

Table S2. Uniquely annotated top down- and up-regulated differentially expressed genes (DEGs) in ovules from apomictic *Limonium multiflorum* (M) in stage S1 (1), relative to the control *L. auriculifolium* (a) ovules in either S1 (1) or S2 (2) stages, and *L. multiflorum* (M) in S2 (2) relative to *L. auriculifolium* (a) in S3/S4 (4). DEGs were annotated according to the *Arabidopsis thaliana* reference genome and are presented in ascending order of log₂ fold-change (log₂FC).

Gene ID	Gene Name	Protein Name	Molecular Function	Log ₂ FC
M1a1				
Down-regulated				
TRINITY_DN5225_c0_g1	<i>DIR1</i>	Putative lipid-transfer protein DIR1	lipid binding; protein binding; ion binding	-9.80
TRINITY_DN40200_c0_g1	<i>AT5G33370</i>	GDSL esterase/lipase At5g33370	hydrolase activity	-8.88
TRINITY_DN253_c1_g1	<i>COBL10</i>	COBRA-like protein 10		-8.86
TRINITY_DN7779_c0_g1	<i>AP3</i>	Floral homeotic protein APETALA 3	transcription regulator activity; protein binding; DNA binding	-8.66
TRINITY_DN8286_c0_g1	<i>DRT100</i>	DNA damage-repair/toleration protein DRT100	nucleotide binding	-8.62
TRINITY_DN8621_c0_g1	<i>AT59</i>	Probable pectate lyase 3	metal ion binding; lyase activity	-8.60
TRINITY_DN1267_c0_g1	<i>PEX4</i>	Pollen-specific leucine-rich repeat extensin-like protein 4	ATP binding; transferase activity	-8.50
TRINITY_DN4212_c0_g1	<i>NOI4</i>	Protein NOI4		-8.47
TRINITY_DN7954_c0_g1	<i>PI</i>	Floral homeotic protein PISTILLATA	transcription regulator activity; protein binding; DNA binding	-8.44
TRINITY_DN185471_c0_g1	<i>AT1G30350</i>	Probable pectate lyase 4	metal ion binding; lyase activity	-8.37
Up-regulated				
TRINITY_DN44719_c0_g1	<i>IQM5</i>	IQ domain-containing protein IQM5		7.37
TRINITY_DN31216_c0_g1	<i>RL6</i>	Protein RADIALIS-like 6	transcription regulator activity	7.52
TRINITY_DN36508_c0_g1	<i>WRKY53</i>	Probable WRKY transcription factor 53	transcription regulator activity; DNA binding	7.62

TRINITY_DN41214_c0_g1	<i>ATM</i>	Serine/threonine-protein kinase ATM	ATP binding; DNA binding; transferase activity	7.84
TRINITY_DN38061_c0_g1	<i>ZFP8</i>	Zinc finger protein 8	transcription regulator activity; ion binding; DNA binding	8.04
TRINITY_DN35799_c0_g1	<i>MSL4</i>	Mechanosensitive ion channel protein 4	transporter activity	8.44
TRINITY_DN13495_c0_g1	<i>AT2G23090</i>	Uncharacterized protein At2g23090		9.13
TRINITY_DN28989_c0_g1	<i>WAKL13</i>	Putative wall-associated receptor kinase-like 13	ATP binding; carbohydrate binding; transferase activity	9.50
TRINITY_DN3514_c2_g1	<i>AT1G50180</i>	Putative disease resistance protein At1g50180	ADP binding; ATP binding	9.69
TRINITY_DN44488_c0_g1	<i>PRB1</i>	Pathogenesis-related protein 1		10.21
M1a2				
Down-regulated				
TRINITY_DN40200_c0_g1	<i>AT5G33370</i>	GDSL esterase/lipase At5g33370	hydrolase activity	-7.61
TRINITY_DN4445_c0_g1	<i>CEP1</i>	KDEL-tailed cysteine endopeptidase CEP1	hydrolase activity	-7.42
TRINITY_DN19789_c0_g1	<i>AT3G01270</i>	Probable pectate lyase 7		-7.32
TRINITY_DN9597_c0_g2	<i>MSBP1</i>	Membrane steroid-binding protein 1	lipid binding	-7.30
TRINITY_DN9027_c0_g3	<i>AP1</i>	Floral homeotic protein APETALA 1	DNA binding; transcription regulator activity; protein binding	-7.24
TRINITY_DN22841_c0_g1	<i>PXG4</i>	Probable peroxygenase 4	ion binding; oxidoreductase activity	-7.14
TRINITY_DN5730_c0_g1	<i>PME38</i>	Putative pectinesterase/pectinesterase inhibitor 38		-7.12
TRINITY_DN9027_c0_g1	<i>SEP1</i>	Developmental protein SEPALLATA 1		-7.09
TRINITY_DN3934_c0_g1	<i>AT3G07850</i>	Exopolygalacturonase clone GBGA483		-6.94
TRINITY_DN8621_c0_g1	<i>AT59</i>	Probable pectate lyase 3		-6.91
Up-regulated				

TRINITY_DN32666_c0_g1	<i>ARI8</i>	Probable E3 ubiquitin-protein ligase ARI8		8.40
TRINITY_DN17343_c0_g1	<i>MYB63</i>	Transcription factor MYB63		8.44
TRINITY_DN42433_c0_g1	<i>CRK32</i>	Putative cysteine-rich receptor-like protein kinase 32		8.78
TRINITY_DN7799_c0_g1	<i>AT1G06650</i>	1-aminocyclopropane-1-carboxylate oxidase homolog 3		8.93
TRINITY_DN13495_c0_g1	<i>AT2G23090</i>	Uncharacterized protein At2g23090	metal cluster binding; oxidoreductase activity; FAD binding; ion binding	9.12
TRINITY_DN6834_c1_g1	<i>DREB1D</i>	Dehydration-responsive element-binding protein 1D	DNA binding; transcription regulator activity; protein binding	9.31
TRINITY_DN40977_c0_g1	<i>ATG8C</i>	Autophagy-related protein 8c		9.52
TRINITY_DN4104_c0_g2	<i>LAC3</i>	Laccase-3	ion binding; oxidoreductase activity	9.93
TRINITY_DN44488_c0_g1	<i>PRB1</i>	Pathogenesis-related protein 1	hydrolase activity	10.21
TRINITY_DN68_c0_g1	<i>PRMT14</i>	Probable histone-arginine methyltransferase 1.4	transferase activity; protein binding	10.27

M2a4

Down-regulated

TRINITY_DN1473_c0_g1	PRE6	Transcription factor PRE6	isomerase activity	-8.30
TRINITY_DN11282_c0_g2	IAA7	Auxin-responsive protein IAA7	DNA binding; transcription regulator activity	-7.13
TRINITY_DN3927_c0_g1	AT3G28060	WAT1-related protein At3g28060	transporter activity	-6.62
TRINITY_DN8876_c0_g1	AT2G27360	GDSL esterase/lipase At2g27360	hydrolase activity	-6.62
TRINITY_DN5904_c0_g1	AT4G00165	Putative lipid-binding protein At4g00165		-6.41
TRINITY_DN44687_c0_g1	ADPG2	Polygalacturonase ADPG2		-6.02
TRINITY_DN6357_c0_g1	PR5K	PR5-like receptor kinase		-5.95
TRINITY_DN9702_c0_g1	JMT	Jasmonate O-methyltransferase		-5.72
TRINITY_DN8238_c0_g2	AT3G03770	Probable inactive leucine-rich repeat receptor-like		-5.70

		protein kinase At3g03770		
TRINITY_DN40496_c0_g1	AT1G04350	1-aminocyclopropane-1-carboxylate oxidase homolog 6		-5.65
Up-regulated				
TRINITY_DN209_c0_g2	<i>ATX5</i>	Histone-lysine N-methyltransferase ATX5		7.64
TRINITY_DN35748_c1_g1	<i>LOV1</i>	Putative inactive disease susceptibility protein LOV1		7.65
TRINITY_DN38698_c0_g1	<i>BSL1</i>	Serine/threonine-protein phosphatase BSL1		7.69
TRINITY_DN28687_c0_g1	<i>GOLS4</i>	Galactinol synthase 4		7.76
TRINITY_DN40624_c0_g1	<i>CAT2</i>	Catalase-2		7.92
TRINITY_DN5170_c0_g1	<i>AT4G16820</i>	Phospholipase A1-Ibeta2, chloroplastic		8.16
TRINITY_DN14944_c1_g1	<i>AT1G78910</i>	RNA pseudouridine synthase 3, mitochondrial		8.30
TRINITY_DN39320_c0_g1	<i>NPF7.3</i>	Protein NRT1/ PTR FAMILY 7.3	transporter activity	9.38
TRINITY_DN6834_c1_g1	<i>DREB1D</i>	Dehydration-responsive element-binding protein 1D	DNA binding; transcription regulator activity	9.79
TRINITY_DN137553_c0_g1	<i>CLPC1</i>	Chaperone protein ClpC1, chloroplastic	ATP binding; hydrolase activity; nucleic acid binding	12.35