Supplemental Materials

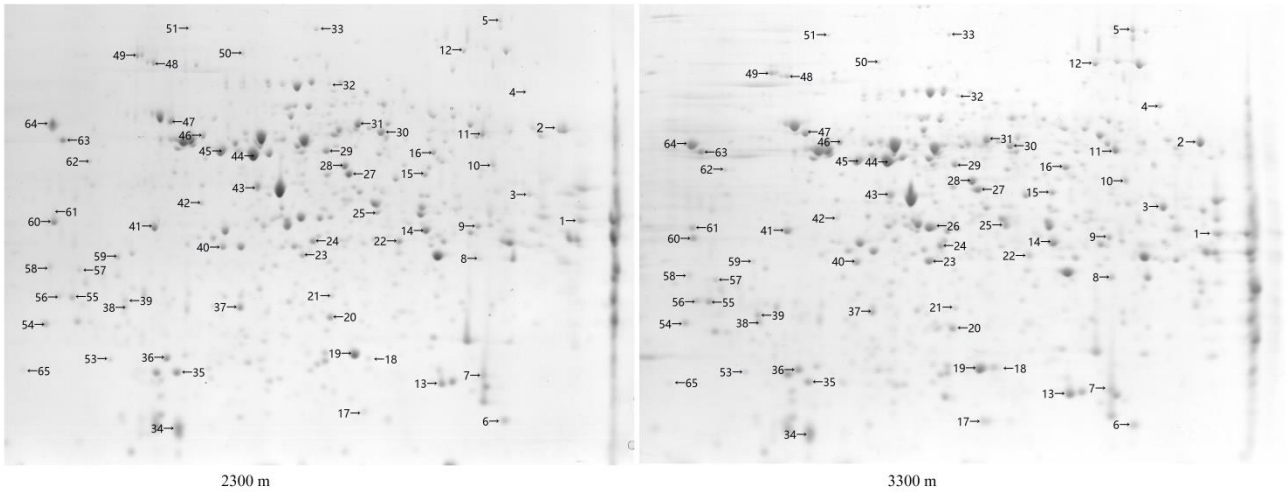


Figure S1. 2-DE gels of proteins extracted from leaves of *S. hexandrum* grown at 2300 and 3300 m.

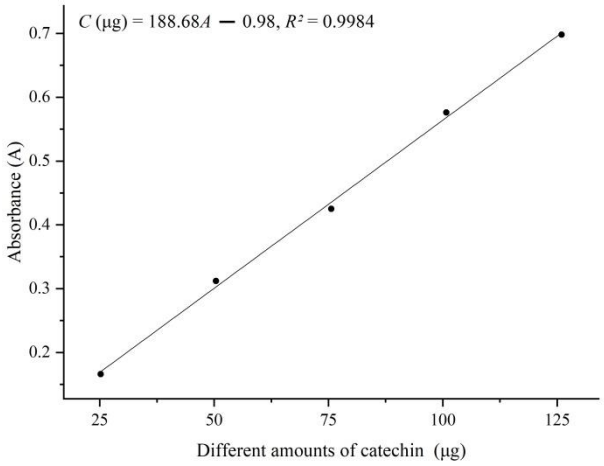


Figure S2. Standard curve of catechin solutions with the range from 25 to 125 μg.

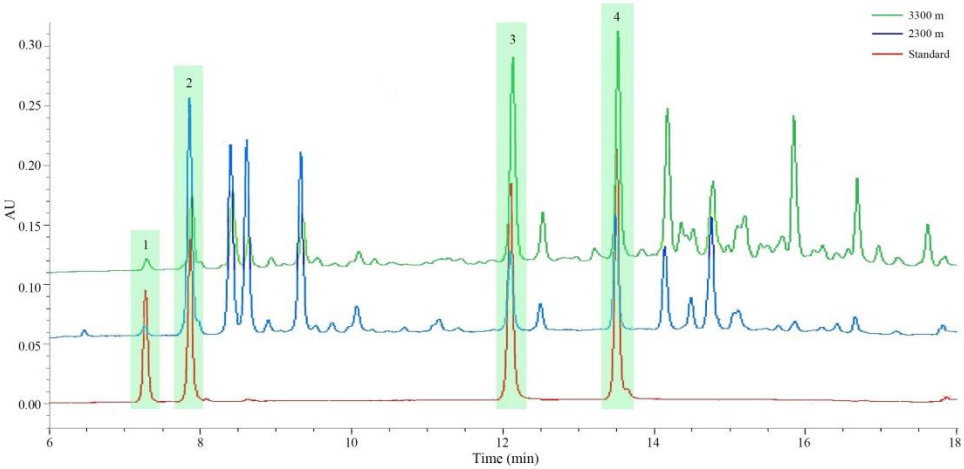


Figure S3. Representative of HPLC chromatogram of reference standards and samples. The numbers 1, 2, 3 and 4 represent the ruin, isoquercetin, quercetin and kaempferol, respectively.

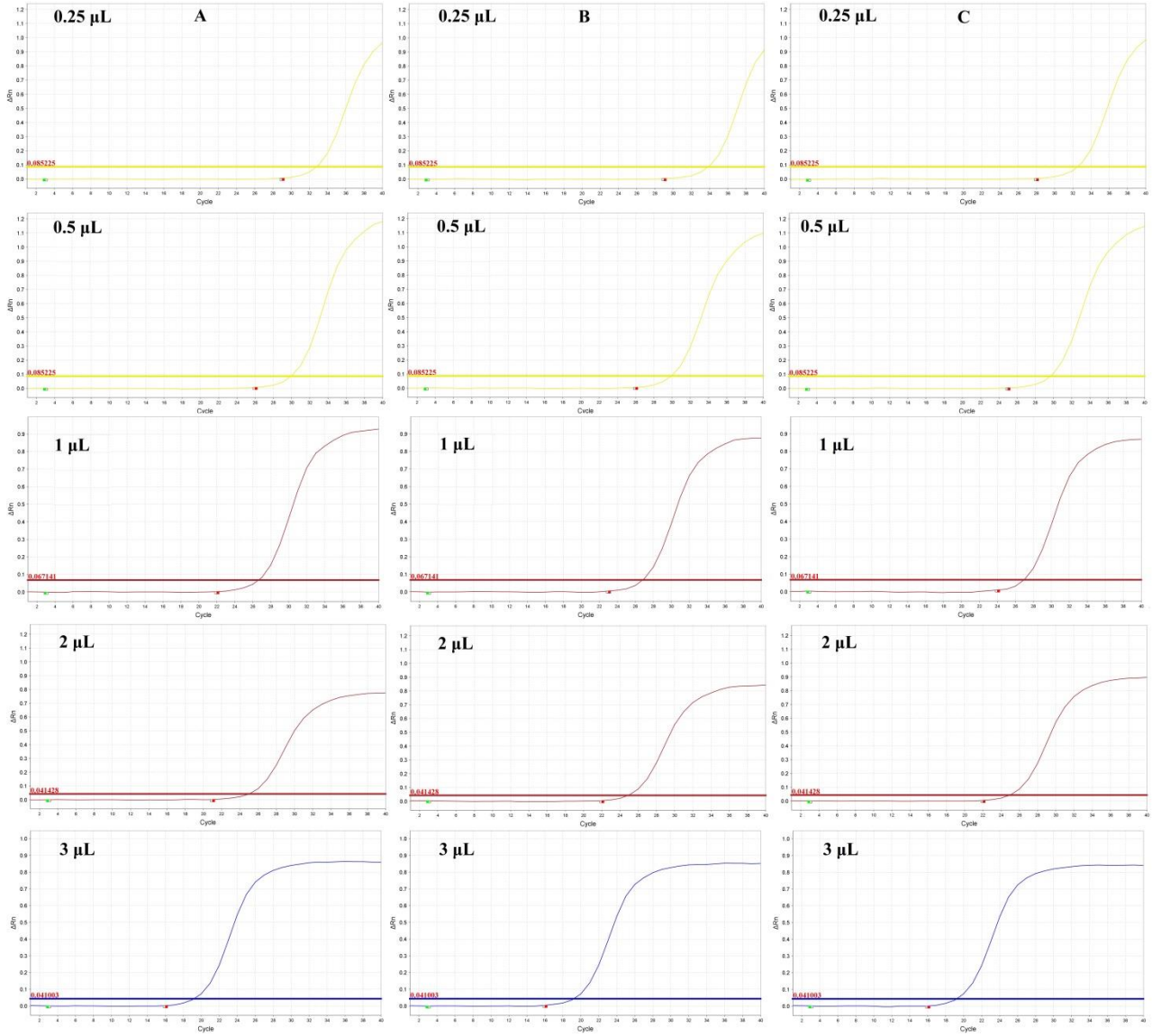


Figure S4. The cycle threshold (Ct) values of *ACT* gene at different volumes (0.25, 0.5, 1.0, 2.0 and 3.0 µL) via PCR amplification with three replications (A, B and C).

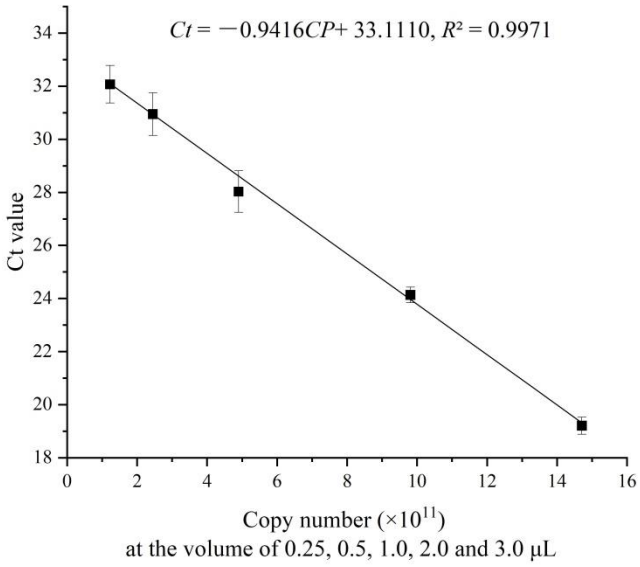


Figure S5. The standard curve of *ACT* gene.

Table S1. Nineteen DEGs involved in light response at 3300 m vs. 2300 m

Genes	Proteins	SwissProt ID	log_2FC (3300 vs. 2300 m)
Photosynthesis (9)			
CAB2	Chlorophyll a-b binding protein 2	P0CJ48	−2.85
CAB3	Chlorophyll a-b binding protein 3	P09756	−2.09
CAB8	Chlorophyll a-b binding protein 8	P27490	9.20
CAB21	Chlorophyll a-b binding protein 21	P27493	10.72
RBCS1	Ribulose bisphosphate carboxylase small chain 1	P16032	−1.73
RBCS4	Ribulose bisphosphate carboxylase small chain 4	Q39746	−2.08
RCAB	Ribulose bisphosphate carboxylase/oxygenase activase	Q42450	−2.40
TPT	Triose phosphate/phosphate translocator	P49132	−2.52
PSBR	Photosystem II 10 kDa polypeptide	P06183	1.93
Light stress (10)			
HSP18.1	18.1 kDa class I heat shock protein	P27879	7.52
HSP90-1	Heat shock protein 90-1	P27323	3.08
HSP22.0	22.0 kDa class IV heat shock protein	P30236	2.28
HSP70	Heat shock 70 kDa protein	O93866	1.54
UBC4	Ubiquitin-conjugating enzyme E2 4	P42748	1.67
ERF5	Ethylene-responsive transcription factor 5	O80341	7.18
ERF9	Ethylene-responsive transcription factor 9	Q9FE67	4.02
TLP	Thaumatin-like protein	Q53MB8	9.28
APX3	L-ascorbate peroxidase 3	Q42564	2.22
EX2	Protein EXECUTER 2	Q657X6	1.30

Abbreviation: FC, fold change.

Table S2. Primer sequences of selected genes used for qRT-PCR validation

Genes	Primer Sequences (5' to 3')	Amplicon size (bp)
ACT	Forward: GCAGGGATCCACGAGACCACC Reverse: CCCACCACTGAGCACATTGTTCC	93
PAL	Forward: TGCCTCGCTACTTACCCTCT Reverse: GGGATTGCTGGGTTTCCACT	200
CHS1	Forward: TCGCACATGCGCTTGAATTT Reverse: GTACCGCAACACCACCAAAC	115
GT6	Forward: CGACGCTATCTTCACCGACA Reverse: CGTCCAGCTCTGTTTCTCGT	112
IFRL	Forward: AGAAGTCACTGCTCCACCCA Reverse: TCAATGTTCTTGCGTCGTCC	128
ANS	Forward: AACAATGCTAGCGGGCAACT Reverse: AGCATATTCGCTTGTCGCCT	129
MYB4	Forward: ACACCGGAAGAAGACACCAG Reverse: TTTTGCTGCACCTCAACAGTC	103
BHLH137	Forward: CAAAACCTTGTTCCGGGCTG Reverse: TCAAGGTCGGAGCCAAAGTC	158
CYP6	Forward: ACCGACGAAATGATCCGAGG Reverse: TTCATCAATCGGTCGGCCTG	171
PPO1	Forward: TGGGGAGAGTTCTTAGGGCT Reverse: ACCCCAGAAAACCGTGTCTC	158
ABCB19	Forward: ACCCGTTTGAGCCATTCACT Reverse: TTCAGGGGCACGAGTCTTTC	150
HSP18.1	Forward: GTCCCAACACAAAAGACCCA Reverse: GTGCCGAAAGAGGAGGTCAA	131
HSP70	Forward: GATTGTCCTCGTCGGTGGTT Reverse: GAGCAGGAGGATCTCGTTGG	187
UBC4	Forward: TGATGAACTGTCGGGTTCTGTT Reverse: ACGCATCATTAACGCAGCAG	160
ERF5	Forward: AGCGATTGAAGCGGCTAGAG Reverse: GTCAACGCTCTGTTCCGTCT	193
ERF9	Forward: CGTGGCTCCAAAGCAAAGAC Reverse: CTTTACGCTCCCGGTGACAT	160
APX3	Forward: GCCCACTGACAAAGCTCTACT Reverse: AACACCGATGACACTGTGGG	193
EX2	Forward: AAAGGTCCAAAGGCTCCCAC Reverse: AGCTTGCACTTACACAGCGA	118