

Figure S1: A volcano plot of significant DGE numbers of CO₂-treated tomatoes on day 7, T1:T2.

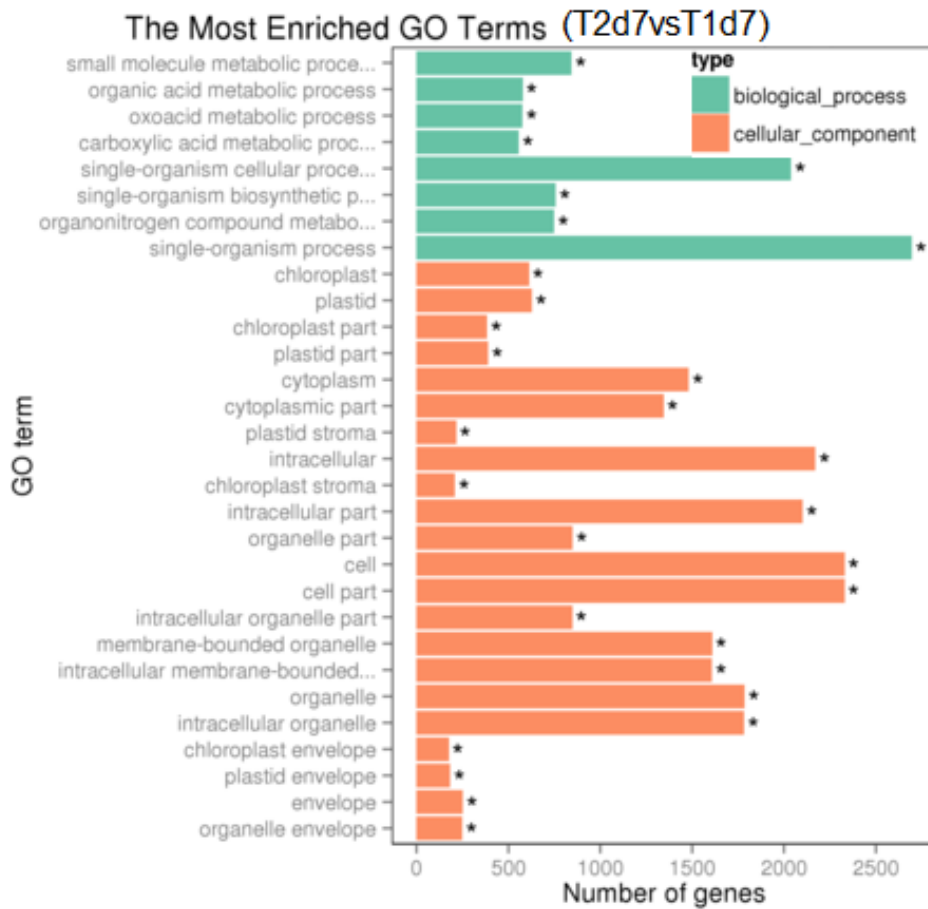


Figure S2: The most enriched GO terms in T1 vs. T2 on d7. Asterisks (*) indicate $q < 0.05$.

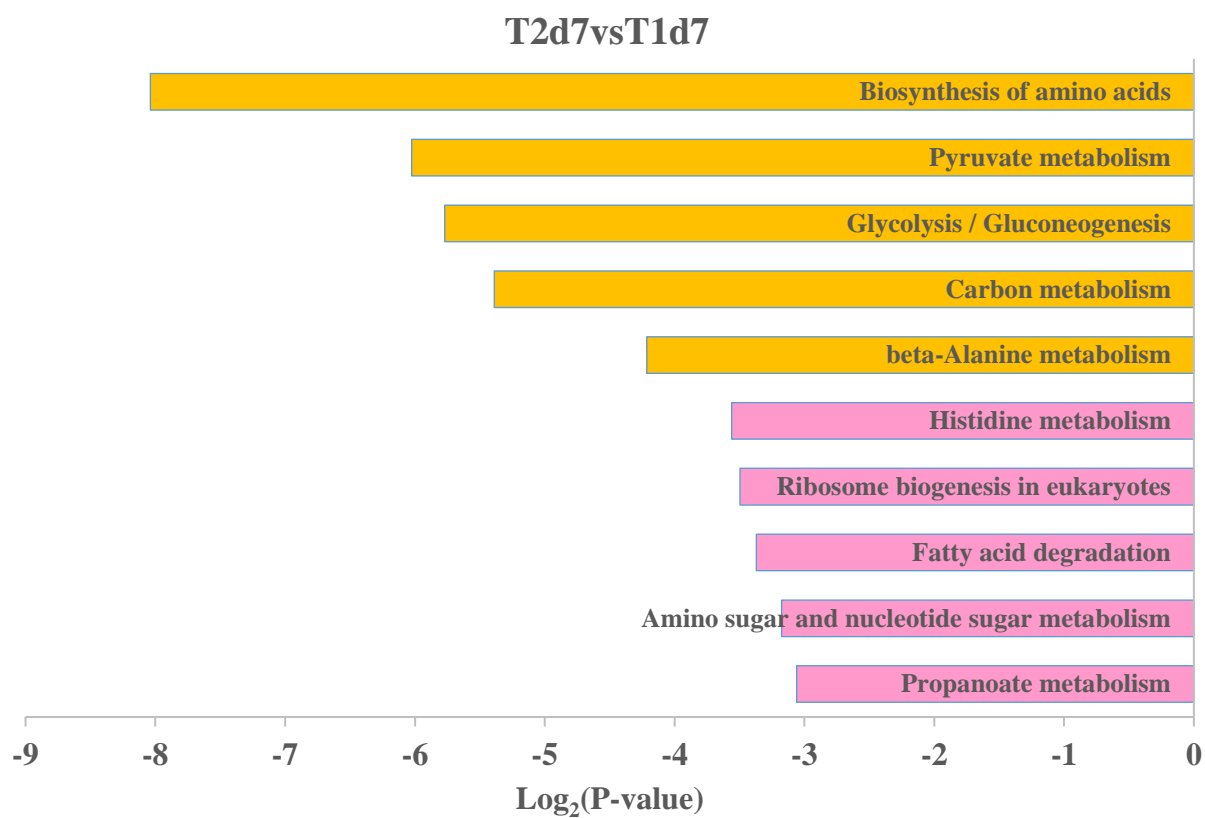


Figure S3: KEGG pathway analysis of T2 vs. T1 on d7; brown bars, $q < 0.05$, $p < 0.05$; pink bars, $q < 0.05$, $p > 0.05$.

Table S1: Primer sequences used in q-PCR assays.

Sequence Description	FWD	REV
Solyc02g061770.2	ATCAATGGTGGAATGGAATG	TACCAGGATCAACTCCCAA
Solyc02g076710.2	CCAACGAAAGAATCATCACC	TGTTTGGTCTCCTGGACAGT
Solyc12g099160.1	GCCAGTATACGAAAGGCTCA	GAGCTTCAACGCAGTCTCTC
Solyc03g115220.2	CCATTGCAGAGCTTATTCGT	CCAGGTCAGATTCCATAACG
Solyc08g005050.2	GCTCATGGAGGAGAACAGA	AAGATCACACCCGAAACAAA
Solyc03g120420.2	AGGATGCCTTTATGCTTGTG	GTAACACAGGGTTGGCATGT
Solyc10g083440.1	TTTGTAAACGCATTGTGGATG	TCCAAACACTTTCCACCATT
Solyc10g075070.1	GAGGGTGTGTGCTGGAGTT	AGGAATGCTTACGCCACAAG
Solyc09g008830.2	TTGGGAACCTCATCACC	TCCCTTTCCATTTCCTCTC
Solyc02g093580.2	TGGTGCGAGTGTTACATTT	AACCGTCGTGGCAATTAGAC
Solyc09g082460.2	CGTTCCTGTGTGGTTTCCT	AAGCCACCCATTCTCTCTT
Solyc09g097760.2	CATCCAAGTGGCAGAACTCA	CAATCTGGTCTAAAAGCAGCAA
Solyc12g006470.1	GCCAGGTGAGACAGAAGAGG	GTCCGCGATGAAAAGAATGT
Solyc09g011540.2	TGAATCGAATCCCGTCCTTA	CTCACTGCATCCAAGCACAT
Solyc03g120320.1	AGGTCACGACGAGGAGAAAA	ACGTGGAAGGATCGAATGAC
Solyc10g054790.1	TGGGAGAACTCCTAGGCTCA	CACTGGAACAACCGCAAGTA
Solyc04g071780.2	CTTTTGCGGAGTCCAAACAT	CCCTAAAGACCACGCGTTTA
Solyc08g077910.2	CTGATGGCAAAGGAACACCT	ATAATGCCTCGTCCTTGCAC
Solyc08g014000.2	TGGTAGACCACCAACACGAA	GGCATGTAATTCAGGGAGGA
Solyc07g064600.2	GCACTGGACATATCGTGGTG	ATACCCGGCCATCAATATCA
Solyc08g005630.2	GCTGGAGCAGAAGAAATTGG	TCCCATGTTTCTCCTTTTGG
Solyc03g093540.1	TCAAATTCCTCCGAAACAGAG	ACCAAACCTCGAGTCCCCTTT
Solyc00g174340.1	TCTTGTGAGGCCCAAAATTC	CCAGCACCAGAATGAATCAA
Solyc04g076860.2	TGGTTTGCCCTGTTTGTAAAT	TTCTGATTGGGGTACTTGGA
Solyc01g006540.2	TGAAGCATTTTCAGCAGTGA	ATCGGATACGACTGATTCCA
Solyc11g011210.1	GCTCAGCAACATCACACAAG	ACAAGGGCATGATTGTTTGT
Solyc03g031630.2	CAATCCTTAGCTTCGTGGAA	CCCTGCAACTCTTCAACAT
Solyc01g099150.2	ATCTCCCAAGTGAAACACCA	TTTGTCTGGATCACCCAAGT
Solyc03g095900.2	GGGGTTTCTTTCAAGTGGTT	ACCTTTTCCCAATATCTCG
Solyc12g042600.1	TGTGGATGGAACCTCGATCTT	CATACCACCCTTCACTCCTG
Solyc08g077910.2	ACACCTACTGGAGCTTGTGG	TAACATGCACCACATCCAAC
Solyc09g008170.1	ATGAACCCTGAAGAGGAACC	GCACGACAAGGAAATTGAAG
Solyc07g040710.2	TGTTTCTCGATGGGCTAGAG	CATAACGATGTCGTGGATCA
Solyc11g005330.1	TACATGTTCAACCACCACTGC	TCTTTTCAATGGAGGAGCTG
Solyc06g069430.2	CCACAACAACCTGGACTCTCC	ACCTTGCTGCTGTGAAGAAC
Solyc08g081170.2	AACCCTTCATTTCCCTTCAC	TCTGAGGGTGTGGGGTAGTA
Solyc06g069520.2	ATTCAGTGCTCAATCCCTTG	GGGACCAACACCCAAGTAGT
Solyc09g091020.2	AGTGGAAGTTTGGACCATGA	ATACAGCTTGTGCCCTGAAG

Table S2: Differential Expression of genes due to CO₂ stress (Fold change).

	Gene ID	Annotation	T1d3 : CTd3	T2d3 : CTd3	T1d7 : CTd7	T2d7 : CTd7
Group 1a	Solyc02g081330	Phytoene synthase 2	0.29	-	0.19	-
	Solyc02g081390	Amine oxidase family protein	0.26	0.23	0.31	-
	Solyc02g084840	Dehydrin DHN1	-	-	10.46	
	Solyc02g091700	Hydroxyproline-rich glycoprotein	0.23	0.13	0.32	-
	Solyc07g040990	Protein phosphatase 2C	0.46	-	-	-
	Solyc07g043590	Amine oxidase family protein	0.39	-	0.29	-
	Solyc07g047790	Chaperone protein htpG	7.84	2.35	4.81	-
	Solyc08g078700	Heat shock protein 22	127.79	-	96.62	-
	Solyc08g079180	Elongation factor G	-	-	0.60	-
	Solyc08g079430	Primary amine oxidase	-	-	2.61	-
	Solyc08g079830	Cu/Zn-superoxide dismutase copper chaperone	0.49	0.33	-	-
	Solyc08g080190	Choline dehydrogenase	0.03	-	0.17	-
	Solyc09g005620	Glutaredoxin	0.43	-	0.30	-
	Solyc09g008770	Group 3 late embryogenesis abundant protein	6.77	-	5.28	-
	Solyc09g009390	Monodehydroascorbate reductase (NADH)-like protein	4.43	-	4.00	-
	Solyc09g010410	BRI1-KD interacting protein 130	-	-	1.88	-
Group 1b	Solyc02g086670	Glycogen synthase kinase	0.21	0.43	0.14	0.91
	Solyc02g087060	Nodulin MtN21 family protein	7.03	19.30	-	-
	Solyc02g087850	Glutaredoxin family protein	-	-	-	0.27
	Solyc02g088630	Glycosyltransferase	-	-	3.18	5.50
	Solyc02g089540	Tomato CONSTANS-like 1	-	1.94	-	3.35
	Solyc02g090680	Cyclin-dependent kinase inhibitor 7	-	23.44	-	-
	Solyc07g006500	Alpha alpha-trehalose-phosphate synthase (UDP-forming)	-	0.41	-	-
	Solyc07g007120	Homeobox protein knotted-1-like 3	1.68	1.81	-	-
	Solyc07g008320	Calcium-transporting ATPase 1	-	2.63	-	-
	Solyc09g007290	Nuclear transcription factor Y subunit B-3	-	0.68	-	-
	Solyc09g009190	1 4-alpha-glucan branching enzyme II	-	1.77	-	-
Group c	Solyc02g084240	H1 histone-like protein	-	2.80	-	0.47
	Solyc02g089620	Proline dehydrogenase	-	-	1.94	0.45
	Solyc02g089900	Receptor-like kinase	-	0.40	4.06	-

	Gene ID	Annotation	T1d3 : CTd3	T2d3 : CTd3	T1d7 : CTd7	T2d7 : CTd7
	Solyc02g090890	Zeaxanthin epoxidase, chloroplastic	6.63	16.54	0.46	-
	Solyc02g093050	WRKY transcription factor 26	-	0.58	4.64	-
	Solyc02g082760	Catalase	0.43	0.43	0.33	-
	Solyc07g005760	Hydroxycinnamoyl CoA shikimate/quinate hydroxycinnamoyltransferase	0.23	0.51	0.22	-
	Solyc07g006890	Cytochrome P450	7.20	14.14	5.98	-
	Solyc07g008310	Rieske (2Fe-2S) domain protein	0.40	0.46	0.20	-
	Solyc08g079100	CRABS CLAW (Fragment)	-	13.21	7.17	-
	Solyc08g082210	Ethylene responsive transcription factor 2b	0.28	0.66	0.03	-
	Solyc08g083130	Homeobox leucine zipper protein	-	11.25	0.07	-
	Solyc09g007850	RNA-binding protein	0.44	0.70	0.34	-
	Solyc09g009040	Delta14-sterol reductase	2.48	2.39	-	-
	Solyc09g011240	Reductase 2	-	1.89	7.24	-

All data shown in this table are statistically significant, "-" indicates statistically not significant.