

Table S6. Uniquely annotated top down- and up-regulated differentially expressed genes (DEGs) in ovules from apomictic *Limonium auriculifolium* (A) in stage S2 (2) relative to S1 (1), and DEGs from ovules in stage S3/S4 (4) relative to either S1 (1) or S2 (2). 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
A2a1				
Down-regulated				
TRINITY_DN8876_c0_g1	<i>AT2G27360</i>	GDSL esterase/lipase At2g27360	hydrolase activity	-5.85
TRINITY_DN11184_c0_g1	<i>AT4G12500</i>	pEARLI1-like lipid transfer protein 3		-5.46
TRINITY_DN31196_c0_g1	<i>SBT5.4</i>	Subtilisin-like protease SBT5.4	hydrolase activity	-5.38
TRINITY_DN604_c0_g1	<i>AT5G45950</i>	GDSL esterase/lipase At5g45950	hydrolase activity	-5.25
TRINITY_DN14059_c0_g1	<i>AT4G28780</i>	GDSL esterase/lipase At4g28780	hydrolase activity	-5.24
TRINITY_DN2678_c0_g2	<i>S-ACP-DES1</i>	Stearoyl-[acyl-carrier-protein] 9-desaturase 1, chloroplastic	oxidoreductase activity; ion binding	-5.00
TRINITY_DN1473_c0_g1	<i>PRE6</i>	Transcription factor PRE6	protein binding	-4.87
TRINITY_DN5904_c0_g1	<i>AT4G00165</i>	Putative lipid-binding protein At4g00165		-4.63
TRINITY_DN664_c0_g1	<i>FACT</i>	Fatty alcohol:caffeoyl-CoA acyltransferase	DNA binding; transcription regulator activity; protein binding; chromatine binding	-4.59
TRINITY_DN166369_c0_g1	<i>UGT89A2</i>	UDP-glycosyltransferase 89A2	transferase activity	-4.44
Up-regulated				
TRINITY_DN7650_c0_g1	<i>VTE5</i>	Phytol kinase 1, chloroplastic	transferase activity	2.80
TRINITY_DN5906_c1_g1	<i>AT2G35920</i>	DExH-box ATP-dependent RNA helicase DExH1	ATP binding; hydrolase activity; RNA binding; helicase activity	2.81
TRINITY_DN41534_c0_g1	<i>UGT73C7</i>	UDP-glycosyltransferase 73C7	transferase activity	2.84

TRINITY_DN2871_c0_g1	<i>AT5G11130</i>	Probable glycosyltransferase At5g11130	transferase activity	2.87
TRINITY_DN51734_c0_g2	<i>LTP11</i>	Non-specific lipid-transfer protein 11	lipid binding	2.89
TRINITY_DN1055_c0_g1	<i>AT2G04020</i>	GDSE esterase/lipase At2g04020	hydrolase activity	3.05
TRINITY_DN7962_c0_g1	<i>PAT1</i>	Anthranilate phosphoribosyltransferase, chloroplastic	transferase activity	3.08
TRINITY_DN13463_c1_g4	<i>RBCL</i>	Ribulose biphosphate carboxylase large chain	ion binding; oxidoreductase activity; RNA binding; lyase activity	3.30
TRINITY_DN1806_c0_g2	<i>NDHH</i>	NAD(P)H-quinone oxidoreductase subunit H, chloroplastic	NAD binding; oxidoreductase activity	3.31
TRINITY_DN5157_c0_g3	<i>PSBC</i>	Photosystem II CP43 reaction center protein	chlorophyll binding; oxidoreductase activity; ion binding; RNA binding	3.65

A4a1

Down-regulated

TRINITY_DN28591_c0_g1	<i>UGT84B1</i>	UDP-glycosyltransferase 84B1	transferase activity	-4.85
TRINITY_DN7605_c3_g1	<i>UBQ11</i>	Polyubiquitin 11	RNA binding; protein tag; protein binding	-4.80
TRINITY_DN184396_c0_g1	<i>AT1G56220</i>	Dormancy-associated protein homolog 3		-4.65
TRINITY_DN51734_c0_g2	<i>LTP11</i>	Non-specific lipid-transfer protein 11	lipid binding	-4.25
TRINITY_DN166189_c1_g1	<i>LTP1</i>	Non-specific lipid-transfer protein 1	protein binding; lipid binding	-4.25
TRINITY_DN105307_c0_g1	<i>PDF2.3</i>	Defensin-like protein 1		-4.17
TRINITY_DN4240_c0_g1	<i>LSU2</i>	Protein RESPONSE TO LOW SULFUR 2		-4.11
TRINITY_DN45272_c0_g1	<i>HPD</i>	4-hydroxyphenylpyruvate dioxygenase	oxidoreductase activity; protein binding; ion binding	-3.95
TRINITY_DN5744_c0_g1	<i>PP2A2</i>	Protein PHLOEM PROTEIN 2-LIKE A2		-3.75
TRINITY_DN16864_c1_g1	<i>EXO</i>	Protein EXORDIUM		-3.46

Up-regulated

TRINITY_DN10706_c0_g1	<i>AT2G17570</i>	Dehydrodolichyl diphosphate synthase 6	transferase activity	3.56
TRINITY_DN31379_c0_g1	<i>TKPR1</i>	Tetraketide alpha-pyrone reductase 1	oxidoreductase activity	3.68
TRINITY_DN44687_c0_g1	<i>ADPG2</i>	Polygalacturonase ADPG2	hydrolase activity	3.78
TRINITY_DN6156_c0_g1	<i>PKSA</i>	Type III polyketide synthase A	transferase activity	3.84
TRINITY_DN6869_c0_g1	<i>A6</i>	Probable glucan endo-1,3-beta-glucosidase A6	hydrolase activity	4.03
TRINITY_DN9952_c0_g1	<i>ABCG26</i>	ABC transporter G family member 26	ATP binding; transporter activity	4.12
TRINITY_DN22852_c0_g1	<i>TA1</i>	Short-chain dehydrogenase reductase ATA1	oxidoreductase activity; protein binding	4.38
TRINITY_DN3406_c2_g2	<i>XTH22</i>	Xyloglucan endotransglucosylase/hydrolase protein 22	hydrolase activity; transferase activity	4.39
TRINITY_DN45712_c0_g1	<i>FAR2</i>	Fatty acyl-CoA reductase 2, chloroplastic	oxidoreductase activity	4.58
TRINITY_DN6357_c0_g1	<i>PR5K</i>	PR5-like receptor kinase	ATP binding; transferase activity	5.18

A2a2

Down-regulated

TRINITY_DN51734_c0_g2	<i>LTP11</i>	Non-specific lipid-transfer protein 11	lipid binding	-7.16
TRINITY_DN166189_c1_g1	<i>LTP1</i>	Non-specific lipid-transfer protein 1	lipid binding; protein binding	-6.96
TRINITY_DN184396_c0_g1	<i>AT1G56220</i>	Dormancy-associated protein homolog 3		-6.68
TRINITY_DN5744_c0_g1	<i>PP2A2</i>	Protein PHLOEM PROTEIN 2-LIKE A2	ion binding; hydrolase activity	-6.29
TRINITY_DN7605_c3_g1	<i>UBQ11</i>	Polyubiquitin 11	RNA binding; protein tag; protein binding	-6.22
TRINITY_DN28591_c0_g1	<i>UGT84B1</i>	UDP-glycosyltransferase 84B1	transferase activity	-5.58
TRINITY_DN16864_c1_g1	<i>EXO</i>	Protein EXORDIUM		-5.55
TRINITY_DN105307_c0_g1	<i>PDF2.3</i>	Defensin-like protein 1		-5.19
TRINITY_DN4240_c0_g1	<i>LSU2</i>	Protein RESPONSE TO LOW SULFUR 2		-4.36
TRINITY_DN35822_c0_g1	<i>PER25</i>	Peroxidase 25	heme binding; ion binding; oxidoreductase activity	-4.13

Up-regulated

TRINITY_DN5909_c0_g2	<i>BG2</i>	Glucan endo-1,3-beta-glucosidase, acidic isoform	hydrolase activity	5.33
TRINITY_DN5487_c0_g1	<i>ROPGEF12</i>	Rop guanine nucleotide exchange factor 12	enzyme regulator activity	5.36
TRINITY_DN8876_c0_g1	<i>AT2G27360</i>	GDSL esterase/lipase At2g27360	hydrolase activity	5.41
TRINITY_DN185471_c0_g1	<i>AT1G30350</i>	Probable pectate lyase 4	ion binding; lyase activity	5.44
TRINITY_DN11348_c0_g1	<i>AT4G10955</i>	GDSL esterase/lipase At4g10955	hydrolase activity	5.48
TRINITY_DN2407_c1_g1	<i>BZIP34</i>	Basic leucine zipper 34	DNA binding; transcription regulator activity	5.59
TRINITY_DN12231_c0_g1	<i>PME13</i>	Probable pectinesterase/pectinesterase inhibitor 13	hydrolase activity	5.63
TRINITY_DN193961_c0_g1	<i>CML16</i>	Probable calcium-binding protein CML16	ion binding; enzyme regulator activity	5.86
TRINITY_DN6869_c0_g1	<i>A6</i>	Probable glucan endo-1,3-beta-glucosidase A6	hydrolase activity	6.00
TRINITY_DN6156_c0_g1	<i>PKSA</i>	Type III polyketide synthase A	transferase activity	6.20