

1 **Supplemental Table S1.** Summary of orthologous gene family clustering

	<i>A. comosus</i>	<i>B. distachyon</i>	<i>O. sativa</i>	<i>O. thomaeum</i>	<i>P. hallii</i>	<i>S. bicolor</i>	<i>S. italica</i>	<i>X. viscosa</i>	<i>Z. marina</i>	<i>A. thaliana</i>
# of genes	27024	34310	39049	28835	33805	34129	34584	25425	20450	27416
# of genes in orthogroups	21778	27612	28492	26459	28195	28451	30811	22699	17580	23424
# of unassigned genes	5246	6698	10557	2376	5610	5678	3773	2726	2870	3992
% of genes in orthogroups	80.6	80.5	73	91.8	83.4	83.4	89.1	89.3	86	85.4
% of unassigned genes	19.4	19.5	27	8.2	16.6	16.6	10.9	10.7	14	14.6
# of orthogroups containing species	11294	12965	13300	13582	13900	13682	14295	10161	9644	10524
% of orthogroups containing species	42.8	49.1	50.4	51.4	52.6	51.8	54.1	38.5	36.5	39.9
# of species-specific orthogroups	61	26	41	12	9	10	13	30	37	51
# of genes in species-specific orthogroups	346	111	157	39	62	39	60	79	230	358
% of genes in species-specific orthogroups	1.3	0.3	0.4	0.1	0.2	0.1	0.2	0.3	1.1	1.3

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3 Continued:

	<i>L. brevidens</i>	<i>L. subrace- mosa</i>	<i>M. polymer- pha</i>	<i>M. truncat- ula</i>	<i>P. patens</i>	<i>S. lepidop- hylla</i>	<i>S. lycopersi- cum</i>	<i>S. moellen- dorffii</i>	<i>V. vinifera</i>
# of genes	27204	33344	19287	50894	32926	27204	34725	22285	26346
# of genes in orthogroups	24055	28783	12536	33838	19780	17755	27020	16550	20958
# of unassigned genes	3149	4561	6751	17056	13146	9449	7705	5735	5388
% of genes in orthogroups	88.4	86.3	65	66.5	60.1	65.3	77.8	74.3	79.5
% of unassigned genes	11.6	13.7	35	33.5	39.9	34.7	22.2	25.7	20.5
# of orthogroups containing species	11150	11454	8704	11657	8950	9478	11459	9149	10818
% of orthogroups containing species	42.2	43.4	33	44.1	33.9	35.9	43.4	34.6	41
# of species-specific orthogroups	7	14	60	171	130	109	61	84	27
# of genes in species-specific orthogroups	40	58	500	1248	610	630	311	451	151
% of genes in species-specific orthogroups	0.1	0.2	2.6	2.5	1.9	2.3	0.9	2	0.6

4 **Supplemental Table S2.** Annotation of ELIPs in the *Selaginella tamariscina* genome.

Contig	Percent identity to <i>S. lepidophylla</i> ortholog	Gene model start (pos.)	Gene model end (pos.)
PUQB01000010.1	41.85	1151807	1151280
PUQB01000010.1	43.01	1180496	1179987
PUQB01000011.1	75.25	565222	565951
PUQB01000011.1	57.71	575975	576733
PUQB01000011.1	57.87	584661	583900
PUQB01000011.1	54.55	588675	587960
PUQB01000011.1	46.98	617860	617180
PUQB01000011.1	68.42	645226	645952
PUQB01000011.1	62.96	663159	662512
PUQB01000029.1	78.13	933789	932897
PUQB01000029.1	78.13	939367	938628
PUQB01000029.1	68.9	947109	946483
PUQB01000029.1	53.18	952759	953412
PUQB01000029.1	61.98	955146	955887
PUQB01000029.1	59.85	960781	961672
PUQB01000029.1	78.13	977377	976563
PUQB01000029.1	66.44	986927	986195
PUQB01000029.1	78.13	989251	988602
PUQB01000029.1	77.78	998816	998708
PUQB01000029.1	65	1000831	999102
PUQB01000029.1	80	1001475	1001534
PUQB01000029.1	70.83	1006939	1007563
PUQB01000029.1	69.62	1009233	1009463
PUQB01000029.1	55.71	1011207	1011901
PUQB01000029.1	42.86	1023659	1024240
PUQB01000029.1	65.85	1025622	1026370
PUQB01000029.1	53.85	1027541	1028212
PUQB01000029.1	42.36	1029037	1029712
PUQB01000054.1	60.71	462437	461937
PUQB01000054.1	75.68	499360	498652
PUQB01000054.1	50.57	504962	505683
PUQB01000054.1	58.25	567722	567111
PUQB01000054.1	43.82	572269	571620
PUQB01000054.1	46.43	573513	574070
PUQB01000054.1	83.82	594021	593444
PUQB01000054.1	57.72	599456	599821
PUQB01000054.1	59.76	617337	618065
PUQB01000054.1	62.28	639096	639748
PUQB01000054.1	54.46	642085	642797

PUQB01000054.1	62.28	654198	654892
PUQB01000054.1	88.52	670340	670880
PUQB01000057.1	50.79	225923	226530
PUQB01000077.1	62.5	97429	96735
PUQB01000077.1	53.27	99214	99799
PUQB01000077.1	84.09	99786	99917
PUQB01000117.1	73.2	143450	142852
PUQB01000148.1	60.24	74544	73804
PUQB01000148.1	56.15	77941	78683
PUQB01000320.1	75.71	212112	211563
PUQB01000320.1	86.76	214576	214373
PUQB01000474.1	42.37	144010	144507
PUQB01000474.1	78.13	186185	185294
PUQB01000474.1	78.13	191770	191037
PUQB01000583.1	49.8	9468	8749
PUQB01000583.1	39.53	11374	11982
PUQB01000588.1	66.67	13407	14005
PUQB01000633.1	47.51	42243	42982
PUQB01000633.1	45.19	70992	70306
PUQB01000633.1	46.28	75133	74670
PUQB01000633.1	51.69	76360	77081
PUQB01000633.1	61.07	97199	96477
PUQB01000633.1	85.96	107714	107884
PUQB01000633.1	57.14	125172	125857
PUQB01000679.1	60.73	302	1042
PUQB01000679.1	61.7	8142	8417
PUQB01000679.1	62.5	10277	10780
PUQB01000679.1	48.05	22552	22782
PUQB01000679.1	49.01	22821	23267
PUQB01000679.1	62.62	24661	25402
PUQB01000679.1	55.33	26725	27303
PUQB01000679.1	51.11	27976	28766
PUQB01000880.1	82.22	6704	6073
PUQB01000880.1	42.78	9120	8554
PUQB01000880.1	60.73	16655	15915
PUQB01000880.1	56.25	23798	23175
PUQB01000880.1	58	29664	30295
PUQB01000880.1	77.65	32121	32752

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7 **Supplementary Table S3.** Summary of expression and physiology data used in this study.

Species	Designation	Stage	RWC (%)	Citation
<i>Boea hygrometrica</i>	F	well-watered	NA	Xiao et al., 2015
	D1	dehydrating	70	
	D2	desiccated	10	
<i>Lindernia brevidens</i>	F	well-watered	80.8	VanBuren et al., 2018b
	D3	dehydrating	53.6	
	D7	dehydrating	22.9	
	D10	desiccated	5.9	
	D14	desiccated	4.2	
	R24	24 hr post rehydration	31.8	
	R48	48 hr post rehydration	44.4	
<i>Oropetium thomaeum</i>	F	well-watered	71.1	VanBuren et al., 2017
	D7	dehydrating	31.6	
	D14	dehydrating	11.6	
	D21	desiccated	7.9	
	D30	desiccated	5.6	
	R24	24 hr post rehydration	38.4	
	R48	48 hr post rehydration	51.8	
<i>Bryum argenteum</i>	D	desiccated	NA	Gao et al., 2015
	R2	2 hr post rehydration	NA	
	R24	24 hr post rehydration	NA	
<i>Selaginella lepidophylla</i>	D	desiccated	11.2	VanBuren et al., 2018c
	R1	1 hr post rehydration	14.3	
	R4	12 hr post rehydration	43.2	
	R24	24 hr post rehydration	68.4	
	R120	120 hr rehydration	75.3	
	D1	desiccated	15.3	
<i>Xerophyta viscosa</i>	F	well-watered	NA	Costa et al., 2017
	D1	dehydrating	80	
	D2	dehydrating	60	
	D3	dehydrating	40	
	D4	dehydrating	20	
	D5	desiccated	4	
	R12	12 hr post rehydration	NA	
	R24	24 hr post rehydration	NA	