

## SUPPLEMENTAL DATA

**Figure S1.** Overview of the DNA array profile by use of the data from late staged ovule from non-emasculated *spl* mutant plants only. The genes of the Venn diagram were  $\geq 2$  fold higher in wild type than in *spl* with P values of  $<0.005$  and signal values of  $> 60$ .

**Figure S2.** GUS expression pattern of the promoter::*GUS* fusion with *At5g40260* in developing anthers. GUS staining of tissues was performed with 5mM potassium ferri-, and ferrocyanide. After staining, anthers were cleared in Hoyer's solution (Liu and Meinke, 1998). Scale bars represent 50  $\mu\text{m}$  in A and D, 20  $\mu\text{m}$  in B and C, and 100  $\mu\text{m}$  in E~I. Floral stages, pollen or stamen developments were referred from papers of Regan and Moffatt (1990), Smyth et al (1990), Bowman et al (1991) and Ma (2005). GUS activity was not detected in flowers at floral stage 7 (A) including in the stamens (B). By contrast, GUS expression is strong within developing anthers of floral stages 8 to early 13 (C- I). A, Vertical view of a stage 7 bud. The flower bud shows that the stamens do not show locule ridges yet. B, Close-up of stamen of floral stage 7, in which archesporial cells divide to make sporogenous and primary parietal cells, did not show any GUS activity. C, Anther of floral stage 8, in which the stamen with visible locules differentiates to anther and filament, shows GUS activity. Especially, GUS expression is clear and strong in the pollen sacs containing microsporocytes. D, Stamen of floral stage early 9, in which microspore mother cells in anthers separate from each other and from tapetum by a callose wall. E, Stamen of floral stage late 9, in which microspore mother cells form tetrads by meiosis. F, Stamen of floral stage 10, during which microspores separate from callose wall and lie in the pollen sac and make round forms and epidermal cells of anther are clearly distinguished. When GUS staining is performed with 7mM potassium ferri-, and ferrocyanide, no GUS activity is observed in the epidermal cells (data not shown). G, Anther of floral stage 11, in which microspores undergo mitotic division and tapetum of the pollen sac degenerates, shows weaker GUS staining than anthers of other floral stages. H, Anther of floral stage 12, in which microspores complete mitotic division and pollen grains desiccate and the tapetum disappears, shows strong GUS staining in the immature pollen. I, Anther of floral stage early 13, in which anther dehiscence occurs, shows strong GUS staining in the pollen. When GUS staining is performed using 7mM potassium ferri-, and ferrocyanide, GUS activity was clearly restricted to the pollen grains (data not shown).

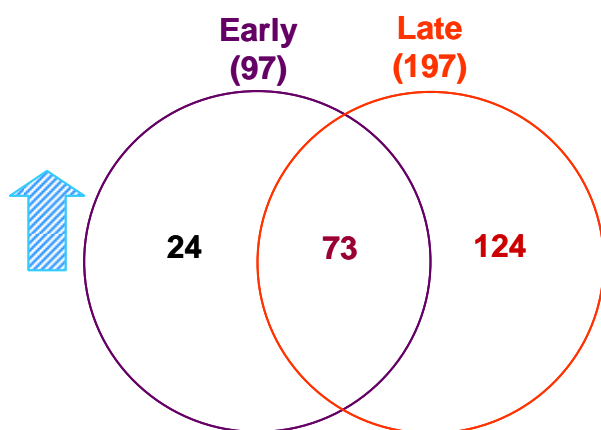
**Table SI.** Correlation coefficients between the arrays

**Table SII.** Mutants analyzed for embryo sac phenotype

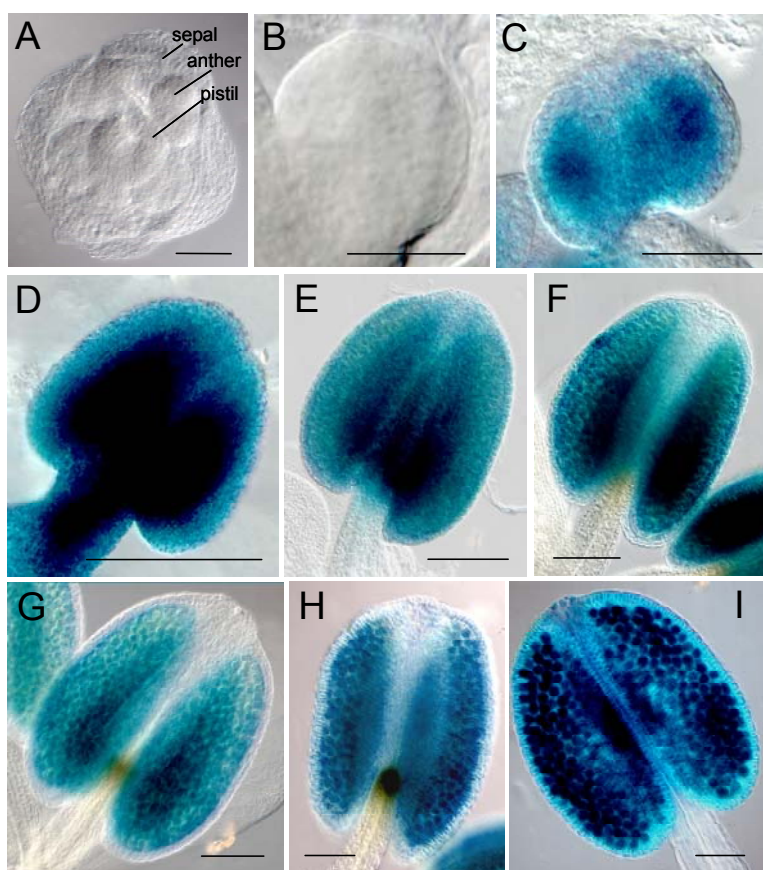
**Table SIII.** Comparison with known genes involved in female gametophyte development

**Table SIV.** Comparative information for embryo sac genes

**Table SV.** The primer sequences used in the promoter::*GUS* fusion



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**Table SI.** Correlation coefficients between the arrays

Divison	Early Staged Ovule						Late Staged Ovule							
	WT <sup>1</sup>	WT <sup>2</sup>	WT <sup>3</sup>	<i>spl</i> <sup>1</sup>	<i>spl</i> <sup>2</sup>	<i>spl</i> <sup>3</sup>	WT <sup>d1</sup>	WT <sup>d2</sup>	WT <sup>d3</sup>	<i>spl</i> <sup>1</sup>	<i>spl</i> <sup>2</sup>	<i>spl</i> <sup>3</sup>	<i>spl</i> <sup>d1</sup>	
Early Staged Ovule	WT <sup>1</sup>	-												
	WT <sup>2</sup>	0.982	-											
	WT <sup>3</sup>	0.980	0.985	-										
	<i>spl</i> <sup>1</sup>	0.970	0.970	0.968	-									
	<i>spl</i> <sup>2</sup>	0.973	0.978	0.973	0.988	-								
	<i>spl</i> <sup>3</sup>	0.942	0.930	0.960	0.989	0.987	-							
Late Staged Ovule	WT <sup>d1</sup>	0.948	0.954	0.945	0.939	0.947	0.942	-						
	WT <sup>d2</sup>	0.933	0.940	0.938	0.922	0.926	0.930	0.976	-					
	WT <sup>d3</sup>	0.955	0.958	0.955	0.954	0.954	0.960	0.986	0.975	-				
	<i>spl</i> <sup>1</sup>	0.943	0.951	0.943	0.960	0.957	0.959	0.972	0.965	0.978	-			
	<i>spl</i> <sup>2</sup>	0.944	0.951	0.941	0.955	0.961	0.956	0.980	0.962	0.980	0.987	-		
	<i>spl</i> <sup>3</sup>	0.936	0.950	0.940	0.951	0.958	0.950	0.980	0.961	0.978	0.987	0.992	-	
	<i>spl</i> <sup>d1</sup>	0.941	0.950	0.945	0.945	0.950	0.950	0.968	0.957	0.957	0.973	0.974	0.972	-
	<i>spl</i> <sup>d2</sup>	0.977	0.960	0.957	0.958	0.962	0.962	0.977	0.966	0.966	0.982	0.983	0.983	0.987

WT<sup>1-3</sup>, array of wild type siblings. *spl* 1-3, array of *spl* mutants. WT<sup>d1-d3</sup>, array of wild type siblings detached anthers. *spl*<sup>d1-d2</sup>, array of *spl* mutants detached anthers

**Table SII.** *Mutants analyzed for embryo sac phenotype*

Gene ID <sup>a</sup>	Description	Insertion Line	Position of Insertion
At1g26795	Self-incompatibility protein-related	SALK_124319	Exon 1
At1g36340	Ubiquitin-conjugating enzyme, E2	SALK_078556	Intron 2
At2g20070	Hypothetical Protein	SALK_038499	Exon 1
At4g22050	Aspartyl protease family protein	SALK_033133	Exon 1
At4g30590	Plastocyanin-like domain-containing protein	SALK_023946	Exon 1
At5g40260	Nodulin MtN3 family protein	SALK_137176	Exon 1
		SALK_092239	Exon 5

<sup>a</sup>*Arabidopsis* genome initiative number

**Table SIII.** Comparison with known genes involved in female gametophyte development

Affymetrix Code <sup>i</sup>	Gene ID <sup>b</sup>	Description	Early staged ovule				Late staged ovule			
			WT <sup>1-3</sup>	<i>spl</i> <sup>1-3</sup>	FC <sup>c</sup>	P value <sup>d</sup>	WT <sup>d1-c</sup>	<i>spl</i> <sup>1-3,1</sup>	FC <sup>c</sup>	P value <sup>d</sup>
255513_at	At4g02060	PRL, DNA replication licensing factor Mcm7	460	475	0.97	0.693433	385	406	0.95	0.590369
248739_at	At5g48030	GFA2, DNAJ heat shock protein	321	412	0.78	0.100869	350	420	0.83	0.054093
264293_at	At1g78770	NOMEGA, Cell division cycle family protein	194	221	0.88	0.229354	195	207	0.94	0.442491
260908_at	At1g02580	MEA, maternal embryogenesis control protein	109	71	1.53	0.024898	<b>93</b>	<b>55</b>	<b>1.67</b>	<b>0.001022</b>
265801_at	At2g35670	FIS2, Fertilization-independent seed 2 protein	39	20	1.95	0.022748	<b>58</b>	<b>16</b>	<b>3.55</b>	<b>0.000000</b>
257987_at	At3g20740	FIE, Fertilization-independent endosperm protein	319	369	0.86	0.170350	306	391	0.78	0.064731

Footnotes are the same in Table2.

**Table SIV. Comparative information for embryo sac genes**

Affymetrix Cod Gene ID <sup>b</sup>	Description	Early Staged Ovule		Late Staged Ovule		Sporophytic Division <sup>c</sup>	Specific Transcriptome		
		FC <sup>c</sup>	P value <sup>d</sup>	FC <sup>c</sup>	P value <sup>d</sup>		Transcriptome	FG <sup>f</sup> or Carpel	MG <sup>g</sup> or Stamen
Unknown protein									
261271_at	At1g26795 Self-incompatibility protein-related	25.3	0.000083	28.2	0.000000	Both			
265133_s_at	At1g51250 Expressed protein	6.1	0.001456	28.2	0.000000	Both			E
259726_at	At1g60985 Expressed protein	5.9	0.002140	21.4	0.000003	Both	0		
265762_at	At2g01240 Reticulon family protein (RTNLB15)	15.1	0.000418	10.3	0.000020	Both	0		
263713_at	At2g20595 Expressed protein	18.9	0.003556	41.4	0.000000	Both	0		
267193_at	At2g30900 Expressed protein	4.3	0.000554	5.4	0.000016	Both	0		C
256719_at	At2g34130 CACTA-like transposase family (Ptta/En/Spm)	10.3	0.000181	11.8	0.000000	Both	0		A
256600_at	At3g14850 Expressed protein	7.6	0.000088	8.5	0.000000	Both			
257889_at	At3g17080 Self-incompatibility protein-related	6.2	0.002931	17.8	0.000000	Both	0		C
251698_at	At3g56610 Expressed protein	32.0	0.004682	46.8	0.000000	Both	0		C
254257_s_at	At4g23350 Expressed protein	3.5	0.003879	15.3	0.000000	Both			
253164_at	At4g35725 Expressed protein	10.4	0.003044	21.2	0.000024	Both			
250871_at	At5g03930 Expressed protein	7.0	0.001971	7.5	0.000002	Both			
250325_s_at	At5g12060 Self-incompatibility protein-related	3.4	0.001255	6.8	0.000001	Both	0		
249855_at	At5g22970 Expressed protein	10.6	0.003517	31.7	0.000001	Both			C
249757_at	At5g24316 Proline-rich family protein	27.7	0.001766	45.6	0.000000	Both			
249401_at	At5g40260 Nodulin MtN3 family protein	15.2	0.000603	14.3	0.000004	Both			E
248284_at	At5g52975 Expressed protein	9.3	0.000353	8.2	0.000001	Both			
262503_at	At1g21670 Expressed protein	4.0	0.000009	1.4	0.031616	Early			
261731_s_at	At1g47780 Acyl-protein thioesterase-related	5.6	0.004140	4.7	0.000003	Early	0		D
249375_at	At5g40730 Arabinogalactan-protein (AGP24)	6.2	0.000342	1.1	0.245297	Early			E
264610_at	At1g04645 Self-incompatibility protein-related	5.7	0.157950	38.1	0.000557	Late			
261846_at	At1g11540 Expressed protein	1.4	0.117890	2.0	0.000012	Late			C
255908_s_at	At1g18010 Expressed protein	2.0	0.018058	2.1	0.000005	Late			
256079_at	At1g20680 Expressed protein	3.9	0.011798	5.7	0.000019	Late	0		
263027_at	At1g24010 Expressed protein	1.9	0.256580	4.3	0.000001	Late			
260942_s_at	At1g45190 Expressed protein	49.3	0.007497	47.1	0.000000	Late	0		
265138_at	At1g51300 Acyl-protein thioesterase-related	4.4	0.015275	9.1	0.000000	Late			
262314_at	At1g70810 C2 domain-containing protein	1.4	0.182775	3.8	0.000004	Late			
262972_at	At1g75620 Glyoxal oxidase-related	1.4	0.205253	3.5	0.000079	Late			
264297_at	At1g78710 Expressed protein	1.9	0.005001	2.5	0.000001	Late	0		
267241_at	At2g02490 Hydroxyproline-rich glycoprotein family protein	10.6	0.052466	37.0	0.000186	Late	0		C
267218_at	At2g02515 Expressed protein	4.2	0.007206	24.8	0.000001	Late	0		
265517_at	At2g06090 Self-incompatibility protein-related	17.8	0.013973	47.4	0.000000	Late			C
264590_at	At2g17710 Expressed protein	0.7	0.361347	2.1	0.000010	Late			
263518_at	At2g21655 Expressed protein	15.8	0.015412	37.6	0.000001	Late	0		C
265674_at	At2g32190 Expressed protein	1.6	0.072973	2.8	0.000267	Late			
265670_s_at	At2g32210 Expressed protein	1.0	0.888298	2.8	0.000186	Late			
265245_at	At2g43060 Expressed protein	0.9	0.564913	2.1	0.000340	Late			
259107_at	At3g05460 Sporozoite surface protein-related	9.4	0.008348	31.1	0.000069	Late	0		
258130_at	At3g24510 Expressed protein	48.6	0.012987	53.8	0.000000	Late	0		C
252253_at	At3g49300 Proline-rich family protein	6.0	0.007754	19.3	0.000044	Late	0		D
251606_at	At3g57840 Self-incompatibility protein-related	2.8	0.058391	12.4	0.000005	Late			
255207_at	At4g07515 Expressed protein	19.8	0.008275	27.0	0.000000	Late	0		
245424_at	At4g17505 Expressed protein	2.8	0.005099	9.4	0.000003	Late	0		C
254494_at	At4g20050 Expressed protein	1.5	0.069310	3.9	0.000001	Late			E
254001_at	At4g26260 Expressed protein	2.8	0.067591	5.9	0.000073	Late	0		D, E
253724_at	At4g29285 Expressed protein	7.3	0.029036	39.5	0.000000	Late			
253656_at	At4g30090 Expressed protein	1.2	0.276358	2.1	0.000137	Late	0		
253401_at	At4g32870 Expressed protein	2.1	0.040870	4.3	0.000012	Late			
246641_s_at	At5g34885 Expressed protein	10.3	0.025229	23.5	0.000000	Late	0		D
249179_at	At5g42955 Expressed protein	19.3	0.014861	38.0	0.000000	Late	0		
248892_at	At5g46300 Expressed protein	11.8	0.014887	23.1	0.000001	Late	0		
Central intermediary metabolism									
259786_at	At1g29660 GDSL-motif lipase/hydrolase family protein	3.4	0.003166	2.1	0.000131	Both			
260124_at	At1g36340 Ubiquitin-conjugating enzyme, E2	15.3	0.001661	13.8	0.000002	Both	0		C
245672_at	At1g56710 Glycoside hydrolase family 28 protein	2.6	0.004220	2.5	0.000298	Both			C
257442_at	At2g28680 Cupin family protein	6.8	0.001424	9.2	0.000008	Both	0		D, E
267408_at	At2g34890 CTP synthase, putative	6.1	0.000651	4.2	0.000011	Both	0		
257243_at	At3g24230 Pectate lyase family protein	5.7	0.003792	3.2	0.000001	Both			
258763_s_at	At3g30540 (1-4)-beta-mannan endohydrolase family	15.9	0.002254	17.4	0.000000	Both	0		
252342_at	At3g48950 Glycoside hydrolase family 28 protein	11.6	0.001576	23.3	0.000000	Both	0		
248925_at	At5g45910 GDSL-motif lipase/ hydrolase-like protein	20.0	0.001613	53.5	0.000000	Both			C
247228_at	At5g65140 Trehalose-6-phosphate phosphatase	8.0	0.000647	2.7	0.000044	Both			
264147_at	At1g02200 CER1 protein	2.4	0.000205	1.0	0.799875	Early			
264146_at	At1g02205 CER1 protein, At1g02200	2.3	0.000021	1.0	0.820363	Early			
259703_at	At1g77790 Glycosyl hydrolase family 17 protein	7.0	0.000428	4.8	0.000000	Early			
267202_s_at	At2g31030 Oxysterol-binding family protein	7.3	0.000864	3.8	0.000005	Early			
260611_at	At2g43670 Glycosyl hydrolase family 17 protein	2.5	0.002326	1.7	0.000212	Early			
252320_at	At3g48580 Xyloglucan:xyloglucosyl transferase, putative	2.4	0.003795	1.5	0.004917	Early			
250082_at	At5g17200 Glycoside hydrolase family 28 protein	4.2	0.002910	1.8	0.000578	Early			

(Table continues on the following page.)



**Table SIV.** (Continued from previous page.)

Affymetrix Cod Gene ID <sup>b</sup>	Description	Early Staged Ovule		Late Staged Ovule		Division <sup>c</sup>	Sporophytic Transcriptome	Specific Transcriptome	
		FC <sup>c</sup>	P value <sup>d</sup>	FC <sup>c</sup>	P value <sup>d</sup>			FG <sup>e</sup> or Carpel	MG <sup>f</sup> or Stamen
Central intermediary metabolism (continued)									
260947_at	At1g06020 PfkB-type carbohydrate kinase family protein	1.5	0.010463	2.6	0.000134	Late	0		
259391_s_at	At1g06350 Fatty acid desaturase family protein	1.7	0.342723	2.2	0.000376	Late			
255956_at	At1g22015 Galactosyltransferase family protein	3.7	0.007113	8.0	0.000000	Late	0		
245792_at	At1g32100 Pinoresinol-lariciresinol reductase, putative	1.0	0.993453	2.7	0.000127	Late			
245794_at	At1g32170 Xyloglucan:xyloglucosyl transferase, putative	1.2	0.363717	2.1	0.000150	Late			
256211_at	At1g50960 Gibberellin 20-oxidase-related	2.2	0.015340	5.4	0.000000	Late			
260333_at	At1g70500 Polygalacturonase, putative / Pectinase, putative	21.7	0.007959	16.0	0.000001	Late			
260066_at	At1g73610 GDSL-motif lipase/hydrolase family protein	2.9	0.035163	8.0	0.000056	Late			
260259_at	At1g74300 Esterase/lipase/thioesterase family protein	1.1	0.690243	2.2	0.000095	Late	0		
265331_at	At2g18420 Gibberellin-responsive protein, putative	1.1	0.777953	4.1	0.000139	Late			E
267607_s_at	At2g26740 Epoxide hydrolase, soluble (sEH)	1.0	0.977676	2.4	0.000242	Late			
267337_at	At2g39980 Transferase family protein	2.0	0.015251	2.3	0.000006	Late			
260559_at	At2g43860 Polygalacturonase, putative / Pectinase, putative	3.0	0.005920	2.3	0.000032	Late	0		
258767_at	At3g10890 (1-4)-beta-mannan endohydrolase, putative	6.3	0.013753	35.1	0.000002	Late	0		E
258151_at	At3g18080 Glycosyl hydrolase family I protein	1.0	0.899935	3.1	0.000003	Late			
257065_at	At3g18220 Phosphatidic acid phosphatase family protein	1.5	0.034020	2.8	0.000003	Late	0		D
251491_at	At3g59480 PfkB-type carbohydrate kinase family protein	9.9	0.032782	2.8	0.001882	Late			E
255550_at	At4g01970 Galactinol-raffinose galactosyltransferase, putative	3.1	0.006794	2.7	0.000170	Late	0		
245349_at	At4g16690 Esterase/ lipase/ thioesterase family protein	1.9	0.193063	2.1	0.000368	Late			
254609_at	At4g18970 GDSL-motif lipase/hydrolase family protein	0.9	0.189942	2.3	0.000085	Late			
246498_at	At5g16230 Acyl-[acyl-carrier-protein] desaturase, putative	1.3	0.219929	3.6	0.001229	Late			
249983_at	At5g18470 Curculin-like (mannose-binding) lectin family protein	1.2	0.486888	2.2	0.001507	Late			
246774_at	At5g27530 Glycoside hydrolase family 28 protein	2.4	0.012277	4.8	0.000001	Late	0		D
249474_s_at	At5g39190 Germin-like protein (GER2)	1.2	0.500732	7.6	0.000004	Late			
248812_at	At5g47330 Palmitoyl protein thioesterase family protein	0.8	0.143704	4.7	0.000004	Late			
248791_at	At5g47350 Palmitoyl protein thioesterase family protein	3.3	0.040644	4.0	0.000003	Late			
Hypothetical protein									
260318_at	At1g63960 Hypothetical Protein	3.2	0.002924	3.5	0.000014	Both	0		
265579_at	At2g20070 Hypothetical Protein	13.8	0.000041	13.4	0.000000	Both	0		
257434_at	At2g21740 Hypothetical Protein	5.0	0.001238	15.3	0.000000	Both	0		
252753_at	At3g43500 Hypothetical Protein	4.0	0.002002	6.6	0.000002	Both	0		
246859_at	At5g25950 Hypothetical Protein	5.4	0.000045	10.9	0.000000	Both	0		
248225_at	At5g53740 Hypothetical Protein	2.3	0.000851	2.1	0.000065	Both			
266706_at	At2g03320 Hypothetical protein	3.5	0.001116	2.8	0.000175	Early	0		
246866_at	At5g25960 Hypothetical protein	11.7	0.000000	4.8	0.000020	Early			
248396_at	At5g52130 Hypothetical protein	5.4	0.000609	3.2	0.000216	Early	0		
257468_at	At1g47470 Hypothetical protein	11.2	0.029273	40.1	0.000000	Late	0		
261313_at	At1g52970 Hypothetical protein	9.9	0.007905	32.1	0.000000	Late			
259944_at	At1g71470 Hypothetical protein	1.2	0.213121	2.1	0.000104	Late			
263895_at	At2g21920 Hypothetical protein	4.2	0.007542	4.2	0.000906	Late			
258798_at	At3g04540 Hypothetical protein	3.7	0.087047	30.9	0.000000	Late	0		C
256773_at	At3g13630 Hypothetical protein	1.1	0.715677	2.2	0.000839	Late	0		D
251607_at	At3g57850 Hypothetical protein	6.6	0.036056	29.4	0.000050	Late	0		
255029_x_at	At4g09470 Hypothetical protein	17.2	0.012714	43.5	0.000003	Late			
255804_at	At4g10220 Hypothetical protein	3.9	0.009652	12.0	0.000003	Late	0		D
254692_at	At4g17860 Hypothetical protein	1.7	0.028983	3.9	0.000008	Late			
246472_at	At5g17130 Hypothetical protein	1.0	0.853233	2.2	0.000487	Late	0		
249157_at	At5g43510 Hypothetical protein	27.3	0.012178	20.1	0.000001	Late	0		
247245_at	At5g64720 Hypothetical protein	6.9	0.010392	24.5	0.000000	Late	0		
Detoxification/ stress response									
264001_at	At2g22420 Peroxidase 17 (PER17)	6.5	0.003718	6.1	0.000007	Both			B
265264_at	At2g42930 Glycosyl hydrolase family protein 17	6.3	0.003492	8.5	0.000007	Both	0		C
254000_at	At4g26250 Galactinol synthase induced by water stress	4.8	0.003892	4.2	0.000004	Both	0		
252951_at	At4g38700 Disease resistance-responsive family protein	2.3	0.004228	6.2	0.000000	Both			
247857_at	At5g58400 Peroxidase, putative	4.4	0.000004	2.9	0.000023	Both			C
261410_at	At1g07610 Metallothionein-like protein 1C (MT-1C)	2.1	0.000832	1.4	0.168590	Early			E
266743_at	At2g02990 Ribonuclease 1 (RNS1)	2.9	0.001354	1.4	0.201557	Early			E
263026_at	At1g24000 Bet v 1 allergen family protein	2.9	0.266278	12.9	0.000001	Late	0		
265920_s_at	At2g15120 Pseudogene, disease-resistance family protein	1.1	0.299880	4.6	0.000933	Late			
266562_at	At2g23970 Defense-related protein, putative	1.1	0.479766	5.1	0.000000	Late	0		D, E
267138_s_at	At2g38210 Ethylene-responsive protein, putative	2.1	0.091609	3.2	0.001233	Late			
266169_at	At2g38900 Serine protease inhibitor	1.1	0.867313	3.3	0.000002	Late	0		
260557_at	At2g43610 Glycoside hydrolase family 19 protein	1.9	0.003261	2.3	0.000002	Late			
258791_at	At3g04720 Hevein-like protein (HEL)	1.0	0.937369	2.6	0.003414	Late			
258172_at	At3g21620 Early-responsive to dehydration protein-related	2.5	0.000597	3.2	0.000002	Late			
254098_at	At4g25100 Superoxide dismutase (Fe), chloroplast (SODB)	2.2	0.060518	5.6	0.000220	Late			
253655_at	At4g30070 Plant defensin-fusion protein, putative	2.5	0.007716	7.4	0.000001	Late	0		
250200_at	At5g14130 Peroxidase, putative	1.4	0.229669	2.6	0.000012	Late			
250083_at	At5g17220 Glutathione S-transferase-like protein	1.1	0.870900	2.3	0.000020	Late			
249560_at	At5g38330 Plant defensin-fusion protein, putative	11.0	0.008435	39.5	0.000000	Late	0		
249527_at	At5g38710 Proline oxidase, putative	3.9	0.006176	4.8	0.000019	Late			

(Table continues on the following page.)

**Table SIV.** (Continued from previous page.)

Affymetrix Cod Gene ID <sup>b</sup>	Description	Early Staged Ovule		Late Staged Ovule		Sporophytic Division <sup>c</sup>	Specific Transcriptome		
		FC <sup>e</sup>	P value <sup>d</sup>	FC <sup>e</sup>	P value <sup>d</sup>		Transcriptome	FG <sup>f</sup> or Carpel	MG <sup>g</sup> or Stamen
Cell structure organization									
260573_at	At2g47280 Pectinesterase family protein	6.4	0.000454	5.5	0.000000	Both	0		D
257878_at	At3g17150 Invertase/pectin methylesterase inhibitor family	15.3	0.004375	29.2	0.000000	Both	0	C	
258438_at	At3g17230 Invertase/pectin methylesterase inhibitor family	14.4	0.000924	24.8	0.000000	Both	0		
251748_at	At3g55680 Invertase/pectin methylesterase inhibitor family	3.2	0.000901	2.8	0.000002	Both	0		
255699_at	At4g00190 Putative pectinesterase	2.8	0.001537	3.7	0.000001	Both	0		
248823_s_at	At5g46960 Invertase/pectin methylesterase inhibitor family	35.1	0.002890	39.4	0.000003	Both	0		
247246_at	At5g64620 Invertase/pectin methylesterase inhibitor family	2.2	0.000298	2.0	0.000000	Both	0		
260802_at	At1g78400 Glycoside hydrolase family 28 protein	8.8	0.000001	1.7	0.001391	Early	0		D
258764_at	At3g10720 Pectinesterase, putative	2.0	0.001974	1.5	0.008263	Early	0	C	
253725_at	At4g29340 Profilin 3 (PRO3) (PFN3)	2.3	0.000446	1.1	0.244366	Early	0		E
264500_at	At1g09370 Pectinesterase inhibitor domain-containing protein	6.0	0.123949	43.8	0.000012	Late	0		
259613_at	At1g48010 Invertase/pectin methylesterase inhibitor family	1.1	0.597625	3.6	0.000000	Late	0		
262083_at	At1g56100 Pectinesterase inhibitor domain-containing protein	2.4	0.444629	3.5	0.000012	Late	0		
245656_at	At1g56620 Pectinesterase inhibitor domain-containing protein	1.9	0.044275	13.3	0.000000	Late	0		
257679_at	At3g20470 Pseudogene, glycine-rich protein	1.2	0.700308	2.2	0.001050	Late	0	C	
245371_at	At4g15750 Invertase/pectin methylesterase inhibitor family	3.2	0.067454	3.1	0.000004	Late	0		
249962_at	At5g18990 Pectinesterase family protein	2.0	0.028245	5.5	0.000041	Late	0		
247377_at	At5g63180 Pectate lyase family protein	1.4	0.147262	2.1	0.000518	Late	0		
Transport									
260319_at	At1g63950 Heavy-metal-associated domain-containing protein	10.9	0.002905	7.9	0.000001	Both	0		
259757_at	At1g77510 Protein disulfide isomerase, putative	2.6	0.000344	2.6	0.000170	Both	0	B	
258760_at	At3g10780 Emp24/gp25L/p24 family protein	4.6	0.001770	5.4	0.000000	Both	0	C	
245892_at	At5g09370 Protease inhibitor/seed storage/lipid transfer protein	6.8	0.004630	12.3	0.000002	Both	0		
263765_at	At2g21540 SEC14 cytosolic factor, putative	2.1	0.000985	1.5	0.002042	Early	0	C	
249346_at	At5g40780 Sugar transporter, putative	4.6	0.002599	1.4	0.054790	Early	0		
264520_at	At1g10010 Lysine and histidine specific transporter, putative	2.6	0.005939	4.8	0.000000	Late	0		
265002_at	At1g24400 Amino acid permease, putative	3.8	0.024933	2.2	0.000005	Late	0		E
259580_at	At1g28030 Lysine and histidine specific transporter	1.2	0.276557	3.0	0.000024	Late	0		
265064_at	At1g61630 Oxidoreductase, 2OG-Fe(II) oxygenase family protein	1.7	0.013220	2.3	0.000179	Late	0		D, E
259844_at	At1g73560 Equilibrative nucleoside transporter, putative (ENT7)	2.2	0.005234	4.9	0.000122	Late	0		
264482_at	At1g77210 Protease inhibitor/seed storage/lipid transfer protein	1.1	0.601658	2.1	0.000012	Late	0		
257366_s_at	At2g03040 Sugar transporter, putative	4.1	0.005632	8.3	0.000008	Late	0		
266276_at	At2g29330 Transmembrane protein-related	2.3	0.007410	2.4	0.000243	Late	0		
254453_at	At4g21120 Tropinone reductase, putative	3.3	0.007991	2.9	0.000000	Late	0		E
246887_at	At5g26250 Amino acid permease family protein	2.6	0.015475	4.0	0.000013	Late	0		D
248275_at	At5g53520 Oligopeptide transporter OPT family protein	1.3	0.204722	3.9	0.000002	Late	0		D
248019_at	At5g56480 Protease inhibitor/seed storage/lipid transfer protein	1.2	0.206709	2.9	0.000015	Late	0		
Protein degradation									
256486_at	At1g31450 Aspartyl protease family protein	14.8	0.001311	35.1	0.000000	Both	0		
245738_at	At1g44130 Nucellin protein, putative	12.3	0.002988	11.2	0.000067	Both	0		
259368_at	At1g69100 Aspartyl protease family protein	42.6	0.003756	29.1	0.000000	Both	0		
252499_s_at	At3g46840 Subtilase family protein	11.6	0.000398	17.2	0.000001	Both	0		
245589_at	At4g15040 Subtilase family protein	7.3	0.000154	4.0	0.000055	Both	0		
254336_at	At4g22050 Aspartyl protease family protein	18.3	0.000096	10.6	0.000000	Both	0		
246684_at	At5g33340 Aspartyl protease family protein	4.0	0.000228	9.1	0.000001	Both	0		
247798_at	At5g58830 Subtilase family protein	5.0	0.002673	17.7	0.000000	Both	0		
254237_at	At4g23520 Cysteine proteinase, putative	2.4	0.000243	1.9	0.000254	Early	0		
247697_at	At5g59810 Subtilase family protein	2.1	0.002288	1.3	0.003872	Early	0	C	
264067_x_at	At2g28010 Aspartyl protease family protein	1.7	0.039844	5.9	0.000004	Late	0		
250345_at	At5g11940 Subtilase family protein	3.9	0.005591	11.4	0.000000	Late	0		D
Signal transduction									
263740_at	At2g20660 Rapid alkalization factor (RALF) family protein	2.4	0.000758	3.8	0.000000	Both	0		
245158_at	At2g33130 RALF family protein	12.8	0.000989	11.4	0.000000	Both	0		
266418_at	At2g38750 Annexin 4 (ANN4)	4.4	0.003825	3.3	0.000001	Both	0		
251514_at	At3g59260 Pirin, putative	6.1	0.001924	5.7	0.000002	Both	0		
255489_at	At4g02650 Epsin N-terminal homology domain-containing protei	20.7	0.004357	39.8	0.000000	Both	0		D, E
245177_at	At5g12380 Annexin, putative	11.2	0.000393	12.8	0.000000	Both	0		
249013_at	At5g44700 Leucine-rich repeat transmembrane protein kinase	2.6	0.001303	2.5	0.000305	Both	0	A	E
261285_at	At1g35720 Annexin 1 (ANN1)	1.4	0.273697	3.6	0.000012	Late	0		
257869_at	At3g25160 ER lumen protein retaining receptor family protein	1.7	0.030431	2.8	0.000020	Late	0		
250090_at	At5g17330 Glutamate decarboxylase 1 (GAD 1)	9.2	0.005864	9.0	0.000000	Late	0	B	
Energy metabolism									
259268_at	At3g01070 Plastocyanin-like domain-containing protein	2.8	0.002166	4.8	0.000001	Both	0		
253634_at	At4g30590 Plastocyanin-like domain-containing protein	12.6	0.000057	12.3	0.000005	Both	0	C	
252897_at	At4g39490 Cytochrome P450 family protein, At4g38480	3.4	0.004614	7.5	0.000000	Both	0		
248236_at	At5g53870 Plastocyanin-like domain-containing protein	20.7	0.000394	4.0	0.000009	Both	0		
262528_at	At1g17260 ATPase 10, plasma membrane-type, putative	1.7	0.385722	3.4	0.000002	Late	0		
261396_at	At1g79800 Plastocyanin-like domain-containing protein	1.2	0.236124	2.2	0.000064	Late	0		D, E
266563_at	At2g23990 Plastocyanin-like domain-containing protein	4.2	0.011017	23.3	0.000015	Late	0		
255690_at	At4g00360 Cytochrome P450, putative	2.1	0.018309	2.7	0.000026	Late	0		
254489_at	At4g20800 FAD-binding domain-containing protein	4.4	0.027803	11.3	0.000000	Late	0		

(Table continues on the following page.)

**Table SIV.** (Continued from previous page.)

Affymetrix Cod Gene ID <sup>b</sup>	Description	Early Staged Ovule		Late Staged Ovule		Sporophytic Division <sup>c</sup>	Sporophytic Transcriptome	Specific Transcriptome	
		FC <sup>e</sup>	P value <sup>d</sup>	FC <sup>e</sup>	P value <sup>d</sup>			FG <sup>f</sup> or Carpel	MG <sup>g</sup> or Stamen
Transcriptional regulation									
267528_at	At2g45650 MADS-box protein (AGL6)	4.2	0.002904	2.1	0.000048	Both	0		
249338_at	At5g41090 No apical meristem (NAM) family protein	9.1	0.000764	5.8	0.000000	Both	0		E
260212_at	At1g74480 RWP-RK domain-containing protein	1.5	0.071151	2.2	0.001510	Late			
266969_at	At2g39540 Gibberellin-regulated family protein	1.1	0.593532	5.6	0.000003	Late			
254619_at	At4g18770 Myb family transcription factor (MYB98)	1.8	0.063530	2.7	0.000002	Late	0		
251114_at	At5g01380 Expressed protein	1.0	0.855505	2.7	0.000211	Late			
248240_at	At5g53950 No apical meristem (NAM) family protein	1.1	0.399544	2.4	0.000013	Late			
Secondary metabolism									
260386_at	At1g74010 Strictosidine synthase family protein	5.1	0.001313	16.4	0.000010	Both			
264401_at	At1g61720 Dihydroflavonol 4-reductase family (BAN)	1.2	0.693582	3.0	0.000017	Late	0		
260335_at	At1g74000 Strictosidine synthase family protein	2.0	0.005947	2.7	0.000038	Late			E
254283_s_at	At4g22870 Leucoanthocyanidin dioxygenase, putative	1.0	0.880918	2.3	0.000118	Late	0		
249215_at	At5g42800 Dihydroflavonol 4-reductase	1.2	0.546725	3.6	0.000030	Late			
Plant development/ Organogenesis									
262113_at	At1g02820 Late embryogenesis abundant 3 family protein	2.5	0.000057	2.8	0.000001	Both			
262659_at	At1g14240 Nucleoside phosphatase family protein	3.3	0.000911	5.8	0.000000	Both			
262549_at	At1g31290 PAZ domain-containing protein	1.4	0.096043	2.7	0.000011	Late			
252234_at	At3g49780 Phytosulfokines 3 (PSK3)	2.0	0.386279	3.8	0.000014	Late			
251301_at	At3g61880 Cytochrome p450, putative	1.9	0.003809	2.2	0.000032	Late			
Protein biosynthesis/ DNA catbolism									
245883_at	At5g09500 40S ribosomal protein S15 (RPS15C)	4.7	0.002080	5.9	0.000028	Early	0		D, E
260438_at	At1g68290 Bifunctional nuclease, putative	1.6	0.093917	5.9	0.000104	Late			

Genes were selected on the basis of the P value of <0.0050, fold change of > 2.0, and signal intensity of >60.0 at wild type siblings. WT<sup>1-3</sup>, mean of signal intensities for array 1-3 of wild type siblings. *spl*<sup>1-3</sup>, mean of signal intensities for array 1-3 of *spl* mutants. WT<sup>d1-d3</sup>, mean of signal intensities for array 1-3 of emasculated wild type siblings. *spl*<sup>1-3, d1-d2</sup>, mean of signal intensities for array 1-3 of not emasculated *spl* and array 1 and 2 of emasculated *spl*. <sup>a</sup>Affymetrix probe set number. <sup>b</sup>Arabidopsis genome initiative number. <sup>c</sup>Fold change for signal intensity of wild type/signal intensity of *spl*. <sup>d</sup>P values calculated by student's t-test for two-sample equal variance. <sup>e</sup>Expressed ovule stage. <sup>f</sup>Female gametophyte. <sup>g</sup>Male gametophyte. 0, It means that the detection call values were not 'present' in all replicates provided or not detect in transcriptome of sporophytic tissue. A, Genes identified from Ds insertional mutants (Pagnussat et al., 2005). B, ESTs of maize embryo sac provided from McCormick's web site. C, Carpel-specific transcriptome (Wellmer et al., 2004). D, Male gametophyte-specific transcriptome (Honys and Twell, 2004). E, Stamen-specific transcriptome (Wellmer et al., 2004).

**Table SV.** The primer sequences used in the promoter::GUS fusion

Gene ID	Primer Name	Primer Sequence (5' to 3')	Mer	TM	RE	Amplicon Size	Total Promoter Size
<i>At1g26795</i>	At1g26795 F	ttgaattctctttcagtgccactaaa	26	62.4	<i>Eco</i> RI	1069 bp	1106 bp
	At1g26795 R	AAGCCATgggtgtgtttacttttaaga	28	64.8	<i>Nco</i> I		
<i>At1g36340</i>	At1g36340 F	ccgaattctgatcattaagttaggggt	28	65.3	<i>Eco</i> RI	1287 bp	1501 bp
	At1g36340 R	TAACCATggttacgagaaatcaccaaac	28	65.9	<i>Nco</i> I		
<i>At2g20070</i>	At2g20070 F	gactcgaatgaacaattattgcttaa	28	60.2	<i>Eco</i> RI	457 bp	556 bp
	At2g20070 R	aaaccatggaacactactacittatata	28	58.8	<i>Nco</i> I		
<i>At4g22050</i>	At4g22050 F	ttctcgaatgaaatcgtacctcttcactt	28	64.7	<i>Eco</i> RI	1359 bp	2772 bp
	At4g22050 R	TATCCATggttgagatgtgaggctcagt	28	68.9	<i>Nco</i> I		
<i>At4g30590</i>	At4g30590 F	ttgaattcagcatgattaaacttgaat	28	62.2	<i>Eco</i> RI	1290 bp	1431 bp
	At4g30590 R	atgccatggtgatgtggttttatatag	28	64.8	<i>Nco</i> I		
<i>At5g40260</i>	At5g40260 F	gtgaattcgaccacaataagtgaatgc	28	64.7	<i>Eco</i> RI	1550 bp	2655 bp
	At5g40260 R	AACCATggtaaaatcgccgtttacaaa	27	67.7	<i>Nco</i> I		

All genes have no *Nor* I and *Sac* I site.