**Supplementary data**

**Table S1. Primers used in this study.**

| Primers | sequence |
|---|---|
| RID1LP1 | 5'-AGCACCCAATCAGGGATATTC-3' |
| RID1RP1 | 5'-ACAGACAACAACAAGGGATGC-3' |
| RID1LP2 | 5'-AGAATATCCCTGATTGGGTGC-3' |
| RID1RP2 | 5'-AACAGAAGTTGGGTGGATGTG-3' |
| T-DNALB | 5'-ATATTGACCATCATACTCATTGC-3' |
| RID1-GC-UP | 5'-GGCTCGAGCAAGCGGTGAGACAGACGTGGAT-3' |
| RID1-GC-DOWN | 5'-AAGGTACCTCACTCTGCCGTTTGGAAATGGTGAG-3' |
| RID1-IF | 5'-GAATTGATTTAGGTGACACTATAGATCCGCGTGAGAAGAGAGAA-3' |
| RID1-IR | 5'-GAATTGTAATACGACTCACTATAGGGTTCTTGCTGGTTTGCATG-3' |
| GFA1-GST-UP | 5'-TTGGATCCATGGAAAGTAGCTTGTATGATGAG-3' |
| GFA1-GST-DOWN | 5'-TTCTCGAGAATCATCTGCAGATGGAGATCGCCT-3' |
| RID1-HIS-UP | 5'-TAGAATTCATGCCATCAATGGCGCAAGGAGAACTCAAG-3' |
| RID1-HIS-DOWN | 5'-AACTCGAGTCACTCTGCCGTTTGGAAATGGTGAGGAGC-3' |
| BIFC-RID1N-UP | 5'-AAACTAGTATGCCATCAATGGCGCAAGGAG-3' |
| BIFC-RID1N-DOWN | 5'-TTGTCGACCTCCTTGCGCCATTGATGGCAT-3' |
| BIFC-GFA1C-UP | 5'-TTGGATCCATGGAAAGTAGCTTGTATGATGAG-3' |
| BIFC-GFA1C-DOWN | 5'-TTCTCGAGAATCATCTGCAGATGGAGATCGCCT-3' |

RID1-AD-UP          5'-TAGAATTCATGCCATCAATGGCGCAAGGAGAAC TCAAG-3'

RID1-AD-DOWN        5'-AACTCGAGTCACTCTGCCGTTTGGAAATGGTGA GGAGC-3'

RID1-1-309-UP       5'-AAGAATTCATGCCATCAATGGCGCAAGGA-3'

RID1-1-309-DOWN     5'-TTTCTCGAGTCTCTCAACAGATTCAATTTC-3'

RID1-265-472-UP     5'-AAGAATTCCTTTACACTGTTCATCCTGAA-3'

RID1-265-472-DOWN   5'-TTGGATCCTATAATCGCCCCCCTTGAAGG-3'

RID1-453-612-UP     5'-TTGAATTCATTGATGATATAGTTGGATTT-3'

RID1-453-612-DOWN   5'-AAGGATCCCCTATATATGTCACGAGCATG-3'

RID1-564-717-UP     5'-TTGAATTCAGTGTTTATCGGGAGTCAGAT-3'

RID1-564-717-DOWN   5'-AAGGATCCCTCTGCCGTTTGGAAATGGTG-3'

RID1-1-271-UP       5'-AAGAATTCATGCCATCAATGGCGCAAGGAGA-3'

RID1-1-271-DOWN     5'-TTGAGCTCTTCAGGATGAACAGTGTAAAGAAT-3'

RID1-272-460-UP     5'-AAGAATTCTCAGATTATGTAGATGCCACCT-3'

RID1-272-460-DOWN   5'-TTGAGCTCAAATCCAACTATATCATCAATCCC-3'

RID1-1-265-UP       5'-AAGAATTCATGCCATCAATGGCGCAAGGAGA-3'

RID1-1-265-DOWN     5'-TTGAGCTCAAGAATGTCAACAGGAAATTGTCGC C-3'

RID1-1-256-UP       5'-AAGAATTCATGCCATCAATGGCGCAAGGAGA-3'

RID1-1-256-DOWN     5'-TTGAGCTCCTGCACATGAACAGCTTTGGCA-3'

RID1-1-181-UP       5'-AAGAATTCATGCCATCAATGGCGCAAGGAGA-3'

RID1 1-181-DOWN     5'-TTGAGCTCTATTTTTTTCAGCAAAGCCAGCAG-3'

RID1 1-271 M$^{267}$-UP     5'-AAGAATTCATGCCATCAATGGCGCAAGGA-3'

RID1 1-271 M$^{267}$-DOWN     5'-TTGAGCTCTTCAGGATGAACAATGTAAAGAAT-3'

RID1 1-271 M$^{266, 267}$-UP     5'-AAGAATTCATGCCATCAATGGCGCAAGGA-3'

RID1 1-271 $M^{266, 267}$-DOWN    5'-TTGAGCTCTTCAGGATGAACAATGAAAAGAA-3'

RID1 1-271 $M^{270, 271}$-UP    5'-AAGAATTCATGCCATCAATGGCGCAAGGA-3'

RID1 1-271 $M^{270, 271}$-DOWN    5'-TTGAGCTCTTTAGAATGAACAGTGTAAAGAA-3'

RID1 1-271 $M^{257, 262, 266}$-UP    5'-AAGGACATTCTTGCCACTGTTCATC-3'

RID1 1-271 $M^{257, 262, 266}$-DOWN    5'-AGGAAATTGTCGCGCCTGCACATGA-3'

RID1 1-271 $M^{266, 270, 271}$-UP    5'-AAGAATTCATGCCATCAATGGCGCAAGGAGA-3'

RID1 1-271 $M^{266, 270, 271}$-DOWN    5'-TTGAGCTCTGCTTTATGAACAGCGGCAAGAAT-3'

RID1 1-271 $M^{257\text{-}271}$-UP    5'-AAGAAGGACAAACTTGCCGCTGTTC-3'

RID1 1-271 $M^{257\text{-}271}$-DOWN    5'-AAATTGTGCCGCCTGCACATGAACA-3'

qTUB2-LP    5'-GAATGCTGATGAGTGCATGG-3'

qTUB2-RP    5'-AGAAGTGAAGACGGGGGAAT-3'

qAT2G01730-LP    5'-GCCCCCTTCAAAATTTTCTC-3'

qAT2G01730-RP    5'-TTGTGAAACTTTGAAGAAGCAAA-3'

qAT3G55630-LP    5'-TGAAACTTGGGAAATTTTTGG-3'

qAT3G55630-RP    5'-CCGGCAAACAAACAGAAAAC-3'

qAT1G09620-LP    5'-CCCACTGGCTCTGTCTCTGT-3'

qAT1G09620-RP    5'-TCTACCAGCTTGGGGAGAGA-3'

qAT4G39260-LP    5'-TTGAGTACCGGTGCTTTGTC-3'

qAT4G39260-RP    5'-CCGTCGAGGATCAGAATCAT-3'

**<span style="color:red">qRT-PCR</span>**

| | |
|---|---|
| AT2G47430-LP | 5'-GTTTCGACTTTGCTCCGAGG-3' |
| AT2G47430-RP | 5'-CAGGACGCAAAAGACCACAA-3' |
| AT2G40910-LP | 5'-ACGCTTCCTTTATGCAATCTCC-3' |
| AT2G40910-RP | 5'-GAGACAACAAAACAGCAATTGGA-3' |
| AT3G62210-LP | 5'-ACACATCGACACACACACAA-3' |
| AT3G62210-RP | 5'-TTGACTACCTCGATCGTTGTT-3' |
| AT5G52820-LP | 5'-TTGCAGAAACATGACGCCTC-3' |
| AT5G52820-RP | 5'-CACCACAACCACACTGCTTA-3' |
| AT1G01960-LP | 5'-TGTTCCATAATGAGTTGATGCCA-3' |
| AT1G01960-RP | 5'-TGCTTGATAGTTGCTTGGACAG-3' |
| AT3G06400-LP | 5'-AATGCAATGGATTCGGCGTT-3' |
| AT3G06400-RP | 5'-ACCATGCGCAGACATTCAAT-3' |
| AT3G03810-LP | 5'-ATACACCCTCCCTAATGGCC-3' |
| AT3G03810-RP | 5'-TCGTTGCTGCCTAAATGCTC-3' |
| AT2G35940-LP | 5'-TCAACCAACAAAGTAACGTGAG-3' |
| AT2G35940-RP | 5'-TTTTGCTCTTCCGATTTCTCAAA-3' |
| AT2G34920-LP | 5'-ACCTGTGCAACAAGGAATAGTG-3' |
| AT2G34920-RP | 5'-CTAGCAAACGCCCCAAACAT-3' |
| AT2G34860-LP | 5'-CATTCTTGTTGGTTCTGTGTGT-3' |
| AT2G34860-RP | 5'-AATTAGAAACCTTTTGCAGCTGA-3' |
| AT2G20490-LP | 5'-TCGGACACATTGAGTTTGGT-3' |
| AT2G20490-RP | 5'-GTGTCAAAACCAAGCGCAAT-3' |
| AT4G00310-LP | 5'-CAGCATTATCCTCCGCCTCT-3' |
| AT4G00310-RP | 5'-ACGACCCATTAACCCTAATCGA-3' |
| AT4G00020-LP | 5'-TAACAACCAAACTCAAGAACCTG-3' |
| AT4G00020-RP | 5'-GCTGTGTGCGCGTTTACATA-3' |
| AT3G60360-LP | 5'-ACTCGAGCTCATCAACTTAACG-3' |
| AT3G60360-RP | 5'-TTCTTTCGTTTCGTCTGTTCG-3' |
| AT3G56990-LP | 5'-ACGAGCCTTTAAGAGACAGGG-3' |

| | |
|---|---|
| AT3G56990-RP | 5'-CCAGGTAAGTTTCACCTCTTGT-3' |
| AT3G59550-LP | 5'-TGGGCATTCATCAAATTCCGA-3' |
| AT3G59550-RP | 5'-TGCAAAATTCTCGAAAAGTCAGA-3' |
| AT3G63130-LP | 5'-TGCAGTGTGATTTTGAGGGT-3' |
| AT3G63130-RP | 5'-TCGAAAACGAAGATGGTGTCG-3' |
| AT4G00140-LP | 5'-TTGCCTTCAAGCCAGAGAGT-3' |
| AT4G00140-RP | 5'-GGTGATGGTGATGAGGACGA-3' |
| AT3G12280-LP | 5'-GAACCATGCCCAACCCATTC-3' |
| AT3G12280-RP | 5'-CCGGAGTGGTGGGTTTTAGA-3' |
| AT1G59680-LP | 5'-TCTTTCACTCCGACGGCTTA-3' |
| AT1G59680-RP | 5'-TGTTTTCTGGCTCGAATCCA-3' |
| AT1G78770-LP | 5'-TTTCACTTGTTTTGATTGGGACT-3' |
| AT1G78770-RP | 5'-TTACCGATAAACCCTAAAACCCT-3' |
| AT1G72970-LP | 5'-TGGTCGTTGATGATTCTGTCT-3' |
| AT1G72970-RP | 5'-GGACTGTGCACTAGTGTCCT-3' |
| AT1G72440-LP | 5'-GAAAACTACGGACCATGCCG-3' |
| AT1G72440-RP | 5'-CCTATCACCACTCTGCTCGT-3' |
| AT4G02060-LP | 5'-TCTCTCTTCTTCTCCGTTCTCG-3' |
| AT4G02060-RP | 5'-GGGAGATTCGCGAAAACCC-3' |
| AT5G66760-LP | 5'-CTCTCTTCCTTCTCCTTCCGT-3' |
| AT5G66760-RP | 5'-TTTGCTCGACTACTAACGCA-3' |
| AT5G52460-LP | 5'-TGTGATCAAACCTAACAGCCA-3' |
| AT5G52460-RP | 5'-ACTTTGTGCATCCAACTCGG-3' |
| AT5G48030-LP | 5'-CTCTCAATTGGTTTCGAATTGGT-3' |
| AT5G48030-RP | 5'-AAACTCAATCACACACAGAACAA-3' |
| AT4G14040-LP | 5'-GCAAAAGCTCTCAAAACATTACC-3' |
| AT4G14040-RP | 5'-AGTCCCTTGGCAATAGTTGG-3' |
| AT4G14220-LP | 5'-AAGCTCTTCGGGGTTTAACG-3' |
| AT4G14220-RP | 5'-CGCAAGGCACAAAATCCGAT-3' |

| | |
|---|---|
| AT4G14790-LP | 5'-GCAACACGAAGCCATCATAAG-3' |
| AT4G14790-RP | 5'-GCAGCTTCTACATCTGTTTCTGT-3' |
| AT4G30930-LP | 5'-TCTCACTCTCACTGATGCTGA-3' |
| AT4G30930-RP | 5'-CACAAATGCAAAGGTTCGTCC-3' |
| AT5G05920-LP | 5'-CTTAACCCAGTGCCCCAAAC-3' |
| AT5G05920-RP | 5'-GCTTTTCCAATTCAGCAACGG-3' |
| AT5G19320-LP | 5'-AGGAAGGAACATCGGTGCTT-3' |
| AT5G19320-RP | 5'-TCCGTTTATTCTCATCGCAAAC-3' |
| AT5G22000-LP | 5'-GCCTTGATTTTGGGGACTCG-3' |
| AT5G22000-RP | 5'-CTCTCCCGCTCCCTAACAAA-3' |
| AT2G01730-LP | 5'-TCAGCTCAACAAAGTCGTGAC-3' |
| AT2G01730-RP | 5'-CAAATTTATCTTCAGGGACAGCA-3' |
| AT3G55630-LP | 5'-TGACTTTTCTGACTTTGTGTGTTC-3' |
| AT3G55630-RP | 5'-CTCGTAAATTTTGGCACGACAC-3' |
| AT1G09620-LP | 5'-AATTCTCTCCCCAAGCTGGT-3' |
| AT1G09620-RP | 5'-GACAGTGCCTACCCCAAAAA-3' |
| AT4G39260-LP | 5'-CCCATCGGTACGTTCATCTT-3' |
| AT4G39260-RP | 5'-TCAGCAAAAACAATCGTGGA-3' |
| TUB2-LP | 5'-TGGCATCAACTTTCATTGGA-3' |
| TUB2-RP | 5'-ATGTTGCTCTCCGCTTCTGT-3' |

**Table S2. Analysis of the genetic transmission of *rid1* alleles**[§]

| Genotype | *RID1*/- | *RID1*/+ | TE (%) |
|---|---|---|---|
| *rid1-2*/+ ♀ × Wild type ♂ | 0 | 123 | 0* |
| *rid1-2*/+ ♀ × Wild type ♂ [¶] | 9 | 162 | 5.6* |

§ The genetic transmission of *RID1* was analyzed by genotyping F1 progeny of the denoted crosses. The transmission efficient (TE) = (*rid1*/+) / (*RID1*/+) × 100% was calculated according to Howden et al. (1998).

¶ The pistils of *rid1-2*/+ plants at floral stage 12 were pollinated with pollen of wild-type plants at 72 h after emasculation.

* indicating the significant difference between the two of them (p < 0.01).

Reference: Howden, R., Park, S.K., Moore, J.M., Orme, J., Grossniklaus, U., et al. (1998) Selection of T-DNA-tagged male and female gametophytic mutants by segregation distortion in *Arabidopsis*. Genetics **149**:621−631.

**Table S3. Down-regulated genes involving in FG development in *rid1*-2/+ and *gfa1*-1/+ mutant ovules identified by qRT-PCR analysis.**

| Gene ID | Protein | Function | Reference |
|---------|---------|----------|-----------|
| At1g01960 | EMBRYO SAC DEVELOPMENT ARREST10 | FG* development | Pagnussat et al., 2005 |
| At1g59680 | EMBRYO SAC DEVELOPMENT ARREST1 | FG development | Pagnussat et al., 2005 |
| At1g72440 | SLOW WALKER2 | FG development and cell cycle progression | Pagnussat et al., 2005; Li et al., 2009 |
| At1g72970 | EMBRYO SAC DEVELOPMENT ARREST17 | FG development | Pagnussat et al., 2005 |
| At1g78770 | ANAPHASE PROMOTING COMPLEX 6 | FG development and cell cycle progression | Kwee et al., 2003 |
| At2g20490 | EMBRYO SAC DEVELOPMENT ARREST27 | FG development. | Pagnussat et al., 2005 |
| At2g34860 | EMBRYO SAC DEVELOPMENT ARREST3 | FG development. | Pagnussat et al., 2005 |
| At2g34920 | EMBRYO SAC DEVELOPMENT ARREST18 | FG and MG[#] development | Pagnussat et al., 2005; Boavida et al., 2009 |
| At2g35940 | BEL-like homeodomain protein 1, EMBRYO SAC DEVELOPMENT ARREST29 | FG development | Pagnussat et al., 2007 |
| At3g03810 | EMBRYO SAC DEVELOPMENT ARREST30 | FG development | Pagnussat et al., 2005 |
| At3g06400 | Chromatin remodeling protein 11, SWI2/SNF2 | FG development | Huanca-Mamani et al., 2005 |
| At3g12280 | RETINOBLASTOMA-RELATED protein RBR1 | FG and MG development, and cell cycle progression | Johnston et al., 2008 |
| At3g56990 | EMBRYO SAC DEVELOPMENT ARREST7 | FG development | Pagnussat et al., 2005 |
| At3g59550 | SISTER CHROMATID COHESION 1 PROTEIN 3 | FG and MG development | Jiang et al., 2007 |
| At3g60360 | EMBRYO SAC DEVELOPMENT ARREST14 | FG development | Pagnussat et al., 2005; Jiang et al., 2007 |
| At3g63130 | RAN GTPase activating protein 1 | FG development and cell cycle | Rodrigo-Peiris et al., 2011 |

| | | progression | |
|---|---|---|---|
| At4g00020 | EMBRYO SAC DEVELOPMENT ARREST20, BREAST CANCER 2 LIKE 2A | FG development | Pagnussat et al., 2005 |
| At4g00140 | EMBRYO SAC DEVELOPMENT ARREST34 | Polar nucleus fusion and FG development | Pagnussat et al., 2005 |
| At4g00310 | EMBRYO SAC DEVELOPMENT ARREST8 | FG development | Pagnussat et al., 2005 |
| At4g02060 | PROLIFERA | FG development and cell cycle progression | Springer et al., 2000 |
| At4g14040 | SELENIUM-BINDING PROTEIN 2, EMBRYO SAC DEVELOPMENT ARREST38 | FG development | Pagnussat et al., 2005 |
| At4g14220 | RING-type E3 ubiquitin ligase RHF1A | FG development and cell cycle progression | Liu et al., 2008 |
| At4g14790 | EMBRYO SAC DEVELOPMENT ARREST15 | FG and MG development. | Pagnussat et al., 2005; Boavida et al., 2009; Gagliardi et al., 1999 |
| At4g30930 | NUCLEAR FUSION DEFECTIVE 1 | FG and MG development | Portereiko et al., 2006 |
| At5g05920 | EMBRYO SAC DEVELOPMENT ARREST22 | FG development | Pagnussat et al., 2005 |
| At5g19320 | RAN GTPase activating protein 2 | FG development and cell cycle progression | Rodrigo-Peiris et al., 2011 |
| At5g22000 | RING-type E3 ubiquitin ligase RING-H2 GROUP F2A | FG development and cell cycle progression | Liu et al., 2008 |
| At5g48030 | GAMETOPHYTIC FACTOR 2 | FG development | Christensen et al., 1998 |
| At5g52460 | EMBRYO SAC DEVELOPMENT ARREST41 | FG development and cell cycle progression | Pagnussat et al., 2005 |
| At5g66760 | SUCCINATE DEHYDROGENASE 1-1 | FG and MG development | León et al., 2007 |

*FG, Female gametophyte; [#] MG, Male gametophyte.

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Kwee, H.S., and Sundaresan, V. (2003). The *NOMEGA* gene required for female gametophyte development encodes the putative APC6/CDC16 component of the Anaphase Promoting Complex in *Arabidopsis*. Plant J. **36**:853–866.

León, G., Holuigue, L., and Jordana, X. (2007). Mitochondrial complex II is essential for gametophyte development in *Arabidopsis*. Plant Physiol. **143**:1534–1546.

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Pagnussat, G.C., Yu, H.J., Ngo, Q.A., Rajani, S., Mayalagu, S., et al. (2005). Genetic and molecular identification of genes required for female gametophyte development and function in *Arabidopsis*. Development **132**:603–614.

Pagnussat, G.C., Yu H.J., and Sundaresan, V. (2007). Cell-fate switch of synergid to egg cell in *Arabidopsis eostre* mutant embryo sacs arises from misexpression of the BEL1-like homeodomain gene *BLH1*. Plant Cell **19**:3578–3592.

Portereiko, M.F., Sandaklie-Nikolova, L., Lloyd, A., Dever, C.A., Otsuga, D., et al. (2006). NUCLEAR FUSION DEFECTIVE1 encodes the *Arabidopsis* RPL21M protein and is required for karyogamy during female gametophyte development and fertilization. Plant Physiol. **141**:957–965.

Rodrigo-Peiris, T., Xu, X.M., Zhao, Q., Wang, H.J., and Meier, I. (2011). RanGAP is required for post-meiotic mitosis in female gametophyte

development in *Arabidopsis thaliana*. J. Exp. Bot. **62**:2705–2714.

**Springer, P.S., Holding, D.R., Groover, A., Yordan, C., and Martienssen, R.A.** (2000). The essential Mcm7 protein PROLIFERA is localized to the nucleus of dividing cells during the G(1) phase and is required maternally for early *Arabidopsis* development. Development **127**:1815–1822.
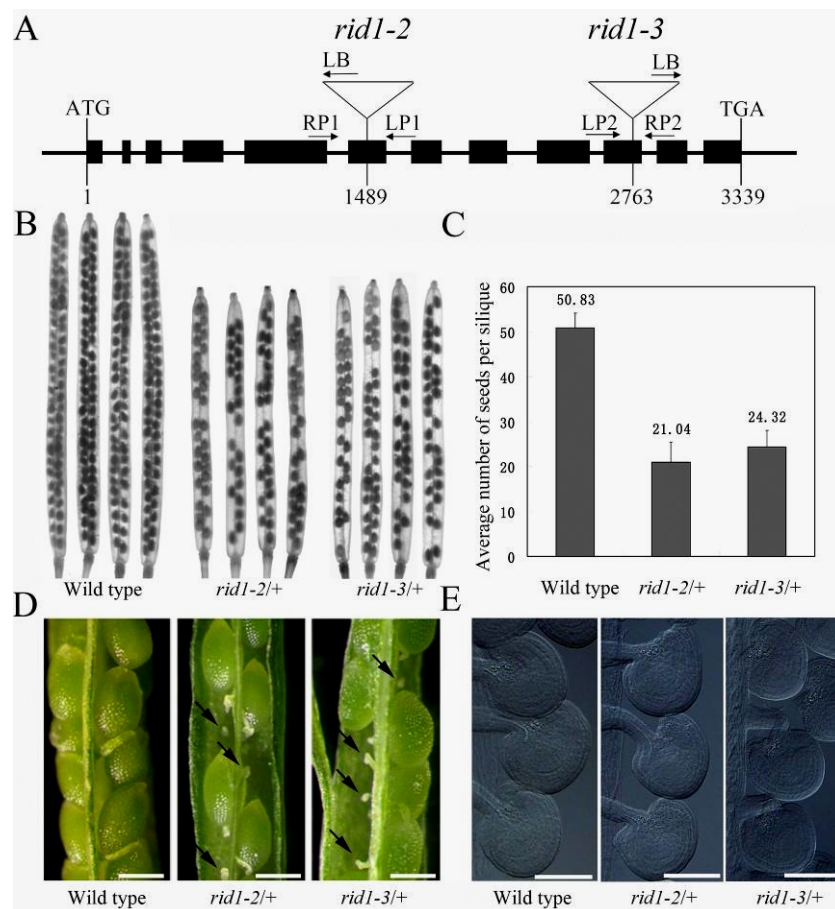
**Figure S1. T-DNA insertion mutant lines of *RID1* and their phenotypes.**

 **(A)** Two T-DNA insertion lines of *RID1*, *rid1-2* and *rid1-3*. Black boxes indicate the exons of *RID1* genomic sequence, and the lines are introns. The triangles represent the locations of the T-DNA insertion in the mutant lines. LBs primers for left border of the T-DNA, RPs and LPs gene-specific primers at downstream and upstream locations, respectively.

**(B)** Mature siliques of wild type and *rid1* mutants.

**(C)** The numbers of seeds in the siliques of *rid1* mutants are about half that of wild type. The data were collected from 150 siliques for each sample.

**(D)** Parts of the young seeds in *rid1* mutant siliques are abortive (arrows). Bar, 100 μm.

**(E)** The morphology of the ovules is normal in the mutant lines. Bar, 20 μm.
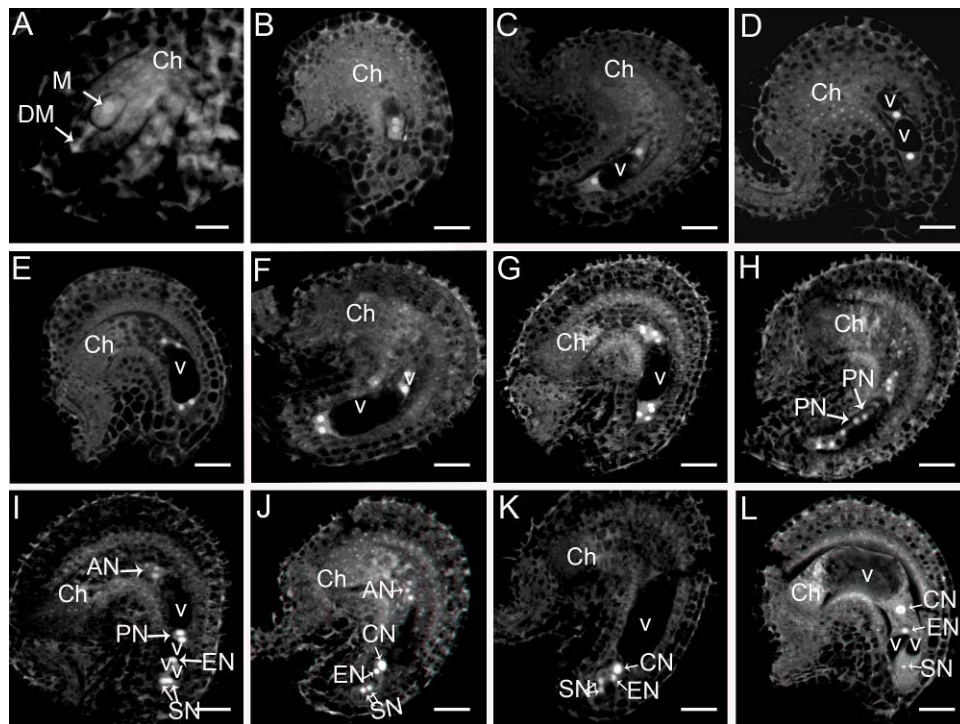
**Figure S2. The stages of FG development of wild-type *Arabidopsis*.**

FG1 (A), FG2 (B and C), FG3 (D), FG4 (E and F), FG5 (G), FG6 (H, I, and J), FG7 (K), and FG8 (L). AN, antipodal nucleus; Ch, chalazal end; CN, central cell nucleus; DM, degenerated megaspores; DS, degenerated synergid; EN, egg cell nucleus; M, megaspore; PN, polar nucleus; SN, synergid nucleus; V, vacuole. Bars, 10 μm.
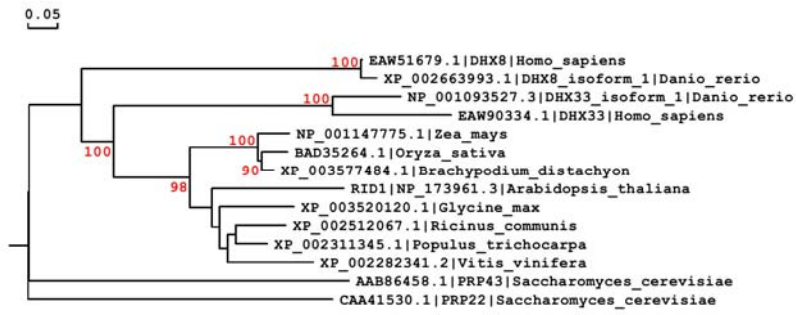
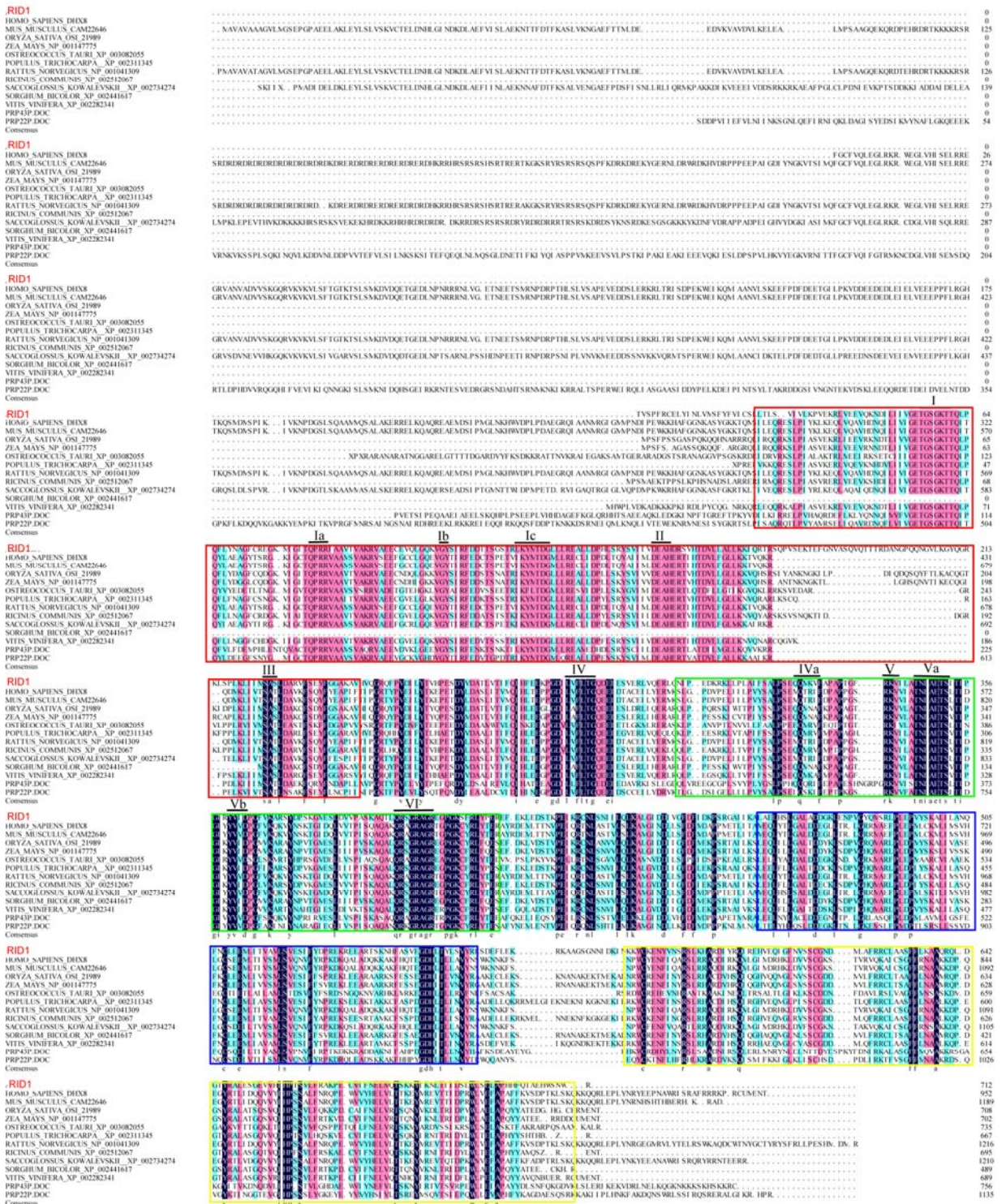**Figure S3. Phylogenetic analysis of RID1 with its orthologs of eukaryotic proteins.**

**Figure S4. Sequence alignment of RID1 and its orthologs.**

The DEXDc, HELICc, HA2, OB-fold domains labeled with red, green, blue, and
yellow squares, respectively. Twelve motifs (I, Ia, Ib, Ic, II, III, IV, IVa, V, Va, Vb and
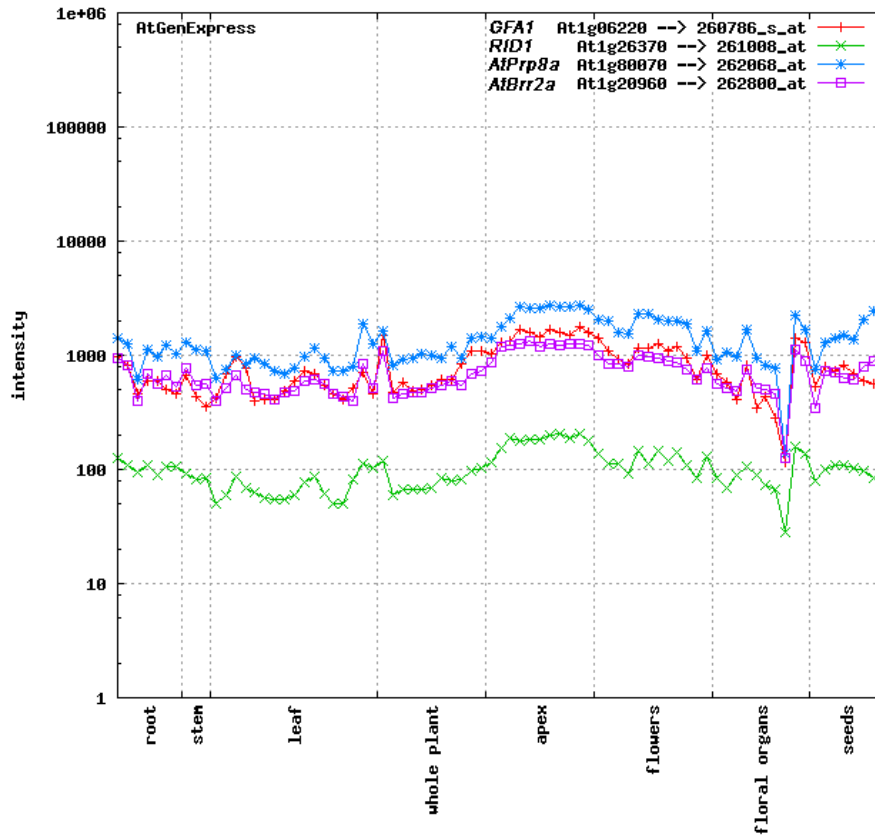VI) in the DEXDc and HELICc domains were labeled in sequence.

**Figure S5. The similar expression patterns among *RID1*, *GFA1*, *AtPRP8*, and *AtBRR2a* during *Arabidopsis* development.**

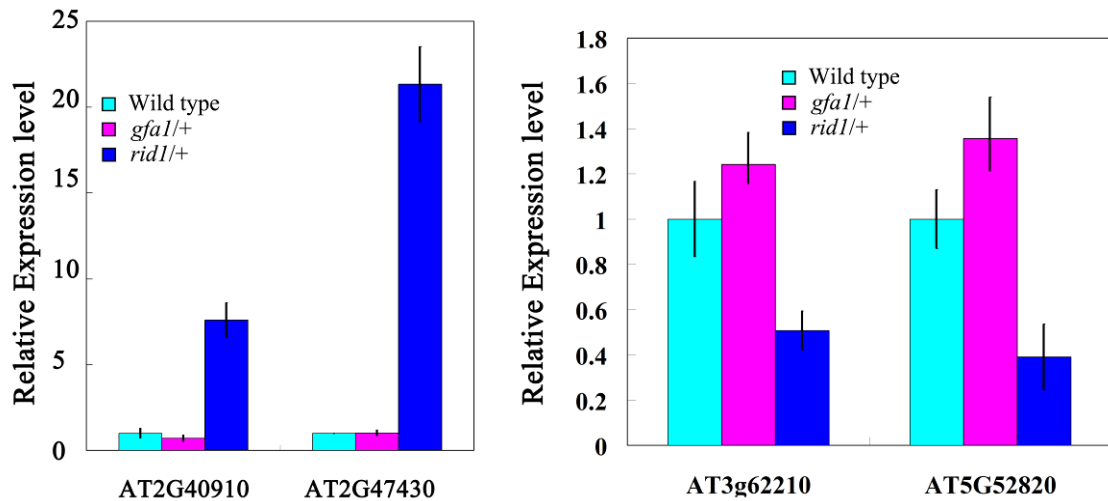The expression patterns were analyzed by AtGenExpress Visualization Tool (http://jsp.weigelworld.org/expviz/expviz.jsp?).

**Figure S6. The genes show abnormal pre-mRNA splicing in either *gfa1-1*/+ or *rid 1-2*/+ mutants.**

The abnormal retentions of first intron in pre-mRNA of RNA splicing-related and female gametophyte development-related genes in *rid1-2*/+ and *gfa1-1*/+ mutants were detected by qRT-PCR analysis. The expression of *TUBULIN2* was used as the internal control. All experiments were repeated three times.
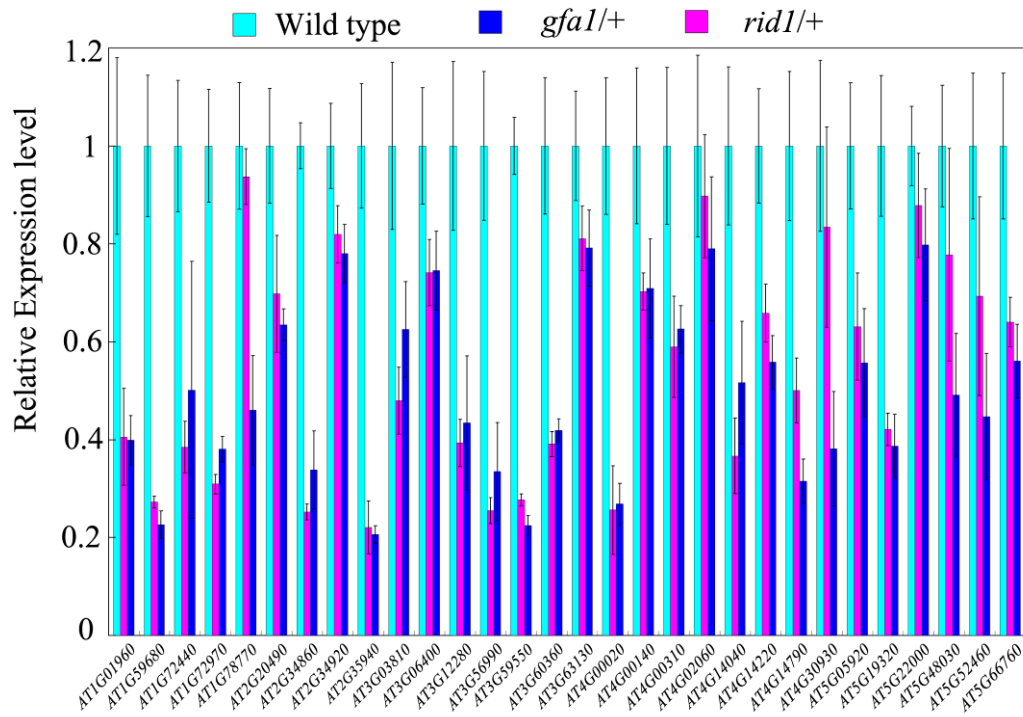
**Figure S7. The genes show reduced expression in *gfa1-1*/+ and *rid1-2*/+ mutants.**
The expressions were detected by qRT-PCR analysis. The expression of *TUBULIN2* was used as the internal control. All experiments were repeated three times.