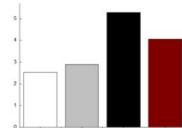
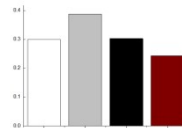
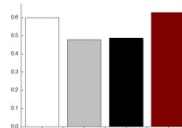
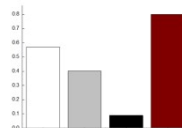
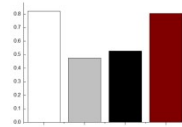
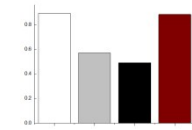
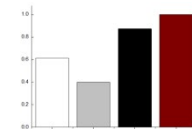
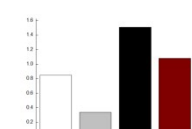
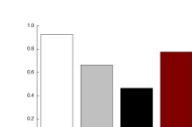
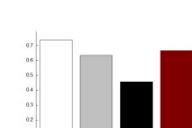
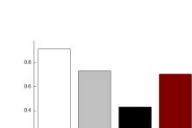


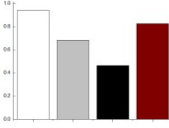
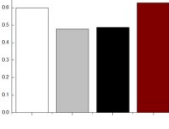
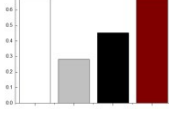
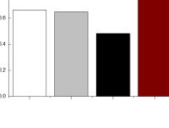
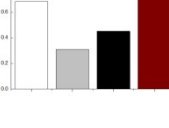
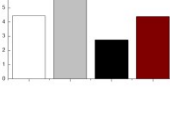
Supplementary table 1. Primers of quantitative RT-PCR for the selected genes

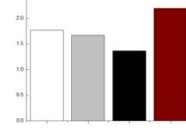
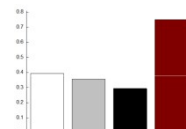
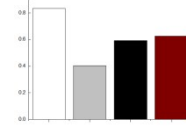
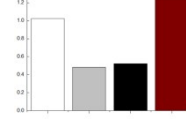
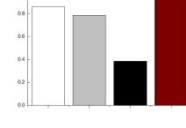
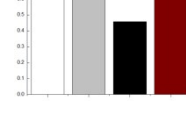
Rrotein ID	Primer F (5'-3')	Primer R (5'-3')
DN13670_c0_g1_i1	ATGGCGGGTATAACCAGCTC	CAATTGGGCCAGAAGATGCT
DN32133_c0_g1_i1	CATTGGCTTCAGCAGCACCT	CCAAATGCCTTTCCAAACTTC CTTTGAATCCACAAGCCAAAT
DN33265_c0_g4_i1	GTGCTGGAGAGGCTGGAAC	C
DN33354_c0_g1_i1	GGCTGATCGGAGAGTGGAGA	TGAAAGCGCATCTTCAAAATC
DN33938_c0_g1_i3	ACGAGGCTGTATCCGCTGAC	CGTTGCTGTTGAGGCAGTTG
DN35749_c0_g2_i4	GGAGTGGCCATACAAGTGTGC	GCTGCATAGGCCTTGTCTT
DN35844_c0_g5_i2	TGTGCTGAGGCTGAGAAGGTC	GAACCGCTGAGGATGCAAT
DN36541_c0_g1_i1	GATGGATCCGCTTCTGCAAT	CCATCATCCGCATACTGTCTG
DN36953_c0_g2_i1	GGGGTGTGGTCAAAGCCTAC	TCCGTGCGACATATTCATCC
DN37718_c0_g2_i3	GCCTTCTACCGCTGTGACATT	TGCAGCATTGCCAAAGATGA
DN38314_c1_g3_i4	TTTCCAAAAGGCGTGAATGT	TTTCCAAAAGGCGTGAATGT
DN38542_c1_g6_i1	CCTTGGTCGCCAAGTCTGA	GTAAGGGGCGGAGAAGAGGA
DN38781_c0_g2_i1	TGACGAGAGGACCGGTAAGC GAGGCCATGATACCTCGAAG	GCGCCGTGTTAGATAACC CACGGCGTCTAACTTCCTCA
DN39221_c0_g1_i3	A	
DN39915_c0_g1_i3	GGTGAACCTGAGCGCGATTA	GACCGGGGTACATTGATACCA
DN40398_c1_g3_i1	TCTTGGCAGCCTTCCGAGT	ACTGGTAAGCCCGTCAGTCC
DN40671_c0_g1_i8	GAAAGGGCCACCTTCATCTC	TTTTCATCCGAGGCAATGGT
DN41597_c1_g1_i1	CTGAAGCAGCGAAACAGGTC	CTCTCGCCAGTACTCACCGT
DN41597_c1_g1_i8	TACATGGCGACGACGACAGT	GCAAGTTCCCCAGTTGTTTCT
DN46943_c0_g1_i1	CTCCTGCCGTGAAGGAATCT	AAGGCGTTATGGTGGTCTCC

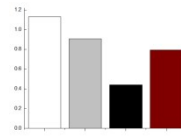
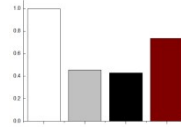
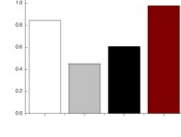
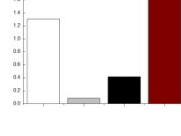
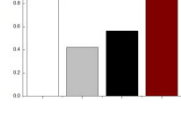
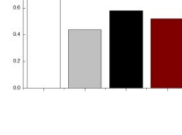
Supplemental Table – Differentially expressed proteins of the strawberry proteome after 7 days of storage in Blank, 2.144 mg/m³, 6.432 mg/m³ and 10.72 mg/m³.

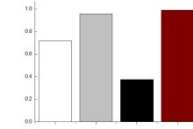
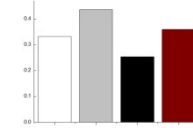
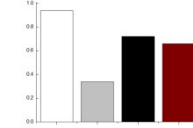
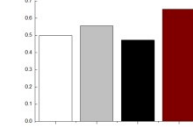
Protein name	Organism	Accession number ^a	Mass/pI ^b	Mascot score ^c	Matched peptides number	Sequence coverage (%)	Protein relative abundance ^d
Ribulose biphosphate carboxylase large chain	Trigonobalanus doichangensis	DN40398_c1_g3_i1	37.20/7.97	1557	10	29.94	
Glucose-1-phosphate adenylyltransferase	Fragaria ananassa	DN33938_c0_g1_i3	57.24/7.42	175	10	21.75	
Pyruvate kinase	Prunus persica	DN36953_c0_g2_i1	70.53/8.43	828	18	39.59	
Nicotinate-nucleotide pyrophosphorylase [carboxylating]	Vitis vinifera	DN38516_c1_g1_i3	31.06/6.24	156	4	15.95	
3-dehydroquinate synthase, chloroplastic	Actinidia chinensis	DN39504_c0_g2_i1	31.06/5.63	147	7	36.49	

Acyl-[acyl-carrier-protein] desaturase	<i>Prunus persica</i>	DN40671_c0_g1_i8	31.06/5.72	2277	23	58.28	
ATP synthase subunit alpha, chloroplastic	<i>Fragaria vesca</i> subsp. <i>vesca</i>	DN38314_c1_g3_i4	31.06/5.06	873	14	30.57	
Chlorophyll a-b binding protein, chloroplastic	<i>Kalanchoe fedtschenkoi</i>	DN37339_c1_g1_i1	31.06/5.26	287	4	11.61	
D-3-phosphoglycerate dehydrogenase	<i>Prunus persica</i>	DN38712_c1_g3_i2	31.06/7.15	1988	19	32.34	
Alpha-1,4 glucan phosphorylase	<i>Cajanus cajan</i>	DN36541_c0_g1_i1	31.06/6.34	391	10	26.79	
Carbamoyl-phosphate synthase large chain	<i>Morus notabilis</i>	DN41489_c0_g5_i2	31.06/6.37	182	8	25.79	

ATP-dependent 6-phosphofruktokinase	Prunus persica	DN39221_c0_g1_i3	31.06/6.62	899	17	40.66	
Pyruvate kinase	Prunus persica	DN36953_c0_g2_i1	31.06/8.43	828	18	39.59	
Pyruvate kinase	Prunus persica	DN35844_c0_g5_i2	31.06/9.17	1272	11	53.15	
Pyruvate kinase	Fragaria ananassa	DN36176_c0_g1_i1	31.06/7.93	1066	12	62.37	
Phosphotransferase	Prunus persica	DN40359_c1_g9_i1	31.06/6.25	693	8	39.26	
Malate synthase	Prunus sibirica	DN33354_c0_g1_i1	31.06/7.9	337	18	35.81	

Citrate synthase	<i>Prunus persica</i>	DN38781_c0_g2_i1	31.06/9.23	255	13	25.42	
Malic enzyme	<i>Malus domestica</i>	DN33265_c0_g4_i1	31.06/6.28	1300	18	35.71	
Succinate dehydrogenase [ubiquinone] iron-sulfur subunit, mitochondrial	<i>Gossypium raimondii</i>	DN46943_c0_g1_i1	31.06/8.79	112	4	10.91	
Malic enzyme	<i>Citrus sinensis</i>	DN41132_c1_g2_i4	31.06/5.5	2739	15	48.90	
Pantothenate kinase 2	<i>Morus notabilis</i>	DN39070_c0_g2_i7	31.06/7.2	903	10	62.68	
UDP-glucuronosyl/UDP-glucosyltransferase	<i>Corchorus olitorius</i>	DN35749_c0_g2_i4	31.06/4.97	83	2	17.73	

UTP--glucose-1-phosphate uridylyltransferase	<i>Pyrus pyrifolia</i>	DN39915_c0 _g1_i3	31.06/8.91	2992	16	74.34	
Cinnamyl-alcohol dehydrogenase isoform 3	<i>Theobroma cacao</i>	DN32133_c0 _g1_i1	38.15/7.05	632	15	51.98	
4-hydroxyphenylpyruvate dioxygenase	<i>Prunus persica</i>	DN38542_c1 _g11_i3	29.84/5.01	403	5	27.88	
4-hydroxyphenylpyruvate dioxygenase	<i>Prunus persica</i>	DN38542_c1 _g6_i1	13.40/7.21	261	3	50.78	
Cytochrome P450	<i>Morus notabilis</i>	DN41597_c1 _g1_i1	49.88/6.42	298	10	25.05	
Cytochrome P450, putative	<i>Ricinus communis</i>	DN41597_c1 _g1_i8	33.10/10.35	305	4	11.11	

CAMTA domain class transcription factor	Malus domestica	DN37953_c0_g10_i2	52.57/7.23	50	3	9.27	
Endoglucanase	Hevea brasiliensis	DN13670_c0_g1_i1	23.45/9.38	117	3	18.80	
Pectinesterase	Prunus persica	DN37718_c0_g2_i3	30.971/9.11	1855	12	47.20	
Reversibly glycosylated polypeptide family	Corchorus capsularis	DN38934_c0_g5_i4	40.706/5.96	1749	22	72.54	

^a Accession numbers according to the detected transcriptome of the strawberry transcriptomic database.

^b Experimental mass (kDa) and isoelectric point (pI) of identified proteins.

^c Mascot score reported after searching against the detected transcriptome of the strawberry transcriptomic database.

^d Relative abundances of normalized protein expression; values are expressed as the mean of three replications. White, grey, black and wine bars show Blank, 2.144 mg/m³, 6.432 mg/m³ and 10.72 mg/m³ ozone treatment storage, respectively.

