

Supplementary Table 1. Primers for RT-PCR used in this study.

Gene ID		Primers
AT3G62030	Forward	5'-TCTGGGGTTTATGCGACCACC-3'
	Reverse	5'-GACCAGCGTTTGCCATGCTC-3'
AT5G01410	Forward	5'-CTGAGGAGGATCCGTGAAGGTG-3'
	Reverse	5'-ACTCGGAGCGATTAGCGAACCT-3'
AT2G33800	Forward	5'-TTGAAGAGCTCTATGGACCTGCGTA-3'
	Reverse	5'-CTCTAGACAATCCTAACCGCTCCT-3'
AT4G20360	Forward	5'-ATCGGAACCATCGGTCATGTTG-3'
	Reverse	5'-GGAACACCAACCTGCTTAGCCA-3'
AT3G01500	Forward	5'-AGCGAAGCATACGACGAGGCTA-3'
	Reverse	5'-TAAGCCCTTTGATCCCACCACA-3'
AT5G66570	Forward	5'-GACCCGTCTTACCTACACCCTTGAC-3'
	Reverse	5'-CCTTTGGTACCTTAGCACCCAAGTC-3'
AT3G11020 (DREB 2B)	Forward	5'-TTGCGACTATAAAGAAGAAG-3'
	Reverse	5'-TCCGCGGTAGGAAAAGTACC-3'
AT2G40340 (DREB 2C)	Forward	5'-GGAGACTTTGGATGCTTG-3'
	Reverse	5'-TTATGTAGATCCATGAACATCTTTG-3'

Supplementary Table 2. Mass spectrometric identification of proteins differentially expressed in wild-type plants in response to heat treatment at 37°C for 24 h.

No <sub>a</sub>	Protein	ID (NCBI)	MW/pI, theor. <sub>b</sub>	MP/DP <sub>c</sub>	SC <sub>d</sub> (%)	Fold change <sub>e</sub>
1	Major latex protein-related	15236566	17518/5.9	14/20	50	+1.52
2	Thioredoxin-dependent peroxidase 1	15218877	17428/5.2	5/13	40	+1.91
3	Germin-like protein	1755188	19223/5.9	4/12	24	+2.70
4	Oxygen-evolving enhancer protein 2	15222166	28095/6.9	12/23	40	-2.38
5	Chaperonin 20	15242045	26785/8.8	7/24	39	-1.82
6	Dehydroascorbate reductase	15223576	23641/5.6	5/5	38	-1.61
7	Cytosolic triose phosphate isomerase	15233272	27169/5.4	10/14	29	+1.81
8	Glutathione transferase 8	18411929	25651/5.8	8/11	37	-1.50
9	Glutathione S-transferase	20197312	24062/6.0	4/6	22	+2.41
10	Manganese superoxide dismutase 1	15228407	25428/8.4	7/16	45	+5.36
11	Ribulose-phosphate 3-epimerase	2499728	29863/8.2	5/22	32	+1.50
12	Ribulose-phosphate 3-epimerase	2499728	29863/8.2	6/17	32	+2.08
13	Glutathione S-transferase 9	15224581	24146/6.2	6/15	43	+1.51
14	RuBisCO large subunit	7525041	52956/5.9	23/31	40	+1.98

15	RuBisCO large subunit	7525041	52956/5.9	12/16	25	+2.29
16	RuBisCO large subunit	7525041	52956/5.9	14/15	32	+2.10
17	Mitochondrial NAD-dependent malate dehydrogenase	21592905	35782/8.5	9/13	33	+3.71
18	Mitochondrial NAD-dependent malate dehydrogenase	21592905	35754/8.5	10/14	36	+2.40
19	Malate dehydrogenase, cytoplasmic 1	11133509	35571/6.1	16/24	66	+2.23
20	LMW heat shock protein	2326354	23594/7.9	8/14	45	+2.40
21	17.6 kDa class I small heat shock protein	15220832	17440/5.2	8/19	46	+13.58
22	17.6 kDa class I small heat shock protein	15220832	17604/5.4	24/40	67	+4.14
23	Heat shock protein 22.0	4538954	21997/5.6	28/36	73	+19.14
24	Heat shock protein 17.6a	3256075	17686/8.2	22/33	82	+6.06
25	17.8 kDa class I heat shock protein	15222395	17828/6.0	14/21	64	+29.20
26	17.6 kDa class II heat shock protein	232274	17623/6.3	6/8	54	+62.60
27	17.6 kDa class I small heat shock protein	15227552	17563/6.3	12/25	59	+36.57
28	Heat shock protein 18	21618106	18121/6.8	27/38	69	+59.80
29	Pyk10-binding protein 1	15228198	32158/5.5	6/18	31	-1.52
30	Stress-inducible protein	79325071	63707/6.0	9/16	20	+1.86

31	Stress-inducible protein	79325071	64520/5.9	14/19	25	+2.28
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a) Numbers correspond to the 2-DE gels shown in Supplementary Fig. 2

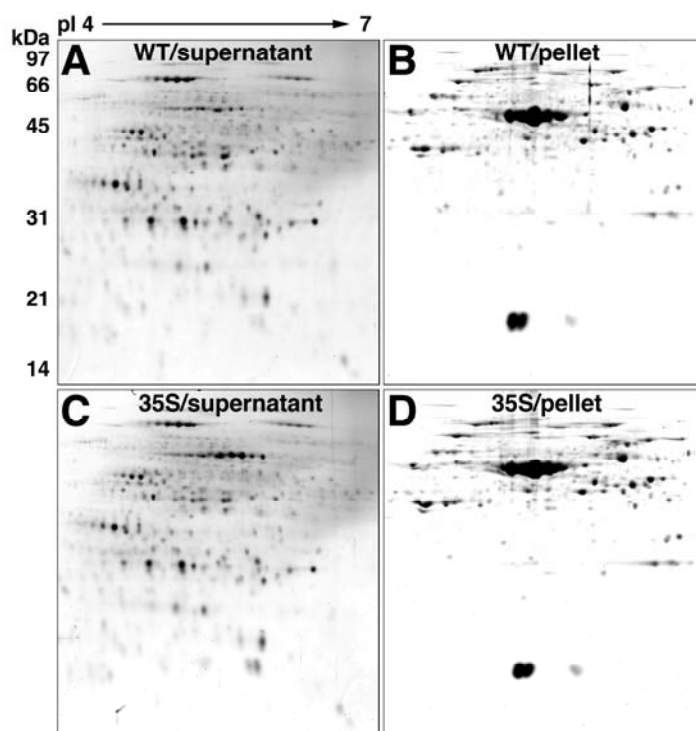
b) Theoretical MW (Da) and pI values

c) Ratio of matched peptides/detected peptides

d) Sequence coverage

e) '+' up regulation; '-' down regulation in wild-type plants after heat treatment for 24h

Supplementary Fig. 1. Representative 2-DE gel images of wild-type and *35S:DREB2C* transgenic plants under normal temperature at 22°C for 24 h. Leaf tissues were fractionated with PEG and the resulting supernatants obtained from wild-type (A) or *35S:DREB2C* plants (C), and pellets from wild-type (B) or *35S:DREB2C* plants (D), were analyzed by 2-DE.



Supplementary Fig. 2. Representative 2-DE gel images of wild-type plants treated or untreated with heat stress at 37°C for 24 h. Leaf tissues were fractionated with PEG and the resulting supernatants obtained from wild-type plants untreated (A) or treated (C) with heat stress, and pellets from wild-type plants untreated (B) or treated (D) with heat stress, were analyzed by 2-DE.

