

Table S7. Uniquely annotated top down- and up-regulate differentially expressed genes (DEGs) in ovules from apomictic *Limonium ovalifolium* (O) in stage S2 (2) relative to S1 (1) and DEGs from 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
O2o1				
Down				
TRINITY_DN166189_c1_g1	<i>LTP1</i>	Non-specific lipid-transfer protein 1	protein binding; lipid binding	-3,53
TRINITY_DN51734_c0_g2	<i>LTP11</i>	Non-specific lipid-transfer protein 11	lipid binding	-3,31
TRINITY_DN16864_c1_g1	<i>EXO</i>	Protein EXORDIUM		-3,05
TRINITY_DN2317_c0_g2	<i>GA2OX6</i>	Gibberellin 2-beta-dioxygenase 6	metal ion binding; oxidoreductase activity	-2,82
TRINITY_DN5744_c0_g1	<i>PP2A2</i>	Protein PHLOEM PROTEIN 2-LIKE A2	ion binding; hydrolase activity	-2,71
TRINITY_DN9463_c0_g1	<i>EMI</i>	Em-like protein GEA1		-2,52
TRINITY_DN79538_c1_g1	<i>COL1</i>	Zinc finger protein CONSTANS-LIKE 1	transcription regulator activity; metal ion binding; DNA binding; protein binding	-2,41
TRINITY_DN89174_c0_g1	<i>FQR1</i>	NAD(P)H dehydrogenase (quinone) FQR1	ribonucleotide binding; oxidoreductase activity	-2,35
TRINITY_DN7605_c3_g1	<i>UBQ11</i>	Polyubiquitin 11	RNA binding; protein tag; protein binding	-2,31
TRINITY_DN13979_c0_g2		Probable inactive nicotinamidase At3g16190		-2,3
Up				
TRINITY_DN19440_c0_g1	<i>PELPK1</i>	Protein PELPK1		3,99
TRINITY_DN150733_c0_g1	<i>TBL31</i>	Protein trichome birefringence-like 31	transferase activity	4,06
TRINITY_DN829_c0_g2	<i>INVA</i>	Alkaline/neutral invertase A, mitochondrial	hydrolase activity	4,24
TRINITY_DN8876_c0_g1	<i>AT2G27360</i>	GDGL esterase/lipase At2g27360	hydrolase activity	4,27
TRINITY_DN8238_c0_g2	<i>AT3G03770</i>	Probable inactive leucine-rich repeat receptor-like protein kinase At3g03770	ATP binding; transferase activity	4,36

TRINITY_DN4747_c0_g1	<i>EXPB3</i>	Expansin-B3		4,37
TRINITY_DN14059_c0_g1	<i>AT4G28780</i>	GDSL esterase/lipase At4g28780	hydrolase activity	4,38
TRINITY_DN1473_c0_g1	<i>PRE6</i>	Transcription factor PRE6	protein binding	4,51
TRINITY_DN604_c0_g1	<i>AT5G45950</i>	GDSL esterase/lipase At5g45950	hydrolase activity	5,73
TRINITY_DN5904_c0_g1	<i>AT4G00165</i>	Putative lipid-binding protein At4g00165		5,82

O4o1

Down

TRINITY_DN51734_c0_g2	<i>LTP11</i>	Non-specific lipid-transfer protein 11	lipid binding	-5,12
TRINITY_DN57_c0_g1	<i>KIN10</i>	SNF1-related protein kinase catalytic subunit alpha KIN10	ATP binding; transferase activity; protein binding	-4,95
TRINITY_DN12370_c0_g1	<i>CSP4</i>	Cold shock domain-containing protein 4	DNA binding; RNA binding; ion binding	-4,8
TRINITY_DN325_c0_g1	<i>XI-B</i>	Myosin-8	ATP-dependent activity; protein binding; ATP binding	-4,13
TRINITY_DN3040_c0_g2	<i>CIPK3</i>	CBL-interacting serine/threonine-protein kinase 3	ATP binding; transferase activity	-4,1
TRINITY_DN1497_c0_g1	<i>RAP2-4</i>	Ethylene-responsive transcription factor RAP2-4	DNA binding; transcription regulator activity	-3,91
TRINITY_DN8323_c0_g1	<i>YYI</i>	Zinc finger transcription factor YY1	transcription regulator activity; metal ion binding; DNA binding	-3,67
TRINITY_DN3733_c0_g2	<i>IAA18</i>	Auxin-responsive protein IAA18	transcription regulator activity	-3,63
TRINITY_DN2881_c0_g1	<i>NHL1</i>	NDR1/HIN1-like protein 1		-3,59
TRINITY_DN2779_c0_g1	<i>RPL11A</i>	60S ribosomal protein L11-1	RNA binding; structural constituent of ribosome	-3,57

Up

TRINITY_DN150733_c0_g1	<i>TBL31</i>	Protein trichome birefringence-like 31	transferase activity	5,5
TRINITY_DN12231_c0_g1	<i>PME13</i>	Probable pectinesterase/pectinesterase inhibitor 13	hydrolase activity	5,52

TRINITY_DN979_c1_g1	<i>ATMG00030</i>	Uncharacterized mitochondrial protein AtMg00030		5,54
TRINITY_DN5904_c0_g1	<i>AT4G00165</i>	Putative lipid-binding protein At4g00165		5,79
TRINITY_DN5664_c0_g1	<i>ATPA</i>	ATP synthase subunit alpha, chloroplastic	ADP binding; ATP binding; RNA binding; ATP-dependent activity; ion binding	5,9
TRINITY_DN1806_c0_g2	<i>NDHH</i>	NAD(P)H-quinone oxidoreductase subunit H, chloroplastic	NAD binding; oxidoreductase activity; quinone binding	5,94
TRINITY_DN1473_c0_g1	<i>PRE6</i>	Transcription factor PRE6	protein binding	6,14
TRINITY_DN47860_c0_g2	<i>PSBE</i>	Cytochrome b559 subunit alpha	oxidoreductase activity; heme binding; ion binding	6,62
TRINITY_DN604_c0_g1	<i>AT5G45950</i>	GDSL esterase/lipase At5g45950	hydrolase activity	6,86
TRINITY_DN2730_c0_g1	<i>CLPP1</i>	Chloroplastic ATP-dependent Clp protease proteolytic subunit 1	enzyme binding; ATP-dependent activity; hydrolase activity	7,17

O4o2

Down

TRINITY_DN2467_c0_g2	<i>XTH10</i>	Probable xyloglucan endotransglucosylase/hydrolase protein 10	hydrolase activity; transferase activity	-4,58
TRINITY_DN57_c0_g1	<i>KIN10</i>	SNF1-related protein kinase catalytic subunit alpha KIN10	ATP binding; transferase activity; protein binding	-4,52
TRINITY_DN3040_c0_g2	<i>CIPK3</i>	CBL-interacting serine/threonine-protein kinase 3	transferase activity	-4,42
TRINITY_DN12370_c0_g1	<i>CSP4</i>	Cold shock domain-containing protein 4	DNA binding; RNA binding; ion binding	-4,28
TRINITY_DN325_c0_g1	<i>XI-B</i>	Myosin-8	ATP-dependent activity; protein binding; ATP binding	-4,1
TRINITY_DN21412_c0_g1	<i>NOP5-1</i>	Probable nucleolar protein 5-1	RNA binding	-3,87
TRINITY_DN1593_c0_g1	<i>DSE1</i>	Protein DECREASED SIZE EXCLUSION LIMIT 1		-3,7

TRINITY_DN6442_c0_g1	<i>A39</i>	Aspartic proteinase 39	hydrolase activity	-3,69
TRINITY_DN2779_c0_g1	<i>RPL11A</i>	60S ribosomal protein L11-1	RNA binding; structural constituent of ribosome	-3,56
TRINITY_DN1497_c0_g1	<i>RAP2-4</i>	Ethylene-responsive transcription factor RAP2-4	transcription regulator activity; DNA binding	-3,46

Up

TRINITY_DN3634_c0_g1	<i>NAD7</i>	NADH dehydrogenase [ubiquinone] iron-sulfur protein 2	oxidoreductase activity; NAD binding	5,18
TRINITY_DN6988_c0_g1	<i>ND2</i>	NADH-ubiquinone oxidoreductase chain 2	oxidoreductase activity	5,5
TRINITY_DN979_c1_g1	<i>ATMG00030</i>	Uncharacterized mitochondrial protein AtMg00030		5,95
TRINITY_DN3643_c2_g1	<i>YCF3</i>	Photosystem I assembly protein Ycf3		6,05
TRINITY_DN5157_c0_g3	<i>PSBC</i>	Photosystem II CP43 reaction center protein	chlorophyll binding; oxidoreductase activity; ion binding; RNA binding	6,23
TRINITY_DN13463_c1_g4	<i>RBCL</i>	Ribulose biphosphate carboxylase large chain	ion binding; oxidoreductase activity; RNA binding; lyase activity	6,23
TRINITY_DN1806_c0_g2	<i>NDHH</i>	NAD(P)H-quinone oxidoreductase subunit H, chloroplastic	NAD binding; oxidoreductase activity; quinone binding	6,23
TRINITY_DN5664_c0_g1	<i>ATPA</i>	ATP synthase subunit alpha, chloroplastic	ADP binding; ATP binding; RNA binding; ATP-dependent activity; transporter activity; ion binding	6,62
TRINITY_DN2730_c0_g1	<i>CLPP1</i>	Chloroplastic ATP-dependent Clp protease proteolytic subunit 1	protein binding; ATP-dependent activity; hydrolase activity	6,96
TRINITY_DN47860_c0_g2	<i>PSBE</i>	Cytochrome b559 subunit alpha	oxidoreductase activity; heme binding; ion binding	7,14
