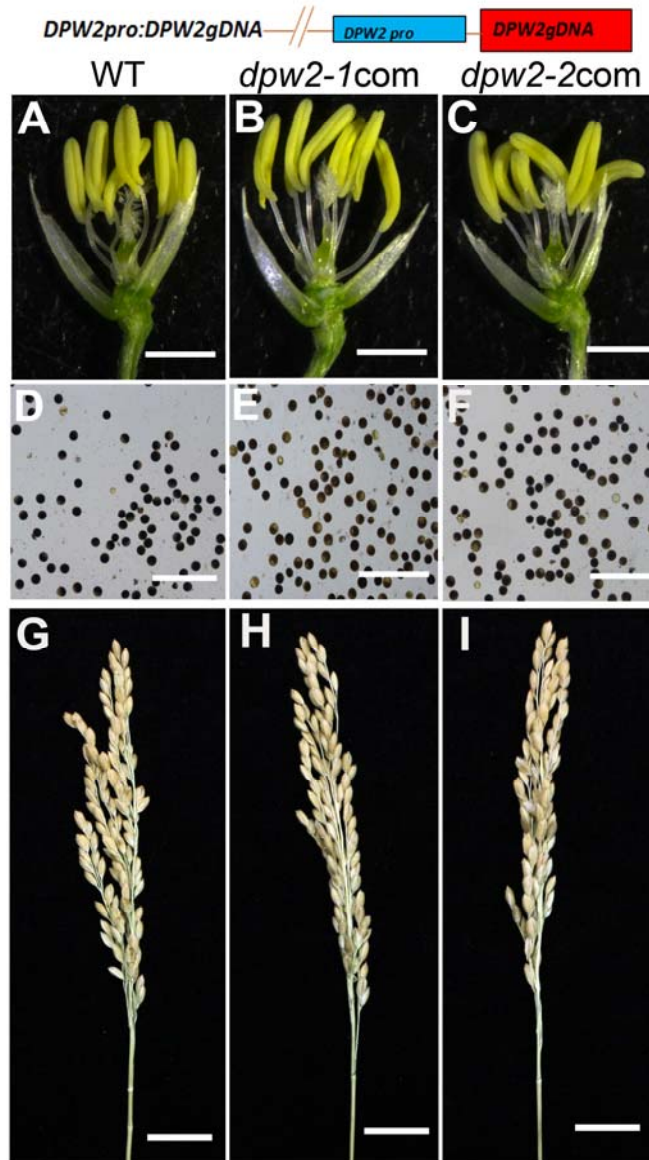
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33 **Supplemental Figure 3.** Complementation of *dpw2-1* and *dpw2-2* mutants by  
 34 *DPW2* genomic DNA.

35 (A) to (C) stage-12 flower from WT (A), *dpw2-1* complemented with the  
 36 ~4.34-kb wild-type genomic fragment (B), and *dpw2-2* complemented with the  
 37 ~4.34-kb wild-type genomic fragment (C).

38 (D) to (F) Pollens stained with 2 % I<sub>2</sub>-KI solution at stage 12 from WT (D),  
 39 *DPW2*-complemented mutant *dpw2-1com* (E), and *DPW2*-complemented  
 40 mutant *dpw-2com* (F) showing mature pollen grains. GDNA, genomic DNA.

41 (G) to (I) Mature panicle from WT (G), *dpw2-1* complemented with the

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42 ~4.34-kb wild-type genomic fragment (H), and *dpw2-2* complemented with the  
43 ~4.34-kb wild-type genomic fragment (I).

44 Bars=1mm in (A) to (C); 200  $\mu$ m in (D) to (F); 2 cm in (G) to (I).

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                *      20      *      40      *      60      *
XP002298644 Pt. : -----MEYSNGN---VFQLVVRQGGFTLVPEAEEKKG-----LYFLSNLQCNIAVIVRT : 47
XP003553956 Gm. : -----MEMANEN---GFQLSVKLSPEFTLVPEAEEKKG-----LYFLSNLQCNIAVIVRT : 47
ATASFT/HHT At. : --MVAENNRNKDVTLSASMDNNNNIKGTNIHLEHQQKFAALVKESESRKQ-----LYFLSNLQCNIAVIVRT : 67
CAT00082 Ca. : -----MENGKSN---TFELTVKQGGFTLVPEAEEKKG-----LYFLSNLQCNIAVIVRT : 47
XP003634222 Vv. : -----MAKASNG---VFELSVRQGGFTLVPEAEEKKG-----LYFLSNLQCNIAVIVRT : 48
AIDCF At. : -----MAD---SFEILVTRKPEVLYVSEASEPKG-----LHFLSNLQCNIAVIVKT : 43
AIFACT At. : -----MVA---SSEFIITRKNDELIPVSETPNG-----HYFLSNLQCNIAVIVKT : 43
XP002449535 Sb. : ---MKQENGGAAVAAA-GEKQQCCQAPPQLVMSVRRGEATLVPEAEEPRGG-----CYLLSNLQCNIAVIVQT : 65
DPW2 Os. : -----MVLGKRGVFTLVPEAEEKKG-----LYFLSNLQCNIAVIVQT : 39
XP002443835 sb. : -----MNNTRRGIHFCF-----QTYVC----- : 19
LOC100273135 Zm. : -----MSVFEMRIKQGGFTLVPEAEEPKG-----LYFLSNLQCNIAVIVQT : 43
XP002993631 Sm. : -----MPVDFK---VELVKEPELVVMEQFVEEQH-----YFLSNLQCNIAVIVMKT : 42
XP001779848 Pp. : -----MKBERGLERLVKADRSNAVPE-----KVVELSSLVVPRVHVQ : 39
HCT Pr. : -----MLITVKNKQVRAAPVQRD-----LWN---SNVLVVPREHTA : 37
AAX83048 Fs. : -----MEKTD---LHNLIEKMYGSLPPPKTT-----LQLSSIDLPGVGRGSIF : 43

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                *      80      *      100      *      120      *      140      *
XP002298644 Pt. : LYCKKSE-----EKGNENAGENVKNAIKRVLVYYPVLAGRLTI---SSE-AKLIHINCT-----GEGAVVVEA : 105
XP003553956 Gm. : VYCKKTA-----ERGNEKAGENVKNAIKRVLVYYPVLAGRLTI---SSE-GKLIHVDCT-----GEGAVVVEA : 105
ATASFT/HHT At. : LYCKKSE-----ERGNEEAVQVIRKALSKVLVYYPVLAGRLTI---SPE-GKLIHVDCT-----GEGAVVVEA : 125
CAT00082 Ca. : LYCKKSG-----EKGNEEAVQVIRKALSKVLVYYPVLAGRLTI---SPE-GKLIHVDCT-----GEGAVVVEA : 105
XP003634222 Vv. : LYCKKSE-----ARGNERAAEIKRDAISKVLVYYPVLAGRLTI---SSE-GKLIHVDCT-----GEGAVVVEA : 106
AIDCF At. : FYVYKSN-----SRNNEESYENVIRKSLSEVLVYYPVLAGRLTI---SPE-GKLIHVDCT-----GEGAVVVEA : 101
AIFACT At. : LYVYKSE-----SRTNQESYENVIRKSLSEVLVYYPVLAGRLTI---SPE-GKLIHVDCT-----GEGAVVVEA : 101
XP002449535 Sb. : VYCKKPP---PSPSSGNGDDDDVVGLRDAIARVLYYHPLAGRLGI---SPE-MKLIHVELT-----GEGAVVVEA : 129
DPW2 Os. : VYCKAAAAG---GGGGG-GAGDPLRESLSRVLVYYPVLAGRLAL---TDD-GKLIHVDCT-----GEGAVVVEA : 99
XP002443835 sb. : ---PRAADD---GGAGRSACDVLRESLAKVLYYYPVLAGRLAN---SDD-GKLIHVDCT-----GEGAVVVEA : 77
LOC100273135 Zm. : VYCKRAADG---GAGGVSACDVLRESLAKVLYYYPVLAGRLAT---SGD-GKLIHVDCT-----GEGAVVVEA : 104
XP002993631 Sm. : IYLYEISS---ARAADNPADVIRQCLSRVLDYYPVLAGRLGI---SSE-GKLIHVDCT-----GEGAVVVEA : 108
XP001779848 Pp. : VIYAYKAS---KGVSYFD---HVVQLGALCRVLTBYRWAGRLMI---DET-CRPIALN-----DGGVVEA : 99
HCT Pr. : SVVYR---PTGSPD---FFSMNLEDAISRLVLYYYPVLAGRLKR---DPE-CRPIALN-----GEGAVVVEA : 96
AAX83048 Fs. : NALLIYNASP---SPTMTSADPAKILIEPAKILVYYPVLAGRLRETN---GDIHVDCA-----GEGAVVVEA : 106

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                *      160      *      180      *      200      *      220
XP002298644 Pt. : EANGAEENG-----DITKED---PDTLGRVMDVPG---ARNILEMPELVAQVTRFCGGFRLGICMNHOMFDG : 169
XP003553956 Gm. : EANGAEENG-----DITKED---PDTLGRVMDVPG---ARNILEMPELVAQVTRFCGGFRLGICMNHOMFDG : 169
ATASFT/HHT At. : EANGAEENG-----DITKED---PDTLGRVMDVVD---ARNILEMPELVAQVTRFCGGFRLGICMNHOMFDG : 189
CAT00082 Ca. : EANGAEENG-----DITKED---PDTLGRVMDVPG---ARNILEMPELVAQVTRFCGGFRLGICMNHOMFDG : 169
XP003634222 Vv. : EANGAEENG-----DITKED---PDTLGRVMDVPG---ARNILEMPELVAQVTRFCGGFRLGICMNHOMFDG : 170
AIDCF At. : EANGAEENG-----DITKED---PDTLGRVMDVPG---ARNILEMPELVAQVTRFCGGFRLGICMNHOMFDG : 167
AIFACT At. : EANGAEENG-----DITKED---PDTLGRVMDVPG---ARNILEMPELVAQVTRFCGGFRLGICMNHOMFDG : 166
XP002449535 Sb. : EANGAEENG-----DITKED---PDTLGRVMDVPG---ARNILEMPELVAQVTRFCGGFRLGICMNHOMFDG : 193
DPW2 Os. : EANGAEENG-----DITKED---PDTLGRVMDVPG---ARNILEMPELVAQVTRFCGGFRLGICMNHOMFDG : 163
XP002443835 sb. : EANGAEENG-----DITKED---PDTLGRVMDVPG---ARNILEMPELVAQVTRFCGGFRLGICMNHOMFDG : 141
LOC100273135 Zm. : EANGAEENG-----DITKED---PDTLGRVMDVPG---ARNILEMPELVAQVTRFCGGFRLGICMNHOMFDG : 168
XP002993631 Sm. : EANGAEENG-----DITKED---PDTLGRVMDVPG---ARNILEMPELVAQVTRFCGGFRLGICMNHOMFDG : 172
XP001779848 Pp. : EANGAEENG-----DITKED---PDTLGRVMDVPG---ARNILEMPELVAQVTRFCGGFRLGICMNHOMFDG : 158
HCT Pr. : EANGAEENG-----DITKED---PDTLGRVMDVPG---ARNILEMPELVAQVTRFCGGFRLGICMNHOMFDG : 158
AAX83048 Fs. : EANGAEENG-----DITKED---PDTLGRVMDVPG---ARNILEMPELVAQVTRFCGGFRLGICMNHOMFDG : 169

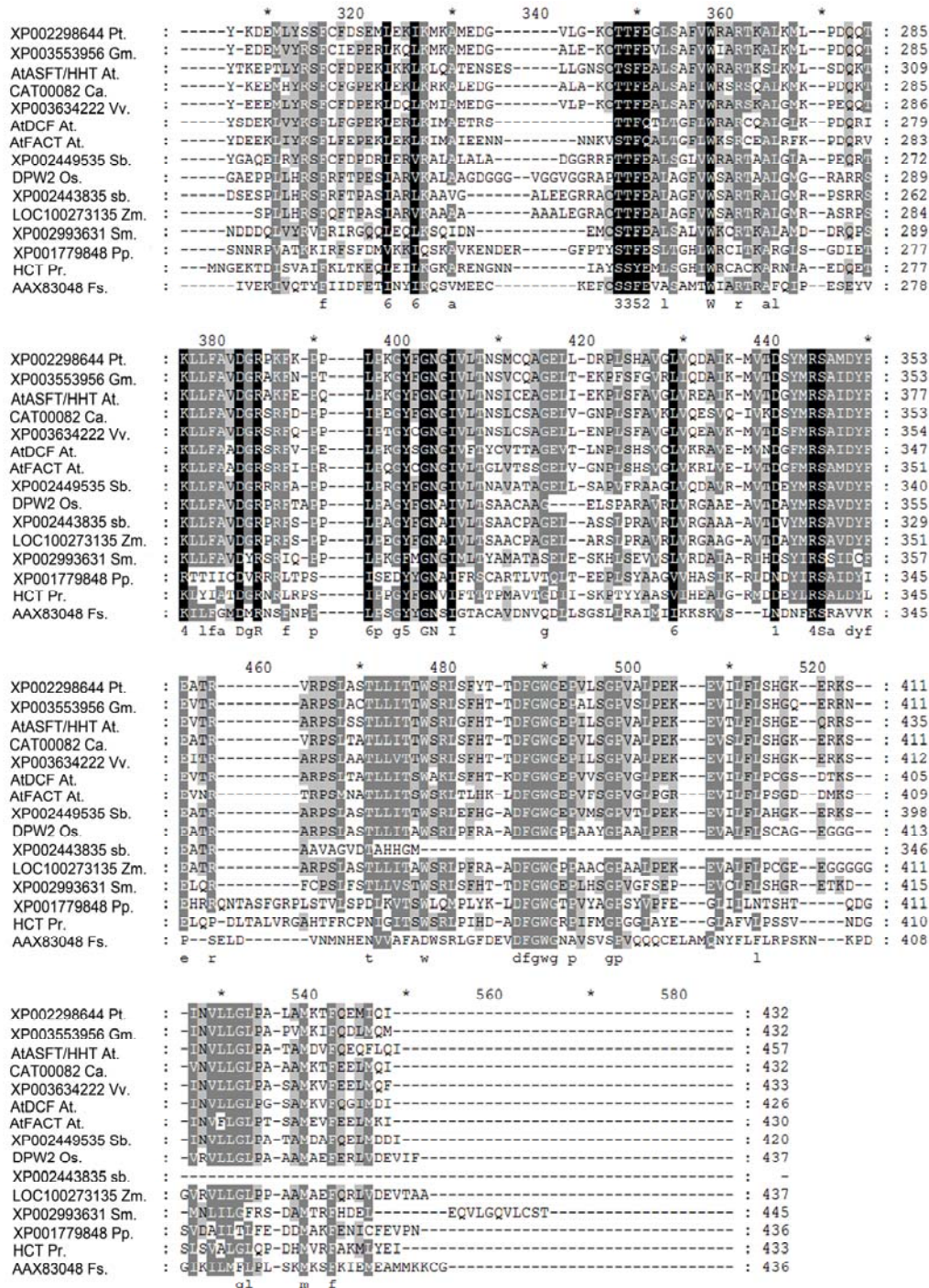
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                *      240      *      260      *      280      *      300
XP002298644 Pt. : IGAMEFVNSWGTARG---LPIKVPFF-----IDRSILKARNPKKIDPEEHEFAEIRKKS---STNDL----- : 226
XP003553956 Gm. : IGAMEFVNSWGTARG---LPIKVPFF-----IDRSILKARNPKKIDPEEHEFAEIRKKS---STNDL----- : 226
ATASFT/HHT At. : IGAMEFVNSWGTARG---LPIKVPFF-----IDRSILKARNPKKIDPEEHEFAEIRKKS---STNDL----- : 246
CAT00082 Ca. : IGAMEFVNSWGTARG---LPIKVPFF-----IDRSILKARNPKKIDPEEHEFAEIRKKS---STNDL----- : 226
XP003634222 Vv. : IGAMEFVNSWGTARG---LPIKVPFF-----IDRSILKARNPKKIDPEEHEFAEIRKKS---STNDL----- : 227
AIDCF At. : IGAMEFVNSWGTARG---LPIKVPFF-----IDRSILKARNPKKIDPEEHEFAEIRKKS---STNDL----- : 224
AIFACT At. : IGAMEFVNSWGTARG---LPIKVPFF-----IDRSILKARNPKKIDPEEHEFAEIRKKS---STNDL----- : 223
XP002449535 Sb. : IGAMEFVNSWGTARG---LPIKVPFF-----IDRSILKARNPKKIDPEEHEFAEIRKKS---STNDL----- : 211
DPW2 Os. : IGAMEFVNSWGTARG---LPIKVPFF-----IDRSILKARNPKKIDPEEHEFAEIRKKS---STNDL----- : 223
XP002443835 sb. : IGAMEFVNSWGTARG---LPIKVPFF-----IDRSILKARNPKKIDPEEHEFAEIRKKS---STNDL----- : 201
LOC100273135 Zm. : IGAMEFVNSWGTARG---LPIKVPFF-----IDRSILKARNPKKIDPEEHEFAEIRKKS---STNDL----- : 226
XP002993631 Sm. : IGAMEFVNSWGTARG---LPIKVPFF-----IDRSILKARNPKKIDPEEHEFAEIRKKS---STNDL----- : 233
XP001779848 Pp. : IGAMEFVNSWGTARG---LPIKVPFF-----IDRSILKARNPKKIDPEEHEFAEIRKKS---STNDL----- : 214
HCT Pr. : IGAMEFVNSWGTARG---LPIKVPFF-----IDRSILKARNPKKIDPEEHEFAEIRKKS---STNDL----- : 215
AAX83048 Fs. : IGAMEFVNSWGTARG---LPIKVPFF-----IDRSILKARNPKKIDPEEHEFAEIRKKS---STNDL----- : 220

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50 **Supplemental Figure 4.** Sequence alignment of DPW2 and 14 DPW2-related  
51 proteins.

52 The alignment was used to produce the NJ phylogenetic tree shown in Figure  
53 4.