Supplementary Table 1 The primers used in qRT-PCR

Melatonin synthase	**Candidate genes**	**Primers**	**Primers sequences**
Tryptophan decarboxylase	*BjuB040500*	*BjTDC* 1-F	5’- ACGCACTCAAAACAAATCCTG -3’
		BjTDC 1-R	5’- GCACCATAGAGCCTTAAGACC -3’
	BjuB028186	*BjTDC* 2-F	5’- TGAGATGTTGAGTGCTGGTC -3’
		BjTDC 2-R	5’- ACTCCACCTCCATTTCCTTTG -3’
Tryptamine 5-hydroxylase	*BjuA011730*	*BjT5H* 1-F	5’- TGTCCAACGAGCAGATCATG -3’
		BjT5H 1-R	5’- CACAAGCAAAGCCACACTC -3’
	BjuB027354	*BjT5H* 2-F	5’- GGTTACACGATCCCAGTCAAG -3’
		BjT5H 2-R	5’- CGGGAGAAACACTTCAGGATC -3’
Serotonin N-acetyltransferase	*BjuA042774*	*BjSNAT* 1-F	5’- CACATGGGAGCAGAAAGTTAAAG -3’
		BjSNAT 1-R	5’-GTACTGGTTCCGTATCGTCATC -3’
	BjuA046012	*BjSNAT* 2-F	5’-CCTGTGGAGTTTACTTTGGTTG -3’
		BjSNAT 2-R	5’-CTAGTTTCGTTAGCGGTCTCC -3’
	BjuA030061	*BjSNAT* 3-F	5’-TCAACGCGATCATATGGGAC -3’
		BjSNAT 3-R	5’-TGTTGCAGATCCCTTTCCTC -3’
	BjuB003067	*BjSNAT* 4-F	5’-GAGAGCTACGGAAGAGAAACG -3’
		BjSNAT 4-R	5’-TGCGAGCTTGGTGATAGAAG -3’
N-acetylserotonin methyltransferase	*BjuA034122*	*BjASMT* 1-F	5’-CGATGACCCTAACTGAACTCTC -3’
		BjASMT 1-R	5’-CGTGTTAGTGTAGCCTGTGG -3’
	BjuB041096	*BjASMT* 2-F	5’-CAAGCCTCTCGACAAAACAAG -3’
		BjASMT 2-R	5’-CATTGATGCCTTTGAAGCCTG -3’
	BjuB047952	*BjASMT* 3-F	5’-CATCTTACTCCATCCTCACCTG -3’
		BjASMT 3-R	5’-GAGACACCATCCTCGTTCTTG -3’
	TUB	*BjTUB*-F	5’-TATCAACTACCAGCCACC -3’
		BjTUB-R	5’-GAACACCTCAGCTACACTC -3’

Supplementary Table 2 DAPs in mustard sprouts under heat stress treatment.

No[a]	Fold change[b]	Description[c]	Cov[d]	MW[e]	pI[f]
Defense/Stress					
A0A178UES7	7.00±0.52	HSP18.2 OS=Arabidopsis thaliana	15.53	18.1	8.38
P31170	6.71±0.25	Heat shock protein 21, chloroplastic	7.05	25.3	7.42
A0A178VX53	4.45±0.09	SHSP domain-containing protein	22.88	17.6	8.40
Q9SYG1	4.24±0.10	17.4 kDa class III heat shock protein	7.10	17.4	8.82
Q9S9N1	4.22±0.09	Heat shock 70 kDa protein 5	13.62	70.9	5.41
Q9FGM9	3.67±0.10	23.5 kDa heat shock protein, mitochondrial	3.81	23.3	8.44
Q96331	3.64±0.09	23.6 kDa heat shock protein, mitochondrial	7.62	23.6	6.96
Q1PER6	3.51±0.02	L-ascorbate peroxidase 2, cytosolic	6.77	28.0	6.81
Q38806	3.05±0.30	Q38806	18.46	22.0	6.57
Q9XIE3	2.80±0.16	17.6 kDa class I heat shock protein 1	6.45	17.6	5.74
Q9LPG9	2.38±0.06	T3F20.15 protein	5.96	45.9	7.50
Q9STH1	1.68±0.25	Hsp70-Hsp90 organizing protein 3	10.75	63.7	6.71
P19036	1.67±0.02	17.4 kDa class I heat shock protein	21.15	17.4	6.62
A0A178WN35	1.64±0.02	Glutathione S-transferase F6	3.85	23.5	4.48
F4K6B6	1.55±0.02	HEAT SHOCK PROTEIN 81-2 (Fragment)	28.43	24.4	7.25
P46422	1.55±0.03	Glutathione S-transferase F2	15.93	12.9	4.77
O04310	0.68±0.03	JAL34 protein	3.83	71.1	5.40
A0A178UMG0	0.67±0.03	Peroxidase	6.33	34.7	6.01
Carbohydrate metabolism					
Q9FK88	1.92±0.09	Alkaline/neutral invertase E, chloroplastic	4.21	69.5	6.23
A0A178UPG9	1.88±0.05	Ribulose-5-phosphate-3-epimerase, chloroplastic	10.00	20.1	7.49
A0A178V4U9	1.79±0.01	Prolyl carboxypeptidase like protein	1.84	54.7	6.00
Q9LIB2	1.60±0.06	Alpha-1,4 glucan phosphorylase	4.16	108.5	5.87
Q9FLH8	1.57±0.02	Probable fructokinase-7	2.92	37.0	6.16
W8PUS4	1.52±0.03	Alpha-1,4 glucan phosphorylase (Fragment)	4.16	108.5	4.83
A0A178W7Z8	0.56±0.02	UDP-glucose 4-epimerase	3.74	38.1	6.80
Q553X7	0.56±0.10	UDP-glucose 4-epimerase	3.74	42.3	7.94
Energy					
A0A1P8AN20	3.06±0.01	Heat shock protein 101	15.18	90.7	6.13
Q9LJ94	2.08±0.03	Spindle assembly abnormal protein	2.67	67.5	5.47
P56761	1.89±0.07	Photosystem II D2 protein (Fragment)	8.78	39.5	5.73
P56778	1.88±0.05	Photosystem II CP43 reaction center protein	9.73	51.8	5.25
Q8HT11	1.89±0.06	Photosystem II CP43 reaction center protein (Fragment)	5.50	44.0	8.37
Q8HS55	1.80±0.05	Photosystem II CP47 reaction center protein (Fragment)	12.31	52.0	6.96
Q0WMN4	1.78±0.04	Peroxisomal 2,4-dienoyl-CoA reductase	3.69	31.8	6.23
Q9LTV6	1.79±0.04	Peroxisomal 2,4-dienoyl-CoA reductase	3.69	31.8	6.62
A0A1P8AS42	1.56±0.19	Glyoxylate reductase 2	32.11	31.3	10.68

Q9LF37	1.74±0.01	Chaperone protein ClpB3, chloroplastic	15.91	108.9	4.54
A0A178WCD6	1.67±0.02	Germin-like protein	7.69	21.5	9.16
A0A178UY46	1.66±0.02	Oxygen-evolving enhancer protein 3-1, chloroplastic	10.76	23.8	9.20
Q8VZ99	1.67±0.03	Germin-like protein	7.69	21.5	9.20
Q9T0A0	1.57±0.08	Long chain acyl-CoA synthetase 4	3.45	74.5	10.26
D7MEV3	1.66±0.03	PSBQA protein	10.76	25.8	5.12
Q9XFT3	1.65±0.03	Oxygen-evolving enhancer protein 3-1, chloroplastic	10.71	23.9	5.72
O22958	1.56±0.04	ATP synthase F1 complex assembly factor	4.44	28.4	5.25
A0A1B1W4S7	1.62±0.03	Photosystem II protein D1	11.61	38.9	8.92
Q9SGT3	1.61±0.02	Obg-like ATPase 1	12.65	45.4	5.25
A0A178WGD0	1.59±0.01	Protein MET1, chloroplastic	20.60	37.4	7.24
P56777	1.57±0.02	Photosystem II CP47 reaction center protein	13.58	56.0	5.44
A0A1B1W4U2	1.52±0.04	Photosystem I P700 chlorophyll a apoprotein A2	6.27	82.4	5.90
F4JCU3	1.51±0.03	Diphosphomevalonate decarboxylase	5.25	46.2	6.20
A0A178VT74	0.64±0.03	Protein MET1, chloroplastic	1.32	138.9	6.80
A0A178V7G4	0.60±0.02	Photosystem I reaction center subunit VI-1, chloroplastic	7.59	15.2	8.70
Q9SUI6	0.59±0.03	Photosystem I reaction center subunit VI-2, chloroplastic	7.59	15.3	8.54
Q9S720	0.43±0.03	PsbP domain-containing protein 3, chloroplastic	5.67	27.5	5.25
Nucleotide metabolism					
B3H4B6	1.76±0.06	Ribosomal protein S25 family protein	22.43	11.9	5.71
A0A1P8APV6	1.70±0.06	RNA-binding protein	3.47	35.6	6.73
F4I3B3	1.57±0.03	Polyadenylate-binding protein	2.47	48.4	6.73
A0A178UWL1	1.74±0.02	40S ribosomal protein S25	22.22	12.0	10.32
A0A178UZI1	1.71±0.03	40S ribosomal protein S25	22.22	12.0	6.43
Q9SX79	1.61±0.08	Polyadenylate-binding protein RBP47C	2.55	48.4	4.81
Q9SX80	1.59±0.04	Polyadenylate-binding protein RBP47C	2.53	48.6	5.29
Q9SI96	1.58±0.06	Histone H2B.3 protein	33.11	16.5	11.87
A0A178VMX3	1.56±0.12	Histone H2B protein	28.26	15.1	6.32
Q9LZ45	1.56±0.09	Histone H2B.9 protein	29.55	14.5	6.19
F4J3P1	1.54±0.02	60S ribosomal protein L23 (Fragment)	26.40	8.1	5.60
A0A1P8ASD0	1.52±0.02	RNA-binding protein 47A	2.44	49.8	8.56
Q9LPD0	1.51±0.01	ATPase ASNA1 homolog protein	4.64	38.7	6.11
P40283	1.48±0.04	Histone H2B.11 protein	33.33	16.4	9.41
Q9SU26	1.53±0.02	Ribonucloprotein	7.81	14.0	9.92
Q9SUY1	1.52±0.01	Ribosomal protein L7Ae-like (Fragment)	9.26	11.6	4.73
Q9M1Q9	0.63±0.04	ABC transporter B family member 21	1.31	140.3	6.46
A0A1I9LR83	0.51±0.01	ADP-ribosylation factor-like A1C	8.48	18.1	4.53
Q8VY57	0.50±0.03	ADP-ribosylation factor-like protein 8a	7.61	20.4	4.86
Amino acid metabolism					

Q9MA84	1.95±0.05	Putative aminopeptidase	3.34	63.0	9.14
Q42523	1.91±0.09	Methylcrotonoyl-CoA carboxylase subunit alpha, mitochondrial	1.36	80.3	6.38
Q9SS45	1.56±0.19	Phenylalanine ammonia-lyase 4	4.10	76.9	10.70
Q9SRY5	1.64±0.02	Glutathione S-transferase F7	3.83	23.6	6.55
Q9FFW8	1.58±0.01	Tryptophan synthase beta chain	3.75	55.7	5.47
Q9SXJ6	1.48±0.10	ATP-dependent Clp protease proteolytic subunit 3, chloroplastic	4.85	33.9	6.35
Q94JT5	1.55±0.02	Cyclase-like protein 2	6.99	30.0	8.63
Q42529	1.59±0.03	Tryptophan synthase alpha chain, chloroplastic	7.05	33.2	6.23
F4K0T5	1.51±0.02	Anthranilate synthase alpha subunit 1	3.69	69.6	4.94
P32068	1.50±0.04	Anthranilate synthase alpha subunit 1, chloroplastic	3.87	66.3	6.21
Q9S7E9	1.50±0.03	Glutamate--glyoxylate aminotransferase 2	30.77	55.3	7.42
Q93WI0	0.67±0.03	Rhodanese-like/PpiC domain-containing protein 12, chloroplastic	4.68	33.0	6.65
A0A2P6QPR2	0.62±0.04	Putative anthranilate synthase	8.25	22.8	8.18
F4IAW5	0.60±0.03	Anthranilate synthase beta subunit 1	5.88	32.1	9.31
Q42565	0.59±0.02	Anthranilate synthase beta subunit 1, chloroplastic	6.16	30.4	9.45
Q9FI78	0.57±0.00	Shikimate O-hydroxycinnamoyltransferase	6.70	48.0	9.38
Q9FE37	0.56±0.02	Anthranilate synthase beta subunit	7.66	24.7	7.52
D7KZM0	0.50±0.02	IAA amidohydrolase	3.85	48.0	6.68
P54968	0.54±0.06	IAA-amino acid hydrolase ILR1	2.71	24.2	5.81
Secondary metabolism					
O65511	1.81±0.02	serine-type peptidase	2.11	95.7	6.68
Q8GZA3	1.77±0.02	Putative prolyl carboxypeptidase	3.20	31.8	6.58
Q94CC6	1.75±0.03	Prolyl carboxypeptidase like protein (Fragment)	1.95	52.1	6.32
B2CU06	1.63±0.03	Superoxide dismutase [Cu-Zn]	57.89	8.0	8.92
A8MRV0	1.46±0.06	RNA binding Plectin/S10 domain-containing protein	11.19	14.3	11.39
Q9SBE3	1.55±0.03	Glutathione S-transferase F2	18.75	11.0	5.05
Q8LDU1	1.48±0.04	Glutamyl-tRNA reductase-binding protein	3.43	35.0	5.41
Q8LCI6	0.58±0.01	IAA-amino acid hydrolase (ILR1)	2.71	48.1	6.54
A0A1I9LLI1	0.56±0.04	Peptidase M20/M25/M40 family protein	3.60	36.3	5.60
Q93Y31	0.51±0.01	ADP-ribosylation factor-like protein 8b	7.61	20.4	4.97
F2XYF7	0.47±0.02	Pyridoxial biosynthesis 2	4.71	27.4	4.96
Q8LAD0	0.46±0.04	Probable pyridoxal 5'-phosphate synthase subunit PDX2	4.71	27.4	4.94
Protein biosynthesis					
Q8RY11	1.95±0.05	Aminopeptidase P2	2.68	67.0	9.13
Q683F9	1.80±0.01	Prolyl carboxypeptidase like protein	1.89	53.7	6.58
Q8GYL5	1.74±0.02	40S ribosomal protein S25-3	17.78	15.2	5.29
Q9SIW5	1.71±0.05	40S ribosomal protein S25-1	22.02	12.1	5.29
A0A1P8AXC2	1.55±0.13	CTP:phosphocholine cytidylyltransferase	2.83	38.4	10.92

Q42347	1.56±0.13	60S ribosomal protein L24-1	14.63	18.8	10.56
Q8LCL3	1.53±0.15	60S ribosomal protein L27-2	5.93	15.6	10.92
Q9LUD4	1.57±0.08	60S ribosomal protein L18a-3	10.00	18.0	10.15
A8MRU9	1.54±0.09	Plastid-lipid associated protein PAP / fibrillin family protein	4.46	29.7	11.87
Q6QJ72	1.49±0.13	Pterin-4-alpha-carbinolamine dehydratase 2, mitochondrial	5.88	21.1	5.29
Q56X13	1.59±0.01	Valyl tRNA synthetase	4.76	23.6	7.24
A0A178UFT0	1.56±0.02	Superoxide dismutase [Fe] 3, chloroplastic	5.70	30.3	5.62
O80480	1.55±0.02	Importin subunit alpha-4	3.35	59.4	10.58
Q8LCY7	1.54±0.02	ATP synthase mitochondrial F1 complex assembly factor 1	4.44	28.3	5.64
Q93YR3	1.54±0.02	FAM10 family protein	2.04	37.8	5.05
P51419	1.48±0.04	60S ribosomal protein	11.11	15.6	6.04
Q8RX55	0.61±0.04	Hydroxyproline O-galactosyltransferase GALT5	3.42	77.3	8.54
Q9FXK1	0.62±0.05	Superoxide dismutase [Fe] 3, chloroplastic	7.23	26.4	6.61
Protein destination and storage					
Q94BZ7	2.34±0.04	DNA gyrase subunit B	2.73	80.8	5.40
A4VCL8	1.79±0.01	Putative prolyl oligopeptidase	1.87	54.2	6.58
O65390	1.72±0.02	Putative aspartic proteinase	19.37	16.0	6.38
A0A178WCQ3	1.68±0.03	Proteasome subunit beta type	11.68	29.6	9.38
Q8VZF3	1.62±0.03	Probable glutamyl endopeptidase, chloroplastic	1.98	106.4	8.92
Q56ZZ7	1.59±0.01	Plastidic glucose transporter 4	2.38	56.9	4.68
A0A178UXW9	1.58±0.02	Ras-related protein RABB1a	6.34	22.9	5.60
Protein folding and degradation					
F4JVJ1	3.32±0.08	DNA gyrase subunit B	2.73	65.8	8.69
P42730	3.12±0.05	Putative prolyl oligopeptidase	13.61	101.2	6.29
Q9LNW0	2.74±0.21	Putative aspartic proteinase	6.37	17.8	8.44
P13853	2.38±0.06	Proteasome subunit beta type	15.29	17.6	6.37
A0A178UMY5	1.65±0.02	Probable glutamyl endopeptidase, chloroplastic	9.68	17.6	5.72
A8MS32	1.46±0.06	Plastidic glucose transporter 4	8.57	15.1	6.25
P55737	1.55±0.03	Ras-related protein RABB1a	31.33	80.0	5.03
Q9ZW27	1.54±0.03	Glutathione S-transferase U4	6.25	25.8	4.98
Transport					
Q84Y95	2.15±0.03	Monothiol glutaredoxin-S14, chloroplastic	10.40	19.3	5.07
Q8HT12	1.89±0.07	Photosystem II D2 protein (Fragment)	9.78	35.2	8.90
Q8L7Z3	1.85±0.03	Anamorsin homolog protein	4.41	29.1	6.90
A0A178VXA5	1.77±0.01	Ribosomal_L28e domain-containing protein	11.19	15.9	6.23
A0A384KU64	1.75±0.01	DOMAIN-CONTAINING TRANSLATION REGULATORY FACTOR 3	1.99	77.3	9.67
Q9LZG7	1.56±0.19	Glutathione S-transferase U27	3.52	26.7	10.58
Q9C7Y4	1.70±0.02	Ferredoxin	6.63	20.4	8.82
Q9M2A0	1.71±0.03	Plasma membrane ATPase	5.91	104.1	9.01

F4IE99	1.69±0.04	2Fe-2S ferredoxin-like superfamily protein	6.19	21.9	9.38
Q84W10	1.54±0.09	zinc ion binding protein	4.67	54.0	11.87
Q84VQ4	1.50±0.10	NAD(P)H-quinone oxidoreductase subunit U, chloroplastic	5.50	24.4	6.37
P56767	1.51±0.03	Photosystem I P700 chlorophyll a apoprotein A2	2.81	51.8	7.05
Q8L8T2	0.68±0.03	Glutaredoxin-C1	14.40	13.6	6.47
Signal transduction and transcription					
Q8LDU4	2.04±0.03	Red chlorophyll catabolite reductase, chloroplastic	3.76	36.4	5.82
Q8W4Q4	1.75±0.02	Ma3 doman-containg translation regulatoty fator 3	1.99	77.4	7.05
Q9SZX0	1.75±0.02	Ma3 doman-containg translation regulatoty fator 3	1.49	104.8	6.70
P38666	1.53±0.15	60S ribosomal protein L24-2	14.72	18.6	10.92
cell growth/division					
A0A178UD67	1.50±0.10	RNA binding Plectin/S10 domain-containing protein	8.33	19.7	7.05
F4I3J0	1.61±0.02	Obg-like ATPase 1	12.59	45.6	5.19
P41127	1.50±0.10	60S ribosomal protein L13-1	7.77	9.1	6.37
Q9LYV6	1.50±0.10	GEM-like protein 5	2.94	30.1	8.07
O81645	1.52±0.06	HP domain-containing protein	1.66	106.4	11.59
O04373	1.52±0.01	IAA-amino acid hydrolase ILR1-like 4	3.18	48.2	5.87
P22954	1.51±0.01	Probable mediator of RNA polymerase II transcription subunit 37c	32.01	71.3	5.85
A8MS28	1.48±0.04	Ribosomal L27e protein family	11.45	15.0	5.87
Q42449	0.61±0.04	Profilin-1	19.08	14.3	9.69
Q948R8	0.56±0.04	Protein TOM THREE HOMOLOG 1	6.14	33.3	5.92
Q9ZUM2	0.54±0.02	Tobamovirus multiplication protein 3	5.94	35.0	5.97
Other					
Q9FK90	1.68±0.26	Zinc finger protein-like	7.74	49.8	8.41
Q42006	1.53±0.15	Chaperonin 62.5K beta chain (Fragment)	15.19	8.5	10.90
R0HLU1	1.67±0.02	SHSP domain-containing protein	21.02	17.6	9.51
Q8GZ70	1.49±0.13	Uncharacterized protein	5.88	21.1	5.29
A0A1P8BC46	1.50±0.10	GRAM domain family protein	3.76	23.6	5.73
D7LDG3	1.48±0.04	LRRNT_2 domain-containing protein	2.08	52.5	6.04
A0A565CCL9	0.67±0.03	NADPH-protochlorophyllide oxidoreductase	21.43	6.2	5.24
Q9LHC4	0.61±0.04	6,7-dimethyl-8-ribityllumazine synthase	5.39	26.6	8.54

a Aceession number according to the UniProtKB database

b The abundance ratio of proteins in mustard sprouts under heat stress treatment compared to control

c Description, Homologue protein name obtained using Arabidopsis database from the UniProtKB

d Sequence coverage

e MW, Theoretical molecular weight

f *pI*, Theoretical isoelectric point