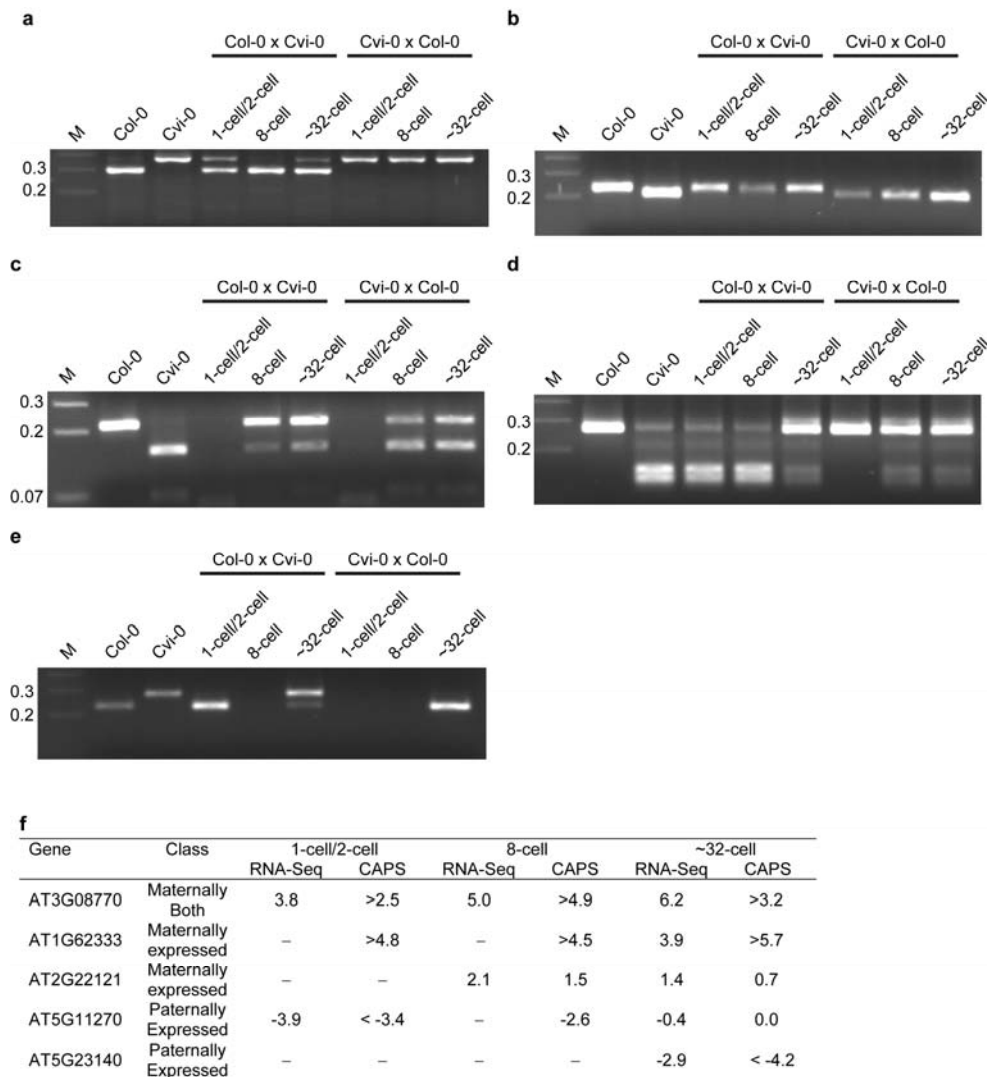
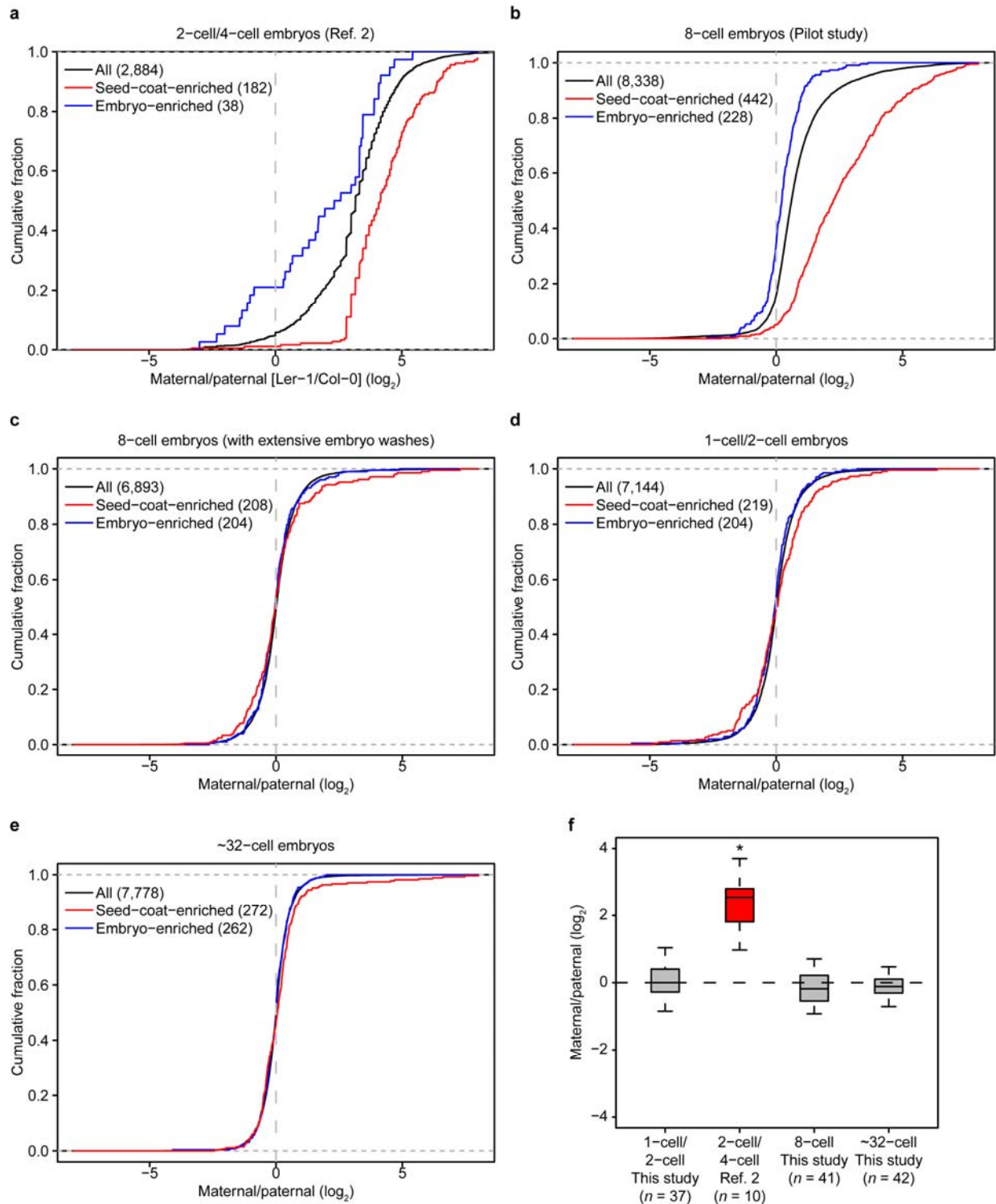


**Supplementary Figure 1 | Transcript levels in RNA-Seq libraries from independent reciprocal crosses were highly correlated. a**, Levels of transcripts, measured in RNA-Seq RPM (reads per million genome- and cDNA-matching reads) from 1-cell/2-cell embryos from Col-0 (maternal) x Cvi-0 (paternal) and Cvi-0 (maternal) x Col-0 (paternal) crosses. Only transcripts that had  $\geq 10$  perfect and unique-matching reads in each cross were considered ( $n = 14,991$ ).  $r$ , Pearson's correlation coefficient. **b**, Levels of transcripts from 8-cell embryos ( $n = 14,771$ ). Otherwise, as in **a**. **c**, Levels of transcripts from ~32-cell embryos ( $n = 15,707$ ). Otherwise, as in **a**.



**Supplementary Figure 2 | Analysis of cleaved amplified polymorphic sequences (CAPS).** **a**, Representative image of digestion products for analysis of *AT3G08770* (a maternally inherited and maternally expressed candidate). After reverse transcription and amplification of the polymorphic sequence, the amplicon was digested with the appropriate restriction enzyme (**Supplementary Tables 3 and 4**) and products were resolved on a 2% agarose gel. Col-0 and Cvi-0 controls, and embryonic stages for reciprocal crosses are indicated. Numbers to the left of gel specify marker (M) sizes in kb. **b**, Representative image of digestion products for analysis of *AT1G62333* (a maternally expressed candidate). Otherwise, as in **a**. **c**, Representative image of digestion products for analysis of *AT2G22121* (a maternally expressed candidate). Otherwise, as in **a**. **d**, Representative image of digestion products for analysis of *AT5G11270* (a paternally inherited candidate). Otherwise, as in **a**. **e**, Representative image of digestion products for analysis of *AT5G23140* (a paternally expressed candidate) Otherwise, as in **a**. **f**, Maternal-to-paternal ratios ( $\log_2$ ) based on RNA-Seq data and replicate sets of CAPS analyses. Bands were quantified, and the average maternal-to-paternal ratios ( $\log_2$ ) for digestion products detected in

both reciprocal crosses (from both replicates) are shown. Undetectable bands were given a value just below the detection limit, and the resulting under-estimated ratios are noted with > or < signs. Class refers to their classification based on RNA-Seq data (**Fig. 3** and **Supplementary Dataset 3**). Dashes indicate transcripts with < 8 reads overlapping SNPs in either cross or undetectable PCR products for the RNA-Seq and CAPS analyses, respectively. Paternally enriched *AT5G23140* transcripts were significantly enriched (Pearson's chi-square test, Benjamini and Hochberg FDR < 0.05) and had 16-fold paternal enrichment in ~32-cell embryos from Col-0 x Cvi-0 crosses, but only 3.5-fold enrichment in ~32-cell embryos from Cvi-0 x Col-0 crosses. Therefore *AT5G23140* was not included in Fig. 3 or Supplementary Dataset 3 because it did not pass the more stringent requirement of being  $\geq 4$ -fold enriched in both crosses.



**Supplementary Figure 3 | Seed-coat mRNA contamination in the embryo mRNA samples of ref. 2 resulted in an over-estimation of maternal contributions to the embryonic transcriptome.** Cumulative distributions of maternal-to-paternal transcript ratios ( $\log_2$ ) for all transcripts (black), seed-coat-enriched transcripts (red) and embryo-enriched transcripts (blue)

are shown for **(a)** transcripts in the 2-cell/4-cell stage dataset of ref. 2., **(b)** transcripts in our pilot 8-cell dataset, acquired without extensive embryo washes, **(c)** transcripts in our subsequent 8-cell dataset, acquired with extensive embryo washes, **(d)** transcripts in our 1-cell/2-cell dataset, acquired with extensive embryo washes and **(e)** transcripts in our ~32-cell dataset, acquired with extensive embryo washes. Ratios for transcripts that had  $\geq 5$  reads overlapping SNPs in the 2-cell/4-cell dataset of ref. 2 ( $n = 2,884$ ), our pilot 8-cell dataset ( $n = 8,338$ ), and subsequent 8-cell ( $n = 6,893$ ), 1-cell/2-cell ( $n = 7,144$ ) and ~32-cell ( $n = 7,778$ ) datasets are plotted in black. Seed-coat-enriched transcripts (red) were transcripts called present in both seed-coat microarray replicates and absent in both embryo microarray replicates (Goldberg-Harada microarray data, NCBI GEO: GSE12404). Conversely, embryo-enriched transcripts (blue) were those called present in both embryo microarray replicates and absent in both seed-coat microarray replicates (Goldberg-Harada data). Within the dataset of ref. 2, seed-coat-enriched transcripts were significantly more maternally enriched than the rest of the 2-cell/4-cell transcriptome ( $P < 10^{-15}$ ; two-sample K-S test), whereas embryo-enriched transcripts were significantly more paternally enriched than the rest of the 2-cell/4-cell transcriptome ( $P = 0.0049$ ; two-sample K-S test). Also note that the ratio between the number of seed-coat-enriched transcripts and the number of embryo-enriched transcripts was 4.8 for the 2-cell/4-cell dataset of ref 2 and 1.9 for our pilot 8-cell dataset; whereas this ratio was 1.1 or less for our libraries generated from extensively washed embryos. **f)** Plots of maternal-to-paternal transcript ratios for a set of genes that segregate as zygotic recessives when mutated<sup>9,12-14</sup> (Supplementary Table 5). The embryonic stage, study and number of transcripts that had at  $\geq 5$  reads overlapping SNPs in datasets from either both reciprocal crosses between Col-0 and Cvi-0 (this study; gray) or the Ler-1 x Col-0 cross (ref. 2; red) are indicated below each plot. Transcripts corresponding to zygotic-recessive preglobular mutants had approximately equal maternal and paternal contributions in our datasets, as expected based on the corresponding mutant Mendelian segregation ratios. In contrast, transcripts corresponding to zygotic-recessive mutants were significantly maternally enriched in the dataset of ref. 2 ( $P = 6.1 \times 10^{-06}$  [indicated by an asterisk]; two-sample Student's *t*-test). For example, maternally and paternally inherited *FACI* alleles both contribute to the initial zygotic division<sup>12</sup>, and as expected, approximately equal amounts of *FACI* maternal and paternal transcripts were detected in our 1-cell/2-cell (~42% maternal), 8-cell (~40% maternal) and ~32-cell (~44% maternal) datasets. In contrast, the dataset of ref. 2 assigns 88% of *FACI* transcripts to the maternal allele. The 25<sup>th</sup>, 50<sup>th</sup> and 75<sup>th</sup> percentiles are indicated by the bottom, dark-stripe and top of the boxes, respectively. The top and bottom whiskers extend from the box to the most extreme values within 1.5 times the interquartile range.

Supplementary Table 1 | Statistics for RNA-Seq libraries

Library <sup>a</sup>	Col-0 x Cvi-0 1-cell/2-cell	Cvi-0 x Col-0 1-cell/2-cell	Col-0 x Cvi-0 8-cell	Cvi-0 x Col-0 8-cell	Col-0 x Cvi-0 ~32-cell	Cvi-0 x Col-0 ~32-cell
Total reads	35,417,281	33,410,806	35,535,355	34,320,868	38,539,815	35,579,678
Unique reads	23,131,163	21,106,332	19,959,582	22,742,359	23,824,934	22,412,159
Col-0 genome- matching reads	12,446,580	12,635,427	11,815,302	14,516,589	15,708,345	16,254,819
Cvi-0 genome- matching reads <sup>b</sup>	12,357,453	12,538,594	11,717,540	14,421,398	15,592,377	16,154,405
Col-0 transcript- matching reads <sup>c</sup>	308,703	281,514	334,967	353,801	607,422	445,168
Cvi-0 transcript- matching reads <sup>b,c</sup>	312,099	289,961	353,635	361,335	619,806	449,021
Reads overlapping genes <sup>d</sup>	10,578,677	10,942,750	10,299,141.5	12,688,761.5	14,641,127.5	14,805,499
Genes with at least 1 read	19,828	19,143	18,831	20,543	20,312	20,575
Genes with at least 10 reads	16,363	16,035	15,311	16,757	16,193	16,700
Reads overlapping SNPs	1,269,420	1,291,815	1,233,554	1,478,544	1,635,774	1,723,732
Reads overlapping Col-0 SNPs	681,278	694,634	666,090	786,190	874,612	912,305
Reads overlapping Cvi-0 SNPs	588,141	597,179	567,464	692,353	761,161	811,423
Genes with at least 5 reads overlapping SNPs	8,273	8,072	7,389	8,705	8,378	8,865

<sup>a</sup> libraries were generated from embryonic RNA from indicated stages and maternal x paternal crosses

<sup>b</sup> Cvi-0 genome and transcripts refer to 'pseudo' Cvi-0 genome and transcript models in which SNPs in the Col-0 genome and transcript models were replaced with Cvi-0 variants as reported by the Ecker lab ([ftp://ftp.arabidopsis.org/home/tair/Sequences/Ecker\\_Cvi\\_snps.txt](ftp://ftp.arabidopsis.org/home/tair/Sequences/Ecker_Cvi_snps.txt))

<sup>c</sup> reads mapped to transcript models, but not genome

<sup>d</sup> based on TAIR10 gene annotations and the average number of reads matching the Col-0 and Cvi-0 genomes

**Supplementary Table 2 | Percentile ranks of RNA Polymerase II transcript levels in early embryos.** Analysis focused on subunits specific to Pol II.

<b>Subunit</b>	<b>Gene</b>	<b>1-cell/2-cell embryos</b>	<b>8-cell embryos</b>	<b>~32-cell embryos</b>
NRPB1	<i>AT4G35800</i>	90.8	89.6	81.8
NRPB2	<i>AT4G21710</i>	89.1	90.2	87.5
NRPB4	<i>AT5G09920</i>	81.9	86.3	91.1
NRPB7	<i>AT5G59180</i>	74.8	80.1	85.7

The average RPM (reads per million total genome- and cDNA-matching reads) overlapping genes were used to calculate percentile ranks (Supplementary Dataset 1). For each stage, only genes with at least 10 overlapping reads in both reciprocal crosses were considered expressed above background and used to calculate percentile ranks.

Supplementary Table 3 | Oligonucleotides used in this study.

Name	Sequence (5' to 3')	Experiment
RPS5A F1	CACCTTGACTCACAATGAGAGAG	Cloning <i>pRPS5A</i>
RPS5A R1	GGCTGTGGTGAGAGAAACAG	Cloning <i>pRPS5A</i>
UBI3 F1	CACCCCAAAGCACATACTTATCGA	Cloning <i>pUBI3</i>
UBI3 R1	TCTTCGCCTGGAGGAGAGAA	Cloning <i>pUBI3</i>
NLSGFP F1	AAGCTTATGGAATCCACCGGAAAAGTGAAGAAGG	Cloning nuclear-localized <i>GFP</i>
NLSGFP R1	GTTTAAACGGTCACTGGATTTTG	Cloning nuclear-localized <i>GFP</i>
GW F1	CACCGTCGACATCACAAGTTTGTACA	Cloning attR1/attR2 Gateway cassette from GWRFa::pET42a
GW R3	GTCGACATCACCACT	Cloning attR1/attR2 Gateway cassette from GWRFa::pET42a
AT3G08770 F1	GGTGAAGCAGCCGTGTCTT	Analyses of cleaved polymorphic sequences
AT3G08770 R1	CAACTAGCAAACCAATGCCC	Analyses of cleaved polymorphic sequences
AT1G62333 F1	TTCCAGGACTTCTTGGGCC	Analyses of cleaved polymorphic sequences
AT1G62333 R1	CTCCGTTTCAACCTACCACC	Analyses of cleaved polymorphic sequences
AT2G22121 F2	TTCTTATTTCTCGTACTCATGC	Analyses of cleaved polymorphic sequences
AT2G22121 R2	TCATAAGTACATACACAATTAGGAGGAC	Analyses of cleaved polymorphic sequences
AT5G11270 F1	AGAAGACGGAGTTCCAGATAAGC	Analyses of cleaved polymorphic sequences
AT5G11270 R1	CGGTTTTCTACAAGACACAATCTCA	Analyses of cleaved polymorphic sequences
AT5G23140 F1	AGTTGGTTAGTTTATGTTAGAAGATGG	Analyses of cleaved polymorphic sequences
AT5G23140 R1	AACACTAGCAATTGAAGGCTCA	Analyses of cleaved polymorphic sequences



**Supplementary Table 4 | Primers and enzymes used for analyses of cleaved polymorphic sequences.**

<b>Gene</b>	<b>Primers</b>	<b>Amplicon size (bp)</b>	<b>Restriction enzyme</b>	<b>Col-0 isoform size(s) after digestion (bp)</b>	<b>Cvi-0 isoform size(s) after digestion (bp)</b>
<i>AT3G08770</i>	AT3G08770 F1/R1	372	AgeI	297, 75	372
<i>AT1G62333</i>	AT1G62333 F1/R1	230	DraIII	230	211, 19
<i>AT2G22121</i>	AT2G22121 F2/R2	213	AccI	213	144, 69
<i>AT5G11270</i>	AT5G11270 F1/R1	270	PleI	270	154, 116
<i>AT5G23140</i>	AT5G23140 F1/R1	280	ApoI	224, 56	280

**Supplementary Table 5 | Maternal-to-paternal ratios ( $\log_2$ ) for transcripts that correspond to preglobular zygotic-recessive genes.** Ratios of transcripts with  $\geq 5$  SNP-overlapping reads from this study and ref. 2 are shown along with evidence that both maternal and paternal alleles are required for normal embryo development and corresponding references.

Gene	1-cell/ 2-cell (this study)	2-cell/ 4-cell (ref. 2)	8-cell (this study)	~32-cell (this study)	Evidence for requirement of both maternal and paternal alleles	References
<i>ATIG03360/ RRP 4</i>	-	-	-	-	~25% of preglobular embryos from self-fertilized heterozygous plants exhibited mutant phenotypes	Muralla et al. <sup>14</sup>
<i>ATIG04950/ EMB 2781</i>	-	-	-	-	~25% of preglobular embryos from self-fertilized heterozygous plants exhibited mutant phenotypes	Muralla et al. <sup>14</sup>
<i>ATIG08560/ KNOLLE</i>	0.26	-	0.24	-0.05	26.2% of < 16-cell embryos from selfed <i>knolle keule</i> plants have cytokinesis defects	Weijers et al. <sup>9</sup>
<i>ATIG09770/ AtCDC 5</i>	0.14	2.04	0.54	0.32	~25% of preglobular embryos from self-fertilized heterozygous plants exhibited mutant phenotypes	Muralla et al. <sup>14</sup>
<i>ATIG10270/ GRP 23</i>	0.27	-	-0.01	-0.17	~25% of preglobular embryos from self-fertilized heterozygous plants exhibited mutant phenotypes	Muralla et al. <sup>14</sup>
<i>ATIG12360/ KEULE</i>	-	-	-0.90	0.16	26.2% of < 16-cell embryos from selfed <i>knolle keule</i> plants have cytokinesis defects	Weijers et al. <sup>9</sup>
<i>ATIG19080/ TTN 10</i>	-	-	-	-	~25% of preglobular embryos from self-fertilized heterozygous plants exhibited mutant phenotypes	Muralla et al. <sup>14</sup>
<i>ATIG21690/ EMB 1968</i>	0.87	-	0.38	0.43	~25% of preglobular embryos from self-fertilized heterozygous plants exhibited mutant phenotypes	Muralla et al. <sup>14</sup>
<i>ATIG31860/ HISN 2</i>	-0.18	-	-0.24	-0.23	~25% of preglobular embryos from self-fertilized heterozygous plants exhibited mutant phenotypes	Muralla et al. <sup>14</sup>
<i>ATIG44900/ MCM 2</i>	0.03	-	-0.30	-0.43	~25% of preglobular embryos from self-fertilized heterozygous plants exhibited mutant phenotypes	Muralla et al. <sup>14</sup>
<i>ATIG48175/ EMB 2191</i>	-	-	0.93	-1.57	~25% of preglobular embryos from self-fertilized heterozygous plants exhibited mutant phenotypes	Muralla et al. <sup>14</sup>
<i>ATIG55350/ EMB 1275</i>	-0.41	-	0.71	0.32	~25% of preglobular embryos from self-fertilized heterozygous plants exhibited mutant phenotypes	Muralla et al. <sup>14</sup>
<i>ATIG55900/ EMB 1860</i>	-0.07	-	-0.55	-0.17	~25% of preglobular embryos from self-fertilized heterozygous plants exhibited mutant phenotypes	Muralla et al. <sup>14</sup>
<i>ATIG59990/ EMB 3108</i>	-	-	-	-	~25% of preglobular embryos from self-fertilized heterozygous plants exhibited mutant phenotypes	Muralla et al. <sup>14</sup>
<i>ATIG63160/ EMB 2811</i>	0.21	-	-0.13	0.17	~25% of preglobular embryos from self-fertilized heterozygous plants exhibited mutant phenotypes	Muralla et al. <sup>14</sup>
<i>ATIG63700/ YDA</i>	0.86	-	-0.28	-0.33	At two days after pollination, 23% of embryos from either <i>yda-1/+</i> x <i>yda-1/+</i>	Lukowitz et al. 2004

<i>AT1G67320/</i> <i>EMB 2813</i>	-	3.70	-	-	or <i>yda-2/+</i> x <i>yda-2/+</i> crosses exhibited defects in the basal cell lineage, while only 2% of embryos from either <i>yda-1/+</i> x wild-type or <i>yda-2/+</i> x wild-type exhibited mutant phenotypes	Muralla et al. <sup>14</sup>
<i>AT1G67630/</i> <i>EMB 2814</i>	0.74	2.39	-2.44	0.48	~25% of preglobular embryos from self-fertilized heterozygous plants exhibited mutant phenotypes	Muralla et al. <sup>14</sup>
<i>AT1G71440/</i> <i>PFI</i>	-	-	-	-	~25% of preglobular embryos from self-fertilized heterozygous plants exhibited mutant phenotypes	Muralla et al. <sup>14</sup>
<i>AT1G77470/</i> <i>EMB 2810</i>	-0.19	-	-0.75	-0.03	~25% of preglobular embryos from self-fertilized heterozygous plants exhibited mutant phenotypes	Muralla et al. <sup>14</sup>
<i>AT2G18390/</i> <i>TTN 5</i>	0.41	-	0.08	-0.11	~25% of preglobular embryos from self-fertilized heterozygous plants exhibited mutant phenotypes	Muralla et al. <sup>14</sup>
<i>AT2G25710/</i> <i>HCS 1</i>	0.29	-	0.10	0.07	~25% of preglobular embryos from self-fertilized heterozygous plants exhibited mutant phenotypes	Muralla et al. <sup>14</sup>
<i>AT2G26060/</i> <i>EMB 1345</i>	-	-	-	-	~25% of preglobular embryos from self-fertilized heterozygous plants exhibited mutant phenotypes	Muralla et al. <sup>14</sup>
<i>AT2G27170/</i> <i>TTN 7</i>	-	-	-	-	~25% of preglobular embryos from self-fertilized heterozygous plants exhibited mutant phenotypes	Muralla et al. <sup>14</sup>
<i>AT2G30200/</i> <i>EMB 3147</i>	-	-	-	-	~25% of preglobular embryos from self-fertilized heterozygous plants exhibited mutant phenotypes	Muralla et al. <sup>14</sup>
<i>AT2G30920/</i> <i>EMB 3002</i>	0.08	-	0.01	0.05	~25% of preglobular embryos from self-fertilized heterozygous plants exhibited mutant phenotypes	Muralla et al. <sup>14</sup>
<i>AT2G32590/</i> <i>EMB 2795</i>	-	-	-1.19	-0.36	~25% of preglobular embryos from self-fertilized heterozygous plants exhibited mutant phenotypes	Muralla et al. <sup>14</sup>
<i>AT2G33800/</i> <i>EMB 3113</i>	-	-	-	-	~25% of preglobular embryos from self-fertilized heterozygous plants exhibited mutant phenotypes	Muralla et al. <sup>14</sup>
<i>AT2G34780/</i> <i>EMB 1611</i>	-	-	-	-	~25% of preglobular embryos from self-fertilized heterozygous plants exhibited mutant phenotypes	Muralla et al. <sup>14</sup>
<i>AT2G36230/</i> <i>HISN 3</i>	-	2.81	-	-	~25% of preglobular embryos from self-fertilized heterozygous plants exhibited mutant phenotypes	Muralla et al. <sup>14</sup>
<i>AT2G38280/</i> <i>FAC 1</i>	-0.42	2.81	-0.38	-0.24	1) ~25% of preglobular embryos from self-fertilized heterozygous plants exhibited mutant phenotypes. 2) 25.5% and 26.6% of zygotes/1-cell embryos from self-fertilized <i>fac1-1/+</i> and <i>fac1-2/+</i> heterozygous plants exhibited mutant phenotypes; 8.1%, 56.3% and 35.6% of <i>fac1-1</i> embryos arrested at unelongated zygote, elongated zygote	1) Muralla et al. <sup>14</sup> , 2) Xu et al. <sup>12</sup>

					and 1-cell stage, respectively; 78.2%, 14.5% and 7.9% of <i>fac1-2</i> embryos arrested at unelongated zygote, elongated zygote and 1-cell stage, respectively; Only 2.8% and 2.1% of ovules aborted from <i>fac1-1/+</i> x Col-0 and Col-0 x <i>fac1-1/+</i> reciprocal crosses demonstrating that the maternal or paternal wild-type allele alone was not sufficient to rescue ovule abortion.	
<i>AT2G38670/</i> <i>PECT 1</i>	-	-	-	-	~25% of preglobular embryos from self-fertilized heterozygous plants exhibited mutant phenotypes	Muralla et al. <sup>14</sup>
<i>AT2G47940/</i> <i>EMB 3117</i>	-0.80	-	-0.76	-0.43	~25% of preglobular embryos from self-fertilized heterozygous plants exhibited mutant phenotypes	Muralla et al. <sup>14</sup>
<i>AT3G02280/</i> <i>ATR 3</i>	0.60	-	0.98	-0.25	~25% of preglobular embryos from self-fertilized heterozygous plants exhibited mutant phenotypes	Muralla et al. <sup>14</sup>
<i>AT3G02660/</i> <i>EMB 2768</i>	0.39	-	0.11	-0.40	~25% of preglobular embryos from self-fertilized heterozygous plants exhibited mutant phenotypes	Muralla et al. <sup>14</sup>
<i>AT3G04680/</i> <i>CLPS 3</i>	1.01	-	0.04	0.17	~25% of preglobular embryos from self-fertilized heterozygous plants exhibited mutant phenotypes	Muralla et al. <sup>14</sup>
<i>AT3G04790/</i> <i>EMB 3119</i>	1.00	-	-	0.32	~25% of preglobular embryos from self-fertilized heterozygous plants exhibited mutant phenotypes	Muralla et al. <sup>14</sup>
<i>AT3G08850/</i> <i>RAPTOR 1</i>	-	-	2.79	-0.43	~25% of preglobular embryos from self-fertilized heterozygous plants exhibited mutant phenotypes	Muralla et al. <sup>14</sup>
<i>AT3G10220/</i> <i>EMB 2804</i>	-	1.81	-	-	~25% of preglobular embryos from self-fertilized heterozygous plants exhibited mutant phenotypes	Muralla et al. <sup>14</sup>
<i>AT3G17300/</i> <i>EMB 2786</i>	-	-	-	-	~25% of preglobular embryos from self-fertilized heterozygous plants exhibited mutant phenotypes	Muralla et al. <sup>14</sup>
<i>AT3G20070/</i> <i>TTN 9</i>	-	-	-	-	~25% of preglobular embryos from self-fertilized heterozygous plants exhibited mutant phenotypes	Muralla et al. <sup>14</sup>
<i>AT3G46740/</i> <i>TOC 75</i>	-0.03	0.97	-0.40	-0.16	~25% of preglobular embryos from self-fertilized heterozygous plants exhibited mutant phenotypes	Muralla et al. <sup>14</sup>
<i>AT3G54670/</i> <i>TTN 8</i>	-	4.09	-	-	~25% of preglobular embryos from self-fertilized heterozygous plants exhibited mutant phenotypes	Muralla et al. <sup>14</sup>
<i>AT3G55010/</i> <i>EMB 2818</i>	0.19	1.51	0.13	-0.29	~25% of preglobular embryos from self-fertilized heterozygous plants exhibited mutant phenotypes	Muralla et al. <sup>14</sup>
<i>AT3G60740/</i> <i>TTN 1</i>	-0.14	-	-0.10	-	~25% of preglobular embryos from self-fertilized heterozygous plants exhibited mutant phenotypes	Muralla et al. <sup>14</sup>
<i>AT4G00620/</i> <i>EMB 3127</i>	-0.17	-	-0.32	0.15	~25% of preglobular embryos from self-fertilized heterozygous plants exhibited mutant phenotypes	Muralla et al. <sup>14</sup>

<i>AT4G02570/</i> <i>AXR 6</i>	-	-	-	-	~25% of preglobular embryos from self-fertilized heterozygous plants exhibited mutant phenotypes	Muralla et al. <sup>14</sup>
<i>AT4G03240/</i> <i>AtFH</i>	-0.16	-	-0.46	0.11	~25% of preglobular embryos from self-fertilized heterozygous plants exhibited mutant phenotypes	Muralla et al. <sup>14</sup>
<i>AT4G05410/</i> <i>YAO</i>	-	-	-	-	~25% of preglobular embryos from self-fertilized heterozygous plants exhibited mutant phenotypes	Muralla et al. <sup>14</sup>
<i>AT4G16370/</i> <i>OPT 3</i>	-	-	-3.38	-0.51	~25% of preglobular embryos from self-fertilized heterozygous plants exhibited mutant phenotypes	Muralla et al. <sup>14</sup>
<i>AT4G21800/</i> <i>QQT 2</i>	0.01	-	0.25	-0.07	~25% of preglobular embryos from self-fertilized heterozygous plants exhibited mutant phenotypes	Muralla et al. <sup>14</sup>
<i>AT4G26900/</i> <i>HISN 4</i>	-1.39	-	1.04	-0.36	~25% of preglobular embryos from self-fertilized heterozygous plants exhibited mutant phenotypes	Muralla et al. <sup>14</sup>
<i>AT4G29910/</i> <i>EMB 2798</i>	-0.57	-	0.77	0.22	~25% of preglobular embryos from self-fertilized heterozygous plants exhibited mutant phenotypes	Muralla et al. <sup>14</sup>
<i>AT4G33680/</i> <i>AGD 2</i>	-	-	-	-	~25% of preglobular embryos from self-fertilized heterozygous plants exhibited mutant phenotypes	Muralla et al. <sup>14</sup>
<i>AT4G36480/</i> <i>EMB 2779</i>	0.76	-	-0.50	0.50	~25% of preglobular embryos from self-fertilized heterozygous plants exhibited mutant phenotypes	Muralla et al. <sup>14</sup>
<i>AT4G39920/</i> <i>POR</i>	-	-	-	-0.41	~25% of preglobular embryos from self-fertilized heterozygous plants exhibited mutant phenotypes	Muralla et al. <sup>14</sup>
<i>AT5G08470/</i> <i>EMB 2817</i>	-	-	-	-	~25% of preglobular embryos from self-fertilized heterozygous plants exhibited mutant phenotypes	Muralla et al. <sup>14</sup>
<i>AT5G10330/</i> <i>HISN 6A</i>	-	-	-	-	~25% of preglobular embryos from self-fertilized heterozygous plants exhibited mutant phenotypes	Muralla et al. <sup>14</sup>
<i>AT5G13010/</i> <i>EMB 3011</i>	-0.39	-	-1.07	-0.69	~25% of preglobular embryos from self-fertilized heterozygous plants exhibited mutant phenotypes	Muralla et al. <sup>14</sup>
<i>AT5G13480/</i> <i>FY</i>	-0.05	-	0.35	-0.33	~25% of preglobular embryos from self-fertilized heterozygous plants exhibited mutant phenotypes	Muralla et al. <sup>14</sup>
<i>AT5G13690/</i> <i>CYL 1</i>	-	-	-	-	~25% of preglobular embryos from self-fertilized heterozygous plants exhibited mutant phenotypes	Muralla et al. <sup>14</sup>
<i>AT5G14800/</i> <i>EMB 2772</i>	-0.38	-	-0.18	0.36	~25% of preglobular embryos from self-fertilized heterozygous plants exhibited mutant phenotypes	Muralla et al. <sup>14</sup>
<i>AT5G15540/</i> <i>EMB 2773</i>	-	-	-	-	~25% of preglobular embryos from self-fertilized heterozygous plants exhibited mutant phenotypes	Muralla et al. <sup>14</sup>
<i>AT5G15920/</i> <i>EMB 2782</i>	-	-	1.19	-	~25% of preglobular embryos from self-fertilized heterozygous plants exhibited mutant phenotypes	Muralla et al. <sup>14</sup>

<i>AT5G22370/</i> <i>EMB 1705</i>	-	-	-	0.00	~25% of preglobular embryos from self-fertilized heterozygous plants exhibited mutant phenotypes	Muralla et al. <sup>14</sup>
<i>AT5G24670/</i> <i>EMB 2820</i>	-1.02	-	-0.16	-0.08	~25% of preglobular embryos from self-fertilized heterozygous plants exhibited mutant phenotypes	Muralla et al. <sup>14</sup>
<i>AT5G27540/</i> <i>EMB 2473</i>	-	-	-	-	~25% of preglobular embryos from self-fertilized heterozygous plants exhibited mutant phenotypes	Muralla et al. <sup>14</sup>
<i>AT5G39750/</i> <i>EMB 3008</i>	-	-	-	-	~25% of preglobular embryos from self-fertilized heterozygous plants exhibited mutant phenotypes	Muralla et al. <sup>14</sup>
<i>AT5G40480/</i> <i>EMB 3012</i>	-	2.70	-	-	~25% of preglobular embryos from self-fertilized heterozygous plants exhibited mutant phenotypes	Muralla et al. <sup>14</sup>
<i>AT5G48840/</i> <i>PTS</i>	-0.25	-	0.28	0.92	~25% of preglobular embryos from self-fertilized heterozygous plants exhibited mutant phenotypes	Muralla et al. <sup>14</sup>
<i>AT5G50390/</i> <i>EMB 3141</i>	-	-	-	-	~25% of preglobular embryos from self-fertilized heterozygous plants exhibited mutant phenotypes	Muralla et al. <sup>14</sup>
<i>AT5G51200/</i> <i>EMB 3142</i>	-0.44	-	-0.23	-0.65	~25% of preglobular embryos from self-fertilized heterozygous plants exhibited mutant phenotypes	Muralla et al. <sup>14</sup>
<i>AT5G53040/</i> <i>GRD/RKD4</i>	-	-	-	-	~60% of <i>grd-3/rkd4-1</i> homozygous embryos exhibited phenotypes at preglobular stages and reciprocal crosses revealed no parent-of-origin effects on embryo development	Waki et al. 2011; Seong et al. 2011
<i>AT5G56270/</i> <i>WRKY2</i>	0.00	-	-1.62	-	26.2% of embryos from <i>wrky2-1</i> x <i>wrky2-1</i> embryos exhibited globular phenotypes, while 0% of embryos from either <i>wrky2-1</i> x wild-type or wild-type x <i>wrky2-1</i> exhibited globular phenotypes	Ueda et al. 2011
<i>AT5G59440/</i> <i>ZEUS 1</i>	-	-	-	-	1) ~25% of preglobular embryos from self-fertilized heterozygous plants exhibited mutant phenotypes; 2) 23.6% of embryos from self-fertilized <i>zeus1/+</i> plants were arrested at elongated zygote stage	1) Muralla et al. <sup>14</sup> , 2) Ronceret et al. <sup>13</sup>