Additional file 11.

	Ortholog of LEA proteins		
Group	Arabidopsis	Thellungiella	Remark
LEA_1	6	133	complete cds: 108
	18	108	
	46	72 , 110	
LEA_2	1	94 , 106, 122, 153	105 and 106 are different translated frames of thellun_all_rep_c15208; 122 and 123 are different translated frames of thellun_all_rep_c20993; 153 and 154 are different translated frames of thellun_all_rep_c28021
		123 , 87, 105, 115, 154	
		196	
	26	63 , 113	113 and 114 are different translated frames of thellun_all_rep_c17285; 141 and 142 are different translated frames of thellun_all_rep_c26673
		142 , 114, 141	
	27	60	complete cds: 60
154.0	2	58	
	37	62	
LEA_3	38	52 , 65, 88, 132, 155, 191	complete cds: 52
	41	54 , 100, 121, 156	complete cds: 54
	7	149 , 66, 67, 185, 189	complete cds: 149; 66 and 67 are different translated frames of thellun_all_rep_c4181
	9	85	400 metalliad to ATOCCOV (no lock) 05 and 00 are different translated frames of the living all cooper
		125 , 86	109 matched to AT22600((no lea); 85 and 86 are different translated frames of thellun_all_c8083
	11	77	
	12	75	
	13		
	19		
LEA_4	23	55 , 74, 112, 187	
		145 , 134, 135, 158, 197	complete cds: 55, 198; 163 and 164 are different translated frames of thellun_all_rep_c34113
		157 , 159	
		198 , 137, 163, 164	
	24	168 , 73, 139	
	25	144 , 143	143 and 144 are different translated frames of thellun_all_c26853
	28		102 matched to AT5G38760, 116 matched to AT5G53820. Both AT5G38760 and AT5G53820 were
			not annotated as LEA (Hundertmark and Hincha, 2008)
	29	84 , 83	83 and 84 are different translated frames of thellun_all_rep_7426
	30	64	complete cds: 64
	36	160	
	39	04	computate ada, 04
	40 42	81 90 , 91	complete cds: 81 90 and 91 are different translated frames of thellun all c8752
	43	30 , 31	30 and 31 are different translated frames of thehun_all_co/32
	48	175	
	.0	114	

LEA_5	20			
LLA_5	35			
AtM	21 22			
Auvi		93		
LEA_6	15		<u></u>	
	16	177 , 56, 82, 169, 184, 186	complete cds: 177	
	17			
	3		<u></u>	
	31	148 , 147	 146, 147, 148 are translated frames of thellun_all_c27216	
SMP	32	146		
SIVIE	47	165		
	49			
	50			
		59 , 120, 138, 162, 174, 179, 192	161 and 162 are different translated frames of thellun_all_rep_c32321; 178 and 179 are different translated frames of thellun_all_rep_c41511	
	4	126 , 61, 126, 150, 161, 166, 178		
		195 , 99, 104, 190		
	5	95 , 97, 151, 173, 176, 194	192 and 193 are different translated frames of cluster216; 194 and 195 are different translated frames of cluster331	
		124 , 111, 118, 131,152		
		130 , 119, 170, 193		
	8	78 , 53, 107, 127		
		98 , 70, 117, 180	complete cds: 199. Sequence 71 is translated frame +1 of thellun_all_rep_c5017 and clustered close to sequence 10. It is highly similar to mitochondrial lipoamide dehydrogenase 1 (AT1G48030) and likely not a LEA ortholog, herby not represented as ortholog of #10 in the Table.	
dehydrin	10	181		
		199 , 68, 69, 76, 92, 101, 128, 140, 171, 182, 188		
	14	89		
	33			
	34	80		
	44	103		
	45			
		57 , 79, 129, 183		
	51	136	complete cds: 57	
		167		
		172		
		40		

Putative Thellungiella LEA proteins were identified by reciprocal BLASTX (E < 10⁻¹⁰) searches of all *T. salsuginea* unigenes against the 51 *Arabidopsis* LEA proteins and resulted in 148 protein sequences as shown in Supplemental Table S2. Empty cells indicate no orthologous protein was found for *T. salsuginea* in the sequence assembly. Cds, coding sequence.