GmSYP24, a putative syntaxin gene, confers osmotic/drought, salt stress tolerances and ABA signal pathway

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Supporting Information

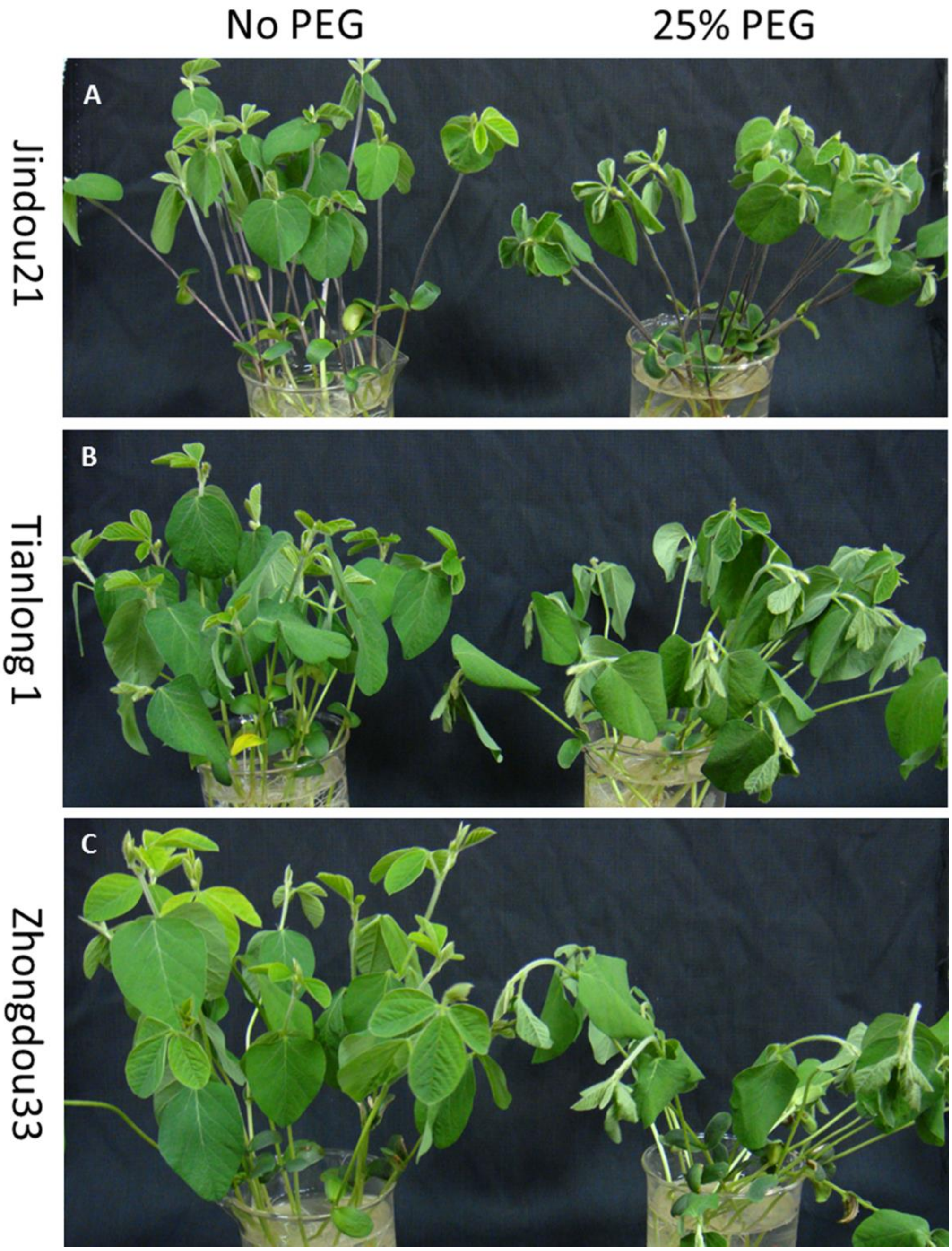

Figure S1. The phenotype of Jindou21, Tianlong1 and Zhongdou33 under 25% PEG or not. (A) Jindou21, (B) Tianlong1, (C) Zhongdou33.

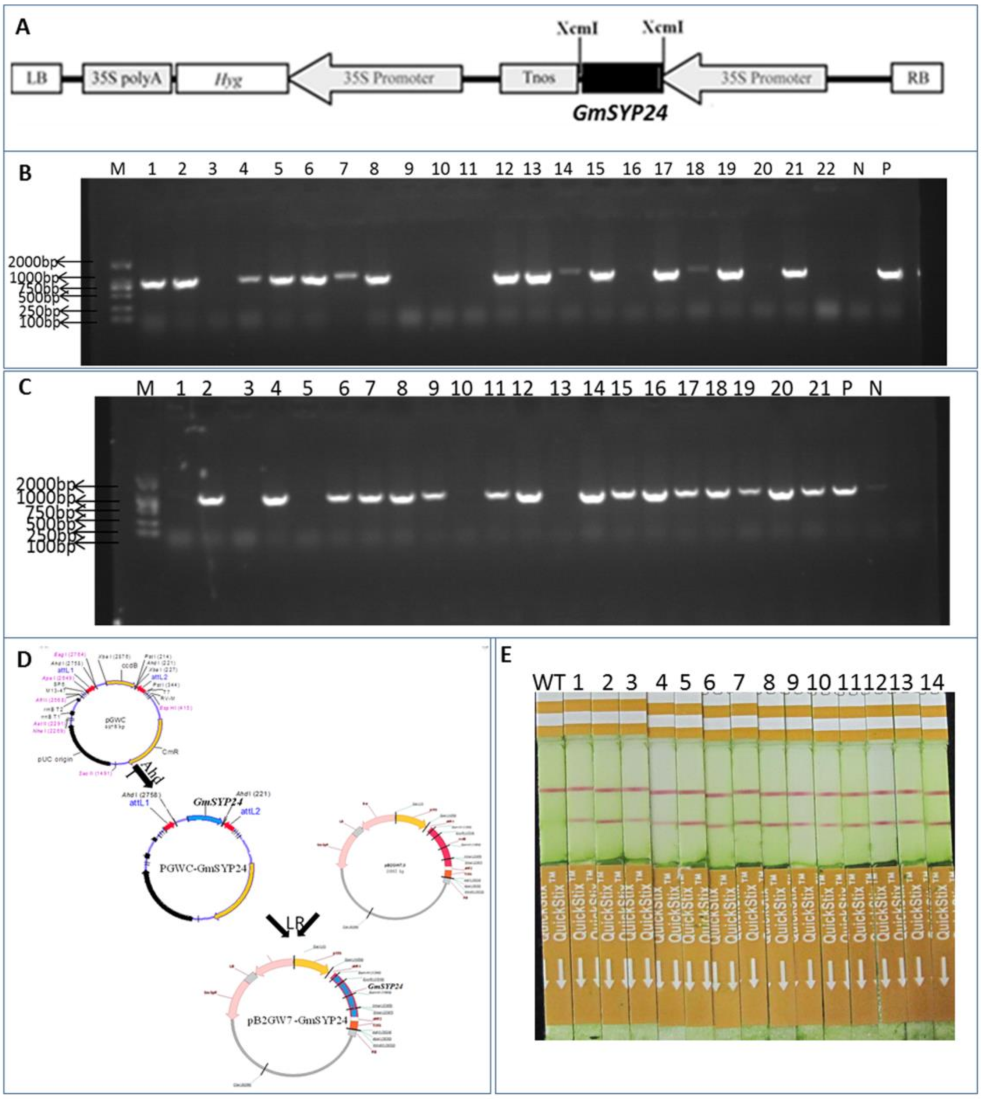

Figure S2. The construction of plant expression vector and molecular detection of transgenic plants. (A) The construct of *GmSYP24* into the pCXSN vector to transform Arabidopsis. (B) The amplification of *GmSYP24* in transgenic Arabidopsis plants. M: 2000 maker; 1-22: transgenic plants; N: negative control; P: positive control. The length of amplified fragment is 775bp (including CDS full-length of *GmSYP24*). (C) The amplification of *GmSYP24* in transgenic soybean plants. M: 2000 maker; 1-21: transgenic plants; P: positive control; N: negative control. The length of amplified fragment is 775bp (including CDS full-length of *GmSYP24*). (D) The construct of *GmSYP24* into the pB2GW7 vector to transform soybean. (E) The Bar protein detection in transgenic soybean of *GmSYP24ox*. WT: wild type plants (negative control); 1-14: transgenic positive plants.

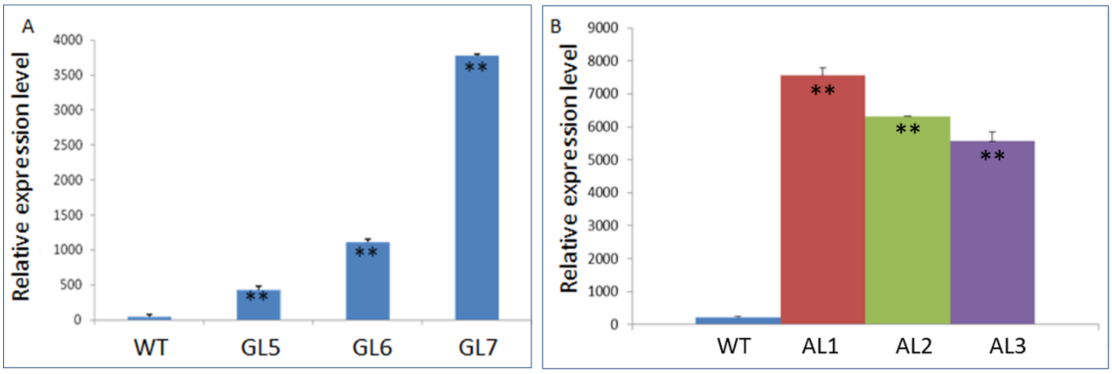

Figure S3. The expression analysis of *GmSYP24* in wild type and three transgenic lines of soybean (A) and Arabidopsis (B). Total RNA was isolated from the leave of greenhouse grown plants. The keephouse gene actin was employed as an internal control. The expression level of these genes in the leave of WT was set to 1. Error bars represent the SDs from three biological replicates. ** indicate significant differences in comparison to WT at $P < 0.01$.

Table S1. LEA2 family genes of soybean were list.

Gene name	Locus name (version Glyma2.0)	the number of LEA2 domain	GenBank Accession No.	Genome Location	The annotation of Arabidopsis homologous genes	Peptide Length	genome sequence	pI	Mw (KD)
GmLEA2-1	Glyma.01G152600	1	XM_003516456	Chr01:48960693-48961382	AT5G45320.1(molecular_function unknown)	229	690	8.95	25.82
GmLEA2-2	Glyma.01G222800	1	XM_006573731	Chr01:55174239-55175109	AT1G64065.1(Late embryogenesis abundant (LEA) hydroxyproline-rich glycoprotein family)	184	871	10.24	20.34
GmLEA2-3	Glyma.01G226100	1		Chr01:55470092-55471377	AT1G64450.1(Glycine-rich protein family)	209	1286	9.51	23.09
GmLEA2-4	Glyma.01G240600	1		Chr01:56444294-56444830	AT4G05220.1(Late embryogenesis abundant (LEA) hydroxyproline-rich glycoprotein family)	178	537	5.2	19.90
GmLEA2-5	Glyma.02G197600	1	XM_003519073	Chr02:37639021-37640558	AT3G11660.1(NDR1/HIN1-like 1)	207	1538	9.79	23.92
GmLEA2-6	Glyma.02G197800	1	XM_003519074	Chr02:37686736-37687986	AT3G11650.1(NDR1/HIN1-like 2, SYNTAXIN)	244	1251	9.26	27.63
GmLEA2-7	Glyma.02G239100	1	NM_001252948	Chr02:42754798-42755899	AT1G65690.1(Late embryogenesis abundant (LEA) hydroxyproline-rich glycoprotein family)	255	1102	10.12	28.77
GmLEA2-8	Glyma.02G274400	1	XM_003519436	Chr02:45751520-45753085	AT2G27080.1(Late embryogenesis abundant (LEA) hydroxyproline-rich glycoprotein family)	273	1566	9.81	30.50
GmLEA2-9	Glyma.02G277300	2	XM_006574374	Chr02:46010712-46013329	AT2G44060.1(Late embryogenesis abundant protein, group 2)	321	2618	4.85	35.82

GmLEA2-10	Glyma.02G303100	1		Chr02:47852657-47854573	AT4G26490.1(Late embryogenesis abundant（LEA）hydroxyproline-rich glycoprotein family)	236	1917	9.96	26.70
GmLEA2-11	Glyma.03G000800	1	XM_003521561	Chr03:113864-115495	AT3G54200.1（Late embryogenesis abundant（LEA）hydroxyproline-rich glycoprotein family）	192	1632	9.17	20.47
GmLEA2-12	Glyma.03G201000	1	XM_003521442	Chr03:40968934-40970257	AT2G35980.1（Late embryogenesis abundant（LEA）hydroxyproline-rich glycoprotein family，syntaxin）	221	1324	9.58	24.94
GmLEA2-13	Glyma.03G201100	1	NM_001253965	Chr03:40972049-40972976	AT2G35980.1(Late embryogenesis abundant（LEA）hydroxyproline-rich glycoprotein family,SYNTAXIN)	227	928	9.31	26.34
GmLEA2-14	Glyma.03G201200	1	XM_003520665	Chr03:40977183-40977806	AT2G35980.1(Late embryogenesis abundant（LEA）hydroxyproline-rich glycoprotein family,SYNTAXIN)	207	624	9.46	24.14
GmLEA2-15	Glyma.03G201300	1		Chr03:40980745-40990121	AT2G35980.1(Late embryogenesis abundant（LEA）hydroxyproline-rich glycoprotein family,SYNTAXIN)	243	9377	9.22	26.77
GmLEA2-16	Glyma.03G201500	1	XM_003521445	Chr03:40986155-40987233	AT2G35980.1(Late embryogenesis abundant（LEA）hydroxyproline-rich glycoprotein family,SYNTAXIN)	229	1079	9.92	28.67
GmLEA2-17	Glyma.03G201600	1	XM_006577032	Chr03:40993013-40994536	AT3G11660.1（NDR1/HIN1-like 1)	252	1524	9.83	21.56
GmLEA2-18	Glyma.03G261400	1	XM_003521778	Chr03:45488450-45489586	AT4G01410.1(Late embryogenesis abundant（LEA）hydroxyproline-rich glycoprotein family)	197	1137	9.66	27.86
GmLEA2-19	Glyma.03G263800	1		Chr03:45666942-45667919	AT2G01080.1 (Late embryogenesis	185	978	8.88	21.09

					abundant (LEA) hydroxyproline-rich glycoprotein family)				
GmLEA2-20	Glyma.04G051600	1	XM_003522201	Chr04:4179782-4181288	AT5G11890.1(molecular_function unknown)	256	1507	9.87	28.23
GmLEA2-21	Glyma.04G103700	1	XM_003523778	Chr04:9701112-9702592	AT2G27080.1(Late embryogenesis abundant (LEA) hydroxyproline-rich glycoprotein family)	255	1481	9.51	28.41
GmLEA2-22	Glyma.04G228200	1		Chr04:49753281-49754534	AT5G53730.1(Late embryogenesis abundant (LEA) hydroxyproline-rich glycoprotein family)	210	1254	9.69	23.26
GmLEA2-23	Glyma.05G094300	1	XM_003525763	Chr05:23964664-23966589	AT1G45688.1(molecular_function unknown)	324	1926	10.06	35.72
GmLEA2-24	Glyma.05G179200	1	XM_006580216	Chr05:36725007-36725747	AT2G27080.1(Late embryogenesis abundant (LEA) hydroxyproline-rich glycoprotein family)	246	741	8.82	26.90
GmLEA2-25	Glyma.05G212600	1	XM_003525320	Chr05:39412222-39413348	AT2G46150.1(Late embryogenesis abundant (LEA) hydroxyproline-rich glycoprotein family)	224	1127	9.28	24.80
GmLEA2-26	Glyma.05G217500	1	XM_003525294	Chr05:39757555-39758761	AT1G64450.1(Glycine-rich protein family)	213	1207	9.54	22.97
GmLEA2-27	Glyma.05G242600	1	XM_003525161	Chr05:41753113- 41754953	AT1G45688.1(molecular_function unknown)	294	1841	9.98	32.78
GmLEA2-28	Glyma.06G052400	1	XM_003525960	Chr06:3947109-3948444	AT5G11890.1(molecular_function unknown)	256	1336	9.87	28.11
GmLEA2-29	Glyma.06G104900	1	XM_003527865	Chr06:8383654-8384433	AT2G27080.1（Late embryogenesis abundant (LEA) hydroxyproline-rich	259	780	9.04	28.59

					glycoprotein family ）				
GmLEA2-30	Glyma.06G136700	1	XM_006580863	Chr06:11191691-11193555	AT5G53730.1（ Late embryogenesis abundant（LEA）hydroxyproline-rich glycoprotein family ）	223	1865	9.1	25.41
GmLEA2-31	Glyma.06G303300	1		Chr06:49275774-49276891	AT3G54200.1（ Late embryogenesis abundant（LEA）hydroxyproline-rich glycoprotein family ）	227	1118	9.65	25.10
GmLEA2-32	Glyma.07G009700	1	XM_006582950	Chr07:728460-730026	AT1G17620.1（ Late embryogenesis abundant（LEA）hydroxyproline-rich glycoprotein family ）	254	1567	9.68	28.02
GmLEA2-33	Glyma.07G049300	1		Chr07:4196836-4197585	AT4G01410.1（ Late embryogenesis abundant（LEA）hydroxyproline-rich glycoprotein family ）	249	750	9.56	27.80
GmLEA2-34	Glyma.07G084600	1	XM_003528883	Chr07:7793897-7796474	AT1G45688.1(molecular_function unknown)	308	2578	9.51	33.71
GmLEA2-35	Glyma.07G087000	1		Chr07:8053652-8055911	AT4G13270.1（ Late embryogenesis abundant（LEA）hydroxyproline-rich glycoprotein family ）	163	2260	9.07	18.36
GmLEA2-36	Glyma.07G099500	1	XM_003528914	Chr07:9419717-9422235	AT1G45688.1(molecular_function unknown)	297	2519	9.93	32.80
GmLEA2-37	Glyma.07G103700	1	XM_003528941	Chr07:9969632-9970849	AT2G35980.1（Late embryogenesis abundant（LEA）hydroxyproline-rich glycoprotein family，syntaxin）	205	1218	9.67	23.52
GmLEA2-38	Glyma.07G103800	1	XM_006583406	Chr07:9985288-9986135	AT2G35980.1(Late embryogenesis abundant（LEA）hydroxyproline-rich glycoprotein family,SYNTAXIN)	209	848	9.43	24.11

GmLEA2-39	Glyma.07G103900	1	XM_003530019	Chr07:9990878-9991757	AT2G35980.1(Late embryogenesis abundant (LEA) hydroxyproline-rich glycoprotein family,SYNTAXIN)	207	880	9.8	24.12
GmLEA2-40	Glyma.08G019000	1	NM_001249306	Chr08:1549130-1550331	AT2G46150.1(Late embryogenesis abundant (LEA) hydroxyproline-rich glycoprotein family)	226	1202	8.98	24.72
GmLEA2-41	Glyma.08G023500	1	XM_003532388	Chr08:1873670-1874780	AT1G64450.1(Glycine-rich protein family)	209	1111	9.54	22.50
GmLEA2-42	Glyma.08G077900	1	XM_003532583	Chr08:5920205-5925896	AT2G01080.1(Late embryogenesis abundant (LEA) hydroxyproline-rich glycoprotein family)	226	5692	9.38	24.70
GmLEA2-43	Glyma.08G136900	1	XM_006586319	Chr08:10465850-10466602	AT2G27080.1(Late embryogenesis abundant (LEA) hydroxyproline-rich glycoprotein family)	250	753	9.07	27.08
GmLEA2-44	Glyma.08G184000	1	XM_003532927	Chr08:14749219-14752814	AT2G01080.1(Late embryogenesis abundant (LEA) hydroxyproline-rich glycoprotein family)	253	3596	9.66	27.33
GmLEA2-45	Glyma.09G071900	1	XM_003534908	Chr09:7418618-7419205	AT3G54200.1(Late embryogenesis abundant (LEA) hydroxyproline-rich glycoprotein family)	195	588	9.21	21.27
GmLEA2-46	Glyma.09G179400	1	XM_006587421	Chr09:40412865-40415233	AT1G45688.1(molecular_function unknown)	297	2369	10.06	32.82
GmLEA2-47	Glyma.09G189900	1	XM_003534146	Chr09:41452904-41455957	AT4G13270.1(Late embryogenesis abundant (LEA) hydroxyproline-rich glycoprotein family)	257	3054	6.73	28.81
GmLEA2-48	Glyma.09G192300	1	XM_003534159	Chr09:41692753-41695528	AT1G45688.1(molecular_function	314	2776	9.82	34.58

					unknown)				
GmLEA2-49	Glyma.09G217800	1	XM_003533428	Chr09:44083696-44084349	AT5G45320.1(molecular_function unknown)	217	654	9.97	24.37
GmLEA2-50	Glyma.10G079400	1	XM_003537055	Chr10:9086412-9087146	AT3G11650.1(NDR1/HIN1-like 2 ,syntaxin)	244	735	9.09	27.57
GmLEA2-51	Glyma.10G079900	1	XM_003535760	Chr10:9245085-9246282	AT2G35980.1(Late embryogenesis abundant (LEA) hydroxyproline-rich glycoprotein family,SYNTAXIN)	227	1198	9.64	26.25
GmLEA2-52	Glyma.10G080000	1	XM_003535761	Chr10:9258476-9260697	AT3G11660.1(NDR1/HIN1-like 1)	209	2222	9.64	26.25
GmLEA2-53	Glyma.10G174100	1	XM_003536133	Chr10:40785837-40786595	AT5G36970.1(NDR1/HIN1-like 25)	252	759	10.02	24.00
GmLEA2-54	Glyma.10G252500	1	XM_003536512	Chr10:48034926-48035710	AT4G05220.1(Late embryogenesis abundant (LEA) hydroxyproline-rich glycoprotein family)	227	785	9.56	26.04
GmLEA2-55	Glyma.11G003000	1		Chr11:188906-189478	AT3G20600.1(Late embryogenesis abundant (LEA) hydroxyproline-rich glycoprotein family)	190	573	9.71	21.64
GmLEA2-56	Glyma.11G020500	1		Chr11:1450017-1450631	AT1G64065.1(Late embryogenesis abundant (LEA) hydroxyproline-rich glycoprotein family)	204	615	9.74	22.98
GmLEA2-57	Glyma.11G020600	1	XM_006591461	Chr11:1453020-1453553	AT1G64065.1(Late embryogenesis abundant (LEA) hydroxyproline-rich glycoprotein family)	177	534	9.87	19.66
GmLEA2-58	Glyma.11G097100	1	XM_003537704	Chr11:7411891-7415860	AT2G41990.1(molecular_function unknown)	321	3970	9.63	36.32
GmLEA2-59	Glyma.11G179900	1	XM_003538046	Chr11:24548259-24549398	AT3G44220.1(Late embryogenesis abundant (LEA) hydroxyproline-rich	214	1140	9.96	23.59

					glycoprotein family)				
GmLEA2-60	Glyma.11G182400	1	XM_003538062	Chr11:24988921-24993379	AT3G44380.1(Late embryogenesis abundant (LEA) hydroxyproline-rich glycoprotein family)	191	4459	6.17	20.94
GmLEA2-61	Glyma.11G199600	1	XM_006591204	Chr11:27769806-27772081	AT2G30505.1(Late embryogenesis abundant (LEA) hydroxyproline-rich glycoprotein family)	249	2276	8.88	27.63
GmLEA2-62	Glyma.11G203000	1	XM_003538305	Chr11:28357079-28358465	AT1G65690.1(Late embryogenesis abundant (LEA) hydroxyproline-rich glycoprotein family)	246	1387	10.03	28.18
GmLEA2-63	Glyma.12G023200	1		Chr12:1701710-1704543	AT2G41990.1(molecular_function unknown)	343	2766	9.8	38.70
GmLEA2-64	Glyma.12G093600	1	XM_003539797	Chr12:7654387-7659033	AT3G44220.1(Late embryogenesis abundant (LEA) hydroxyproline-rich glycoprotein family)	213	4647	9.96	23.56
GmLEA2-65	Glyma.12G187600	1	XM_006592709	Chr12:34865817-34869986	AT3G44220.1(Late embryogenesis abundant (LEA) hydroxyproline-rich glycoprotein family)	221	4170	9.34	24.63
GmLEA2-66	Glyma.12G194700	1	XM_003539456	Chr12:35653530-35654090	AT2G46150.1(Late embryogenesis abundant (LEA) hydroxyproline-rich glycoprotein family)	186	561	8.42	20.54
GmLEA2-67	Glyma.12G202900	1		Chr12:36333664-36334359	AT1G65690.1(Late embryogenesis abundant (LEA) hydroxyproline-rich glycoprotein family)	166	696	8.88	18.60
GmLEA2-68	Glyma.13G000500	1		Chr13:154446-155404	AT3G54200.1(Late embryogenesis abundant (LEA) hydroxyproline-rich	207	959	9.23	22.14

					glycoprotein family)				
GmLEA2-69	Glyma.13G248600	1	XM_003541708	Chr13:35666896-35668024	AT5G22870.1(Late embryogenesis abundant (LEA) hydroxyproline-rich glycoprotein family)	203	1129	9.71	23.25
GmLEA2-70	Glyma.13G298800	1	XM_006595387	Chr13:39723376-39724074	AT1G65690.1(Late embryogenesis abundant (LEA) hydroxyproline-rich glycoprotein family)	232	699	7.93	26.32
GmLEA2-71	Glyma.13G307700	1	XM_003541896	Chr13:40333363-40333923	AT2G46150.1(Late embryogenesis abundant (LEA) hydroxyproline-rich glycoprotein family)	186	561	7.93	26.32
GmLEA2-72	Glyma.13G307900	1		Chr13:40339771-40340331	AT2G46150.1(Late embryogenesis abundant (LEA) hydroxyproline-rich glycoprotein family)	186	561	9.03	20.37
GmLEA2-73	Glyma.13G313600	1	XM_003543371	Chr13:40891153-40892294	AT2G27260.1(Late embryogenesis abundant (LEA) hydroxyproline-rich glycoprotein family)	271	1142	10.01	30.00
GmLEA2-74	Glyma.13G313700	1	XM_003543372	Chr13:40902956-40904226	AT3G44220.1(Late embryogenesis abundant (LEA) hydroxyproline-rich glycoprotein family)	218	1271	9.36	24.01
GmLEA2-75	Glyma.13G349900	1	XM_003543546	Chr13:43954196-43955906	AT1G17620.1(Late embryogenesis abundant (LEA) hydroxyproline-rich glycoprotein family)	254	1711	10.24	27.84
GmLEA2-76	Glyma.13G357600	1		Chr13:44542513-44544526	AT1G45688.1(molecular_function unknown)	302	2014	9.62	33.33
GmLEA2-77	Glyma.13G359200	1	XM_006595073	Chr13:44651121-44653243	AT1G52330.1(Late embryogenesis abundant (LEA) hydroxyproline-rich	201	2123	10.06	22.71

					glycoprotein family)				
GmLEA2-78	Glyma.14G010800	1	XM_003545035	Chr14:824392-825474	AT4G26490.1(Late embryogenesis abundant (LEA) hydroxyproline-rich glycoprotein family)	230	1083	9.85	26.19
GmLEA2-79	Glyma.14G037300	2	NM_001254648	Chr14:2808746-2811889	AT2G44060.1(Late embryogenesis abundant protein, group 2)	320	3144	4.8	35.65
GmLEA2-80	Glyma.14G041700	1	XM_003545437	Chr14:3150091-3152649	AT2G27080.1(Late embryogenesis abundant (LEA) hydroxyproline-rich glycoprotein family)	273	2559	9.65	30.38
GmLEA2-81	Glyma.14G160000	1		Chr14:36711633-36712196	AT3G54200.1(Late embryogenesis abundant (LEA) hydroxyproline-rich glycoprotein family)	187	564	9.39	20.81
GmLEA2-82	Glyma.14G208000	1	XM_003544903	Chr14:47379161-47380263	AT1G65690.1(Late embryogenesis abundant (LEA) hydroxyproline-rich glycoprotein family,SYNTAXIN)	260	1103	10.15	29.48
GmLEA2-83	Glyma.15G015800	1	NM_001254412	Chr15:1250483-1253447	AT1G45688.1(molecular_function unknown)	309	2965	9.95	34.24
GmLEA2-84	Glyma.15G024400	1	XM_006597127	Chr15:1962152-1963820	AT1G17620.1(Late embryogenesis abundant (LEA) hydroxyproline-rich glycoprotein family)	254	1669	10.28	27.92
GmLEA2-85	Glyma.15G048800	1	XM_003547015	Chr15:3852038-3855379	AT2G01080.1(Late embryogenesis abundant (LEA) hydroxyproline-rich glycoprotein family)	260	3342	9.66	27.89
GmLEA2-86	Glyma.15G065400	1	XM_003545751	Chr15:4971607-4972756	AT5G22870.1(Late embryogenesis abundant (LEA) hydroxyproline-rich glycoprotein family)	203	1150	9.62	23.24

GmLEA2-87	Glyma.16G031000	1	XM_003548573	Chr16:2934876-2936089	AT2G46150.1(Late embryogenesis abundant (LEA) hydroxyproline-rich glycoprotein family)	219	1214	10.2	24.19
GmLEA2-88	Glyma.16G031300	1	NM_001251006	Chr16:2949165-2950467	AT1G01470.1(Late embryogenesis abundant protein)	152	1303	5.16	16.69
GmLEA2-89	Glyma.16G221900	1	XM_003548290	Chr16:37848866-37850458	AT3G54200.1(Late embryogenesis abundant (LEA) hydroxyproline-rich glycoprotein family)	192	1593	9.3	20.54
GmLEA2-90	Glyma.17G172900	1	XM_003550013	Chr17:17752933-17754945	AT1G45688.1(molecular_function unknown)	323	2013	10.01	35.52
GmLEA2-91	Glyma.18G047800	1	XM_003553105	Chr18:4153739-4154925	AT1G65690.1(Late embryogenesis abundant (LEA) hydroxyproline-rich glycoprotein family)	244	1187	9.97	27.86
GmLEA2-92	Glyma.18G073200	1	XM_003552938	Chr18:6901495-6902707	AT4G26490.1(Late embryogenesis abundant (LEA) hydroxyproline-rich glycoprotein family)	258	1213	10.05	29.48
GmLEA2-93	Glyma.18G218700	1		Chr18:50553919-50555110	AT3G05975.1(Late embryogenesis abundant (LEA) hydroxyproline-rich glycoprotein family)	221	1192	9.83	24.28
GmLEA2-94	Glyma.18G218800	1	XM_003551579	Chr18:50556074-50559120	AT3G54200.1(Late embryogenesis abundant (LEA) hydroxyproline-rich glycoprotein family)	196	3047	8.6	21.38
GmLEA2-95	Glyma.18G238700	1		Chr18:52756503-52759147	AT1G01470.1(Late embryogenesis abundant protein)	176	1617	5.83	18.93
GmLEA2-96	Glyma.19g198600	1		Chr19:45575608-45576562	AT2G35980.1(Late embryogenesis abundant (LEA) hydroxyproline-rich	216	955	9.63	24.48

					glycoprotein family,SYNTAXIN)				
GmLEA2-97	Glyma.19G198700	1	NM_001252717	Chr19:45578902-45579788	AT2G35980.1(Late embryogenesis abundant (LEA) hydroxyproline-rich glycoprotein family,SYNTAXIN)	227	887	9.34	26.41
GmLEA2-98	Glyma.19G198800	1	XM_003554413	Chr19:45582865-45583763	AT2G35980.1（Late embryogenesis abundant (LEA) hydroxyproline-rich glycoprotein family，syntaxin）	227	899	9.34	26.43
GmLEA2-99	Glyma.19G198900	1		Chr19:45588629-45590084	AT3G11660.1（NDR1/HIN1-like 1)	210	1456	9.81	23.91
GmLEA2-100	Glyma.19G260500	1	XM_003554739	Chr19:50373544-50374912	AT4G01410.1（Late embryogenesis abundant (LEA) hydroxyproline-rich glycoprotein family）	197	1369	9.89	21.54
GmLEA2-101	Glyma.20G044800	2	NM_001254150	Chr20:8268501-8275551	AT2G44060.1(Late embryogenesis abundant protein, group 2)	312	7051	4.72	34.36
GmLEA2-102	Glyma.20G140900	1	XM_003555974	Chr20:37967537-37968547	AT4G05220.1(Late embryogenesis abundant (LEA) hydroxyproline-rich glycoprotein family)	227	1011	9.36	26.06
GmLEA2-103	Glyma.20G216300	1	XM_003556371	Chr20:45204176-45205311	AT5G36970.1(NDR1/HIN1-like 25)	250	1136	9.83	27.94
GmLEA2-104	uncharacterized protein LOC100797168	1	XM_006599136	Chr16:18333921-18335433	AT5G45320(Late embryogenesis abundant protein, group 2)	207	1513	9.23	22.77
GmLEA2-105	protein YLS9-like	1	XM_006577031	Chr3:42994014-42994917	AT2G35980(NDR1/HIN1-like 10)	227	904	9.5	26.22
GmLEA2-106	uncharacterized protein LOC100784646	1	XM_003548348	Chr16:1579950-1580875	AT4G01410(late embryogenesis abundant hydroxyproline-rich glycoprotein)	250	926	9.51	27.90
GmLEA2-107	uncharacterized protein	1	XM_006589805	Chr10:9182898-9183497	AT2G27260(late embryogenesis abundant hydroxyproline-rich	199	600	8.84	22.42

	LOC102663298				glycoprotein)				
GmLEA2-108	protein YLS9-like	1	XM_003533271	Chr9:37252919-37253898	AT2G35980(NDR1/HIN1-like 10)	178	537	9.44	21.08
GmLEA2-109	uncharacterized protein LOC100777620	1	XM_003526081	Chr06:43350865-43360367	AT2G01080.1(Late embryogenesis abundant (LEA) hydroxyproline-rich glycoprotein family)	624	1875	8.12	68.95
GmLEA2-110	uncharacterized protein LOC100807939	1	XM_003543336	Chr13:39157431-39157958	AT3G54200(late embryogenesis abundant hydroxyproline-rich glycoprotein)	175	528	8.57	19.28
GmLEA2-111	uncharacterized protein LOC102659599	1	XM_006574253	Chr01:55422524-55423102	AT3G54200(late embryogenesis abundant hydroxyproline-rich glycoprotein)	192	579	8.13	21.16
GmLEA2-112	uncharacterized protein LOC100804569	1	XM_003543939	Chr13:11874210-11876570	AT3G54200(late embryogenesis abundant hydroxyproline-rich glycoprotein)	376	1333	9.57	40.96
GmLEA2-113	uncharacterized protein LOC100800449	1	XM_006593218	Chr12:35682617-35682985	AT3G54200(late embryogenesis abundant hydroxyproline-rich glycoprotein)	122	369	7.75	13.47

Table S2. The coding sequences and protein sequences of LEA2 gene family.

The coding sequences

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Table S3. Pairwise identities between homologous pairs of soybean LEA2 proteins.

Gene name	Score	Expect	Identities	Positives	Gaps	Duplication pattern
GmLEA2-5/52	397bits (1019)	5.00E-146	189/207(91%)	198/207 (95%)	0/207 (0%)	
GmLEA2-17/99	384 bits (985)	5.00E-140	188/197(95%)	193/197 (97%)	0/197 (0%)	segmental
GmLEA2-59/64	387 bits (994)	4.00E-142	202/214(94%)	207/214 (96%)	1/214 (0%)	
GmLEA2-65/74	329 bits (844)	5.00E-119	178/221(81%)	202/221 (91%)	3/221 (1%)	segmental
GmLEA2-22/30	344 bits (883)	4.00E-125	170/177(96%)	173/177 (97%)	1/177 (0%)	
GmLEA2-18/100	376 bits (966)	2.00E-138	184/197(93%)	193/197 (97%)	0/197 (0%)	segmental
GmLEA2-33/106	424 bits (1091)	2.00E-155	226/249(91%)	237/249 (95%)	2/249 (0%)	segmental
GmLEA2-54/102	460 bits (1183)	3E-170	218/227(96%)	221/227 (97%)	0/227 (0%)	segmental
GmLEA2-34/48	497 bits (1279)	0	271/314(86%)	280/314 (89%)	6/314 (1%)	
GmLEA2-76/83	525 bits (1351)	0	264/305(87%)	274/305 (89%)	10/305 (3%)	segmental
GmLEA2-58/63	494bits (1272)	3.00E-180	286/347(82%)	292/347 (84%)	30/347 (8%)	
GmLEA2-23/90	594 bits (1531)	0	311/324(96%)	316/324 (97%)	1/324 (0%)	
GmLEA2-36/46	559 bits (1441)	0	283/297(95%)	291/297 (97%)	0/297 (0%)	
GmLEA2-4/55	212 bits (540)	3.00E-74	105/124(85%)	112/124 (90%)	0/124 (0%)	segmental
GmLEA2-69/86	391bits (1004)	5.00E-144	186/203(92%)	197/203 (97%)	0/203 (0%)	segmental
GmLEA2-37/39	353 bits (905)	1.00E-128	179/209(86%)	185/209 (88%)	10/209 (4%)	tandem
GmLEA2-6/50	390 bits (1001)	5.00E-142	212/246(86%)	222/246 (90%)	4/246 (1%)	
GmLEA2-12/96	395 bits (1015)	5E-145	202/221(91%)	208/221 (94%)	5/221 (2%)	segmental
GmLEA2-13/97	434 bits (1116)	4E-160	208/227(92%)	217/227 (95%)	0/227 (0%)	segmental
GmLEA2-16/98	448 bits (1153)	1E-165	213/229(93%)	222/229 (96%)	2/229 (0%)	segmental
GmLEA2-15/105	401 bits	6E-147	194/197(98%)	195/197	0/197	tandem

	(1031)			(98%)	(0%)	
GmLEA2-21/29	413 bits (1061)	9E-151	206/241(85%)	220/241 (91%)	3/241 (1%)	segmental
GmLEA2-24/43	389 bits (998)	2E-141	208/250(83%)	222/250 (88%)	6/250 (2%)	segmental
GmLEA2-67/70	249 bits (635)	4E-88	143/232(62%)	154/232 (66%)	66/232 (28%)	segmental
GmLEA2-8/80	443 bits (1139)	4E-162	256/273(94%)	262/273 (95%)	0/273 (0%)	segmental
GmLEA2-53/103	406 bits (1043)	3E-148	228/253(90%)	237/253 (93%)	4/253 (1%)	segmental
GmLEA2-7/82	448 bits (1153)	1E-164	242/260(93%)	252/260 (96%)	5/260 (1%)	
GmLEA2-62/91	431 bits (1107)	4E-158	229/246(93%)	236/246 (95%)	2/246 (0%)	
GmLEA2-20/28	522 bits (1345)	0	250/256(98%)	253/256 (98%)	0/256 (0%)	segmental
GmLEA2-75/84	504 bits (1299)	0	244/254(96%)	248/254 (97%)	0/254 (0%)	segmental
GmLEA2-44/85	373 bits (957)	7E-135	232/260(89%)	236/260 (90%)	7/260 (2%)	segmental
GmLEA2-1/49	407 bits (1045)	2E-149	198/216(92%)	205/216 (94%)	3/216 (1%)	
GmLEA2-10/78	449 bits (1154)	1E-165	218/224(97%)	222/224 (99%)	0/224 (0%)	segmental
GmLEA2-73/107						
GmLEA2-60/61						
GmLEA2-26/41	356 bits (914)	7E-130	185/190(97%)	189/190 (99%)	0/190 (0%)	segmental
GmLEA2-2/57	271 bits (694)	1E-97	137/186(74%)	151/186 (81%)	11/186 (5%)	
GmLEA2-110/113	232 bits (592)	2E-83	114/122(93%)	118/122 (96%)	0/122 (0%)	segmental
GmLEA2-66/72	336 bits (862)	7E-123	166/186(89%)	171/186 (91%)	0/186 (0%)	segmental
GmLEA2-25/40	376 bits (965)	3E-137	201/227(89%)	212/227 (93%)	4/227 (1%)	segmental
GmLEA2-45/81	288 bits (736)	1E-103	144/161(89%)	149/161 (92%)	0/161 (0%)	
GmLEA2-11/112	374 bits (959)	2E-134	187/192(97%)	189/192 (98%)	0/192 (0%)	
GmLEA2-35/47	272 bits (695)	6E-97	137/151(91%)	141/151 (93%)	1/151 (0%)	

GmLEA2-88/95	266 bits (680)	5E-96	131/152(86%)	141/152(92%)	0/152(0%)	
GmLEA2-9/79	617bits (1590)	0	313/319(98%)	315/319(98%)	0/319(0%)	segmental

Table S4. The amino acid sequences of Arabidopsis proteins of LEA2 domain.
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>AT3G05975.1
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>AT3G11650.1
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>AT3G11660.1
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>AT3G20590.1
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>AT3G20600.1
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>AT3G52470.1
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>AT4G01410.1
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GIPVSPEVANGLKNDEAYGVVLMRVVIFGRLRWKAGAIKTGRYGFYARCDVWLRFNPSSNGQVPLLAPSTCKV
DV
>AT4G05220.1
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QCF
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>AT4G26490.1
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>AT4G35170.1
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DQIPLYGGVPALFGQRAEPDQVVLPLNLTFTLRARAYVLGRLVKTTFHSNIKCSITFYGDKLGKTLDLSKSCSDH
>AT5G22200.1
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>AT5G21130.1
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>AT5G06330.1
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DF
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>AT5G45320.1
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>AT5G53730.1
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>glycine-rich uncharacterized protein
MAKPHDRRRSSGRTNLASCAVATVFLLILLVVLLVVYFTVFKPKDPKISVNAVQLPSFAVSNNTANFSFSQYVAVR
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DFTVTPRNPDSPYFPGYPESPDLPGNPGSPDFSGNPGPPSFPRNPGSPEFPGNPGAPIIPRNPGSPEFPINPPRN
PGAPVIPRNPNPPVFPGNPRSMGPPGFPGIGGPPGFPGTPFGGGGTGPTLGDGYANPGFGYGNRVGPTM
EIESKMELAGRVKVLHVFTHHVVAKSDCRVTVSIADGSVLGFHC
```

Table S5. The mutants selection of four homologous genes of *GmSYP24*.

gene name	mutant name	insertion type	Amplification primers	expression level
AT2G35460	SALK_064143	exon insertion	LP AGGGTGGTGGCTTAGATATCG; RP CGTGCCAATCTACATCTCTCC	downregulated 6.4 times
	SALK_069015	promoter insertion	LP ACAAACCAAGGCACTTCTACG; RP CTGAGTCAGACCCAGCAAAAG	upregulated 16.4 times
	SALK_073333	exon insertion	LP GAACCAAGACCAACCTATGCC; RP TTCACGTCGATCCTGTAAACC	downregulated 2.4 times
	SALK_106063	exon insertion	LP TGATATTCTCCTTGGGTTCCC; RP CGTGCCAATCTACATCTCTCC	upregulated 24.5 times
AT3G11650	SALK_008804	promoter insertion	LPTTTAGTGTAGTTCCATGAAACTAGGG; RPATGAGGATGTTGCAGATCAGG	upregulated 3.2 times
	SALK_129820	promoter insertion	LPTGAGAAACCTAACTTTGGATTTCC; RP TATAGCTGCGGTGAGCCTTAG	upregulated 11.5 times
AT5G06320	SALK_150318	exon insertion	LPGAGACGTCAGAAAACTCCGTG; RPAACTCACCGAATTCACACTCG	downreguated 2.6 times
	SALK_035427	exon insertion	LPTCTCTGATGGACATCCTGACC; RP:AACTCACCGAATTCACACTCG	downreguated 1.4 times
AT2G35980	CS423587	exon insertion	LPCATCGTCCTGATCTGCTTAGG; RPCTCCCAAAGGCTACTACCGAC	No homozygous transgenic lines
	SALK_132320	unknown insertion site	LPAGTCTACGACGCTGAGCTGAC; RPCTGAAACTCTTTCAACGCTGC	No homozygous transgenic lines
LBPrimer: ATTTTGCCGATTTCGGAAC				

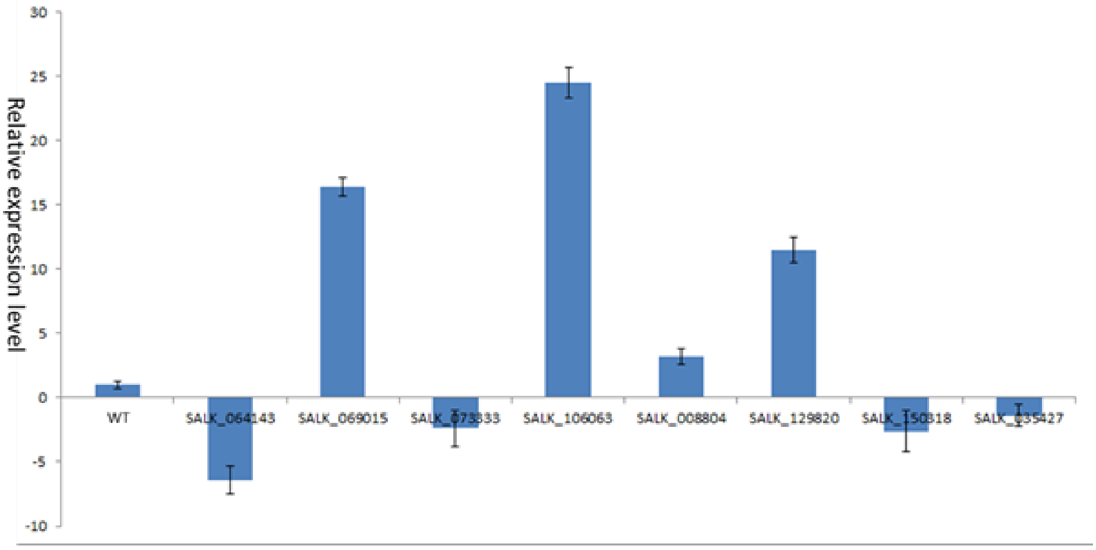
30
25
20
15
10
5
0
-5
-10
Relative expression level
WT
SALK_064143
SALK_069015
SALK_073333
SALK_106063
SALK_008804
SALK_129820
SALK_150318
SALK_035427

Table S6. Genes that were up-regulated in the GmSYP24ox transgenic plants under drought.

Locus	log2.Fold_change.	P-value	Q-value	Blast swissprot
Glyma.01G015400.Wm82.a2.v1	2.2027	1.4076E-07	7.7824E-06	unknown
Glyma.01G023300.Wm82.a2.v1	1.7189	9.05E-07	2.08E-05	sp|Q8W486|Y1491_ARATH Uncharacterized protein At1g04910 OS=Arabidopsis thaliana GN=At1g04910 PE=2 SV=1//2.97641e-83
Glyma.01G126600.Wm82.a2.v1	3.5778	1.55E-31	2.54E-29	sp|Q9C523|DIR19_ARATH Dirigent protein 19 OS=Arabidopsis thaliana GN=DIR19 PE=2 SV=1//5.46253e-61
Glyma.01G127200.Wm82.a2.v1	2.444	4.15E-64	1.67E-61	sp|Q9FI66|DIR3_ARATH Dirigent protein 3 OS=Arabidopsis thaliana GN=DIR3 PE=3 SV=1//1.68406e-49
Glyma.01G185800.Wm82.a2.v1	1.3681	0.00011231	0.0034201	sp|P22335|HSF24_SOLPE Heat shock factor protein HSF24 OS=Solanum peruvianum GN=HSF24 PE=2 SV=1//2.27036e-80
Glyma.01G228700.Wm82.a2.v1	1.5952	5.47E-54	1.88E-51	sp|P30081|CHS7_SOYBN Chalcone synthase 7 OS=Glycine max GN=CHS7 PE=3 SV=1//0
Glyma.01G232400.Wm82.a2.v1	1.7658	1.66E-11	7.50E-10	sp|P31687|4CL2_SOYBN 4-coumarate--CoA ligase 2 OS=Glycine max PE=2 SV=2//0
Glyma.02G208400.Wm82.a2.v1	1.4087	1.39E-19	1.22E-17	sp|P27608|AROF_TOBAC Phospho-2-dehydro-3-deoxyheptonate aldolase 1, chloroplastic OS=Nicotianatabacum GN=DHAPS-1 PE=2 SV=1//0
Glyma.03G174300.Wm82.a2.v1	1.8271	6.00E-08	3.47E-06	sp|Q9LZD3|E70A1_ARATH Exocyst complex component EXO70A1 OS=Arabidopsis thaliana GN=EXO70A1 PE=1 SV=1//3.9145e-68

Glyma.03G213300.Wm82.a2.v1	6.3721	8.55E-11	7.37E-09	sp|O82245|TSPO_ARATH Translocator protein homolog OS=Arabidopsis thaliana GN=TSPO PE=1 SV= 1//2.54929e-44
Glyma.04G050300.Wm82.a2.v1	1.5345	4.81E-06	0.00020339	sp|Q9FU27|C3H2_ORYSJ Zinc finger CCCH domain-containing protein 2 OS=Oryza sativa subsp. japonica GN=Os01g0192000 PE=2 SV=1//1.22277e-61
Glyma.04G089700.Wm82.a2.v1	1.7043	8.67E-11	7.43E-09	sp|Q9T074|PCKA_ARATH Phosphoenolpyruvate carboxykinase [ATP] OS=Arabidopsis thaliana GN= PCKA PE=1 SV=1//0
Glyma.04G104200.Wm82.a2.v1	1.9169	6.64E-06	0.00026914	sp|Q9Y7K5|YGI3_SCHPO Uncharacterized WD repeat-containing protein C2A9.03 OS= Schizosaccharomycespombe (strain 972/ ATCC 24843) GN=SPBC2A9.03 PE=3 SV=2//2.58827e-38
Glyma.05G044200.Wm82.a2.v1	1.2521	8.28E-06	0.00033017	sp|Q53EL6|PDCD4_HUMAN Programmed cell death protein 4 OS=Homo sapiens GN=PDCD4 PE=1 SV =2//4.99051e-26
Glyma.05G056300.Wm82.a2.v1	2.8705	5.76E-59	3.99E-56	sp|P29001|INVA_VIGRR Acid beta-fructofuranosidase OS=Vignaradiata var. radiata GN=INVA PE=1 SV=1//0
Glyma.05G180100.Wm82.a2.v1	1.8907	4.48E-17	6.31E-15	sp|O65201|ACOX2_ARATH Acyl-coenzyme A oxidase 2, peroxisomal OS=Arabidopsis thaliana GN=ACX2 PE=1 SV=2//0
Glyma.06G021200.Wm82.a2.v1	5.2677	1.13E-115	2.16E-112	sp|Q0JIL1|NRX2_ORYSJ Probable nucleoredoxin 2 OS=Oryza sativa subsp. japonica GN=Os01g0794400 PE=2 SV=1//1.57959e-114
Glyma.06G059600.Wm82.a2.v1	1.2725	1.36E-25	3.43E-23	sp|Q940T9|COL4_ARATH Zinc finger protein CONSTANS-LIKE 4 OS=Arabidopsis thaliana

				GN=COL4 PE=2 SV=2//5.89374e-93
Glyma.06G105200.Wm82.a2.v1	3.4919	5.25E-09	3.50E-07	sp|Q9Y7K5|YGI3_SCHPO Uncharacterized WD repeat-containing protein C2A9.03 OS=Schizosac -charomycespombe (strain 972 / ATCC 24843) GN=SPBC2A9.03 PE=3 SV=2//1.32105e-38
Glyma.06G216700.Wm82.a2.v1	1.6107	2.45E-09	1.75E-07	sp|Q94A82|NUD19_ARATH Nudix hydrolase 19, chloroplastic OS=Arabidopsis thaliana GN=NUDT19 PE=1 SV=1//0
Glyma.06G239900.Wm82.a2.v1	1.9392	6.81E-47	3.70E-44	sp|Q9T076|ENL2_ARATH Early nodulin-like protein 2 OS=Arabidopsis thaliana GN=At4g27520 PE=1 SV=1//1.22676e-40
Glyma.07G126800.Wm82.a2.v1	1.7026	5.75E-06	0.00023712	sp|O82199|C3H20_ARATH Zinc finger CCCH domain-containing protein 20 OS=Arabidopsis thaliana GN=At2g19810 PE=2 SV=1//1.47867e-130
Glyma.07G261500.Wm82.a2.v1	4.8253	2.20E-47	6.18E-45	sp|P92980|APR3_ARATH 5'-adenylylsulfate reductase 3, chloroplastic OS=Arabidopsis thaliana GN= APR3 PE=2 SV=2//0
Glyma.08G056600.Wm82.a2.v1	6.1673	3.13E-09	2.17E-07	sp|Q9C942|CSE_ARATH Caffeoylshikimate esterase OS=Arabidopsis thaliana GN=CSE PE=1 SV= 1//8.87112e-34
Glyma.09G010500.Wm82.a2.v1	2.291	1.91E-14	2.25E-12	unknown
Glyma.09G069800.Wm82.a2.v1	1.2887	4.74E-37	1.93E-34	sp|Q8RWQ9|ALEUL_ARATH Thiol protease aleurain-like OS=Arabidopsis thaliana GN=At3g45310 PE=2 SV=1//7.6746e-178
Glyma.09G173300.Wm82.a2.v1	2.3094	6.58E-05	0.002114	unknown
Glyma.09G190600.Wm82.a2.v1	2.1601	2.60E-20	4.51E-18	sp|Q9LV52|HSFC1_ARATH Heat stress transcription

				factor C-1 OS=Arabidopsis thaliana GN=HSFC1 PE=2 SV=1//1.19541e-70
Glyma.09G199000.Wm82.a2.v1	1.5502	1.39E-17	2.05E-15	sp|Q8W486|Y1491_ARATH Uncharacterized protein At1g04910 OS=Arabidopsis thaliana GN=At1g04910 PE=2 SV=1//2.47287e-83
Glyma.09G205700.Wm82.a2.v1	2.2597	4.26E-08	1.22E-06	sp|Q500U8|TKPR1_ARATH Tetraketide alpha-pyrone reductase 1 OS=Arabidopsis thaliana GN=TKPR1 PE=1 SV=1//1.00335e-34
Glyma.09G269600.Wm82.a2.v1	1.8934	2.60E-06	5.49E-05	sp|Q40316|VESTR_MEDSA Vestitone reductase OS=Medicago sativa PE=1 SV=1//4.14286e-173
Glyma.10G001700.Wm82.a2.v1	2.8948	3.19E-89	4.14E-86	sp|Q9XIW0|CIPK7_ARATH CBL-interacting serine/threonine-protein kinase 7 OS=Arabidopsis thaliana GN=CIPK7 PE=1 SV=1//4.03366e-150
Glyma.10G291400.Wm82.a2.v1	1.1681	1.53E-06	3.37E-05	sp|Q9C942|CSE_ARATH Caffeoylshikimate esterase OS=Arabidopsis thaliana GN=CSE PE=1 SV=1//4.32716e-49
Glyma.11G010500.Wm82.a2.v1	1.4475	1.45E-05	0.00025842	sp|P31687|4CL2_SOYBN 4-coumarate--CoA ligase 2 OS=Glycine max PE=2 SV=2//0
Glyma.11G011500.Wm82.a2.v1	1.5424	2.81E-46	7.52E-44	sp|P23569|CHSY_PUEML Chalcone synthase OS=Puerariamontana var. lobata GN=CHS PE=2 SV=1//0
Glyma.11G063600.Wm82.a2.v1	3.3452	1.78E-08	1.11E-06	sp|Q9SYY4|ELO3L_ARATH Elongation of fatty acids protein 3-like OS=Arabidopsis thaliana GN=HOS3 PE=2 SV=1//6.67054e-118
Glyma.11G070500.Wm82.a2.v1	3.4429	8.37E-13	4.30E-11	sp|P52575|IFR_MEDSA Isoflavone reductase OS=Medicago sativa GN=IFR PE=1 SV=1//0

Glyma.11G119500.Wm82.a2.v1	1.4381	3.36E-07	8.35E-06	sp|Q8VZ80|PLT5_ARATH Polyol transporter 5 OS=Arabidopsis thaliana GN=PLT5 PE=1 SV=2//0
Glyma.11G208700.Wm82.a2.v1	1.1571	5.10E-05	0.0016717	unknown
Glyma.12G117000.Wm82.a2.v1	2.1039	1.20E-10	1.02E-08	sp|Q9FE67|ERF80_ARATH Ethylene-responsive transcription factor 9 OS=Arabidopsis thaliana GN=ERF9 PE=2 SV=1//7.38365e-29
Glyma.12G134300.Wm82.a2.v1	1.9234	0.00015715	0.0045974	unknown
Glyma.13G145000.Wm82.a2.v1	1.2321	8.23E-17	5.84E-15	sp|P19142|PAL2_PHAVU Phenylalanine ammonia-lyase class 2 OS=Phaseolus vulgaris PE=3 SV=1//0
Glyma.13G360600.Wm82.a2.v1	1.2766	1.34E-05	0.00050859	sp|Q9M8L2|FBK30_ARATH F-box/kelch-repeat protein At1g80440 OS=Arabidopsis thaliana GN=At1g80440 PE=2 SV=1//6.28671e-123
Glyma.14G010500.Wm82.a2.v1	2.5757	2.96E-17	4.27E-15	sp|Q84VX0|RFS1_ARATH Probable galactinol--sucrose galactosyltransferase 1 OS=Arabidopsis thaliana GN=RFS1 PE=2 SV=1//0
Glyma.14G038200.Wm82.a2.v1	1.3152	8.78E-07	4.23E-05	sp|Q06445|CYTI_VIGUN Cysteine proteinase inhibitor OS=Vignaunguiculata PE=3 SV=1//6.14795e-42
Glyma.14G087600.Wm82.a2.v1	2.3909	2.12E-06	9.62E-05	sp|Q9STX1|ACBP3_ARATH Acyl-CoA-binding domain-containing protein 3 OS=Arabidopsis thaliana GN=ACBP3 PE=1 SV=1//3.08907e-32
Glyma.15G072400.Wm82.a2.v1	2.9506	7.98E-19	1.27E-16	sp|P24805|TSJT1_TOBAC Stem-specific protein TSJT1 OS=Nicotianatabacum GN=TSJT1 PE=2 SV=1//2.56932e-32
Glyma.16G100400.Wm82.a2.v1	2.5454	6.16E-30	1.92E-27	sp|A3FPF2|DEF_NELNU Defensin-like protein OS=Nelumbonucifera PE=3 SV=1//3.46437e-14
Glyma.17G034900.Wm82.a2.v1	4.633	5.36E-103	4.84E-100	sp|Q9NZT1|CALL5_HUMAN Calmodulin-like protein 5

				OS=Homo sapiens GN=CALML5 PE=1 SV=2//1.53851e-13
Glyma.17G096700.Wm82.a2.v1	1.4622	1.27E-22	2.61E-20	sp|Q02283|HAT5_ARATH Homeobox-leucine zipper protein HAT5 OS=Arabidopsis thaliana GN=HAT5 PE=1 SV=1//9.02554e-41
Glyma.17G235300.Wm82.a2.v1	1.6879	1.59E-16	2.11E-14	sp|J9U5U9|DAD2_PETHY Probable strigolactone esterase DAD2 OS=Petunia hybrida GN=DAD2 PE=1 SV=1//1.42839e-159
Glyma.18G009700.Wm82.a2.v1	1.02	1.68E-28	2.33E-26	sp|Q7FAH2|G3PC2_ORYSJ Glyceraldehyde-3-phosphate dehydrogenase 2, cytosolic OS=Oryza sativa subsp. japonica GN=GAPC2 PE=1 SV=1//0
Glyma.18G061100.Wm82.a2.v1	3.9037	0	0	sp|P49093|ASNS2_LOTJA Asparagine synthetase [glutamine-hydrolyzing] 2 OS=Lotus japonicus GN=AS2 PE=2 SV=2//0
Glyma.18G193400.Wm82.a2.v1	1.8893	4.58E-08	1.31E-06	sp|Q9SR40|LAC7_ARATH Laccase-7 OS=Arabidopsis thaliana GN=LAC7 PE=2 SV=1//0
Glyma.19G076500.Wm82.a2.v1	3.5398	8.84E-06	0.00034992	unknown
Glyma.19G089800.Wm82.a2.v1	2.2837	3.22E-38	1.39E-35	sp|P92941|CLCA_ARATH Chloride channel protein CLC-a OS=Arabidopsis thaliana GN=CLC-A PE=1 SV=2//0
Glyma.19G099400.Wm82.a2.v1	1.1542	4.22E-05	0.0014111	sp|Q9LW26|Y3684_ARATH Acyltransferase-like protein At3g26840, chloroplastic OS=Arabidopsis thaliana GN=At3g26840 PE=2 SV=1//0
Glyma.19G125300.Wm82.a2.v1	1.2203	1.84E-05	0.00067755	sp|O80683|CAB25_ARATH Calmodulin-binding protein 25 OS=Arabidopsis thaliana GN=CAMBP25 PE=1

				SV=1//2.72625e-22
Glyma.19G198600.Wm82.a2.v1	2.8398	3.65E-213	1.08E-209	sp|Q9SJ52|YLS9_ARATH Protein YLS9 OS= Arabidopsis thaliana GN=YLS9 PE=2 SV= 1// 2.36052e-62
Glyma.19G217700.Wm82.a2.v1	4.7525	1.38E-06	6.44E-05	sp|Q93XK2|STSYN_PEA Stachyose synthase OS= Pisumsativum GN=STS1 PE=1 SV=1//0
Glyma.19G245400.Wm82.a2.v1	3.3694	9.67E-08	2.64E-06	sp|P02877|HEVE_HEVBR Pro-hevein OS= Hevea-brasiliensis GN=HEV1 PE=1 SV= 2//3.75062e-99
Glyma.20G135200.Wm82.a2.v1	1.5041	1.37E-10	5.49E-09	unknown
Glyma.20G158400.Wm82.a2.v1	1.9212	0.00016959	0.0048902	unknown

Table S8. Genes that were up-regulated in the GmSYP24ox transgenic plants under ABA.

Locus	log2.Fold_change	P-value	Q-value	Blast swissprot
Glyma.01G006000.Wm82.a2.v1	1.6235	0.000451	0.0045645	unknown
Glyma.01G115900.Wm82.a2.v1	1.5826	1.76E-124	1.37E-121	sp|Q9XF88|CB4B_ARATH Chlorophyll a-b binding protein CP29.2, chloroplastic OS=Arabidopsis thaliana GN=LHCB4.2 PE=1 SV=1//3.49966e-165
Glyma.02G213700.Wm82.a2.v1	3.3283	4.45E-19	3.04E-17	sp|Q94CE3|BCA5_ARATH Beta carbonic anhydrase 5, chloroplastic OS=Arabidopsis thaliana GN=BCA5 PE=2 SV=1//2.9914e-97
Glyma.04G020300.Wm82.a2.v1	1.3446	6.09E-104	3.42E-101	sp|P17340|PLAS_SOLLC Plastocyanin, chloroplastic OS=Solanum lycopersicum GN=PETE PE=2 SV=1//1.86003e-69
Glyma.04G118700.Wm82.a2.v1	2.5952	1.86E-15	9.58E-14	sp|P17407|21KD_DAUCA 21 kDa protein OS=Daucuscarota PE=2 SV=1//7.00889e-71
Glyma.04G179500.Wm82.a2.v1	3.6466	2.41E-18	1.56E-16	sp|Q93X17|SNAK2_SOLTU Snakin-2 OS=Solanum tuberosum GN=SN2 PE=1 SV=1//3.43079e-22
Glyma.05G168400.Wm82.a2.v1	2.1553	1.10E-79	4.37E-77	sp|Q9ZTS2|FER_CAPAN Ferredoxin, chloroplastic OS=Capsicum annuum GN=AP1 PE=1 SV=1//3.53401e-71
Glyma.05G218400.Wm82.a2.v1	1.6683	5.64E-28	6.29E-26	sp|Q9FLE8|Y5986_ARATH Uncharacterized protein At5g39865 OS=Arabidopsis thaliana GN=At5g39865 PE=2 SV=1//1.12827e-26
Glyma.05G224500.Wm82.a2.v1	4.1785	3.41E-07	6.84E-06	sp|Q8H1S0|MIOX4_ARATH Inositol oxygenase 4 OS=Arabidopsis thaliana GN=MIOX4 PE=2 SV=1//7.88763e-179
Glyma.06G050100.Wm82.a2.v1	4.3766	8.92E-05	0.001091	sp|Q9M439|BCAT2_ARATH

				Branched-chain-amino-acid aminotransferase 2, chloroplastic OS=Arabidopsis thaliana GN=BCAT2 PE=1 SV=1//6.11164e-166
Glyma.06G102100.Wm82.a2.v1	3.2377	2.67E-50	5.85E-48	sp|Q9ZPE7|EXO_ARATH Protein EXORDIUM OS=Arabidopsis thaliana GN=EXO PE=2 SV=1//3.98167e-140
Glyma.06G117200.Wm82.a2.v1	3.7351	3.97E-28	4.47E-26	sp|Q0WPW4|ACCO5_ARATH 1-aminocyclopropane-1-carboxylate oxidase 5 OS=Arabidopsis thaliana GN=At1g77330 PE=2 SV=1//8.60588e-159
Glyma.06G121100.Wm82.a2.v1	2.6421	3.17E-06	5.33E-05	sp|P00303|BABL_CUCSA Basic blue protein OS=Cucumissativus PE=1 SV=1//6.00089e-48
Glyma.06G185300.Wm82.a2.v1	2.6502	8.36E-50	1.77E-47	sp|Q93X17|SNAK2_SOLTU Snakin-2 OS=Solanum tuberosum GN=SN2 PE=1 SV=1//1.98791e-22
Glyma.07G125600.Wm82.a2.v1	2.1205	1.39E-07	2.97E-06	unknown
Glyma.07G150400.Wm82.a2.v1	3.7216	4.92E-144	4.56E-141	sp|Q9SRM5|CPR49_ARATH GDSL esterase/lipase CPRD49 OS=Arabidopsis thaliana GN=CPRD49 PE=2 SV=1//1.65434e-91
Glyma.08G152500.Wm82.a2.v1	1.0563	7.67E-08	6.03E-06	sp|Q66GR3|BH130_ARATH Transcription factor bHLH130 OS=Arabidopsis thaliana GN=BHLH130 PE=1 SV=1//5.36096e-38
Glyma.08G171000.Wm82.a2.v1	3.8824	6.56E-23	5.55E-21	unknown
Glyma.08G200100.Wm82.a2.v1	2.9297	9.84E-202	1.45E-198	sp|P10743|VSPB_SOYBN Stem 31 kDa glycoprotein OS=Glycine max GN=VSPB PE=2 SV=1//0
Glyma.09G005700.Wm82.a2.v1	1.6272	5.01E-11	5.90E-09	sp|Q9C519|WRKY6_ARATH WRKY transcription factor 6 OS=Arabidopsis thaliana GN=WRKY6 PE=1

				SV=1//5.28188e-122
Glyma.09G089700.Wm82.a2.v1	1.3209	1.15E-12	1.66E-10	sp|Q93VD3|CIPKN_ARATH CBL-interacting serine/threonine-protein kinase 23 OS=Arabidopsis thaliana GN=CIPK23 PE=1 SV=1//0
Glyma.10G200700.Wm82.a2.v1	1.5059	4.85E-08	3.90E-06	sp|Q84WB7|GT645_ARATH Glycosyltransferase family protein 64 protein C5 OS=Arabidopsis thaliana GN=At5g04500 PE=2 SV=1//0
Glyma.11G088600.Wm82.a2.v1	2.058	4.28E-09	1.17E-07	sp|O14197|YDQ4_SCHPO Uncharacterized transporter C5D6.04 OS=Schizosaccharomycespombe (strain 972 / ATCC 24843) GN=SPAC5D6.04 PE=3 SV=1//2.83664e-06
Glyma.11G207500.Wm82.a2.v1	1.7387	1.94E-06	0.00011766	sp|Q9CAL3|CRK2_ARATH Cysteine-rich receptor-like protein kinase 2 OS=Arabidopsis thaliana GN=CRK2 PE=2 SV=1//2.1279e-108
Glyma.13G212600.Wm82.a2.v1	2.593	5.59E-14	2.59E-12	sp|Q8RXC8|RBK2_ARATH Receptor-like cytosolic serine/threonine-protein kinase RBK2 OS=Arabidopsis thaliana GN=RBK2 PE=1 SV=1//3.78835e-156
Glyma.14G086300.Wm82.a2.v1	2.3803	1.30E-286	3.99E-283	sp|Q8GXG1|ASPGB_ARATH Probable isoaspartyl peptidase/L-asparaginase 2 OS=Arabidopsis thaliana GN=At3g16150 PE=2 SV=2//0
Glyma.14G087200.Wm82.a2.v1	2.8531	7.43E-43	1.33E-40	sp|Q948Z4|SNAK1_SOLTU Snakin-1 OS=Solanum tuberosum GN=SN1 PE=1 SV=1//5.29715e-31
Glyma.14G093100.Wm82.a2.v1	1.1126	3.75E-15	6.99E-13	sp|P43399|MT1_TRIRP Metallothionein-like protein 1 OS=Trifoliumrepens GN=MT1B PE=3 SV=1//1.07989e-13
Glyma.14G220000.Wm82.a2.v1	1.6715	3.33E-10	1.06E-08	sp|B6ETT4|SYT2_ARATH Synaptotagmin-2

				OS=Arabidopsis thaliana GN=SYT2 PE=2 SV=1//0
Glyma.15G072400.Wm82.a2.v1	2.9329	1.03E-17	6.42E-16	sp|P24805|TSJT1_TOBAC Stem-specific protein TSJT1 OS=Nicotianatabacum GN=TSJT1 PE=2 SV=1//2.56932e-32
Glyma.15G110300.Wm82.a2.v1	1.2815	2.83E-06	0.00016449	sp|Q9C519|WRKY6_ARATH WRKY transcription factor 6 OS=Arabidopsis thaliana GN=WRKY6 PE=1 SV=1//2.29689e-126
Glyma.16G173000.Wm82.a2.v1	2.8834	5.88E-09	5.28E-07	sp|P36908|CHIA_CICAR Acidic endochitinase OS=Cicer arietinum PE=2 SV=1//2.03516e-138
Glyma.16G205200.Wm82.a2.v1	1.542	4.37E-74	1.53E-71	sp|Q9XF89|CB5_ARATH Chlorophyll a-b binding protein CP26, chloroplastic OS=Arabidopsis thaliana GN=LHCB5 PE=1 SV=1//5.02959e-141
Glyma.17G237100.Wm82.a2.v1	3.0164	1.24E-62	3.50E-60	sp|Q948Z4|SNAK1_SOLTU Snakin-1 OS=Solanum tuberosum GN=SN1 PE=1 SV=1//1.19277e-25
Glyma.18G259400.Wm82.a2.v1	2.2789	1.13E-07	2.45E-06	sp|P46690|GASA4_ARATH Gibberellin-regulated protein 4 OS=Arabidopsis thaliana GN=GASA4 PE=1 SV=2//1.72057e-37
Glyma.19G147400.Wm82.a2.v1	2.0514	6.18E-44	1.17E-41	sp|P48631|FD6E2_SOYBN Omega-6 fatty acid desaturase, endoplasmic reticulum isozyme 2 OS=Glycine max GN=FAD2-2 PE=2 SV=1//0
Glyma.20G027200.Wm82.a2.v1	2.1882	1.62E-53	3.83E-51	unknown
Glyma.20G167500.Wm82.a2.v1	3.1219	2.25E-21	1.76E-19	unknown

Table S9 The expression level of aquaporins in the GmSYP24ox transgenic line under osmotic/drought, salt or ABA stress.

S24N1L vs S24L				
Locus	log2.Fold_change.	pvalue	qvalue	Blast swiss prot
Glyma.19G181300.Wm82.a2.v1	-1.8936	3.12E-31	1.09E-29	sp|P43286|PIP21_ARATH Aquaporin PIP2-1 OS=Arabidopsis thaliana GN=PIP2-1 PE=1 SV=1//1.21882e-159
Glyma.03G078700.Wm82.a2.v1	-1.5052	2.96E-05	0.0001612	sp|Q39196|PIP14_ARATH Probable aquaporin PIP1-4 OS=Arabidopsis thaliana GN=PIP1.4 PE=1 SV=1//0
Glyma.03G180900.Wm82.a2.v1	5.659	7.52E-06	4.52E-05	sp|Q9ATM4|PIP27_MAIZE Aquaporin PIP2-7 OS=Zea mays GN=PIP2-7 PE=2 SV=1//7.13148e-158
Glyma.12G075400.Wm82.a2.v1	-3.3361	6.17E-17	1.14E-15	sp|Q9ATM4|PIP27_MAIZE Aquaporin PIP2-7 OS=Zea mays GN=PIP2-7 PE=2 SV=1//7.87722e-176
Glyma.12G172500.Wm82.a2.v1	2.2324	1.60E-35	6.52E-34	sp|Q9ATM4|PIP27_MAIZE Aquaporin PIP2-7 OS=Zea mays GN=PIP2-7 PE=2 SV=1//0
Glyma.01G208200.Wm82.a2.v1	-2.2134	0.0010242	0.0039515	sp|P21653|TIP1_TOBAC Probable aquaporin TIP-type RB7-5A OS=Nicotiana tabacum PE=2 SV=1//8.56123e-108
Glyma.04G083200.Wm82.a2.v1	-3.1633	1.23E-07	9.65E-07	sp|O82316|TIP41_ARATH Aquaporin TIP4-1 OS=Arabidopsis thaliana GN=TIP4-1 PE=2 SV=1//2.71385e-104
Glyma.06G084600.Wm82.a2.v1	-6.4231	5.57E-09	5.22E-08	sp|O82316|TIP41_ARATH Aquaporin TIP4-1 OS=Arabidopsis thaliana GN=TIP4-1 PE=2 SV=1//5.03132e-112
Glyma.11G034000.Wm82.a2.v1	-4.7633	1.79E-61	1.30E-59	sp|Q41975|TIP22_ARATH Probable aquaporin TIP2-2 OS=Arabidopsis thaliana GN=TIP2-2 PE=1 SV=2//1.28753e-108
Glyma.12G023600.Wm82.a2.v1	2.612	0.0008194	0.0032401	sp|Q9ATL5|TIP42_MAIZE Aquaporin TIP4-2 OS=Zea mays GN=TIP4-2 PE=2 SV=1//1.41957e-16
Glyma.13G146300.Wm82.a2.v1	-1.9586	1.21E-07	9.50E-07	sp|P25818|TIP11_ARATH Aquaporin TIP1-1 OS=Arabidopsis thaliana

				GN=TIP1-1 PE=1 SV=1//3.98186e-100
Glyma.13G224900.Wm82.a2.v1	-3.8681	3.57E-07	2.63E-06	sp|Q8LFP7|NIP12_ARATH Aquaporin NIP1-2 OS=Arabidopsis thaliana GN=NIP1-2 PE=2 SV=2//2.31568e-131
Glyma.16G210000.Wm82.a2.v1	6.1432	9.63E-09	8.73E-08	sp|P23958|TIPA_PHAVU Probable aquaporin TIP-type alpha OS=Phaseolus vulgaris PE=1 SV=1//1.5688e-132
Glyma.19G186100.Wm82.a2.v1	-1.4319	8.73E-28	2.68E-26	sp|Q9FY14|TIP1_MEDTR Probable aquaporin TIP-type OS=Medicago truncatula GN=AQP1 PE=1 SV=1//1.79911e-139
S24N2L vs S24L				
Locus	log2.Fold_change.	pvalue	qvalue	Blast swiss prot
Glyma.03G078700.Wm82.a2.v1	-2.7425	1.31E-09	5.11E-09	sp|Q39196|PIP14_ARATH Probable aquaporin PIP1-4 OS=Arabidopsis thaliana GN=PIP1.4 PE=1 SV=1//0
Glyma.03G180900.Wm82.a2.v1	7.1414	6.07E-10	2.46E-09	sp|Q9ATM4|PIP27_MAIZE Aquaporin PIP2-7 OS=Zea mays GN=PIP2-7 PE=2 SV=1//7.13148e-158
Glyma.10G211000.Wm82.a2.v1	-2.0288	2.78E-06	6.99E-06	sp|P43287|PIP22_ARATH Aquaporin PIP2-2 OS=Arabidopsis thaliana GN=PIP2-2 PE=1 SV=2//3.46181e-175
Glyma.11G228000.Wm82.a2.v1	3.6206	0.0020952	0.0029389	sp|P25794|PIP2_PEA Probable aquaporin PIP-type 7a OS=Pisum sativum GN=TRG-31 PE=2 SV=2//0
Glyma.12G075400.Wm82.a2.v1	-6.0915	1.45E-19	1.20E-18	sp|Q9ATM4|PIP27_MAIZE Aquaporin PIP2-7 OS=Zea mays GN=PIP2-7 PE=2 SV=1//7.87722e-176
Glyma.12G172500.Wm82.a2.v1	2.7414	1.10E-30	1.47E-29	sp|Q9ATM4|PIP27_MAIZE Aquaporin PIP2-7 OS=Zea mays GN=PIP2-7 PE=2 SV=1//0
Glyma.14G061500.Wm82.a2.v1	-3.4944	3.14E-256	5.83E-254	sp|P25794|PIP2_PEA Probable aquaporin PIP-type 7a OS=Pisum sativum GN=TRG-31 PE=2 SV=2//0
Glyma.19G181300.Wm82.a2.v1	-1.8146	2.39E-41	4.34E-40	sp|P43286|PIP21_ARATH Aquaporin PIP2-1 OS=Arabidopsis thaliana GN=PIP2-1 PE=1 SV=1//1.21882e-159
Glyma.20G179700.Wm82.a2.v1	-1.2547	1.07E-09	4.23E-09	sp|Q9SV31|PIP25_ARATH Probable aquaporin PIP2-5 OS=Arabidopsis

				thaliana GN=PIP2-5 PE=1 SV=1//2.42474e-174
Glyma.01G208200.Wm82.a2.v1	-3.2561	3.87E-05	7.96E-05	sp|P21653|TIP1_TOBAC Probable aquaporin TIP-type RB7-5A OS=Nicotiana tabacum PE=2 SV=1//8.56123e-108
Glyma.03G185900.Wm82.a2.v1	-3.9833	3.58E-49	7.75E-48	sp|Q9FY14|TIP1_MEDTR Probable aquaporin TIP-type OS=Medicago truncatula GN=AQP1 PE=1 SV=1//4.13105e-138
Glyma.04G083200.Wm82.a2.v1	-2.4955	5.31E-08	1.71E-07	sp|O82316|TIP41_ARATH Aquaporin TIP4-1 OS=Arabidopsis thaliana GN=TIP4-1 PE=2 SV=1//2.71385e-104
Glyma.06G084600.Wm82.a2.v1	-7.8808	5.20E-08	1.68E-07	sp|O82316|TIP41_ARATH Aquaporin TIP4-1 OS=Arabidopsis thaliana GN=TIP4-1 PE=2 SV=1//5.03132e-112
Glyma.10G221100.Wm82.a2.v1	4.4345	1.72E-08	5.90E-08	sp|Q9SV84|NIP51_ARATH Probable aquaporin NIP5-1 OS=Arabidopsis thaliana GN=NIP5-1 PE=2 SV=1//9.09463e-136
Glyma.11G034000.Wm82.a2.v1	-7.0479	1.24E-57	3.10E-56	sp|Q41975|TIP22_ARATH Probable aquaporin TIP2-2 OS=Arabidopsis thaliana GN=TIP2-2 PE=1 SV=2//1.28753e-108
Glyma.13G146300.Wm82.a2.v1	-3.9189	6.20E-13	3.32E-12	sp|P25818|TIP11_ARATH Aquaporin TIP1-1 OS=Arabidopsis thaliana GN=TIP1-1 PE=1 SV=1//3.98186e-100
Glyma.13G224900.Wm82.a2.v1	-4.0888	6.06E-08	1.93E-07	sp|Q8LFP7|NIP12_ARATH Aquaporin NIP1-2 OS=Arabidopsis thaliana GN=NIP1-2 PE=2 SV=2//2.31568e-131
Glyma.16G210000.Wm82.a2.v1	8.4148	1.80E-29	2.32E-28	sp|P23958|TIPA_PHAVU Probable aquaporin TIP-type alpha OS=Phaseolus vulgaris PE=1 SV=1//1.5688e-132
Glyma.19G186100.Wm82.a2.v1	-2.6303	2.21E-58	5.61E-57	sp|Q9FY14|TIP1_MEDTR Probable aquaporin TIP-type OS=Medicago truncatula GN=AQP1 PE=1 SV=1//1.79911e-139
S24P4L vs S24L				
Locus	log2.Fold_change.	pvalue	qvalue	Blast swiss prot
Glyma.02G255000.Wm82.a2.v1	1.9736	3.38E-84	3.88E-81	sp|P25794|PIP2_PEA Probable aquaporin PIP-type 7a OS=Pisum sativum GN=TRG-31 PE=2 SV=2//0
Glyma.03G078700.Wm82.a2.v1	1.4195	4.37E-06	0.000186	sp|Q39196|PIP14_ARATH Probable aquaporin PIP1-4 OS=Arabidopsis

			6	thaliana GN=PIP1.4 PE=1 SV=1//0
Glyma.10G211000.Wm82.a2.v1	4.0029	4.72E-76	4.87E-73	sp|P43287|PIP22_ARATH Aquaporin PIP2-2 OS=Arabidopsis thaliana GN=PIP2-2 PE=1 SV=2//3.46181e-175
Glyma.13G325900.Wm82.a2.v1	1.4467	3.06E-25	7.46E-23	sp|Q9ATM4|PIP27_MAIZE Aquaporin PIP2-7 OS=Zea mays GN=PIP2-7 PE=2 SV=1//0
Glyma.14G061500.Wm82.a2.v1	1.2008	1.02E-85	1.20E-82	sp|P25794|PIP2_PEA Probable aquaporin PIP-type 7a OS=Pisum sativum GN=TRG-31 PE=2 SV=2//0
Glyma.16G155100.Wm82.a2.v1	3.5931	2.60E-06	0.0001151	sp|P43287|PIP22_ARATH Aquaporin PIP2-2 OS=Arabidopsis thaliana GN=PIP2-2 PE=1 SV=2//3.48282e-165
Glyma.20G179700.Wm82.a2.v1	1.7429	1.13E-14	1.36E-12	sp|Q9SV31|PIP25_ARATH Probable aquaporin PIP2-5 OS=Arabidopsis thaliana GN=PIP2-5 PE=1 SV=1//2.42474e-174
Glyma.03G185900.Wm82.a2.v1	1.1109	7.58E-14	8.41E-12	sp|Q9FY14|TIP1_MEDTR Probable aquaporin TIP-type OS=Medicago truncatula GN=AQP1 PE=1 SV=1//4.13105e-138
Glyma.11G143100.Wm82.a2.v1	4.8672	1.73E-14	2.06E-12	sp|O82598|TIP13_ARATH Aquaporin TIP1-3 OS=Arabidopsis thaliana GN=TIP1-3 PE=1 SV=1//6.95573e-136
Glyma.13G333100.Wm82.a2.v1	2.8634	3.84E-16	4.97E-14	sp|O82598|TIP13_ARATH Aquaporin TIP1-3 OS=Arabidopsis thaliana GN=TIP1-3 PE=1 SV=1//1.6409e-139
S24P4R vs S24R				
Locus	log2.Fold_change.	pvalue	qvalue	Blast swiss prot
Glyma.03G078700.Wm82.a2.v1	1.5271	0.0001767	0.002433	sp|Q39196|PIP14_ARATH Probable aquaporin PIP1-4 OS=Arabidopsis thaliana GN=PIP1.4 PE=1 SV=1//0
Glyma.11G023200.Wm82.a2.v1	-1.6612	9.01E-24	1.01E-21	sp|Q7XSQ9|PIP12_ORYSJ Probable aquaporin PIP1-2 OS=Oryza sativa subsp. japonica GN=PIP1-2 PE=2 SV=3//1.77595e-180
Glyma.12G172500.Wm82.a2.v1	-1.0375	4.25E-09	1.43E-07	sp|Q9ATM4|PIP27_MAIZE Aquaporin PIP2-7 OS=Zea mays GN=PIP2-7 PE=2 SV=1//0
Glyma.13G325900.Wm82.a2.v1	-1.5726	1.18E-124	1.58E-121	sp|Q9ATM4|PIP27_MAIZE Aquaporin PIP2-7 OS=Zea mays GN=PIP2-7

				PE=2 SV=1//0
Glyma.16G155000.Wm82.a2.v1	1.8013	2.20E-07	5.70E-06	sp|P43287|PIP22_ARATH Aquaporin PIP2-2 OS=Arabidopsis thaliana GN=PIP2-2 PE=1 SV=2//2.43539e-164
Glyma.16G155100.Wm82.a2.v1	2.4703	1.20E-05	0.0002187	sp|P43287|PIP22_ARATH Aquaporin PIP2-2 OS=Arabidopsis thaliana GN=PIP2-2 PE=1 SV=2//3.48282e-165
Glyma.01G208200.Wm82.a2.v1	-1.5375	5.57E-84	3.40E-81	sp|P21653|TIP1_TOBAC Probable aquaporin TIP-type RB7-5A OS=Nicotiana tabacum PE=2 SV=1//8.56123e-108
Glyma.11G034000.Wm82.a2.v1	-1.494	1.88E-75	9.91E-73	sp|Q41975|TIP22_ARATH Probable aquaporin TIP2-2 OS=Arabidopsis thaliana GN=TIP2-2 PE=1 SV=2//1.28753e-108
Glyma.11G143100.Wm82.a2.v1	1.5806	0.0001159	0.0016699	sp|O82598|TIP13_ARATH Aquaporin TIP1-3 OS=Arabidopsis thaliana GN=TIP1-3 PE=1 SV=1//6.95573e-136
Glyma.13G333100.Wm82.a2.v1	5.1343	4.70E-22	4.78E-20	sp|O82598|TIP13_ARATH Aquaporin TIP1-3 OS=Arabidopsis thaliana GN=TIP1-3 PE=1 SV=1//1.6409e-139
Glyma.19G186100.Wm82.a2.v1	-1.1421	7.19E-119	8.07E-116	sp|Q9FY14|TIP1_MEDTR Probable aquaporin TIP-type OS=Medicago truncatula GN=AQP1 PE=1 SV=1//1.79911e-139
Glyma.09G238200.Wm82.a2.v1	-5.6833	1.15E-78	6.44E-76	sp|Q6Z2T3|NIP21_ORYSJ Aquaporin NIP2-1 OS=Oryza sativa subsp. japonica GN=NIP2-1 PE=1 SV=1//3.71203e-92
Glyma.18G259500.Wm82.a2.v1	-2.9387	1.15E-10	4.72E-09	sp|Q6Z2T3|NIP21_ORYSJ Aquaporin NIP2-1 OS=Oryza sativa subsp. japonica GN=NIP2-1 PE=1 SV=1//1.04006e-92
Glyma.19G108400.Wm82.a2.v1	-1.2588	1.13E-13	6.26E-12	sp|Q9ATM2|SIP12_MAIZE Aquaporin SIP1-2 OS=Zea mays GN=SIP1-2 PE=2 SV=1//6.2894e-74
S24P10L vs S24L				
Locus	log2.Fold_change.	pvalue	qvalue	Blast swiss prot
Glyma.02G255000.Wm82.a2.v1	1.4353	1.97E-30	2.14E-28	sp|P25794|PIP2_PEA Probable aquaporin PIP-type 7a OS=Pisum sativum GN=TRG-31 PE=2 SV=2//0
Glyma.03G180900.Wm82.a2.v1	7.1822	7.94E-16	4.08E-14	sp|Q9ATM4|PIP27_MAIZE Aquaporin PIP2-7 OS=Zea mays GN=PIP2-7

				PE=2 SV=1//7.13148e-158
Glyma.10G211000.Wm82.a2.v1	2.814	3.89E-23	3.19E-21	sp|P43287|PIP22_ARATH Aquaporin PIP2-2 OS=Arabidopsis thaliana GN=PIP2-2 PE=1 SV=2//3.46181e-175
Glyma.16G155100.Wm82.a2.v1	3.2682	0.0001118	0.0014843	sp|P43287|PIP22_ARATH Aquaporin PIP2-2 OS=Arabidopsis thaliana GN=PIP2-2 PE=1 SV=2//3.48282e-165
Glyma.02G255000.Wm82.a2.v1	1.4353	1.97E-30	2.14E-28	sp|P25794|PIP2_PEA Probable aquaporin PIP-type 7a OS=Pisum sativum GN=TRG-31 PE=2 SV=2//0
Glyma.19G181300.Wm82.a2.v1	1.6089	1.07E-36	1.53E-34	sp|P43286|PIP21_ARATH Aquaporin PIP2-1 OS=Arabidopsis thaliana GN=PIP2-1 PE=1 SV=1//1.21882e-159
Glyma.04G083200.Wm82.a2.v1	-3.9144	3.74E-08	9.09E-07	sp|O82316|TIP41_ARATH Aquaporin TIP4-1 OS=Arabidopsis thaliana GN=TIP4-1 PE=2 SV=1//2.71385e-104
Glyma.06G084600.Wm82.a2.v1	-3.3701	7.72E-08	1.80E-06	sp|O82316|TIP41_ARATH Aquaporin TIP4-1 OS=Arabidopsis thaliana GN=TIP4-1 PE=2 SV=1//5.03132e-112
Glyma.11G034000.Wm82.a2.v1	-2.1254	1.34E-34	1.72E-32	sp|Q41975|TIP22_ARATH Probable aquaporin TIP2-2 OS=Arabidopsis thaliana GN=TIP2-2 PE=1 SV=2//1.28753e-108
Glyma.11G143100.Wm82.a2.v1	3.2988	0.0001835	0.0023031	sp|O82598|TIP13_ARATH Aquaporin TIP1-3 OS=Arabidopsis thaliana GN=TIP1-3 PE=1 SV=1//6.95573e-136
Glyma.13G333100.Wm82.a2.v1	1.9577	1.36E-05	0.0002197	sp|O82598|TIP13_ARATH Aquaporin TIP1-3 OS=Arabidopsis thaliana GN=TIP1-3 PE=1 SV=1//1.6409e-139
Glyma.13G224900.Wm82.a2.v1	-1.929	0.0002146	0.0026527	sp|Q8LFP7|NIP12_ARATH Aquaporin NIP1-2 OS=Arabidopsis thaliana GN=NIP1-2 PE=2 SV=2//2.31568e-131
S24P10R vs S24R				
Locus	log2.Fold_change.	pvalue	qvalue	Blast swiss prot
Glyma.01G220600.Wm82.a2.v1	-1.0456	5.90E-07	1.34E-05	sp|Q39196|PIP14_ARATH Probable aquaporin PIP1-4 OS=Arabidopsis thaliana GN=PIP1.4 PE=1 SV=1//0
Glyma.05G208700.Wm82.a2.v1	-1.5477	1.53E-09	5.24E-08	sp|Q7XSQ9|PIP12_ORYSJ Probable aquaporin PIP1-2 OS=Oryza sativa

				subsp. japonica GN=PIP1-2 PE=2 SV=3//0
Glyma.11G023200.Wm82.a2.v1	-1.1189	1.33E-15	8.09E-14	sp|Q7XSQ9|PIP12_ORYSJ Probable aquaporin PIP1-2 OS=Oryza sativa subsp. japonica GN=PIP1-2 PE=2 SV=3//1.77595e-180
Glyma.11G146500.Wm82.a2.v1	-1.2914	1.01E-06	2.22E-05	sp|Q9ATM4|PIP27_MAIZE Aquaporin PIP2-7 OS=Zea mays GN=PIP2-7 PE=2 SV=1//0
Glyma.13G325900.Wm82.a2.v1	-1.4212	2.08E-116	1.61E-113	sp|Q9ATM4|PIP27_MAIZE Aquaporin PIP2-7 OS=Zea mays GN=PIP2-7 PE=2 SV=1//0
Glyma.01G208200.Wm82.a2.v1	-2.1452	7.68E-132	7.48E-129	sp|P21653|TIP1_TOBAC Probable aquaporin TIP-type RB7-5A OS=Nicotiana tabacum PE=2 SV=1//8.56123e-108
Glyma.04G083200.Wm82.a2.v1	-1.474	2.51E-35	4.18E-33	sp|O82316|TIP41_ARATH Aquaporin TIP4-1 OS=Arabidopsis thaliana GN=TIP4-1 PE=2 SV=1//2.71385e-104
Glyma.08G203000.Wm82.a2.v1	-1.985	4.72E-06	9.12E-05	sp|Q41951|TIP21_ARATH Aquaporin TIP2-1 OS=Arabidopsis thaliana GN=TIP2-1 PE=1 SV=2//7.86985e-112
Glyma.11G034000.Wm82.a2.v1	-1.8039	5.70E-101	3.48E-98	sp|Q41975|TIP22_ARATH Probable aquaporin TIP2-2 OS=Arabidopsis thaliana GN=TIP2-2 PE=1 SV=2//1.28753e-108
Glyma.19G186100.Wm82.a2.v1	-1.0718	4.28E-119	3.43E-116	sp|Q9FY14|TIP1_MEDTR Probable aquaporin TIP-type OS=Medicago truncatula GN=AQP1 PE=1 SV=1//1.79911e-139
Glyma.09G238200.Wm82.a2.v1	-7.2272	9.14E-74	3.40E-71	sp|Q6Z2T3|NIP21_ORYSJ Aquaporin NIP2-1 OS=Oryza sativa subsp. japonica GN=NIP2-1 PE=1 SV=1//3.71203e-92
Glyma.16G043800.Wm82.a2.v1	1.1158	2.22E-05	0.0003689	sp|Q9ATM2|SIP12_MAIZE Aquaporin SIP1-2 OS=Zea mays GN=SIP1-2 PE=2 SV=1//1.074e-64
Glyma.18G259500.Wm82.a2.v1	-3.0228	4.15E-11	1.70E-09	sp|Q6Z2T3|NIP21_ORYSJ Aquaporin NIP2-1 OS=Oryza sativa subsp. japonica GN=NIP2-1 PE=1 SV=1//1.04006e-92
S24A1L vs S24L				
Locus	log2.Fold_change.	pvalue	qvalue	Blast swiss prot
Glyma.01G220600.Wm82.a2.v1	2.85	6.43E-07	1.23E-05	sp|Q39196|PIP14_ARATH Probable aquaporin PIP1-4 OS=Arabidopsis

				thaliana GN=PIP1.4 PE=1 SV=1//0
Glyma.02G255000.Wm82.a2.v1	1.7729	2.59E-58	6.95E-56	sp|P25794|PIP2_PEA Probable aquaporin PIP-type 7a OS=Pisum sativum GN=TRG-31 PE=2 SV=2//0
Glyma.03G180900.Wm82.a2.v1	6.4452	1.44E-10	4.81E-09	sp|Q9ATM4|PIP27_MAIZE Aquaporin PIP2-7 OS=Zea mays GN=PIP2-7 PE=2 SV=1//7.13148e-158
Glyma.08G015300.Wm82.a2.v1	5.6265	1.71E-15	8.82E-14	sp|Q7XSQ9|PIP12_ORYSJ Probable aquaporin PIP1-2 OS=Oryza sativa subsp. japonica GN=PIP1-2 PE=2 SV=3//0
Glyma.05G208700.Wm82.a2.v1	3.5809	2.30E-16	1.28E-14	sp|Q7XSQ9|PIP12_ORYSJ Probable aquaporin PIP1-2 OS=Oryza sativa subsp. japonica GN=PIP1-2 PE=2 SV=3//0
Glyma.10G211000.Wm82.a2.v1	2.0977	9.87E-11	3.34E-09	sp|P43287|PIP22_ARATH Aquaporin PIP2-2 OS=Arabidopsis thaliana GN=PIP2-2 PE=1 SV=2//3.46181e-175
Glyma.11G146500.Wm82.a2.v1	3.1783	6.24E-07	1.20E-05	sp|Q9ATM4|PIP27_MAIZE Aquaporin PIP2-7 OS=Zea mays GN=PIP2-7 PE=2 SV=1//0
Glyma.12G075400.Wm82.a2.v1	2.3425	1.19E-38	1.89E-36	sp|Q9ATM4|PIP27_MAIZE Aquaporin PIP2-7 OS=Zea mays GN=PIP2-7 PE=2 SV=1//7.87722e-176
Glyma.12G172500.Wm82.a2.v1	1.0966	1.02E-07	2.25E-06	sp|Q9ATM4|PIP27_MAIZE Aquaporin PIP2-7 OS=Zea mays GN=PIP2-7 PE=2 SV=1//0
Glyma.13G325900.Wm82.a2.v1	1.2707	1.42E-16	8.00E-15	sp|Q9ATM4|PIP27_MAIZE Aquaporin PIP2-7 OS=Zea mays GN=PIP2-7 PE=2 SV=1//0
Glyma.14G061500.Wm82.a2.v1	1.0535	8.51E-54	2.04E-51	sp|P25794|PIP2_PEA Probable aquaporin PIP-type 7a OS=Pisum sativum GN=TRG-31 PE=2 SV=2//0
Glyma.19G181300.Wm82.a2.v1	2.5944	1.80E-154	1.79E-151	sp|P43286|PIP21_ARATH Aquaporin PIP2-1 OS=Arabidopsis thaliana GN=PIP2-1 PE=1 SV=1//1.21882e-159
Glyma.20G179700.Wm82.a2.v1	1.5905	6.58E-11	2.26E-09	sp|Q9SV31|PIP25_ARATH Probable aquaporin PIP2-5 OS=Arabidopsis thaliana GN=PIP2-5 PE=1 SV=1//2.42474e-174
Glyma.03G185900.Wm82.a2.v1	3.0357	1.05E-211	1.82E-208	sp|Q9FY14|TIP1_MEDTR Probable aquaporin TIP-type OS=Medicago

				truncatula GN=AQP1 PE=1 SV=1//4.13105e-138
Glyma.07G018000.Wm82.a2.v1	4.7891	2.60E-13	1.13E-11	sp|Q41951|TIP21_ARATH Aquaporin TIP2-1 OS=Arabidopsis thaliana GN=TIP2-1 PE=1 SV=2//9.26677e-112
Glyma.08G203000.Wm82.a2.v1	2.5759	9.56E-05	0.001159	sp|Q41951|TIP21_ARATH Aquaporin TIP2-1 OS=Arabidopsis thaliana GN=TIP2-1 PE=1 SV=2//7.86985e-112
Glyma.11G034000.Wm82.a2.v1	1.0229	4.45E-13	1.90E-11	sp|Q41975|TIP22_ARATH Probable aquaporin TIP2-2 OS=Arabidopsis thaliana GN=TIP2-2 PE=1 SV=2//1.28753e-108
Glyma.15G018100.Wm82.a2.v1	5.3221	2.62E-23	2.29E-21	sp|Q41951|TIP21_ARATH Aquaporin TIP2-1 OS=Arabidopsis thaliana GN=TIP2-1 PE=1 SV=2//3.77304e-115
Glyma.19G186100.Wm82.a2.v1	3.1099	0	0	sp|Q9FY14|TIP1_MEDTR Probable aquaporin TIP-type OS=Medicago truncatula GN=AQP1 PE=1 SV=1//1.79911e-139
Glyma.06G307000.Wm82.a2.v1	2.6283	4.46E-05	0.0005873	sp|Q9ATM2|SIP12_MAIZE Aquaporin SIP1-2 OS=Zea mays GN=SIP1-2 PE=2 SV=1//7.29961e-66
S24A1R vs S24R				
Locus	log2.Fold_change.	pvalue	qvalue	Blast swiss prot
Glyma.02G255000.Wm82.a2.v1	1.2037	3.02E-111	7.42E-108	sp|P25794|PIP2_PEA Probable aquaporin PIP-type 7a OS=Pisum sativum GN=TRG-31 PE=2 SV=2//0
Glyma.16G155000.Wm82.a2.v1	1.4911	8.41E-06	0.0004411	sp|P43287|PIP22_ARATH Aquaporin PIP2-2 OS=Arabidopsis thaliana GN=PIP2-2 PE=1 SV=2//2.43539e-164
Glyma.09G238200.Wm82.a2.v1	-1.9697	1.01E-34	5.32E-32	sp|Q6Z2T3|NIP21_ORYSJ Aquaporin NIP2-1 OS=Oryza sativa subsp. japonica GN=NIP2-1 PE=1 SV=1//3.71203e-92
Glyma.19G108400.Wm82.a2.v1	-1.0846	9.63E-10	9.73E-08	sp|Q9ATM2|SIP12_MAIZE Aquaporin SIP1-2 OS=Zea mays GN=SIP1-2 PE=2 SV=1//6.2894e-74
S24A3L vs S24L				
Locus	log2.Fold_change.	pvalue	qvalue	Blast swiss prot
Glyma.03G180900.Wm82.a2.v1	6.7068	1.76E-13	1.44E-11	sp|Q9ATM4|PIP27_MAIZE Aquaporin PIP2-7 OS=Zea mays GN=PIP2-7

				PE=2 SV=1//7.13148e-158
Glyma.05G208700.Wm82.a2.v1	3.0156	1.63E-11	1.11E-09	sp|Q7XSQ9|PIP12_ORYSJ Probable aquaporin PIP1-2 OS=Oryza sativa subsp. japonica GN=PIP1-2 PE=2 SV=3//0
Glyma.08G015300.Wm82.a2.v1	4.6566	3.94E-09	2.04E-07	sp|Q7XSQ9|PIP12_ORYSJ Probable aquaporin PIP1-2 OS=Oryza sativa subsp. japonica GN=PIP1-2 PE=2 SV=3//0
Glyma.12G075400.Wm82.a2.v1	1.5905	2.01E-17	2.31E-15	sp|Q9ATM4|PIP27_MAIZE Aquaporin PIP2-7 OS=Zea mays GN=PIP2-7 PE=2 SV=1//7.87722e-176
Glyma.19G181300.Wm82.a2.v1	1.9465	1.08E-83	8.12E-81	sp|P43286|PIP21_ARATH Aquaporin PIP2-1 OS=Arabidopsis thaliana GN=PIP2-1 PE=1 SV=1//1.21882e-159
Glyma.03G185900.Wm82.a2.v1	1.6317	1.03E-44	3.33E-42	sp|Q9FY14|TIP1_MEDTR Probable aquaporin TIP-type OS=Medicago truncatula GN=AQP1 PE=1 SV=1//4.13105e-138
Glyma.07G018000.Wm82.a2.v1	3.7763	2.79E-07	1.07E-05	sp|Q41951|TIP21_ARATH Aquaporin TIP2-1 OS=Arabidopsis thaliana GN=TIP2-1 PE=1 SV=2//9.26677e-112
Glyma.15G018100.Wm82.a2.v1	4.2759	1.73E-12	1.29E-10	sp|Q41951|TIP21_ARATH Aquaporin TIP2-1 OS=Arabidopsis thaliana GN=TIP2-1 PE=1 SV=2//3.77304e-115
Glyma.19G186100.Wm82.a2.v1	1.3203	3.59E-36	8.72E-34	sp|Q9FY14|TIP1_MEDTR Probable aquaporin TIP-type OS=Medicago truncatula GN=AQP1 PE=1 SV=1//1.79911e-139
S24A3R vs S24R				
Locus	log2.Fold_change.	pvalue	qvalue	Blast swiss prot
Glyma.10G211000.Wm82.a2.v1	-1.2424	2.93E-15	2.64E-13	sp|P43287|PIP22_ARATH Aquaporin PIP2-2 OS=Arabidopsis thaliana GN=PIP2-2 PE=1 SV=2//3.46181e-175
Glyma.01G208200.Wm82.a2.v1	-1.8079	8.46E-97	8.56E-94	sp|P21653|TIP1_TOBAC Probable aquaporin TIP-type RB7-5A OS=Nicotiana tabacum PE=2 SV=1//8.56123e-108
Glyma.03G185900.Wm82.a2.v1	-1.1135	4.80E-98	5.24E-95	sp|Q9FY14|TIP1_MEDTR Probable aquaporin TIP-type OS=Medicago truncatula GN=AQP1 PE=1 SV=1//4.13105e-138
Glyma.04G083200.Wm82.a2.v1	-2.1545	3.31E-50	1.45E-47	sp|O82316|TIP41_ARATH Aquaporin TIP4-1 OS=Arabidopsis thaliana

				GN=TIP4-1 PE=2 SV=1//2.71385e-104
Glyma.06G084600.Wm82.a2.v1	-1.6221	1.78E-11	1.13E-09	sp|O82316|TIP41_ARATH Aquaporin TIP4-1 OS=Arabidopsis thaliana GN=TIP4-1 PE=2 SV=1//5.03132e-112
Glyma.07G018000.Wm82.a2.v1	1.4453	6.43E-07	2.33E-05	sp|Q41951|TIP21_ARATH Aquaporin TIP2-1 OS=Arabidopsis thaliana GN=TIP2-1 PE=1 SV=2//9.26677e-112
Glyma.11G034000.Wm82.a2.v1	-1.3318	1.20E-58	6.71E-56	sp|Q41975|TIP22_ARATH Probable aquaporin TIP2-2 OS=Arabidopsis thaliana GN=TIP2-2 PE=1 SV=2//1.28753e-108
Glyma.09G238200.Wm82.a2.v1	-5.1685	9.41E-78	7.36E-75	sp|Q6Z2T3|NIP21_ORYSJ Aquaporin NIP2-1 OS=Oryza sativa subsp. japonica GN=NIP2-1 PE=1 SV=1//3.71203e-92
Glyma.15G003900.Wm82.a2.v1	1.9064	0.0001142	0.0025937	sp|Q9SAI4|NIP61_ARATH Aquaporin NIP6-1 OS=Arabidopsis thaliana GN=NIP6-1 PE=1 SV=1//2.87757e-112
Glyma.18G259500.Wm82.a2.v1	-2.1677	8.39E-08	3.47E-06	sp|Q6Z2T3|NIP21_ORYSJ Aquaporin NIP2-1 OS=Oryza sativa subsp. japonica GN=NIP2-1 PE=1 SV=1//1.04006e-92

Table S10. The information of all primers in the manuscript.

SYP24-F1	ACATCATTTCCCACTCCCG
SYP24-R1	GGACCTATGTCCAAAAGTAACCA
SYP24-F2	TCTGGCTCATAGTCCGTCCG
SYP24-R2	GCCTCTTGTTGGGGTTTCG
SYP24-F3	cgacgacaagaccgtgACATCATTTCCCACTCCCG
SYP24-R3	gaggagaagagccgtGGACCTATGTCCAAAAGTAACCA
Atactin-F	GAAGTTCAATGTTTCGTTTCATGT
Atactin-R	GGATTATACAAGGCCCCAAAA
Gmactin-F	ATCTTGACTGAGCGTGGTTATTCC
Gmactin-R	GCTGGTCCTGGCTGTCTCC
RD29AF	GGCGTAACAGGTAAACCTAGAG
RD29AR	TCCGATGTAAACGTCGTCC
RD22F	GGTTCGGAAGAAGCGGAG
RD22R	GAAACAGCCCTGACGTGATAT
COR47F	GGAGTACAAGAACAACGTTCCCGA
COR47R	TGTCGTCGCTGGTGATTCCTCT
NCED3F	CAGCTTGTAGCTTTTGGGCTGTA
NCED3R	TAACAGAAACCAGCTGAGCTCGA
COR15AF	GGCCACAAAGAAAGCTTCAG
COR15AR	CTTGTTTGCGGCTTCTTTTC
KIN1F	AACAAGAATGCCTTCCAAGC
KIN1R	CGCATCCGATACACTCTTTCC
P5CSF	GCGCATAGTTTCTGATGCAA
P5CSR	TGCAACTTCGTGATCCTCTG
ABI1F	AGAGTGTGCCTTTGTATGGTTTTA
ABI1R	CATCCTCTCTCTACAATAGTTCGCT
ABI2F	GATGGAAGATTCTGTCTCAACGATT
ABI2R	GTTTCTCCTTCACTATCTCCTCCG
ABI4F	ACTCCAAGTTCCGTTACCGTG
ABI4R	GGGGTTAAGTTGAGCTGAGCA
ABI5F	CAATAAGAGAGGGATAGCGAACGAG
ABI5R	CGTCCATTGCTGTCTCCTCCA
ABF4F	AACAACTTAGGAGGTGGTGGTC
ABF4R	CTTCAGGAGTTCATCCATGTTC
ABA3F	TGCACACAACGTCACTTTCCATATA
ABA3R	GACCGTAGCTCAGAATGGGATAACT
CIPK3F	AGAATCTTAGATCCGAATCCGATGAC
CIPK3R	CCTCCTCTCAATGTTATCCTTGTTTC
RGALF	CCCGGTTCCATCGATAAGTTTT
RGALR	TCGCATGCCACAAGGTTTAGTAT
IAA28F	ACCAATTCACTTCCAACAACAAC
IAA28R	CTTGCCATGTTTTCTAGGTGAG

Cu/Zn SODF	ATGGCGAAAGGAGTTGCAGT
Cu/Zn SODR	TTAGCCCTGGAGACCAATGA