Comparative transcriptome analysis between an evolved abscisic acid-overproducing mutant *Botrytis cinerea* TBC-A and its ancestral strain *Botrytis cinerea* TBC-6

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Supplementary information

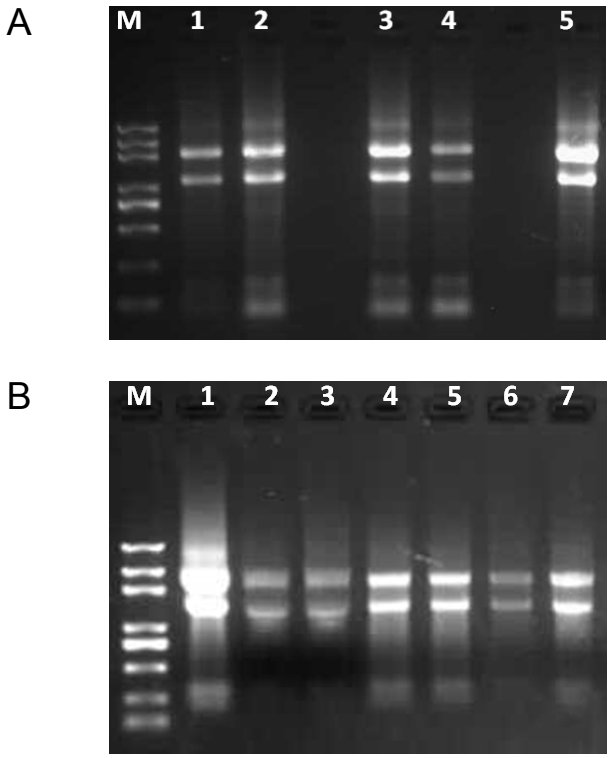

Figure S1. Electrophoresis images of the *Botrytis cinerea* TBC-A and TBC-6 RNA samples subjected to transcriptome sequencing. **(A)** Electrophoresis image of the 5 *Botrytis cinerea* TBC-6 RNA samples used for RNA sequencing. M: Marker; Lane 1: TBC-6-17 h total RNA sample; Lane 2: TBC-6-41 h total RNA sample; Lane 3: TBC-6-72 h total RNA sample; Lane 4: TBC-6-96 h total RNA sample; Lane 5: TBC-6-120 h total RNA sample. **(B)** Electrophoresis image of the 7 *Botrytis cinerea* TBC-A RNA samples used for RNA sequencing. M: Marker; Lane 1: TBC-A-17 h total RNA sample; Lane 2: TBC-A-41 h total RNA sample; Lane 3: TBC-A-48 h total RNA sample; Lane 4: TBC-A-52 h total RNA sample; Lane 5: TBC-A-72 h total RNA sample; Lane 6: TBC-A-96 h total RNA sample; Lane 7: TBC-A-120 h total RNA sample.

Table S1. Summary of the RNA-seq data, quality control and mapping to TBC-A genome sequence.

Sample name	Raw reads	Average length	Total clean reads	Uniquely mapped reads to TBC-A genome sequence	Q20	Q30
TBC-6-17h	24000000	2*100	23630320	14452630 (61.16%)	0.988587095	0.9361843
TBC-6-41h	24000000	2*100	23475792	15024842 (64.00%)	0.997205152	0.9830862
TBC-6-72h	24000000	2*100	23363414	14453926 (61.87%)	0.991609146	0.9534694
TBC-6-96h	24000000	2*100	23391082	14764162 (63.12%)	0.991628653	0.9536873
TBC-6-120h	24000000	2*100	23357358	14797260 (63.35%)	0.991563893	0.9533049
TBC-A-17h	24000000	2*100	23474688	15714974 (66.94%)	0.991703904	0.9538087
TBC-A-41h	24000000	2*100	23150542	14392496 (62.17%)	0.985030105	0.924453
TBC-A-48h	24000000	2*100	23138952	16924790 (73.14%)	0.983330119	0.9161745
TBC-A-52h	24000000	2*100	23141932	14885364 (64.32%)	0.984177622	0.9205756
TBC-A-72h	24000000	2*100	23225008	15037280 (64.75%)	0.984892502	0.9234146
TBC-A-96h	24000000	2*100	23161708	14473394 (62.49%)	0.984537598	0.9220141
TBC-A-120h	24000000	2*100	23166820	14680694 (63.37%)	0.984639111	0.9228005

Table S8. The primers used in this study for quantitative real-time PCR analysis.

Primer name	5'-3' DNA sequence
RT-PDC-F	AGACGCTGGAAGTGACAGTAGAAC
RT-PDC-R	CCAAGGCGGATCATTGTGCTTAC
RT-ALDH-F	ACCGTTGTTACTGGAGGTGAGAG
RT-ALDH-R	GGTGGAGAACTTGGCGATGGA
RT-ACS-F	CGCTCTCCGATCCAAGTGTAGTC
RT-ACS-R	CGCCAGTCCTCCAACATTGCTA
RT-CRC-F	GTTTCTTCTCCGCCATTCCACAAA
RT-CRC-R	TTCACCACATCGACACCACCATT
RT-CAT-F	GCCAGCAGTCGGAATCCTTACAT
RT-CAT-R	CGCCATCACCGTGCCAGTATT
RT-YAT-F	GCTCAACACAACCGTCCTCTCA
RT-YAT-R	TGTCTGGCGATGCTTACTACTGG
RT-ACAT-F	ACACGAGAACAACAAGACGAATACG
RT-ACAT-R	CGAAGCATTGGCAGCGGTAAT
RT-FPPS-F	TTGACAGCACCAGAGGACAAGG
RT-FPPS-R	GGCGACAGGAAGGTAGAAGGAAT
RT-BC1G_15246-F	CCATCGCAACAGTCGGTAAGGT
RT-BC1G_15246-R	CCATCCGCATCATCCGTACTAATC
RT-CS-F	ACTTCGCCAACCAACTCGGATT
RT-CS-R	ACCAGCAGCAAGGGACAACATT
RT-Amy3-F	AAGCCAAGCACAACTACTCCTCTC
RT-Amy3-R	GTGTTGCGTATGTGGAATCGTCATT
RT-CelB-F	CTAGTTCGGCGGCAACCTCAA
RT-CelB-R	GTAGCAGGAGTGACAGCAGGATT
RT-PYK-F	CCACCGCAATGGATCACTTAGTTAC
RT-PYK-R	CGACGATAGTTCTTGGTAGGCTTGA
RT-ICL-F	ATGCCGAGAGCCGAACAAGAA
RT-ICL-R	CTTCACCACATCCACACCGAGAT
RT-MLS-F	GCAGAAGTGAGTCGTTCGCAATT
RT-MLS-R	ATCCGCCTGTTCCTTGAGTAATCT
RT-ACAC-F	CTGGTAAGGACGACGATGAAGGAT
RT-ACAC-R	CGGCAGGTGTGATGTTCTCAACT
RT-HMGCR-F	ACAGAGTCACATGGCACATAACAG
RT-HMGCR-R	GCTGGAGACAAGGCTGCTATACC
RT-HMGCS-F	GCTCTACAACGACTATCTTGCCAAC
RT-HMGCS-R	CTCAACAAACCAACCAATCCACCAT
RT-Rco-3-F	GGTGGTGGTCTCTTCTTCCTTCC
RT-Rco-3-R	TGGTTGGCGATGATCTCAGTAAGTT
RT-Bcaba1-F	TTAATGGCGGTAGCAGAGCATCAT
RT-Bcaba1-R	GCACCAGTGTAGAGCGAATAGCA
RT-Bcaba2-F	AATTGTTCCTCCAGGTGGCTCTG

RT-Bcaba2-R	CTAGGTCCAAGACTGAATGGCTGAG
RT-Bcaba3-F	CACTGCCAGCAACAACCTCCT
RT-Bcaba3-R	CGCCTTGTCCGCCGTGATTA
RT-Bcaba4-F	CACCAATGCTAAAGACTGCCGAAA
RT-Bcaba4-R	TCTCCATCCGCCATCAATGCTAAT
RT-tubA-F	GCGTTCGTGCATTGGTATGT
RT-tubA-R	CACGGGCCTCAGAGAATTCA

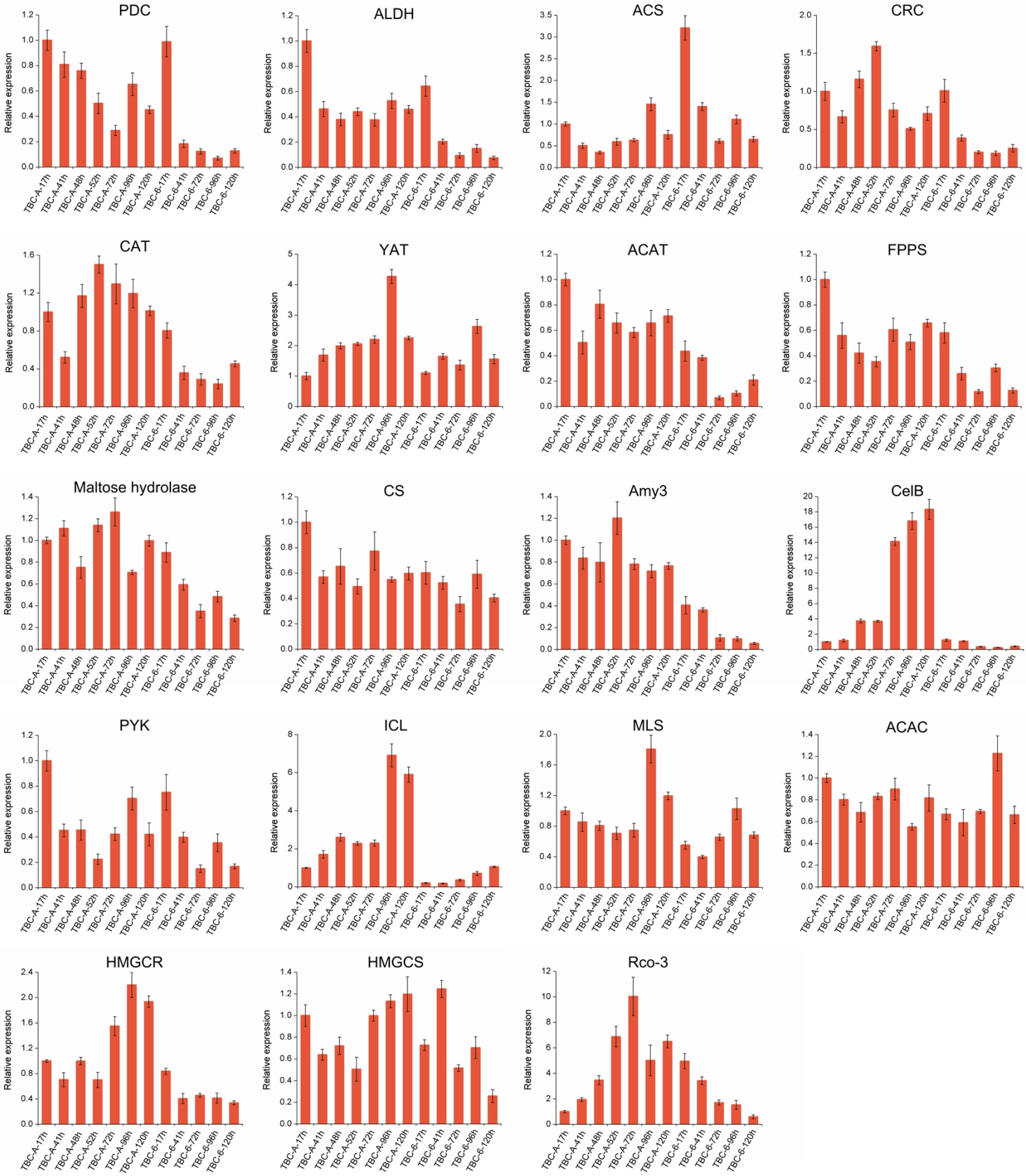

Figure S2. Validation of the RNA sequencing data using quantitative real-time PCR analysis. These selected DEGs encode PDC (pyruvate decarboxylase, encoded by BC1G_11347), ALDH (aldehyde dehydrogenase,

encoded by BC1G_06362), ACS (acetyl-coenzyme A synthetase, encoded by BC1G_07090), CRC (mitochondrial carnitine carrier, encoded by BC1G_14666), CAT (carnitine O-acetyltransferase, encoded by BC1G_14516), YAT (putative mitochondrial carnitine O-acetyltransferase, encoded by BC1G_02490), ACAT (acetyl-CoA acetyltransferase, encoded by BC1G_02275), FPPS (farnesyl pyrophosphate synthase, encoded by BC1G_02940), Maltose hydrolase (encoded by BC1G_15246), CS (citrate synthase, encoded by BC1G_02443), Amy3 (alpha-amylase A type-3, encoded by BC1G_06463), CelB (endoglucanase B, encoded by BC1G_07822), PYK (pyruvate kinase, encoded by BC1G_05305), ICL (isocitrate lyase, encoded by BC1G_13616), MLS (malate synthase, encoded by BC1G_09443), ACAC (acetyl-CoA carboxylase, encoded by BC1G_11289), HMGCR (3-hydroxy-3-methylglutaryl-coenzyme A reductase, encoded by BC1G_01518), HMGCS (hydroxymethylglutaryl -CoA synthase, encoded by BC1G_09652), Rco-3 (probable glucose transporter rco-3, encoded by BC1G_03115) and BcABA3 (*B.cinerea* ABA3 protein, encoded by BC1G_07534). The *B. cinerea* tubulin gene (BC1G_05600) was used as the internal control gene. Data represent mean ± SD of three independent replicates.