

Table S9. Over-representation analysis (ORA) performed by gProfiler of transcription factors (TFs) differentially expressed genes (DEGs) in ovules of *Limonium* plants, namely apomictic *L. multiflorum* (M) and sexual *L. auriculifolium* (a) and *L. ovalifolium* (o). DEGs were filtered by $|\log_2 \text{fold-change} (\log_2 \text{FC})| > 2$. *Arabidopsis thaliana* most similar homolog of each differentially expressed gene (DEG) was mapped to the respective functional annotation. Significantly (FDR < 0.01) KEGG and WikiPathways metabolic pathways and the respective DEGs from **M1a1**, **M1a2**, **M1o1**, **M1o2**, **M2a4** and **M2o4** (Red: up-regulated DEGs; blue: down-regulated DEGs).

Gene ID	Gene Name	Protein Name	Log2FC					
			M1a1	M1a2	M1o1	M1o2	M2a4	M2o4
Flower Development [WP:WP618]								
TRINITY_DN6666_c0_g1	AG	Floral homeotic protein AGAMOUS						-2,4
TRINITY_DN9027_c0_g3	API	Floral homeotic protein APETALA 1	-7,1	-7,2	-7,2	-6,3		
TRINITY_DN7779_c0_g1	AP3	Floral homeotic protein APETALA 3					-4,2	-3,2
TRINITY_DN7954_c0_g1	PI	Floral homeotic protein PISTILLATA	-8,4	-6,5	-7,1	-8,3		-3,4
TRINITY_DN12350_c0_g1	RAP2-7	Ethylene-responsive transcription factor RAP2-7					-4,2	
TRINITY_DN9027_c0_g1	SEP1	Developmental protein SEPALLATA 1	-7,9		-7,6	-8,1		
TRINITY_DN31040_c0_g1	SEP3	Developmental protein SEPALLATA 3					-2,4	
TRINITY_DN2251_c0_g1	SOC1	MADS-box protein SOC1						
TRINITY_DN29363_c0_g1	SVP	MADS-box protein SVP						
Flower Development (Initiation) [WP:WP2108]								
TRINITY_DN6666_c0_g1	AG	Floral homeotic protein AGAMOUS						-2,4
TRINITY_DN9027_c0_g3	API	Floral homeotic protein APETALA 1	-7,1	-7,2	-7,2	-6,3		
TRINITY_DN2754_c0_g1	AP2	Floral homeotic protein APETALA 2						2,1
TRINITY_DN7779_c0_g1	AP3	Floral homeotic protein APETALA 3					-2,5	-3,2
TRINITY_DN7954_c0_g1	PI	Floral homeotic protein PISTILLATA						-3,4
TRINITY_DN12350_c0_g1	RAP2-7	Ethylene-responsive transcription factor RAP2-7	6,4		6,5	4,6	4,6	
TRINITY_DN31040_c0_g1	SEP3	Developmental protein SEPALLATA 3					-2,4	

Lysine degradation [KEGG:00310]						
TRINITY_DN8133_c0_g1	<i>ASHR1</i>	Histone-lysine N-methyltransferase ASHR1	10,1			
TRINITY_DN1656_c0_g1	<i>ATXR3</i>	Histone-lysine N-methyltransferase ATXR3	2,1			
TRINITY_DN15991_c0_g1	<i>ATXR5</i>	Histone-lysine N-methyltransferase EZA1	6,8			
TRINITY_DN14929_c0_g1	<i>EZA1</i>	Histone-lysine N-methyltransferase EZA1	2,9			
TRINITY_DN22984_c0_g1	<i>SUVH6</i>	Histone-lysine N-methyltransferase, H3 lysine-9 specific SUVH6	7,2			
TRINITY_DN393_c0_g2	<i>SUVH9</i>	Histone-lysine N-methyltransferase family member SUVH9	10,4			
TRINITY_DN10785_c0_g1	<i>SUVR3</i>	Histone-lysine N-methyltransferase SUVR3	7,1			
MAPK signaling pathway - plant [KEGG:04016]						
TRINITY_DN11495_c0_g1	<i>EIN4</i>	Protein EIN4	10,5			
TRINITY_DN9787_c0_g1	<i>AT1G66345</i>	Pentatricopeptide repeat-containing protein At1g66345	9,6			
TRINITY_DN7020_c3_g1	<i>MYC2</i>	Transcription factor MYC2	2,6			
TRINITY_DN10939_c0_g2	<i>WRKY29</i>	Probable WRKY transcription factor 29	8,1			
TRINITY_DN42768_c0_g1	<i>WRKY33</i>	Probable WRKY transcription factor 33	2,8			
Plant hormone signal transduction [KEGG:04075]						
TRINITY_DN5251_c0_g1	<i>AHK3</i>	Histidine kinase 3	2,6	2,4	2,6	9,8
TRINITY_DN5309_c0_g1	<i>AHK4</i>	Histidine kinase 4		-3,8	-2,2	
TRINITY_DN106_c0_g1	<i>ARF1</i>	Auxin response factor 1				2,7
TRINITY_DN21549_c0_g1	<i>ARR11</i>	Two-component response regulator ARR11				8,3
TRINITY_DN12286_c0_g1	<i>ARR17</i>	Two-component response regulator ARR17			-4,1	
TRINITY_DN7878_c1_g2	<i>ARR9</i>	Two-component response regulator ARR9	-2,3	-2,4		8,6
TRINITY_DN13746_c0_g1	<i>BZR2</i>	Protein BRASSINAZOLE-RESISTANT 2				7,6
TRINITY_DN56546_c0_g1	<i>DPBF3</i>	ABSCISIC ACID-INSENSITIVE 5-like protein 2				6,7
TRINITY_DN11495_c0_g1	<i>EIN4</i>	Protein EIN4				10,5

TRINITY_DN5700_c2_g1	<i>ERF2</i>	Ethylene-responsive transcription factor 2		2,2	10,8
TRINITY_DN9787_c0_g1	<i>AT1G66345</i>	Pentatricopeptide repeat-containing protein At1g66345			9,6
TRINITY_DN5071_c0_g1	<i>GBF4</i>	G-box-binding factor 4			11,7
TRINITY_DN6334_c0_g1	<i>IAA14</i>	Auxin-responsive protein IAA14	-3,4	-2,8	
TRINITY_DN16729_c0_g1	<i>IAA27</i>	Auxin-responsive protein IAA27		-4,2	-3,1
TRINITY_DN243_c0_g4	<i>IAA3</i>	Auxin-responsive protein IAA3		-2,2	
TRINITY_DN11282_c0_g2	<i>IAA7</i>	Auxin-responsive protein IAA7		-7,1	-5
TRINITY_DN7020_c3_g1	<i>MYC2</i>	Transcription factor MYC2		2,8	2,6
TRINITY_DN9310_c0_g1	<i>NPR5</i>	Regulatory protein NPR5		-2	
TRINITY_DN2328_c0_g1	<i>TGA1</i>	Transcription factor TGA1			11,1
TRINITY_DN10239_c0_g1	<i>TGA2</i>	Transcription factor TGA2	2,1		2,8
TRINITY_DN20363_c0_g1	<i>TGA6</i>	Transcription factor TGA6			3,1