

Supplementary Table 1 The primers used in qRT-PCR analysis

Name of the gene	GenBank ID	Primer pairs
<i>aact</i>	FJ947159.3	5'-GTATCGTTGGGTCATCCTCTTG-3' 5'-TCCTCCTCCGTTGCAAATAC-3'
<i>hmgr</i>	HM222606.1	5'-CATGGTCTCAAAGGGAGTACAG-3' 5'-TTCTTGTCGGAGCAGTAGTTG-3'
<i>mvk</i>	JQ670899.1	5'-CTTACTGGCACTGTCTGATTCT-3' 5'-GAGGGCTTTCCTGGATTAT-3'
<i>mdc</i>	JN116821.1	5'-CACTGGGACGACCTTGTATT-3' 5'-GTACCACTTCCCTGGCTCTATG-3'
<i>fpps</i>	GU385740.1	5'-GAGCCTGAGAAGATTGGAAAGA-3' 5'-CTTCCCGTAGTGCTCGAATAAA-3'
<i>sqs</i>	GU734711.1	5'-CTCCGTGATGCTGTACGTATTT-3' 5'-TCGATGGAAAGCCTTCAGAATAG-3'
<i>bas</i>	GU734709.1	5'-CTGCCAAGGACGAAATACA-3' 5'-GCTTTATCCAGAGGCGTAGTG-3'
<i>ugt 1</i>	FJ586244.3	5'-TACGTGTCGTTGGGAAGTATTG-3' 5'-CTTGTCTGTTCTGAAGCTCTTA-3'
<i>ugt 2</i>	FJ586245.3	5'-CCGGTTCACCTCGTTGGATTT-3' 5'-CCACTCGCTCTACGCATATTTTC-3'
<i>dxs</i>	FJ883018.2	5'-CCATCAGATGAAGCAGAGCTAAT-3' 5'-AAGAGCTCCCACACCATTTC-3'
<i>dahs</i>	HQ687488.1	5'-GGGTTACGCAGTGGAATCTT-3' 5'-GTCCAGCAGCCTCCATAAAT-3'
<i>fgt</i>	FJ586246.1	5'-GGTGTATTGGGCCATTGTATCT-3' 5'-CAACAGAACCCGGATCCATATC-3'
<i>pr 1</i>	JN642525.1	5'-CCTCAACCATAGCTTCTCATCC-3' 5'-GTTCCACACGAGAGGTTTCA-3'
<i>18S rDNA</i>	AY492095.1	5'-GAGAAGTCCACTGAACCTTATCA-3' 5'-ATCCTTCCGCAGGTTTAC-3'
<i>26S rDNA</i>	AY492095.1	5'-TCGTTGAGCTCATCTTAGGAC-3' 5'-AGGGAACGGGCTTGGCAGAATC-3'
<i>β-actin</i>	-----	5'-TCCATAATGAAGTGTGATGT-3' 5'-GGACCTGACTCGTCATACTC-3'

Supplementary Table 2 Differentially abundant proteins among the leaf proteome of Bm-NT, BmAt-n and BmAt-ncrypt plant lines which could not be identified using MALDI-TOF MS/MS analysis

Spot No	Name of the predicted protein	Organism	Localization	Accession number*	Mass score	Theo. pI #	Expt. pI †	Matched peptides	Sequence coverage (%)
2	Hypothetical protein CHLNCDRAFT_33359	Chlorella variabilis	Chloroplast	gi 307102515	133	48.2/5.05	71.2/5.74	5	8
16	Hypothetical protein OsI_11553	Oryza sativa Indica	Chloroplast	gi 125543849	90	70.7/9.12	72.5/5.73	7	23
20	Predicted protein [CCE9901]	Ostreococcus lucimarinus	Cytoplasm	gi 145348257	182	49.8/5.68	53.9/5.32	3	42
22	Unknown	Solanum tuberosum	Cytoplasm	gi 77999255	182	38.4/8.52	51.9/6.83	5	10
30	Predicted protein	Ostreococcus lucimarinus CCE9901	Cytoplasm	gi 145345374	77	41.8/9.17	41.2/5.63	6	36
32	Predicted protein	Micromonas	Cytoplasm	gi 3032	88	30.4/	28.3/	4	7

		pusilla CCMP1545	plas m	90552		5.75	5.27		
36	Unnamed protein product	Vitis vinifera	Chlo ropla st	gi 3021 41995	118	37.5/ 6.65	28.3/ 6.07	4	20
40	Hypothetical protein SORBIDRAFT_02 g008800	Sorghum bicolor	Cyto plas m	gi 2420 48156	112	50.3/ 8.25	66.8/ 7.44	8	12

* GenBank ID

Theo. Mr./pI: Theoretical molecular weight/isoelectric point

† Expt. Mr./pI: Experimental molecular weight/isoelectric point

Supplementary Table 3 Signature peptides of the unidentified protein spots as identified by MALDI-TOF MS/MS analysis

Protein spot	Signature peptides
Spot 2	RLKDLVLRW RQEIVFIGASMDRA
Spot 16	GVGSGAMSPRDS FISLAELLPDHA TEDFSCKNLELRA AAEDVNLVPRLIAAIA GPANRLLRGLARRLGSL PRSGSGVGSGAMSPRDSYASVRREN
Spot 20	KDVQSWMTWYKT RAGEIVCEPPLKELIRS KHGYQVLTRPGEQVDKI
Spot 22	RELNAMNKLQTKK KVAPEVIAEYTVRA KGILAADESTGTIGKRL
Spot 30	RYGLTDMRKA MDGATTTASGKRA RLIGAKCSLMARV KKATAGMSSASAVRA RTASDGPVSGTDSVFSERRG
Spot 32	RIDAADPPPKRA RAFGGSTTEDLLRV
Spot 36	RVPQWEKA KDKFTA VGFGPRQ RFSSEISRPENKG
Spot 40	RSGVRYVTNGLKV KVVVMTHAYGNRS RAMQFPNTNLLDRLPRY KKAIDMLPGIDPQIMHLRM