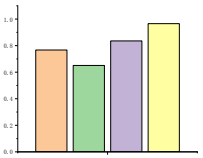
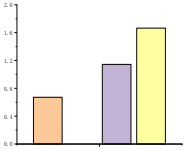
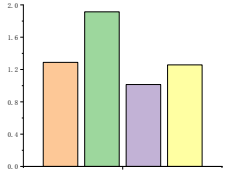
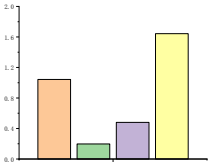
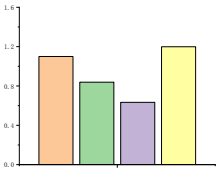
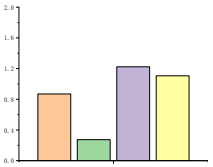
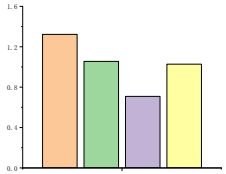
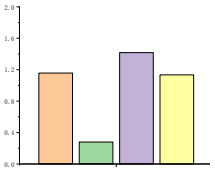
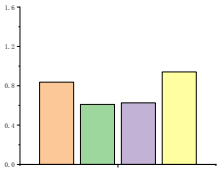
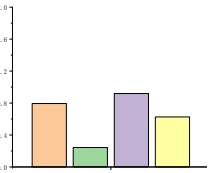
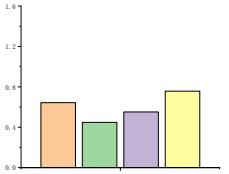
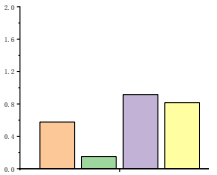
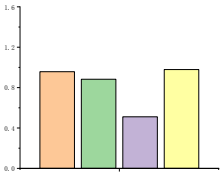
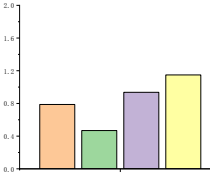
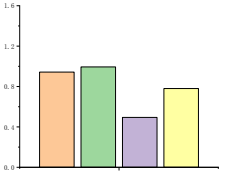
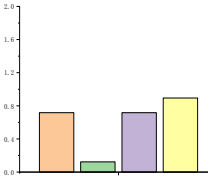
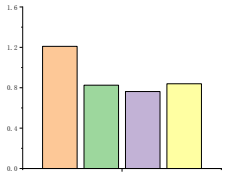
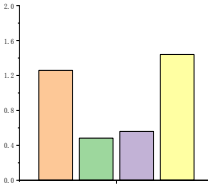
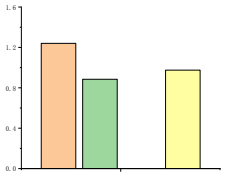
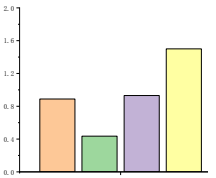
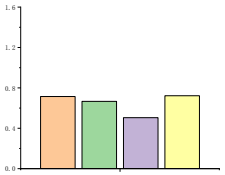
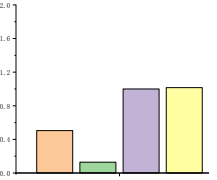
Electronic Supplementary Material (ESI) for RSC Advances.

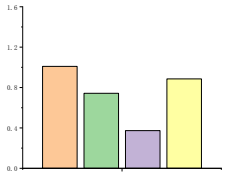
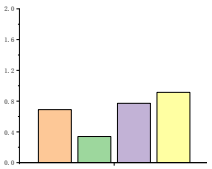
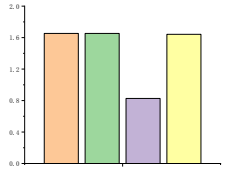
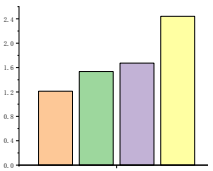
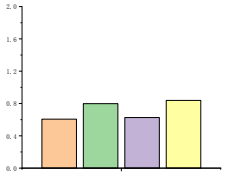
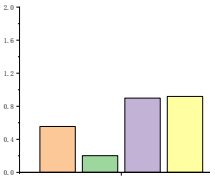
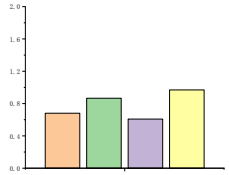
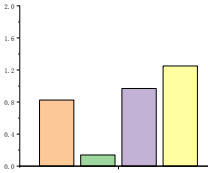
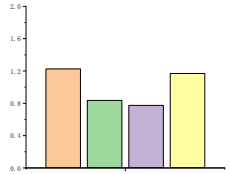
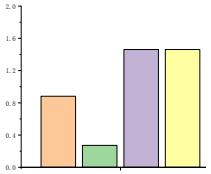
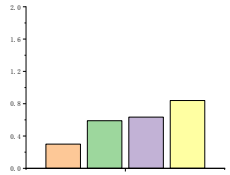
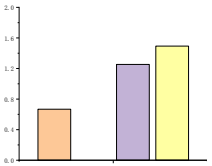
Supplementary table 1. Primers of quantitative RT-PCR for the selected genes

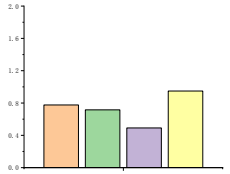
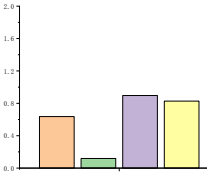
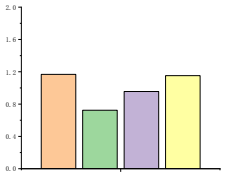
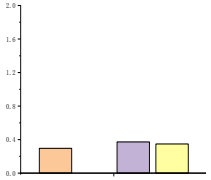
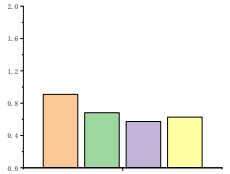
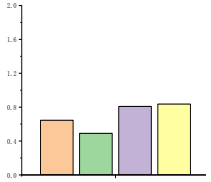
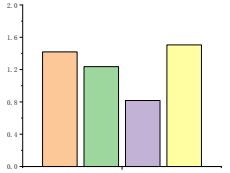
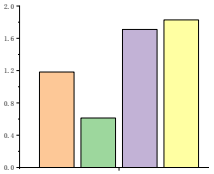
Rrotein ID	Primer F (5'-3')	Primer R (5'-3')
DN40748_c0_g4_i2	GCCGATTACCAGCTCACTAAG	GTTGTTCTCGGCCAAGTCCT
DN40748_c0_g4_i1	GGCCGATTACCAGCTCACTA	GTTGTTCTCGGCCAAGTCCT
DN33720_c0_g3_i1	GGAAGGAGGAGTCGAAGATCA	GCCAAGCAGGATATGGTTGA
DN35956_c0_g1_i4	AGACGGCCGAGGAGTTGAC	GCCCGTCAGCGGTAGTATC
DN35956_c0_g1_i1	GGTGAGGGGGATGGAGATAC	GCCCGTCAGCGGTAGTATC
DN40748_c0_g26_i1	TCCGTCAAGCGTCTCATGAT	GGTCACGGCAGTGATCTCAG
DN35005_c0_g4_i2	TGGTGAAGCCTGATGGTGTT	AATCTCTGGGGCACTGGAAG
DN32105_c0_g1_i3	GGCGGCGACTCACTTGAC	CATAGGTGTGGCGACATGGA
DN35005_c0_g5_i3	TCACTTGACGCTGTGGAAGG	TTCTCAGGGTCCTTGGACTCA
DN38477_c2_g5_i1	ATGAGCGGAGCAGAGAAGGT	GTCACGAACTGAAGCCTTGAC
DN37789_c0_g1_i9	TCTACCTCGATGGCTTGACCT	GGCCAATGCATGAGAATTGT
DN37915_c0_g1_i2	CGAACATGACGATGGCTCTT	GCCTGGAGGAAGCTTGAATC
DN38764_c0_g6_i3	TCATGAAGTTTCCGTTCAGCTC	TCTGTTGTGGGAGGTTGATGA
DN37722_c0_g3_i3	GGCGCGAGATTGTGACCTAC	AACCCCATCAGCTCGTCACT
DN37722_c0_g2_i2	ATTGGCGCGAGATTGTGAC	TCGTCACTGTACTGCGTTGTCA
DN40983_c0_g8_i2	GAGGTCAGCTGCTTGGTCACT	ACATGAGCCGAGAGTGAAGC
DN37999_c0_g2_i3	CCGAAGAGGAGCTCGTTAACA	CACCTTGATGTCCTCCGAGTC
DN37999_c0_g1_i1	GAAGGGCCTCAAGTACCTACC	ATGCCATGGTTGACAAGGTG
DN37999_c0_g2_i2	AGGAAGCAGCCGTCGAATG	CCTTCTGCTCAATGGGAAGAT
DN38544_c0_g9_i1	ATCGAGCTAGACGACGTCACC	CTTCAAGGCAAAGCAAATCG
DN38261_c0_g1_i1	GGCCTCCTCGTCACCTTCT	AGCGGATGAATCCATCTCCA

Supplemental Table 2 – Differentially expressed proteins of the strawberry proteome after 7 days and 21 days of storage in Blank, 1 ppm, 3 ppm and 5 ppm.

Protein name	Organism	Accession number [a]	Mass/pI [b]	Mascot score [c]	Matched peptides number	Sequence coverage (%)	Protein relative abundance day 7[d]	Protein relative abundance day 21[d]
Q4AE08	Fragaria ananassa	DN40748_c0_g4_i2	24.36/ 8.41	1681	13	71.8		
Q4AE08	Fragaria ananassa	DN40748_c0_g4_i1	18.853/8.53	1830	10	63.5		
H6SV47	Prunus persica	DN33720_c0_g3_i1	23.50/4.92	2052	9	56.13		
Q4AE12	Fragaria ananassa	DN35956_c0_g1_i4	25.55/5.21	1027	14	60.34		
Q4AE11	Fragaria ananassa	DN35956_c0_g1_i1	25.39/5.33	781	13	55.70		

Q4AE08	Fragaria ananassa	DN40748_c0_g26_i1	20.76 /5.22	828	6	34.54		
Q5UL14	Fragaria ananassa	DN35005_c0_g4_i2	27.21/8.21	1283	16	59.59		
A0A0A0PTJ7	Fragaria ananassa	DN32105_c0_g1_i3	21.55/5.94	806	8	45.83		
A0A0A0PTJ7	Fragaria ananassa	DN35005_c0_g5_i3	22.91/6.57	739	6	26.70		
A0A0B0N5I9	Gossypium arboreum	DN38477_c2_g5_i1	24.39/8.22	67	4	12.61		
A0A089WWI7	Betula pendula	DN37789_c0_g1_i9	18.59/4.7	965	7	57.06		

V9I5V0	Caragana korshinskii	DN37915_c0_g1_i2	55.02/8.53	96	9	20.16		
Q66PF3	Fragaria ananassa	DN38764_c0_g6_i3	47.72/5.5	40	6	13.07		
Q66ME9	Fragaria ananassa	DN37722_c0_g3_i3	21.85/7.11	2003	13	83.16		
Q66ME9	Fragaria ananassa	DN37722_c0_g2_i2	23.65/5.15	1870	15	80.77		
Q5UL10	Fragaria ananassa	DN40983_c0_g8_i2	50.18/6	2091	15	32.83		
J7HBV7	Fragaria ananassa	DN37999_c0_g2_i3	19.82/4.83	917	13	86.93		

Q5UL08	Fragaria ananassa	DN37999_c0_g1_i1	28.33/6.43	1057	10	46.43		
Q5UL08	Fragaria ananassa	DN37999_c0_g2_i2	18.53/4.88	392	12	85.98		
W9R8W2	Morus notabilis	DN38544_c0_g9_i1	58.77/6.55	476	17	40.08		
Q66PF4	Fragaria ananassa	DN38261_c0_g1_i1	61.36/5.3	2916	26	41.26		

[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. Red, green, purple and yellow bars show Blank, 1 ppm, 3 ppm and 5 ppm ozone treatment storage, respectively.