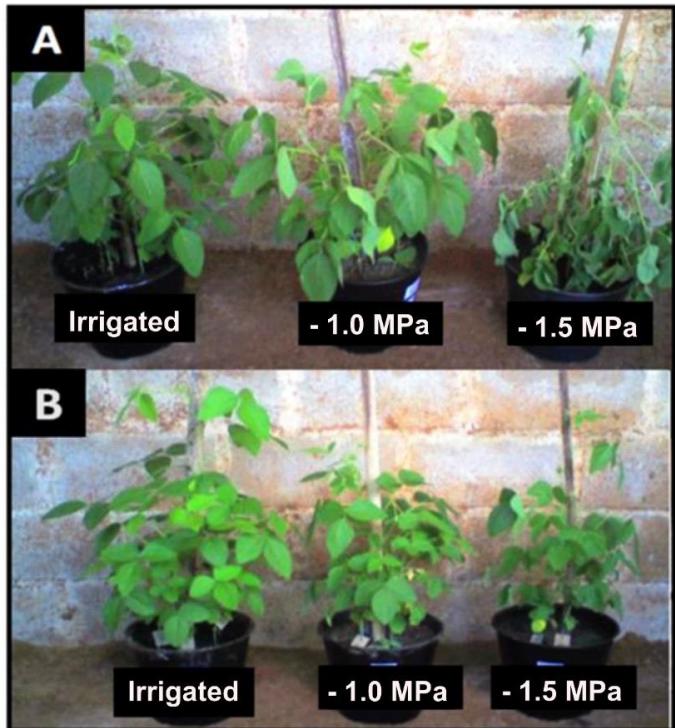
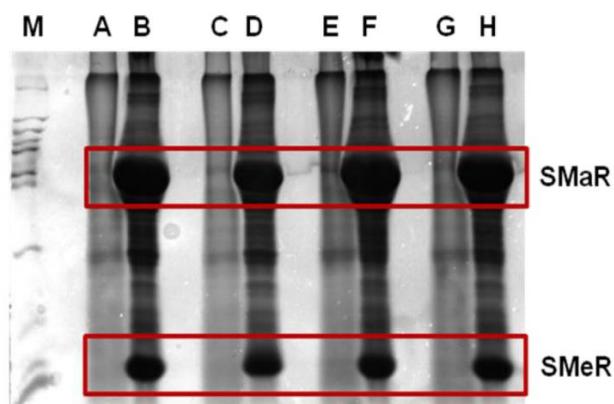


Proteomic and Metabolomic Analysis of a Drought Tolerant Soybean Cultivar from Brazilian Savanna

Supplementary Materials

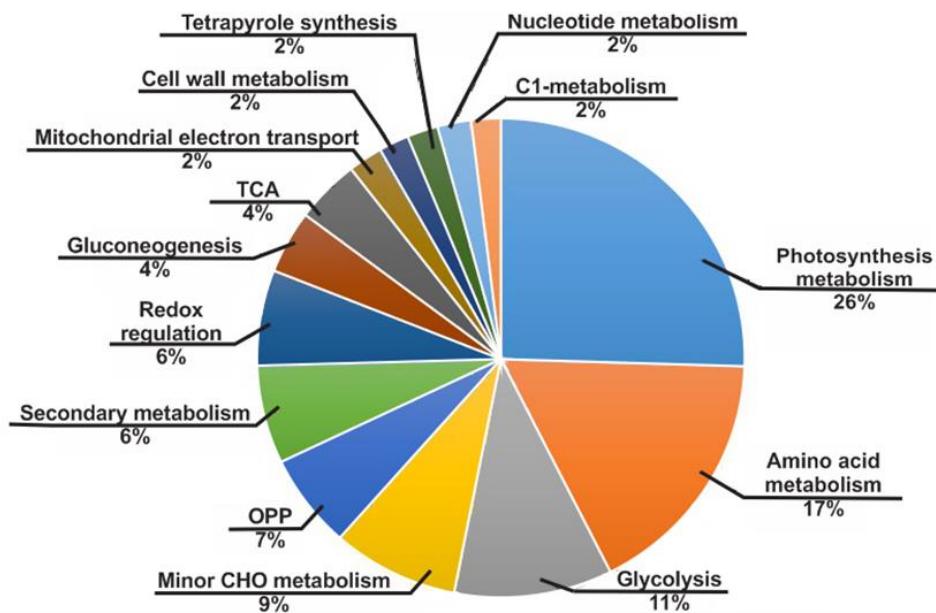


Supplementary Figure S1: Leaf turgor of the soybean leaves under drought and water supply. The drought sensitive BR 16 in **(A)** and tolerant Embrapa 48 in **(B)**. The drought tolerance and sensitivity are shown by wilting of the leaves, especially at severe stress (-1.5 MPa) for BR 16 genotype.

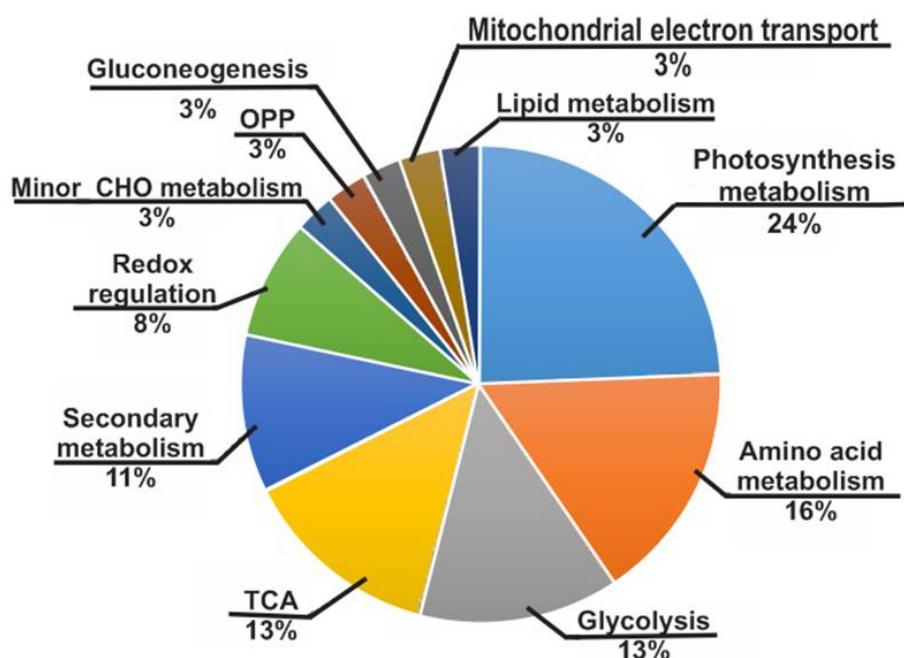


Supplementary Figure S2: SDS-PAGE 1D profiles of the protein extracts fractionated with PEG and stained by Coomassie blue. The leaf with the most abundant proteins were differentially precipitated in the PEG-pellet fractions, as indicated by the presence and absence of the bands corresponding small (SMeR) and larger (SMaR) RUBISCO subunits. The capital letter corresponds to the 150 ug protein/lane of the each samples: in **(A)** BR 16 IR PEG- supernaut, in **(B)** BR 16 IR PEG-pellet, in **(C)** BR16 NI -1,0MPa PEG-supernaut, in **(D)** BR16 NI -1,0MPa PEG-pellet, in **(E)** Embrapa 48 IR PEG- supernaut, **(F)** Emprapa 48 IR PEG-pellet, in **(G)** Embrapa 48 NI -1,0MPa PEG-supernaut, in **(H)** Embrapa 48 NI -1,0MPa PEG-pellet, in **(M)** molecular-weight marker.

(A)

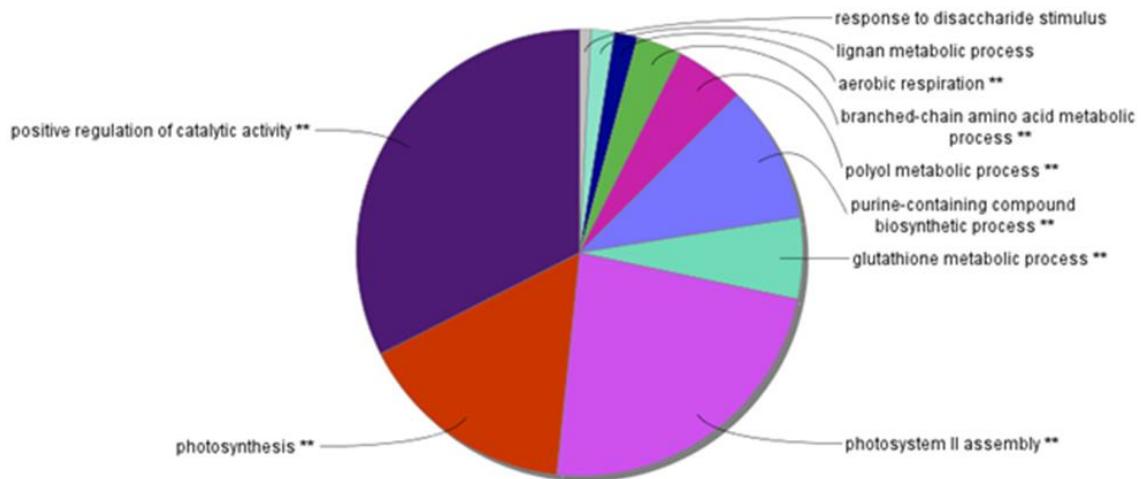


(B)

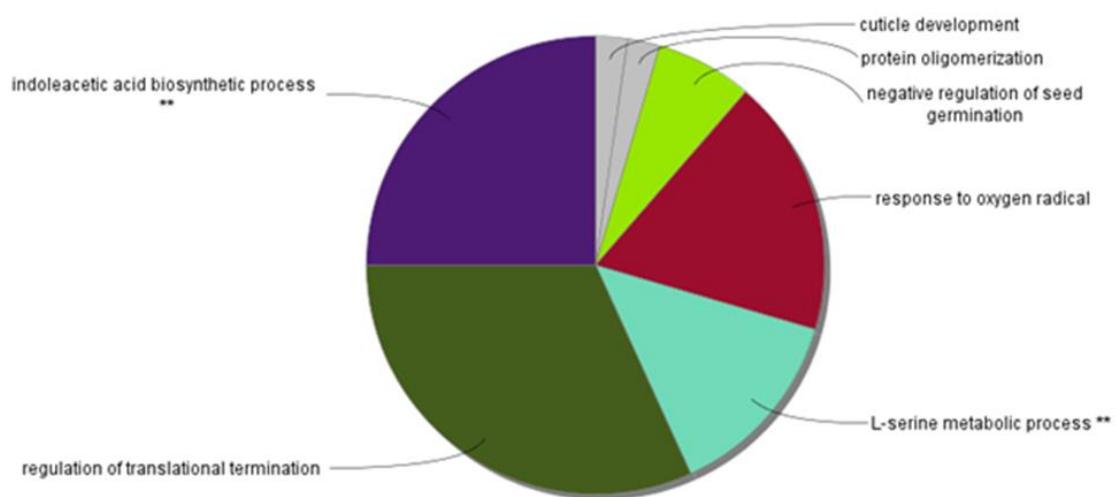


Supplementary Figure S3: Gene Ontology (GO) classification of the differentially expressed proteins identified from the leaves of soybean Embrapa 48 **(A)** and BR 16 **(B)** genotypes under drought stress.

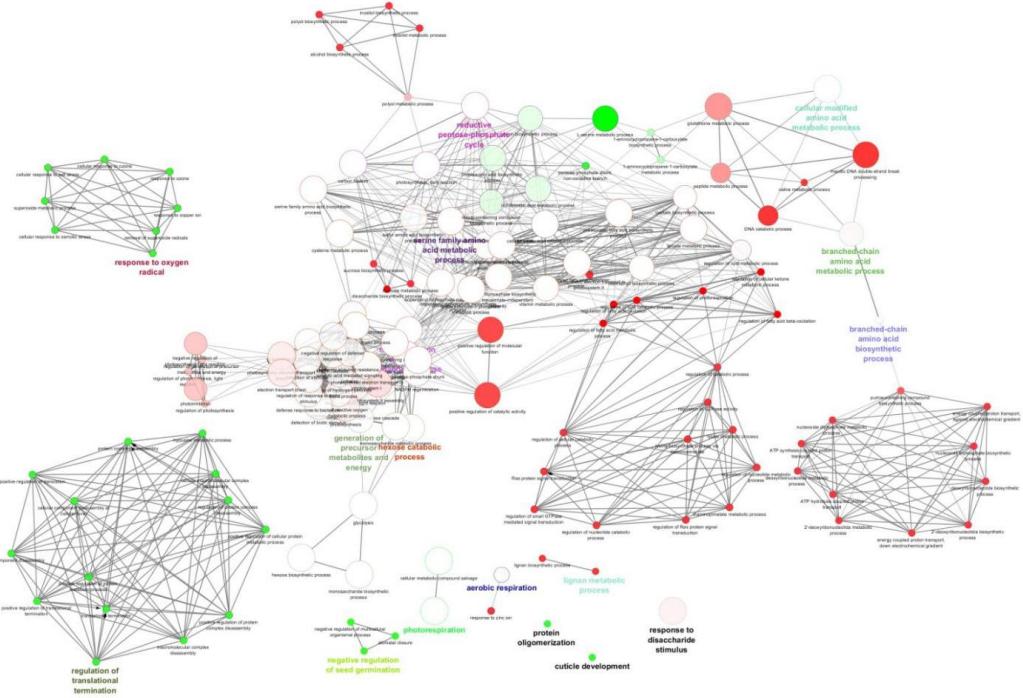
(A)



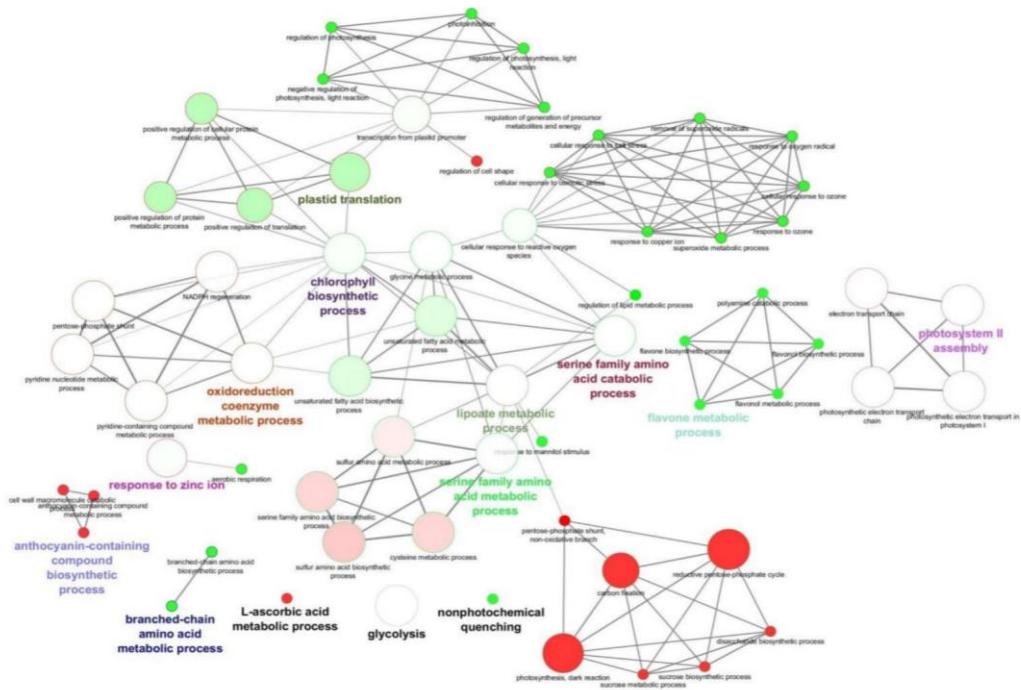
(B)



Supplementary Figure S4: Biological processes enriched by ClueGO analysis of the proteins that were up-regulated in the Embrapa 48 **(A)** and BR16 **(B)** genotypes under drought stress.

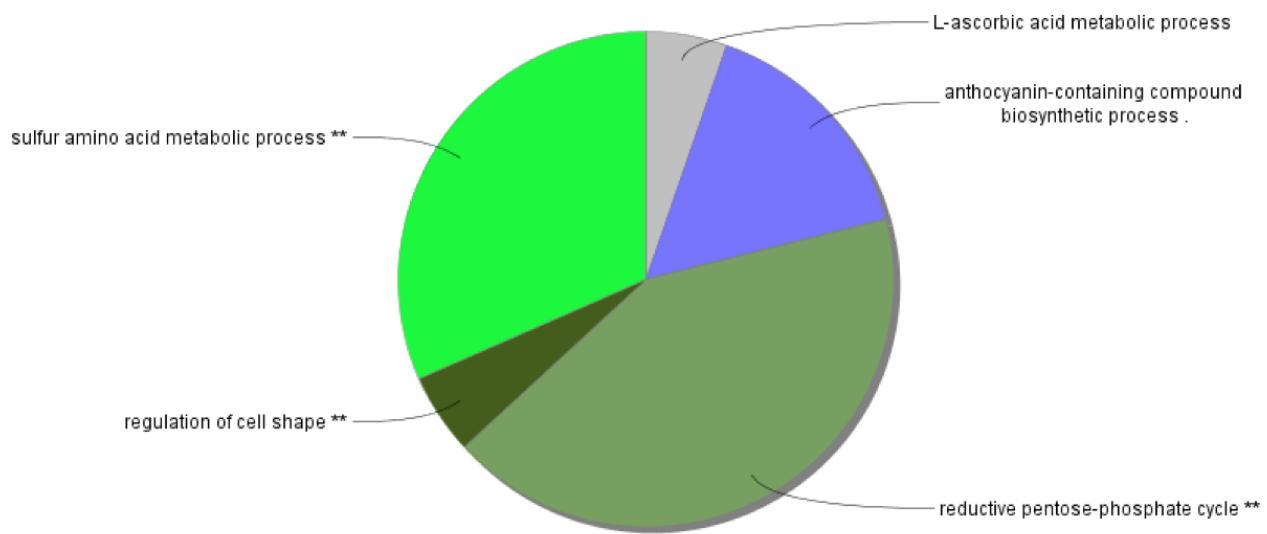


Supplementary Figure S5: Clustering analysis generated by *ClueGO plugin* showing functionally grouped networks of the enriched GO terms using a *kappa score* level ≥ 0.3 . Green and red circle clusters are shown for up-regulated proteins from BR 16 and Embrapa 48, respectively. The larger circles indicate that the biological process was more enriched. White circles and those showing a mix of green and red were not specific for the genotypes.

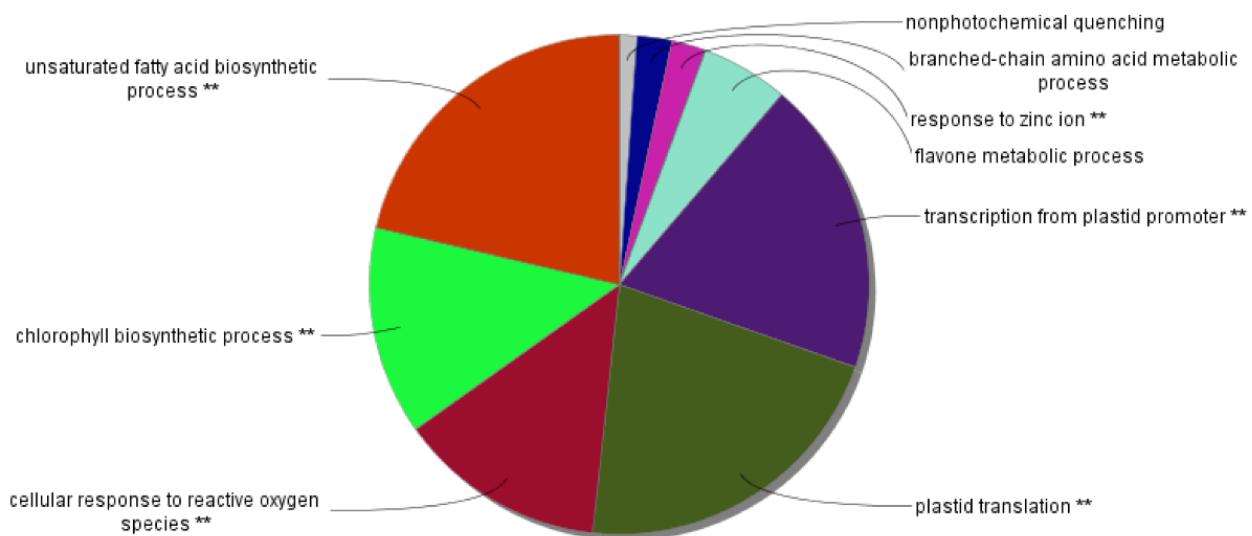


Supplementary Figure S6: Clustering analysis generated by ClueGO showing functionally grouped networks of the enriched GO terms using a *kappa score* level ≥ 0.3 . Green and red clusters are shown for down-regulated proteins from BR 16 and Embrapa 48, respectively.

(A)

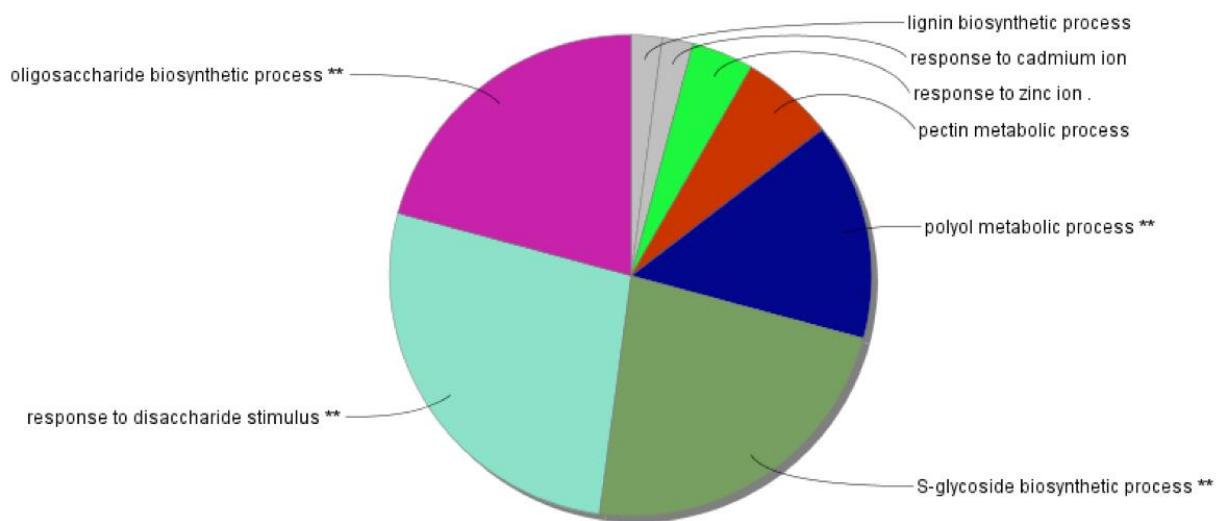


(B)

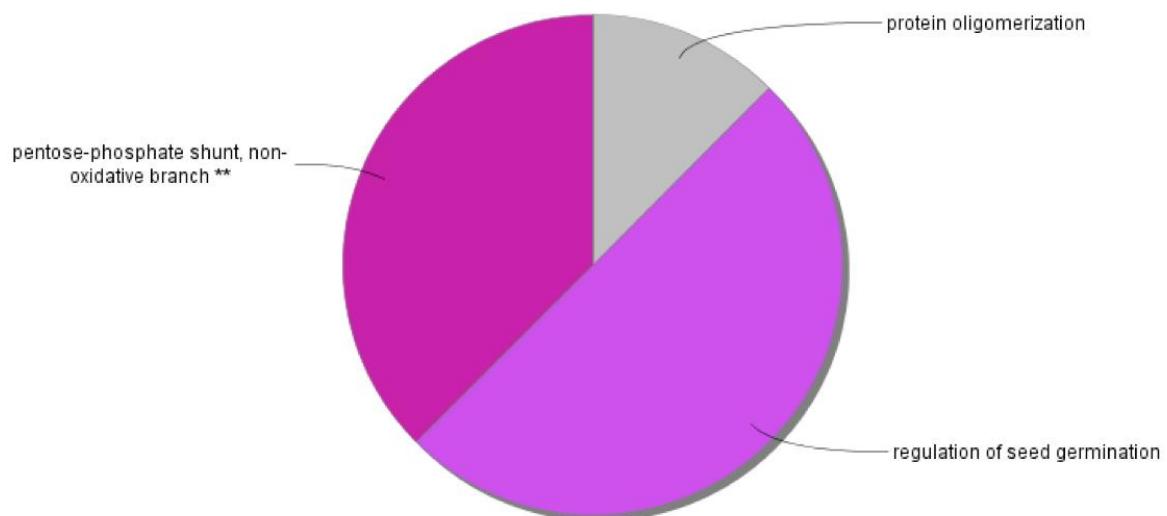


Supplementary Figure S7: Biological Processes enriched generated ClueGO analysis from the proteins that were down-regulated of the Embrapa 48 (A) and BR 16 (B) genotypes under drought stress.

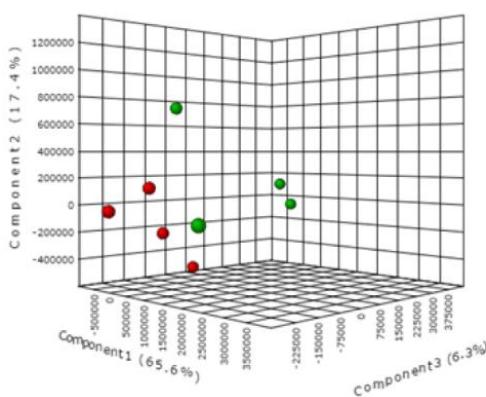
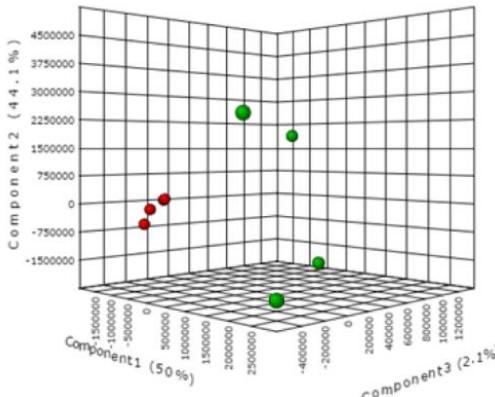
(A)



(B)

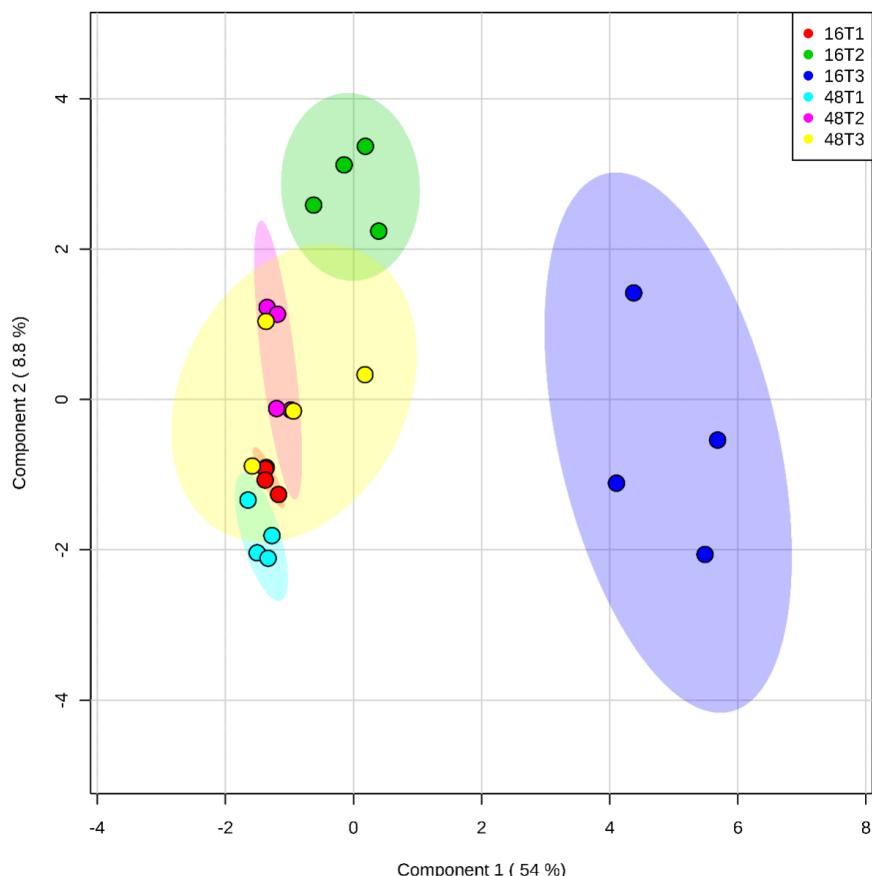


Supplementary Figure S8: Biological Process enriched generated ClueGO analysis from the phosphoproteins that were UP-regulated of the Embrapa 48 (A) and BR 16 (B) genotypes under drought stress.

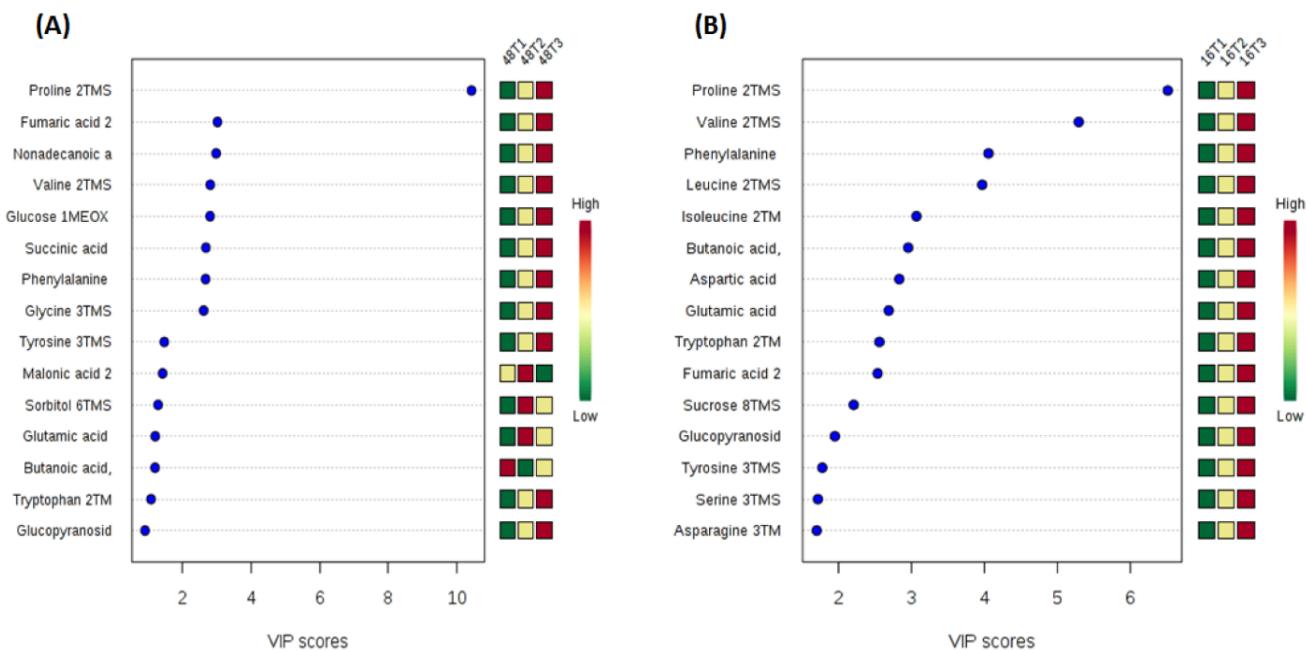
(A)**(B)**

Supplementary Figure S9: Clustering analysis by tridimensional score plot *PCA* for the metabolite abundances of the soybean leaves identified by GC/MS. Four replicates are showed of the treatments of the genotypes Embrapa 48 in **(A)** and BR16 in **(B)** when plants under irrigation (T1) and non-irrigation (T3: -1.5MPa).

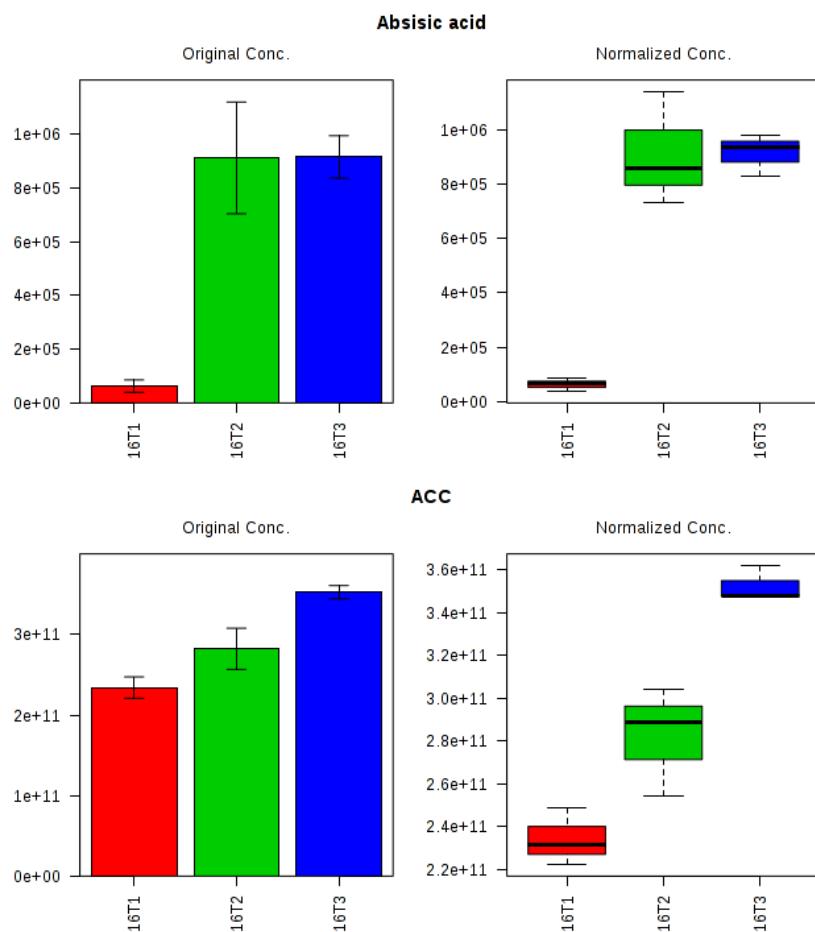
Scores Plot

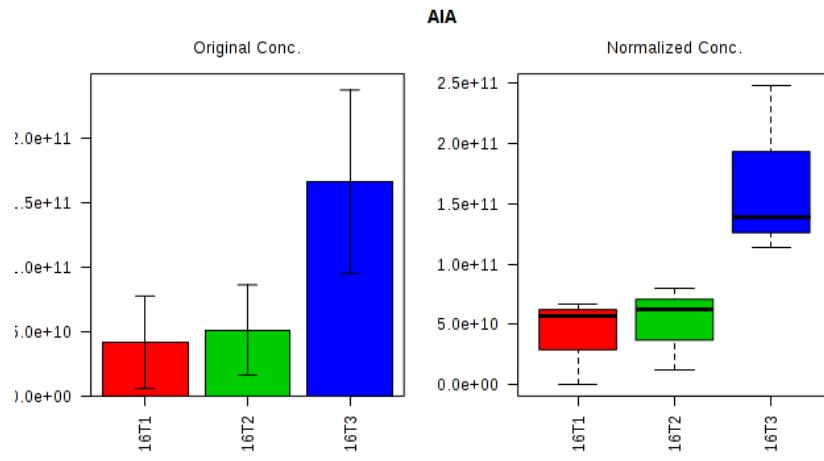


Supplementary Figure S10: Clustering analysis by *bidimensional score plot* PLS-DA for the metabolite abundances of the soybean leaves identified by GC/MS. Four replicates are showed of the treatments of the genotypes Embrapa 48 and BR 16 when plants under irrigation (T1) and non-irrigation (T2: -1.0MPa and T3: -1.5MPa). Colored circles indicate the genotypes and treatments according to the captions at the top of figure: 16 for BR 16 and 48 for Embrapa 48.



Supplementary Figure S11: Determination of the metabolites that contributed for sample distributions on the PLS-DA plot (Figure 10). The relative abundance of the metabolites is indicated, as well as the VIP scores of the Embrapa 48 **(A)** and BR 16 **(B)** when plants are under irrigation (T1) and non-irrigation (T2: -1.0MPa and T3: -1.5M





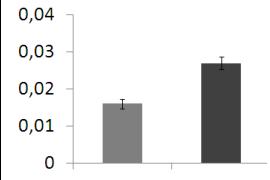
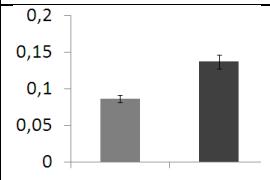
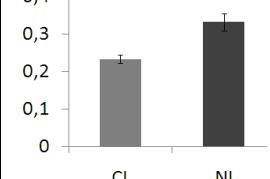
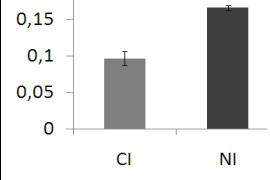
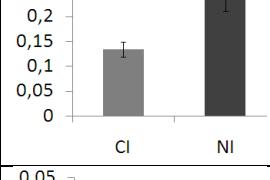
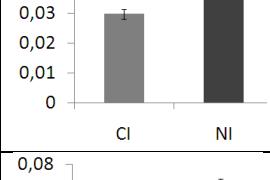
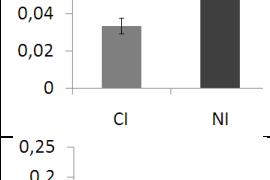
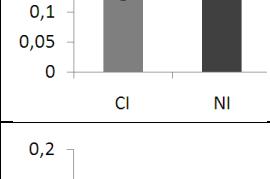
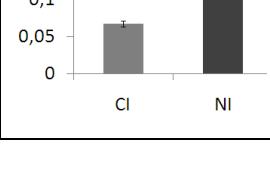
Supplementary Figure S12: Absolute abundance of the phytohormones Abscisic Acid (ABA), ACC and AIA of the soybean leaves quantified by LC/MS. The treatment irrigated (T1), under moderate (T2, -1.0MPa) and severe (T3, -1.5MPa) drought stress are indicated.

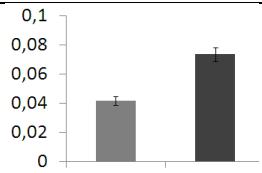
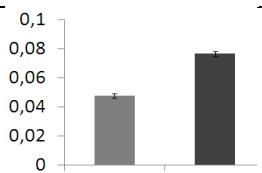
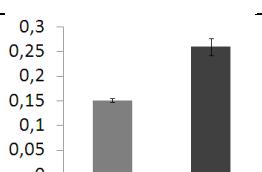
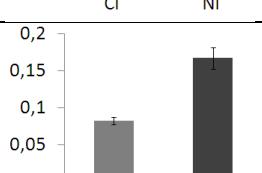
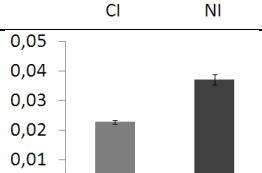
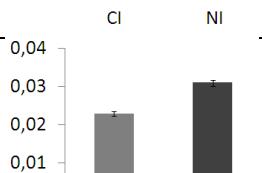
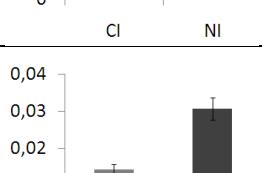
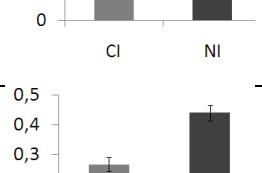
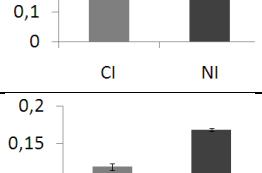
Supplementary Table S1: Transition list of the ions monitored for quantification analysis of the phytohormones from soybean leaves by MRM. The scan mode, the mass of the molecular ion and respective fragment ions are indicated.

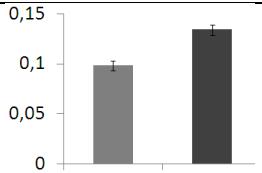
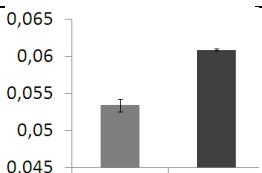
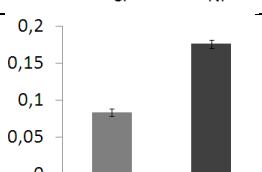
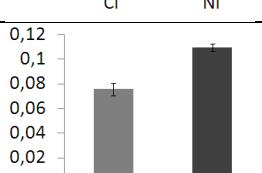
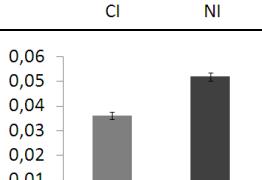
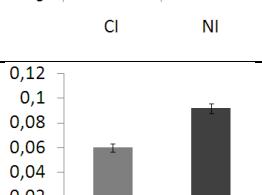
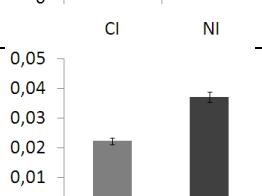
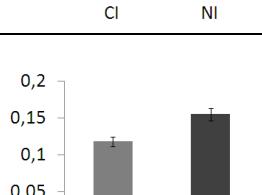
PHYTOHORMNES	MS1	MS2	SCAN MODE
Zeatina	220	202	Positive
ACC	106	56	Positive
AIA	176	130	Positive
ABA	263	153	Negative
AS	137	93	Negative
GA4	331	213	Negative
JA-ILE	322	130	Negative
MeJa	225	151	Negative
JA	209	59	Negative
NAA	185	141	Negative

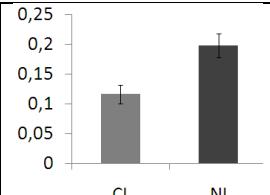
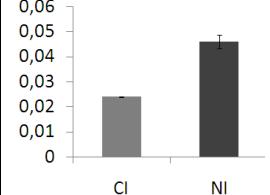
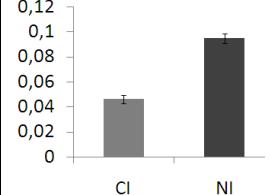
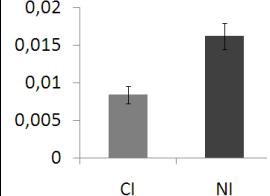
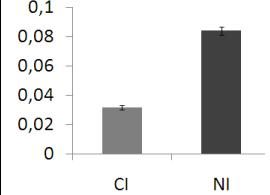
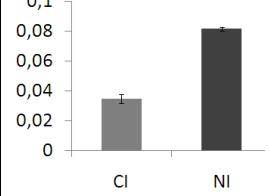
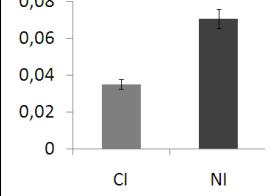
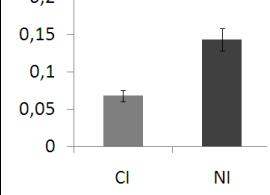
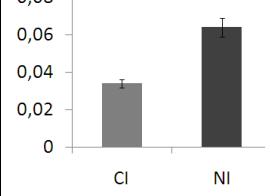
Supplementary Table S2. Differentially expressed proteins of the soybean leaves from the Embrapa 48 identified by mass spectrometry. The protein abundances are indicate as % volume average of the spots from three biological replicated generated by *ImageMaster* software. CI for irrigated control and NI for non-irrigated (-1,0 MPa)

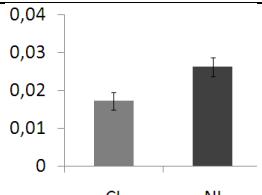
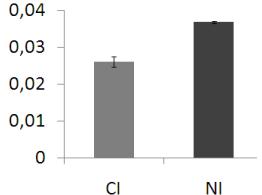
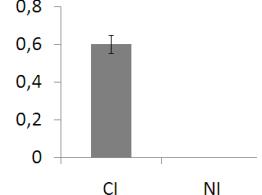
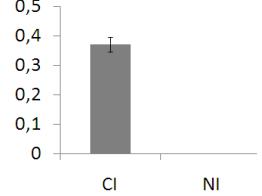
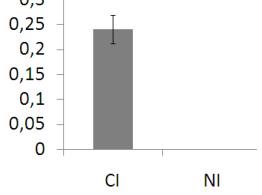
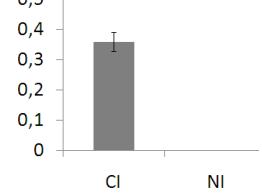
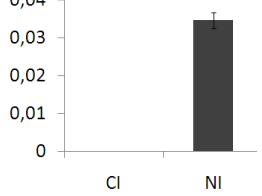
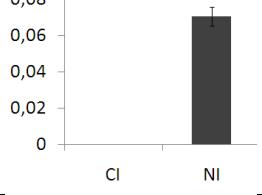
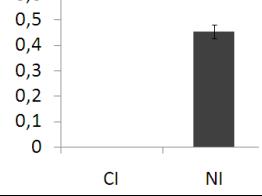
Spot ID	Protein	MM(Da)	PI	Glyma 1.1 Accession number	Coverage (%)	Unique peptides	Protein Abundance % Volume ± SD*						
855	Adenine nucleotide alpha hydrolases-like superfamily protein	18.679,4	6,00	Glyma03g16510.1	22	3	<table border="1"> <caption>Abundance Data for Spot 855</caption> <thead> <tr> <th>Condition</th> <th>Abundance (%)</th> </tr> </thead> <tbody> <tr> <td>CI</td> <td>~0.015</td> </tr> <tr> <td>NI</td> <td>~0.035</td> </tr> </tbody> </table>	Condition	Abundance (%)	CI	~0.015	NI	~0.035
Condition	Abundance (%)												
CI	~0.015												
NI	~0.035												

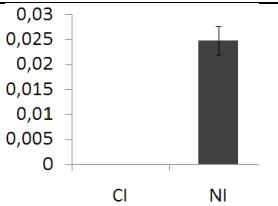
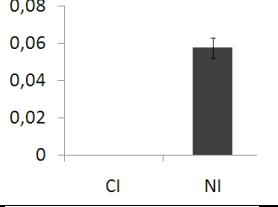
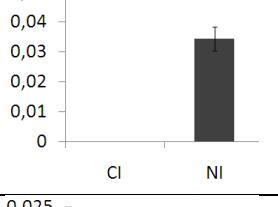
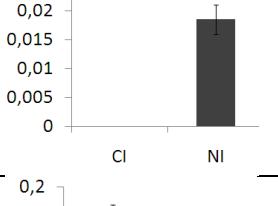
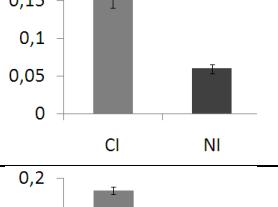
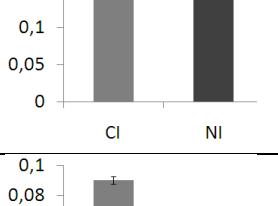
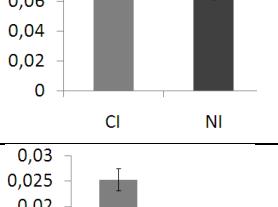
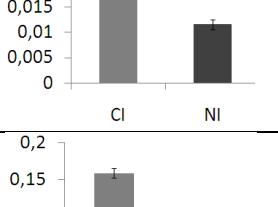
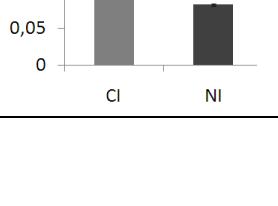
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252	Alanine-2-oxoglutarate aminotransferase 2	53.524,9	5,61	Glyma01g0326 0.1	43	16	
87	Ascorbate peroxidase 1	27.052,6	5,70	Glyma11g1568 0.5	28	5	
81	Chalcone-flavanone isomerase family protein	23.496,0	4,84	Glyma06g1482 0.1	21	3	
289	Chaperonin-60 alpha	61.705,7	4,81	Glyma12g0831 0.1	40	19	
696	Chloroplast RNA-binding protein 31B	32.914,1	4,25	Glyma05g0280 0.1	23	5	
690	Chloroplastic drought-induced stress protein of 32 KD	33.170,7	5,08	Glyma14g3994 0.1	16	4	
695	Chloroplastic drought-induced stress protein of 32 KD	33.170,7	5,13	Glyma14g3994 0.1	34	8	
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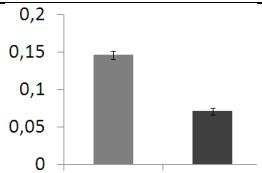
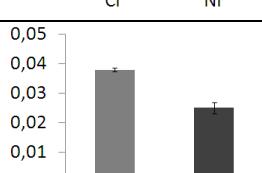
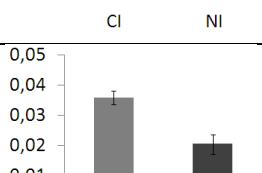
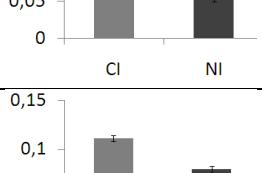
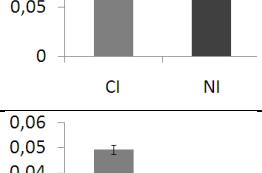
44	Glutathione peroxidase 6	18.503,6	5,58	Glyma01g4284 0.1	32	7	
61	Glutathione S-transferase TAU 19	25.559,9	6,05	Glyma15g4020 0.1	26	5	
914	Glutathione-disulfide reductase	53.992,6	5,77	Glyma16g2721 0.1	19	6	
851	Glycine decarboxylase complex H	21.955,5	4,28	Glyma01g4081 0.1	22	3	
887	Glyoxylate reductase 1	30.856,0	6,61	Glyma07g0657 0.1	46	8	
159	Malate dehydrogenase	43.147,8	5,60	Glyma17g1088 0.1	36	10	
661	Mog1/PsbP/DUF1795-like photosystem II reaction Center PsbP family protein	27.566,1	5,50	Glyma04g4201 0.2	16	3	
138	NAD(P)-binding Rossmann-fold superfamily protein	34.960,2	5,80	Glyma11g2946 0.1	29	9	
141	NAD(P)-linked oxidoreductase superfamily protein	35.210,4	6,33	Glyma03g1161 0.1	40	9	

158	NAD(P)-linked oxidoreductase superfamily protein	36.090,4	6,42	Glyma16g3457 0.1	25	9	
34	Peroxiredoxin IIF	21.169,7	6,01	Glyma13g2771 0.1	24	3	
150	Peroxisomal NAD-malate dehydrogenase II	37.462,1	6,96	Glyma07g3043 0.1	31	7	
194	PfkB-like carbohydrate kinase family protein	43.603,1	5,25	Glyma10g0472 0.1	32	8	
303	Phosphoglycerate mutase, 2,3-bisphosphoglycerate-independent	60.869,6	5,58	Glyma09g4069 0.1	18	6	
36	Photosynthetic electron transfer C	24.187,0	5,54	Glyma12g3258 0.1	16	3	
864	Photosynthetic electron transfer C	24.187,0	5,57	Glyma12g3258 0.1	16	3	
903	Pyridoxal phosphate (PLP)-dependent transferases superfamily protein	49.925,7	6,11	Glyma08g0679 0.1	38	11	

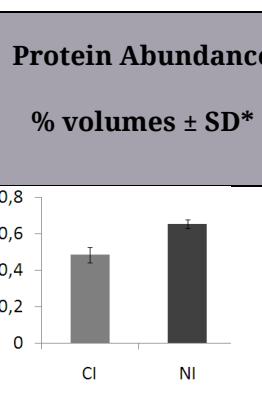
885	Pyrophosphorylase 6	32.335,0	4,05	Glyma13g3266 0.1	32	8	
854	Ribonuclease E inhibitor RraA/Dimethyl menaquinone	22.554,8	5,69	Glyma15g0690 0.1	37	6	
241	S-adenosylmethionine synthetase family protein	43.052,9	5,62	Glyma15g2189 0.1	19	6	
778	Sugar isomerase (SIS) family protein	62.657,2	6,26	Glyma04g0349 0.1	12	4	
294	TCP-1/cpn60 chaperonin family protein	62.841,5	5,28	Glyma08g1876 0.1	34	16	
295	TCP-1/cpn60 chaperonin family protein	62.841,5	5,22	Glyma08g1876 0.1	22	10	
848	Thioredoxin-dependent peroxidase 1	17.366,6	5,76	Glyma07g0924 0.1	37	4	
850	Thioredoxin-dependent peroxidase 1	17.366,6	5,45	Glyma07g0924 0.1	38	5	
249	Thylakoid rhodanese-like	47.570,4	4,76	Glyma16g0294 0.1	22	8	

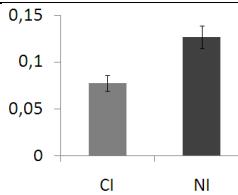
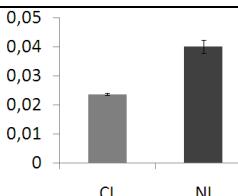
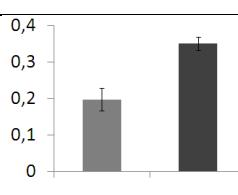
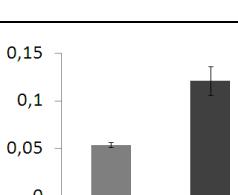
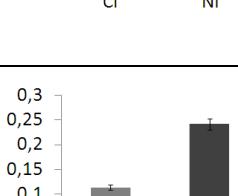
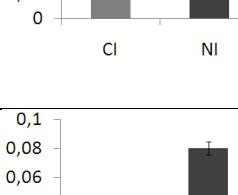
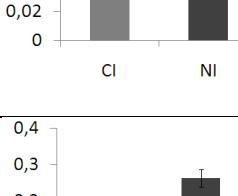
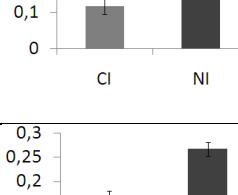
835	Transcriptional coactivator/pterin dehydratase	28.602,2	5,26	Glyma10g2271 0.2	19	3	
151	Zinc-binding dehydrogenase family protein	37.921,1	6,26	Glyma03g2389 0.1	41	9	
872	Carbonic anhydrase 1	36.750,6	6,92	Glyma19g0105 0.1	39	11	
881	Carbonic anhydrase 1	36.750,6	6,86	Glyma19g0105 0.1	27	7	
888	Carbonic anhydrase 1	36.750,6	6,95	Glyma19g0105 0.1	24	6	
861	Rotamase CYP 3	20.715,4	6,94	Glyma11g1048 0.2	28	4	
774	ATP synthase subunit alpha	55.739,4	5,03	Glyma12g3610 6.1	15	6	
775	ATP synthase subunit alpha	55.739,4	5,19	Glyma12g3610 6.1	27	10	
703	Ferredoxin-NADP(+) oxidoreductase 1	40.440,3	5,72	Glyma02g0535 0.1	43	10	

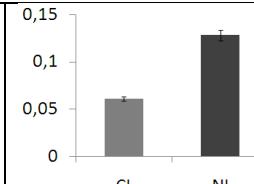
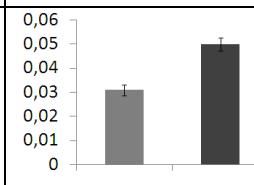
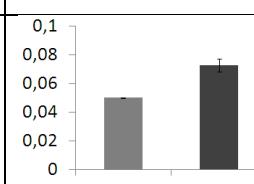
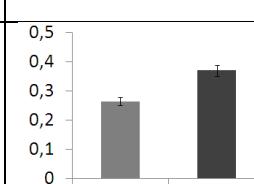
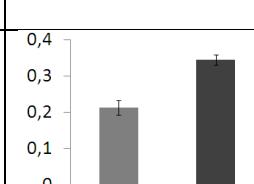
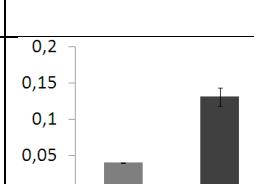
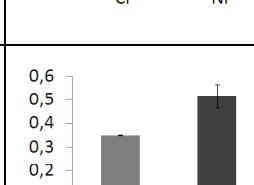
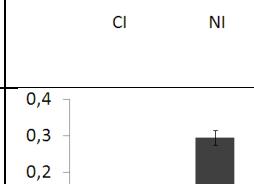
699	Fibrillin	33.660,3	4,44	Glyma09g0108 0.1	22	5	
694	Gamma carbonic anhydrase 1	29.992,2	6,52	Glyma04g0331 0.3	16	4	
773	Ketol-acid reductoisomerase	62.786,3	5,84	Glyma12g1442 0.1	13	5	
790	NAD-dependent malic enzyme 1	68.984,8	5,33	Glyma03g2463 0.1	19	9	
3	Allene oxide cyclase 3	27.671,2	5,94	Glyma13g0749 0.1	23	4	
69	Carbonic anhydrase 1	36.750,6	6,64	Glyma19g0105 0.1	22	6	
59	Chalcone-flavanone isomerase family protein	23.265,4	6,44	Glyma20g3856 0.1	66	12	
197	Chaperonin 20	26.669,9	5,19	Glyma15g1997 0.1	36	6	
199	Glyceraldehyde-3-phosphate dehydrogenase B subunit	48.432,0	6,46	Glyma08g0185 0.1	26	9	

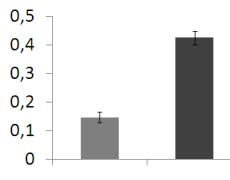
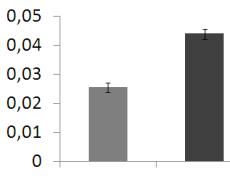
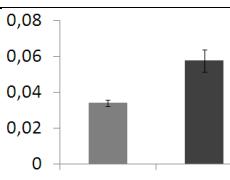
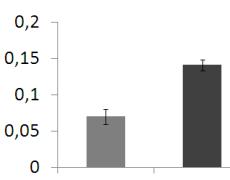
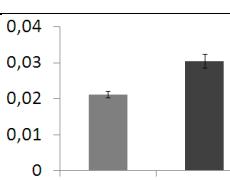
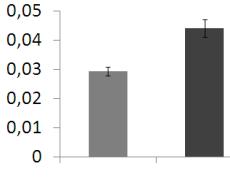
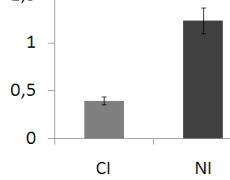
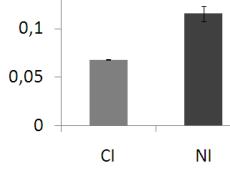
211	Glyceraldehyd e-3-phosphate dehydrogenase B subunit	48.432,0	6,45	Glyma08g0185 0.1	32	11	
116	NAD(P)-binding Rossmann-fold superfamily protein	32.287,8	5,49	Glyma07g0809 0.1	41	8	
96	Phosphomann omutase	28.019,6	6,05	Glyma18g4639 0.1	37	7	
55	Photosystem II subunit P-1	28.434,7	5,69	Glyma18g1441 0.1	31	6	
67	Photosystem II subunit P-1	28.017,9	5,94	Glyma02g4519 0.1	28	6	
16	TCP-1/cpn60 chaperonin family protein	62.841,5	5,01	Glyma08g1876 0.1	35	14	

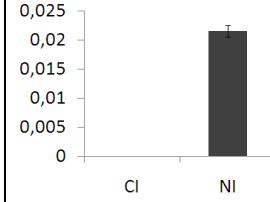
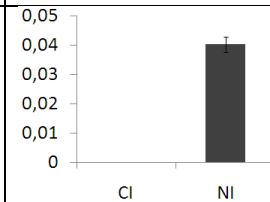
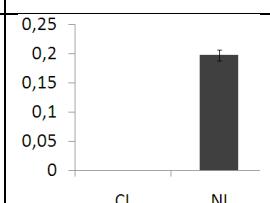
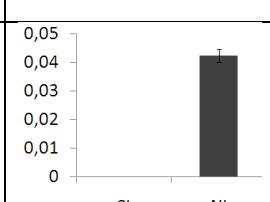
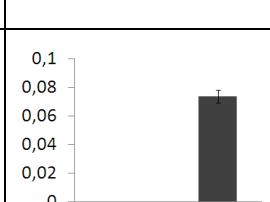
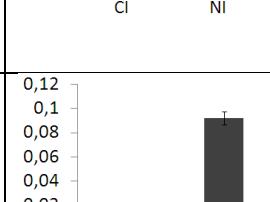
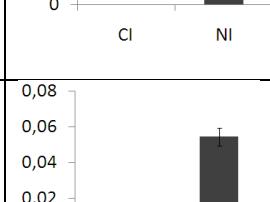
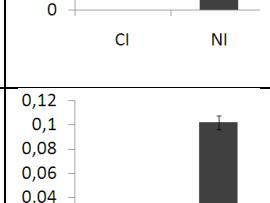
Supplementary Table S3. Differentially expressed proteins of the soybean leaves from BR 16 identified by mass spectrometry. The protein abundances are indicate as % volume average of the spots from three biological replicated generated by ImageMaster software. CI for irrigated control and NI for non-irrigated (-1,0 MPa).

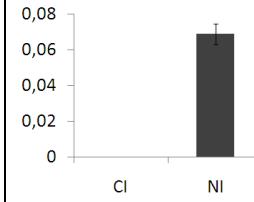
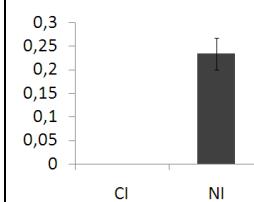
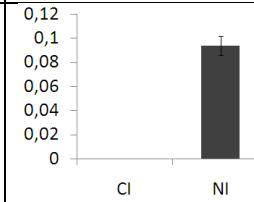
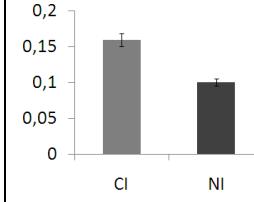
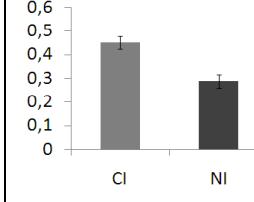
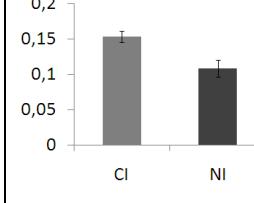
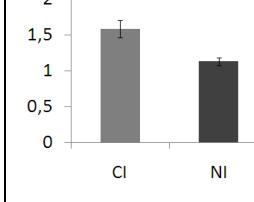
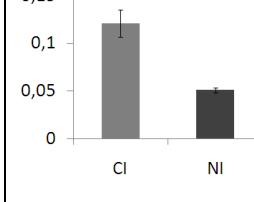
Spot ID	Protein	MM (Da)	PI	Accession Number	Coverage (%)	Unique Peptides	Protein Abundance % volumes ± SD*
520	Aldolase superfamily protein	38.421,4	6,11	Glyma14g014 70.1	47	12	

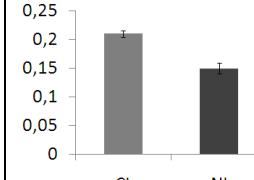
1013	Alkenal reductase	37.930,1	6,05	Glyma03g240 20.1	29	6	
467	Alpha/beta-Hydrolases superfamily protein	34.562,8	6,24	Glyma17g062 00.1	23	4	
1126	Chaperonin 20	26.669,9	5,54	Glyma15g199 70.1	45	9	
349	Chloroplastic drought-induced stress protein of 32 KD	33.170,7	5,27	Glyma14g399 40.1	25	4	
475	Chloroplastic drought-induced stress protein of 32 KD	33.170,7	5,17	Glyma14g399 40.1	26	7	
959	Copper/zinc superoxide dismutase 2	21.647,8	5,31	Glyma11g198 40.1	25	3	
440	D-ribulose-5-phosphate-3-epimerase	29.883,3	5,81	Glyma17g1099 0.5	26	4	
627	D-ribulose-5-phosphate-3-epimerase	29.883,3	5,98	Glyma17g1099 0.5	19	3	

961	eukaryotic translation initiation factor 5A3 isoform X1	17.469,9	5,44	Glyma04g329 50.3	37	4	
350	Glutathione peroxidase 6	18.503,6	5,68	Glyma01g428 40.1	28	6	
433	Glutathione S-transferase TAU 19	25.559,9	6,07	Glyma15g402 00.1	26	5	
353	Lactate/Malate dehydrogenase family protein	36.141,9	6,11	Glyma12g195 20.1	19	3	
579	Lipoamide dehydrogenase 2	52.887,5	6,76	Glyma17g042 10.1	23	7	
973	Matrix metalloproteinase	34.057,7	6,42	Glyma02g379 90.1	25	4	
489	NAD(P)-binding Rossmann-fold superfamily protein	34.960,2	5,83	Glyma11g294 60.1	25	7	
1015	O-acetylserine (thiol) lyase (OAS-TL) isoform A1	34.313,7	5,57	Glyma19g431 50.1	48	12	

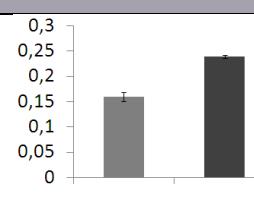
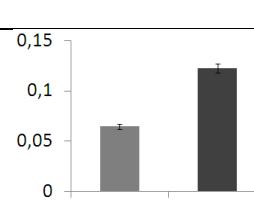
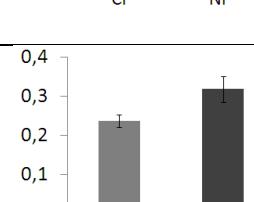
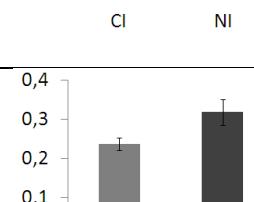
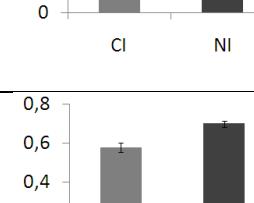
525	Oxidoreductase, zinc-binding dehydrogenase family protein	41.969,2	5,89	Glyma18g190 50.1	53	4	
365	Phosphoglycerate mutase, 2,3-bisphosphoglycerate-independent	60.869,6	5,61	Glyma09g406 90.1	15	5	
1075	Photosynthetic electron transfer C	24.187,0	5,61	Glyma12g325 80.1	14	3	
553	S-adenosylmethionine synthetase family protein	43.052,9	5,66	Glyma15g218 90.1	15	6	
583	Sugar isomerase (SIS) family protein	62.657,2	6,26	Glyma04g034 90.1	14	4	
952	Transcriptional coactivator/pterin dehydratase	28.602,2	5,36	Glyma10g227 10.2	17	3	
454	Triosephosphate isomerase	33.124,0	5,56	Glyma03g343 00.1	54	11	
458	Triosephosphate isomerase	33.124,0	5,83	Glyma03g343 00.1	27	5	

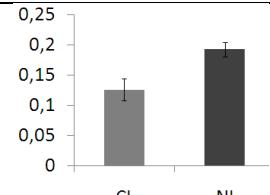
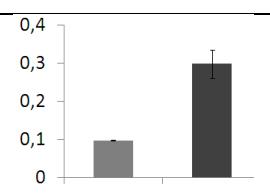
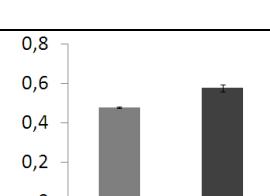
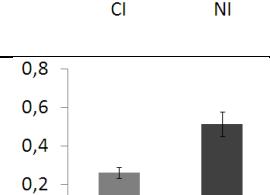
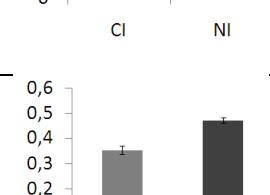
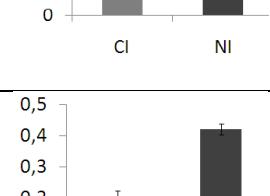
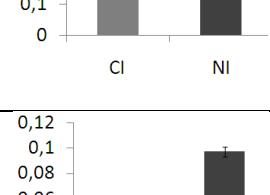
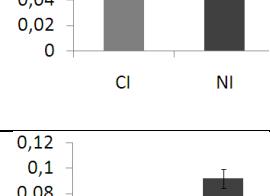
1039	3-ketoacyl-acyl Carrier protein synthase I	49.705,6	6,29	Glyma08g089 10.1	13	3	
1041	Alanine:glyoxylate aminotransferase	44.326,8	6,84	Glyma18g147 40.2	18	4	
979	Ascorbate peroxidase 4	37.752,3	5,71	Glyma02g371 60.1	38	9	
1003	Carbonic anhydrase 2	30.350,5	6,20	Glyma01g037 20.1	24	3	
986	Chloroplastic drought-induced stress protein of 32 KD	33.170,7	5,22	Glyma14g399 40.1	25	4	
1009	Cysteine synthase D1	34.565,4	5,43	Glyma10g301 40.1	17	3	
1051	Dehydratase family	64.116,5	5,41	Glyma13g278 10.1	15	5	
994	Gamma carbonic anhydrase 1	29.992,2	6,48	Glyma04g033 10.3	18	4	

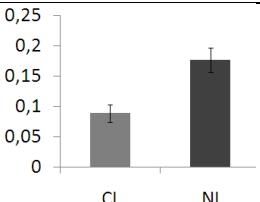
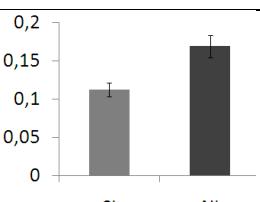
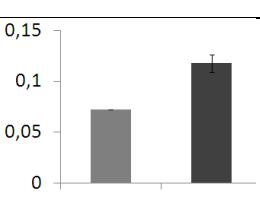
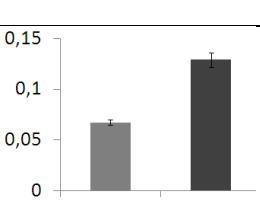
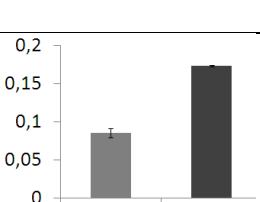
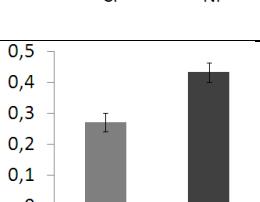
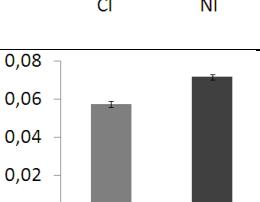
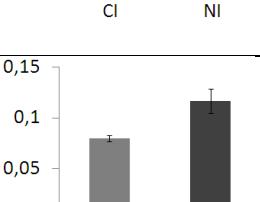
957	Mog1/PsbP/D UF1795-like photosystem II reaction Center PsbP family protein	27.566,1	5,57	Glyma04g420 10.2	14	3	
1010	NAD(P)- binding Rossmann- fold superfamily protein	35.127,5	5,51	Glyma18g065 10.1	47	8	
928	O- acetylserine (thiol) lyase B	41.648,6	5,36	Glyma02g156 40.1	43	11	
436	Carbonic anhydrase 1	35.445,0	5,76	Glyma19g010 50.10	16	3	
997	Carbonic anhydrase 1	35.445,0	6,59	Glyma19g010 50.10	36	7	
510	Chloroplast stem-loop binding protein of 41 kDa	42.237,7	6,34	Glyma19g415 40.2	11	3	
515	Fructose- bisphosphat e aldolase 2	42.952,7	5,93	Glyma11g118 70.1	15	5	
1060	Heat shock protein 70	71.089,6	5,10	Glyma12g069 10.1	34	5	

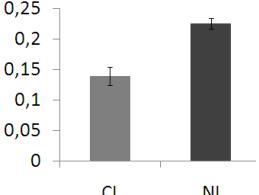
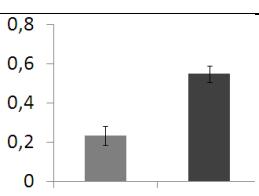
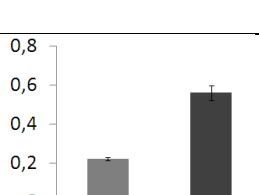
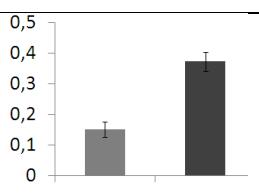
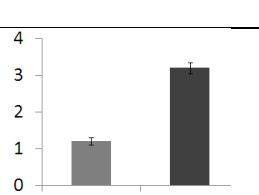
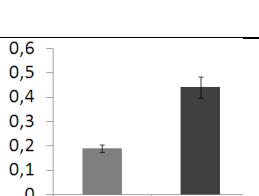
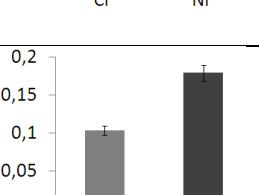
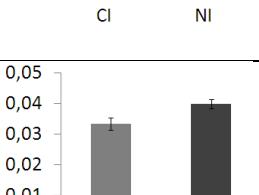
409	Photosynthetic electron transfer C	24.187,0	6,17	Glyma12g325 80.1	23	3	
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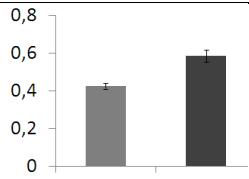
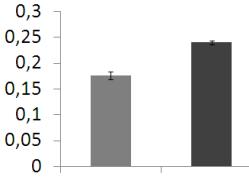
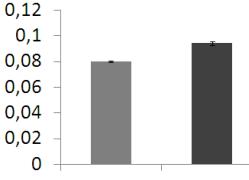
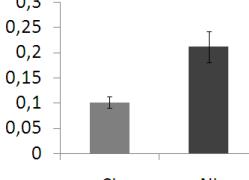
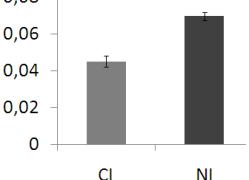
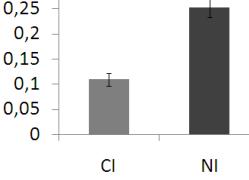
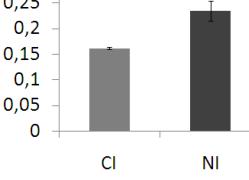
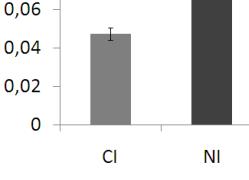
Supplementary Table S4. Differentially expressed phosphoproteins of the soybean leaves from Embrapa 48 identified by mass spectrometry. The protein abundances are indicate as % volume average of the spots from three biological replicated generated by *ImageMaster* software of the 2DE gels. CI for irrigated control and NI for non-irrigated (-1,0 MPa).

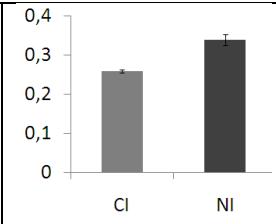
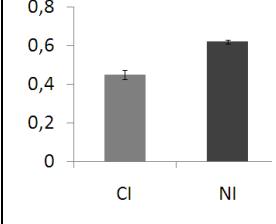
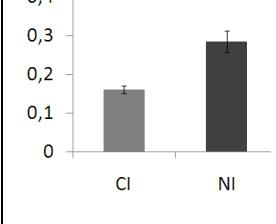
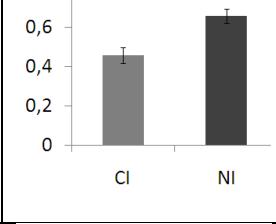
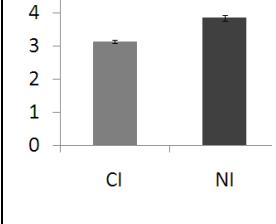
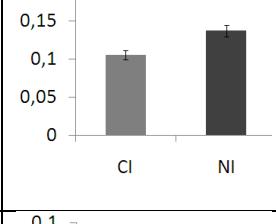
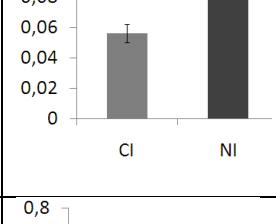
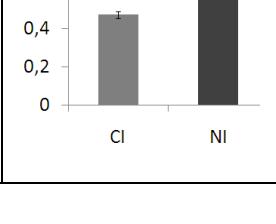
Spot ID	Protein	MM (Da)	PI	Glyma 1.1 Accession Number	Coverage (%)	Unique Peptides	Protein Abundance % volumes ± SD*
250	Alanine-2-oxoglutarate aminotransferase 2	53.524,9	5,76	Glyma01g03260.1	46	14	
148	Alkenal reductase	37.930,1	5,57	Glyma03g24020.1	57	14	
87	Ascorbate peroxidase 1	27.052,6	5,71	Glyma11g15680.5	28	5	
87	Ascorbate peroxidase 1	27.052,6	5,69	Glyma11g15680.5	28	5	
268	ATP synthase alpha/beta family protein	59.836,9	5,16	Glyma10g41330.1	48	17	

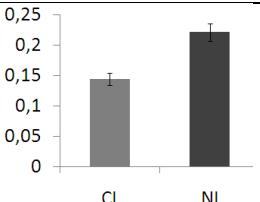
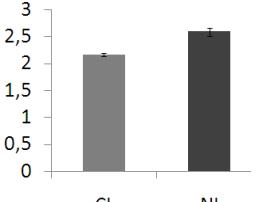
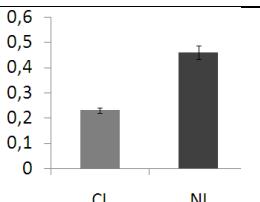
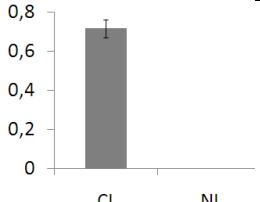
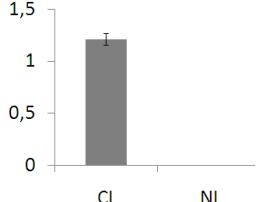
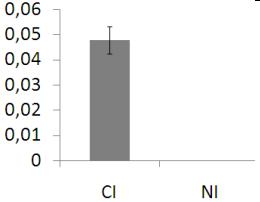
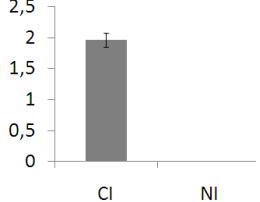
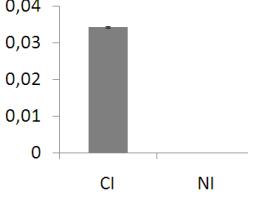
269	ATP synthase alpha/beta family protein	59.836,9	5,08	Glyma10g 41330.1	44	16	
282	ATP synthase subunit alpha	55.739,4	5,08	Glyma12g 36106.1	31	12	
93	Carbonic anhydrase 1	36.750,6	6,25	Glyma19g 01050.1	43	11	
672	Chaperonin 20	26.669,9	5,50	Glyma15g 19970.1	58	12	
63	Chaperonin 20	26.669,9	5,28	Glyma15g 19970.1	40	10	
327	Cobalamin-independant synthase family protein	84.284,5	6,37	Glyma16g 04240.1	40	22	
330	Cobalamin-independant synthase family protein	84.284,5	6,31	Glyma16g 04240.1	10	6	
331	Cobalamin-independant synthase family protein	84.284,5	6,26	Glyma16g 04240.1	10	5	

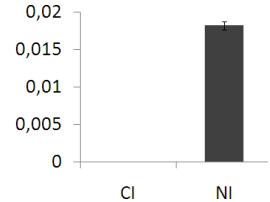
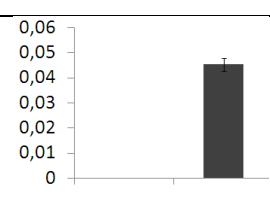
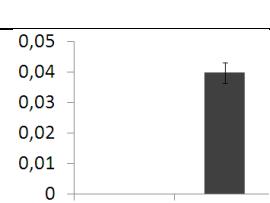
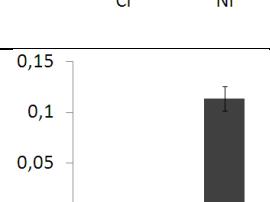
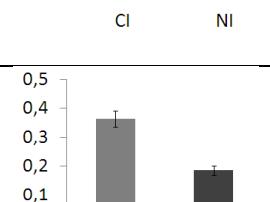
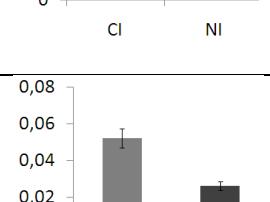
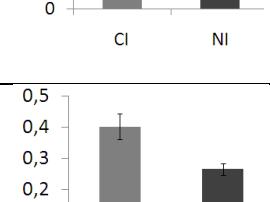
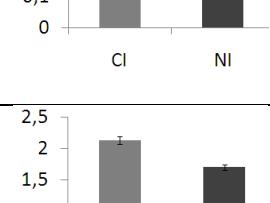
329	Cobalamin-independent synthase family protein	84.284,5	6,44	Glyma16g 04240.1	11	7	
342	Glycine decarboxylase P-protein 2	114.623, 1	6,60	Glyma17g 34690.1	21	17	
340	Glycine decarboxylase P-protein 2	114.623, 1	6,31	Glyma17g 34690.1	16	12	
829	Glycine decarboxylase P-protein 2	114.623, 1	6,82	Glyma17g 34690.1	21	16	
279	Myo-inositol-1-phosphate syntase 3	56.421,3	5,61	Glyma05g 31450.1	30	13	
138	NAD(P)-binding Rossmann-fold superfamily protein	34.960,2	5,79	Glyma11g 29460.1	29	9	
111	NAD(P)-binding Rossmann-fold superfamily protein	32.735,8	5,62	Glyma09g 39850.1	31	7	
153	NAD(P)-linked oxidoreductase superfamily protein	34.875,8	6,53	Glyma01g 24931.1	51	12	

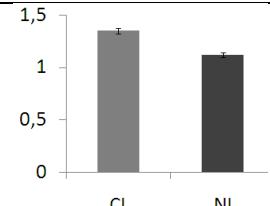
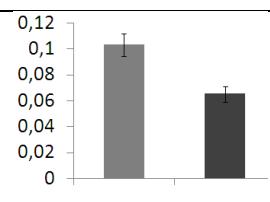
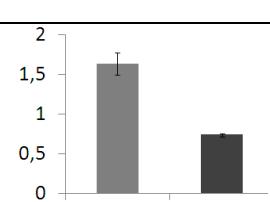
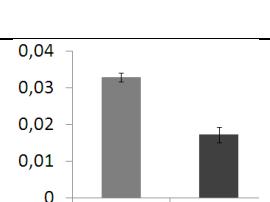
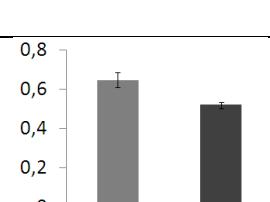
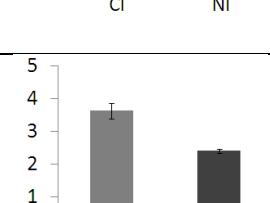
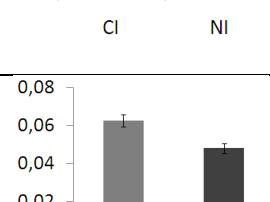
156	NAD(P)-linked oxidoreductase superfamily protein	36.090,4	6,69	Glyma16g 34570.1	25	9	
195	O-methyltransferase 1	40.920,6	5,82	Glyma12g 12230.1	41	11	
186	O-methyltransferase 1	41.510,4	6,24	Glyma06g 45043.1	32	3	
256	Phosphoglycerate kinase family protein	50.268,2	6,29	Glyma08g 17610.1	15	4	
258	Phosphoglycerate kinase family protein	50.268,2	6,17	Glyma08g 17610.1	12	3	
259	Phosphoglycerate kinase family protein	50.268,2	6,06	Glyma08g 17610.1	17	5	
266	Phosphoglycerate kinase family protein	50.268,2	5,98	Glyma08g 17610.1	11	3	
299	Phosphoglycerate mutase, 2,3-bisphosphoglycerate-independent	60.869,6	5,75	Glyma09g 40690.1	14	7	

120	Photosystem II subunit O-2	35.059,5	4,84	Glyma16g 25860.1	39	8	
70	Photosystem II subunit P-1	28.017,9	5,25	Glyma02g 45190.1	30	7	
5	Plastid-lipid associated protein PAP / fibrillin family protein	39.645,0	4,14	Glyma01g 01910.1	22	6	
698	Pyrophosphorylase 6	32.335,0	5,04	Glyma13g 32660.1	32	8	
212	Rubisco activase	53.938,4	5,28	Glyma18g 04081.1	33	11	
1	Stress responsive alpha-beta barrel domain protein	27.656,7	5,26	Glyma17g 05840.3	24	4	
322	Transketolase	80.228,0	5,66	Glyma10g 43990.1	14	7	
323	Transketolase	80.228,0	5,60	Glyma10g 43990.1	10	6	

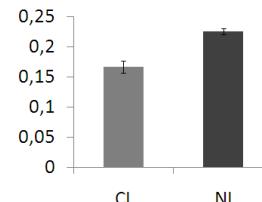
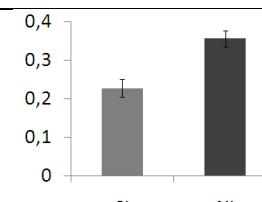
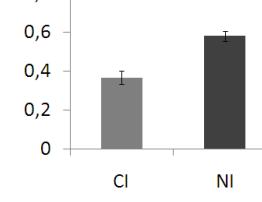
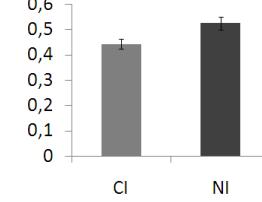
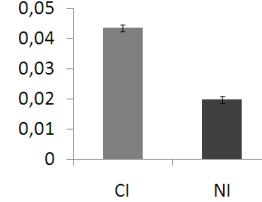
320	Transketolase	80.228,0	5,86	Glyma10g 43990.1	18	10	
318	Transketolase	80.228,0	5,94	Glyma10g 43990.1	15	8	
921	Transketolase	80.228,0	5,89	Glyma10g 43990.1	17	9	
316	Transketolase	80.228,0	5,80	Glyma10g 43990.1	18	10	
72	Triosephosphate isomerase	33.124,0	5,53	Glyma03g 34300.1	35	7	
80	Triosephosphate isomerase	27.196,9	5,98	Glyma15g 04290.1	55	11	
126	Uridylytransferase-related	33.070,8	4,43	Glyma15g 00560.1	33	8	
214	Phosphoribulokinase	45.270,9	4,95	Glyma01g 01370.1	32	10	

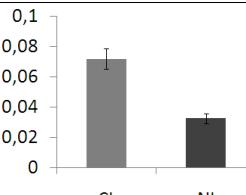
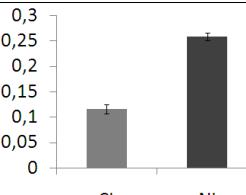
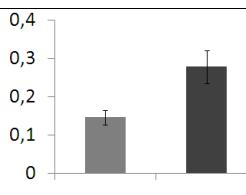
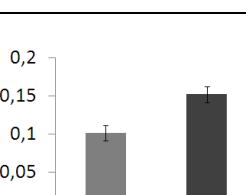
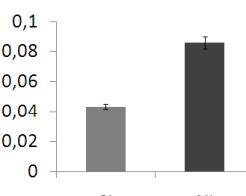
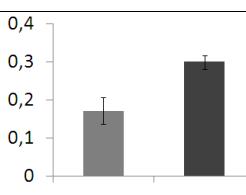
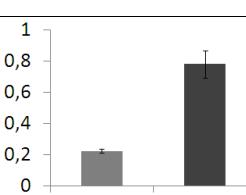
216	Phosphoribulo kinase	45.270,9	4,89	Glyma01g 01370.1	25	8	
219	Phosphoribulo kinase	45.270,9	5,06	Glyma01g 01370.1	28	8	
255	Phosphoglycerate kinase family protein	50.268,2	6,10	Glyma08g 17610.1	11	3	
895	Aldolase superfamily protein	38.421,4	6,49	Glyma14g 01470.1	39	10	
897	Aldolase-type TIM barrel family protein	40.795,8	6,95	Glyma15g 40140.1	60	16	
839	Carbonic anhydrase 1	36.750,6	6,05	Glyma19g 01050.1	32	8	
900	Hydroxypyruvate reductase	42.201,8	6,96	Glyma20g 24200.2	62	16	
837	Ribose 5-phosphate isomerase, type A protein	29.783,0	4,50	Glyma03g 40640.1	22	4	

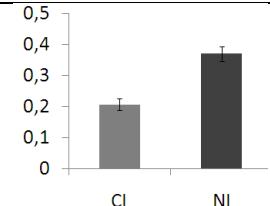
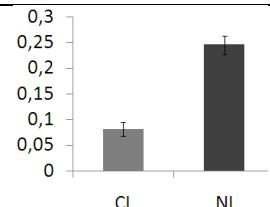
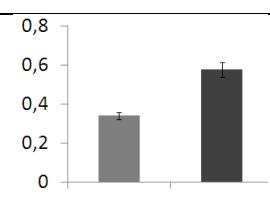
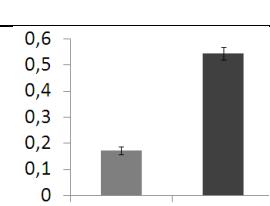
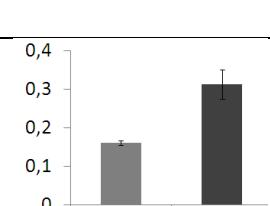
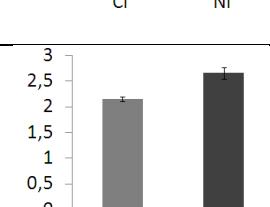
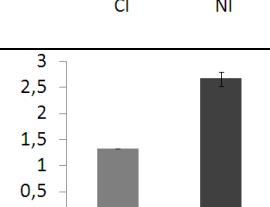
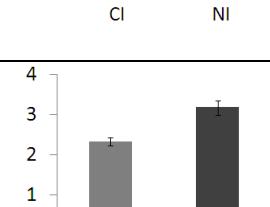
647	Cobalamin-independent synthase family protein	84.284,5	6,19	Glyma16g 04240.1	10	6	
805	Cobalamin-independent synthase family protein	84.284,5	6,51	Glyma16g 04240.1	10	5	
803	Cobalamin-independent synthase family protein	84.284,5	6,22	Glyma16g 04240.1	12	8	
720	Sedoheptulose-bisphosphatase	41.833,9	4,69	Glyma11g 34900.1	21	7	
128	6-phosphogluconate dehydrogenase family protein	34.935,9	6,96	Glyma05g 35880.1	25	5	
761	ATP synthase alpha/beta family protein	59.836,9	5,04	Glyma10g 41330.1	36	12	
177	Chloroplast stem-loop binding protein of 41 KDa	43.766,8	6,36	Glyma02g 16620.1	39	11	
178	Fructose-bisphosphate aldolase 2	42.952,7	5,88	Glyma11g 11870.1	44	14	

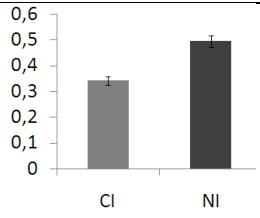
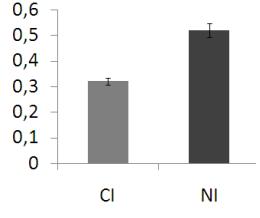
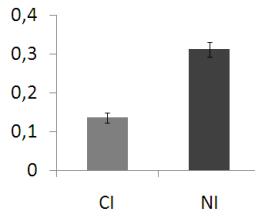
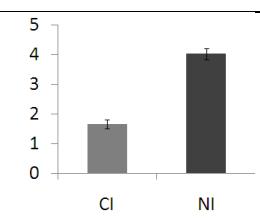
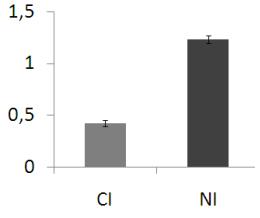
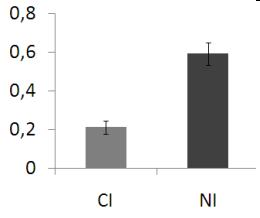
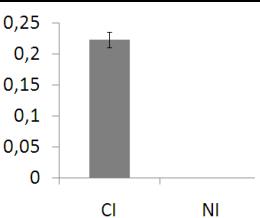
174	Fructose-bisphosphate aldolase 2	42.952,7	5,65	Glyma11g 11870.1	28	13	
224	Glutamate-1-semialdehyde 2,1-aminomutase 2	50.044,0	5,85	Glyma04g 00420.1	43	13	
904	Glycine cleavage T-protein family	44.338,2	6,97	Glyma07g 39190.1	43	14	
307	NAD(P)-binding Rossmann-fold superfamily protein	55.753,1	5,35	Glyma12g 05030.1	24	9	
222	Phosphoglycerate kinase family protein	50.268,2	5,59	Glyma08g 17610.1	44	14	
200	Phosphoglycerate kinase family protein	50.268,2	5,68	Glyma08g 17610.1	52	19	
319	Transketolase	80.228,0	6,03	Glyma10g 43990.1	17	9	

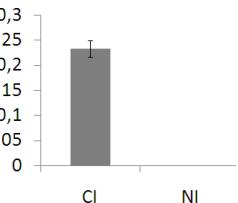
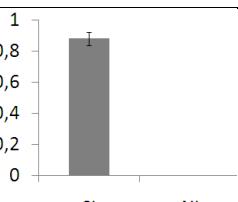
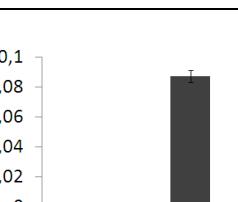
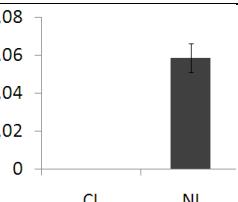
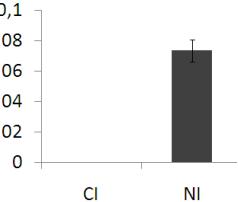
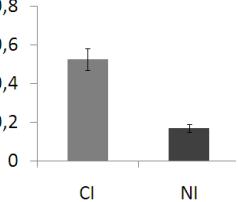
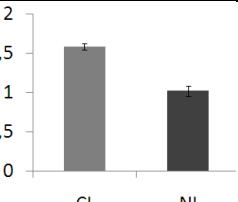
Supplementary Table S5. Differentially expressed phosphoproteins of the soybean leaves from BR 16 identified by mass spectrometry. The protein abundances are indicate as % volume average of the spots from three biological replicated generated by ImageMaster software of the 2DE gels. CI for irrigated control and NI for non-irrigated (-1,0 MPa) .

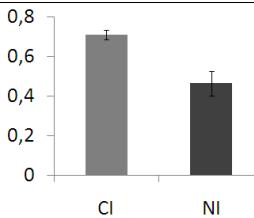
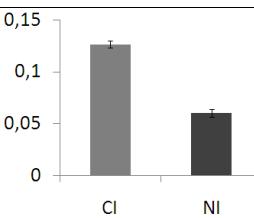
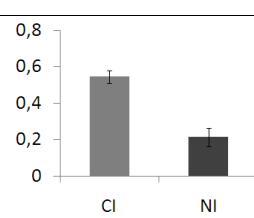
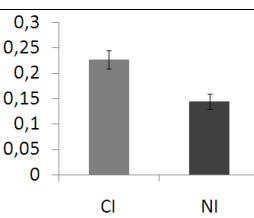
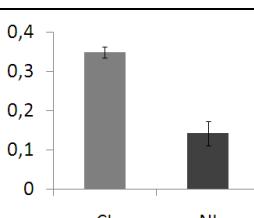
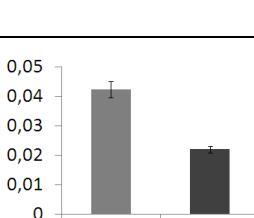
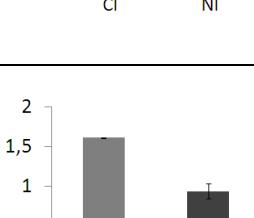
Spot ID	Protein	MM (Da)	PI	Glyma 1.1 Accession Number	Coverage (%)	Unique Peptides	Protein Abundance % volumes ± SD*
557	Alanine-2-oxoglutarate aminotransferase 2	53.524,9	5,81	Glyma01g03260.1	25	8	
459	Ascorbate peroxidase 1	27.052,6	5,76	Glyma11g15680.5	20	5	
468	Carbonic anhydrase 1	35.445,0	7,00	Glyma19g01050.10	31	10	
441	D-ribulose-5-phosphate-3-epimerase	29.883,3	6,14	Glyma17g10990.5	33	5	
1211	Glycine decarboxylase P-protein 2	114.623,1	6,53	Glyma17g34690.1	9	4	

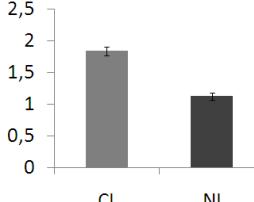
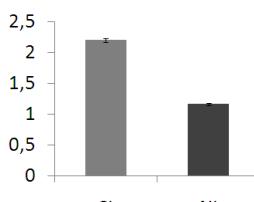
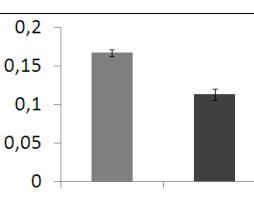
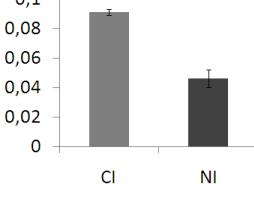
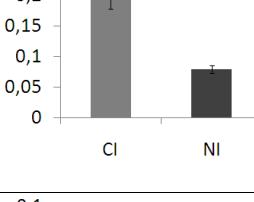
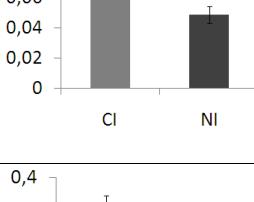
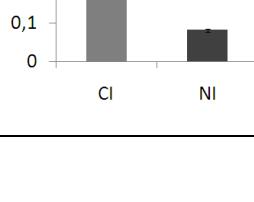
1213	Glycine decarboxylase P-protein 2	114.623,1	6,60	Glyma17g34 690.1	14	10	
600	Heat shock cognate protein 70-1	71.501,7	5,05	Glyma19g35 560.1	36	16	
599	Heat shock cognate protein 70-1	71.501,7	4,99	Glyma19g35 560.1	20	6	
493	NAD(P)-linked oxidoreductase superfamily protein	35.210,4	6,39	Glyma03g11 610.1	34	9	
1054	NADP-malic enzyme 4	65.028,0	6,17	Glyma01g01 180.1	38	13	
521	O-methyltransferase 1	41.510,4	6,29	Glyma06g45 043.1	26	6	
531	Phosphoglycerate kinase family protein	50.067,9	5,56	Glyma15g41 540.1	34	10	

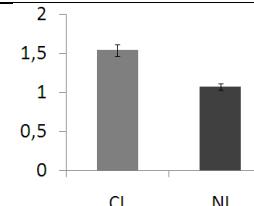
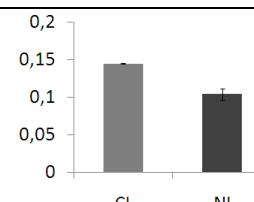
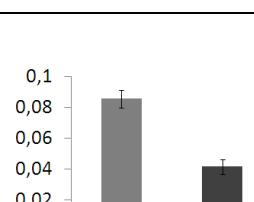
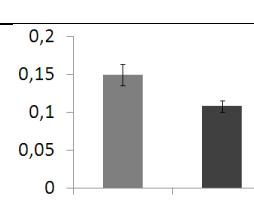
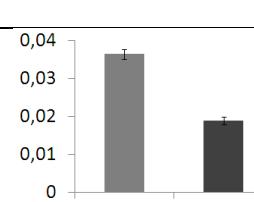
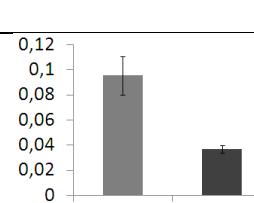
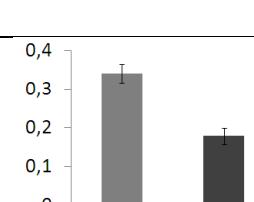
529	Phospho glycerate kinase family protein	50.067,9	5,68	Glyma15g41 540.1	22	7	
533	Phospho glycerate kinase family protein	50.067,9	5,39	Glyma15g41 540.1	39	11	
1166	Phospho glycerate kinase family protein	50.067,9	5,43	Glyma15g41 540.1	29	10	
542	Phosphor ibulokina se	45.270,9	4,95	Glyma01g01 370.1	39	10	
543	Phosphor ibulokina se	45.270,9	4,85	Glyma01g01 370.1	33	8	
544	Phosphor ibulokina se	45.270,9	5,05	Glyma01g01 370.1	47	12	
486	Photosyst em II subunit O-2	34.628,9	5,13	Glyma02g06 830.1	13	4	
488	Photosyst em II subunit O-2	34.628,9	4,99	Glyma02g06 830.1	28	3	

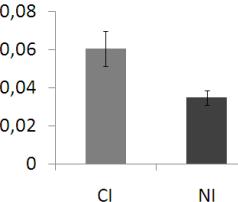
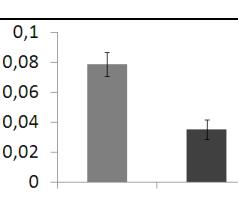
1155	Photosystem II subunit O-2	34.628,9	5,42	Glyma02g06830.1	16	4	
368	Photosystem II subunit P-1	28.017,9	6,99	Glyma02g45190.1	19	3	
449	Ribose 5-phosphate isomerase, type A protein	29.783,0	4,59	Glyma03g40640.1	47	7	
444	Triosephosphate isomerase	33.124,0	5,61	Glyma03g34300.1	37	7	
454	Triosephosphate isomerase	33.124,0	5,56	Glyma03g34300.1	54	11	
464	Triosephosphate isomerase	33.124,0	5,51	Glyma03g34300.1	27	6	
1090	Lactate/Malate dehydrogenase family protein	35.467,6	6,22	Glyma02g00810.1	18	3	

1089	Lactate/ Malate dehydrogenase family protein	35.467,6	6,21	Glyma02g00 810.1	22	4	
485	Photosystem II subunit O-2	34.628,9	5,33	Glyma02g06 830.1	19	5	
981	Stress responsive alpha- beta barrel domain protein	27.656,7	5,01	Glyma17g05 840.3	18	3	
1046	TCP- 1/cpn60 chaperon in family protein	62.841,5	5,30	Glyma08g18 760.1	23	9	
1047	TCP- 1/cpn60 chaperon in family protein	62.841,5	5,23	Glyma08g18 760.1	39	15	
548	1-deoxy- D- xylulose 5- phosphate reductoisomerase	50.541,7	5,66	Glyma16g10 880.1	23	8	
571	ATP synthase alpha/beta family protein	59.836,9	5,49	Glyma10g41 330.1	26	7	

352	ATP synthase alpha/beta family protein	59.836,9	5,41	Glyma10g41 330.1	35	12	
1183	ATP synthase alpha/beta beta family protein	59.836,9	5,49	Glyma10g41 330.1	39	13	
469	Carbonic anhydrase 1	35.445,0	6,63	Glyma19g01 050.10	32	7	
586	Chaperonin-60 alpha	63.626,1	4,81	Glyma11g20 180.1	43	18	
511	Chloroplast stem-loop binding protein of 41KDa	43.766,8	6,46	Glyma02g16 620.1	23	4	
400	Copper/zinc superoxide dismutase 2	21.647,8	5,30	Glyma11g19 840.1	25	4	
569	Cytosolic NADP+-dependent isocitrate dehydrogenase	46.081,5	6,23	Glyma02g40 820.1	16	5	

515	Fructose-bisphosphate aldolase 2	42.952,7	5,93	Glyma11g11 870.1	44	14	
623	Glyceraldehyde 3-phosphate dehydrogenase A subunit 2	43.202,5	6,59	Glyma16g04 940.1	21	5	
619	Glycine decarboxylase P-protein 2	114.623,1	6,84	Glyma17g34 690.1	17	10	
620	Glycine decarboxylase P-protein 2	114.623,1	6,64	Glyma17g34 690.1	14	8	
621	Glycine decarboxylase P-protein 2	114.623,1	6,84	Glyma17g34 690.1	10	6	
572	Ketol-acid reductoisomerase	63.385,9	6,33	Glyma12g33 760.1	6	3	
579	Lipoamide dehydrogenase 2	52.887,5	6,72	Glyma17g04 210.1	23	7	

546	O-methyltransferase 1	40.920,6	5,83	Glyma12g12 230.1	30	3	
622	Photosystem II subunit P-1	28.017,9	5,99	Glyma02g45 190.1	28	6	
536	Plastid-lipid associated protein PAP / fibrilin family protein	39.645,0	4,09	Glyma01g01 910.1	18	5	
418	Rotamase CYP 4	29.017,0	5,03	Glyma10g27 990.1	16	3	
1092	Transketolase	80.080,0	5,78	Glyma20g38 720.1	6	3	
1082	Transketolase	80.080,0	5,75	Glyma20g38 720.1	10	5	
607	Transketolase	80.080,0	5,99	Glyma20g38 720.1	10	5	

1201	Transketolase	80.080.0	5,95	Glyma20g38720.1	13	6	
462	Triosephosphate isomerase	27.196,9	6,43	Glyma15g04290.1	72	13	

Supplementary Table S6: Phosphorylated sites predicted *in silico* to the protein sequences of BR 16, stained as phosphoprotein in 2DE gels, and present in plant phosphoprotein database P3DB.

Spot ID	Phosphoprotein	Acesso	Number of Predict Phosphorylated Sites Over 70% specificity	Number of Predict Phosphorylated Sites Over 95% specificity	Plant species and detected phosphorylated sites Present Plant Databases P3DB
444	Triosephosphate isomerase	Glyma03g34300.1	4	1	<i>Arabidopsis thaliana</i> – 1 (1 proteína)
441	D-ribulose-5-phosphate-3-epimerase	Glyma17g10990.5	11	1	-
469	Carbonic anhydrase 1	Glyma19g01050.10	26	3	<i>Arabidopsis thaliana</i> – 8 (1 proteínas)
462	Triosephosphate isomerase	Glyma15g04290.1	2	0	<i>Arabidopsis thaliana</i> – 1 (1 proteína)
579	Lipoamide dehydrogenase 2	Glyma17g04210.1	9	0	<i>Arabidopsis thaliana</i> – 2 e 2 (2 proteínas)
622	Photosystem II subunit P-1	Glyma02g45190.1	14	3	<i>Arabidopsis thaliana</i> – 5 (1 proteína)

623	Glyceraldehyde 3-phosphate dehydrogenase A subunit 2	Glyma16g04940.1	13	0	<i>Arabidopsis thaliana</i> – 6 (1 proteína) <i>Medicago truncatula</i> – 4 (1 proteína)
400	Copper/zinc superoxide dismutase 2	Glyma11g19840.1	11	0	-
542	Phosphoribulokinase	Glyma01g01370.1	7	1	<i>Arabidopsis thaliana</i> – 1 e 5 (2 proteínas) <i>Medicago truncatula</i> – 1, 1 e 6 (3 proteínas)
543	Phosphoribulokinase	Glyma01g01370.1	7	1	<i>Arabidopsis thaliana</i> – 1 e 5 (2 proteínas) <i>Medicago truncatula</i> – 1, 1 e 6 (3 proteínas)
544	Phosphoribulokinase	Glyma01g01370.1	7	1	<i>Arabidopsis thaliana</i> – 1 e 5 (2 proteínas) <i>Medicago truncatula</i> – 1, 1 e 6 (3 proteínas)
511	Chloroplast stem-loop binding protein of 41KDa	Glyma02g16620.1	14	1	<i>Arabidopsis thaliana</i> – 2 (1 proteína)
571	ATP synthase alpha/beta family protein	Glyma10g41330.1	22	1	<i>Arabidopsis thaliana</i> – 1, 1 e 1 (3 proteínas) <i>Medicago truncatula</i> – 10 (1 proteína)

352	ATP synthase alpha/beta family protein	Glyma10g41330.1	22	1	<i>Arabidopsis thaliana</i> – 1, 1 e 1 (3 proteínas) <i>Medicago truncatula</i> – 10 (1 proteína)
118 3	ATP synthase alpha/beta family protein	Glyma10g41330.1	22	1	<i>Arabidopsis thaliana</i> – 1, 1 e 1 (3 proteínas) <i>Medicago truncatula</i> – 10 (1 proteína)
515	Fructose-bisphosphate aldolase 2	Glyma11g11870.1	13	1	-
531	Phosphoglycerate kinase family protein	Glyma15g41540.1	18	4	<i>Medicago truncatula</i> – 8 (1 proteína)
569	Cytosolic NADP ⁺ -dependent isocitrate dehydrogenase	Glyma02g40820.1	10	0	<i>Medicago truncatula</i> – 3 (1 proteína)
546	O-methyltransferase 1	Glyma12g12230.1	3	0	<i>Arabidopsis thaliana</i> – 1 (1 proteína) <i>Medicago truncatula</i> – 1 e 1 (2 proteínas)
486	Photosystem II subunit O-2	Glyma02g06830.1	16	0	-
488	Photosystem II subunit O-2	Glyma02g06830.1	16	0	-
454	Triosephosphate isomerase	Glyma03g34300.1	4	1	<i>Arabidopsis thaliana</i> – 1 (1 proteína)

464	Triosephosphate isomerase	Glyma03g34300.1	4	1	<i>Arabidopsis thaliana</i> – 1 (1 proteína)
521	O-methyltransferase 1	Glyma06g45043.1	4	0	<i>Arabidopsis thaliana</i> – 1 (1 proteína) <i>Medicago truncatula</i> – 1 e 1 (2 proteínas)
572	Ketol-acid reductoisomerase	Glyma12g33760.1	16	0	<i>Medicago truncatula</i> – 2 (1 proteína)
548	1-deoxy-D-xylulose 5-phosphate reductoisomerase	Glyma16g10880.1	16	3	<i>Medicago truncatula</i> – 1 (1 proteína)
109 2	Transketolase	Glyma20g38720.1	20	3	<i>Arabidopsis thaliana</i> – 1, 1, 2 e 5 (4 proteínas) <i>Medicago truncatula</i> – 1 e 5 (2 proteínas)
108 2	Transketolase	Glyma20g38720.1	20	3	<i>Arabidopsis thaliana</i> – 1, 1, 2 e 5 (4 proteínas) <i>Medicago truncatula</i> – 1 e 5 (2 proteínas)
607	Transketolase	Glyma20g38720.1	20	3	<i>Arabidopsis thaliana</i> – 1, 1, 2 e 5 (4 proteínas) <i>Medicago truncatula</i> – 1 e 5 (2 proteínas)
418	Rotamase CYP 4	Glyma10g27990.1	1	6	-

109 0	Lactate/Malate dehydrogenase family protein	Glyma02g00810.1	1	0	<i>Arabidopsis thaliana</i> – 1, 1, 4 e 5 (4 proteínas) <i>Glycine max</i> – 1 (1 proteína) <i>Medicago truncatula</i> – 4, 6 e 7 (3 proteínas)
108 9	Lactate/Malate dehydrogenase family protein	Glyma02g00810.1	1	0	<i>Arabidopsis thaliana</i> – 1, 1, 4 e 5 (4 proteínas) <i>Glycine max</i> – 1 (1 proteína) <i>Medicago truncatula</i> – 4, 6 e 7 (3 proteínas)
120 1	Transketolase	Glyma20g38720.1	20	3	<i>Arabidopsis thaliana</i> – 1, 1, 2 e 5 (4 proteínas) <i>Medicago truncatula</i> – 1 e 5 (2 proteínas)
619	Glycine decarboxylase P-protein 2	Glyma17g34690.1	23	2	-
620	Glycine decarboxylase P-protein 2	Glyma17g34690.1	23	2	-
621	Glycine decarboxylase P-protein 2	Glyma17g34690.1	23	2	-
121 1	Glycine decarboxylase P-protein 2	Glyma17g34690.1	23	2	-

121 3	Glycine decarboxylase P- protein 2	Glyma17g34690.1	23	2	-
105 4	NADP-malic enzyme 4	Glyma01g01180.1	12	2	<i>Glycine max</i> – 1 (1 proteína)
104 6	TCP-1/cpn60 chaperonin family protein	Glyma08g18760.1	13	0	<i>Arabidopsis</i> <i>thaliana</i> – 1, 1, 1 e 1 (4 proteínas) <i>Glycine max</i> – 1 (1 proteína) <i>Medicago</i> <i>truncatula</i> – 1, 1, 1 e 1 (4 proteínas)
104 7	TCP-1/cpn60 chaperonin family protein	Glyma08g18760.1	13	0	<i>Arabidopsis</i> <i>thaliana</i> – 1, 1, 1 e 1 (4 proteínas) <i>Glycine max</i> – 1 (1 proteína) <i>Medicago</i> <i>truncatula</i> – 1, 1, 1 e 1 (4 proteínas)
600	Heat shock cognate protein 70-1	Glyma19g35560.1	17	1	<i>Arabidopsis</i> <i>thaliana</i> – 2 (1 proteína) <i>Medicago</i> <i>truncatula</i> – 2, 2 e 8 (3 proteínas)
599	Heat shock cognate protein 70-1	Glyma19g35560.1	17	1	<i>Arabidopsis</i> <i>thaliana</i> – 2 (1 proteína) <i>Medicago</i> <i>truncatula</i> – 2, 2 e 8 (3 proteínas)

586	Chaperonin-60 alpha	Glyma11g20180.1	20	3	<i>Arabidopsis thaliana</i> – 2 (1 proteína) <i>Glycine max</i> – 1 (1 proteína) <i>Medicago truncatula</i> – 2 (1 proteína)
485	Photosystem II subunit O-2	Glyma02g06830.1	16	0	-
981	Stress responsive alpha-beta barrel domain protein	Glyma17g05840.3	9	1	<i>Arabidopsis thaliana</i> – 2 (1 proteína)
529	Phosphoglycerate kinase family protein	Glyma15g41540.1	18	4	<i>Medicago truncatula</i> – 8 (1 proteína)
368	Photosystem II subunit P-1	Glyma02g45190.1	14	3	<i>Arabidopsis thaliana</i> – 5 (1 proteína)
536	Plastid-lipid associated protein PAP / fibrilin family protein	Glyma01g01910.1	28	9	<i>Arabidopsis thaliana</i> – 1 e 3 (2 proteínas)
449	Ribose 5-phosphate isomerase, type A protein	Glyma03g40640.1	10	2	<i>Arabidopsis thaliana</i> – 1 (1 proteína) <i>Medicago truncatula</i> – 1 e 2 (2 proteínas)
115 5	Photosystem II subunit O-2	Glyma02g06830.1	16	0	-
533	Phosphoglycerate kinase family protein	Glyma15g41540.1	18	4	<i>Medicago truncatula</i> – 8 (1 proteína)
116 6	Phosphoglycerate kinase family protein	Glyma15g41540.1	18	4	<i>Medicago truncatula</i> – 8 (1 proteína)

557	Alanine-2-oxoglutarate aminotransferase 2	Glyma01g03260.1	8	0	<i>Arabidopsis thaliana</i> – 5 (1 proteína)
459	Ascorbate peroxidase 1	Glyma11g15680.5	5	0	<i>Medicago truncatula</i> – 5 (1 proteína)
493	NAD(P)-linked oxidoreductase superfamily protein	Glyma03g11610.1	3	0	<i>Arabidopsis thaliana</i> – 1 (1 proteína) <i>Medicago truncatula</i> – 2, 2, 2, 2, 2, 3, 5 e 6 (9 proteínas)
468	Carbonic anhydrase 1	Glyma19g01050.10	26	3	<i>Arabidopsis thaliana</i> – 8 (1 proteína)

Supplementary Table S7: Phosphorylated sites predicted *in silico* to the protein sequences of Embrapa 48, stained as phosphoprotein in 2DE gels, and present in plant phosphoprotein database P3DB

Spot ID	Phosphoprotein	Accession Number	Number of Predict Phosphorylated Sites Over 70% specificity	Number of Predict Phosphorylated Sites Over 95% specificity	Plant species and detected phosphorylated sites Present in the Plant Databases P3DB
319	Transketolase	Glyma10g43990.1	23	1	<i>Arabidopsis thaliana</i> – 1, 1, 2 e 5 (4 proteínas) <i>Medicago truncatula</i> – 1 e 5 (2 proteínas)
320	Transketolase	Glyma10g43990.1	23	1	<i>Arabidopsis thaliana</i> – 1, 1, 2 e 5 (4 proteínas) <i>Medicago truncatula</i> – 1 e 5 (2 proteínas)
318	Transketolase	Glyma10g43990.1	23	1	<i>Arabidopsis thaliana</i> – 1, 1, 2 e 5 (4 proteínas) <i>Medicago truncatula</i> – 1 e 5 (2 proteínas)

921	Transketolase	Glyma10g4 3990.1	23	1	<i>Arabidopsis thaliana</i> – 1, 1, 2 e 5 (4 proteínas) <i>Medicago truncatula</i> – 1 e 5 (2 proteínas)
316	Transketolase	Glyma10g4 3990.1	23	1	<i>Arabidopsis thaliana</i> – 1, 1, 2 e 5 (4 proteínas) <i>Medicago truncatula</i> – 1 e 5 (2 proteínas)
72	Triosephosphate isomerase	Glyma03g3 4300.1	4	1	<i>Arabidopsis thaliana</i> – 1 (1 proteína)
672	Chaperonin 20	Glyma15g1 9970.1	6	0	<i>Arabidopsis thaliana</i> – 1 (1 proteína)
279	Myo-inositol-1-phosphate syntase 3	Glyma05g3 1450.1	7	0	-
222	Phosphoglycerate kinase family protein	Glyma08g1 7610.1	16	4	<i>Medicago truncatula</i> – 8 (1 proteína)
200	Phosphoglycerate kinase family protein	Glyma08g1 7610.1	16	4	<i>Medicago truncatula</i> – 8 (1 proteína)
224	Glutamate-1-semialdehyde 2,1-aminomutase 2	Glyma04g0 0420.1	14	1	<i>Medicago truncatula</i> – 3 (1 proteína)
895	Aldolase superfamily protein	Glyma14g0 1470.1	10	1	<i>Arabidopsis thaliana</i> – 3, 4, 4, 4, 4, 7 e 7 (7 proteínas) <i>Medicago truncatula</i> – 1, 1 e 27 (3 proteínas) <i>Glycine max</i> – 1 e 1 (2 proteínas)
153	NAD(P)-linked oxidoreductase superfamily protein	Glyma01g2 4931.1	4	0	<i>Arabidopsis thaliana</i> – 1 (1 proteína) <i>Medicago truncatula</i> – 2, 2, 2, 2, 2, 2, 3, 5 e 6 (9 proteínas)
80	Triosephosphate isomerase	Glyma15g0 4290.1	2	0	<i>Arabidopsis thaliana</i> – 1 (1 proteína)

138	NAD(P)-binding Rossmann-fold superfamily protein	Glyma11g2 9460.1	4	0	<i>Arabidopsis thaliana</i> – 0, 1, 1, 3, 3, 4, 4, 5, 5, 6 e 9 (12 proteínas) <i>Medicago truncatula</i> – 1, 1, 1, 1, 1, 1, 2, 4 e 4 (10 proteínas) <i>Glycine max</i> – 1 e 1 (2 proteínas)
268	ATP synthase alpha/beta family protein	Glyma10g4 1330.1	22	1	<i>Arabidopsis thaliana</i> – 1, 1 e 1 (3 proteínas) <i>Medicago truncatula</i> – 10 (1 proteína)
269	ATP synthase alpha/beta family protein	Glyma10g4 1330.1	22	1	<i>Arabidopsis thaliana</i> – 1, 1 e 1 (3 proteínas) <i>Medicago truncatula</i> – 10 (1 proteína)
126	Uridylytransferase-related	Glyma15g0 0560.1	13	2	-
5	Plastid-lipid associated protein PAP / fibrillin family protein	Glyma01g0 1910.1	28	9	<i>Arabidopsis thaliana</i> – 1 e 3 (2 proteínas)
720	Sedoheptulose-bisphosphatase	Glyma11g3 4900.1	20	2	<i>Medicago truncatula</i> – 1 (1 proteína)
178	Fructose-bisphosphate aldolase 2	Glyma11g1 1870.1	13	1	-
174	Fructose-bisphosphate aldolase 2	Glyma11g1 1870.1	13	1	-
195	O-methyltransferase 1	Glyma12g1 2230.1	3	0	<i>Arabidopsis thaliana</i> – 1 (1 proteína) <i>Medicago truncatula</i> – 1 e 1 (2 proteínas)
87	Ascorbate peroxidase 1	Glyma11g1 5680.5	5	0	<i>Medicago truncatula</i> – 5 (1 proteína)

111	NAD(P)-binding Rossmann-fold superfamily protein	Glyma09g39850.1	3	0	<i>Arabidopsis thaliana</i> – 0, 1, 1, 3, 3, 4, 4, 5, 5, 6 e 9 (12 proteínas) <i>Medicago truncatula</i> – 1, 1, 1, 1, 1, 1, 2, 4 e 4 (10 proteínas) <i>Glycine max</i> – 1 e 1 (2 proteínas)
177	Chloroplast stem-loop binding protein of 41 KDa	Glyma02g16620.1	14	1	<i>Arabidopsis thaliana</i> – 2 (1 proteína)
900	Hydroxypyruvate reductase	Glyma20g24200.2	5	0	-
897	Aldolase-type TIM barrel family protein	Glyma15g40140.1	3	0	<i>Medicago truncatula</i> – 2 e 9 (2 proteínas)
904	Glycine cleavage T-protein family	Glyma07g39190.1	8	1	-
327	Cobalamin-independant synthase family protein	Glyma16g04240.1	10	1	<i>Arabidopsis thaliana</i> – 2 e 2 (2 proteínas) <i>Brassica napus</i> – 2 (1 proteína) <i>Glycine max</i> – 1 (1 proteína) <i>Medicago truncatula</i> – 5 e 10 (2 proteínas)
647	Cobalamin-independant synthase family protein	Glyma16g04240.1	10	1	<i>Arabidopsis thaliana</i> – 2 e 2 (2 proteínas) <i>Brassica napus</i> – 2 (1 proteína) <i>Glycine max</i> – 1 (1 proteína) <i>Medicago truncatula</i> – 5 e 10 (2 proteínas)
250	Alanine-2-oxoglutarate aminotransferase 2	Glyma01g03260.1	8	0	-

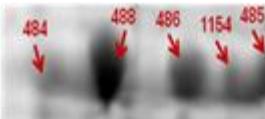
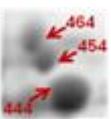
186	O-methyltransferase 1	Glyma06g4 5043.1	4	0	<i>Arabidopsis thaliana</i> – 1 (1 proteína) <i>Medicago truncatula</i> – 1 e 1 (2 proteínas)
63	Chaperonin 20	Glyma15g1 9970.1	6	0	<i>Arabidopsis thaliana</i> – 1 (1 proteína)
70	Photosystem II subunit P-1	Glyma02g4 5190.1	14	3	<i>Arabidopsis thaliana</i> – 5 (1 proteína)
1	Stress responsive alpha-beta barrel domain protein	Glyma17g0 5840.3	9	1	<i>Arabidopsis thaliana</i> – 1 (1 proteína)
87	Ascorbate peroxidase 1	Glyma11g1 5680.5	5	0	<i>Medicago truncatula</i> – 5 (1 proteína)
342	Glycine decarboxylase P-protein 2	Glyma17g3 4690.1	23	2	-
156	NAD(P)-linked oxidoreductase superfamily protein	Glyma16g3 4570.1	1	0	<i>Arabidopsis thaliana</i> – 1 (1 proteína) <i>Medicago truncatula</i> – 2, 2, 2, 2, 2, 2, 3, 5 e 6 (9 proteínas)
93	Carbonic anhydrase 1	Glyma19g0 1050.1	25	3	<i>Arabidopsis thaliana</i> – 8 (1 proteína)
340	Glycine decarboxylase P-protein 2	Glyma17g3 4690.1	23	2	-
829	Glycine decarboxylase P-protein 2	Glyma17g3 4690.1	23	2	-
330	Cobalamin-independant synthase family protein	Glyma16g0 4240.1	10	1	<i>Arabidopsis thaliana</i> – 2 e 2 (2 proteínas) <i>Brassica napus</i> – 2 (1 proteína) <i>Glycine max</i> – 1 (1 proteína) <i>Medicago truncatula</i> – 5 e 10 (2 proteínas)

331	Cobalamin-independent synthase family protein	Glyma16g04240.1	10	1	<i>Arabidopsis thaliana</i> – 2 e 2 (2 proteínas) <i>Brassica napus</i> – 2 (1 proteína) <i>Glycine max</i> – 1 (1 proteína) <i>Medicago truncatula</i> – 5 e 10 (2 proteínas)
329	Cobalamin-independent synthase family protein	Glyma16g04240.1	10	1	<i>Arabidopsis thaliana</i> – 2 e 2 (2 proteínas) <i>Brassica napus</i> – 2 (1 proteína) <i>Glycine max</i> – 1 (1 proteína) <i>Medicago truncatula</i> – 5 e 10 (2 proteínas)
805	Cobalamin-independent synthase family protein	Glyma16g04240.1	10	1	<i>Arabidopsis thaliana</i> – 2 e 2 (2 proteínas) <i>Brassica napus</i> – 2 (1 proteína) <i>Glycine max</i> – 1 (1 proteína) <i>Medicago truncatula</i> – 5 e 10 (2 proteínas)
803	Cobalamin-independent synthase family protein	Glyma16g04240.1	10	1	<i>Arabidopsis thaliana</i> – 2 e 2 (2 proteínas) <i>Brassica napus</i> – 2 (1 proteína) <i>Glycine max</i> – 1 (1 proteína) <i>Medicago truncatula</i> – 5 e 10 (2 proteínas)

322	Cobalamin-independent synthase family protein	Glyma16g04240.1	10	1	<i>Arabidopsis thaliana</i> – 2 e 2 (2 proteínas) <i>Brassica napus</i> – 2 (1 proteína) <i>Glycine max</i> – 1 (1 proteína) <i>Medicago truncatula</i> – 5 e 10 (2 proteínas)
839	Carbonic anhydrase 1	Glyma19g01050.1	25	3	<i>Arabidopsis thaliana</i> – 8 (1 proteínas)
120	Photosystem II subunit O-2	Glyma16g25860.1	15	2	-
128	6-phosphogluconate dehydrogenase family protein	Glyma05g35880.1	6	0	<i>Arabidopsis thaliana</i> – 1 e 1 (2 proteínas)
148	Alkenal reductase	Glyma03g24020.1	5	0	-
212	Rubisco activase	Glyma18g04081.1	6	1	<i>Arabidopsis thaliana</i> – 1, 1 e 8 (3 proteínas) <i>Medicago truncatula</i> – 1 e 2 (2 proteínas)
255	Phosphoglycerate kinase family protein	Glyma08g17610.1	16	4	<i>Medicago truncatula</i> – 8 (1 proteína)
256	Phosphoglycerate kinase family protein	Glyma08g17610.1	16	4	<i>Medicago truncatula</i> – 8 (1 proteína)
258	Phosphoglycerate kinase family protein	Glyma08g17610.1	16	4	<i>Medicago truncatula</i> – 8 (1 proteína)
259	Phosphoglycerate kinase family protein	Glyma08g17610.1	16	4	<i>Medicago truncatula</i> – 8 (1 proteína)
266	Phosphoglycerate kinase family protein	Glyma08g17610.1	16	4	<i>Medicago truncatula</i> – 8 (1 proteína)

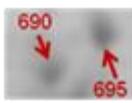
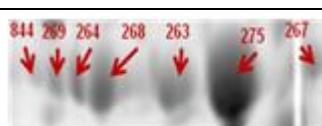
282	ATP synthase subunit alpha	Glyma12g36106.1	9	1	<i>Arabidopsis thaliana</i> – 1 (1 proteína)
299	Phosphoglycerate mutase, 2,3-bisphosphoglycerate-independent	Glyma09g40690.1	5	0	<i>Arabidopsis thaliana</i> – 1, 1 e 1 (3 proteínas) <i>Glycine max</i> – 1 (1 proteína) <i>Medicago truncatula</i> – 3 (1 proteína)
307	NAD(P)-binding Rossmann-fold superfamily protein	Glyma12g05030.1	46	12	<i>Arabidopsis thaliana</i> – 0, 1, 1, 3, 3, 3, 4, 4, 5, 5, 6 e 9 (12 proteínas) <i>Medicago truncatula</i> – 1, 1, 1, 1, 1, 1, 1, 2, 4 e 4 (10 proteínas) <i>Glycine max</i> – 1 e 1 (2 proteínas)
698	Pyrophosphorylase 6	Glyma13g32660.1	8	1	-
761	ATP synthase alpha/beta family protein	Glyma10g41330.1	22	1	<i>Arabidopsis thaliana</i> – 1, 1 e 1 (3 proteínas) <i>Medicago truncatula</i> – 10 (1 proteína)
837	Ribose 5-phosphate isomerase, type A protein	Glyma03g40640.1	10	2	<i>Arabidopsis thaliana</i> – 1 (1 proteína) <i>Medicago truncatula</i> – 1 e 2 (2 proteínas)
323	Cobalamin-independent synthase family protein	Glyma16g04240.1	10	1	-

Supplementary Table S8: Protein isoforms from BR 16 detected in the 2DE gels and identified by mass spectrometry.

Protein	Number of Detected Isoforms	Spot Numbers
Phosphoribulokinase	3	
ATP synthase alpha/beta family protein	4	
Glycine decarboxylase P-protein 2	5	
Heat shock cognate protein 70-1	4	
Phosphoglycerate kinase family protein	4	
Photosystem II subunit O-2	6	
TCP-1/cpn60 chaperonin family protein	2	
Transketolase	8	
Triosephosphate isomerase	3	

Cytosolic NADP ⁺ -dependent isocitrate dehydrogenase	3	
Chloroplastic drought-induced stress protein of 32 KD	3	
NAD(P)-binding Rossmann-fold superfamily protein	6	
Cobalamin-independent synthase family protein	4	

Supplementary Table S9: Protein isoforms from Embrapa 48 detected in the 2DE gels and identified by mass spectrometry.

Protein	Detected Isoforms	Spot Numbers
ATP synthase subunit alpha	3	
Chloroplastic drought-induced stress protein of 32 KD	2	
Glyceraldehyde-3-phosphate dehydrogenase B subunit	4	
TCP-1/cpn60 chaperonin family protein	2	
ATP synthase alpha/beta family protein	7	

Cobalamin-independent synthase family protein	7	
Transketolase	9	
Glycine decarboxylase P-protein 2	7	
Phosphoglycerate kinase family protein	6	
Fructose-bisphosphate aldolase 2	3	
Phosphoribulokinase	5	
Sedoheptulose-bisphosphatase	3	
Photosystem II subunit O-2	4	