

Supplementary Table1: Peptide data summary of aluminum regulated proteins detected in soybean line PI 416937 in time-course Al stress experiment

Peptide data summary									
Spot	Accession	Protein ID/functional class ^a							
			Peptide count	Protein score	Protein score C.I. %	Ion score	Ion score C.I. %	e-value soya ^b	% identity soya ^c
5	gi/126411	Lipoxygenase(PM)	4	97	100	61	99.2	0	100
8	gi/42820320	Copper amino oxidase (DD)	17	375	100	216	100	0	96.1
15	gi/225425555	Theoredoxin (DD)	2	66	83.7	57	99.2	0	66.2
16	gi/224115920	Protein phosphatase 2A (ST)	6	135	100	76	100	0	92.8
17	gi/22331670	Serine/threonine protein kinase (ST)	4	48	0.0	-	-	7.7e-164	57
18	gi/15225438	Malate oxidoreductase (E)	6	80	99.3	38	43	0	86.6
20	gi/162458207	Enolase (E)	4	116	100	88	100	0	89.4
21	gi/223548395	26S protease subunit 6a (PD)	14	303	100	161	100	0	97
22	gi/2511541	DNA-binding protein gbp16 (UN)	3	88	99.9	65	99.8	4.4e-172	85.6
23	gi/4836923	CREB binding protein (TF)	6	60	30.6	-	-	1.1e-178	48.3
24	gi/223548531	S-adenosyle methionase synthase (PM)	11	341	100	240	100	0	96.9
25	gi/224285989	Amidase (PM)	3	49	0.0	-	-	2.3e-137	58.9
26	gi/3024127	S-adenosyle methione synthase (PM)	9	267	100	174	100	0	95.9
27	gi/223548639	Transaldolase (PM)	6	98	100	49	96.3	0	85
30	gi/211970690	Formate dehydrogenase (PM)	2	70	94.1	60	99.6	0	90.1
31	gi/1498340	Actin (CS)	13	363	100	209	100	0	98.8
33	gi/157346459	NADH:flavin oxidoreductase (DD)	4	72	96.3	44	83.9	4e-180	83.7
34	gi/242462	Lipoxygenase (PM)	5	104	100	78	100	0	99.5
35	gi/195637880	Pyruvate dehydrogenase E1 (E)	5	75	98	38	41	5.9e-179	83.8
36	gi/9230771	Cyt phosphoglysrate kinase (PM)	4	131	100	91	100	0	93.3
37	gi/49257111	Disulfide isomerase-like (PD)	6	231	100	176	100	0	100
38	gi/168029670	Unknown (UN)	6	64	74.8	-	-	-	-
39	gi/126508778	Cystine synthase (PM)	4	65	79.5	34	0.0	1.4-162	99.7
42	gi/3273828	Malate dehydrogenase (E)	5	66	84.8	43	85.9	0	99.3
43	gi/186506243	Aaldo/keto reductase (PM)	5	110	100	74	100	2.8e-114	68.5
44	gi/134559418	(+)-pulegone reductase (SM)	2	90	99.9	70	100	9.1e-129	65.5
45	gi/108864466	Unknown (UN)	7	57	0.0	-	-	-	-
46	gi/2687724	NADPH:isoflavonre reductase (SM)	15	483	100	289	100	0	99.7
50	gi/393401	Alpha tubulin (CS)	10	210	100	84	100	2.4e-139	98.3
55	gi/3023196	14-3-like protein C (ST)	5	132	100	81	100	2.1e-140	99.2
56	gi/6469121	Plasma memberane polypeptide (UN)	1	75	98.1	69	99.9	4.8e-45	77.1
61	gi/186507172	BRCA1 C terminal (CD)	7	52	0.0	-	-	2.9e-155	50.6
62	gi/6690745	Rresistance protein (DD))	7	94	100	-	-	1e-41	48.8
64	gi/3023194	14-3-3-like protein A (ST)	6	268	100	205	100	1.3e-135	98.4
65	gi/125550993	Unknown (UN)	4	63	71.1	-	-	-	-
67	gi/225455804	Hypothetical protein	10	73	97	-	-	1.1e-149	46.6
70	gi/226866	31 kD protein (UN)	7	315	100	221	100	8.9e-142	99.6
75	gi/11385431	Glutathione S-transferase 8 (DD)	6	114	100	66	99.9	3.1e-128	99.6
78	gi/224087343	WD40 protein/RNA processing (TF)	5	45	0.0	-	-	0	76.5
79	gi/194705252	Cytidylyl transferase (SM)	3	38	0.0	-	-	5.2e-162	89.6
81	gi/1170781	Gluthatione-S-transferase 3 (DD)	2	66	82.6	49	88.6	2.8e-120	100
82	gi/11385435	Guthione S-transferase 10 (DD)	2	74	97.7	53	97.7	4.2e-113	100
83	gi/399240	20 kDa chaperonin (UN)	1	67	87.1	51	96.4	3.1e-5	95.2
84	gi/224135489	Beta glucosidase (PM)	3	66	85.5	-	-	1.8e-38	83.3
85	gi/11385459	Gluthstione aS-transferase 22 (DD)	8	482	100	377	100	3.4e-12	100
89	gi/28192427	Dehydroascorbate reductase (DD)	2	112	100	95	100	6.3e-93	76.9
90	gi/30682123	Adenine phosphoribosyl transferase, ATP4 (PM)	2	99	100	83	100	3.2e-62	82.4
91	gi/17380185	Proteasome subunit beta-1 (PD)	4	219	100	186	100	6.6e-123	91.5
92	gi/21068664	Quinine oxidoreductase (DD)	4	179	100	142	100	1.2e-101	95.1

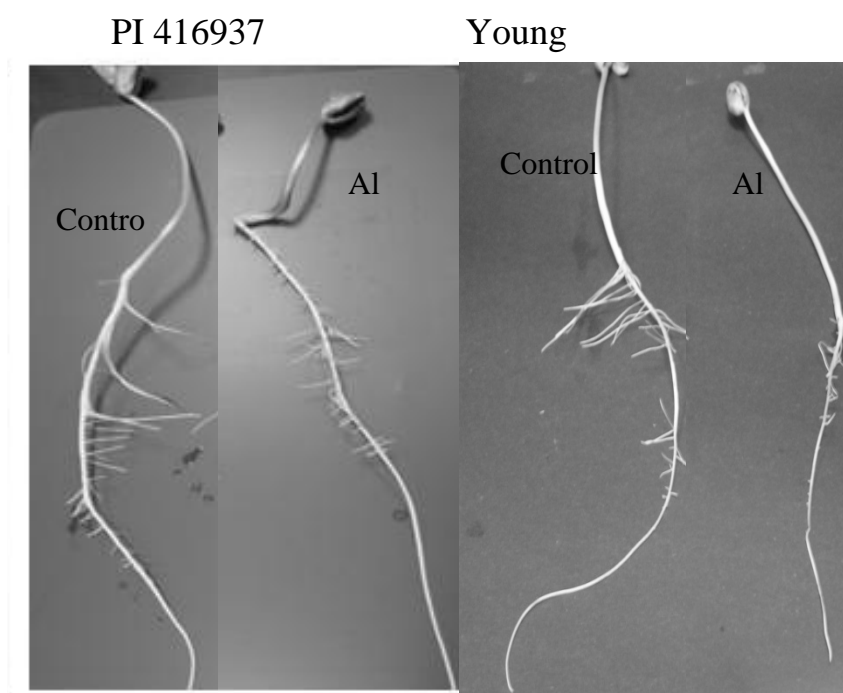
^aPM = primary metabolism, SM = Secondary metabolism, E = energy, PD = protein destination, TF = transcription factor,

CS = cell structure, ST = signal transduction, DD, = disease/defense, CD = cell division, UN = unknown function; ^cxpression fold change at each time point, negative values = down-regulation, positive values = up-regulation, fold change significance cutoff is ± 1.3 , SE = standard error, nd = not detected. ^b the probability that the match with soybean protein in soybean genome data base is by chance. ^c % sequence identity with soybean protein in soybean genome database.

Supplementary Table 2: Peptide data summary of aluminum regulated proteins detected in soybean cultivar Young in time-course Al stress experiment

Spot	Accession	Protein ID/functional class ^a	Peptide data summary						
			Peptide count	Protein score	Protein score C.I. %	Ion score	Ion score C.I. %	e-value soya ^b	% identity soya ^c
3	gi/27883937	Phosphoribosylformyl glycine synthase (PM)	9	80	99.4	12	0.0	0	94.0
2	gi/224160640	Zinc knuckle (UN)	5	53	0.0	-	-	5.1e-29	49.2
87	gi/11385431	Glutathione (DD)	7	206	100	139	100	3.1e-128	99.6
100	gi/156938901	Profilin (CS)	3	230	100	193	100	4.6e-64	100
103	gi/79321519	Heat shock protein 91 (PD)	15	119	100	42	88.3	0	81.8
104	gi/153805634	Unknown (UN)	10	59	22.2	-	-	-	-
106	gi/15219879	Apoptotic ATPase (DD)	7	60	30.6	-	-	2.5e-98	35.1
107	gi/30696901	Xylose isomerase (PM)	3	230	100	193	100	8.8e-116	81.5
109	gi/168030956	Serine/threonine protein kinase ((ST)	6	56	0.0	-	-	4.6e-102	59.0
112	gi/436169	Lipoxygenase (PM)	10	129	100	65	99.9	-	-
113	gi/77552532	Unknown (UN)	3	54	0.0	-	-	2.4e-177	82.2
116	gi/2232254	NADH:flavin oxidoreductase (UN)	3	50	0.0	-	-	0	96.7
118	gi/223541365	Transitional endoplasmic reticulum ATPase (CS)	28	324	100	84	100	0	96.7
119	gi/223974443	Unknown (UN)	4	58	0.0	-	-	-	-
133	gi/42820320	Copper amino oxidase (DD)	5	81	99.4	43	80	0	96.1
136	gi/195636596	T-complex protein 1 alpha (PD)	13	152	100	49	96.1	0	88.6
137	gi/125574688	Glutathione-S-transferase (DD)	4	56	0.0	-	-	3.1e-22	49.5
140	gi/74053562	Tubulin beta-3-chain (CS)	19	289	100	96	100	0	99.3
147	gi/5225811	Unknown (UN)	7	53	0.0	-	-	-	-
151	gi/124112056	Septum site determining protein (CS)	8	60	30.6	-	-	5.6e-61	63.5
155	gi/87240711	V-ATPase subunit C (DD)	5	66	84.5	29	0.0	0	86.1
156	gi/1346698	Phosphoglycerate kinase (PM)	6	154	100	121	100	0	90.5
157	gi/1582580	Caffeic acid O-methyl transferase (SM)	5	140	100	92	100	0	90.1
158	gi/1346028	Polyprenyl synthetase (SM)	5	58	10.6	13	0.0	0	90.6
166	gi/3023197	14-3-3-like (ST)	6	136	100	84	100	9.5e-146	100
167	gi/393401	Alpha tubulin (CS)	13	187	100	25	0.0	2.4e-139	98.3
172	gi/78146198	MADS box protein/transcription factor (TF)	7	56	0.0	-	-	3.3e-77	63.9
185	gi/115511406	Acriduoytase dioxygenase (PM)	5	103	100	50	94.6	6.4e-92	88.5
186	gi/224105487	Unknown (UN)	4	58	0.0	-	-	-	-
187	gi/145352433	Unknown (UN)	5	51	0.0	-	-	-	-
188	gi/17380185	Proteasome subunit beta type-1 (PD)	4	341	100	308	100	6.6e-123	91.5
191	gi/223543735	Proteasome subunit beta type (PD)	5	127	100	60	99.5	1.3e-110	93.0
193	gi/145340582	Unknown (UN)	4	58	4.3	39	52.9	-	-
195	gi/209778987	Putative rab1C protein (IT)	4	72	95.9	20	0.0	6.3e-67	90.1
196	gi/18395025	20S proteasome beta subunit C (PD)	8	307	100	200	100	1.5e-113	93.1
197	gi/125577605	DNJ/HSP40 (DD)	7	65	80.5	-	-	6.8e-47	42.4
198	gi/34485411	Resistance protein (DD)	7	56	0.0	-	-	1.9e-15	35.5
200	gi/20140683	Translationally-controlled tumor protein homolog (CD)	12	497	100	343	100	2.5e-79	100
201	gi/40644130	Allene oxide cyclase (PM)	4	109	100	71	100	1.4e-84	71.8
204	gi/223510245	unknown	7	62	63.6	-	-	-	-
206	gi/197294157	Hypothetical protein (UN)	8	55	0.0	-	-	5.4e-29	63.1
212	gi/110931690	MYB transcription factor (TF)	8	56	0.0	-	-	1e-139	100
214	gi/18143656	Mcp20 (PD)	5	114	100	57	99.3	9.4e-119	99.5
218	gi/829282	Eukaryotic initiation factor A (PS)	5	138	100	75	100	1.9e-72	91.0
220	gi/15238219	Unknown (UN)	6	57	0.0	-	-	-	-
225	gi/223547693	Electron transporter (E)	2	95	100	78	100	1.3e-60	78.8
226	gi/145345251	Glycogen synthase kinase-3 (PM)	3	49	0.0	-	-	1.4e-132	64.8

^aPM = primary metabolism, SM = Secondary metabolism, E = energy, PD = protein destination, TF = transcription factor, CS = cell structure, ST = signal transduction, DD = disease/defense, CD = cell division, UN = unknown function; ^bexpression fold change at each time point, negative values = down-regulation, positive values = up-regulation, fold change significance cutoff is ± 1.3 , SD = standard error, nd = not detected. ^c the probability that the match with soybean protein in soybean genome data base is by chance. ^d % sequence identity with soybean protein in soybean genome database.



Supplementary Figure 1: Representative pictures of control and Al- treated roots of PI 416937 and Young