Transcriptional analysis of the Arabidopsis ovule by Massively Parallel Signature Sequencing.

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Supplementary Table 1

Supplementary table 1 . Transcriptional activity of wild type ovules signatures from unnanotated regions.

[a]MPSS signatures.

[b]Activity in transcripts per Million. AGM. *agamous* infloresence. AP1. *apetala1-10* infloresence. AP3. *apetala3-6* infloresence. CAS. Callus. GSE. Germinating seedlings. INS. Infloresences. LES. Leaves. ROS. Roots. S04. Leaves, 4 hr after salicylic acid treatment. S52. Leaves, 52 hr after salicylic acid treatment. SAP. *superman/apetala* infloresence. SIS. Siliques. OVL. Wild type ovules.SPL. *sporocyteless* ovule

SIGNATURE[a]	Transcriptional activity[b]													
	AGM	AP1	AP3	CAS	GSE	INS	LES	ROS	S04	S52	SAP	SIS	OVL	SPL
GATCCAACTGGTTTTGT	3	2	4	0	0	0	0	0	0	0	3	0	19	0
GATCTGTCTTCTTAGTT	8	2	15	3	0	2	1	5	0	5	0	0	1	0
GATCTCAAACGAGTAAC	11	0	5	0	0	1	0	0	0	4	0	0	30	0
GATCTGCAAGACGAAAA	208	135	103	42	19	263	221	951	163	267	83	34	183	120
GATCATTTGTTGCAATA	5	5	6	11	0	0	0	5	5	0	0	35	9	0
GATCTGCTTTTGTCGCA	12	0	1	0	5	0	5	2	0	1	0	0	9	7
GATCCAAACCTAATACC	13	5	1	50	0	5	30	0	0	3	3	29	30	16
GATCCAATCTTTGTTGC	8	0	13	12	0	0	8	0	0	0	0	54	12	0
GATCTGTTGTTGGACCT	18	46	61	0	13	12	32	21	51	23	26	23	95	10
GATCTTCAACAAGGTGA	6	1	8	7	0	2	11	0	0	4	1	1	1	0
GATCTTCAACATTTGAC	9	0	4	12	2	0	0	1	0	0	0	0	25	0
GATCTTCCCTTTTCTTG	20	1	19	17	0	0	0	7	0	0	0	35	3	26
GATCTTCGTGAACTTTG	7	2	4	0	0	0	0	0	0	0	0	2	1	0

Supplementary Table 1

SIGNATURE[a]	Transcriptional activity[b]													
	AGM	AP1	AP3	CAS	GSE	INS	LES	ROS	S04	S52	SAP	SIS	OVL	SPL
GATCTTCGTTGGTGACC	1	2	0	5	0	3	3	22	0	3	1	0	7	11
GATCCATCAGGGGAGGA	14	7	4	21	0	3	0	6	3	0	0	1	14	35
GATCTTGTGGATGCCCT	3	10	7	31	0	3	12	13	0	0	0	2	29	37
GATCTTGTTGGTGGCAG	13	12	8	14	0	7	0	6	0	24	0	6	163	38
GATCCCAACTAAACAAA	9	8	3	0	4	5	6	0	78	62	26	15	1	0
GATCCCAAGATGCTGAG	9	12	4	105	0	2	34	1	0	0	1	60	5	19
GATCTTGTTTCCGACGA	13	28	35	15	80	43	4	25	6	14	10	19	72	25
GATCCCATCTGGGAACG	4	16	16	12	0	3	2	6	7	0	19	0	5	3
GATCCCCAATGATTTTC	5	2	9	60	0	2	1	31	3	40	17	0	42	2
GATCCCCTTTCGAAGTT	18	29	4	0	113	12	14	12	0	0	18	0	1	0
GATCCCGAAAACTAACC	51	38	18	10	65	22	1	18	14	53	80	52	260	167
GATCCGAATCAATTCTC	3	5	4	0	0	1	0	0	0	0	0	10	27	1
GATCCGAGTGGTACATT	10	4	3	0	0	4	1	6	1	0	0	0	9	0
GATCAAAACTCCAACAG	6	2	9	29	0	13	0	2	4	17	0	0	1	39
GATCAAAATTTGAGAGG	7	0	12	0	2	7	1	0	1	0	0	0	5	0
GATCAAACACAAACTCA	15	3	0	0	7	5	8	6	27	3	2	20	25	0
GATCAAACTCTTTTACC	15	5	0	0	76	17	51	5	27	1	9	13	2	0
GATCCGGGAAATACTGA	3	0	0	0	0	0	0	0	0	0	0	0	17	0

Supplementary Table 1

SIGNATURE[a]	Transcriptional activity[b]													
	AGM	AP1	AP3	CAS	GSE	INS	LES	ROS	S04	S52	SAP	SIS	OVL	SPL
GATCACTTAGCAGGAGA	3	1	0	0	0	4	0	0	0	0	0	0	3	0
GATCCTAACCGTTGTCC	60	35	26	138	0	82	42	80	17	40	48	81	60	65
GATCCTAAGCTCATGAA	9	8	24	29	0	12	3	6	0	1	35	4	19	3
GATCAGAGTTTCTTCAT	2	0	2	0	0	0	0	3	0	0	0	6	2	0
GATCCTACATTCTCTTT	27	8	4	3	5	3	4	0	110	7	12	5	5	0
GATCCTCAAGTGTGATG	13	2	8	3	7	0	0	16	0	9	23	0	32	0
GATCCTCTCAGCTATTC	20	29	5	0	0	10	6	0	0	5	46	96	317	39
GATCAACGATTCCATCC	9	0	6	0	0	0	19	0	0	0	4	15	5	3
GATCCTGAAGATTAAGT	10	7	8	61	0	11	2	43	0	0	0	12	1	2
GATCCTGCGGACCAATG	4	0	0	0	0	0	0	0	0	0	0	0	1	0
GATCCTGTCAACGAACC	14	10	5	15	0	13	24	24	0	5	0	5	57	21
GATCCTTCCCTTGGAAT	8	7	2	0	0	4	0	0	0	2	37	0	43	16
GATCAAGTTTCAGAGTC	2	2	0	0	18	2	0	0	0	0	12	0	38	23
GATCAATAAAGTGTGCC	33	2	10	92	0	4	66	23	7	4	0	89	27	65
GATCCTTGTTTCCCTTT	23	57	77	25	2	66	9	60	42	7	22	22	35	18
GATCCTTTCTTGGCGAA	11	2	10	0	0	3	3	0	0	0	6	0	51	57
GATCAATGCCAAGTCTC	23	7	24	63	0	9	1	34	4	1	2	65	94	87
GATCACAACCAACGAAA	3	4	0	0	0	0	0	0	5	1	0	0	1	1

Supplementary Table 1

SIGNATURE[a]	Transcriptional activity[b]													
	AGM	AP1	AP3	CAS	GSE	INS	LES	ROS	S04	S52	SAP	SIS	OVL	SPL
GATCACAGTCACTTGCT	16	17	23	0	53	13	62	0	12	37	16	43	21	6
GATCCTTTTGACAGGAC	11	4	15	29	0	3	0	4	0	0	7	6	12	16
GATCGAAGGTGTATGTG	842	181	127	32	1496	57	335	27	5933	3376	865	585	11	0
GATCGACGGTGGTTAGT	171	59	44	287	9	22	36	24	25	16	109	56	121	116
GATCACCAAAATCAGGA	9	4	27	0	2	17	12	18	12	3	0	3	69	5
GATCACCATCTTGTTCG	7	16	1	0	7	13	1	29	0	0	2	1	23	6
GATCGAGGTCTCTCTTT	13	4	10	9	9	10	1	26	4	18	0	0	24	17
GATCGCAAGACTCGTGC	43	58	44	95	43	36	29	186	3	15	28	51	131	160
GATCGCAAGAGGATAAT	3	0	0	1	0	1	0	2	0	0	7	0	10	0
GATCACTCTTCAACCAA	3	1	4	52	0	0	8	17	0	2	0	15	41	15
GATCGGTTTCGTGGCTG	7	0	0	0	0	0	0	0	0	0	0	0	1	1
GATCGGAACTCATCCTT	8	24	4	0	0	1	0	15	12	0	1	0	3	0
GATCGGAAGCGTCGATG	12	12	36	63	3	22	21	64	19	0	6	46	22	145
GATCGGAAGTTTGCTCA	41	95	31	29	0	27	10	27	21	17	30	15	45	73
GATCAGCACACGTGGTA	5	1	2	0	0	0	2	0	8	0	0	0	2	0
GATCTGAAAATCTTTGC	4	0	0	0	0	2	0	0	0	0	0	0	2	0
GATCGTCGACTCCTTGT	472	280	318	119	31	277	235	321	157	227	106	137	414	220
GATCATAATGAGAGACA	6	0	10	0	0	3	10	0	0	0	1	0	14	0

Supplementary Table 1

SIGNATURE[a]	Transcriptional activity[b]													
	AGM	AP1	AP3	CAS	GSE	INS	LES	ROS	S04	S52	SAP	SIS	OVL	SPL
GATCATCGACAGCCTCC	11	23	13	10	3	24	0	34	0	0	16	46	67	80
GATCATCGGAGGTACTG	1	2	10	0	0	0	0	11	0	9	0	0	16	16
GATCTACGGAGCCATTT	47	11	32	124	108	2	1	48	42	3	18	18	139	213
GATCTCTTTTTTTGGTC	3	0	0	0	0	0	0	17	0	0	0	0	1	0
GATCTGAAGAAACCAAC	22	37	52	16	33	30	8	34	12	10	74	30	17	14
GATCATGCCTAATCTGC	22	13	19	81	1	17	8	59	18	2	4	134	177	119
GATCTGATGCTTGTTGG	7	2	5	0	2	3	3	31	10	0	36	7	1	48
GATCTTTACTTTTTCCT	2	0	9	0	0	2	2	0	0	0	15	74	5	0
GATCTTTATGTTAGTTC	3	0	5	0	0	2	0	0	0	0	2	0	1	0
GATCAAACATGGGTTTC	10	10	15	29	5	6	35	64	12	18	29	6	88	21
GATCTTGTCTTCTTTTG	12	0	1	0	0	8	17	0	0	0	0	0	6	0
GATCTTGTGGCTAAAAA	5	12	0	0	0	2	11	0	0	0	0	0	6	0
GATCTTTACTGGTGAAA	22	7	15	0	0	16	0	0	0	0	8	0	1	1
GATCACCTCTGATTGAG	3	6	12	18	0	5	22	14	0	3	1	0	6	10
GATCCATCATCCATGTT	1	0	0	0	0	2	0	10	0	0	0	0	12	0
GATCTTCATCGGTCACT	9	2	2	0	2	0	3	10	1	0	0	0	1	14
GATCTTCCGCCATCGCT	6	12	10	20	0	3	0	0	3	0	13	9	66	3

Supplementary Table 1

SIGNATURE[a]	Transcriptional activity[b]													
	AGM	AP1	AP3	CAS	GSE	INS	LES	ROS	S04	S52	SAP	SIS	OVL	SPL
GATCCGGTTAAAATTCC	35	59	19	174	90	39	11	212	33	11	48	16	12	50
GATCCGATTCGTTCTCT	1	0	3	0	16	5	0	0	0	0	18	0	2	0
GATCCGCCATGGAAGGA	3	12	1	0	0	0	0	0	0	0	6	0	1	21
GATCGTCTCTTCTTCTT	3	0	0	0	0	2	0	0	0	0	5	0	2	0
GATCAAGTTTAGTGCCT	14	17	33	0	0	8	9	15	3	0	0	34	41	20
GATCAATTCGCTTAACT	4	19	11	0	0	5	3	16	0	0	17	8	34	21
GATCGTTACTCACTCCA	5	1	0	1	0	5	0	0	0	0	0	0	1	0
GATCTACAATTTTGACG	9	8	18	59	0	6	47	35	1	9	13	73	45	7
GATCTTGAAGGTAGCCT	6	21	20	0	0	24	2	2	10	0	0	0	3	0
GATCCCATAGCAGGCCG	5	2	0	16	0	0	0	0	0	0	0	74	2	1
GATCCCCAGGACTTATG	13	15	5	6	0	8	19	3	163	22	14	74	61	3
GATCTCCATACTTGGCT	9	4	0	0	0	8	0	0	0	1	5	14	9	0
GATCCTCCTAGGAGAGG	4	27	28	5	6	6	63	45	43	2	41	11	2	34
GATCCTCTCAAAACCGC	6	6	0	0	0	0	0	2	0	25	0	0	3	2
GATCTTAATGGTCTTTG	1	5	6	0	10	0	26	9	0	30	0	0	5	0
GATCAATTCTTCTCTCA	1	1	5	81	0	7	1	0	0	0	0	6	9	12
GATCTTCGAGATACCGG	1	0	0	0	2	17	0	0	0	0	0	0	1	0

Supplementary Table 1

SIGNATURE[a]	Transcriptional activity[b]													
	AGM	AP1	AP3	CAS	GSE	INS	LES	ROS	S04	S52	SAP	SIS	OVL	SPL
GATCATTGGATTGTCTC	1	0	5	0	0	0	6	0	0	0	8	0	32	1
GATCCAAAGAAGTGACA	3	1	0	0	0	0	0	2	0	0	14	33	6	0
GATCAAGTTTGCTTCTG	5	2	4	0	0	0	0	15	0	0	0	0	69	6
GATCAATGTCCAAGGAC	2	0	0	0	0	0	0	0	0	0	0	0	21	0
GATCCTTCGCCGGGATA	1	0	0	0	0	2	2	3	0	0	0	0	14	0
GATCCTTCTCTTTTTCT	1	0	0	0	0	0	0	2	0	0	0	0	12	0
GATCTTGGTCTGTGGTG	2	2	1	0	0	4	0	7	0	0	3	0	6	0
GATCGAAGTTCATAGGT	4	0	0	0	1	0	1	2	0	9	0	29	2	0
GATCCTTCTGAGCCTTC	1	11	6	3	22	2	8	6	0	0	0	7	6	4
GATCGTTGGTTGCGTTT	1	0	0	0	0	0	6	2	1	0	3	0	5	83
GATCATCAACTCAATCA	6	4	2	0	31	5	0	0	1	0	0	0	6	0
GATCTTGACTGGTCTGA	1	2	6	0	0	0	0	2	0	0	0	34	15	8
GATCTAAGTAGATTCGG	45	114	313	80	281	35	70	229	46	93	205	0	435	390
GATCTATTGTGAGTTTC	2	2	4	0	0	0	0	4	0	0	0	2	7	0
GATCTCATGGAGTGTAG	3	0	0	0	0	0	0	0	0	0	0	0	9	0
GATCAAAGCCACCAAGT	1	1	0	0	0	0	0	1	0	0	0	0	16	6
GATCAAATACTCAGAGA	3	3	13	3	0	3	0	0	0	0	0	0	2	0

Supplementary Table 1

SIGNATURE[a]	Transcriptional activity[b]													
	AGM	AP1	AP3	CAS	GSE	INS	LES	ROS	S04	S52	SAP	SIS	OVL	SPL
GATCCGTAGTGGGTTGC	1	4	3	2	5	6	0	0	0	0	2	4	1	0
GATCCAGCTTGAGGGGG	1	0	0	0	0	0	0	0	0	0	0	0	40	0
GATCGGAGTCGAAATCA	1	3	2	0	2	0	3	0	0	0	16	0	5	10
GATCTGCAAATCGGTAG	3	4	15	39	3	9	0	0	0	0	0	0	63	50
GATCTGCGACTGAAATA	8	1	3	0	0	3	2	0	0	4	0	0	8	0
GATCCAAAGCAGAAGAT	0	2	6	7	0	0	3	0	0	12	0	0	12	17
GATCTGAGCCAAAACCG	0	19	1	0	0	8	0	0	0	0	11	24	8	25
GATCCACAACCGTGGTT	0	3	0	0	0	0	0	0	0	0	0	0	8	0
GATCCGTTCAATCAACA	0	2	0	0	0	5	0	3	0	0	0	0	1	0
GATCCCTCGCAAAAAAT	0	5	1	0	0	0	0	0	0	0	0	0	3	0
GATCCCTCTCCTGAATT	0	2	2	1	3	0	0	4	0	0	0	0	47	1
GATCCGACTCCTACGAA	0	2	0	0	0	20	0	0	0	0	16	0	1	0
GATCCGGCATTAGTCGT	0	1	19	50	0	0	0	0	0	0	0	0	11	15
GATCTGTCTTAGTCCCC	0	15	8	7	1	14	0	5	0	38	7	4	56	103
GATCAGCCTTAGTCACG	0	3	0	0	0	0	0	0	0	0	0	0	9	0
GATCGCGTTTTGAAGGA	0	2	5	0	14	2	1	0	0	0	0	0	9	0
GATCGGCTTTCGTCCAA	0	2	0	24	0	0	0	0	3	0	0	0	2	0

Supplementary Table 1

SIGNATURE[a]	Transcriptional activity[b]													
	AGM	AP1	AP3	CAS	GSE	INS	LES	ROS	S04	S52	SAP	SIS	OVL	SPL
GATCATACCTAAGCAAA	0	2	3	0	1	9	0	0	0	0	0	0	25	0
GATCGCAGCCATGTTCC	0	3	0	0	14	0	0	20	0	0	9	10	24	6
GATCGGAAAACAAATTG	0	2	24	0	0	2	5	0	10	0	8	0	2	0
GATCGGAAAACTTTGAA	0	4	6	5	0	0	2	2	10	1	1	20	1	0
GATCGGAGAAAAAGGAT	0	3	0	14	8	0	0	10	0	0	1	0	3	9
GATCTAGTCTCCAAGAT	0	2	0	3	0	0	0	0	0	0	0	0	4	0
GATCTCATCTGAACCAC	0	2	6	8	0	0	0	2	0	0	2	35	4	0
GATCTTGCTTGAACCAA	0	15	18	0	0	25	20	11	0	20	17	38	5	0
GATCCAATCAGAGTCAA	0	7	0	3	0	0	0	0	0	0	8	0	12	0
GATCTGTTTATCAGTTC	0	3	2	0	0	0	5	31	0	0	1	12	18	0
GATCTTCCCTCGGGTAC	0	2	7	7	0	1	0	0	0	0	0	11	19	3
GATCTTCTACTGTTGCC	0	4	0	3	0	0	0	0	0	0	0	0	12	0
GATCTTGAAACTGTCGG	0	2	0	13	3	6	0	2	0	0	0	0	12	0
GATCCAGCGTGGTGGAC	0	6	0	0	0	0	0	0	0	0	24	0	1	0
GATCTCCACTGCAGTGA	0	5	0	0	0	0	0	0	0	0	0	0	16	2
GATCAGTGAAACGAGAA	0	1	0	0	1	0	0	0	0	0	0	0	1	1
GATCTCTCTGTACAGTT	0	5	2	12	2	10	3	16	0	0	1	0	38	63

Supplementary Table 1

SIGNATURE[a]	Transcriptional activity[b]													
	AGM	AP1	AP3	CAS	GSE	INS	LES	ROS	S04	S52	SAP	SIS	OVL	SPL
GATCTCTTCACTAAGCT	0	3	15	0	0	12	0	0	0	0	2	105	134	32
GATCTCGGTGTGGGTGG	0	2	0	0	0	0	0	0	0	0	0	0	22	0
GATCCACGTTCGGTTGA	0	1	0	10	0	0	0	0	14	0	2	5	1	1
GATCCAAAAGCCTGCGG	0	2	0	9	4	0	0	3	12	0	0	16	13	11
GATCTACAAAACTTCAG	0	1	0	0	0	0	0	0	0	0	0	0	26	3
GATCCAAGAAACAAGTT	0	2	3	0	0	0	4	2	0	0	0	0	3	0
GATCTTCCTATACAAGT	0	1	1	0	0	2	0	10	0	0	20	0	2	0
GATCTTGTTGTCTCGGG	0	5	0	0	44	2	0	0	0	1	2	0	1	0
GATCCCTACATGGCTTG	0	2	0	8	0	0	2	0	0	0	0	0	29	38
GATCACTCCTCTCTGAT	0	1	0	21	0	0	39	3	0	0	0	0	24	0
GATCTCTCGCTCTCTCC	0	1	0	0	0	0	3	2	0	0	0	0	7	33
GATCAAATGGTATCACC	0	2	3	0	0	1	0	0	0	0	2	0	6	0
GATCCTTCGATGTCAAT	0	1	2	35	0	0	1	8	0	16	0	0	2	0
GATCTTCGTTTGAGTTG	0	1	0	3	0	2	8	0	0	0	6	0	1	0
GATCACTTTTACGCTTG	0	1	0	0	0	0	0	0	0	0	0	0	9	0
GATCAGTTCGCCCTTTC	0	1	0	0	0	0	0	0	0	0	0	0	6	3
GATCGACAAGTCCAGAG	0	2	1	0	0	2	6	0	0	0	0	0	4	10

Supplementary Table 1

SIGNATURE[a]	Transcriptional activity[b]													
	AGM	AP1	AP3	CAS	GSE	INS	LES	ROS	S04	S52	SAP	SIS	OVL	SPL
GATCCACTGCCAGGTCA	0	2	6	0	0	0	0	0	0	0	0	2	25	6
GATCAAAGCTCAAGGTA	0	5	0	0	0	2	0	0	0	0	25	0	2	0
GATCGGTTCGAGAGTCG	0	4	4	13	18	1	3	29	0	3	18	0	44	46
GATCGGCGGCGGCTAAT	0	1	0	0	0	0	0	0	0	0	2	0	1	0
GATCACGAGTAGAGAGA	0	1	4	0	1	0	0	0	0	0	0	0	2	0
GATCGGCGATAAGTTAA	0	0	1	0	0	0	0	6	0	0	0	0	1	1
GATCCGTACGGTTGCTA	0	0	3	0	0	0	4	19	0	0	6	4	4	0
GATCACAAAGAGTTTCT	0	0	2	0	0	0	0	0	0	0	0	0	2	0
GATCACACTCGACAAAA	0	0	4	0	0	3	0	0	0	0	0	0	6	0
GATCCTATACTTCTTTA	0	0	22	0	0	9	0	0	0	0	30	0	5	0
GATCTTTTTTGATAGCT	0	0	30	75	0	1	0	0	0	0	49	3	15	10
GATCAAACATCTAGTTA	0	0	1	0	0	1	28	16	0	0	0	38	2	0
GATCTGGGTTCTTGTTG	0	0	1	0	0	0	0	2	0	0	38	0	2	0
GATCAGAATCTGGAAAT	0	0	4	0	0	0	0	2	0	0	0	0	12	0
GATCAGAAATCTCAGTT	0	0	3	0	0	0	0	0	0	3	0	0	28	0
GATCATAGCGAGATTGA	0	0	5	1	0	0	0	0	0	0	3	6	5	0
GATCCGACAGAACCCGA	0	0	4	0	0	0	0	0	0	0	0	3	1	0

Supplementary Table 1

SIGNATURE[a]	Transcriptional activity[b]													
	AGM	AP1	AP3	CAS	GSE	INS	LES	ROS	S04	S52	SAP	SIS	OVL	SPL
GATCTGAGTTATGGATT	0	0	6	0	0	0	4	0	0	0	0	0	2	0
GATCAGCTATGGCTAAG	0	0	2	0	2	1	0	2	0	14	0	0	5	7
GATCGGTGTGTGTTGCA	0	0	2	0	0	1	0	0	0	0	35	0	19	5
GATCATCCACACGACCT	0	0	1	0	0	0	0	4	1	1	0	0	4	0
GATCTGCAAAAGAAGAA	0	0	5	0	4	1	0	0	0	0	0	0	30	0
GATCATTGTGAGGAATC	0	0	2	0	0	0	0	0	0	0	0	0	48	0
GATCCAACTCACAACTC	0	0	1	0	0	0	0	0	0	0	0	0	18	0
GATCCTAATGGGTGGTG	0	0	2	0	0	0	0	0	0	0	0	0	8	0
GATCCTGAATATACCGA	0	0	2	30	11	0	8	0	0	0	0	0	1	19
GATCGTTCTAATGACCA	0	0	1	0	0	0	0	2	0	3	0	13	1	0
GATCTATAACAACTGAC	0	0	1	0	0	1	0	0	0	0	0	0	8	0
GATCAGTTGTTCACTTT	0	0	5	0	0	0	0	0	0	0	0	0	1	1
GATCTGAACAATTGTGG	0	0	0	0	0	0	0	0	0	0	0	0	20	0
GATCTGGTGTTGTTGGG	0	0	0	8	0	0	0	0	0	0	0	0	5	2
GATCTGTGTTACCAAAC	0	0	0	0	3	0	15	0	0	0	0	0	4	0
GATCTTCATAAACTTTT	0	0	0	1	0	0	0	0	0	0	0	0	54	0
GATCTTCGATAACCTTT	0	0	0	0	0	3	0	5	0	0	0	1	11	0

Supplementary Table 1

SIGNATURE[a]	Transcriptional activity[b]													
	AGM	AP1	AP3	CAS	GSE	INS	LES	ROS	S04	S52	SAP	SIS	OVL	SPL
GATCTTCTCCTTCTTCC	0	0	0	2	0	0	0	0	0	0	0	0	1	0
GATCCAGCTTTAGTCGT	0	0	0	3	0	1	4	0	0	0	0	0	7	0
GATCCTTGAGAAATCTG	0	0	0	0	0	0	1	25	7	0	0	4	6	2
GATCGGCCAGTGGAAAG	0	0	0	0	0	0	0	1	0	0	0	0	3	5
GATCAGAGAAACCACTT	0	0	0	0	0	0	0	0	0	0	0	0	1	0
GATCAGCTTTTTCTTTT	0	0	0	0	0	0	0	3	0	0	0	0	2	0
GATCTCACTTGTTTCAA	0	0	0	0	0	0	9	0	0	0	0	0	1	0
GATCTCGAACGCTACCG	0	0	0	0	0	0	0	0	0	0	0	0	24	0
GATCCTTGGTTATTCTC	0	0	0	0	0	0	0	18	0	0	0	0	3	0
GATCATAGATGTGTGTA	0	0	0	8	8	2	0	0	0	0	0	0	3	0
GATCCCTCATTAGCCAA	0	0	0	0	0	5	0	0	0	0	0	0	1	15
GATCGGTTTCAGATTTG	0	0	0	0	0	0	0	0	0	0	0	16	9	9
GATCCTTTGGTTTTTCT	0	0	0	0	0	0	0	0	0	0	0	0	2	0
GATCGAACTTTGAGGCT	0	0	0	0	0	3	0	0	0	0	0	0	19	7
GATCCACTCGCACAAAG	0	0	0	0	0	0	0	0	0	0	0	0	1	0
GATCTCTGCAAAATCAG	0	0	0	3	0	1	0	0	0	0	0	0	1	0
GATCAATGCAAGGAAAA	0	0	0	0	0	0	0	0	0	0	0	0	16	0

Supplementary Table 1

SIGNATURE[a]	Transcriptional activity[b]													
	AGM	AP1	AP3	CAS	GSE	INS	LES	ROS	S04	S52	SAP	SIS	OVL	SPL
GATCCTCTCTTGCTCTC	0	0	0	1	0	0	0	0	0	0	0	0	1	11
GATCAAGCTTCGGTTGT	0	0	0	5	0	0	7	0	0	0	0	0	2	28
GATCCGCTTTGCAGCTT	0	0	0	24	0	0	1	1	0	0	0	0	1	0
GATCCTTTGTTTCTCGC	0	0	0	4	0	0	0	0	0	0	0	0	1	0
GATCGATAGGAGCATAC	0	0	0	2	0	0	0	16	16	1	0	0	2	5
GATCTGATGTAGACATG	0	0	0	2	0	0	0	0	0	0	0	0	1	0
GATCAGCCGGCAACGTC	0	0	0	6	0	0	50	0	33	0	22	105	148	89
GATCTATGTTAGTGTTG	0	0	0	20	0	1	0	2	0	0	0	0	11	0
GATCTAGATTCTTCCGC	0	0	0	2	24	3	3	4	0	0	0	0	5	0
GATCAGTGTGAGAAACA	0	0	0	1	0	1	0	0	0	0	0	0	8	0
GATCAGCCATGGAGGAC	0	0	0	0	66	18	0	6	1	32	0	0	29	2
GATCTGCTCTATTACTG	0	0	0	0	4	0	0	18	0	0	0	0	2	0
GATCATCAAACCTTCAT	0	0	0	0	4	0	0	6	0	0	0	0	18	0
GATCGCTATGACTATAG	0	0	0	0	36	1	0	0	16	5	0	0	2	0
GATCACGTTGGAACTGT	0	0	0	0	1	3	0	0	0	0	12	0	1	0
GATCGACTCGATTTTGT	0	0	0	0	0	0	0	0	0	0	0	0	4	0
GATCTTCTCTGTTTTGA	0	0	0	0	0	3	0	0	0	0	3	0	35	0

Supplementary Table 1

SIGNATURE[a]	Transcriptional activity[b]													
	AGM	AP1	AP3	CAS	GSE	INS	LES	ROS	S04	S52	SAP	SIS	OVL	SPL
GATCTCTGAGGCCTTTT	0	0	0	0	0	0	0	0	0	0	0	0	18	0
GATCCAATGCTTTTCAA	0	0	0	0	0	0	0	0	0	0	0	0	18	0
GATCACAACGGTCATTA	0	0	0	0	0	0	0	0	0	0	0	0	25	0
GATCCTTGTTTTACTCC	0	0	0	0	0	4	0	0	0	0	0	0	9	0
GATCACAACCGTTGGTT	0	0	0	0	0	2	0	0	0	0	0	0	27	0
GATCCTGTCTCCCTAGA	0	0	0	0	0	3	0	0	0	0	2	12	44	0
GATCTGAGTTTGAGGCT	0	0	0	0	0	0	0	0	0	0	0	5	6	0
GATCTACGTCGATGCGC	0	0	0	0	0	0	0	3	0	0	0	0	1	0
GATCCACCAAATCTTGA	0	0	0	0	0	0	0	7	0	0	0	0	9	0
GATCACTGACGGTATCT	0	0	0	0	0	0	3	0	0	0	0	0	30	0
GATCAGGAAAGGTCAAG	0	0	0	0	0	0	3	0	0	0	0	0	53	15
GATCTAGAGACGCAATT	0	0	0	0	0	0	4	0	0	0	0	10	2	0
GATCAGAACCAAGTCAG	0	0	0	0	0	0	0	0	1	0	0	0	4	9
GATCCAGATGAACTCTT	0	0	0	0	0	0	0	0	0	0	0	0	9	0
GATCTCTCCGGTCGATT	0	0	0	0	0	0	0	0	0	0	8	0	9	0
GATCCATATCTCAGTAT	0	0	0	0	0	0	0	0	0	0	0	0	1	0
GATCAATTCCAATGTGC	0	0	0	0	0	0	0	0	0	0	0	26	2	0

Supplementary Table 1

SIGNATURE[a]	Transcriptional activity[b]													
	AGM	AP1	AP3	CAS	GSE	INS	LES	ROS	S04	S52	SAP	SIS	OVL	NZZ
GATCCTCTGTGTGTGTG	0	0	0	0	0	0	0	0	0	0	10	2	22	0
GATCACTTTTTTTTTTG	0	0	0	0	0	0	0	0	0	7	0	0	28	0
GATCTTTTGTTCACCTA	0	0	0	0	0	0	0	2	0	0	5	3	190	0
GATCACGTTTGATTAGC	0	0	0	0	0	0	0	1	0	0	0	0	2	17
GATCCATTTGGTTGACT	0	0	0	0	0	0	0	20	0	0	0	0	2	0
GATCTCATTGGGCCGGG	0	0	0	0	0	0	0	24	0	0	4	0	14	7
GATCAAGGCAGTGGATT	0	0	0	0	0	0	0	3	0	0	1	0	4	0
GATCTGTTAAGGGTTGG	0	0	0	0	0	0	0	0	0	0	2	0	13	0
GATCGATGTCGCGGTGG	0	0	0	0	0	0	0	0	0	0	0	0	1	0
GATCAAGACAGCCAAAA	0	0	0	0	0	0	0	0	0	0	0	0	8	0
GATCATGCATAAGGTCG	0	0	0	0	0	0	0	0	0	0	0	0	9	52
GATCCGGCTTGACACGC	0	0	0	0	0	0	0	0	0	0	0	0	1	11
GATCGTTGTGGTTCTTT	0	0	0	0	0	0	0	0	0	0	0	0	6	5
GATCCTGCGCTGAAGGA	0	0	0	0	0	0	0	0	0	0	0	0	21	11
GATCCTTCGACGGTTCT	0	0	0	0	0	0	0	0	0	0	0	0	9	12
GATCGATAAAAACTTCA	0	0	0	0	0	0	0	0	0	0	0	0	6	1
GATCACAAAAGAGGTGA	0	0	0	0	0	0	0	0	0	0	0	0	45	4

Supplementary Table 1

SIGNATURE[a]	Transcriptional activity[b]													
	AGM	AP1	AP3	CAS	GSE	INS	LES	ROS	S04	S52	SAP	SIS	OVL	SPL
GATCCGCTTTAACTTAA	0	0	0	0	0	0	0	0	0	0	0	0	42	1
GATCCATATGTGGTGGG	0	0	0	0	0	0	0	0	0	0	0	0	9	0
GATCTCTTGATAAGGCT	0	0	0	0	0	0	0	0	0	0	0	0	5	0
GATCAGACAGCAGTGCT	0	0	0	0	0	0	0	0	0	0	0	0	60	0
GATCATCTCGGCCCATG	0	0	0	0	0	0	0	0	0	0	0	0	40	0
GATCATGTCCGTCGCCG	0	0	0	0	0	0	0	0	0	0	0	0	12	0
GATCCACGTTGTCGGAA	0	0	0	0	0	0	0	0	0	0	0	0	6	0
GATCCATACCCTTTGCA	0	0	0	0	0	0	0	0	0	0	0	0	7	0
GATCCTGCGTTCTTGAG	0	0	0	0	0	0	0	0	0	0	0	0	6	0
GATCGTTCCTGGAGTAC	0	0	0	0	0	0	0	0	0	0	0	0	19	0
GATCTGTTGTGGGTTGG	0	0	0	0	0	0	0	0	0	0	0	0	4	0

Supplementary Table 2

Supplementary table 2 . *sporocyteless* ovules signatures from unnanotated regions.

[a]MPSS 17pb signatures.

[b]Activity in transcripts per Million. AGM. *agamous* infloresence.AP1. *apetala1-10* infloresence. AP3. *apetala3-6* infloresence. CAS. Callus. GSE. Germinating seedlings. INS. Infloresences. LES. Leaves. ROS. Roots. S04. Leaves, 4 hr after salicylic acid treatment. S52. Leaves, 52 hr after salicylic acid treatment. SAP. *superman/apetala* infloresence. SIS. Siliques. OVL. Wild type ovules.SPL. *sporocyteless* ovules.

SIGNATURE[a]	Transcriptional activity[b]													
	AGM	AP1	AP3	CAS	GSE	INS	LES	ROS	S04	S52	SAP	SIS	OVL	SPL
GATCTATGGAATCGAGT	4	3	7	14	0	0	30	13	0	13	0	21	0	1
GATCTGCAAGACGAAAA	208	135	103	42	19	263	221	951	163	267	83	34	183	120
GATCTGCTTTTGTCGCA	12	0	1	0	5	0	5	2	0	1	0	0	9	7
GATCCAAACCTAATACC	13	5	1	50	0	5	30	0	0	3	3	29	30	16
GATCTGTTGTTGGACCT	18	46	61	0	13	12	32	21	51	23	26	23	95	10
GATCTTATCGGCCGGCA	2	0	4	0	0	1	0	8	5	44	10	0	0	8
GATCTTCCCTTTTCTTG	20	1	19	17	0	0	0	7	0	0	0	35	3	26
GATCTTCGCAAGAGAAT	1	2	0	0	2	0	0	0	0	7	2	0	0	2
GATCTTCGTTGGTGACC	1	2	0	5	0	3	3	22	0	3	1	0	7	11
GATCCATCAGGGGAGGA	14	7	4	21	0	3	0	6	3	0	0	1	14	35
GATCTTGTGGATGCCCT	3	10	7	31	0	3	12	13	0	0	0	2	29	37
GATCTTGTTGGTGGCAG	13	12	8	14	0	7	0	6	0	24	0	6	163	38
GATCCCAAGATGCTGAG	9	12	4	105	0	2	34	1	0	0	1	60	5	19

Supplementary Table 2

SIGNATURE[a]	Transcriptional activity[b]													
	AGM	AP1	AP3	CAS	GSE	INS	LES	ROS	S04	S52	SAP	SIS	OVL	SPL
GATCTTGTTTCCGACGA	13	28	35	15	80	43	4	25	6	14	10	19	72	25
GATCCCATCTGGGAACG	4	16	16	12	0	3	2	6	7	0	19	0	5	3
GATCCCCAATGATTTTC	5	2	9	60	0	2	1	31	3	40	17	0	42	2
GATCCCGAAAACTAACC	51	38	18	10	65	22	1	18	14	53	80	52	260	167
GATCCCTTGAGCAAAAC	6	0	2	0	0	0	0	0	0	0	0	0	0	1
GATCCGAATCAATTCTC	3	5	4	0	0	1	0	0	0	0	0	10	27	1
GATCCGATGCGAACAAT	21	24	5	16	27	3	0	34	7	0	63	0	0	14
GATCAAAACTCCAACAG	6	2	9	29	0	13	0	2	4	17	0	0	1	39
GATCAAAAGTTCCAAAC	5	0	0	0	20	0	1	0	0	0	0	0	0	1
GATCCTAACCGTTGTCC	60	35	26	138	0	82	42	80	17	40	48	81	60	65
GATCCTAAGCTCATGAA	9	8	24	29	0	12	3	6	0	1	35	4	19	3
GATCCTCTCAGCTATTC	20	29	5	0	0	10	6	0	0	5	46	96	317	39
GATCATTGGTTCTTGCA	1	3	2	3	0	0	0	0	0	0	0	0	0	2
GATCAACGATTCCATCC	9	0	6	0	0	0	19	0	0	0	4	15	5	3
GATCCTGAAGATTAAGT	10	7	8	61	0	11	2	43	0	0	0	12	1	2
GATCAAGACTTGACTCT	43	16	28	0	2	36	2	28	11	0	7	16	0	6
GATCCTGTCAACGAACC	14	10	5	15	0	13	24	24	0	5	0	5	57	21
GATCCTTCCCTTGGAAT	8	7	2	0	0	4	0	0	0	2	37	0	43	16

Supplementary Table 2

SIGNATURE[a]	Transcriptional activity[b]													
	AGM	AP1	AP3	CAS	GSE	INS	LES	ROS	S04	S52	SAP	SIS	OVL	SPL
GATCAAGTTTCAGAGTC	2	2	0	0	18	2	0	0	0	0	12	0	38	23
GATCAATAAAGTGTGCC	33	2	10	92	0	4	66	23	7	4	0	89	27	65
GATCCTTGTTTCCCTTT	23	57	77	25	2	66	9	60	42	7	22	22	35	18
GATCCTTTCTTGGCGAA	11	2	10	0	0	3	3	0	0	0	6	0	51	57
GATCCGACTACATCAAG	9	1	0	0	0	0	0	0	0	0	0	0	0	5
GATCCGCTTGAGACTGG	3	0	5	0	0	5	1	0	0	0	26	0	0	36
GATCAATGCCAAGTCTC	23	7	24	63	0	9	1	34	4	1	2	65	94	87
GATCACAACCAACGAAA	3	4	0	0	0	0	0	0	5	1	0	0	1	1
GATCACAGTCACTTGCT	16	17	23	0	53	13	62	0	12	37	16	43	21	6
GATCCTTTTGACAGGAC	11	4	15	29	0	3	0	4	0	0	7	6	12	16
GATCCTTTTGACCATCC	17	2	2	8	0	7	20	0	0	2	45	27	0	38
GATCCGGTGGAGCAAGA	2	0	0	0	0	4	0	0	1	0	0	0	0	5
GATCCTAACGACGTCGT	1	1	0	0	0	0	3	2	0	0	31	0	0	20
GATCGAATCCAATATCT	7	0	0	0	0	3	0	2	0	0	0	0	0	1
GATCGACGGTGGTTAGT	171	59	44	287	9	22	36	24	25	16	109	56	121	116
GATCACCAAAATCAGGA	9	4	27	0	2	17	12	18	12	3	0	3	69	5
GATCACCATCTTGTTCG	7	16	1	0	7	13	1	29	0	0	2	1	23	6
GATCGAGGTCTCTCTTT	13	4	10	9	9	10	1	26	4	18	0	0	24	17

Supplementary Table 2

SIGNATURE[a]	Transcriptional activity[b]													
	AGM	AP1	AP3	CAS	GSE	INS	LES	ROS	S04	S52	SAP	SIS	OVL	SPL
GATCGCAAGACTCGTGC	43	58	44	95	43	36	29	186	3	15	28	51	131	160
GATCGAAACCTTCGCAA	2	0	0	0	0	0	5	34	0	0	2	0	0	12
GATCGACATTGTATCTC	1	0	2	0	0	0	0	0	0	0	0	0	0	2
GATCGGACTATGCAAAT	2	0	0	0	2	13	0	2	0	13	0	0	0	2
GATCACTCTTCAACCAA	3	1	4	52	0	0	8	17	0	2	0	15	41	15
GATCGGGGATTGGGAGA	3	0	0	0	0	0	0	0	44	0	0	0	0	1
GATCGGTTTCGTGGCTG	7	0	0	0	0	0	0	0	0	0	0	0	1	1
GATCGGAAGCGTCGATG	12	12	36	63	3	22	21	64	19	0	6	46	22	145
GATCGGAAGTTTGCTCA	41	95	31	29	0	27	10	27	21	17	30	15	45	73
GATCGGCAAAGGTGGAG	13	0	5	191	11	19	3	0	0	0	0	0	0	36
GATCGGCGGAAGGGAAA	10	2	0	19	0	0	0	0	0	0	0	0	0	1
GATCGTCGACTCCTTGT	472	280	318	119	31	277	235	321	157	227	106	137	414	220
GATCGTCGTGTCAAGGC	28	0	0	0	11	0	0	0	0	0	0	0	0	12
GATCATCGACAGCCTCC	11	23	13	10	3	24	0	34	0	0	16	46	67	80
GATCATCGGAGGTACTG	1	2	10	0	0	0	0	11	0	9	0	0	16	16
GATCTACGGAGCCATTT	47	11	32	124	108	2	1	48	42	3	18	18	139	213
GATCTGAAAAGCAAGGA	16	19	0	0	0	0	0	3	0	5	0	0	0	4
GATCTGAAGAAACCAAC	22	37	52	16	33	30	8	34	12	10	74	30	17	14

Supplementary Table 2

SIGNATURE[a]	Transcriptional activity[b]													
	AGM	AP1	AP3	CAS	GSE	INS	LES	ROS	S04	S52	SAP	SIS	OVL	SPL
GATCATGCCTAATCTGC	22	13	19	81	1	17	8	59	18	2	4	134	177	119
GATCTGATGCTTGTTGG	7	2	5	0	2	3	3	31	10	0	36	7	1	48
GATCAAACATGGGTTTC	10	10	15	29	5	6	35	64	12	18	29	6	88	21
GATCTTTACTGGTGAAA	22	7	15	0	0	16	0	0	0	0	8	0	1	1
GATCACCTCTGATTGAG	3	6	12	18	0	5	22	14	0	3	1	0	6	10
GATCACGGAGACTGAGT	3	2	0	0	0	0	1	4	0	0	0	0	0	4
GATCTTCATCGGTCACT	9	2	2	0	2	0	3	10	1	0	0	0	1	14
GATCTTCCGCCATCGCT	6	12	10	20	0	3	0	0	3	0	13	9	66	3
GATCCGGTTAAAATTCC	35	59	19	174	90	39	11	212	33	11	48	16	12	50
GATCCGCCATGGAAGGA	3	12	1	0	0	0	0	0	0	0	6	0	1	21
GATCAGCAGAAGAAAGA	7	25	0	0	0	0	0	0	0	3	10	26	0	2
GATCAAGTTTAGTGCCT	14	17	33	0	0	8	9	15	3	0	0	34	41	20
GATCAATTCGCTTAACT	4	19	11	0	0	5	3	16	0	0	17	8	34	21
GATCTCTCTGCCTAAAA	2	2	0	0	0	5	3	0	0	0	0	0	0	2
GATCGTTTTTTCCAATT	3	0	4	6	2	0	0	6	0	6	0	0	0	18
GATCTAAGAACTTGGAA	3	1	12	0	0	0	0	0	0	1	34	0	0	2
GATCTAAGTTGCTTGAA	10	9	0	0	16	0	0	25	2	0	0	0	0	2
GATCTACAATTTTGACG	9	8	18	59	0	6	47	35	1	9	13	73	45	7

Supplementary Table 2

SIGNATURE[a]	Transcriptional activity[b]													
	AGM	AP1	AP3	CAS	GSE	INS	LES	ROS	S04	S52	SAP	SIS	OVL	SPL
GATCCCATAGCAGGCCG	5	2	0	16	0	0	0	0	0	0	0	74	2	1
GATCCCCAGGACTTATG	13	15	5	6	0	8	19	3	163	22	14	74	61	3
GATCCTCCTAGGAGAGG	4	27	28	5	6	6	63	45	43	2	41	11	2	34
GATCCTCTCAAAACCGC	6	6	0	0	0	0	0	2	0	25	0	0	3	2
GATCAATTCTTCTCTCA	1	1	5	81	0	7	1	0	0	0	0	6	9	12
GATCTTCTCATCTACCC	1	0	3	6	0	0	0	0	0	0	2	0	0	6
GATCATTGGATTGTCTC	1	0	5	0	0	0	6	0	0	0	8	0	32	1
GATCCAAAGCAACCTCA	1	3	0	0	0	0	0	3	0	0	0	0	0	28
GATCAAGTTTGCTTCTG	5	2	4	0	0	0	0	15	0	0	0	0	69	6
GATCATTGTTTCTGGTG	1	0	4	0	0	5	0	10	0	0	0	11	0	12
GATCTTCTGAAACTGGG	3	19	5	45	2	3	0	5	0	0	6	1	0	8
GATCCTTCTGAGCCTTC	1	11	6	3	22	2	8	6	0	0	0	7	6	4
GATCGTTGGTTGCGTTT	1	0	0	0	0	0	6	2	1	0	3	0	5	83
GATCGGAGGCTGGAGAG	1	2	0	3	3	3	0	0	0	0	0	0	0	6
GATCTTGACTGGTCTGA	1	2	6	0	0	0	0	2	0	0	0	34	15	8
GATCTAAGTAGATTCGG	45	114	313	80	281	35	70	229	46	93	205	0	435	390
GATCTATTTATCCCTGA	2	0	0	0	10	2	0	0	29	11	2	4	0	1

Supplementary Table 2

SIGNATURE[a]	Transcriptional activity[b]													
	AGM	AP1	AP3	CAS	GSE	INS	LES	ROS	S04	S52	SAP	SIS	OVL	SPL
GATCATGAGTTCTCGGA	1	2	9	0	0	0	0	2	0	0	0	0	0	1
GATCAAAGCCACCAAGT	1	1	0	0	0	0	0	1	0	0	0	0	16	6
GATCAAAGGAAGACACC	3	9	3	1	0	3	5	2	0	0	2	0	0	9
GATCTGTGTTGAGAATG	5	26	24	0	5	12	9	34	0	0	6	0	0	1
GATCCGAAAATTTTCCC	2	0	0	0	0	0	0	14	0	0	0	0	0	2
GATCGGAGTCGAAATCA	1	3	2	0	2	0	3	0	0	0	16	0	5	10
GATCCAGTAACTGCTGA	2	16	3	0	0	6	0	0	0	0	0	0	0	3
GATCTGCAAATCGGTAG	3	4	15	39	3	9	0	0	0	0	0	0	63	50
GATCATTGCGTTTGGTT	0	1	3	0	0	4	0	4	0	0	1	0	0	6
GATCCAAAGCAGAAGAT	0	2	6	7	0	0	3	0	0	12	0	0	12	17
GATCCGGTGAGGAAGAA	0	4	1	30	0	0	2	5	0	18	0	0	0	6
GATCTGAGCCAAAACCG	0	19	1	0	0	8	0	0	0	0	11	24	8	25
GATCCCTCTCCTGAATT	0	2	2	1	3	0	0	4	0	0	0	0	47	1
GATCCGGCATTAGTCGT	0	1	19	50	0	0	0	0	0	0	0	0	11	15
GATCTGTCTTAGTCCCC	0	15	8	7	1	14	0	5	0	38	7	4	56	103
GATCCTAGAGGTGCAGG	0	2	2	0	0	4	0	0	0	0	0	0	0	5
GATCGCAGCCATGTTCC	0	3	0	0	14	0	0	20	0	0	9	10	24	6

Supplementary Table 2

SIGNATURE[a]	Transcriptional activity[b]													
	AGM	AP1	AP3	CAS	GSE	INS	LES	ROS	S04	S52	SAP	SIS	OVL	SPL
GATCGGAGAAAAAGGAT	0	3	0	14	8	0	0	10	0	0	1	0	3	9
GATCTGCAACGCGTAAA	0	1	0	14	0	0	0	1	1	0	15	0	0	11
GATCTTCCCTCGGGTAC	0	2	7	7	0	1	0	0	0	0	0	11	19	3
GATCCACGGCAACCTTT	0	19	13	8	0	2	0	7	0	0	44	15	0	13
GATCTCCACTGCAGTGA	0	5	0	0	0	0	0	0	0	0	0	0	16	2
GATCTCTCTGTACAGTT	0	5	2	12	2	10	3	16	0	0	1	0	38	63
GATCTCTTCACTAAGCT	0	3	15	0	0	12	0	0	0	0	2	105	134	32
GATCCACGTTCGGTTGA	0	1	0	10	0	0	0	0	14	0	2	5	1	1
GATCAGTGAAACGAGAA	0	1	0	0	1	0	0	0	0	0	0	0	1	1
GATCATAATCCTGAGTC	0	2	4	0	0	0	0	0	0	0	0	0	0	1
GATCGGACAAAAGTCGC	0	1	0	0	10	0	0	0	0	0	0	0	0	22
GATCGTCTTCTTCTTTC	0	1	5	8	0	0	0	0	0	0	2	0	0	3
GATCCAAAAGCCTGCGG	0	2	0	9	4	0	0	3	12	0	0	16	13	11
GATCTACAAAACTTCAG	0	1	0	0	0	0	0	0	0	0	0	0	26	3
GATCGGGATAAAAACGG	0	2	0	0	0	0	0	0	0	0	0	0	0	25
GATCGGTGAGAATGGGG	0	10	0	0	0	0	0	0	0	0	0	0	0	17
GATCTCGACCGAACTAT	0	1	0	0	0	2	0	0	0	2	15	0	0	7

Supplementary Table 2

SIGNATURE[a]	Transcriptional activity[b]													
	AGM	AP1	AP3	CAS	GSE	INS	LES	ROS	S04	S52	SAP	SIS	OVL	SPL
GATCGTCTCCGAGTCTA	0	4	0	0	0	0	0	0	0	0	0	0	0	3
GATCTTGAAGGGACATT	0	2	15	0	0	24	3	0	2	3	0	0	0	1
GATCCCTACATGGCTTG	0	2	0	8	0	0	2	0	0	0	0	0	29	38
GATCCCTCCAGAGTCCA	0	1	1	0	0	0	3	2	0	0	0	0	0	36
GATCCGTTGGTCGGAAG	0	4	0	0	0	0	0	0	0	0	0	0	0	24
GATCTCTCGCTCTCTCC	0	1	0	0	0	0	3	2	0	0	0	0	7	33
GATCCGCTTCTGAGGCT	0	1	0	77	0	0	0	17	0	0	0	0	0	1
GATCAGTTCGCCCTTTC	0	1	0	0	0	0	0	0	0	0	0	0	6	3
GATCGACAAGTCCAGAG	0	2	1	0	0	2	6	0	0	0	0	0	4	10
GATCCACTGCCAGGTCA	0	2	6	0	0	0	0	0	0	0	0	2	25	6
GATCGAGTGCCTGTAGA	0	4	1	0	0	1	0	0	0	0	10	0	0	1
GATCAAAGACTTGATTT	0	6	9	0	0	0	0	1	0	0	0	0	0	1
GATCTGTAGCTGCTCTC	0	4	0	1	0	0	0	0	3	8	0	15	0	2
GATCCTTTGTTGTTGCG	0	1	0	0	0	0	0	0	0	0	2	0	0	8
GATCGGTTCGAGAGTCG	0	4	4	13	18	1	3	29	0	3	18	0	44	46
GATCAGAACAGACCGCA	0	1	0	0	0	19	0	2	0	0	0	5	0	2
GATCGCTTGGAAGCGTT	0	1	1	0	0	2	7	9	11	0	0	1	0	1

Supplementary Table 2

SIGNATURE[a]	Transcriptional activity[b]													
	AGM	AP1	AP3	CAS	GSE	INS	LES	ROS	S04	S52	SAP	SIS	OVL	SPL
GATCAACGCAGACAATT	0	1	0	0	0	0	0	0	0	0	0	0	0	12
GATCTCTCAGGAAATGC	0	1	1	0	0	0	0	0	0	0	15	2	0	1
GATCCGCTCGATGGGCG	0	0	3	0	0	3	0	0	0	0	0	0	0	14
GATCGGCGATAAGTTAA	0	0	1	0	0	0	0	6	0	0	0	0	1	1
GATCATGTCTCGGTCCA	0	0	5	0	0	3	0	0	0	0	0	0	0	2
GATCTTTTTTGATAGCT	0	0	30	75	0	1	0	0	0	0	49	3	15	10
GATCTGAGCCTTCCTCT	0	0	2	103	0	0	1	10	0	0	0	0	0	7
GATCTGTCATGCCCAGT	0	0	2	0	0	0	0	0	0	0	0	0	0	11
GATCCTTATCAAAACCG	0	0	1	0	0	0	0	0	0	0	0	0	0	17
GATCAGCTATGGCTAAG	0	0	2	0	2	1	0	2	0	14	0	0	5	7
GATCTTTTCCCGAACCT	0	0	3	3	0	0	0	0	0	0	7	0	0	11
GATCGGTGTGTGTTGCA	0	0	2	0	0	1	0	0	0	0	35	0	19	5
GATCCCGGAGAAAGTTG	0	0	5	0	5	1	0	6	0	4	0	0	0	12
GATCCTGAATATACCGA	0	0	2	30	11	0	8	0	0	0	0	0	1	19
GATCTGAGGAACAGAAG	0	0	5	0	0	0	0	3	0	0	1	0	0	6
GATCAACAACGCTCAAG	0	0	2	0	0	0	0	6	0	0	0	0	0	23
GATCAGTAAAGTCTCCA	0	0	1	0	6	0	1	0	0	0	0	0	0	2
GATCAGTTGTTCACTTT	0	0	5	0	0	0	0	0	0	0	0	0	1	1

Supplementary Table 2

SIGNATURE[a]	Transcriptional activity[b]													
	AGM	AP1	AP3	CAS	GSE	INS	LES	ROS	S04	S52	SAP	SIS	OVL	SPL
GATCTCGCTTTGACGGT	0	0	0	0	0	0	0	0	0	0	0	0	0	1
GATCATTGAAAGTTAGT	0	0	0	10	0	5	44	38	0	0	0	0	0	2
GATCTGGTGTTGTTGGG	0	0	0	8	0	0	0	0	0	0	0	0	5	2
GATCTGTTGATTGGACT	0	0	0	2	0	0	0	0	0	0	0	0	0	3
GATCTTCAACCAACCAA	0	0	0	9	0	0	0	0	0	0	0	0	0	31
GATCCAGAAGAAAAGCA	0	0	0	0	0	0	0	0	0	0	0	0	0	15
GATCGGCTGAGGAAGAA	0	0	0	0	0	0	8	3	0	0	0	0	0	10
GATCAAGTAATGCCGTA	0	0	0	0	0	0	0	0	0	0	0	0	0	3
GATCAATCGCCATTATG	0	0	0	0	20	0	0	0	0	0	0	0	0	19
GATCACAACAAATGCAA	0	0	0	0	0	0	0	0	0	0	0	0	0	1
GATCCTTGAGAAATCTG	0	0	0	0	0	0	1	25	7	0	0	4	6	2
GATCGGCCAGTGGAAAG	0	0	0	0	0	0	0	1	0	0	0	0	3	5
GATCTAGGGTTTCTAGT	0	0	0	9	0	0	3	0	0	0	0	0	0	3
GATCTATATTGGTACCA	0	0	0	0	0	0	1	6	0	0	2	0	0	4
GATCAAATGGCTGTTTC	0	0	0	0	0	0	0	11	0	0	0	1	0	6
GATCCCTCATTAGCCAA	0	0	0	0	0	5	0	0	0	0	0	0	1	15
GATCGGTTTCAGATTTG	0	0	0	0	0	0	0	0	0	0	0	16	9	9
GATCGTACGGCTGTTTG	0	0	0	0	0	0	0	0	0	0	0	0	0	12

Supplementary Table 2

SIGNATURE[a]	Transcriptional activity[b]													
	AGM	AP1	AP3	CAS	GSE	INS	LES	ROS	S04	S52	SAP	SIS	OVL	SPL
GATCGAACTTTGAGGCT	0	0	0	0	0	3	0	0	0	0	0	0	19	7
GATCTGCTAGTTCCAAA	0	0	0	0	0	0	0	0	0	0	0	0	0	4
GATCTGCTGTTCCGGCA	0	0	0	0	0	0	0	10	1	0	0	0	0	16
GATCCAACGATTCATCG	0	0	0	2	0	0	0	0	0	0	2	0	0	2
GATCAATCAAGAAGAGA	0	0	0	0	0	10	10	0	0	3	0	0	0	1
GATCCTCTCTTGCTCTC	0	0	0	1	0	0	0	0	0	0	0	0	1	11
GATCCTGTGATGAGCAG	0	0	0	18	0	0	0	0	0	0	0	0	0	1
GATCAATCTACGGTGGA	0	0	0	3	0	0	0	0	0	0	0	0	0	5
GATCAAGCTTCGGTTGT	0	0	0	5	0	0	7	0	0	0	0	0	2	28
GATCTTTCGTGATGCTT	0	0	0	12	0	0	1	0	0	0	0	73	0	9
GATCGATAGGAGCATAC	0	0	0	2	0	0	0	16	16	1	0	0	2	5
GATCGTCTGACTCGACT	0	0	0	1	0	0	0	5	0	0	0	0	0	1
GATCAGCCGGCAACGTC	0	0	0	6	0	0	50	0	33	0	22	105	148	89
GATCTGTCCACAACTGC	0	0	0	8	0	0	0	0	0	0	0	0	0	2
GATCAGCCATGGAGGAC	0	0	0	0	66	18	0	6	1	32	0	0	29	2
GATCGGCGGTGCAGTGG	0	0	0	0	50	0	0	0	0	0	0	0	0	9
GATCGGAAACTCTCTCT	0	0	0	3	0	0	0	3	27	0	1	0	0	10
GATCGTGACGAACTGAG	0	0	0	0	8	0	0	0	0	0	0	0	0	5

Supplementary Table 2

SIGNATURE[a]	Transcriptional activity[b]													
	AGM	AP1	AP3	CAS	GSE	INS	LES	ROS	S04	S52	SAP	SIS	OVL	SPL
GATCTAATGAGAACGCA	0	0	0	0	2	0	0	0	0	0	0	0	0	11
GATCGAAGTATCTCGTC	0	0	0	0	1	0	0	0	0	0	0	0	0	11
GATCGAAGTTCCGAGGA	0	0	0	0	3	2	0	0	0	0	0	0	0	16
GATCTTATGTTGTGTGT	0	0	0	0	2	0	0	0	0	1	0	0	0	27
GATCAGGAAAATGAGTT	0	0	0	0	0	0	0	0	0	0	0	0	0	10
GATCTGTGAGAATACCT	0	0	0	0	0	0	1	0	0	0	0	0	0	1
GATCTAGTGAGTTAGAC	0	0	0	0	0	0	0	0	0	0	13	0	0	3
GATCTAGAAAGAGGAGC	0	0	0	0	0	0	11	0	0	0	0	0	0	11
GATCCGATTCTGTCCGC	0	0	0	0	0	0	2	0	0	0	0	0	0	7
GATCGTACCTTTCCTTC	0	0	0	0	0	0	0	0	0	0	0	0	0	4
GATCAGAATCACACGTT	0	0	0	0	0	0	0	0	0	0	0	0	0	9
GATCATATGGACAACAA	0	0	0	0	0	2	0	0	0	0	0	0	0	1
GATCAGGCAACCCACAA	0	0	0	0	0	4	0	0	3	0	0	0	0	9
GATCTATGTCCACAACC	0	0	0	0	0	2	0	0	0	0	0	0	0	7
GATCCCCAAATCCCTGA	0	0	0	0	0	2	0	1	0	2	2	0	0	18
GATCATGTTTTTTTTTC	0	0	0	0	0	0	0	0	0	0	1	0	0	5
GATCCTCTCTAGTTGCC	0	0	0	0	0	0	0	0	0	0	0	0	0	8
GATCGAAGCAGAACAGC	0	0	0	0	0	0	0	0	0	0	6	23	0	11

Supplementary Table 2

SIGNATURE[a]	Transcriptional activity[b]													
	AGM	AP1	AP3	CAS	GSE	INS	LES	ROS	S04	S52	SAP	SIS	OVL	SPL
GATCACGTTTGATTAGC	0	0	0	0	0	0	0	1	0	0	0	0	2	17
GATCTCATTGGGCCGGG	0	0	0	0	0	0	0	24	0	0	4	0	14	7
GATCAACTTGGGATTGA	0	0	0	0	0	0	0	0	0	3	0	0	0	16
GATCGTGCAGTCTGAAA	0	0	0	0	0	0	0	0	0	0	6	0	0	1
GATCGCTAGTGTCTTGA	0	0	0	0	0	0	9	0	0	0	0	0	0	6
GATCATCTCAACTTCTC	0	0	0	0	0	0	9	0	0	0	0	0	0	5
GATCAGGAAAGGTCAAG	0	0	0	0	0	0	3	0	0	0	0	0	53	15
GATCTCTGATTGGGTGT	0	0	0	0	0	0	0	0	0	0	0	0	0	4
GATCAGAACCAAGTCAG	0	0	0	0	0	0	0	0	1	0	0	0	4	9
GATCTCTCCGTCTGATT	0	0	0	0	0	0	0	0	0	0	0	0	0	11
GATCATTTGCGTAAACC	0	0	0	0	0	0	0	0	0	0	3	0	0	25
GATCCATTCTCGATGGG	0	0	0	0	0	0	0	0	0	0	2	0	0	18
GATCTGAAAGTCCCAGT	0	0	0	0	0	0	0	0	0	0	0	0	0	32
GATCTTATCCCAGGCCG	0	0	0	0	0	0	0	0	0	0	0	0	0	9
GATCATGCATAAGGTCG	0	0	0	0	0	0	0	0	0	0	0	0	9	52
GATCCAAGTCAAGCCAA	0	0	0	0	0	0	0	0	0	0	0	0	0	14
GATCCCGCCCAAGACAG	0	0	0	0	0	0	0	0	0	0	0	0	0	15
GATCCGCTGCTTACTGC	0	0	0	0	0	0	0	0	0	0	0	0	0	23

Supplementary Table 2

SIGNATURE[a]	Transcriptional activity[b]													
	AGM	AP1	AP3	CAS	GSE	INS	LES	ROS	S04	S52	SAP	SIS	OVL	SPL
GATCCGGCTTGACACGC	0	0	0	0	0	0	0	0	0	0	0	0	1	11
GATCCTTACATGACGAA	0	0	0	0	0	0	0	0	0	0	0	0	0	11
GATCCTTTGGAACTTCT	0	0	0	0	0	0	0	0	0	0	0	0	0	7
GATCGTTGTGGTTCTTT	0	0	0	0	0	0	0	0	0	0	0	0	6	5
GATCTTCTGTGTGCGTG	0	0	0	0	0	0	0	0	0	0	0	0	0	13
GATCCTTCTGAGTGGCA	0	0	0	0	0	0	0	0	0	0	0	0	0	6
GATCATCCAAAGTAAGC	0	0	0	0	0	0	0	0	0	0	0	0	0	16
GATCCAGTCTTGAGCTG	0	0	0	0	0	0	0	0	0	0	0	0	0	8
GATCCGTGAAAGAGTCT	0	0	0	0	0	0	0	0	0	0	0	0	0	10
GATCCTGCGCTGAAGGA	0	0	0	0	0	0	0	0	0	0	0	0	21	11
GATCCTTCGACGGTTCT	0	0	0	0	0	0	0	0	0	0	0	0	9	12
GATCGATAAAAACTTCA	0	0	0	0	0	0	0	0	0	0	0	0	6	1
GATCAAGCCCCAAATTC	0	0	0	0	0	0	0	0	0	0	0	0	0	11
GATCGGCACCATGGGGC	0	0	0	0	0	0	0	0	0	0	0	0	0	9
GATCACAAAAGAGGTGA	0	0	0	0	0	0	0	0	0	0	0	0	45	4

Supplementary Table 3

Supplemententery table 3. Transcriptional activity of non-ovule genes in diverse MPSS collections.

GENE ID[a]	Transcriptional activity[b]												
	AGM	AP1	AP3	CAS	GSE	INS	LES	ROS	S04	S52	SAP	SIS	OVL
At5g67060	0	3	2	0	66	4	0	0	20	0	0	0	0
At3g50330	0	1	0	1	77	5	5	4	0	0	0	0	0
At1g20130	0	1518	0	0	0	774	1	0	0	0	1124	0	0
At3g271025	0	5	0	0	0	9	0	0	0	0	7	6	0
At5g07550	32	1759	0	0	0	9516	58	0	0	0	11209	0	0
At2g19070	2	582	0	0	0	650	0	0	0	0	978	0	0
At1g33430	0	264	0	0	0	206	0	0	0	0	355	0	0
At1g72290	0	15	129	0	0	13	0	0	0	0	8	0	0

[a] TheArabidopsis Genome Initiative Number.

[b] Activity in transcripts per Million. AGM. *agamous* infloresence.AP1. *apetala 1-10* infloresence. AP3. *apetala 3-6* infloresence. CAS. Callus. GSE. Germinating seedlings. INS. Infloresences. LES. Leaves. ROS. Roots. S04. Leaves, 4 hr after salicylic acid treatment. S52. Leaves, 52 hr after salicylic acid treatment. SAP. *superman/apetala* infloresence. SIS. Siliques. OVL. Wild type ovules.SPL. *sporocyteless* ovules.

Supplementary table 4. List of MPSS differentially expressed genes between wild-type and *sporocyteless* ovule.

GENE ID[a]	Transcriptional activity[b]		PREDICTED FUNCTION[c]
	Wild type ovule	*sp/* ovule	
At1g01050	39	0	AtPPa1 (Arabidopsis thaliana pyrophosphorylase 1
At1g01060	198	0	LHY (LATE ELONGATED HYPOCOTYL
At1g01360	9	0	Unknown protein
At1g01490	39	1	Heavy-metal-associated domain-containing protein
At1g01920	19	0	SET domain-containing protein
At1g02060	18	0	Pentatricopeptide (PPR) repeat-containing protein
At1g02065	30	0	SPL8 (SQUAMOSA PROMOTER BINDING PROTEIN-LIKE 8)
At1g02790	46	0	PGA4 (POLYGALACTURONASE 4); polygalacturonase
At1g03030	23	0	Phosphoribulokinase/uridine kinase family protein
At1g03250	38	0	Unknown protein
At1g03350	36	0	BSD domain-containing protein
At1g03440	12	0	Leucine-rich repeat family protein
At1g03610	43	0	Unknown protein
At1g03630	9	0	POR C (PROTOCHLOROPHYLLIDE OXIDOREDUCTASE)
At1g04280	14	0	Unknown protein
At1g04410	451	17	Malate dehydrogenase, cytosolic, putative
At1g04510	9	0	Encodes MAC3A, a U-box proteins with homology to the yeast and human E3 ubiquitin ligase Prp19.
At1g04830	25	1	RabGAP/TBC domain-containing protein
At1g05500	54	0	NTMC2T2.1
At1g05540	79	0	Unknown protein
At1g05710	137	0	Ethylene-responsive protein, putative
At1g05805	18	0	Basic helix-loop-helix (bhlh) family protein
At1g06040	48	0	STO (SALT TOLERANCE); DNA binding / protein binding/ transcription factor/ zinc ion binding
At1g06070	9	0	Bzip transcription factor, putative (bzip69)
At1g06250	12	0	Lipase class 3 family protein
At1g06470	24	0	Phosphate translocator-related
At1g06960	89	3	Small nuclear ribonucleoprotein U2B, putative / spliceosomal protein, putative
At1g07020	87	3	Unknown protein
At1g07090	9	0	LSH6 (LIGHT SENSITIVE HYPOCOTYLS 6)
At1g07180	32	0	NDA1 (ALTERNATIVE NAD(P)H DEHYDROGENASE 1); NADH dehydrogenase
At1g07530	9	0	SCL14 (SCARECROW-LIKE 14); transcription factor
At1g07960	17	0	ATPDIL5-1 (PDI-like 5-1)
At1g08680	62	1	ZIGA4 (ARF GAP-like zinc finger-containing protein ZiGA4); ARF GTPase activator/ DNA binding / zinc ion binding
At1g09080	33	0	BIP3; ATP binding

Supplementary Table 4

GENE ID[a]	Transcriptional activity[b]		PREDICTED FUNCTION[c]
	Wild type ovule	*spl* ovule	
At1g09570	11	0	PHYA (PHYTOCHROME A); G-protein coupled photoreceptor/ protein histidine kinase/ red or far-red light photoreceptor/ signal transducer
At1g09575	10	0	Unknown protein
At1g09710	22	0	DNA binding
At1g10455	14	0	Unknown protein
At1g10538	27	0	Pseudogene of CPL4 (phosphoprotein phosphatase)
At1g10590	35	0	DNA-binding protein-related
At1g10650	9	0	Protein binding / zinc ion binding
At1g10710	19	0	Computational predictions suggested the presence of a small cysteine-rich protein beginning in intron 9 (Silverstein 2007), but subsequent analysis revealed that this region contains a tenth exon for the At1g10710 gene.
At1g10730	14	0	Clathrin adaptor complexes medium subunit family protein
At1g10840	12	0	TIF3H1; translation initiation factor
At1g11200	14	0	Unknown protein
At1g11260	38	0	STP1 (SUGAR TRANSPORTER 1); carbohydrate transmembrane transporter/ sugar:hydrogen symporter
At1g11362	14	0	Enzyme inhibitor/ pectinesterase
At1g11800	14	0	Endonuclease/exonuclease/phosphatase family protein
At1g11900	9	0	Pentatricopeptide (PPR) repeat-containing protein
At1g12080	74	0	Unknown protein
At1g12300	16	0	Pentatricopeptide (PPR) repeat-containing protein
At1g12310	14	0	Calmodulin, putative
At1g12400	25	0	DNA binding
At1g12610	40	0	DDF1 (DWARF AND DELAYED FLOWERING 1); DNA binding
At1g12750	14	0	ATRBL6 (ARABIDOPSIS RHOMBOID-LIKE PROTEIN 6)
At1g12775	13	0	Pentatricopeptide repeat protein (PPR)
At1g12820	101	3	AFB3 (AUXIN SIGNALING F-BOX 3); auxin binding / ubiquitin-protein ligase
At1g13170	10	0	ORP1D (OSBP(OXYSTEROL BINDING PROTEIN)-RELATED PROTEIN 1D); oxysterol binding
At1g13210	23	0	ACA.l (autoinhibited Ca2+/ATPase II); ATPase, coupled to transmembrane movement of ions, phosphorylative mechanism / calmodulin binding
At1g13450	11	0	DNA binding protein GT-1
At1g13750	30	0	Calcineurin-like phosphoesterase family protein
At1g14200	41	0	Zinc finger (C3HC4-type RING finger) family protein
At1g14260	19	0	Zinc finger (C3HC4-type RING finger) family protein
At1g14280	37	0	PKS2 (PHYTOCHROME KINASE SUBSTRATE 2)
At1g14530	11	0	THH1 (TOM THREE HOMOLOG 1); virion binding
At1g14650	26	0	SWAP (Suppressor-of-White-APricot)/surp domain-containing protein / ubiquitin family protein.

Supplementary Table 4

GENE ID[a]	Transcriptional activity[b]		PREDICTED FUNCTION[c]
	Wild type ovule	*sp/* ovule	
At1g15020	47	0	Thioredoxin family protein
At1g15220	14	0	CCMH; oxidoreductase
At1g15350	14	0	Unknown protein
At1g15690	185	2	AVP1; atpase/ hydrogen-translocating pyrophosphatase
At1g15780	64	0	Unknown protein
At1g16170	10	0	Unknown protein
At1g16300	11	0	GAPCP-2; NAD or NADH binding / binding / catalytic/ glyceraldehyde-3-phosphate dehydrogenase (phosphorylating)/ glyceraldehyde-3-phosphate dehydrogenase
At1g16390	11	0	ATOCT3 (ARABIDOPSIS THALIANA ORGANIC CATION/CARNITINE TRANSPORTER 3
At1g16445	21	0	Methylase-related
At1g16590	20	0	REV7; DNA binding
At1g16630	10	0	Unknown protein
At1g17130	10	0	Cell cycle control protein-related
At1g17400	22	0	Unknown protein
At1g17550	88	1	HAB2; catalytic/ protein serine/threonine phosphatase
At1g17890	43	1	GER2; binding / catalytic/ coenzyme binding
At1g17930	16	0	Unknown protein
At1g18075	43	0	MIR159/MIR159B; miRNA
At1g18500	27	1	MAML-4 (METHYLTHIOALKYLMALATE SYNTHASE-LIKE 4); 2-isopropylmalate synthase
At1g18610	13	0	Galactose oxidase/kelch repeat superfamily protein
At1g18840	19	0	IQD30; calmodulin binding
At1g19350	14	0	BES1 (BRI1-EMS-SUPPRESSOR 1); protein binding / transcription factor/ transcription regulator
At1g19450	13	0	Integral membrane protein, putative / sugar transporter family protein
At1g19690	73	0	Binding / catalytic/ coenzyme binding
At1g19790	15	0	Srs7 (shi-related sequence 7)
At1g19990	63	0	Unknown protein
At1g20000	11	0	TAF11b (TBP-ASSOCIATED FACTOR 11b); DNA binding / RNA polymerase II transcription factor/ transcription initiation factor
At1g20140	33	0	ASK4 (ARABIDOPSIS SKP1-LIKE 4); protein binding / ubiquitin-protein ligase
At1g20220	14	0	Nucleic acid binding
At1g20830	9	0	Unknown protein
At1g21080	20	0	DNAJ heat shock N-terminal domain-containing protein
At1g21390	18	0	Emb2170 (embryo defective 2170)
At1g21400	21	0	2-oxoisovalerate dehydrogenase, putative / 3-methyl-2-oxobutanoate dehydrogenase, putative / branched-chain alpha-keto acid dehydrogenase E1 alpha subunit, putative
At1g21460	28	0	Nodulin mtn3 family protein

Supplementary Table 4

GENE ID[a]	Transcriptional activity[b]		PREDICTED FUNCTION[c]
	Wild type ovule	*spl* ovule	
At1g21700	15	0	ATSWI3C (SWITCH/SUCROSE NONFERMENTING 3C); DNA binding
At1g22140	79	2	Unknown protein
At1g22275	12	0	ZYP1b
At1g22970	21	0	Unknown protein
At1g23350	18	0	Invertase/pectin methylesterase inhibitor family protein
At1g23550	37	0	SRO2 (SIMILAR TO RCD ONE 2); NAD+ ADP-ribosyltransferase
At1g23790	43	1	Unknown protein
At1g23960	132	3	Unknown protein
At1g24070	22	0	ATCSLA10; cellulose synthase/ transferase, transferring glycosyl groups
At1g24120	39	1	ARL1 (ARG1-LIKE 1); heat shock protein binding / unfolded protein binding
At1g24160	10	0	Unknown protein
At1g24490	9	0	ALB4 (ALBINA 4)
At1g25490	11	0	RCN1 (ROOTS CURL IN NPA); protein phosphatase type 2A regulator
At1g26480	30	1	GRF12 (GENERAL REGULATORY FACTOR 12); protein binding / protein phosphorylated amino acid binding
At1g26610	21	0	Zinc finger (C2H2 type) family protein
At1g26620	15	0	Unknown protein
At1g26795	97	0	Self-incompatibility protein-related
At1g27030	16	0	Unknown protein
At1g27390	54	1	TOM20-2 (TRANSLOCASE OUTER MEMBRANE 20-2); P-P-bond-hydrolysis-driven protein transmembrane transporter/ metal ion binding
At1g27520	18	0	Glycoside hydrolase family 47 protein
At1g27530	77	3	Unknown function
At1g28330	802	29	DYL1 (DORMANCY-ASSOCIATED PROTEIN-LIKE 1)
At1g28440	51	0	HSL1 (HAESA-Like 1); ATP binding / kinase/ protein serine/threonine kinase
At1g28760	11	0	Unknown protein
At1g29060	21	0	Target SNARE coiled-coil domain protein
At1g29140	23	0	Pollen Ole e 1 allergen and extensin family protein
At1g29260	37	1	PEX7; peroxisome matrix targeting signal-2 binding / protein binding
At1g29330	15	0	ERD2 (ENDOPLASMIC RETICULUM RETENTION DEFECTIVE 2); KDEL sequence binding / receptor
At1g29357	26	1	other RNA
At1g30440	9	0	Phototropic-responsive NPH3 family protein
At1g30970	16	0	SUF4 (suppressor of FRIGIDA4/ transcription factor
At1g31330	210	2	PSAF (photosystem I subunit F)
At1g31660	9	0	Unknown function.
At1g31760	129	3	SWIB complex BAF60b domain-containing protein

Supplementary Table 4

GENE ID[a]	Transcriptional activity[b]		PREDICTED FUNCTION[c]
	Wild type ovule	*spl* ovule	
At1g31810	24	0	Actin binding
At1g32120	14	0	Unknown protein
At1g32300	11	0	FAD-binding domain-containing protein
At1g32310	32	0	Unknown protein
At1g32390	21	0	Transposable element gene
At1g32460	15	0	Unknown protein
At1g32470	19	0	Glycine cleavage system H protein, mitochondrial, putative
At1g33230	14	0	TMPIT-like protein
At1g33360	31	0	ATP-dependent Clp protease ATP-binding subunit ClpX, putative
At1g33970	22	0	Avirulence-responsive protein, putative / avirulence induced gene protein, putative / AIG protein, putative
At1g34210	25	0	SERK2 (SOMATIC EMBRYOGENESIS RECEPTOR-LIKE KINASE 2); kinase
At1g34380	19	0	5'-3' exonuclease family protein
At1g34550	12	0	EMB2756 (EMBRYO DEFECTIVE 2756)
At1g35180	11	0	TRAM, LAG1 and CLN8 (TLC) lipid-sensing domain containing protein
At1g43886	35	1	Transposable element gene
At1g44900	61	0	ATP binding / DNA binding / DNA-dependent ATPase
At1g45000	53	0	26S proteasome regulatory complex subunit p42D, putative
At1g45180	11	0	Zinc finger (C3HC4-type RING finger) family protein
At1g46264	69	1	AT-HSFB4; DNA binding / transcription factor
At1g47128	107	1	RD21 (responsive to dehydration 21); cysteine-type endopeptidase/ cysteine-type peptidase
At1g47240	14	0	NRAMP2; inorganic anion transmembrane transporter/ metal ion transmembrane transporter
At1g47450	26	0	Unknown protein
At1g47470	21	0	Unknown protein
At1g47670	63	0	Amino acid transporter family protein
At1g47780	53	0	Acyl-protein thioesterase-related
At1g47830	30	1	Clathrin coat assembly protein, putative
At1g47930	15	0	pseudogene, glutamyl-tRNA synthetase, similar to GI:3435196 from (Arabidopsis thaliana
At1g48460	29	0	Unknown protein
At1g48560	15	0	Unknown protein
At1g48600	19	0	Phosphoethanolamine N-methyltransferase 2, putative (NMT2)
At1g48900	54	0	Signal recognition particle 54 kDa protein 3 / SRP54 (SRP-54C)
At1g48950	26	1	Zinc ion binding
At1g49650	19	0	Cell death associated protein-related
At1g49920	46	0	Zinc finger protein-related
At1g50000	30	0	Methyltransferase
At1g50010	9	0	TUA2; structural constituent of cytoskeleton

Supplementary Table 4

GENE ID[a]	Transcriptional activity[b]		PREDICTED FUNCTION[c]
	Wild type ovule	*spl* ovule	
At1g50250	54	0	FTSH1 (FtsH protease 1); ATP-dependent peptidase/ ATPase/ metallopeptidase
At1g50440	14	0	Zinc finger (C3HC4-type RING finger) family protein
At1g50500	14	0	HIT1 (HEAT-INTOLERANT 1); transporter
At1g50510	10	0	Indigoidine synthase A family protein
At1g51100	27	0	Unknown protein
At1g51440	13	0	Lipase class 3 family protein
At1g51550	10	0	F-box family protein
At1g51570	83	2	C2 domain-containing protein
At1g52190	39	0	Proton-dependent oligopeptide transport (POT) family protein
At1g52220	137	2	Unknown function
At1g52250	9	0	Dynein light chain type 1 family protein
At1g52347	16	0	Unknown gene
At1g52590	12	0	Putative thiol-disulphide oxidoreductase
At1g52730	17	0	Transducin family protein / WD-40 repeat family protein
At1g53120	34	1	RNA-binding S4 domain-containing protein
At1g53170	13	0	ERF8; DNA binding / transcription factor/ transcription repressor
At1g53300	30	0	TTL1 (TETRATRICOPETIDE-REPEAT THIOREDOXIN-LIKE 1); binding
At1g53440	74	2	Leucine-rich repeat family protein / protein kinase family protein
At1g53645	38	0	Hydroxyproline-rich glycoprotein family protein
At1g53760	14	0	Unknown protein
At1g54260	76	3	Histone H1/H5 family protein
At1g54570	11	0	Esterase/lipase/thioesterase family protein
At1g54580	477	0	ACP2 (ACYL CARRIER PROTEIN 2); acyl carrier
At1g54630	10	0	ACP3 (ACYL CARRIER PROTEIN 3); acyl carrier
At1g54830	13	0	NF-YC3 (NUCLEAR FACTOR Y, SUBUNIT C3); DNA binding / transcription factor
At1g54850	19	0	HSP20-like chaperones superfamily protein
At1g55170	10	0	Unknown protein
At1g55260	43	1	Lipid binding
At1g55680	69	0	WD-40 repeat family protein
At1g55810	58	1	Uracil phosphoribosyltransferase, putative
At1g55820	9	0	Protein of Unknown function DUF1296
At1g56020	19	0	Unknown protein
At1g56180	39	0	Unknown protein
At1g56450	35	0	20S proteasome beta subunit PBG1 (PBG1)
At1g56610	9	0	Syntaxin-related family protein
At1g57590	11	0	Carboxylesterase
At1g58220	18	0	Myb family transcription factor

Supplementary Table 4

GENE ID[a]	Transcriptional activity[b]		PREDICTED FUNCTION[c]
	Wild type ovule	*spl* ovule	
At1g58227	9	0	Binding
At1g58250	19	0	SABRE, putative gene of Unknown function, homologous to maize apt1 gene.
At1g58520	12	0	Hydrolase, acting on ester bonds / lipase
At1g59520	18	0	Encodes CW7
At1g60000	12	0	29 kDa ribonucleoprotein, chloroplast, putative / RNA-binding protein cp29, putative
At1g60160	13	0	Potassium transporter family protein
At1g60650	14	0	Glycine-rich RNA-binding protein, putative
At1g60740	33	1	Peroxiredoxin type 2, putative
At1g60860	47	0	AGD2 (ARF-GAP DOMAIN 2); ARF GTPase activator/ protein binding / zinc ion binding
At1g60940	84	1	SNRK2.10 (SNF1-RELATED PROTEIN KINASE 2.10); kinase
At1g60960	34	1	IRT3; cation transmembrane transporter/ metal ion transmembrane transporter
At1g60970	13	0	Clathrin adaptor complex small chain family protein
At1g60990	15	0	Aminomethyltransferase
At1g61665	11	0	Pseudogene, similar to serine/threonine kinase,
At1g61790	183	3	OST3/OST6 family protein
At1g62130	9	0	AAA-type ATPase family protein
At1g62520	25	1	Unknown protein
At1g62730	12	0	Transferase
At1g62860	27	0	Pseudogene of pentatricopeptide (PPR) repeat-containing protein
At1g63130	24	0	Pentatricopeptide (PPR) repeat-containing protein
At1g63220	116	4	C2 domain-containing protein
At1g63490	30	1	Transcription factor jumonji (jmjC) domain-containing protein
At1g63500	26	0	ATP binding.
At1g64050	21	0	Unknown protein
At1g64230	32	1	Ubiquitin-conjugating enzyme, putative
At1g64280	17	0	NPR1 (NONEXPRESSER OF PR GENES 1); protein binding / transcription activator
At1g64520	72	1	RPN12a (Regulatory Particle non-ATPase 12a); peptidase
At1g64740	33	0	TUA1 (ALPHA-1 TUBULIN); structural constituent of cytoskeleton
At1g65240	46	1	Aspartyl protease family protein
At1g66150	25	0	TMK1 (TRANSMEMBRANE KINASE 1); transmembrane receptor protein serine/threonine kinase
At1g66660	20	0	Seven in absentia (SINA) protein, putative
At1g67325	15	0	Binding / zinc ion binding
At1g67570	30	0	UUnknown protein
At1g67650	12	0	7S RNA binding
At1g67660	9	0	DNA binding / nuclease
At1g67750	43	0	Pectate lyase family protein

Supplementary Table 4

GENE ID[a]	Transcriptional activity[b]		PREDICTED FUNCTION[c]
	Wild type ovule	*sp* ovule	
At1g68020	11	0	ATTPS6; alpha,alpha-trehalose-phosphate synthase (UDP-forming)/ transferase, transferring glycosyl groups / trehalose-phosphatase
At1g68440	17	0	Unknown protein
At1g69230	19	0	SP1L2 (SPIRAL1-LIKE2)
At1g69400	25	0	Transducin family protein / WD-40 repeat family protein
At1g69850	11	0	ATNRT1:2 (ARABIDOPSIS THALIANA NITRATE TRANSPORTER 1:2); calcium ion binding / transporter
At1g70100	22	0	Unknown protein
At1g70250	21	0	Receptor serine/threonine kinase, putative
At1g70280	16	0	NHL repeat-containing protein
At1g70500	34	1	Polygalacturonase, putative / pectinase, putative
At1g70560	52	0	TAA1 (TRYPTOPHAN AMINOTRANSFERASE OF ARABIDOPSIS 1)
At1g70660	75	3	MMZ2 (MMS ZWEI HOMOLOGE 2);ubiquitin-protein ligase
At1g71030	20	0	MYBL2 (ARABIDOPSIS MYB-LIKE 2); DNA binding / transcription factor
At1g71260	68	1	ATWHY2 (A. THALIANA WHIRLY 2); DNA binding
At1g71310	22	0	Unknown protein
At1g71380	14	0	ATCEL3 (ARABIDOPSIS THALIANA CELLULASE 3); catalytic/ hydrolase, hydrolyzing O-glycosyl compounds
At1g71430	17	0	Unknown protein
At1g71730	14	0	Unknown protein
At1g71750	34	0	Phosphoribosyltransferase family protein
At1g72300	25	0	Leucine-rich repeat transmembrane protein kinase, putative
At1g72550	35	0	tRNA synthetase beta subunit family protein
At1g72880	16	0	Acid phosphatase survival protein sure, putative
At1g73450	9	0	Protein kinase, putative
At1g73885	20	0	Unknown protein
At1g73910	17	0	ATARP4A (Actin-related proteins 4A); protein binding / structural constituent of cytoskeleton
At1g74180	27	0	AtRLP14 (Receptor Like Protein 14); protein binding
At1g74390	56	1	Exonuclease family protein
At1g74700	21	0	TRZ1 (TRNASE Z 1); 3'-tRNA processing endoribonuclease
At1g74840	72	0	Myb family transcription factor
At1g75020	60	1	LPAT4 (LYSOPHOSPHATIDYL ACYLTRANSFERASE 4); acyltransferase
At1g75150	11	0	Unknown protein
At1g75780	27	1	TUB1; GTP binding / GTPase/ structural molecule
At1g75840	45	1	ARAC5 (RAC-LIKE GTP BINDING PROTEIN 5); GTP binding / GTPase
At1g75980	41	0	Single hybrid motif superfamily protein
At1g76100	50	0	PETE1 (PLASTOCYANIN 1); copper ion binding / electron carrier
At1g76130	24	0	AMY2 (ALPHA-AMYLASE-LIKE 2); alpha-amylase/ calcium ion

binding / catalytic/ cation binding

GENE ID[a]	Transcriptional activity[b]		PREDICTED FUNCTION[c]
	Wild type ovule	*sp*/ ovule	
At1g76185	14	0	Unknown protein
At1g76600	18	0	Unknown protein
At1g76830	13	0	F-box family protein
At1g77380	9	0	AAP3; amino acid transmembrane transporter
At1g77720	10	0	Protein kinase family protein
At1g77760	33	0	NIA1 (NITRATE REDUCTASE 1); nitrate reductase
At1g78560	18	0	Bile acid:sodium symporter family protein
At1g79070	33	1	SNARE-associated protein-related
At1g79410	15	0	AtOCT5 (Arabidopsis thaliana ORGANIC CATION/CARNITINE TRANSPORTER5); carbohydrate transmembrane transporter/ sugar:hydrogen symporter
At1g79690	31	1	atnudt3 (Arabidopsis thaliana Nudix hydrolase homolog 3); hydrolase
At1g79710	17	0	Integral membrane transporter family protein
At1g79810	29	1	TED3 (REVERSAL OF THE DET PHENOTYPE 3); protein binding / zinc ion binding
At1g80370	31	1	CYCA2;4 (Cyclin A2;4); cyclin-dependent protein kinase regulator
At1g80460	45	0	NHO1 (nonhost resistance to P. s. phaseolicola 1); carbohydrate kinase/ glycerol kinase
At1g80490	28	0	TPR1 (TOPLESS-RELATED 1)
At1g80620	21	0	Ribosomal protein S15 family protein
At1g80690	10	0	Unknown protein
At2g01400	27	0	Unknown protein
At2g01490	46	1	Phytanoyl-coa dioxygenase (phyh) family protein
At2g01830	13	0	WOL (WOODEN LEG); cytokinin receptor/ osmosensor/ phosphoprotein phosphatase/ protein histidine kinase
At2g02090	27	0	ETL1; ATP binding / DNA binding / helicase/ nucleic acid binding
At2g02400	41	0	cinnamoyl-CoA reductase family
At2g02740	27	0	WHY3 (WHIRLY 3); DNA binding
At2g02910	100	3	Protein of Unknown function DUF616 .
At2g03270	9	0	DNA-binding protein, putative
At2g03420	12	0	Unknown protein
At2g03550	38	0	Hydrolase
At2g03810	72	1	18S pre-ribosomal assembly protein gar2-related
At2g03840	24	0	TET13 (TETRASPANIN13)
At2g04037	30	1	Unknown protein
At2g04039	12	0	Unknown protein
At2g04235	21	0	Unknown protein
At2g04280	19	0	Unknown protein
At2g06090	13	0	Self-incompatibility protein-related
At2g09800	15	0	Transposable element gene
At2g10340	14	0	Unknown protein

Supplementary Table 4

GENE ID[a]	Transcriptional activity[b]		PREDICTED FUNCTION[c]
	Wild type ovule	*spl* ovule	
At2g10405	12	0	Transposable element gene
At2g11140	41	1	Transposable element gene
At2g12462	19	0	Unknown protein
At2g13360	12	0	AGT (ALANINE:GLYOXYLATE AMINOTRANSFERASE);
At2g13610	26	0	ABC transporter family protein
At2g13960	16	0	Myb family transcription factor
At2g14120	49	1	Dynamin-like protein 2b (ADL2b)
At2g14170	73	0	ALDH6B2; 3-chloroallyl aldehyde dehydrogenase/ methylmalonate-semialdehyde dehydrogenase (acylating)/ oxidoreductase
At2g14255	42	0	Zinc ion binding
At2g14560	12	0	LURP1 (LATE UPREGULATED IN RESPONSE TO HYALOPERONOSPORA PARASITICA)
At2g15440	15	0	Unknown protein
At2g15695	69	2	Unknown protein
At2g15960	22	0	Unknown protein
At2g16050	18	0	Cysteine/Histidine-rich C1 domain family protein
At2g16370	106	2	THY-1 (THYMIDYLATE SYNTHASE 1); dihydrofolate reductase/ thymidylate synthase
At2g16400	16	0	BLH7 (bell1-like homeodomain 7); DNA binding / transcription factor
At2g16570	9	0	ATASE1 (GLN PHOSPHORIBOSYL PYROPHOSPHATE AMIDOTRANSFERASE 1); amidophosphoribosyltransferase
At2g16800	14	0	High-affinity nickel-transport family protein
At2g17130	11	0	IDH2 (ISOCITRATE DEHYDROGENASE SUBUNIT 2); isocitrate dehydrogenase (NAD+)/ oxidoreductase, acting on the CH-OH group of donors, NAD or NADP as acceptor
At2g17210	15	0	Pentatricopeptide (PPR) repeat-containing protein
At2g17390	14	0	AKR2B (ANKYRIN REPEAT-CONTAINING 2B); protein binding / transcription regulator
At2g17420	29	1	NTRA (NADPH-DEPENDENT THIOREDOXIN REDUCTASE A); thioredoxin-disulfide reductase
At2g17530	53	0	Protein kinase family protein
At2g17570	31	0	Undecaprenyl pyrophosphate synthetase family protein / UPP synthetase family protein
At2g18040	33	0	PIN1AT (PEPTIDYLPROLYL CIS/TRANS ISOMERASE, NIMA-INTERACTING 1); peptidyl-prolyl cis-trans isomerase
At2g18330	28	1	AAA-type ATPase family protein
At2g18700	65	2	ATTPS11; transferase, transferring glycosyl groups
At2g18890	11	0	Protein kinase family protein
At2g19340	75	3	Membrane protein, putative
At2g19660	15	0	DC1 domain-containing protein
At2g19760	24	0	PRF1 (PROFILIN 1); actin binding
At2g20050	22	0	ATP binding / cAMP-dependent protein kinase regulator/ catalytic/ protein kinase/ protein serine/threonine phosphatase
At2g20690	19	0	Lumazine-binding family protein
At2g20790	73	0	Protein binding

Supplementary Table 4

GENE ID[a]	Transcriptional activity[b]		PREDICTED FUNCTION[c]
	Wild type ovule	*spl* ovule	
At2g20800	32	0	NDB4 (NAD(P)H dehydrogenase B4); NADH dehydrogenase
At2g20960	11	0	pEARLI4
At2g21120	24	0	Unknown protein
At2g21250	73	0	Mannose 6-phosphate reductase (NADPH-dependent), putative
At2g21440	27	0	RNA recognition motif (RRM)-containing protein
At2g21540	11	0	SFH3 (SEC14-LIKE 3); phosphatidylinositol transporter
At2g21580	41	0	40S ribosomal protein S25 (RPS25B)
At2g21655	35	0	Unknown protein
At2g22120	18	0	Protein binding / zinc ion binding
At2g22170	27	0	Lipid-associated family protein
At2g22240	51	0	MIPS2 (MYO-INOSITOL-1-PHOSTPATE SYNTHASE 2); binding / catalytic/ inositol-3-phosphate synthase
At2g22310	13	0	ATUBP4 (ARABIDOPSIS THALIANA UBIQUITIN-SPECIFIC PROTEASE 4); ubiquitin-specific protease
At2g22490	14	0	CYCD2;1 (Cyclin D2;1); cyclin-dependent protein kinase regulator/ protein binding
At2g22540	20	0	SVP (SHORT VEGETATIVE PHASE); transcription factor/ translation repressor, nucleic acid binding
At2g22650	24	0	FAD-dependent oxidoreductase family protein
At2g22940	15	0	BEST Arabidopsis thaliana protein match is: zinc finger (C3HC4-type RING finger)
At2g23040	9	0	Unknown protein
At2g23142	19	0	Plant self-incompatibility protein S1 family
At2g23310	17	0	ATRER1C1
At2g23340	15	0	AP2 domain-containing transcription factor, putative
At2g23460	40	0	XLG1 (EXTRA-LARGE G-PROTEIN 1); guanyl nucleotide binding / signal transducer
At2g23530	18	0	Zinc-finger domain of monoamine-oxidase A repressor R1
At2g24205	13	0	Encodes a ECA1 gametogenesis related family protein
At2g24270	113	0	ALDH11A3; 3-chloroallyl aldehyde dehydrogenase/ glyceraldehyde-3-phosphate dehydrogenase (NADP+)
At2g24360	15	0	Serine/threonine/tyrosine kinase, putative
At2g24450	30	0	FLA3 (FASCICLIN-LIKE ARABINOGALACTAN PROTEIN 3 PRECURSOR)
At2g24830	11	0	Zinc finger (CCCH-type) family protein / D111/G-patch domain-containing protein
At2g25010	59	0	Unknown protein
At2g25300	50	0	Transferase, transferring glycosyl groups / transferase, transferring hexosyl groups
At2g25320	18	0	TRAF-like family protein
At2g25590	70	2	Agenet domain-containing protein
At2g26360	26	0	Mitochondrial substrate carrier family protein
At2g26450	10	0	Pectinesterase family protein
At2g26920	26	0	Ubiquitin-associated (UBA)/TS-N domain-containing protein
At2g26970	16	0	Exonuclease family protein

Supplementary Table 4

GENE ID[a]	Transcriptional activity[b]		PREDICTED FUNCTION[c]
	Wild type ovule	*spl* ovule	
At2g25650	109	2	NA-binding storekeeper protein-related
At2g26080	66	0	AtGLDP2 (Arabidopsis thaliana glycine decarboxylase P-protein 2); ATP binding / glycine dehydrogenase (decarboxylating)
At2g27500	15	0	Glycosyl hydrolase family 17 protein
At2g27900	31	0	Unknown protein
At2g28110	41	1	FRA8 (FRAGILE FIBER 8); glucuronosyltransferase/ transferase
At2g28380	27	0	DRB2 (DSRNA-BINDING PROTEIN 2); double-stranded RNA binding
At2g28480	29	0	RNA binding
At2g28680	19	0	Cupin family protein
At2g28800	39	1	ALB3 (ALBINO 3); P-P-bond-hydrolysis-driven protein transmembrane transporter
At2g28930	14	0	APK1B; ATP binding / kinase/ protein kinase/ protein serine/threonine kinase
At2g29080	12	0	Ftsh3 (FtsH protease 3); ATP-dependent peptidase/ ATPase
At2g29200	20	0	APUM1 (Arabidopsis Pumilio 1); RNA binding / binding
At2g29660	35	0	Zinc finger (C2H2 type) family protein
At2g29700	25	0	ATPH1 (ARABIDOPSIS THALIANA PLECKSTRIN HOMOLOGUE 1); phosphoinositide binding
At2g29970	32	0	Heat shock protein-related
At2g30200	19	0	[acyl-carrier-protein] S-malonyltransferase/ binding / catalytic/ transferase
At2g30270	25	1	Unknown protein
At2g30984	11	0	Potential natural antisense gene, locus overlaps with At2g30985
At2g31141	24	0	Unknown protein
At2g31530	12	0	EMB2289 (EMBRYO DEFECTIVE 2289); P-P-bond-hydrolysis-driven protein transmembrane transporter
At2g31870	30	0	TEJ (Sanskrit for 'bright'); poly(ADP-ribose) glycohydrolase
At2g31985	22	0	Unknown protein
At2g32400	34	0	GLR5 (GLUTAMATE RECEPTOR 5); intracellular ligand-gated ion channel
At2g32560	9	0	F-box family protein
At2g32600	42	0	hydroxyproline-rich glycoprotein family protein
At2g32720	131	0	CB5-B (CYTOCHROME B5 ISOFORM B); heme binding
At2g33400	92	1	Unknown protein
At2g33610	12	0	ATSWI3B (SWITCH SUBUNIT 3); DNA binding
At2g33775	17	0	RALFL19 (ralf-like 19); signal transducer
At2g33980	9	0	Atnudt22 (Arabidopsis thaliana Nudix hydrolase homolog 22); hydrolase
At2g35030	10	0	Pentatricopeptide (PPR) repeat-containing protein
At2g35240	30	0	Plastid developmental protein DAG, putative
At2g35250	9	0	Unknown protein
At2g35330	82	1	Protein binding / zinc ion binding
At2g35470	54	1	Unknown protein

Supplementary Table 4

GENE ID[a]	Transcriptional activity[b]		PREDICTED FUNCTION[c]
	Wild type ovule	*spl* ovule	
At2g35550	32	0	BPC7 (BASIC PENTACYSTEINE 7); DNA binding / transcription factor
At2g34680	24	0	AIR9; protein binding
At2g34690	118	3	ACD11 (ACCELERATED CELL DEATH 11); sphingosine transmembrane transporter
At2g34700	16	0	Pollen Ole e 1 allergen and extensin family protein
At2g35690	27	1	ACX5 (ACYL-COA OXIDASE 5); FAD binding / acyl-CoA dehydrogenase/ acyl-CoA oxidase/ electron carrier/ oxidoreductase/ oxidoreductase, acting on the CH-CH group of donors
At2g35840	25	0	Sucrose-phosphatase 1 (SPP1)
At2g36610	78	0	ATHB22 (ARABIDOPSIS THALIANA HOMEOBOX PROTEIN 22); DNA binding / transcription factor
At2g36810	13	0	Binding
At2g36835	25	0	Unknown protein
At2g37050	33	0	Kinase
At2g37060	54	1	NF-YB8 (NUCLEAR FACTOR Y, SUBUNIT B8); transcription factor
At2g37120	34	1	DNA-binding S1FA family protein
At2g37470	23	0	Histone H2B, putative
At2g37520	24	0	PHD finger family protein
At2g37550	26	0	AGD7; ARF GTPase activator/ DNA binding / zinc ion binding
At2g37640	26	0	EXP3
At2g37740	9	0	ZFP10 (ZINC-FINGER PROTEIN 10); nucleic acid binding / transcription factor/ zinc ion binding
At2g37840	18	0	Protein kinase family protein
At2g37890	17	0	Mitochondrial substrate carrier family protein
At2g38140	48	0	PSRP4 (PLASTID-SPECIFIC RIBOSOMAL PROTEIN 4); structural constituent of ribosome
At2g38280	10	0	FAC1 (EMBRYONIC FACTOR1); AMP deaminase
At2g38410	11	0	VHS domain-containing protein / GAT domain-containing protein
At2g38630	27	0	Transducin/WD40 repeat-like superfamily protein
At2g38680	14	0	5'-nucleotidase/ magnesium ion binding
At2g39140	9	0	SVR1 (SUPPRESSOR OF VARIEGATION 1); RNA binding / pseudouridine synthase
At2g39270	42	0	Adenylate kinase family protein
At2g39390	80	0	60S ribosomal protein L35 (RPL35B)
At2g39740	11	0	Unknown protein
At2g39930	180	6	ISA1 (ISOAMYLASE 1); alpha-amylase/ isoamylase
At2g40095	18	0	Unknown protein
At2g40760	46	0	Rhodanese-like domain-containing protein
At2g40765	46	1	Unknown protein
At2g40780	13	0	RNA binding / translation initiation factor
At2g40880	9	0	ATCYSA (CYSTATIN A); cysteine-type endopeptidase inhibitor
At2g40935	32	0	Unknown protein

Supplementary Table 4

GENE ID[a]	Transcriptional activity[b]		PREDICTED FUNCTION[c]
	Wild type ovule	*spl* ovule	
At2g40950	21 53	0 1	EEL (ENHANCED EM LEVEL); DNA binding / transcription factor BZIP17; DNA binding / transcription activator/ transcription factor
At2g41650	9	0	Unknown protein
At2g41710	144	4	Ovule development protein, putative
At2g42005	85	0	Amino acid transporter family protein
At2g42070	17	0	ATNUDX23 (ARABIDOPSIS THALIANA NUDIX HYDROLASE HOMOLOG 23); FAD diphosphatase/ hydrolase
At2g42570	57	1	Unknown protein
At2g42590	91	0	GRF9 (GENERAL REGULATORY FACTOR 9); calcium ion binding / protein binding / protein phosphorylated amino acid binding
At2g42620	33	0	MAX2 (MORE AXILLARY BRANCHES 2); ubiquitin-protein ligase
At2g42640	28	0	ATP binding / protein kinase/ protein serine/threonine kinase/ protein tyrosine kinase
At2g42650	57	0	60S ribosomal protein-related
At2g42740	66	0	RPL16A; structural constituent of ribosome
At2g43230	45	0	Serine/threonine protein kinase, putative
At2g43250	27	0	Unknown protein
At2g43330	32	0	INT1 (INOSITOL TRANSPORTER 1); carbohydrate transmembrane transporter/ myo-inositol:hydrogen symporter/ sugar:hydrogen symporter
At2g43530	29	1	Trypsin inhibitor, putative
At2g44440	42	0	Emsy N terminus domain-containing protein / ENT domain-containing protein
At2g44490	35	0	PEN2 (PENETRATION 2); hydrolase, hydrolyzing O-glycosyl compounds / thioglucosidase
At2g44740	24	0	CYCP4;1 (cyclin p4;1); cyclin-dependent protein kinase
At2g45160	150	6	Scarecrow transcription factor family protein
At2g45260	12	0	Unknown protein
At2g45720	29	1	Armadillo/beta-catenin repeat family protein
At2g45870	35	0	Unknown protein
At2g46020	23	0	Transcription regulatory protein SNF2, putative
At2g46030	50	1	UBC6 (ubiquitin-conjugating enzyme 6); ubiquitin-protein ligase
At2g46040	18	0	ARID/BRIGHT DNA-binding domain-containing protein / ELM2 domain-containing protein
At2g46200	32	0	Unknown protein
At2g46490	110	4	Unknown protein
At2g46590	49	1	DAG2 (DOF AFFECTING GERMINATION 2); DNA binding / transcription factor
At2g46830	49	0	CCA1 (CIRCADIAN CLOCK ASSOCIATED 1); DNA binding / transcription activator/ transcription factor/ transcription repressor
At2g46950	23	0	CYP709B2; electron carrier/ heme binding / iron ion binding / monooxygenase/ oxygen binding
At2g47010	32	0	Unknown protein
At2g47030	11	0	VGDH1; enzyme inhibitor/ pectinesterase

Supplementary Table 4

GENE ID[a]	Transcriptional activity[b]		PREDICTED FUNCTION[c]
	Wild type ovule	*sp/* ovule	
At2g47180	18	0	AtGolS1 (Arabidopsis thaliana galactinol synthase 1); transferase, transferring glycosyl groups / transferase, transferring hexosyl groups
At2g47400	253	10	CP12-1
At2g47420	58	0	Dimethyladenosine transferase, putative
At2g47450	50	1	CAO (CHAOS); chromatin binding
At2g47900	21	0	AtTLP3 (TUBBY LIKE PROTEIN 3); phosphoric diester hydrolase/ transcription factor
At2g48030	18	0	Endonuclease/exonuclease/phosphatase family protein
At3g01230	22	0	Unknown protein
At3g01270	16	0	Pectate lyase family protein
At3g01330	26	0	DEL3 (DP-E2F-LIKE PROTEIN 3); DNA binding / transcription factor
At3g01380	17	0	Catalytic/ transferase
At3g01410	40	0	RNase H domain-containing protein
At3g01460	31	0	MBD9; DNA binding / methyl-CpG binding
At3g01760	23	0	Lysine and histidine specific transporter, putative
At3g01810	22	0	Unknown function
At3g02065	19	0	DEAD/DEAH box helicase family protein
At3g02070	22	0	OTU-like cysteine protease family protein
At3g02100	16	0	UDP-glucoronosyl/UDP-glucosyl transferase family protein
At3g02180	67	1	SP1L3 (SPIRAL 1-LIKE3)
At3g02340	16	0	Zinc finger (C3HC4-type RING finger) family protein
At3g02460	54	0	Plant adhesion molecule, putative
At3g02560	53	1	40S ribosomal protein S7 (RPS7B)
At3g02970	9	0	EXL6 (EXORDIUM LIKE 6)
At3g03170	10	0	Unknown protein
At3g03272	18	0	Encodes a ECA1 gametogenesis related family protein
At3g03440	21	0	Armadillo/beta-catenin repeat family protein
At3g03630	19	0	CS26; cysteine synthase
At3g04040	40	0	Unknown protein
At3g04090	65	0	SIP1A (SMALL AND BASIC INTRINSIC PROTEIN 1A); water channel
At3g04350	22	0	Unknown protein
At3g04460	11	0	PEX12; protein binding / zinc ion binding
At3g04605	17	0	Transposable element gene
At3g04640	32	0	Glycine-rich protein
At3g04700	22	0	Unknown protein
At3g04780	63	2	Encodes a protein with little sequence identity with any other protein of known structure or function.
At3g05050	10	0	Protein kinase family protein
At3g05460	18	0	Sporozoite surface protein-related
At3g05685	56	2	Cystatin/monellin superfamily protein

Supplementary Table 4

GENE ID[a]	Transcriptional activity[b]		PREDICTED FUNCTION[c]
	Wild type ovule	*spl* ovule	
At3g05720	31	0	IMPA-7 (IMPORTIN ALPHA ISOFORM 7); binding / protein transporter
At3g05770	14	0	Unknown protein
At3g05970	11	0	LACS6 (long-chain acyl-CoA synthetase 6); long-chain-fatty-acid-CoA ligase
At3g06000	22	0	Leucine-rich repeat family protein
At3g06020	10	0	Unknown protein
At3g06300	13	0	AT-P4H-2 (A. THALIANA P4H ISOFORM 2); oxidoreductase
At3g06420	30	1	ATG8H (autophagy 8h); microtubule binding
At3g06580	35	0	GALK; ATP binding / galactokinase
At3g06660	32	1	PAPA-1-like family protein / zinc finger (HIT type) family protein
At3g06778	25	0	Heat shock protein binding / unfolded protein binding
At3g06780	18	0	Glycine-rich protein
At3g06790	57	0	Plastid developmental protein DAG, putative
At3g06940	10	0	Transposable element gene
At3g07005	24	0	LCR43 (Low-molecular-weight cysteine-rich 43)
At3g07160	86	0	ATGSL10 (glucan synthase-like 10); 1,3-beta-glucan synthase
At3g07370	22	0	CHIP (CARBOXYL TERMINUS OF HSC70-INTERACTING PROTEIN); ubiquitin-protein ligase
At3g07460	84	0	Unknown protein
At3g07520	22	0	GLR1.4 (GLUTAMATE RECEPTOR 1.4); cation channel/ intracellular ligand-gated ion channel
At3g07820	9	0	Polygalacturonase 3 (PGA3) / pectinase
At3g07880	27	1	Rho GDP-dissociation inhibitor family protein
At3g08960	61	0	Binding / protein transporter
At3g09035	35	0	Legume lectin family protein
At3g09070	50	0	Glycine-rich protein
At3g09740	120	4	SYP71 (SYNTAXIN OF PLANTS 71); protein transporter
At3g09770	28	0	Zinc finger (C3HC4-type RING finger) family protein
At3g09900	31	0	ATRABE1E (ARABIDOPSIS RAB GTPASE HOMOLOG E1E); GTP binding
At3g10250	19	0	Unknown protein
At3g10410	18	0	scpl49 (serine carboxypeptidase-like 49); serine-type carboxypeptidase
At3g10420	30	1	Sporulation protein-related
At3g10760	15	0	Myb family transcription factor
At3g11420	22	0	Fringe-related protein
At3g11590	22	0	Unknown protein
At3g11890	15	0	Sterile alpha motif (SAM) domain-containing protein
At3g12100	19	0	Cation efflux family protein / metal tolerance protein, putative
At3g12180	9	0	Cornichon family protein
At3g12260	54	2	Complex 1 family protein / LVR family protein
At3g12350	53	0	F-box family protein

Supplementary Table 4

GENE ID[a]	Transcriptional activity[b]		PREDICTED FUNCTION[c]
	Wild type ovule	*spl* ovule	
At3g12360	39	0	ITN1 (INCREASED TOLERANCE TO NACL); protein binding
At3g12530	10	0	PSF2
At3g12560	31	1	TRFL9 (TRF-LIKE 9); DNA bending/ DNA binding / telomeric DNA binding
At3g12690	10	0	AGC1.5 (AGC KINASE 1.5); kinase
At3g12820	17	0	AtMYB10 (myb domain protein 10); DNA binding / transcription factor
At3g12930	34	1	Nascent polypeptide-associated complex (NAC), alpha subunit family protein
At3g13030	33	0	hAT dimerisation domain-containing protein
At3g13050	16	0	Transporter-related
At3g13120	45	0	30S ribosomal protein S10, chloroplast, putative
At3g13350	33	0	High mobility group (HMG1/2) family protein / ARID/BRIGHT DNA-binding domain-containing protein
At3g13360	53	0	WIP3 (WPP-domain Interacting Protein 3)
At3g13390	13	0	sks11 (SKU5 Similar 11); copper ion binding / oxidoreductase
At3g13440	11	0	Methyltransferase/ nucleic acid binding
At3g13570	21	0	SCL30a; RNA binding / nucleic acid binding / nucleotide binding
At3g13782	12	0	NAP1;4 (NUCLEOSOME ASSEMBLY PROTEIN1;4); DNA binding / chromatin binding
At3g14090	10	0	ATEXO70D3 (exocyst subunit EXO70 family protein D3); protein binding
At3g14100	93	0	Oligouridylate-binding protein, putative
At3g14380	17	0	Integral membrane family protein
At3g15030	15	0	TCP4 (TCP family transcription factor 4); transcription factor
At3g15160	15	0	Unknown protein
At3g15355	12	0	UBC25 (UBIQUITIN-CONJUGATING ENZYME 25); small conjugating protein ligase
At3g15450	312	7	Unknown protein
At3g15630	111	0	Unknown protein
At3g16020	13	0	Phospholipase C
At3g16130	29	0	ROPGEF13; Rho guanyl-nucleotide exchange factor
At3g16190	36	0	Isochorismatase hydrolase family protein
At3g16200	33	0	Unknown protein
At3g16220	15	0	Predicted eukaryotic LigT
At3g16480	15	0	MPPalpha (mitochondrial processing peptidase alpha subunit); catalytic/ metal ion binding / metalloendopeptidase/ zinc ion binding
At3g16730	31	0	Unknown protein
At3g16850	66	1	Glycoside hydrolase family 28 protein / polygalacturonase (pectinase) family protein
At3g17030	43	0	Nucleic acid-binding proteins superfamily
At3g17160	120	0	Unknown protein
At3g17205	12	0	UPL6 (UBIQUITIN PROTEIN LIGASE 6); ubiquitin-protein ligase

Supplementary Table 4

GENE ID[a]	Transcriptional activity[b]		PREDICTED FUNCTION[c]
	Wild type ovule	*spl* ovule	
At3g17210	14	0	HS1 (HEAT STABLE PROTEIN 1)
At3g17450	28	1	hAT dimerisation domain-containing protein
At3g17970	25	0	AtToc64-III (Arabidopsis thaliana translocon at the outer membrane of chloroplasts 64-III); binding / carbon-nitrogen ligase, with glutamine as amido-N-donor
At3g18350	10	0	Unknown protein
At3g18480	38	0	AtCASP (Arabidopsis thaliana CCAAT-displacement protein alternatively spliced product)
At3g18535	24	0	Other RNA
At3g19360	16	0	Zinc finger (CCCH-type) family protein
At3g19970	16	0	Unknown protein
At3g20170	41	0	Armadillo/beta-catenin repeat family protein
At3g20250	50	1	APUM5 (Arabidopsis Pumilio 5); RNA binding / binding
At3g20395	30	0	Protein binding / zinc ion binding
At3g20540	47	0	POLGAMMA1 (polymerase gamma 1); 3'-5' exonuclease/ DNA binding
At3g20650	34	0	mRNA capping enzyme family protein
At3g20680	14	0	Unknown protein
At3g20720	48	0	Unknown protein
At3g20890	30	1	RNA binding / nucleic acid binding / nucleotide binding
At3g20920	14	0	Translocation protein-related
At3g20970	43	1	NFU4; structural molecule
At3g21055	25	0	PSBTN (photosystem II subunit T)
At3g21175	28	0	ZML1 (ZIM-LIKE 1); sequence-specific DNA binding / transcription factor/ zinc ion binding
At3g21215	26	0	RNA-binding protein, putative
At3g21630	23	0	CERK1 (CHITIN ELICITOR RECEPTOR KINASE 1); kinase/ receptor signaling protein/ transmembrane receptor protein kinase
At3g21740	90	0	APO4 (ACCUMULATION OF PHOTOSYSTEM ONE 4)
At3g22160	16	0	VQ motif-containing protein
At3g22425	14	0	IGPD; imidazoleglycerol-phosphate dehydratase
At3g22430	20	0	Unknown protein
At3g22760	33	0	SOL1; transcription factor
At3g22810	9	0	Phosphoinositide binding
At3g22880	52	2	DMC1 (DISRUPTION OF MEIOTIC CONTROL 1)
At3g23030	15	0	IAA2 (INDOLE-3-ACETIC ACID INDUCIBLE 2)
At3g23080	30	1	Polyketide cyclase/dehydrase and lipid transport superfamily protein
At3g23100	21	0	XRCC4; protein C-terminus binding
At3g23710	26	1	Chloroplast inner membrane import protein Tic22, putative
At3g23805	35	0	RALFL24 (ralf-like 24); signal transducer
At3g24230	117	3	Pectate lyase family protein

Supplementary Table 4

GENE ID[a]	Transcriptional activity[b]		PREDICTED FUNCTION[c]
	Wild type ovule	*spl* ovule	
At3g24480	84	1	Leucine-rich repeat family protein / extensin family protein
At3g24510	136	4	Encodes a defensin-like (DEFL) family protein.
At3g24927	27	0	Pseudogene of Unknown protein
At3g25260	12	0	Proton-dependent oligopeptide transport (POT) family protein
At3g25590	9	0	Unknown protein
At3g25717	19	0	RTFL16 (ROTUNDIFOLIA LIKE 16)
At3g26020	12	0	Serine/threonine protein phosphatase 2A (PP2A) regulatory subunit B', putative
At3g26070	66	2	Plastid-lipid associated protein PAP / fibrillin family protein
At3g26410	12	0	Methyltransferase/ nucleic acid binding
At3g26618	9	0	ERF1-3 (eukaryotic release factor 1-3); translation release factor
At3g26910	24	0	Hydroxyproline-rich glycoprotein family protein
At3g27300	30	0	G6PD5 (glucose-6-phosphate dehydrogenase 5); glucose-6-phosphate dehydrogenase
At3g27990	14	0	Unknown gene
At3g28050	13	0	Nnodulin MtN21 family protein
At3g28345	17	0	ABC transporter family protein
At3g28450	32	1	Leucine-rich repeat transmembrane protein kinase, putative
At3g28560	10	0	BCS1 AAA-type ATPase
At3g28690	14	0	Protein kinase, putative
At3g28840	24	0	Unknown protein
At3g28917	11	0	MIF2 (MINI ZINC FINGER 2); DNA binding
At3g28970	9	0	AAR3 (antiauxin-resistant 3)
At3g28980	17	0	Unknown protein
At3g29020	9	0	MYB110 (myb domain protein 110); DNA binding / transcription factor
At3g29160	44	0	AKIN11 (Arabidopsis SNF1 kinase homolog 11); protein binding / protein kinase
At3g29260	14	0	Short-chain dehydrogenase/reductase (SDR) family protein
At3g29270	12	0	Ubiquitin-protein ligase
At3g29370	11	0	Unknown protein
At3g29375	16	0	XH domain-containing protein
At3g42670	23	0	CHR38 (CHROMATIN REMODELING 38); ATP binding / DNA binding / helicase/ nucleic acid binding
At3g43220	28	1	Phosphoinositide phosphatase family protein
At3g43850	21	0	Unknown protein
At3g43860	22	0	AtGH9A4 (Arabidopsis thaliana Glycosyl Hydrolase 9A4); catalytic/ hydrolase, hydrolyzing O-glycosyl compounds
At3g44330	16	0	Unknown function
At3g44735	11	0	PSK1; growth factor
At3g44850	19	0	Protein kinase-related

Supplementary Table 4

GENE ID[a]	Transcriptional activity[b]		PREDICTED FUNCTION[c]
	Wild type ovule	*spl* ovule	
At3g45040	22	0	Phosphatidate cytidylyltransferase family protein
At3g46668	16	0	Other RNA
At3g47342	30	0	snoRNA
At3g47450	27	0	NOA1 (NO ASSOCIATED 1); GTPase/ nitric-oxide synthase
At3g47620	12	0	AtTCP14 (TEOSINTE BRANCHED1, CYCLOIDEA and PCF (TCP) 14); transcription factor
At3g47730	22	0	ATATH1; ATPase, coupled to transmembrane movement of substances / transporter
At3g48030	36	0	Hypoxia-responsive family protein / zinc finger (C3HC4-type RING finger) family protein
At3g48530	19	0	KING1 (SNF1-RELATED PROTEIN KINASE REGULATORY SUBUNIT GAMMA 1)
At3g48610	11	0	Phosphoesterase family protein
At3g48690	17	0	CXE12; carboxylesterase
At3g48860	52	0	Unknown protein
At3g48880	12	0	F-box family protein
At3g48890	17	0	ATMP2; heme binding
At3g48950	11	0	Glycoside hydrolase family 28 protein / polygalacturonase (pectinase) family protein
At3g49050	14	0	Lipase class 3 family protein / calmodulin-binding heat-shock protein, putative
At3g49051	26	0	Unknown protein
At3g49100	20	0	signal recognition particle 9 kDa protein, putative / SRP9, putative
At3g49350	9	0	RAB GTPase activator
At3g49420	45	0	Got1-like family protein
At3g49920	9	0	VDAC5 (VOLTAGE DEPENDENT ANION CHANNEL 5); voltage-gated anion channel
At3g50050	9	0	Aspartyl protease family protein
At3g50665	22	0	pre-tRNA; tRNA-Glu (anticodon: TTC)
At3g51440	22	0	Strictosidine synthase family protein
At3g51450	25	0	Strictosidine synthase family protein
At3g51500	9	0	Unknown protein
At3g51980	45	0	Binding
At3g52060	9	0	Unknown protein
At3g52070	43	0	Unknown protein
At3g52072	17	0	Potential natural antisense gene, locus overlaps with AT3G52070
At3g52280	11	0	GTE6 (GENERAL TRANSCRIPTION FACTOR GROUP E6); DNA binding / H3/H4 histone acetyltransferase
At3g52290	28	0	IQD3 (IQ-domain 3); calmodulin binding
At3g52560	123	2	UEV1D-4 (UBIQUITIN E2 VARIANT 1D-4); protein binding / ubiquitin-protein ligase
At3g52800	20	0	Zinc finger (AN1-like) family protein
At3g53110	10	0	LOS4 (LOW EXPRESSION OF OSMOTICALLY RESPONSIVE GENES 4); ATP-dependent helicase/ RNA helicase/ RNA-dependent ATPase

Supplementary Table 4

GENE ID[a]	Transcriptional activity[b]		PREDICTED FUNCTION[c]
	Wild type ovule	*spl* ovule	
At3g53340	74	0	NF-YB10 (NUCLEAR FACTOR Y, SUBUNIT B10); transcription factor
At3g53420	130	0	PIP2A (PLASMA MEMBRANE INTRINSIC PROTEIN 2A); water channel
At3g53620	10	0	AtPPa4 (Arabidopsis thaliana pyrophosphorylase 4); inorganic diphosphatase
At3g54420	27	0	ATEP3; chitinase
At3g55060	34	0	Unknown protein
At3g56010	12	0	Unknown protein
At3g56030	9	0	Pentatricopeptide (PPR) repeat-containing protein
At3g56070	26	0	ROC2 (ROTAMASE CYCLOPHILIN 2); cyclosporin A binding / peptidyl-prolyl cis-trans isomerase
At3g56110	82	1	PRA1.B1 (PRENYLATED RAB ACCEPTOR 1.B1)
At3g56170	17	0	CAN (CA-2+ DEPENDENT NUCLEASE); nuclease
At3g56180	11	0	Unknown protein
At3g57060	33	1	Binding
At3g57280	14	0	Unknown protein
At3g57420	53	0	Unknown protein
At3g57550	14	0	AGK2 (GUANYLATE KINASE); guanylate kinase
At3g58010	12	0	Unknown protein
At3g58110	18	0	Unknown protein
At3g58580	23	0	Hydrolase
At3g58660	14	0	60S ribosomal protein-related
At3g58710	20	0	WRKY69; transcription factor
At3g58760	11	0	Ankyrin protein kinase, putative
At3g59260	17	0	Pirin, putative
At3g59390	12	0	Unknown protein
At3g59430	31	0	Unknown protein
At3g59630	13	0	Diphthamide synthesis DPH2 family protein
At3g59660	39	1	C2 domain-containing protein / GRAM domain-containing protein
At3g59960	38	0	ASHH4 (HISTONE-LYSINE N-METHYLTRANSFERASE ASHH4); histone-lysine N-methyltransferase
At3g60140	12	0	DIN2 (DARK INDUCIBLE 2); catalytic/ cation binding / hydrolase, hydrolyzing O-glycosyl compounds
At3g60500	31	0	CER7 (ECERIFERUM 7); 3'-5'-exoribonuclease/ RNA binding
At3g60520	26	0	Unknown protein
At3g60900	50	0	FLA10
At3g60965	27	1	Transposable element gene
At3g61060	139	0	AtPP2-A13 (Arabidopsis thaliana phloem protein 2-A13); carbohydrate binding
At3g61070	51	2	PEX11E
At3g61120	30	0	AGL13 (AGAMOUS-LIKE 13); DNA binding / transcription factor
At3g61160	33	0	Shaggy-related protein kinase beta / ASK-beta (ASK2)
At3g61300	35	1	C2 domain-containing protein

Supplementary Table 4

GENE ID[a]	Transcriptional activity[b]		PREDICTED FUNCTION[c]
	Wild type ovule	*spl* ovule	
At3g61420	10	0	BSD domain (BTF2-like transcription factors, Synapse-associated proteins and DOS2-like proteins)
At3g61570	11	0	GDAP1 (GRIP-RELATED ARF-BINDING DOMAIN-CONTAINING ARABIDOPSIS PROTEIN 1); protein binding
At3g61710	25	0	Autophagy protein Apg6 family
At3g61860	43	1	RSP31; RNA binding / nucleic acid binding / nucleotide binding
At3g62060	14	0	Pectinacetylesterase family protein
At3g62310	99	0	RNA helicase, putative
At3g62400	12	0	Unknown protein
At3g62420	170	0	ATBZIP53 (BASIC REGION/LEUCINE ZIPPER MOTIF 53); DNA binding / protein heterodimerization/ sequence-specific DNA binding / transcription factor
At3g62860	11	0	Esterase/lipase/thioesterase family protein
At3g63000	40	0	NPL41 (NPL4-LIKE PROTEIN 1)
At3g63010	84	1	GID1B (GA INSENSITIVE DWARF1B); hydrolase
At3g63440	27	0	CKX6 (CYTOKININ OXIDASE/DEHYDROGENASE 6); cytokinin dehydrogenase
At3g63450	62	1	RNA binding / nucleic acid binding / nucleotide binding
At4g00030	11	0	Plastid-lipid associated protein PAP / fibrillin family protein
At4g00120	11	0	IND (INDEHISCENT); DNA binding / transcription factor
At4g00270	60	0	DNA-binding storekeeper protein-related
At4g00380	13	0	XH/XS domain-containing protein / XS zinc finger domain-containing protein
At4g00450	27	0	CRP (CRYPTIC PRECOCIOUS)
At4g00467	40	0	Calcium-dependent lipid-binding (CaLB domain) family protein
At4g00905	38	1	NC domain-containing protein-related
At4g01180	11	0	XH/XS domain-containing protein
At4g01200	14	0	C2 domain-containing protein
At4g01250	22	0	WRKY22; transcription factor
At4g01710	49	1	CRK (CROOKED); actin binding
At4g01897	30	0	Unknown protein
At4g02040	25	0	Unknown protein
At4g02060	82	1	PRL (PROLIFERA); ATP binding / DNA binding / DNA-dependent ATPase/ nucleoside-triphosphatase/ nucleotide binding
At4g02200	14	0	Drought-responsive family protein
At4g02250	22	0	invertase/pectin methylesterase inhibitor family protein
At4g02400	25	0	U3 ribonucleoprotein (Utp) family protein
At4g02440	38	1	EID1 (EMPFINDLICHER IM DUNKELROTEN LICHT 1); ubiquitin-protein ligase
At4g02630	10	0	Protein kinase family protein
At4g02650	100	0	Epsin N-terminal homology (ENTH) domain-containing protein / clathrin assembly protein-related
At4g02655	100	0	Unknown protein
At4g02800	11	0	Unknown protein

Supplementary Table 4

GENE ID[a]	Transcriptional activity[b]		PREDICTED FUNCTION[c]
	Wild type ovule	*spl* ovule	
At4g02840	53	0	Small nuclear ribonucleoprotein D1, putative / snRNP core protein D1, putative / Sm protein D1, putative
At4g02940	11	0	Oxidoreductase, 2OG-Fe(II) oxygenase family protein
At4g03140	22	0	Binding / catalytic/ oxidoreductase
At4g03230	22	0	ATP binding / kinase/ protein kinase/ protein serine/threonine kinase/ protein tyrosine kinase/ sugar binding
At4g03240	17	0	FH (FRATAXIN HOMOLOG)
At4g03960	11	0	Tyrosine specific protein phosphatase family protein
At4g04320	9	0	Malonyl-CoA decarboxylase family protein
At4g04610	59	1	APR1 (APS REDUCTASE 1); adenylyl-sulfate reductase
At4g04670	53	2	Met-10+ like family protein / kelch repeat-containing protein
At4g04870	60	0	CLS (CARDIOLIPIN SYNTHASE); cardiolipin synthase/ phosphatidyltransferase
At4g05020	45	0	NDB2 (NAD(P)H dehydrogenase B2); FAD binding / disulfide oxidoreductase/ oxidoreductase
At4g05410	64	2	Transducin family protein / WD-40 repeat family protein
At4g07390	49	0	PQ-loop repeat family protein / transmembrane family protein
At4g08240	11	0	Unknown protein
At4g08690	14	0	SEC14 cytosolic factor family protein / phosphoglyceride transfer family protein
At4g08810	94	2	SUB1; calcium ion binding
At4g08980	12	0	F-box family protein (FBW2)
At4g09153	33	0	LCR36 (Low-molecular-weight cysteine-rich 36)
At4g09530	19	0	Auxin-responsive family protein
At4g10040	11	0	CYTC-2 (cytochrome c-2); electron carrier/ heme binding / iron ion binding
At4g10650	21	0	GTP binding
At4g10710	85	0	SPT16 (global transcription factor C)
At4g11060	32	0	MTSSB (mitochondrially targeted single-stranded DNA binding protein); single-stranded DNA binding
At4g11090	60	0	Unknown protein
At4g11330	16	0	ATMPK5 (MAP KINASE 5); MAP kinase/ kinase
At4g11570	17	0	Haloacid dehalogenase-like hydrolase family protein
At4g11760	57	0	LCR17 (Low-molecular-weight cysteine-rich 17)
At4g11790	43	0	Ran-binding protein 1 domain-containing protein / RanBP1 domain-containing protein
At4g11800	30	1	Hydrolase/ protein serine/threonine phosphatase
At4g11960	17	0	PGRL1B (PGR5-Like B)
At4g11980	21	0	ATNUDX14 (ARABIDOPSIS THALIANA NUDIX HYDROLASE HOMOLOG 14); ADP-glucose pyrophosphohydrolase/ ADP-ribose pyrophosphohydrolase/ ADP-sugar diphosphatase/ hydrolase
At4g12130	33	0	Aminomethyltransferase
At4g12340	28	1	Copper ion binding
At4g12650	69	0	Endomembrane protein 70 protein family
At4g12860	18	0	UNE14 (unfertilized embryo sac 14); calcium ion binding

Supplementary Table 4

GENE ID[a]	Transcriptional activity[b]		PREDICTED FUNCTION[c]
	Wild type ovule	*spl* ovule	
At4g13230	11	0	Late embryogenesis abundant domain-containing protein / LEA domain-containing protein
At4g13270	19	0	Unknown protein
At4g13690	45	0	Unknown protein
At4g13780	52	1	Methionine--tRNA ligase, putative / methionyl-tRNA synthetase, putative / MetRS, putative
At4g14070	9	0	AAE15 (acyl-activating enzyme 15); long-chain-fatty-acid-[acyl-carrier-protein] ligase
At4g14110	10	0	COP9 (CONSTITUTIVE PHOTOMORPHOGENIC 9); metalloendopeptidase/ protein binding
At4g14210	29	1	PDS3 (PHYTOENE DESATURASE 3); phytoene dehydrogenase
At4g14340	11	0	CKI1 (CASEIN KINASE I); kinase/ protein serine/threonine kinase
At4g14342	27	0	pre-mRNA splicing factor 10 kDa subunit, putative
At4g14570	59	0	Acylaminoacyl-peptidase-related
At4g14760	122	2	Kinase interacting (KIP1-like) family protein
At4g14900	21	0	Hydroxyproline-rich glycoprotein family protein
At4g14950	81	0	Unknown protein
At4g14960	28	0	TUA6; structural constituent of cytoskeleton
At4g15010	34	0	Mitochondrial substrate carrier family protein
At4g15640	14	0	Unknown protein
At4g15750	28	0	invertase/pectin methylesterase inhibitor family protein
At4g15885	18	0	Kinesin motor protein-related
At4g15940	65	2	Fumarylacetoacetate hydrolase family protein
At4g15955	43	0	Epoxide hydrolase-related
At4g16155	28	0	Dihydrolipoyl dehydrogenase
At4g16480	38	0	INT4 (INOSITOL TRANSPORTER 4); carbohydrate transmembrane transporter/ myo-inositol:hydrogen symporter/ sugar:hydrogen symporter
At4g16515	14	0	Unknown protein
At4g16570	50	2	PRMT7 (PROTEIN ARGININE METHYLTRANSFERASE 7); methyltransferase
At4g16640	18	0	Matrix metalloproteinase, putative
At4g16710	29	0	Glycosyltransferase family protein 28
At4g16980	13	0	Arabinogalactan-protein family
At4g17180	12	0	Glycosyl hydrolase family 17 protein
At4g17270	9	0	Mo25 family protein
At4g17695	12	0	KAN3 (KANADI 3); DNA binding / transcription factor
At4g18060	70	0	Clathrin binding
At4g18375	45	0	KH domain-containing protein
At4g18970	79	3	GDSL-motif lipase/hydrolase family protein
At4g19020	30	1	CMT2 (chromomethylase 2); DNA binding / chromatin binding
At4g19090	23	0	Unknown protein
At4g19185	45	0	Integral membrane family protein

Supplementary Table 4

GENE ID[a]	Transcriptional activity[b]		PREDICTED FUNCTION[c]
	Wild type ovule	*spl* ovule	
At4g19191	31	0	Pentatricopeptide (PPR) repeat-containing protein
At4g19220	18	0	Pentatricopeptide (PPR) repeat-containing protein
At4g19400	25	1	Actin binding
At4g19490	35	1	Protein binding
At4g19870	25	0	Kelch repeat-containing F-box family protein
At4g20130	120	2	PTAC14 (PLASTID TRANSCRIPTIONALLY ACTIVE14)
At4g20150	246	0	Unknown protein
At4g20362	11	0	other RNA
At4g20410	29	0	GSNAP (GAMMA-SOLUBLE NSF ATTACHMENT PROTEIN); binding / transporter
At4g20820	15	0	FAD-binding domain-containing protein
At4g21150	42	1	HAP6 (HAPLESS 6); dolichyl-diphosphooligosaccharide-protein glycotransferase
At4g21170	15	0	Pentatricopeptide (PPR) repeat-containing protein
At4g21350	14	0	PUB8 (PLANT U-BOX 8); binding / protein binding / ubiquitin-protein ligase/ zinc ion binding
At4g21610	37	1	LOL2 (LSD ONE LIKE 2); transcription factor
At4g21630	77	0	Subtilase family protein
At4g21710	66	0	NRPB2; DNA binding / DNA-directed RNA polymerase
At4g21730	26	0	Pseudogene of N-ethylmaleimide sensitive factor (NSF)
At4g21790	120	1	TOM1 (TOBAMOVIRUS MULTIPLICATION 1); protein binding
At4g21880	9	0	Pentatricopeptide (PPR) repeat superfamily-protein
At4g22105	84	0	SCRL26 (SCR-Like 26)
At4g22200	9	0	AKT2/3 (ARABIDOPSIS POTASSIUM TRANSPORT 2/3); cyclic nucleotide binding / inward rectifier potassium channel/ protein binding
At4g22280	12	0	F-box family protein
At4g22390	30	0	F-box associated ubiquitination effector family protein
At4g22830	9	0	Unknown protein
At4g23400	9	0	PIP1;5 (PLASMA MEMBRANE INTRINSIC PROTEIN 1;5); water channel
At4g23520	10	0	Cysteine proteinase, putative
At4g23530	13	0	Unknown protein
At4g23740	12	0	Lleucine-rich repeat transmembrane protein kinase, putative
At4g23940	23	0	FtsH protease, putative
At4g23960	19	0	F-box family protein
At4g24080	15	0	ALL1 (Aldolase like); carbon-carbon lyase/ catalytic
At4g24750	24	0	Rhodanese/Cell cycle control phosphatase superfamily protein
At4g25120	33	0	ATP binding / ATP-dependent DNA helicase/ DNA binding / hydrolase
At4g25520	9	0	SLK1 (SEUSS-LIKE 1); transcription regulator
At4g25570	70	1	ACYB-2; carbon-monoxide oxygenase

Supplementary Table 4

GENE ID[a]	Transcriptional activity[b]		PREDICTED FUNCTION[c]
	Wild type ovule	*spl* ovule	
At4g25700	49	1	BETA-OHASE 1 (BETA-HYDROXYLASE 1); carotene beta-ring hydroxylase
At4g25770	21	0	Unknown protein
At4g25840	11	0	GPP1 (glycerol-3-phosphatase 1); catalytic/ hydrolase
At4g25850	9	0	ORP4B (OSBP(OXYSTEROL BINDING PROTEIN)-RELATED PROTEIN 4B); oxysterol binding
At4g26070	11	0	MEK1 (MAP KINASE/ ERK KINASE 1); MAP kinase kinase/ kinase/ protein binding
At4g26180	9	0	Mitochondrial substrate carrier family protein
At4g26500	30	1	CPSUFE (CHLOROPLAST SULFUR E); enzyme activator/ transcription regulator
At4g26550	22	0	Got1/Sft2-like vescicle transport protein family
At4g26610	19	0	D6PKL1 (D6 PROTEIN KINASE LIKE 1); kinase
At4g26640	17	0	WRKY20; transcription factor
At4g26660	23	0	Unknown function
At4g27090	46	1	60S ribosomal protein L14 (RPL14B)
At4g27270	21	0	Quinone reductase family protein
At4g27280	53	0	Calcium-binding EF hand family protein
At4g27350	14	0	Unknown protein
At4g27540	27	0	PRA1.H (PRENYLATED RAB ACCEPTOR 1.H)
At4g27580	20	0	Unknown protein
At4g27654	33	1	Unknown protein
At4g27660	36	0	Unknown protein
At4g28010	14	0	Pentatricopeptide (PPR) repeat-containing protein
At4g28020	95	0	Unknown protein
At4g28290	12	0	Unknown protein
At4g28610	186	2	PHR1 (PHOSPHATE STARVATION RESPONSE 1); transcription factor
At4g28630	22	0	ATM1 (ABC TRANSPORTER OF THE MITOCHONDRION); ATPase, coupled to transmembrane movement of substances / transporter
At4g28730	25	0	Glutaredoxin family protein
At4g28775	30	0	Unknown protein
At4g28950	14	0	ROP9 (RHO-RELATED PROTEIN FROM PLANTS 9); GTP binding
At4g29100	23	0	Ethylene-responsive family protein
At4g29160	41	1	SNF7.1
At4g29340	19	0	PRF4 (PROFILIN 4); actin binding
At4g29735	245	5	Unknown protein
At4g29810	28	0	ATMKK2 (ARABIDOPSIS THALIANA MAP KINASE KINASE 2); MAP kinase kinase/ kinase
At4g29960	14	0	Unknown protein
At4g29990	11	0	Light repressible receptor protein kinase

Supplementary Table 4

GENE ID[a]	Transcriptional activity[b]		PREDICTED FUNCTION[c]
	Wild type ovule	*spl* ovule	
At4g30190	9	0	AHA2; ATPase/ hydrogen-exporting ATPase, phosphorylative mechanism
At4g30220	36	1	RUXF (SMALL NUCLEAR RIBONUCLEOPROTEIN F)
At4g30360	12	0	ATCNGC17; calmodulin binding / cyclic nucleotide binding / ion channel
At4g30430	10	0	TET9 (TETRASPANIN9)
At4g30600	49	1	Signal recognition particle receptor alpha subunit family protein
At4g30610	25	0	BRS1 (BRI1 SUPPRESSOR 1); serine-type carboxypeptidase
At4g30662	39	0	Unknown protein
At4g30970	19	0	Unknown protein
At4g31010	20	0	RNA binding
At4g31040	10	0	Proton extrusion protein-related
At4g31600	21	0	UDP-glucuronic acid/UDP-N-acetylgalactosamine transporter-related
At4g31650	15	0	Transcriptional factor B3 family protein
At4g31750	22	0	WIN2 (HOPW1-1-INTERACTING 2); protein serine/threonine phosphatase
At4g31820	71	0	ENP (ENHANCER OF PINOID); protein binding / signal transducer
At4g32130	12	0	Carbohydrate binding
At4g32170	14	0	CYP96A2; electron carrier/ heme binding / iron ion binding / monooxygenase/ oxygen binding
At4g32190	34	1	Centromeric protein-related
At4g32490	10	0	Plastocyanin-like domain-containing protein
At4g32530	69	0	Vacuolar ATP synthase, putative / V-atpase, putative
At4g32590	30	0	Ferredoxin-related
At4g32600	35	1	Zinc finger (C3HC4-type RING finger) family protein
At4g33460	9	0	ATNAP13; transporter
At4g33490	11	0	Apartic-type endopeptidase
At4g33630	12	0	EX1 (EXECUTER1)
At4g34090	39	0	Unknown protein
At4g34180	42	0	Cyclase family protein
At4g34480	9	0	Catalytic/ cation binding / hydrolase, hydrolyzing O-glycosyl compounds
At4g34870	107	1	ROC5 (ROTAMASE CYCLOPHILIN 5); peptidyl-prolyl cis-trans isomerase
At4g35020	20	0	ARAC3 (ARABIDOPSIS RAC-LIKE 3); GTP binding / GTPase
At4g35335	17	0	Nucleotide-sugar transmembrane transporter/ sugar:hydrogen symporter
At4g35770	202	0	SEN1 (SENESCENCE 1)
At4g35785	12	0	Nucleic acid binding / nucleotide binding
At4g35800	26	1	NRPB1 (RNA POLYMERASE II LARGE SUBUNIT); DNA binding / DNA-directed RNA polymerase
At4g35840	27	0	Zinc finger (C3HC4-type RING finger) family protein
At4g36240	45	0	Zinc finger (GATA type) family protein
At4g36280	35	0	ATP-binding region, ATPase-like domain-containing protein

Supplementary Table 4

GENE ID[a]	Transcriptional activity[b]		PREDICTED FUNCTION[c]
	Wild type ovule	*spl* ovule	
At4g36470	11	0	S-adenosyl-L-methionine:carboxyl methyltransferase family protein
At4g36940	43	0	NAPRT1 (NICOTINATE PHOSPHORIBOSYLTRANSFERASE 1); nicotinate phosphoribosyltransferase
At4g37445	11	0	BEST Arabidopsis thaliana protein match is: calcium-binding EF hand family protein
At4g37460	36	1	SRFR1 (SUPPRESSOR OF RPS4-RLD 1); protein complex scaffold
At4g37800	11	0	Xyloglucan:xyloglucosyl transferase, putative / xyloglucan endotransglycosylase, putative / endo-xyloglucan transferase, putative
At4g38090	25	0	Unknown protein
At4g38150	28	0	Pentatricopeptide (PPR) repeat-containing protein
At4g38230	14	0	CPK26; ATP binding / calcium ion binding / calmodulin-dependent protein kinase/ kinase/ protein kinase
At4g38360	24	0	Unknown protein
At4g38380	10	0	Antiporter/ drug transporter
At4g38470	28	1	Protein kinase family protein
At4g38520	58	0	Protein phosphatase 2C family protein / PP2C family protein
At4g38650	14	0	Glycosyl hydrolase family 10 protein
At4g38790	27	0	ER lumen protein retaining receptor family protein
At4g38800	40	0	ATMTN1; catalytic/ methylthioadenosine nucleosidase
At4g39550	36	0	Kelch repeat-containing F-box family protein
At4g39780	11	0	AP2 domain-containing transcription factor, putative
At4g39800	19	0	MIPS1 (MYO-INOSITOL-1-PHOSTPATE SYNTHASE 1); inositol-3-phosphate synthase
At4g39865	11	0	pre-tRNA
At4g39890	17	0	AtRABH1c (Arabidopsis Rab GTPase homolog H1c); GTP binding / protein binding
At5g01075	9	0	Beta-galactosidase
At5g01370	26	0	Unknown protein
At5g01650	18	0	Macrophage migration inhibitory factor family protein / MIF family protein
At5g01800	9	0	Saposin B domain-containing protein
At5g01810	12	0	CIPK15 (CBL-INTERACTING PROTEIN KINASE 15); kinase/ protein kinase
At5g01860	25	0	Zinc finger (C2H2 type) family protein
At5g02180	20	0	Amino acid transporter family protein
At5g02410	25	1	DIE2/ALG10 family
At5g02560	13	0	HTA12; DNA binding
At5g02850	18	0	Hydroxyproline-rich glycoprotein family protein
At5g02950	61	2	PWWP domain-containing protein
At5g03070	45	0	IMPA-9 (IMPORTIN ALPHA ISOFORM 9); binding
At5g03320	18	0	Protein kinase, putative
At5g03330	29	0	OTU-like cysteine protease family protein
At5g03520	40	0	ATRAB8C; GTP binding

Supplementary Table 4

GENE ID[a]	Transcriptional activity[b]		PREDICTED FUNCTION[c]
	Wild type ovule	*spl* ovule	
At5g04770	10	0	CAT6 (CATIONIC AMINO ACID TRANSPORTER 6); amino acid transmembrane transporter/ basic amino acid transmembrane transporter/ cationic amino acid transmembrane transporter
At5g04930	63	1	ALA1 (aminophospholipid ATPase1); ATPase, coupled to transmembrane movement of ions, phosphorylative mechanism
At5g05090	25	0	Myb family transcription factor
At5g05100	74	0	Nucleic acid binding
At5g05365	38	0	Metal ion binding
At5g05760	42	0	SYP31 (SYNTAXIN OF PLANTS 31); SNAP receptor
At5g06220	34	1	LETM1-like protein
At5g06310	27	0	AtPOT1b (protection of telomeres 1b); DNA binding
At5g06350	11	0	Binding
At5g06660	10	0	Unknown protein
At5g06810	10	0	Mitochondrial transcription termination factor-related / mTERF-related
At5g06870	36	0	PGIP2 (POLYGALACTURONASE INHIBITING PROTEIN 2); protein binding
At5g07350	73	0	Tudor domain-containing protein / nuclease family protein
At5g07710	24	0	Exonuclease family protein
At5g07810	22	0	SNF2 domain-containing protein / helicase domain-containing protein / HNH endonuclease domain-containing protein
At5g07910	55	0	Leucine-rich repeat family protein
At5g07950	28	0	Unknown protein
At5g07960	76	0	Unknown protein
At5g08090	9	0	Unknown protein
At5g08100	84	0	L-asparaginase / L-asparagine amidohydrolase
At5g08120	22	0	MBP2C (MICROTUBULE BINDING PROTEIN 2C); protein binding
At5g08340	30	0	Riboflavin biosynthesis protein-related
At5g08350	53	0	GRAM domain-containing protein / ABA-responsive protein-related
At5g08565	39	0	Positive transcription elongation factor/ zinc ion binding
At5g08710	15	0	Regulator of chromosome condensation (RCC1) family protein / UVB-resistance protein-related
At5g08720	9	0	BEST Arabidopsis thaliana protein match is: Polyketide cyclase / dehydrase and lipid transport protein
At5g09260	12	0	VPS20.2 (VACUOLAR PROTEIN SORTING-ASSOCIATED PROTEIN 20.2)
At5g09580	21	0	Unknown protein
At5g10290	9	0	Leucine-rich repeat family protein / protein kinase family protein
At5g10620	11	0	Methyltransferases
At5g10630	9	0	Elongation factor 1-alpha, putative / EF-1-alpha, putative
At5g10790	14	0	UBP22 (UBIQUITIN-SPECIFIC PROTEASE 22); ubiquitin thiolesterase/ ubiquitin-specific protease/ zinc ion binding
At5g10910	18	0	mraW methylase family protein

Supplementary Table 4

GENE ID[a]	Transcriptional activity[b]		PREDICTED FUNCTION[c]
	Wild type ovule	*spl* ovule	
At5g11020	15	0	ATP binding / kinase/ protein kinase/ protein serine/threonine kinase/ protein tyrosine kinase
At5g11180	24	0	ATGLR2.6; intracellular ligand-gated ion channel
At5g11380	16	0	DXPS3 (1-deoxy-D-xylulose 5-phosphate synthase 3); 1-deoxy-D-xylulose-5-phosphate synthase
At5g11490	17	0	Adaptin family protein
At5g11810	23	0	Unknown protein
At5g11870	12	0	Alkaline phytoceramidase (aPHC)
At5g12290	9	0	DGS1 (DGD1 SUPPRESSOR 1)
At5g12380	58	0	Annexin, putative
At5g12970	14	0	C2 domain-containing protein
At5g13150	27	0	ATEXO70C1 (exocyst subunit EXO70 family protein C1); protein binding
At5g13200	29	0	GRAM domain-containing protein / ABA-responsive protein-related
At5g13440	26	0	Ubiquinol-cytochrome C reductase iron-sulfur subunit, mitochondrial, putative / Rieske iron-sulfur protein, putative
At5g13490	193	7	Encodes mitochondrial ADP/ATP carrier
At5g13650	26	0	Elongation factor family protein
At5g13710	16	0	SMT1 (STEROL METHYLTRANSFERASE 1); sterol 24-C-methyltransferase
At5g13770	22	0	Pentatricopeptide (PPR) repeat-containing protein
At5g13790	13	0	AGL15 (AGAMOUS-LIKE 15); DNA binding / transcription factor
At5g13860	30	0	ELC-Like (ELCH-like); small conjugating protein ligase
At5g14280	9	0	DNA-binding storekeeper protein-related
At5g14500	15	0	Aldose 1-epimerase family protein
At5g14860	18	0	Transferase, transferring glycosyl groups
At5g14910	11	0	Heavy-metal-associated domain-containing protein
At5g15260	97	3	Structural constituent of ribosome
At5g15760	25	0	Plastid-specific 30S ribosomal protein 3, putative / PSRP-3, putative
At5g15770	23	0	AtGNA1 (Arabidopsis thaliana glucose-6-phosphate acetyltransferase 1); N-acetyltransferase/ glucosamine 6-phosphate N-acetyltransferase
At5g15810	15	0	N2,N2-dimethylguanosine tRNA methyltransferase family protein
At5g15860	13	0	ATPCME (PRENYLCYSTEINE METHYLESTERASE); prenylcysteine methylesterase
At5g16250	47	0	Unknown protein
At5g16260	9	0	RNA recognition motif (RRM)-containing protein
At5g16390	25	0	CAC1 (CHLOROPLASTIC ACETYLCOENZYME A CARBOXYLASE 1); acetyl-CoA carboxylase/ biotin binding
At5g16500	14	0	Protein kinase family protein
At5g16560	9	0	KAN (KANADI); transcription factor
At5g16660	35	0	Unknown protein
At5g16720	29	0	Unknown protein

Supplementary Table 4

GENE ID[a]	Transcriptional activity[b]		PREDICTED FUNCTION[c]
	Wild type ovule	*spl* ovule	
At5g16820	37	1	HSF3 (HEAT SHOCK FACTOR 3); DNA binding / transcription factor
At5g17090	26	1	Cystatin/monellin superfamily protein
At5g17210	126	2	Unknown protein
At5g17300	33	0	Myb family transcription factor
At5g17710	32	0	EMB1241 (embryo defective 1241); adenyl-nucleotide exchange factor/ chaperone binding / protein binding / protein homodimerization
At5g17770	13	0	ATCBR (ARABIDOPSIS THALIANA NADH:CYTOCHROME B5 REDUCTASE 1); cytochrome-b5 reductase
At5g17790	25	0	VAR3 (VARIEGATED 3); binding / zinc ion binding
At5g18220	18	0	Glycosyl hydrolase family 17 protein
At5g18255	72	2	other RNA
At5g18440	11	0	Unknown protein
At5g18480	24	0	PGSIP6 (PLANT GLYCOGENIN-LIKE STARCH INITIATION PROTEIN 6); transferase, transferring glycosyl groups / transferase, transferring hexosyl groups
At5g18630	114	1	Lipase class 3 family protein
At5g18810	12	0	SCL28; RNA binding / nucleic acid binding / nucleotide binding
At5g18840	13	0	Sugar transporter, putative
At5g19151	104	2	Unknown protein
At5g19210	14	0	DEAD/DEAH box helicase, putative
At5g19670	14	0	Exostosin family protein
At5g19790	25	0	RAP2.11 (related to AP2 11); DNA binding / transcription factor
At5g19810	34	0	Proline-rich extensin-like family protein
At5g19910	11	0	SOH1 family protein
At5g20150	12	0	SPX1 (SPX DOMAIN GENE 1)
At5g20250	681	18	DIN10 (DARK INDUCIBLE 10); hydrolase, hydrolyzing O-glycosyl compounds
At5g20500	31	0	glutaredoxin, putative
At5g20510	22	0	AL5 (ALFIN-LIKE 5); DNA binding / methylated histone residue binding
At5g20660	23	0	24 kDa vacuolar protein, putative
At5g20830	60	2	SUS1 (SUCROSE SYNTHASE 1); UDP-glycosyltransferase/ sucrose synthase
At5g21080	35	0	Unknown protein
At5g21140	26	1	emb1379 (embryo defective 1379)
At5g21160	79	2	La domain-containing protein / proline-rich family protein
At5g21900	34	0	Unknown protein
At5g22060	75	0	ATJ2; protein binding
At5g22400	14	0	Rac GTPase activating protein, putative
At5g22450	52	2	Unknown protein
At5g22460	109	0	Esterase/lipase/thioesterase family protein

Supplementary Table 4

GENE ID[a]	Transcriptional activity[b]		PREDICTED FUNCTION[c]
	Wild type ovule	*spl* ovule	
At5g22830	21	0	ATMGT10 (MAGNESIUM (MG) TRANSPORTER 10); magnesium ion transmembrane transporter
At5g22875	17	0	Unknown protein
At5g23090	30	0	NF-YB13 (NUCLEAR FACTOR Y, SUBUNIT B13); transcription factor
At5g23380	24	0	Unknown protein
At5g23395	128	0	Encodes Mia40, a component of the mitochondrial intermembrane space assembly machinery involved in the import pathway of the small intermembrane space proteins.
At5g23850	27	0	Unknown function.
At5g23870	37	1	Pectinacetylesterase family protein
At5g24400	22	0	emb2024 (embryo defective 2024); 6-phosphogluconolactonase/ catalytic
At5g24735	49	0	Unknown gene
At5g25060	13	0	RNA recognition motif (RRM)-containing protein
At5g25080	31	0	Sas10/Utp3/C1D family
At5g25090	132	5	Plastocyanin-like domain-containing protein
At5g25100	81	1	Endomembrane protein 70, putative
At5g25780	30	0	EIF3B-2 (EUKARYOTIC TRANSLATION INITIATION FACTOR 3B-2); nucleic acid binding / protein binding / translation initiation factor
At5g25920	14	0	BEST Arabidopsis thaliana protein match is: Eukaryotic aspartyl protease family protein
At5g26200	13	0	Mitochondrial substrate carrier family protein
At5g26210	38	0	AL4 (ALFIN-LIKE 4); DNA binding / methylated histone residue binding
At5g26820	46	0	ATIREG3 (IRON-REGULATED PROTEIN 3)
At5g26910	15	0	Unknown protein
At5g27380	10	0	GSH2 (GLUTATHIONE SYNTHETASE 2); glutathione synthase
At5g27400	52	0	Unknown protein
At5g27440	14	0	Unknown protein
At5g27730	11	0	Unknown protein
At5g27750	59	0	F-box family protein
At5g27830	14	0	Unknown function
At5g27970	27	0	Binding
At5g28000	40	0	Bet v I allergen family protein
At5g28020	39	0	CYSD2 (CYSTEINE SYNTHASE D2); catalytic/ cysteine synthase/ pyridoxal phosphate binding
At5g28626	11	0	Transposable element gene
At5g28840	10	0	GME (GDP-D-MANNOSE 3',5'-EPIMERASE); GDP-mannose 3,5-epimerase/ NAD or NADH binding / catalytic
At5g33340	23	0	CDR1 (CONSTITUTIVE DISEASE RESISTANCE 1); aspartic-type endopeptidase
At5g35680	17	0	Eukaryotic translation initiation factor 1A, putative / eIF-1A, putative / eIF-4C, putative

Supplementary Table 4

GENE ID[a]	Transcriptional activity[b]		PREDICTED FUNCTION[c]
	Wild type ovule	*spl* ovule	
At5g36170	13	0	HCF109 (HIGH CHLOROPHYLL FLUORESCENT 109); translation release factor/ translation release factor, codon specific
At5g37130	15	0	Protein prenylyltransferase superfamily protein
At5g37190	11	0	CIP4 (COP1-interacting protein 4); transcription cofactor
At5g37380	12	0	DNAJ heat shock N-terminal domain-containing protein
At5g37540	10	0	Aspartyl protease family protein
At5g37710	15	0	Lipase class 3 family protein / calmodulin-binding heat-shock protein, putative
At5g37890	59	1	Seven in absentia (SINA) protein, putative
At5g38460	19	0	ALG6, ALG8 glycosyltransferase family protein
At5g38850	20	0	Disease resistance protein (TIR-NBS-LRR class), putative
At5g38860	13	0	BIM3 (BES1-interacting Myc-like protein 3); DNA binding / transcription factor
At5g38970	39	0	BR6OX1 (BRASSINOSTEROID-6-OXIDASE 1); monooxygenase/ oxygen binding
At5g39840	9	0	ATP-dependent RNA helicase, mitochondrial, putative
At5g40150	14	0	Peroxidase, putative
At5g40200	36	0	DegP9 (DegP protease 9); catalytic/ protein binding / serine-type endopeptidase/ serine-type peptidase
At5g40380	13	0	Protein kinase family protein
At5g40760	72	0	G6PD6 (GLUCOSE-6-PHOSPHATE DEHYDROGENASE 6); glucose-6-phosphate dehydrogenase
At5g41020	9	0	Myb family transcription factor
At5g41600	9	0	BTI3 (VIRB2-INTERACTING PROTEIN 3)
At5g41980	36	0	Unknown protein
At5g42030	49	0	ABIL4 (ABL INTERACTOR-LIKE PROTEIN 4)
At5g42060	44	0	Unknown protein
At5g42242	9	0	LCR57 (Low-molecular-weight cysteine-rich 57)
At5g43280	53	0	ATDCI1 (DELTA(3,5),DELTA(2,4)-DIENOYL-COA ISOMERASE 1); delta3,5-delta2,4-dienoyl-CoA isomerase/ enoyl-CoA hydratase
At5g43430	35	0	ETFBETA; electron carrier
At5g43513	141	3	Encodes a defensin-like (DEFL) family protein.
At5g44040	13	0	Unknown protein
At5g44495	14	0	Encodes a ECA1 gametogenesis related family protein
At5g44500	10	0	Small nuclear ribonucleoprotein associated protein B, putative / snRNP-B, putative / Sm protein B, putative
At5g44760	24	0	C2 domain-containing protein
At5g44860	18	0	Unknown protein
At5g44980	13	0	F-box family protein
At5g45050	14	0	TTR1; protein binding / transcription factor
At5g45110	10	0	NPR3 (NPR1-LIKE PROTEIN 3); protein binding
At5g45170	18	0	CbbY protein-related
At5g45260	19	0	RRS1 (RESISTANT TO RALSTONIA SOLANACEARUM 1); DNA binding / transcription factor

Supplementary Table 4

GENE ID[a]	Transcriptional activity[b]		PREDICTED FUNCTION[c]
	Wild type ovule	*spl* ovule	
At5g45590	18	0	Unknown protein
At5g45750	9	0	AtRABA1c (Arabidopsis Rab GTPase homolog A1c); GTP binding
At5g45775	130	5	60S ribosomal protein L11 (RPL11D)
At5g45790	14	0	Ubiquitin thiolesterase
At5g46590	14	0	Anac096 (Arabidopsis NAC domain containing protein 96); transcription factor
At5g46700	9	0	TRN2 (TORNADO 2)
At5g46730	18	0	Glycine-rich protein
At5g46790	16	0	Unknown protein
At5g46960	39	0	Invertase/pectin methylesterase inhibitor family protein
At5g47110	13	0	lil3 protein, putative
At5g47240	66	0	Atnudt8 (Arabidopsis thaliana Nudix hydrolase homolog 8); hydrolase
At5g47250	11	0	Disease resistance protein (CC-NBS-LRR class), putative
At5g47370	17	0	HAT2; DNA binding / transcription factor/ transcription repressor
At5g47520	18	0	AtRABA5a (Arabidopsis Rab GTPase homolog A5a); GTP binding
At5g47700	155	0	60S acidic ribosomal protein P1 (RPP1C)
At5g47810	12	0	PFK2 (PHOSPHOFRUCTOKINASE 2); 6-phosphofructokinase
At5g48090	20	0	ELP1 (EDM2-LIKE PROTEIN1)
At5g48290	9	0	Heavy-metal-associated domain-containing protein
At5g48520	26	0	Unknown protein
At5g48530	43	0	Unknown protein
At5g48840	19	0	PANC (ARABIDOPSIS HOMOLOG OF BACTERIAL PANC); pantoate-beta-alanine ligase/ protein homodimerization
At5g49010	47	1	SLD5 (SYNTHETIC LETHALITY WITH DPB11-1 5)
At5g49015	14	0	Expressed protein
At5g49215	21	0	Glycoside hydrolase family 28 protein / polygalacturonase (pectinase) family protein
At5g49220	13	0	Unknown protein
At5g49400	34	0	Zinc knuckle (CCHC-type) family protein
At5g49640	45	1	Unknown protein
At5g49880	11	0	Mitotic checkpoint family protein
At5g50340	9	0	ATP binding / damaged DNA binding / nucleoside-triphosphatase/ nucleotide binding
At5g50430	35	1	UBC33 (ubiquitin-conjugating enzyme 33); ubiquitin-protein ligase
At5g50930	26	0	DNA binding
At5g50970	11	0	WD-40 repeat family protein
At5g51020	39	0	CRL (CRUMPLED LEAF)
At5g51451	17	0	Unknown protein
At5g51700	26	0	PBS2 (PPHB SUSCEPTIBLE 2); protein binding / zinc ion binding
At5g51890	24	0	Peroxidase
At5g52030	11	0	TraB protein-related

Supplementary Table 4

GENE ID[a]	Transcriptional activity[b]		PREDICTED FUNCTION[c]
	Wild type ovule	*sp/* ovule	
At5g52810	30	0	Ornithine cyclodeaminase/mu-crystallin family protein
At5g52860	33	0	ABC transporter family protein
At5g53060	43	1	KH domain-containing protein
At5g53080	12	0	Kinesin light chain-related
At5g53280	68	1	PDV1 (PLASTID DIVISION1)
At5g53440	17	0	Unknown protein
At5g53470	17	0	ACBP1 (ACYL-COA BINDING PROTEIN 1); acyl-CoA binding / lead ion binding
At5g53650	24	0	Unknown protein
At5g53940	33	1	Yippee family protein
At5g54160	60	0	ATOMT1 (O-METHYLTRANSFERASE 1); caffeate O-methyltransferase/ myricetin 3'-O-methyltransferase/ quercetin 3-O-methyltransferase
At5g54500	14	0	FQR1 (FLAVODOXIN-LIKE QUINONE REDUCTASE 1); FMN binding / oxidoreductase, acting on NADH or NADPH, quinone or similar compound as acceptor
At5g54760	14	0	Eukaryotic translation initiation factor SUI1, putative
At5g54870	35	0	Unknown protein
At5g55000	79	0	FIP2; protein binding / voltage-gated potassium channel
At5g55120	131	3	VTC5 (VITAMIN C DEFECTIVE 5); GDP-D-glucose phosphorylase/ galactose-1-phosphate guanylyltransferase (GDP)/ quercetin 4'-O-glucosyltransferase
At5g55160	34	0	SUMO2 (SMALL UBIQUITIN-LIKE MODIFIER 2); protein binding / protein tag
At5g55210	41	0	Unknown protein
At5g55700	21	0	BAM4 (BETA-AMYLASE 4); beta-amylase/ catalytic/ cation binding
At5g55930	25	1	OPT1 (OLIGOPEPTIDE TRANSPORTER 1); oligopeptide transporter
At5g55940	11	0	emb2731 (embryo defective 2731)
At5g55990	9	0	CBL2 (CALCINEURIN B-LIKE 2); calcium ion binding
At5g56020	35	1	Got1/Sft2-like vescicle transport protein family
At5g56120	14	0	Unknown protein
At5g56130	14	0	Transducin family protein / WD-40 repeat family protein
At5g56350	23	0	Pyruvate kinase, putative
At5g56550	17	0	OXS3 (OXIDATIVE STRESS 3)
At5g56880	15	0	Unknown protein
At5g56890	16	0	Protein kinase family protein
At5g57070	12	0	Hhydroxyproline-rich glycoprotein family protein
At5g57160	13	0	ATLIG4; DNA ligase (ATP)/ protein binding
At5g57280	31	0	Methyltransferase
At5g57290	43	0	60S acidic ribosomal protein P3 (RPP3B)
At5g57410	30	1	Unknown protein
At5g57590	30	0	BIO1 (biotin auxotroph 1); adenosylmethionine-8-amino-7-oxononanoate transaminase

Supplementary Table 4

GENE ID[a]	Transcriptional activity[b]		PREDICTED FUNCTION[c]
	Wild type ovule	*spl* ovule	
At5g57940	10	0	ATCNGC5 (CYCLIC NUCLEOTIDE GATED CHANNEL 5); calmodulin binding / cyclic nucleotide binding / potassium channel
At5g57960	28	0	GTP-binding family protein
At5g58640	21	0	Selenoprotein-related
At5g58750	40	0	Wound-responsive protein-related
At5g59030	28	0	COPT1 (copper transporter 1); copper ion transmembrane transporter
At5g59290	35	0	UXS3 (UDP-GLUCURONIC ACID DECARBOXYLASE 3); UDP-glucuronate decarboxylase/ catalytic
At5g59440	23	0	ZEU1 (ZEUS1); ATP binding / thymidylate kinase
At5g59470	24	0	PQ-loop repeat family protein / transmembrane family protein
At5g59550	65	0	Zinc finger (C3HC4-type RING finger) family protein
At5g59810	29	0	SBT5.4; identical protein binding / serine-type endopeptidase
At5g59960	27	0	Unknown protein
At5g60170	83	3	RNA binding / nucleic acid binding / nucleotide binding / protein binding / zinc ion binding
At5g60200	27	0	Dof-type zinc finger domain-containing protein
At5g60340	11	0	MaoC-like dehydratase domain-containing protein
At5g60460	13	0	Sec61beta family protein
At5g60553	19	0	Encodes a defensin-like (DEFL) family protein.
At5g60600	24	0	HDS (4-HYDROXY-3-METHYLBUT-2-ENYL DIPHOSPHATE SYNTHASE); 4 iron, 4 sulfur cluster binding / 4-hydroxy-3-methylbut-2-en-1-yl diphosphate synthase
At5g60630	39	1	Unknown protein
At5g60640	61	0	ATPDIL1-4 (PDI-LIKE 1-4); protein disulfide isomerase
At5g60690	17	0	REV (REVOLUTA); DNA binding / lipid binding / transcription factor
At5g60880	32	0	Unknown protein
At5g60963	11	0	pre-tRNA
At5g61530	12	0	Small G protein family protein / RhoGAP family protein
At5g61800	14	0	Pentatricopeptide (PPR) repeat-containing protein
At5g61820	13	0	Unknown function
At5g61840	64	0	GUT1; catalytic/ glucuronoxylan glucuronosyltransferase
At5g61920	38	1	Unknown protein
At5g61930	50	0	APO3 (ACCUMULATION OF PHOTOSYSTEM ONE 3)
At5g61990	14	0	Pentatricopeptide (PPR) repeat-containing protein
At5g62000	35	1	ARF2 (AUXIN RESPONSE FACTOR 2); protein binding / transcription factor
At5g58920	37	0	Unknown protein
At5g62080	12	0	Protease inhibitor/seed storage/lipid transfer protein (LTP) family protein
At5g62170	30	1	Unknown protein

Supplementary Table 4

GENE ID[a]	Transcriptional activity[b]		PREDICTED FUNCTION[c]
	Wild type ovule	*spl* ovule	
At5g62200	31	0	Embryo-specific protein-related
At5g62280	42	0	Unknown protein
At5g62550	11	0	Unknown protein
At5g62610	180	2	Basic helix-loop-helix (bHLH) family protein
At5g62710	17	0	Leucine-rich repeat family protein / protein kinase family protein
At5g62910	58	2	Protein binding / zinc ion binding
At5g62920	12	0	ARR6 (RESPONSE REGULATOR 6); transcription regulator/ two-component response regulator
At5g62940	76	0	Dof-type zinc finger domain-containing protein
At5g62980	82	0	Dihydroneopterin aldolase, putative
At5g63060	16	0	Transporter
At5g63063	11	0	Encodes a Plant thionin family protein
At5g63087	26	0	Encodes a Plant thionin family protein
At5g63180	24	0	Pectate lyase family protein
At5g63300	12	0	Structural constituent of ribosome
At5g63490	33	0	CBS domain-containing protein / octicosapeptide/Phox/Bemp1 (PB1) domain-containing protein
At5g63500	43	0	Unknown protein
At5g63760	92	2	IBR domain-containing protein
At5g63800	9	0	MUM2 (MUCILAGE-MODIFIED 2); beta-galactosidase
At5g63870	19	0	PP7 (SERINE/THREONINE PHOSPHATASE 7); protein serine/threonine phosphatase
At5g63920	52	0	DNA topoisomerase III alpha, putative
At5g64050	39	0	ERS (GLUTAMATE TRNA SYNTHETASE); glutamate-tRNA ligase
At5g64150	30	0	Methylase family protein
At5g64250	60	0	2-nitropropane dioxygenase family / NPD family.
At5g64280	12	0	DiT2.2 (dicarboxylate transporter 2.2); oxoglutarate:malate antiporter
At5g64440	42	1	AtFAAH (Arabidopsis thaliana fatty acid amide hydrolase); N-(long-chain-acyl)ethanolamine deacylase/ amidase
At5g64572	40	0	Potential natural antisense gene, locus overlaps with At5g64570.
At5g64650	17	0	Ribosomal protein L17 family protein
At5g65080	20	0	MAF5 (MADS AFFECTING FLOWERING 5); transcription factor
At5g65180	17	0	ENTH/VHS family protein
At5g65470	12	0	Unknown protein
At5g65520	89	0	Tetratricopeptide repeat (TPR)-like superfamily protein
At5g65540	49	0	Unknown protein
At5g65650	25	0	Unknown protein
At3g01740	109	0	Unknown protein
At5g65685	38	0	Soluble glycogen synthase-related
At5g65690	16	0	PCK2 (PHOSPHOENOLPYRUVATE CARBOXYKINASE 2); ATP binding / phosphoenolpyruvate carboxykinase (ATP)/ phosphoenolpyruvate carboxykinase/ purine nucleotide binding

Supplementary Table 4

GENE ID[a]	Transcriptional activity[b]		PREDICTED FUNCTION[c]
	Wild type ovule	*spl* ovule	
At5g65730	9	0	Xyloglucan:xyloglucosyl transferase, putative / xyloglucan endotransglycosylase, putative / endo-xyloglucan transferase, putative
At5g65850	17	0	F-box family protein
At5g65900	27	0	DEAD/DEAH box helicase, putative
At5g66000	9	0	Unknown protein
At5g66130	11	0	ATRAD17 (ARABIDOPSIS THALIANA RADIATION SENSITIVE)
At5g66500	13	0	Pentatricopeptide (PPR) repeat-containing protein
At5g66770	57	0	Scarecrow transcription factor family protein
At5g66810	11	0	Unknown function
At5g67130	40	0	Phospholipase C/ phosphoric diester hydrolase
At5g67470	11	0	Formin homology 2 domain-containing protein / FH2 domain-containing protein
At5g67580	19	0	TRB2; DNA binding / double-stranded telomeric DNA binding / protein homodimerization/ single-stranded telomeric DNA binding / transcription factor
AtCg00030	50	1	Lysine tRNA
AtCg00160	14	0	Chloroplast ribosomal protein S2

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[a] TheArabidopsis Genome Initiative Number.

[b] Activity in transcripts per Million.

[c] From The Arabidopsis Information Resource (www.arabidopsis.org).

Supplementary Table5. Fisher exact test for 1,301 *spl* downregulated genes.

	Raw transcriptional activity		
Gene ID[a]	Wild Type ovules[b]	*spl* ovules[b]	Fisher pvalue
AT1G01050	51	0	4.18E-16
AT1G01060	274	0	2.35E-83
AT1G01360	13	0	1.20E-04
AT1G01490	53	1	2.93E-15
AT1G01920	27	0	7.22E-09
AT1G02060	25	0	2.89E-08
AT1G02065	41	0	4.33E-13
AT1G02790	62	0	2.01E-19
AT1G03030	30	0	8.99E-10
AT1G03250	53	0	1.04E-16
AT1G03350	48	0	3.36E-15
AT1G03440	16	0	1.50E-05
AT1G03610	57	0	6.48E-18
AT1G03630	12	0	2.41E-04
AT1G04280	19	0	1.86E-06
AT1G04410	625	20	1.75E-157
AT1G04510	12	0	2.41E-04
AT1G04830	33	1	2.02E-09
AT1G05500	71	0	3.89E-22
AT1G05540	113	0	8.41E-35
AT1G05710	180	0	5.24E-55
AT1G05805	23	0	1.16E-07
AT1G06040	63	0	1.01E-19
AT1G06070	16	1	1.43E-04
AT1G06250	16	0	1.50E-05
AT1G06470	31	0	4.49E-10
AT1G06960	117	5	3.75E-29
AT1G07020	129	4	1.06E-33
AT1G07090	13	0	1.20E-04
AT1G07180	42	0	2.16E-13
AT1G07530	12	0	2.41E-04
AT1G07960	22	0	2.32E-07
AT1G08680	86	0	1.17E-26
AT1G09080	44	0	5.39E-14
AT1G09570	15	0	3.00E-05
AT1G09575	13	0	1.20E-04
AT1G09710	29	0	1.80E-09
AT1G10455	20	0	9.31E-07

Supplementary Table 5

	Raw transcriptional activity		
Gene ID[a]	Wild Type ovules[b]	*spl* ovules[b]	Fisher pvalue
AT1G10538	39	2	3.95E-10
AT1G10590	49	0	1.68E-15
AT1G10650	12	0	2.41E-04
AT1G10710	27	0	7.22E-09
AT1G10730	19	0	1.86E-06
AT1G10840	16	0	1.50E-05
AT1G11200	19	0	1.86E-06
AT1G11260	53	0	1.04E-16
AT1G11362	19	0	1.86E-06
AT1G11800	20	0	9.31E-07
AT1G11900	12	0	2.41E-04
AT1G12080	97	0	5.62E-30
AT1G12300	22	0	2.32E-07
AT1G12310	19	0	1.86E-06
AT1G12400	33	1	2.02E-09
AT1G12610	52	0	2.09E-16
AT1G12750	20	0	9.31E-07
AT1G12775	18	0	3.73E-06
AT1G12820	139	3	7.48E-38
AT1G13170	14	0	6.00E-05
AT1G13210	30	0	8.99E-10
AT1G13450	16	0	1.50E-05
AT1G13750	42	0	2.16E-13
AT1G14200	58	0	3.24E-18
AT1G14260	25	0	2.89E-08
AT1G14280	49	0	1.68E-15
AT1G14530	15	0	3.00E-05
AT1G14650	37	0	6.96E-12
AT1G15020	62	0	2.01E-19
AT1G15220	19	0	1.86E-06
AT1G15350	19	0	1.86E-06
AT1G15690	243	3	1.67E-68
AT1G15780	90	0	7.25E-28
AT1G16170	13	0	1.20E-04
AT1G16300	15	0	3.00E-05
AT1G16390	14	0	6.00E-05
AT1G16445	29	0	1.80E-09
AT1G16590	28	0	3.60E-09
AT1G16630	14	0	6.00E-05
AT1G17130	13	0	1.20E-04

Supplementary Table 5

	Raw transcriptional activity		
Gene ID[a]	Wild Type ovules[b]	*spl* ovules[b]	Fisher pvalue
AT1G17400	31	0	4.49E-10
AT1G17550	122	1	1.02E-35
AT1G17890	58	2	1.54E-15
AT1G17930	21	5	1.50E-03
AT1G18075	56	0	1.30E-17
AT1G18500	35	1	5.32E-10
AT1G18610	17	0	7.48E-06
AT1G18840	26	0	1.44E-08
AT1G19350	19	0	1.86E-06
AT1G19450	18	0	3.73E-06
AT1G19690	101	0	3.49E-31
AT1G19790	20	0	9.31E-07
AT1G19990	88	0	2.91E-27
AT1G20000	14	0	6.00E-05
AT1G20140	44	0	5.39E-14
AT1G20220	20	0	9.31E-07
AT1G20830	15	0	3.00E-05
AT1G21080	26	0	1.44E-08
AT1G21390	23	0	1.16E-07
AT1G21400	28	0	3.60E-09
AT1G21460	38	0	3.48E-12
AT1G21700	21	0	4.65E-07
AT1G22140	110	2	1.10E-30
AT1G22275	17	0	7.48E-06
AT1G22970	28	0	3.60E-09
AT1G23350	24	0	5.79E-08
AT1G23550	49	0	1.68E-15
AT1G23790	56	2	5.79E-15
AT1G23960	174	5	1.65E-45
AT1G24070	29	0	1.80E-09
AT1G24120	52	1	5.76E-15
AT1G24160	13	0	1.20E-04
AT1G24490	12	0	2.41E-04
AT1G25490	15	0	3.00E-05
AT1G26480	42	2	5.64E-11
AT1G26610	28	0	3.60E-09
AT1G26620	20	0	9.31E-07
AT1G26795	134	0	3.91E-41
AT1G27030	21	0	4.65E-07
AT1G27390	75	1	9.47E-22

Supplementary Table 5

	Raw transcriptional activity		
Gene ID[a]	Wild Type ovules[b]	*spl* ovules[b]	Fisher pvalue
AT1G27520	25	0	2.89E-08
AT1G27530	105	3	5.93E-28
AT1G28330	1078	39	3.80E-265
AT1G28440	67	0	6.25E-21
AT1G28760	15	0	3.00E-05
AT1G29060	29	0	1.80E-09
AT1G29140	30	0	8.99E-10
AT1G29260	49	2	5.82E-13
AT1G29330	19	0	1.86E-06
AT1G29357	36	1	2.73E-10
AT1G30440	13	0	1.20E-04
AT1G30970	21	0	4.65E-07
AT1G31330	292	2	9.66E-85
AT1G31660	13	0	1.20E-04
AT1G31760	169	6	6.83E-43
AT1G31810	32	0	2.24E-10
AT1G32120	18	0	3.73E-06
AT1G32300	14	0	6.00E-05
AT1G32310	45	0	2.69E-14
AT1G32390	27	0	7.22E-09
AT1G32460	20	0	9.31E-07
AT1G32470	27	0	7.22E-09
AT1G33230	19	0	1.86E-06
AT1G33360	42	0	2.16E-13
AT1G33970	31	0	4.49E-10
AT1G34210	33	0	1.12E-10
AT1G34380	26	0	1.44E-08
AT1G34550	17	0	7.48E-06
AT1G35180	15	0	3.00E-05
AT1G43886	49	1	4.37E-14
AT1G44900	82	0	1.87E-25
AT1G45000	74	0	4.85E-23
AT1G45180	14	0	6.00E-05
AT1G46264	90	2	7.98E-25
AT1G47128	141	1	2.19E-41
AT1G47240	18	0	3.73E-06
AT1G47450	36	0	1.39E-11
AT1G47470	29	0	1.80E-09
AT1G47670	87	0	5.82E-27
AT1G47780	69	0	1.56E-21

Supplementary Table 5

	Raw transcriptional activity		
Gene ID[a]	Wild Type ovules[b]	*spl* ovules[b]	Fisher pvalue
AT1G47830	39	1	3.66E-11
AT1G47930	21	0	4.65E-07
AT1G48460	38	0	3.48E-12
AT1G48560	21	0	4.65E-07
AT1G48600	26	0	1.44E-08
AT1G48900	75	0	2.42E-23
AT1G48950	34	2	9.90E-09
AT1G49650	26	0	1.44E-08
AT1G49920	61	0	4.03E-19
AT1G50000	40	0	8.67E-13
AT1G50010	12	0	2.41E-04
AT1G50250	74	0	4.85E-23
AT1G50440	19	0	1.86E-06
AT1G50500	20	0	9.31E-07
AT1G50510	13	0	1.20E-04
AT1G51100	37	0	6.96E-12
AT1G51440	18	0	3.73E-06
AT1G51550	14	0	6.00E-05
AT1G51570	115	2	3.71E-32
AT1G52190	51	0	4.18E-16
AT1G52220	191	4	9.77E-52
AT1G52250	12	0	2.41E-04
AT1G52347	22	0	2.32E-07
AT1G52590	17	0	7.48E-06
AT1G52730	23	0	1.16E-07
AT1G53120	45	2	7.98E-12
AT1G53170	18	0	3.73E-06
AT1G53300	39	0	1.74E-12
AT1G53440	97	3	1.22E-25
AT1G53645	53	0	1.04E-16
AT1G53760	23	0	1.16E-07
AT1G54260	100	5	2.37E-24
AT1G54570	14	0	6.00E-05
AT1G54580	661	0	4.44E-200
AT1G54630	14	0	6.00E-05
AT1G54830	17	0	7.48E-06
AT1G54850	27	0	7.22E-09
AT1G55170	14	0	6.00E-05
AT1G55260	58	1	9.91E-17
AT1G55680	61	0	4.03E-19

Supplementary Table 5

	Raw transcriptional activity		
Gene ID[a]	Wild Type ovules[b]	*spl* ovules[b]	Fisher pvalue
AT1G55810	76	1	4.79E-22
AT1G55820	12	0	2.41E-04
AT1G56020	25	0	2.89E-08
AT1G56180	54	0	5.20E-17
AT1G56450	49	0	1.68E-15
AT1G56610	13	0	1.20E-04
AT1G57590	15	0	3.00E-05
AT1G58220	25	0	2.89E-08
AT1G58227	12	0	2.41E-04
AT1G58250	26	0	1.44E-08
AT1G58520	16	0	1.50E-05
AT1G59520	24	0	5.79E-08
AT1G60000	16	0	1.50E-05
AT1G60160	17	0	7.48E-06
AT1G60650	19	0	1.86E-06
AT1G60740	44	2	1.53E-11
AT1G60860	65	0	2.51E-20
AT1G60940	117	1	3.15E-34
AT1G60960	45	2	7.98E-12
AT1G60970	17	0	7.48E-06
AT1G60990	20	0	9.31E-07
AT1G61670	39	13	2.64E-04
AT1G61790	241	4	2.03E-66
AT1G62130	13	0	1.20E-04
AT1G62520	34	1	1.04E-09
AT1G62730	17	0	7.48E-06
AT1G62860	37	0	6.96E-12
AT1G63130	32	2	3.56E-08
AT1G63220	152	6	4.94E-38
AT1G63490	40	1	1.87E-11
AT1G63500	34	0	5.59E-11
AT1G64050	27	0	7.22E-09
AT1G64230	43	1	2.49E-12
AT1G64280	23	0	1.16E-07
AT1G64520	94	2	5.40E-26
AT1G64740	43	0	1.08E-13
AT1G65240	61	1	1.29E-17
AT1G66150	35	0	2.79E-11
AT1G66660	26	0	1.44E-08
AT1G67325	21	0	4.65E-07

Supplementary Table 5

	Raw transcriptional activity		
Gene ID[a]	Wild Type ovules[b]	*spl* ovules[b]	Fisher pvalue
AT1G67570	41	0	4.33E-13
AT1G67650	16	0	1.50E-05
AT1G67660	12	0	2.41E-04
AT1G67750	57	0	6.48E-18
AT1G68020	15	0	3.00E-05
AT1G68440	24	0	5.79E-08
AT1G69230	26	0	1.44E-08
AT1G69400	35	0	2.79E-11
AT1G69850	14	0	6.00E-05
AT1G70100	30	0	8.99E-10
AT1G70250	29	0	1.80E-09
AT1G70280	21	0	4.65E-07
AT1G70500	58	2	1.54E-15
AT1G70560	68	0	3.12E-21
AT1G70660	99	3	3.23E-26
AT1G71030	26	0	1.44E-08
AT1G71260	94	1	2.20E-27
AT1G71310	29	0	1.80E-09
AT1G71380	18	0	3.73E-06
AT1G71430	24	0	5.79E-08
AT1G71730	18	0	3.73E-06
AT1G71750	47	0	6.72E-15
AT1G72300	34	0	5.59E-11
AT1G72550	49	0	1.68E-15
AT1G72880	21	0	4.65E-07
AT1G73450	13	0	1.20E-04
AT1G73885	28	0	3.60E-09
AT1G73910	22	0	2.32E-07
AT1G74180	37	0	6.96E-12
AT1G74390	78	1	1.23E-22
AT1G74700	27	0	7.22E-09
AT1G74840	94	0	4.51E-29
AT1G75020	79	1	6.19E-23
AT1G75150	15	0	3.00E-05
AT1G75780	36	2	2.74E-09
AT1G75840	59	1	5.03E-17
AT1G75980	57	0	6.48E-18
AT1G76100	68	0	3.12E-21
AT1G76130	34	0	5.59E-11
AT1G76185	19	0	1.86E-06

Supplementary Table 5

	Raw transcriptional activity		
Gene ID[a]	Wild Type ovules[b]	*spl* ovules[b]	Fisher pvalue
AT1G76600	23	5	5.38E-04
AT1G76830	17	0	7.48E-06
AT1G77380	12	0	2.41E-04
AT1G77720	14	0	6.00E-05
AT1G77760	46	0	1.35E-14
AT1G78560	26	0	1.44E-08
AT1G79070	46	1	3.31E-13
AT1G79410	20	0	9.31E-07
AT1G79690	43	1	2.49E-12
AT1G79710	23	0	1.16E-07
AT1G79810	42	1	4.88E-12
AT1G80370	43	2	2.94E-11
AT1G80460	59	0	1.62E-18
AT1G80490	39	0	1.74E-12
AT1G80620	29	0	1.80E-09
AT1G80690	14	0	6.00E-05
AT2G01400	38	0	3.48E-12
AT2G01490	61	2	2.11E-16
AT2G01830	17	0	7.48E-06
AT2G02090	36	0	1.39E-11
AT2G02400	55	0	2.60E-17
AT2G02740	37	0	6.96E-12
AT2G02910	139	4	1.36E-36
AT2G03270	12	0	2.41E-04
AT2G03420	16	0	1.50E-05
AT2G03550	53	0	1.04E-16
AT2G03810	101	0	3.49E-31
AT2G03840	31	0	4.49E-10
AT2G04037	42	0	2.16E-13
AT2G04039	17	0	7.48E-06
AT2G04235	28	0	3.60E-09
AT2G04280	25	0	2.89E-08
AT2G06090	17	0	7.48E-06
AT2G09800	21	0	4.65E-07
AT2G10340	20	0	9.31E-07
AT2G10405	16	0	1.50E-05
AT2G11140	57	1	1.95E-16
AT2G12462	26	0	1.44E-08
AT2G13360	16	0	1.50E-05
AT2G13610	38	0	3.48E-12

Supplementary Table 5

	Raw transcriptional activity		
Gene ID[a]	Wild Type ovules[b]	*spl* ovules[b]	Fisher pvalue
AT2G13960	22	0	2.32E-07
AT2G14120	64	3	3.33E-16
AT2G14170	101	0	3.49E-31
AT2G14255	58	0	3.24E-18
AT2G14560	17	0	7.48E-06
AT2G15440	20	0	9.31E-07
AT2G15695	95	2	2.75E-26
AT2G15960	30	0	8.99E-10
AT2G16050	25	0	2.89E-08
AT2G16370	147	2	1.34E-41
AT2G16400	21	0	4.65E-07
AT2G16570	13	0	1.20E-04
AT2G16800	19	0	1.86E-06
AT2G17130	15	0	3.00E-05
AT2G17210	20	0	9.31E-07
AT2G17390	19	0	1.86E-06
AT2G17420	38	1	7.15E-11
AT2G17530	69	0	1.56E-21
AT2G17570	41	0	4.33E-13
AT2G18040	43	0	1.08E-13
AT2G18330	40	1	1.87E-11
AT2G18700	86	2	1.18E-23
AT2G18890	15	0	3.00E-05
AT2G19340	99	5	4.52E-24
AT2G19660	21	0	4.65E-07
AT2G19760	33	0	1.12E-10
AT2G20050	28	0	3.60E-09
AT2G20690	27	0	7.22E-09
AT2G20790	102	0	1.74E-31
AT2G20800	42	0	2.16E-13
AT2G20960	15	0	3.00E-05
AT2G21120	33	0	1.12E-10
AT2G21250	96	0	1.12E-29
AT2G21440	36	0	1.39E-11
AT2G21540	15	0	3.00E-05
AT2G21580	56	0	1.30E-17
AT2G21655	48	0	3.36E-15
AT2G22120	24	0	5.79E-08
AT2G22170	38	0	3.48E-12
AT2G22240	71	0	3.89E-22

Supplementary Table 5

	Raw transcriptional activity		
Gene ID[a]	Wild Type ovules[b]	*spl* ovules[b]	Fisher pvalue
AT2G22310	18	0	3.73E-06
AT2G22490	19	0	1.86E-06
AT2G22540	27	0	7.22E-09
AT2G22650	32	1	3.94E-09
AT2G22940	20	0	9.31E-07
AT2G23040	13	0	1.20E-04
AT2G23142	25	0	2.89E-08
AT2G23310	22	0	2.32E-07
AT2G23340	21	0	4.65E-07
AT2G23460	52	1	5.76E-15
AT2G23530	25	0	2.89E-08
AT2G24205	18	0	3.73E-06
AT2G24270	149	0	1.17E-45
AT2G24360	20	0	9.31E-07
AT2G24450	40	0	8.67E-13
AT2G24830	15	0	3.00E-05
AT2G25010	77	0	6.03E-24
AT2G25300	70	0	7.79E-22
AT2G25320	25	3	1.49E-05
AT2G25590	96	2	1.40E-26
AT2G25650	151	2	8.78E-43
AT2G26080	91	0	3.62E-28
AT2G26360	34	0	5.59E-11
AT2G26450	13	0	1.20E-04
AT2G26920	37	0	6.96E-12
AT2G26970	22	0	2.32E-07
AT2G27500	21	0	4.65E-07
AT2G27900	43	0	1.08E-13
AT2G28110	54	2	2.17E-14
AT2G28380	36	0	1.39E-11
AT2G28480	38	0	3.48E-12
AT2G28680	25	0	2.89E-08
AT2G28800	51	1	1.13E-14
AT2G28930	18	0	3.73E-06
AT2G29080	17	0	7.48E-06
AT2G29200	27	0	7.22E-09
AT2G29660	49	0	1.68E-15
AT2G29700	34	0	5.59E-11
AT2G29970	45	0	2.69E-14
AT2G30200	26	0	1.44E-08

Supplementary Table 5

	Raw transcriptional activity		
Gene ID[a]	Wild Type ovules[b]	*spl* ovules[b]	Fisher pvalue
AT2G30270	33	1	2.02E-09
AT2G30984	15	0	3.00E-05
AT2G31141	32	0	2.24E-10
AT2G31530	16	0	1.50E-05
AT2G31870	42	0	2.16E-13
AT2G31985	31	0	4.49E-10
AT2G32400	47	3	1.88E-11
AT2G32560	13	0	1.20E-04
AT2G32600	58	0	3.24E-18
AT2G32720	182	0	1.31E-55
AT2G33400	128	1	1.66E-37
AT2G33610	16	0	1.50E-05
AT2G33775	23	0	1.16E-07
AT2G33980	12	0	2.41E-04
AT2G34670	11	47	2.03E-06
AT2G34690	163	4	1.46E-43
AT2G34700	22	0	2.32E-07
AT2G35030	13	0	1.20E-04
AT2G35240	42	0	2.16E-13
AT2G35250	12	0	2.41E-04
AT2G35330	113	1	4.89E-33
AT2G35470	71	2	2.72E-19
AT2G35550	42	0	2.16E-13
AT2G35690	37	1	1.40E-10
AT2G35840	34	0	5.59E-11
AT2G36610	108	0	2.71E-33
AT2G36810	17	0	7.48E-06
AT2G36835	33	0	1.12E-10
AT2G37050	43	0	1.08E-13
AT2G37060	113	1	4.89E-33
AT2G37120	45	1	6.49E-13
AT2G37470	30	0	8.99E-10
AT2G37520	33	0	1.12E-10
AT2G37550	34	0	5.59E-11
AT2G37640	34	0	5.59E-11
AT2G37740	12	0	2.41E-04
AT2G37840	24	0	5.79E-08
AT2G37890	22	0	2.32E-07
AT2G38140	67	0	6.25E-21
AT2G38280	14	0	6.00E-05

Supplementary Table 5

	Raw transcriptional activity		
Gene ID[a]	Wild Type ovules[b]	*spl* ovules[b]	Fisher pvalue
AT2G38410	14	0	6.00E-05
AT2G38630	38	0	3.48E-12
AT2G38680	18	0	3.73E-06
AT2G39140	12	0	2.41E-04
AT2G39270	57	0	6.48E-18
AT2G39390	105	0	2.17E-32
AT2G39740	15	0	3.00E-05
AT2G39930	250	0	4.07E-76
AT2G40095	23	0	1.16E-07
At2g40760	46	0	1.35E-14
AT2G40765	61	2	2.11E-16
AT2G40780	17	0	7.48E-06
AT2G40880	12	0	2.41E-04
AT2G40935	44	0	5.39E-14
AT2G40950	70	2	5.30E-19
AT2G41070	29	0	1.80E-09
AT2G41650	12	0	2.41E-04
AT2G41710	199	5	9.17E-53
AT2G42005	118	0	2.61E-36
AT2G42070	23	0	1.16E-07
AT2G42570	75	1	9.47E-22
AT2G42590	125	0	2.02E-38
AT2G42620	43	0	1.08E-13
AT2G42640	39	0	1.74E-12
AT2G42650	79	0	1.50E-24
AT2G42740	86	0	1.17E-26
AT2G43230	62	0	2.01E-19
AT2G43250	36	0	1.39E-11
AT2G43330	44	0	5.39E-14
AT2G43530	38	2	7.54E-10
AT2G44440	55	0	2.60E-17
AT2G44490	47	0	6.72E-15
AT2G44740	32	0	2.24E-10
AT2G45160	197	10	1.40E-46
AT2G45260	16	0	1.50E-05
AT2G45720	38	1	7.15E-11
AT2G45870	48	0	3.36E-15
AT2G46020	32	0	2.24E-10
AT2G46030	69	1	5.64E-20
AT2G46040	23	0	1.16E-07

Supplementary Table 5

	Raw transcriptional activity		
Gene ID[a]	Wild Type ovules[b]	*spl* ovules[b]	Fisher pvalue
AT2G46200	42	0	2.16E-13
AT2G46490	152	5	3.69E-39
AT2G46590	68	0	3.12E-21
AT2G46830	68	0	3.12E-21
AT2G46950	30	0	8.99E-10
AT2G47010	44	0	5.39E-14
AT2G47030	15	0	3.00E-05
AT2G47180	23	0	1.16E-07
AT2G47400	350	13	9.67E-87
AT2G47420	80	0	7.52E-25
AT2G47450	66	2	7.62E-18
AT2G47900	27	0	7.22E-09
AT2G48030	23	0	1.16E-07
AT3G01230	29	0	1.80E-09
AT3G01270	22	0	2.32E-07
AT3G01330	34	0	5.59E-11
AT3G01380	23	1	1.51E-06
AT3G01410	52	0	2.09E-16
AT3G01460	69	0	1.56E-21
AT3G01740	151	0	2.92E-46
AT3G01760	32	0	2.24E-10
AT3G01810	30	0	8.99E-10
AT3G02065	29	0	1.80E-09
AT3G02070	31	1	7.66E-09
AT3G02100	21	0	4.65E-07
AT3G02180	88	1	1.33E-25
AT3G02340	22	0	2.32E-07
AT3G02460	75	0	2.42E-23
AT3G02560	73	1	3.70E-21
AT3G02970	13	0	1.20E-04
AT3G03170	13	0	1.20E-04
AT3G03272	24	0	5.79E-08
AT3G03440	27	0	7.22E-09
AT3G03630	26	0	1.44E-08
AT3G04040	56	0	1.30E-17
AT3G04090	90	0	7.25E-28
AT3G04350	30	0	8.99E-10
AT3G04460	15	0	3.00E-05
AT3G04605	22	0	2.32E-07
AT3G04640	44	0	5.39E-14

Supplementary Table 5

	Raw transcriptional activity		
Gene ID[a]	Wild Type ovules[b]	*spl* ovules[b]	Fisher pvalue
AT3G04700	30	0	8.99E-10
AT3G04780	86	3	1.79E-22
AT3G05050	13	0	1.20E-04
AT3G05460	25	0	2.89E-08
AT3G05685	73	4	9.26E-18
AT3G05720	41	0	4.33E-13
AT3G05770	20	0	9.31E-07
AT3G05970	14	0	6.00E-05
AT3G06000	29	0	1.80E-09
AT3G06020	13	0	1.20E-04
AT3G06300	17	0	7.48E-06
AT3G06420	42	1	4.88E-12
AT3G06580	46	0	1.35E-14
AT3G06660	42	2	5.64E-11
AT3G06778	34	0	5.59E-11
AT3G06780	25	0	2.89E-08
AT3G06790	77	0	6.03E-24
AT3G06940	13	0	1.20E-04
AT3G07005	31	0	4.49E-10
AT3G07160	121	0	3.25E-37
AT3G07370	29	0	1.80E-09
AT3G07460	116	0	1.05E-35
AT3G07520	29	0	1.80E-09
AT3G07820	12	0	2.41E-04
AT3G07880	37	1	1.40E-10
AT3G08960	85	0	2.33E-26
AT3G09035	49	0	1.68E-15
AT3G09070	70	0	7.79E-22
AT3G09740	166	7	6.21E-41
AT3G09770	39	0	1.74E-12
AT3G09900	43	0	1.08E-13
AT3G10250	25	0	2.89E-08
AT3G10410	24	0	5.79E-08
AT3G10420	39	1	3.66E-11
AT3G10760	21	0	4.65E-07
AT3G11420	29	0	1.80E-09
AT3G11590	29	0	1.80E-09
AT3G11890	20	0	9.31E-07
AT3G12100	27	0	7.22E-09
AT3G12180	12	0	2.41E-04

Supplementary Table 5

	Raw transcriptional activity		
Gene ID[a]	Wild Type ovules[b]	*spl* ovules[b]	Fisher pvalue
AT3G12260	73	0	9.70E-23
AT3G12350	69	0	1.56E-21
AT3G12360	51	0	4.18E-16
AT3G12530	13	0	1.20E-04
AT3G12560	42	1	4.88E-12
AT3G12690	13	0	1.20E-04
AT3G12820	28	0	3.60E-09
AT3G12930	45	1	6.49E-13
AT3G13030	43	0	1.08E-13
AT3G13050	21	0	4.65E-07
AT3G13120	62	0	2.01E-19
AT3G13350	44	0	5.39E-14
AT3G13360	74	0	4.85E-23
AT3G13390	19	0	1.86E-06
AT3G13440	15	1	2.71E-04
AT3G13570	27	0	7.22E-09
AT3G13782	17	0	7.48E-06
AT3G14090	13	0	1.20E-04
AT3G14100	122	0	1.62E-37
AT3G14380	23	0	1.16E-07
AT3G15030	20	0	9.31E-07
AT3G15160	22	0	2.32E-07
AT3G15355	16	0	1.50E-05
AT3G15450	426	11	4.50E-111
AT3G15630	160	0	5.64E-49
AT3G16020	18	0	3.73E-06
AT3G16130	38	0	3.48E-12
AT3G16190	48	0	3.36E-15
AT3G16200	46	0	1.35E-14
AT3G16220	20	0	9.31E-07
AT3G16480	20	0	9.31E-07
AT3G16730	43	1	2.49E-12
AT3G16850	91	1	1.71E-26
AT3G17030	59	0	1.62E-18
AT3G17160	166	0	8.74E-51
AT3G17205	17	0	7.48E-06
AT3G17210	19	0	1.86E-06
AT3G17450	38	1	7.15E-11
AT3G17970	34	0	5.59E-11
AT3G18350	14	0	6.00E-05

Supplementary Table 5

	Raw transcriptional activity		
Gene ID[a]	Wild Type ovules[b]	*spl* ovules[b]	Fisher pvalue
AT3G18480	53	0	1.04E-16
AT3G18535	33	0	1.12E-10
AT3G19360	22	0	2.32E-07
AT3G19970	22	0	2.32E-07
AT3G20170	56	0	1.30E-17
AT3G20250	69	1	5.64E-20
AT3G20395	40	0	8.67E-13
AT3G20540	65	0	2.51E-20
AT3G20650	47	0	6.72E-15
AT3G20680	20	0	9.31E-07
AT3G20720	67	0	6.25E-21
AT3G20890	39	1	3.66E-11
AT3G20920	19	0	1.86E-06
AT3G20970	59	0	1.62E-18
AT3G21055	34	0	5.59E-11
AT3G21175	37	1	1.40E-10
AT3G21215	36	0	1.39E-11
AT3G21630	30	0	8.99E-10
AT3G21740	125	0	2.02E-38
AT3G22160	21	0	4.65E-07
AT3G22425	19	0	1.86E-06
AT3G22430	26	0	1.44E-08
AT3G22760	46	0	1.35E-14
AT3G22810	12	0	2.41E-04
AT3G22880	73	3	9.33E-19
AT3G23030	20	0	9.31E-07
AT3G23080	41	1	9.56E-12
AT3G23100	27	0	7.22E-09
AT3G23710	36	1	2.73E-10
AT3G23805	48	0	3.36E-15
AT3G24230	162	4	2.86E-43
AT3G24480	117	1	3.15E-34
AT3G24510	189	5	7.40E-50
AT3G24927	38	0	3.48E-12
AT3G25260	16	0	1.50E-05
AT3G25590	12	0	2.41E-04
AT3G25717	25	0	2.89E-08
AT3G26020	17	0	7.48E-06
AT3G26070	92	3	3.37E-24
AT3G26410	17	0	7.48E-06

Supplementary Table 5

	Raw transcriptional activity		
Gene ID[a]	Wild Type ovules[b]	*spl* ovules[b]	Fisher pvalue
AT3G26618	12	0	2.41E-04
AT3G26910	31	0	4.49E-10
AT3G27300	41	0	4.33E-13
AT3G27990	19	0	1.86E-06
AT3G28050	18	0	3.73E-06
AT3G28345	24	0	5.79E-08
AT3G28450	42	1	4.88E-12
AT3G28560	13	0	1.20E-04
AT3G28690	20	0	9.31E-07
AT3G28840	33	0	1.12E-10
AT3G28917	15	0	3.00E-05
AT3G28970	12	0	2.41E-04
AT3G28980	23	0	1.16E-07
AT3G29020	13	0	1.20E-04
AT3G29160	58	0	3.24E-18
AT3G29260	19	0	1.86E-06
AT3G29270	16	0	1.50E-05
AT3G29370	14	0	6.00E-05
AT3G29375	22	0	2.32E-07
AT3G42670	30	0	8.99E-10
AT3G43220	39	2	3.95E-10
AT3G43850	29	0	1.80E-09
AT3G43860	29	0	1.80E-09
AT3G44330	22	0	2.32E-07
AT3G44735	14	0	6.00E-05
AT3G44850	26	0	1.44E-08
AT3G45040	29	0	1.80E-09
AT3G46668	23	0	1.16E-07
AT3G47342	41	0	4.33E-13
AT3G47450	36	0	1.39E-11
AT3G47620	16	0	1.50E-05
AT3G47730	30	0	8.99E-10
AT3G48030	50	0	8.37E-16
AT3G48530	26	0	1.44E-08
AT3G48610	15	0	3.00E-05
AT3G48690	23	0	1.16E-07
AT3G48860	72	0	1.94E-22
AT3G48880	17	0	7.48E-06
AT3G48890	23	0	1.16E-07
AT3G48950	14	0	6.00E-05

Supplementary Table 5

	Raw transcriptional activity		
Gene ID[a]	Wild Type ovules[b]	*spl* ovules[b]	Fisher pvalue
AT3G49050	18	0	3.73E-06
AT3G49051	36	0	1.39E-11
AT3G49100	28	0	3.60E-09
AT3G49350	12	0	2.41E-04
AT3G49420	63	0	1.01E-19
AT3G49920	12	0	2.41E-04
AT3G50050	13	0	1.20E-04
AT3G50665	29	0	1.80E-09
AT3G51440	31	0	4.49E-10
AT3G51450	35	0	2.79E-11
AT3G51500	12	0	2.41E-04
AT3G51980	61	0	4.03E-19
AT3G52060	12	0	2.41E-04
AT3G52070	57	0	6.48E-18
AT3G52072	23	0	1.16E-07
AT3G52280	15	0	3.00E-05
AT3G52290	39	0	1.74E-12
AT3G52560	170	2	2.06E-48
AT3G52800	28	0	3.60E-09
AT3G53110	16	0	1.50E-05
AT3G53340	103	0	8.71E-32
AT3G53420	172	0	1.36E-52
AT3G53620	17	0	7.48E-06
AT3G54420	37	0	6.96E-12
AT3G55060	47	0	6.72E-15
AT3G56010	16	0	1.50E-05
AT3G56030	13	0	1.20E-04
AT3G56070	34	0	5.59E-11
AT3G56110	109	3	4.11E-29
AT3G56170	24	0	5.79E-08
AT3G56180	15	0	3.00E-05
AT3G57060	46	0	1.35E-14
AT3G57280	20	0	9.31E-07
AT3G57420	74	0	4.85E-23
AT3G57550	20	0	9.31E-07
AT3G58010	16	0	1.50E-05
AT3G58110	23	0	1.16E-07
AT3G58580	30	0	8.99E-10
AT3G58660	20	0	9.31E-07
AT3G58710	28	0	3.60E-09

Supplementary Table 5

	Raw transcriptional activity		
Gene ID[a]	Wild Type ovules[b]	*spl* ovules[b]	Fisher pvalue
AT3G58760	14	0	6.00E-05
AT3G59260	23	0	1.16E-07
AT3G59390	16	0	1.50E-05
AT3G59430	43	2	2.94E-11
AT3G59630	18	0	3.73E-06
AT3G59660	54	1	1.49E-15
AT3G59960	53	0	1.04E-16
AT3G60140	16	0	1.50E-05
AT3G60500	41	0	4.33E-13
AT3G60520	36	0	1.39E-11
AT3G60900	68	0	3.12E-21
AT3G60965	39	2	3.95E-10
AT3G61060	192	0	1.26E-58
AT3G61070	67	4	4.32E-16
AT3G61120	41	0	4.33E-13
AT3G61160	43	0	1.08E-13
AT3G61300	48	1	8.59E-14
AT3G61420	13	0	1.20E-04
AT3G61570	15	0	3.00E-05
AT3G61710	33	0	1.12E-10
AT3G61860	57	2	2.99E-15
AT3G62060	19	0	1.86E-06
AT3G62310	131	1	2.11E-38
AT3G62400	16	0	1.50E-05
AT3G62420	236	0	6.78E-72
AT3G62860	14	0	6.00E-05
AT3G63000	55	0	2.60E-17
AT3G63010	110	2	1.10E-30
AT3G63440	38	0	3.48E-12
AT3G63450	81	7	2.26E-17
AT4G00030	14	0	6.00E-05
AT4G00120	14	0	6.00E-05
AT4G00270	79	0	1.50E-24
AT4G00380	17	0	7.48E-06
AT4G00450	37	0	6.96E-12
AT4G00467	56	0	1.30E-17
AT4G00905	52	2	8.10E-14
AT4G01180	14	0	6.00E-05
AT4G01200	18	0	3.73E-06
AT4G01250	29	0	1.80E-09

Supplementary Table 5

	Raw transcriptional activity		
Gene ID[a]	Wild Type ovules[b]	*spl* ovules[b]	Fisher pvalue
AT4G01710	65	1	8.56E-19
AT4G01897	39	0	1.74E-12
AT4G02040	34	0	5.59E-11
AT4G02060	114	1	2.46E-33
AT4G02200	19	0	1.86E-06
AT4G02250	30	0	8.99E-10
AT4G02400	33	0	1.12E-10
AT4G02440	53	2	4.19E-14
AT4G02630	22	0	2.32E-07
At4g02650	139	0	1.21E-42
AT4G02655	139	0	1.21E-42
AT4G02800	15	0	3.00E-05
AT4G02840	74	0	4.85E-23
AT4G02940	15	0	3.00E-05
AT4G03140	31	0	4.49E-10
AT4G03230	30	0	8.99E-10
AT4G03240	24	0	5.79E-08
AT4G03960	15	0	3.00E-05
AT4G04320	12	0	2.41E-04
AT4G04610	77	1	2.42E-22
AT4G04670	70	3	6.65E-18
AT4G04870	83	0	9.36E-26
AT4G05020	63	0	1.01E-19
AT4G05410	84	3	6.71E-22
AT4G07390	68	0	3.12E-21
AT4G08240	15	0	3.00E-05
AT4G08690	20	0	9.31E-07
AT4G08810	130	2	1.41E-36
AT4G08980	16	0	1.50E-05
AT4G09153	44	0	5.39E-14
AT4G09530	26	0	1.44E-08
AT4G10040	15	0	3.00E-05
AT4G10650	29	0	1.80E-09
AT4G10710	112	0	1.68E-34
AT4G11060	42	0	2.16E-13
AT4G11090	83	0	9.36E-26
AT4G11330	22	0	2.32E-07
AT4G11570	23	0	1.16E-07
AT4G11760	79	0	1.50E-24
AT4G11790	60	0	8.07E-19

Supplementary Table 5

	Raw transcriptional activity		
Gene ID[a]	Wild Type ovules[b]	*spl* ovules[b]	Fisher pvalue
AT4G11800	42	1	4.88E-12
AT4G11960	22	0	2.32E-07
AT4G11980	27	0	7.22E-09
AT4G12130	43	0	1.08E-13
AT4G12340	40	1	1.87E-11
AT4G12650	95	0	2.25E-29
AT4G12860	25	0	2.89E-08
AT4G13230	15	0	3.00E-05
AT4G13270	25	0	2.89E-08
AT4G13690	63	0	1.01E-19
AT4G13780	72	1	7.31E-21
AT4G14070	12	0	2.41E-04
AT4G14110	13	0	1.20E-04
AT4G14210	38	1	7.15E-11
AT4G14340	14	0	6.00E-05
AT4G14342	35	0	2.79E-11
AT4G14570	81	0	3.75E-25
AT4G14760	160	3	5.24E-44
AT4G14900	28	0	3.60E-09
AT4G14950	115	0	2.10E-35
AT4G14960	37	0	6.96E-12
AT4G15010	47	0	6.72E-15
AT4G15640	18	0	3.73E-06
AT4G15750	37	0	6.96E-12
AT4G15885	25	0	2.89E-08
AT4G15940	90	2	7.98E-25
AT4G15955	59	0	1.62E-18
AT4G16155	37	0	6.96E-12
AT4G16480	53	0	1.04E-16
AT4G16515	19	0	1.86E-06
AT4G16570	69	0	1.56E-21
AT4G16640	24	0	5.79E-08
AT4G16710	40	0	8.67E-13
AT4G16980	17	0	7.48E-06
AT4G17180	16	0	1.50E-05
AT4G17270	12	0	2.41E-04
AT4G17695	16	0	1.50E-05
AT4G18060	92	0	1.81E-28
AT4G18375	63	0	1.01E-19
AT4G18970	104	5	1.78E-25

Supplementary Table 5

	Raw transcriptional activity		
Gene ID[a]	Wild Type ovules[b]	*spl* ovules[b]	Fisher pvalue
AT4G19020	39	1	3.66E-11
AT4G19090	30	0	8.99E-10
AT4G19185	63	0	1.01E-19
AT4G19191	43	0	1.08E-13
AT4G19220	25	0	2.89E-08
AT4G19400	35	1	5.32E-10
AT4G19490	52	1	5.76E-15
AT4G19870	33	0	1.12E-10
AT4G20130	166	4	1.96E-44
AT4G20150	342	0	7.30E-104
AT4G20362	15	0	3.00E-05
AT4G20410	38	0	3.48E-12
AT4G20820	20	0	9.31E-07
AT4G21150	59	1	5.03E-17
AT4G21170	20	0	9.31E-07
AT4G21350	19	0	1.86E-06
AT4G21610	51	1	1.13E-14
AT4G21630	107	0	5.42E-33
AT4G21710	95	0	2.25E-29
AT4G21730	34	0	5.59E-11
AT4G21790	166	1	7.42E-49
AT4G21880	12	0	2.41E-04
AT4G22105	116	0	1.05E-35
AT4G22200	13	0	1.20E-04
AT4G22280	17	0	7.48E-06
AT4G22390	39	0	1.74E-12
AT4G22830	12	0	2.41E-04
AT4G23400	12	0	2.41E-04
AT4G23520	14	0	6.00E-05
AT4G23530	19	0	1.86E-06
AT4G23740	16	0	1.50E-05
AT4G23940	30	0	8.99E-10
AT4G23960	26	0	1.44E-08
AT4G24080	21	0	4.65E-07
AT4G24750	34	0	5.59E-11
AT4G25120	44	0	5.39E-14
AT4G25520	12	0	2.41E-04
AT4G25570	97	1	2.82E-28
AT4G25700	68	1	1.11E-19
AT4G25770	29	0	1.80E-09

Supplementary Table 5

	Raw transcriptional activity		
Gene ID[a]	Wild Type ovules[b]	*spl* ovules[b]	Fisher pvalue
AT4G25840	15	0	3.00E-05
AT4G25850	12	0	2.41E-04
AT4G26070	15	0	3.00E-05
AT4G26180	12	0	2.41E-04
AT4G26500	40	2	2.07E-10
AT4G26550	29	0	1.80E-09
AT4G26610	26	0	1.44E-08
AT4G26640	24	0	5.79E-08
AT4G26660	36	0	1.39E-11
AT4G27090	62	2	1.09E-16
AT4G27270	29	0	1.80E-09
AT4G27280	72	4	1.76E-17
AT4G27350	19	0	1.86E-06
AT4G27540	35	0	2.79E-11
AT4G27580	28	0	3.60E-09
AT4G27654	43	1	2.49E-12
AT4G27660	50	0	8.37E-16
AT4G28010	20	0	9.31E-07
AT4G28020	132	0	1.57E-40
AT4G28290	17	0	7.48E-06
AT4G28610	258	3	5.97E-73
AT4G28630	30	0	8.99E-10
AT4G28730	35	0	2.79E-11
AT4G28775	40	0	8.67E-13
AT4G28950	19	0	1.86E-06
AT4G29100	32	0	2.24E-10
AT4G29160	57	1	1.95E-16
AT4G29340	25	0	2.89E-08
AT4G29735	340	6	1.11E-92
AT4G29810	37	0	6.96E-12
AT4G29960	19	0	1.86E-06
AT4G29990	14	0	6.00E-05
AT4G30190	13	0	1.20E-04
AT4G30220	47	2	2.16E-12
AT4G30360	16	0	1.50E-05
AT4G30430	13	0	1.20E-04
AT4G30600	68	1	1.11E-19
AT4G30610	33	0	1.12E-10
AT4G30662	51	0	4.18E-16
AT4G30970	26	0	1.44E-08

Supplementary Table 5

	Raw transcriptional activity		
Gene ID[a]	Wild Type ovules[b]	*spl* ovules[b]	Fisher pvalue
AT4G31010	28	0	3.60E-09
AT4G31040	17	0	7.48E-06
AT4G31600	27	0	7.22E-09
AT4G31650	20	0	9.31E-07
AT4G31750	31	0	4.49E-10
AT4G31820	103	0	8.71E-32
AT4G32130	16	0	1.50E-05
AT4G32170	19	0	1.86E-06
AT4G32190	45	2	7.98E-12
AT4G32490	13	0	1.20E-04
AT4G32530	96	9	8.18E-20
AT4G32590	41	0	4.33E-13
AT4G32600	48	1	8.59E-14
AT4G33460	12	0	2.41E-04
AT4G33490	15	0	3.00E-05
AT4G33630	17	0	7.48E-06
AT4G34090	54	0	5.20E-17
AT4G34180	58	1	9.91E-17
AT4G34480	13	0	1.20E-04
AT4G34870	143	1	5.53E-42
AT4G35020	26	0	1.44E-08
AT4G35335	23	0	1.16E-07
AT4G35770	265	0	1.22E-80
AT4G35785	17	2	3.97E-04
AT4G35800	35	1	5.32E-10
AT4G35840	37	0	6.96E-12
AT4G36240	63	0	1.01E-19
AT4G36280	48	0	3.36E-15
AT4G36470	14	0	6.00E-05
AT4G36940	60	0	8.07E-19
AT4G37445	15	0	3.00E-05
AT4G37460	48	1	8.59E-14
AT4G37800	15	0	3.00E-05
AT4G38090	34	0	5.59E-11
AT4G38150	39	0	1.74E-12
AT4G38230	18	0	3.73E-06
AT4G38360	33	0	1.12E-10
AT4G38380	13	0	1.20E-04
AT4G38470	39	1	3.66E-11
AT4G38520	83	0	9.36E-26

Supplementary Table 5

	Raw transcriptional activity		
Gene ID[a]	Wild Type ovules[b]	*spl* ovules[b]	Fisher pvalue
AT4G38650	20	0	9.31E-07
AT4G38790	41	0	4.33E-13
AT4G38800	55	0	2.60E-17
AT4G39550	47	0	6.72E-15
AT4G39780	15	0	3.00E-05
AT4G39800	25	0	2.89E-08
AT4G39865	15	0	3.00E-05
AT4G39890	24	0	5.79E-08
AT5G01075	13	0	1.20E-04
AT5G01370	34	0	5.59E-11
AT5G01650	25	0	2.89E-08
AT5G01800	12	0	2.41E-04
AT5G01810	16	0	1.50E-05
AT5G01860	33	0	1.12E-10
AT5G02180	26	0	1.44E-08
AT5G02410	33	1	2.02E-09
AT5G02560	18	0	3.73E-06
AT5G02850	24	0	5.79E-08
AT5G02950	80	4	1.01E-19
AT5G03070	63	0	1.01E-19
AT5G03320	25	0	2.89E-08
AT5G03330	40	1	1.87E-11
AT5G03520	53	0	1.04E-16
AT5G04770	14	0	6.00E-05
AT5G04930	87	1	2.63E-25
AT5G05090	33	0	1.12E-10
AT5G05100	103	0	8.71E-32
AT5G05365	53	0	1.04E-16
AT5G05760	58	0	3.24E-18
AT5G06220	45	1	6.49E-13
AT5G06310	37	0	6.96E-12
AT5G06350	14	0	6.00E-05
AT5G06660	14	0	6.00E-05
AT5G06810	13	0	1.20E-04
AT5G06870	50	0	8.37E-16
AT5G07350	101	0	3.49E-31
AT5G07710	33	0	1.12E-10
AT5G07810	30	0	8.99E-10
AT5G07910	76	0	1.21E-23
AT5G07950	39	0	1.74E-12

Supplementary Table 5

	Raw transcriptional activity		
Gene ID[a]	Wild Type ovules[b]	*spl* ovules[b]	Fisher pvalue
AT5G07960	105	0	2.17E-32
AT5G08090	13	0	1.20E-04
AT5G08100	117	3	1.95E-31
AT5G08120	29	0	1.80E-09
AT5G08340	42	0	2.16E-13
AT5G08350	73	0	9.70E-23
AT5G08565	53	0	1.04E-16
AT5G08710	21	0	4.65E-07
AT5G08720	12	0	2.41E-04
AT5G09260	17	0	7.48E-06
AT5G09580	27	0	7.22E-09
AT5G10290	12	0	2.41E-04
AT5G10620	16	0	1.50E-05
AT5G10630	13	0	1.20E-04
AT5G10790	19	0	1.86E-06
AT5G10910	23	0	1.16E-07
AT5G11020	19	0	1.86E-06
AT5G11180	31	0	4.49E-10
AT5G11380	22	0	2.32E-07
AT5G11490	24	0	5.79E-08
AT5G11810	32	0	2.24E-10
AT5G11870	16	0	1.50E-05
AT5G12290	12	0	2.41E-04
AT5G12380	76	0	1.21E-23
AT5G12970	27	0	7.22E-09
AT5G13150	37	0	6.96E-12
AT5G13200	40	0	8.67E-13
AT5G13440	34	0	5.59E-11
AT5G13490	253	12	2.78E-60
AT5G13650	34	0	5.59E-11
AT5G13710	22	0	2.32E-07
AT5G13770	31	0	4.49E-10
AT5G13790	18	0	3.73E-06
AT5G13860	40	0	8.67E-13
AT5G14280	13	0	1.20E-04
AT5G14500	21	0	4.65E-07
AT5G14860	23	0	1.16E-07
AT5G14910	15	0	3.00E-05
AT5G15260	135	4	1.95E-35
AT5G15760	34	0	5.59E-11

Supplementary Table 5

	Raw transcriptional activity		
Gene ID[a]	Wild Type ovules[b]	*spl* ovules[b]	Fisher pvalue
AT5G15770	30	0	8.99E-10
AT5G15810	22	0	2.32E-07
AT5G15860	18	0	3.73E-06
AT5G16250	65	0	2.51E-20
AT5G16260	12	0	2.41E-04
AT5G16390	34	0	5.59E-11
AT5G16500	18	0	3.73E-06
AT5G16560	12	0	2.41E-04
AT5G16660	48	0	3.36E-15
AT5G16720	38	0	3.48E-12
AT5G16820	52	1	5.76E-15
AT5G17090	34	1	1.04E-09
AT5G17210	175	2	6.78E-50
AT5G17300	43	0	1.08E-13
AT5G17710	42	0	2.16E-13
AT5G17770	18	0	3.73E-06
AT5G17790	34	0	5.59E-11
AT5G18220	25	0	2.89E-08
AT5G18255	97	3	1.22E-25
AT5G18440	15	0	3.00E-05
AT5G18480	31	0	4.49E-10
AT5G18630	158	1	1.83E-46
AT5G18810	17	0	7.48E-06
AT5G18840	17	1	7.50E-05
AT5G19151	137	3	2.87E-37
AT5G19210	18	0	3.73E-06
AT5G19670	20	0	9.31E-07
AT5G19790	35	0	2.79E-11
AT5G19810	47	0	6.72E-15
AT5G19910	15	2	1.30E-03
AT5G20150	16	0	1.50E-05
AT5G20250	943	21	1.67E-248
AT5G20500	57	0	6.48E-18
AT5G20510	31	0	4.49E-10
AT5G20660	30	0	8.99E-10
AT5G20830	89	2	1.56E-24
AT5G21080	48	0	3.36E-15
AT5G21140	35	2	5.21E-09
AT5G21160	104	4	1.59E-26
AT5G21900	45	0	2.69E-14

Supplementary Table 5

	Raw transcriptional activity		
Gene ID[a]	Wild Type ovules[b]	*spl* ovules[b]	Fisher pvalue
AT5G22060	104	0	4.35E-32
AT5G22400	19	0	1.86E-06
AT5G22450	68	4	2.28E-16
AT5G22460	151	0	2.92E-46
AT5G22830	27	0	7.22E-09
AT5G22875	23	0	1.16E-07
AT5G23090	42	0	2.16E-13
AT5G23380	33	0	1.12E-10
AT5G23395	177	0	4.21E-54
AT5G23850	37	0	6.96E-12
AT5G23870	51	1	1.13E-14
AT5G24400	65	0	2.51E-20
AT5G24735	64	0	5.02E-20
AT5G25060	18	0	3.73E-06
AT5G25080	41	0	4.33E-13
AT5G25090	183	5	4.08E-48
AT5G25100	107	2	8.33E-30
AT5G25780	39	0	1.74E-12
AT5G25920	19	0	1.86E-06
AT5G26200	17	0	7.48E-06
AT5G26210	53	0	1.04E-16
AT5G26820	64	0	5.02E-20
AT5G26910	21	0	4.65E-07
AT5G27380	13	0	1.20E-04
AT5G27400	72	1	7.31E-21
AT5G27440	18	0	3.73E-06
AT5G27730	14	0	6.00E-05
AT5G27750	77	15	1.85E-11
AT5G27830	19	0	1.86E-06
AT5G27970	38	0	3.48E-12
AT5G28000	56	0	1.30E-17
AT5G28020	54	0	5.20E-17
AT5G28626	15	0	3.00E-05
AT5G28840	14	0	6.00E-05
AT5G33340	30	0	8.99E-10
AT5G35680	22	0	2.32E-07
AT5G36170	18	0	3.73E-06
AT5G37130	20	0	9.31E-07
AT5G37190	17	0	7.48E-06
AT5G37380	19	0	1.86E-06

Supplementary Table 5

	Raw transcriptional activity		
Gene ID[a]	Wild Type ovules[b]	*spl* ovules[b]	Fisher pvalue
AT5G37540	13	0	1.20E-04
AT5G37710	21	3	1.54E-04
AT5G37890	82	1	8.00E-24
AT5G38460	26	0	1.44E-08
AT5G38850	28	0	3.60E-09
AT5G38860	17	0	7.48E-06
AT5G38970	54	0	5.20E-17
AT5G39840	13	0	1.20E-04
AT5G40150	20	0	9.31E-07
AT5G40200	50	0	8.37E-16
AT5G40380	18	0	3.73E-06
AT5G40760	98	0	2.81E-30
AT5G41020	12	0	2.41E-04
AT5G41600	12	0	2.41E-04
AT5G41980	50	0	8.37E-16
AT5G42030	66	0	1.25E-20
AT5G42060	61	0	4.03E-19
AT5G42242	12	0	2.41E-04
AT5G43280	73	0	9.70E-23
AT5G43430	49	0	1.68E-15
AT5G43513	196	4	3.36E-53
AT5G44040	17	0	7.48E-06
AT5G44495	19	0	1.86E-06
AT5G44500	13	0	1.20E-04
AT5G44760	33	0	1.12E-10
AT5G44860	23	0	1.16E-07
AT5G44980	17	0	7.48E-06
AT5G45050	20	0	9.31E-07
AT5G45110	13	0	1.20E-04
AT5G45170	24	0	5.79E-08
AT5G45260	26	0	1.44E-08
AT5G45590	25	0	2.89E-08
AT5G45750	12	0	2.41E-04
AT5G45775	181	6	2.45E-46
AT5G45790	19	0	1.86E-06
AT5G46590	19	0	1.86E-06
AT5G46700	12	0	2.41E-04
AT5G46730	23	0	1.16E-07
AT5G46790	21	0	4.65E-07
AT5G46960	51	0	4.18E-16

Supplementary Table 5

	Raw transcriptional activity		
Gene ID[a]	Wild Type ovules[b]	*spl* ovules[b]	Fisher pvalue
AT5G47110	18	0	3.73E-06
AT5G47240	92	0	1.81E-28
AT5G47250	14	0	6.00E-05
AT5G47370	25	0	2.89E-08
AT5G47520	24	0	5.79E-08
AT5G47700	215	0	1.46E-65
AT5G47810	17	0	7.48E-06
AT5G48090	26	0	1.44E-08
AT5G48290	12	0	2.41E-04
AT5G48520	36	0	1.39E-11
AT5G48530	59	0	1.62E-18
AT5G48840	27	0	7.22E-09
AT5G49010	62	2	1.09E-16
AT5G49015	19	0	1.86E-06
AT5G49215	29	0	1.80E-09
AT5G49220	18	0	3.73E-06
AT5G49400	47	0	6.72E-15
AT5G49640	63	2	5.60E-17
AT5G49880	14	0	6.00E-05
AT5G50340	13	0	1.20E-04
AT5G50430	46	2	4.15E-12
AT5G50930	34	0	5.59E-11
AT5G50970	18	0	3.73E-06
AT5G51020	54	0	5.20E-17
AT5G51451	23	0	1.16E-07
AT5G51700	37	0	6.96E-12
AT5G51890	40	0	8.67E-13
AT5G52030	15	0	3.00E-05
AT5G52810	42	0	2.16E-13
AT5G52860	44	0	5.39E-14
AT5G53060	57	0	6.48E-18
AT5G53080	18	0	3.73E-06
AT5G53280	89	1	6.70E-26
AT5G53440	23	0	1.16E-07
AT5G53470	23	0	1.16E-07
AT5G53650	33	0	1.12E-10
AT5G53940	43	2	2.94E-11
AT5G54160	79	0	1.50E-24
AT5G54500	18	0	3.73E-06
AT5G54760	20	0	9.31E-07

Supplementary Table 5

	Raw transcriptional activity		
Gene ID[a]	Wild Type ovules[b]	*spl* ovules[b]	Fisher pvalue
AT5G54870	49	0	1.68E-15
AT5G55000	110	0	6.75E-34
AT5G55120	172	5	6.26E-45
AT5G55160	45	0	2.69E-14
AT5G55210	66	0	1.25E-20
AT5G55700	27	0	7.22E-09
AT5G55930	34	1	1.04E-09
AT5G55940	15	0	3.00E-05
AT5G55990	12	0	2.41E-04
AT5G56020	49	1	4.37E-14
AT5G56120	19	2	1.19E-04
AT5G56130	18	0	3.73E-06
AT5G56350	30	0	8.99E-10
AT5G56550	22	0	2.32E-07
AT5G56580	188	67	1.15E-14
AT5G56890	21	0	4.65E-07
AT5G57070	16	0	1.50E-05
AT5G57160	18	0	3.73E-06
AT5G57280	41	0	4.33E-13
AT5G57290	60	0	8.07E-19
AT5G57410	42	1	4.88E-12
AT5G57590	41	0	4.33E-13
AT5G57940	14	0	6.00E-05
AT5G57960	37	0	6.96E-12
AT5G58640	28	0	3.60E-09
AT5G58750	56	0	1.30E-17
AT5G58920	51	0	4.18E-16
AT5G59030	42	0	2.16E-13
AT5G59290	48	0	3.36E-15
AT5G59440	30	0	8.99E-10
AT5G59470	33	0	1.12E-10
AT5G59550	91	0	3.62E-28
AT5G59810	62	0	2.01E-19
AT5G59960	48	0	3.36E-15
AT5G60170	116	4	5.84E-30
AT5G60200	38	0	3.48E-12
AT5G60340	35	0	2.79E-11
AT5G60460	18	0	3.73E-06
AT5G60553	26	0	1.44E-08
AT5G60600	33	0	1.12E-10

Supplementary Table 5

	Raw transcriptional activity		
Gene ID[a]	Wild Type ovules[b]	*spl* ovules[b]	Fisher pvalue
AT5G60630	54	1	1.49E-15
AT5G60640	80	0	7.52E-25
AT5G60690	24	0	5.79E-08
AT5G60880	45	0	2.69E-14
At5g60963	15	0	3.00E-05
AT5G61530	17	0	7.48E-06
AT5G61800	20	0	9.31E-07
AT5G61820	18	0	3.73E-06
AT5G61840	89	0	1.45E-27
AT5G61920	50	1	2.23E-14
AT5G61930	70	0	7.79E-22
AT5G61990	19	0	1.86E-06
AT5G62000	48	1	8.59E-14
AT5G62080	16	0	1.50E-05
AT5G62170	39	2	3.95E-10
AT5G62200	41	0	4.33E-13
AT5G62280	55	0	2.60E-17
AT5G62550	15	0	3.00E-05
AT5G62610	249	4	8.92E-69
AT5G62710	22	0	2.32E-07
AT5G62910	76	4	1.34E-18
AT5G62920	17	0	7.48E-06
AT5G62940	105	0	2.17E-32
AT5G62980	114	0	4.20E-35
AT5G63060	21	0	4.65E-07
AT5G63063	15	0	3.00E-05
AT5G63087	34	0	5.59E-11
AT5G63180	32	0	2.24E-10
AT5G63300	16	0	1.50E-05
AT5G63490	49	0	1.68E-15
AT5G63500	60	0	8.07E-19
AT5G63760	123	2	1.63E-34
AT5G63800	12	0	2.41E-04
AT5G63870	26	0	1.44E-08
AT5G63920	68	0	3.12E-21
AT5G64050	51	0	4.18E-16
AT5G64150	40	0	8.67E-13
AT5G64250	83	0	9.36E-26
AT5G64280	17	0	7.48E-06
AT5G64440	55	1	7.56E-16

Supplementary Table 5

	Raw transcriptional activity		
Gene ID[a]	Wild Type ovules[b]	*spl* ovules[b]	Fisher pvalue
AT5G64572	58	0	3.24E-18
AT5G64650	23	0	1.16E-07
AT5G65080	28	0	3.60E-09
AT5G65180	23	0	1.16E-07
AT5G65470	16	0	1.50E-05
AT5G65520	124	0	4.05E-38
AT5G65540	65	0	2.51E-20
AT5G65650	34	0	5.59E-11
AT5G65685	54	0	5.20E-17
AT5G65690	22	0	2.32E-07
AT5G65730	12	0	2.41E-04
AT5G65850	24	0	5.79E-08
AT5G65900	35	0	2.79E-11
AT5G66000	12	0	2.41E-04
AT5G66130	14	0	6.00E-05
AT5G66500	18	0	3.73E-06
AT5G66770	79	0	1.50E-24
AT5G66810	15	0	3.00E-05
AT5G67130	53	0	1.04E-16
AT5G67460	196	75	7.86E-14
AT5G67580	25	0	2.89E-08
ATCG00030	68	1	1.11E-19
ATCG00160	19	0	1.86E-06

[a] TheArabidopsis Genome Initiative Number

[b]Raw Transcriptional activity (Total signatures per gene).

c Fisher exact test p-Value.

Supplementary table 6. Insertional lines screened looking for female gametophytic defects.

GENE ID	STOCK
At1g01060	SALK_149287
At1g02060	SAIL_423_B07
At1g03250	SALK_017923
At1g05540	SALK_023237
At1g05750	SALK_104250
At1g05805	SALK_106364
At1g06250	SALK_083919
At1g07020	SALK_066870
At1g08680	SALK_116821
At1g08970	SALK_058903
At1g09710	SALK_106866
At1g10590	SALK_010814
At1g12080	SALK_ 138122
At1g12120	SALK_083872
At1g12400	SAIL_364_A08
At1g12610	SALK_114390
At1g13210	SALK_121697
At1g14200	SALK_095353
At1g14260	SALK_118406
At1g15220	SALK_046392
At1g15690	SALK_046492
At1g15780	SALK_059783
At1g17120	SALK_133128
At1g17400	SALK_119273
At1g18610	SALK_003526
At1g19790	SALK_151552
At1g19990	SALK_065338
At1g20140	SALK_114528
At1g21390	SALK_061442
At1g21400	SALK_071180
At1g22275	SALK_045440
At1g22970	SALK_120579
At1g23550	SAIL_361_A07
At1g23790	SALK_050121
At1g23960	SALK_111586
At1g24120	SALK_059216
At1g26480	SALK_110798

STOCK

Supplementary Table 6

GENE ID	
At1g26620	SALK_035172
At1g28440	SALK_108127
At1g29060	SALK_141347
At1g29260	SALK_005354
At1g30970	SALK_056285
At1g32300	SALK_060116
At1g32310	SALK_018488
At1g34210	SALK_003614
At1g43886	SALK_020396
At1g44900	SALK_054614
At1g45000	SALK_101982
At1g47450	SALK_124353
At1g47470	SALK_114435
At1g47670	CS859439
At1g47780	SALK_102031
At1g48240	SALK_092845
At1g48460	SALK_014132
At1g49410	SALK_110615
At1g49920	SALK_024493
At1g50250	SALK_133555
At1g51100	SAIL_697_B12
At1g51440	SALK_012430
At1g51960	SALK_106850
At1g52220	SALK_052057
At1g53300	SALK_081417
At1g53440	SALK_130548
At1g55260	SALK_067741
At1g55680	SALK_142665c
At1g55810	SALK_118929
At1g56180	SALK_053826
At1g60560	SALK_023519
At1g60970	SALK_067179
At1g62520	SALK_117636
At1g62680	SALK_139736
At1g62860	SALK_043644
At1g63220	SALK_120441
At1g63490	SALK_089978
At1g64520	SALK_134934
At1g65240	SAIL_161_A07
At1g67570	SALK_060234

Supplementary Table 6

GENE ID	STOCK
At1g67750	SALK_095735
At1g69400	SALK_053743
At1g70250	SAIL_125_D06
At1g70500	SALK_117236
At1g70560	SALK_022743
At1g71310	SALK_089362
At1g71865	SALK_032816
At1g72880	SALK_061696
At1g74180	SAIL_904_H11
At1g74390	SALK_086424
At1g75020	SALK_115626
At1g75260	SALK_113793
At1g75430	SALK_030336
At1g75980	SALK_023922
At1g76130	SALK_008656
At1g76830	SALK_021998
At1g78400	SALK_071023
At1g78560	SALK_008931
At1g79410	SALK_045609
At1g79810	SALK_062976
At2g01400	SALK_124838
At2g02740	SALK_005345
At2g02910	SALK_098750
At2g03260	SALK_056388
At2g03550	SALK_009690
At2g03810	SALK_042890
At2g03840	SALK_011012
At2g04235	SALK_091108
At2g06090	SAIL_652_G04
At2g07340	SALK_013585
At2g09800	SALK_059493
At2g10340	SALK_056999
At2g11140	SALK_131580
At2g13610	SALK_126034
At2g14170	SALK_093983
At2g15695	SALK_044186
At2g16370	SALK_054193
At2g18330	SALK_140302
At2g18700	SALK_082979
At2g20515	SALK_094958

Supplementary Table 6

GENE ID	STOCK
At2g20800	SAIL_543_F10
At2g21580	SALK_001420
At2g22940	SALK_058177
At2g23530	SALK_086420
At2g24270	SALK_147202
At2g25300	SALK_044399
At2g25650	SALK_032610
At2g27900	SALK_113195
At2g28110	SALK_120296
At2g28480	SALK_021339
At2g28680	SALK_077956
At2g28800	SALK_044418
At2g29660	SALK_119814
At2g29700	SALK_035930
At2g29970	SALK_122196
At2g30700	SALK_024519
At2g32720	SALK_041099
At2g33400	SALK_60675
At2g34420	SALK_049351
At2g34690	SAIL_915_B04
At2g35250	SALK_121861
At2g35330	CS24712
At2g35550	SALK_018618
At2g36835	SALK_065861
At2g37050	SALK_070810
At2g37120	SALK_123257
At2g37470	SALK_003306
At2g37550	SALK_127233
At2g37740	SALK_086072
At2g38140	SALK_129668
At2g38630	SAIL_792_C08
At2g38680	SALK_078575
At2g39270	SALK_117901
At2g39390	SALK_068525
At2g39930	SALK_006623
At2g40095	SALK_113359
At2g40765	SALK_018191
At2g40950	SALK_104326
At2g42005	SALK_063680
At2g42070	SAIL_539_H02

Supplementary Table 6

GENE ID	STOCK
At2g42280	SALK_024023
At2g42570	SALK_117521
At2g42590	SALK_129360
At2g42630	SALK_126902
At2g42650	SALK_019141
At2g42740	SALK_120345
At2g43230	SALK_033102
At2g43250	SALK_144233
At2g43330	SALK_018591
At2g43420	SALK_129508
At2g45720	SALK_041473
At2g45870	SALK_006759
At2g46200	SALK_099276
At2g46220	SALK_091794
At2g46830	SALK_067039
At2g46950	SALK_124250
At2g47010	SALK_045432
At2g47400	SALK_008459
At2g47420	SALK_133845
At2g47450	SAIL_783_F08
At3g01230	SALK_054861
At3g01330	SALK_063981
At3g01740	SALK_015764
At3g02130	SALK_062412
At3g02560	SALK_008899
At3g02960	SALK_071540
At3g03440	SALK_014623
At3g03630	SALK_034133
At3g04040	SALK_093343
At3g04640	SALK_026582
At3g04780	SALK_086281
At3g05460	SALK_009445
At3g05685	SALK_036718
At3g05720	SALK_020428
At3g05770	SALK_069840
At3g06420	SALK_026217
At3g06660	SALK_084123
At3g07480	SALK_015333c
At3g08550	SALK_087345
At3g08955	SAIL_737_F07

Supplementary Table 6

GENE ID	STOCK
At3g09070	SALK_139301
At3g09770	CS24715
At3g09900	SALK_076104
At3g11590	SALK_083658
At3g11600	SALK_93234
At3g12930	SALK_121803
At3g13120	SALK_145158
At3g13360	SAIL_106_E08
At3g15450	SALK_017321
At3g15630	SALK_077838
At3g16020	SALK_067113
At3g16130	SALK_032681
At3g16200	SALK_015388
At3g16730	SALK_059304
At3g16770	SALK_030459
At3g17030	SALK_042356
At3g17160	SALK_119732
At3g17450	SALK_052525
At3g18480	SALK_052760
At3g20170	SALK_042301
At3g20540	SALK_134274
At3g20720	SALK_128547
At3g22760	SALK_045808
At3g23080	SALK_062475
At3g24230	SALK_030175
At3g24510	SALK_094671
At3g24927	SALK_078437
At3g26340	SALK_081100
At3g28450	SALK_111477
At3g28560	SAIL_805_E02
At3g29160	SALK_114798
At3g47450	SALK_071384
At3g47730	SALK_090081
At3g48530	SALK_074554
At3g48860	SALK_138077
At3g48950	SALK_011242
At3g49420	SALK_128874
At3g49720	SAIL_505_E11
At3g51980	SALK_032235
At3g52070	SALK_021882

Supplementary Table 6

GENE ID	STOCK
At3g53420	SALK_088839
At3g54420	SALK_091602
At3g55060	SAIL_693_H10
At3g57420	SALK_045404
At3g58010	SALK_024284
At3g59260	SAIL_1243_E02
At3g59430	SALK_086046
At3g59660	SALK_072823
At3g59960	SALK_131038
At3g60140	SALK_029737
At3g60500	SALK_031994
At3g60520	SALK_126470
At3g60965	SALK_028867
At3g61300	SALK_012154
At3g61710	SALK_109281
At3g61860	SALK_085956
At3g62420	SALK_004675
At4g00270	SALK_013473
At4g00450	SALK_108241
At4g00905	SALK_069026
At4g01180	SALK_037188
At4g01897	SALK_095650
At4g02040	SALK_021719
At4g02250	SALK_139236
At4g04610	SAIL_326_H07
At4g04870	SALK_139314
At4g05020	SALK_064041
At4g10650	SALK_121198
At4g11060	SAIL_378_E03
At4g11090	SALK_022579
At4g11760	SALK_003342
At4g11800	SALK_044295
At4g11820	SALK_078721
At4g12650	SALK_023139
At4g13230	SALK_077261
At4g13690	SALK_024568
At4g13780	SALK_135441
At4g14500	SALK_018403
At4g14570	SALK_080653
At4g14950	SALK_069718

Supplementary Table 6

GENE ID	STOCK
At4g15750	SALK_038767
At4g15950	SALK_020157
At4g16155	SALK_083571
At4g16480	SALK_082659
At4g16640	SAIL_586_G10
At4g18375	SALK_016188
At4g19490	SALK_036485
At4g20150	SALK_088793
At4g21150	SALK_017994
At4g21630	SALK_127987
At4g21710	SALK_078769
At4g21730	SALK_108222
At4g22390	SALK_101810
At4g23520	SALK_09710
At4g23960	SALK_024220
At4g24610	SALK_113528
At4g25570	SALK_058385
At4g25630	SALK_114637
At4g25700	SALK_094002
At4g26550	SALK_143326
At4g27020	SALK_000824
At4g27090	SALK_048998
At4g27280	SALK_048098
At4g28020	SALK_096057
At4g28610	SALK_067629
At4g29340	SAIL_682_E05
At4g30430	SALK_142164
At4g30600	SALK_034609
At4g31250	SALK_105100
At4g31600	SALK_120828
At4g32530	SAIL_1155_B10
At4g32600	SALK_069389
At4g34090	SALK_068115
At4g34180	SALK_096799
At4g35020	SALK_091737
At4g35800	SALK_088125
At4g35840	CS24978
At4g36240	SALK_018414
At4g36280	SALK_062270
At4g38090	SALK_029673

Supplementary Table 6

GENE ID	STOCK
At4g38150	SALK_098509
At4g38380	SALK_019192
At4g38520	SALK_049798
At5g01370	SALK_003831
At5g01860	SALK_122390
At5g02180	SALK_071622
At5g02410	SALK_051207
At5g03070	SALK_005888
At5g03455	SALK_005882
At5g03520	SALK_062100
At5g04460	SALK_117733
At5g04930	SALK_002106
At5g05090	SALK_118637
At5g05100	SALK_051913
At5g05760	SALK_057421
At5g06220	SALK_012033
At5g06500	SALK_075694
At5g06620	SALK_065711
At5g06870	SALK_023011
At5g07810	SALK_137595
At5g07890	SALK_127886
At5g07910	SALK_070294
At5g07950	SALK_006685
At5g08340	SALK_076455
At5g08565	SAIL_838_D04
At5g08590	SALK_024421
At5g09230	SALK:149295
At5g09580	SALK_147007
At5g12380	SALK_062276
At5g13200	SALK_013073
At5g13440	SALK_096795
At5g13490	SALK_046870
At5g15320	SALK_116411
At5g15750	SALK_122900
At5g15760	SALK_139455
At5g16250	SALK_031814
At5g16390	SALK_120571
At5g16500	SALK_055909
At5g16720	SALK_024827
At5g17090	SALK_068375

Supplementary Table 6

GENE ID	STOCK
At5g17210	SALK_058503
At5g17300	SALK_025754
At5g17790	SALK_000790
At5g18630	SALK_125679
At5g19650	SALK_136444
At5g19790	SALK_101209
At5g20050	SALK_000490
At5g20720	SALK_083054
At5g21080	SALK_148611
At5g21140	SALK_015925
At5g21900	SALK_025534
At5g22060	SALK_000821
At5g23395	SALK_026945
At5g23580	SALK_090011
At5g23850	SALK_145225
At5g25100	SALK_052385
At5g25780	SALK_009083
At5g25920	SALK_089179
At5g27400	SALK_019618
At5g27970	SALK_003367
At5g28000	SALK_006136
At5g33340	SALK_050514
At5g35935	SALK_021335
At5g37381	SALK_071806
At5g38970	SALK_148384
At5g39590	SALK_082749
At5g41980	SALK_146017
At5g42030	SAIL_623_E12
At5g43280	SALK_002674
At5g44760	SALK_104320
At5g44790	SALK_006331
At5g44980	SALK_077681
At5g45150	SALK_005745
At5g45260	SALK_065748
At5g45775	SALK_123502
At5g45790	SALK_095684
At5g46590	SALK_078797
At5g47240	SALK_046577
At5g47250	SALK_098936
At5g47700	SALK_059356

Supplementary Table 6

GENE ID	STOCK
At5g48090	SALK_112608
At5g48140	SALK_065870
At5g48520	SALK_045375
At5g49215	SALK_056269
At5g49640	SALK_058837
At5g51020	SALK_088835
At5g51630	SALK_124803
At5g52860	SALK_148022
At5g53280	SALK_117722
At5g54160	CS25167
At5g54780	SALK_141450
At5g55210	SALK_060883
At5g55990	SALK_15142
At5g56020	SALK_142246
At5g56880	SAIL_105_H08
At5g57160	SALK_044027
At5g57280	SALK_071938
At5g57290	SALK_120009
At5g57410	SALK_074089
At5g57590	SALK_059607
At5g58510	SALK_100935
At5g58920	SALK_068750
At5g59030	SALK_067183
At5g59810	SALK_025087
At5g59960	SALK_041674
At5g60200	SALK_022367
At5g60630	SALK_116512
At5g60640	SALK_073313
At5g60880	SALK_070834
At5g60963	SALK_148180
At5g61930	SALK_088641
At5g62170	SALK_047222
At5g62200	SALK_022266
At5g62940	SALK_008810
At5g62980	SALK_147446
At5g63490	SALK_129317
At5g63500	SALK_113863
At5g64050	SALK_073242
At5g64370	SALK_016594
At5g64440	SALK_118043

Supplementary Table 6

GENE ID	STOCK
At5g65520	SALK_138023
At5g65540	SALK_107533
At5g65650	SALK_074259
At5g65700	SALK_107016
At5g65850	SALK_091257
At5g65900	SALK_140168
At5g66410	SAIL_625_D11
At5g66770	SALK_132051
At5g67130	SAIL_760_G05
At5g67580	SALK_057545
At1g61790	SALK_064315

Supplementary Table 7. Classification of MPSS differentially expressed genes between wild-type and *spl* ovules.

Class name	Number of genes (%)[a]	Description[b]
Signalling	97 (7.5%)[a]	Kinase and leucine-rich repeat domain proteins; calmodulins, armadillo proteins; hormone-related and stress-induced.
Cell cycle	11(0.85%)[a]	Proteins involved in the mitotic cell cycle.
Organelle processes	56 (4.3%)[a]	Proteins involved in organellar activity, mainly chloroplast and mitochondria.
RNA binding	76 (5.8%)[a]	RNA binding domain proteins; RNA helicases, Pumilio proteins, RNA methyltransferases; ribosomal proteins and RNA capping enzymes.
DNA binding	50 (3.8%)[a]	Proteins containing DNA binding domains that are not transcription factors.
Transcription factors	72 (5.6%)[a]	Transcription Factors.
Nucleic acid-interacting	14 (1%)[a]	Exonucleases, DNA methyltransferases and endonucleases.
Chromatin related	16 (1.2%)[a]	Histone and histone interacting proteins.
Housekeeping processes	210 (16.15%)[a]	Proteins involved in cellular trafficking, ubiquitination, photosynthesis, pathogen response, multimerization, chaperones.
Metabolism	237 (18.2%)[a]	Metabolic proteins; epimerases, transferases, hydrolases, lipases, AMP binding proteins, etc.
Others	222 (17%)[a]	Include all the genes that could not be classified in other category.
Non Pfam domains	240 (18.5%)[a]	Include all genes that contained non Pfam domain and couldn´t be classified.
Total genes	1301	

[a] Represents percentage of genes on every Pfam class.

[b] Description is based on Pfam domains containing.

Supplementary Table 8. PPR genes downregulated in the *sporocyteless* ovule.

Gene ID	Transcriptional activity (TPM)		Predicted function
	Wild type ovule	*spl* ovule	
At1g02060	18	0	Pentatricopeptide (PPR) repeat-containing protein
At1g11900	9	0	Pentatricopeptide (PPR) repeat-containing protein
At1g12300	16	0	Pentatricopeptide (PPR) repeat-containing protein
At1g12775	13	0	Pentatricopeptide (PPR) repeat-containing protein
At1g63130	24	0	Pentatricopeptide (PPR) repeat-containing protein
At2g17210	15	0	Pentatricopeptide (PPR) repeat-containing protein
At2g35030	10	0	Pentatricopeptide (PPR) repeat-containing protein
At3g56030	9	0	Pentatricopeptide (PPR) repeat-containing protein
At4g19191	31	0	Pentatricopeptide (PPR) repeat-containing protein
At4g19220	18	0	Pentatricopeptide (PPR) repeat-containing protein
At4g21170	15	0	Pentatricopeptide (PPR) repeat-containing protein
At4g21880	9	0	Pentatricopeptide (PPR) repeat-containing protein
At4g28010	14	0	Pentatricopeptide (PPR) repeat-containing protein
At4g38150	28	0	Pentatricopeptide (PPR) repeat-containing protein
At5g13770	22	0	Pentatricopeptide (PPR) repeat-

			containing protein
At5g61800	14	0	Pentatricopeptide (PPR) repeat-containing protein
At5g61990	14	0	Pentatricopeptide (PPR) repeat-containing protein
At5g66500	13	0	Pentatricopeptide (PPR) repeat-containing protein

Supplementary Table 9

Supplementary Table 9. Primers used in RT-PCR experiments.

GENE ID[a]	Forward primer	Reverse primer
At3g22760	5’-ATGCTTTGCTGCTGGATTTT-3’	5’-TTACAGCCTCGTTTGTGTCG-3’
At5g55210	5’-AGTGGCCGTGTAAGGAAATG-3’	5’- CTCTGTCTCACCGGAACCAT-3’
At5g16720	5’- GATCAAATTTCAGGGCGTGT-3’	5’- CGGATCAAGCTCCTTAGTCG-3’
At4g23960	5’- GCAATTGTTTCCGGAGGTTA-3’	5’- CGGAGTTCCACCATTTGTTT-3’
At5g 01860	5’- AGAGTTCCGCTTCCTGTTCA-3’	5’- CTGCTGAAGGAAAGTCCAC’-3
At3g07820	5’-CAATGCAGCTTGGAGAGTCA -3’	5’- CCAACACGTTGATGTGGAA-3’
At4g38380	5’- GGTGCTCCTGCTTATGTGGT-3’	5’- GCATCAAAATGGCAACAGTG-3’
At3g16130	5’- CGATGAAATGCTCCTCGATT-3’	5’- AGCACTTGGCACACACACTC-3’
At4g31600	5’- TGTGCTGGTGGAGAAGTCTG-3’	5’- AGGACAATGCCCATAACCAG-3’
At3g55060	5’- TGCGAAAAAGAAGCGGATAG-3’	5’- GCATCGAGATGAATGATTGC-3
At4g38520	5’- ACCGTTCAGCAAGCCATTAC-3’	5’- CGCGGATGATTCTGGACTAT-3’
At1g28330	5’-CGTAAGATCACCACCCAACC-3’	5’- GACGCTCCTCCACACGTTAT-3’
ACTIN 2	5’-TCCCTCAGCACATTCCAGCAG-3’	5’-AACGATTCCTGGACCTGCCTC-3’

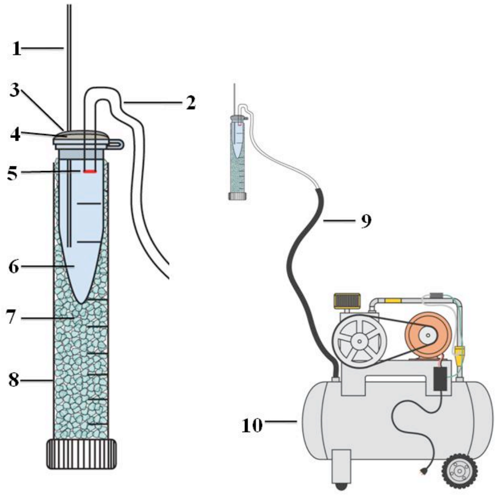
[a] Arabidopsis Genome Initiative Number

Supplementary Table 10

Supplementary Table 10. Primers and restriction sites used for promoter ::fusion plasmid construction.

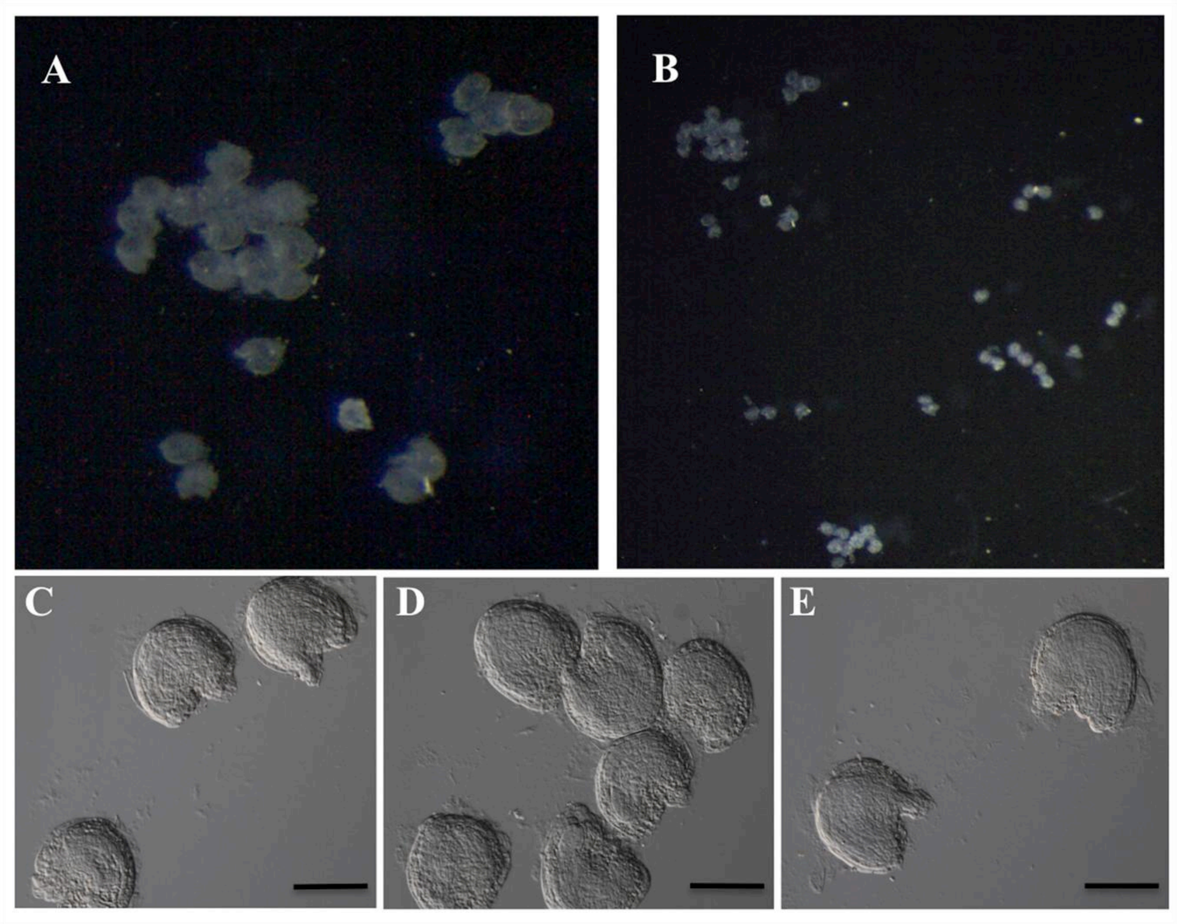
GENE ID	FORWARD PRIMERS	Restriction site	REVERSE PRIMERS	Restriction site
At3g01740	5’-GCGTCGACTCGACTACGAGTATTCACAACGA-3’	SalI	5’-GCGGATCCTTTTTGGCCTTGATGGAGTT-3’	BamHI
At3g53420	5’-GCAAGCTTACCTTTTGCCAACACAGACC-3’	HindIII	5’-GCGGATCCAGCTCCGCTCCATCAATAAA-3’	BamHI
At3g62310	5’-GCAAGCTTTATGCCCGTATGGGATTGTT-3’	HindIII	5’-GCGGATCCTCTACGAGGCTGTGTGCATC-3’	BamHI
At2g40880	5’-GCAAGCTTTCTCCACCGGAAAAACAAAC-3’	HindIII	5’-GCTCTAGATACCTGCTCCCTTGCTTTG-3’	XbaI
At1g31760	5’-GCAAGCTTCCTGACCATGGCTCTCCTTA-3’	HindIII	5’-GCTCTAGACCACGAGTGAGTTCCCTTTC-3’	XbaI
At4g38150	5’-GCGTCGACACGCCACTACAACACACCAA-3’	SalI	5’-GCGGATCCAGGAAGCCATCGTCAGACAG-3’	BamHI
At4g38380	5’-GCGTCGACGCAGAGGAGAAGTTGGTTGC-3’	SalI	5’-GCGGATCCGCAATGGCTGGAAGAGAGAG-3’	BamHI
At5g13490	5’-GCGTCGACGCCTTCCCAACCATTACTGA-3’	SalI	5’-GCGGATCCCCTCTCCACAACGAACCAAT-3’	BamHI
At5g22460	5’-GCAAGCTTTTTGGAGTCTCTCGGCACTT-3’	HindIII	5’-GCGGATCCATCGGCGAGTTCTTGAATGT-3’	BamHI

Supplementary Figures.



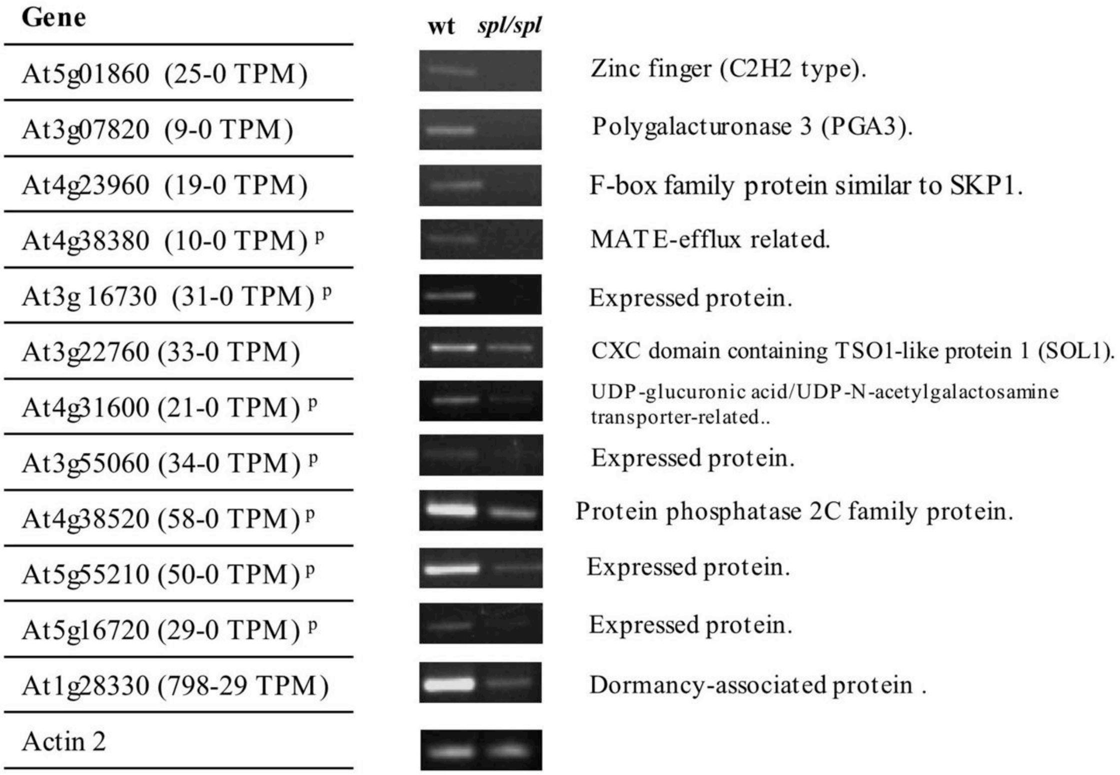
Supplementary Figure 1.Micro-aspirator device for ovules of Arabidopsis.

The micro-aspirator device consists of an aspiration/collection tube and a vacuum pump. The aspiration/collection tube is made of a 1.5 mL microcentrifuge tube that serves as the collection chamber. The lid of the microcentrifuge tube has a 2 mm perforation and a 5 mm perforation. A 5 cm (10 µl capacity) glass capillary tube is inserted in the 2 mm perforation and a standard plastic intravenous line (IVL) hose is inserted in the 5 mm perforation. The glass capillary tube inside the microcentrifuge tube should reach the 100 µl mark while the IVL hose should be approximately 1 cm from the lid. Perforations on the lid are sealed with adhesive epoxy resin. Once resin has polymerized, the microcentrifuge tube must be completely sealed by adding a layer of transparent silicone sealant on top of the resin layer and by covering the lid with parafilm. In contrast to must epoxy resins that tend to crack at low temperatures, silicone sealant resist low temperatures necessary for sample preservation. The aspiration/collection tube is subsequently placed inside a 15 mL conical falcon tube (with cap). The conical base of the tube is sliced to allow the aspiration/collection tube to fit (only the lid of the aspiration/collection tube should be surfacing out of the falcon tube). The falcon tube is filled with ground-to-powder dry ice and the cap is secured. Before securing the cap, it is important to perforate the cap to allow release of CO_2. This arrangement allows the falcon tube and the aspiration/collection tube to work as a single unit and to be held as a pen. The other end of the IV hose is connected to vacuum pump capable of ensuring a steady pressure of 0.3 to 0.6 Kg.cm^{-2} necessary to detach an ovule from the placental tissue by transversally sectioning its funiculus. After an ovule collecting session, the lid of the tube can be carefully removed by cutting the tube hinge. The lid with the capillary tube and the IVL hose can be saved and reused for subsequent sessions. Ovules are flash frozen in liquid nitrogen and preserved at -80°C. Detail: 1.- Glass capillary tube; 2.- Plastic IVL hose; 3.- Silicone sealant; 4.- Epoxy resin; 5.- Nylon mesh filter; 6.- Microcentrifuge tube; 7.- Ground dry ice; 8.- 15 mL falcon tube; 9.- Pump hose; 10.- Vacuum pump.



Supplementary Figure 2. Integrity of micro-aspirated wild type ovules.

Ovules were aspirated using the device shown in Suppl Fig. 1 and observed under stero-microscope (A and B) or Nomarsky optics in 50% Glycerol (C to E). Scale bar: 1cm=74.5 µm.



Supplementary Figure 3. RT-PCR of differentially expressed genes in wild-type and *sporocyteless* ovules.