



# Transcriptome analysis of prestorage 1-MCP and high CO<sub>2</sub> treated 'Madoka' peach fruit explains the reduction in chilling injury and improvement of storage period by delaying ripening

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**Table S1.** List of commonly expressed and identified DEGs in the comparison of CS vs. CO<sub>2</sub> + CS and 1-MCP + CS ‘Madoka’ peach fruit after 12 days storage.

1

| Gene_id      | mRNA_accession | Protein accession | Gene descriptions  | Log fold change |       | p value         |       |
|--------------|----------------|-------------------|--|-----------------|-------|-----------------|-------|
|              |                |                   |  | CO <sub>2</sub> | 1-MCP | CO <sub>2</sub> | 1-MCP |
| Up-regulated |                |                   |  |                 |       |                 |       |
| LOC18790383  | XM_020555209.1 | XP_020410798.1    | ethylene-responsive transcription factor ERF113                    | 6.81            | 6.62  | 0.042           | 0.042 |
| LOC18781898  | XM_007215803.2 | XP_007215865.1    | thaumatin-like protein 1   | 6.73            | 8.94  | 0.034           | 0.033 |
| LOC18790734  | XM_007222992.2 | XP_007223054.2    | esterase   | 6.67            | 6.62  | 0.039           | 0.038 |
| LOC18777635  | XM_007209805.2 | XP_007209867.1    | beta-amylase 3, chloroplastic                                      | 6.48            | 6.13  | 0.001           | 0.001 |
| LOC18788559  | XM_007225606.2 | XP_007225668.1    | putative beta-D-xylosidase   | 6.32            | 5.20  | 0.001           | 0.001 |
| LOC18767585  | XM_007200356.2 | XP_007200418.1    | ethylene-responsive transcription factor ERF071                    | 6.26            | 7.52  | 0.001           | 0.001 |
| LOC18766816  | XM_007201832.2 | XP_007201894.1    | expansin-like A2   | 5.78            | 6.46  | 0.001           | 0.001 |
| LOC18776099  | XM_007210904.2 | XP_007210966.2    | E3 ubiquitin-protein ligase BOI, transcript variant X1             | 5.73            | 6.10  | 0.001           | 0.001 |
| LOC18789693  | XM_007222580.2 | XP_007222642.1    | transcription factor MYB1R1  | 5.57            | 6.17  | 0.001           | 0.001 |
| LOC18792372  | XM_007222812.2 | XP_007222874.1    | zinc finger protein ZAT10  | 5.36            | 6.02  | 0.001           | 0.007 |
| LOC18789880  | XM_007222978.2 | XP_007223040.1    | probable galacturonosyltransferase-like 9                          | 4.85            | 5.57  | 0.003           | 0.002 |
| LOC18790715  | XM_007222877.2 | XP_007222939.1    | lipase   | 4.58            | 4.44  | 0.001           | 0.001 |
| LOC18781566  | XM_007215176.2 | XP_007215238.1    | gamma aminobutyrate transaminase 3, chloroplastic                  | 4.46            | 3.64  | 0.023           | 0.006 |
| LOC18767804  | XM_007199131.2 | XP_007199193.2    | bifunctional riboflavin biosynthesis protein RIBA 1, chloroplastic | 4.23            | 4.52  | 0.001           | 0.001 |
| LOC18768297  | XM_007200926.2 | XP_007200988.1    | scopoletin glucosyltransferase                                     | 4.13            | 4.78  | 0.002           | 0.001 |
| LOC18783318  | XM_007214979.2 | XP_007215041.1    | allene oxide cyclase, chloroplastic                                | 3.93            | 5.10  | 0.002           | 0.001 |
| LOC18768213  | XM_020570312.1 | XP_020425901.1    | pleiotropic drug resistance protein 1                              | 3.78            | 4.53  | 0.001           | 0.001 |
| LOC18791409  | XM_007222632.2 | XP_007222694.1    | E3 ubiquitin-protein ligase ATL6                                   | 3.72            | 5.12  | 0.001           | 0.001 |
| LOC18773198  | XM_007205323.2 | XP_007205385.1    | omega-3 fatty acid desaturase, chloroplastic                       | 3.71            | 3.49  | 0.001           | 0.002 |
| LOC18793580  | XM_007227653.2 | XP_007227715.1    | transcription factor MYB44   | 3.67            | 4.31  | 0.014           | 0.045 |
| LOC18767634  | XM_007199720.2 | XP_007199782.1    | lysine histidine transporter-like 8                                | 3.62            | 4.73  | 0.017           | 0.004 |
| LOC18789531  | XM_007222768.2 | XP_007222830.1    | cinnamoyl-CoA reductase-like SNL6, transcript variant X3           | 3.36            | 3.83  | 0.043           | 0.031 |
| LOC18789736  | XM_007223025.2 | XP_007223087.1    | jasmonate O-methyltransferase                                      | 3.26            | 3.48  | 0.005           | 0.004 |
| LOC18776076  | XM_007209268.2 | XP_007209330.1    | bZIP transcription factor 60                                       | 3.06            | 4.40  | 0.026           | 0.027 |

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| Gene_id               | mRNA_accession | Protein accession | Gene descriptions   | Log fold change |       | p value         |       |
|-----------------------|----------------|-------------------|---|-----------------|-------|-----------------|-------|
|                       |                |                   |   | CO <sub>2</sub> | 1-MCP | CO <sub>2</sub> | 1-MCP |
| LOC18771212           | XM_007204294.2 | XP_007204356.2    | <i>glucan endo-1,3-beta-glucosidase 14</i>  | 3.01            | 2.16  | 0.007           | 0.049 |
| LOC18789209           | XM_007223513.2 | XP_007223575.1    | <i>cell wall / vacuolar inhibitor of fructosidase 1</i>                             | 2.90            | 4.31  | 0.006           | 0.001 |
| LOC109946619          | XM_020555005.1 | XP_020410594.1    | <i>endoglucanase 10</i>   | 2.90            | 3.17  | 0.003           | 0.001 |
| LOC18773658           | XM_020565001.1 | XP_020420590.1    | <i>AP2-likeethylene-responsive transcription factor TOE3, transcript variant X2</i> | 2.88            | 3.37  | 0.042           | 0.026 |
| LOC18774914           | XM_007205621.2 | XP_007205683.1    | <i>methylesterase 17</i>  | 2.83            | 2.89  | 0.009           | 0.008 |
| LOC18768526           | XM_007200507.2 | XP_007200569.1    | <i>E3 ubiquitin-protein ligase CHIP</i>   | 2.45            | 2.94  | 0.009           | 0.012 |
| LOC18775963           | XM_007209024.2 | XP_007209086.1    | <i>4-coumarate--CoA ligase-like 9</i>   | 2.16            | 3.13  | 0.026           | 0.006 |
| LOC18786692           | XM_007218108.2 | XP_007218170.1    | <i>glycosyltransferase family 64 protein C4</i>                                     | 2.01            | 2.40  | 0.041           | 0.013 |
| <b>Down-regulated</b> |                |                   |   |                 |       |                 |       |
| LOC18776275           | XM_007210219.2 | XP_007210281.1    | <i>endoglucanase 6</i>  | -7.12           | -5.09 | 0.001           | 0.001 |
| LOC18774729           | XM_007205678.2 | XP_007205740.1    | <i>expansin-A6</i>  | -6.04           | -4.03 | 0.001           | 0.001 |
| LOC18770721           | XM_020567830.1 | XP_020423419.1    | <i>beta-galactosidase 3</i>   | -5.69           | -4.96 | 0.040           | 0.002 |
| LOC18771540           | XM_007204321.2 | XP_007204383.1    | <i>12-oxophytodienoate reductase 3</i>  | -5.24           | -3.58 | 0.001           | 0.004 |
| LOC18773967           | XM_007205700.2 | XP_007205762.1    | <i>expansin-A4</i>  | -5.08           | -3.46 | 0.001           | 0.001 |
| LOC18785045           | XM_007217890.2 | XP_007217952.1    | <i>anthocyanidin 3-O-glucosyltransferase 2</i>                                      | -4.92           | -4.60 | 0.001           | 0.001 |
| LOC18775995           | XM_007209069.2 | XP_007209131.1    | <i>methanol O-anthraniloyltransferase</i>   | -4.66           | -3.29 | 0.001           | 0.003 |
| LOC18774870           | XM_007208112.2 | XP_007208174.1    | <i>probable linoleate 9S-lipoxygenase 5</i>   | -4.44           | -4.32 | 0.001           | 0.001 |
| LOC18784809           | XM_007220569.2 | XP_007220631.1    | <i>jasmonic acid-amido synthetase JAR1, transcript variant X2</i>                   | -4.33           | -3.27 | 0.002           | 0.010 |
| LOC18775065           | XM_020566833.1 | XP_020422422.1    | <i>pectin acetylesterase 12</i>   | -4.17           | -5.51 | 0.001           | 0.001 |
| LOC18786085           | XM_007218621.2 | XP_007218683.1    | <i>cinnamoyl-CoA reductase 1</i>  | -4.00           | -4.51 | 0.006           | 0.003 |
| LOC18783897           | XM_007215328.2 | XP_007215390.2    | <i>probable galacturonosyltransferase 15</i>  | -3.68           | -3.21 | 0.001           | 0.003 |
| LOC18782821           | XM_007215891.2 | XP_007215953.1    | <i>glutathione S-transferase F12</i>  | -3.66           | -4.09 | 0.001           | 0.001 |
| LOC18770980           | XM_007204516.2 | XP_007204578.1    | <i>3-hydroxy-3-methylglutaryl-coenzyme A reductase 1</i>                            | -3.63           | -2.92 | 0.002           | 0.003 |
| LOC18788884           | XM_007222255.2 | XP_007222317.1    | <i>dihydroflavonol 4-reductase</i>  | -3.56           | -3.46 | 0.002           | 0.004 |

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| Gene_id     | mRNA_accession | Protein accession | Gene descriptions   | Log fold change |       | p value         |       |
|-------------|----------------|-------------------|---|-----------------|-------|-----------------|-------|
|             |                |                   |   | CO <sub>2</sub> | 1-MCP | CO <sub>2</sub> | 1-MCP |
| LOC18783067 | XM_007215424.2 | XP_007215486.1    | ATP-dependent 6-phosphofructokinase 6   | -3.35           | -2.96 | 0.001           | 0.005 |
| LOC18789799 | XM_020555946.1 | XP_020411535.1    | 1-aminocyclopropane-1-carboxylate oxidase homolog 1, transcript variant X1        | -3.19           | -3.36 | 0.024           | 0.002 |
| LOC18769691 | XM_007204670.2 | XP_007204732.1    | soluble inorganic pyrophosphatase   | -3.15           | -3.36 | 0.010           | 0.004 |
| LOC18781238 | XM_007214493.2 | XP_007214555.2    | glycogen phosphorylase 1  | -3.14           | -3.02 | 0.006           | 0.007 |
| LOC18778082 | XM_007210461.2 | XP_007210523.1    | glyceraldehyde-3-phosphate dehydrogenase, cytosolic                               | -3.06           | -2.47 | 0.015           | 0.044 |
| LOC18779670 | XM_007211818.2 | XP_007211880.1    | pyrophosphate-fructose 6-phosphate 1-phosphotransferase subunit beta              | -3.03           | -2.75 | 0.004           | 0.010 |
| LOC18781433 | XM_007214656.2 | XP_007214718.1    | glyceraldehyde-3-phosphate dehydrogenase GAPCP1, chloroplastic                    | -2.71           | -2.13 | 0.011           | 0.047 |
| LOC18783403 | XM_007215938.2 | XP_007216000.1    | glucose-1-phosphate adenylyltransferase small subunit, chloroplastic/amyloplastic | -2.55           | -2.33 | 0.016           | 0.028 |
| LOC18769676 | XM_007204579.2 | XP_007204641.1    | subtilisin-like protease SBT3.5   | -2.52           | -3.44 | 0.009           | 0.003 |
| LOC18793152 | XM_007223728.2 | XP_007223790.1    | endo-1,3;1,4-beta-D-glucanase   | -2.35           | -2.08 | 0.015           | 0.029 |
| LOC18781318 | XM_007211928.2 | XP_007211990.1    | DAG protein, chloroplastic  | -2.28           | -2.42 | 0.017           | 0.032 |
| LOC18789462 | XM_007225326.2 | XP_007225388.1    | calcium-transporting ATPase 1, chloroplastic                                      | -2.09           | -2.00 | 0.038           | 0.048 |
| LOC18791377 | XM_020554552.1 | XP_020410141.1    | phosphoenolpyruvate carboxylase 4   | -2.09           | -2.17 | 0.049           | 0.043 |

**Table S2.** List of exclusively expressed and identified DEGs in the comparison of control vs. CS with control vs. 1-MCP+ CS ‘Madoka’ peach fruit after 12 days storage.

| Gene_id             | mRNA accession | Protein accession | Gene descriptions   | Log fold change | p value |
|---------------------|----------------|-------------------|---|-----------------|---------|
| <b>Up-regulated</b> |                |                   |   |                 |         |
| LOC18771354         | XM_007202534.2 | XP_007202596.2    | <i>cold shock protein CS66</i>  | 4.52            | 0.000   |
| LOC18792096         | XM_007223262.2 | XP_007223324.1    | <i>NAC transcription factor 29</i>                                    | 4.42            | 0.049   |
| LOC18774119         | XM_007205943.2 | XP_007206005.1    | <i>vegetative cell wall protein gp1</i>                               | 3.84            | 0.009   |
| LOC18772963         | XM_007207282.2 | XP_007207344.1    | <i>probable aquaporin PIP2-5</i>                                      | 3.71            | 0.008   |
| LOC18781808         | XM_007215851.2 | XP_007215913.1    | <i>26.5 kDa heat shock protein, mitochondrial</i>                     | 3.62            | 0.015   |
| LOC18771504         | XM_007203666.2 | XP_007203728.1    | <i>UDP-glycosyltransferase 73C3</i>                                   | 3.58            | 0.010   |
| LOC18783057         | XM_007217136.2 | XP_007217198.1    | <i>non-specific lipid-transfer protein 2</i>                          | 3.28            | 0.003   |
| LOC18784147         | XM_007215806.2 | XP_007215868.1    | <i>B-box zinc finger protein 24</i>                                   | 3.28            | 0.005   |
| LOC18766758         | XM_007201292.2 | XP_007201354.1    | <i>NDR1/HIN1-like protein 13</i>                                      | 3.22            | 0.003   |
| LOC18782396         | XM_007217705.2 | XP_007217767.1    | <i>zinc finger AN1 domain-containing stress-associated protein 12</i> | 3.18            | 0.019   |
| LOC18768241         | XM_007201304.2 | XP_007201366.1    | <i>peroxidase 12</i>  | 3.11            | 0.010   |
| LOC18770453         | XM_007203623.2 | XP_007203685.1    | <i>protein EARLY-RESPONSIVE TO DEHYDRATION 7, chloroplastic</i>       | 3.09            | 0.006   |
| LOC18769499         | XM_007202413.2 | XP_007202475.1    | <i>aquaporin TIP1-1</i>   | 3.07            | 0.042   |
| LOC18772208         | XM_007205406.2 | XP_007205468.2    | <i>F-box/kelch-repeat protein At1g15670</i>                           | 3.07            | 0.005   |
| LOC18769333         | XM_007202197.2 | XP_007202259.1    | <i>fructose-bisphosphate aldolase, cytoplasmic isozyme</i>            | 3.02            | 0.003   |
| LOC18781387         | XM_007211912.2 | XP_007211974.1    | <i>polyphenol oxidase, chloroplastic</i>                              | 3.00            | 0.031   |
| LOC18784924         | XM_007218708.2 | XP_007218770.1    | <i>protein SRC2</i>   | 2.95            | 0.011   |
| LOC18779840         | XM_020563111.1 | XP_020418700.1    | <i>VQ motif-containing protein 4</i>                                  | 2.94            | 0.029   |
| LOC18773341         | XM_007207361.2 | XP_007207423.1    | <i>UDP-glycosyltransferase 71K1, transcript variant X1</i>            | 2.90            | 0.033   |
| LOC18766770         | XM_007201642.2 | XP_007201704.2    | <i>chaperonin CPN60-2, mitochondrial</i>                              | 2.86            | 0.004   |
| LOC18785553         | XM_007217962.2 | XP_007218024.1    | <i>UDP-glucuronate 4-epimerase 3</i>                                  | 2.79            | 0.009   |
| LOC18783598         | XM_007217098.2 | XP_007217160.1    | <i>homeobox-leucine zipper protein GLABRA 2</i>                       | 2.75            | 0.014   |
| LOC18766694         | XM_020569952.1 | XP_020425541.1    | <i>BTB/POZ domain-containing protein At1g63850</i>                    | 2.72            | 0.009   |

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| Gene_id      | mRNA accession | Protein accession | Gene descriptions  | Log fold change | p value |
|--------------|----------------|-------------------|--|-----------------|---------|
| LOC18780582  | XM_007211964.2 | XP_007212026.1    | <i>probable polygalacturonase</i>  | 2.71            | 0.016   |
| LOC18785140  | XM_007218771.2 | XP_007218833.1    | <i>ethylene-responsive transcription factor 2</i>                                    | 2.69            | 0.016   |
| LOC18782289  | XM_007215565.2 | XP_007215627.1    | <i>probable 2-oxoglutarate-dependent dioxygenase At5g05600</i>                       | 2.68            | 0.013   |
| LOC18772792  | XM_020566162.1 | XP_020421751.1    | <i>glycine-rich RNA-binding protein RZ1A</i>   | 2.67            | 0.016   |
| LOC18785398  | XM_020556175.1 | XP_020411764.1    | <i>probable serine/threonine-protein kinase PBL9</i>                                 | 2.63            | 0.007   |
| LOC18774023  | XM_020566630.1 | XP_020422219.1    | <i>ethylene-responsive transcription factor RAP2-7, transcript variant X1</i>        | 2.60            | 0.046   |
| LOC18767475  | XM_020569665.1 | XP_020425254.1    | <i>magnesium transporter MRS2-3</i>  | 2.58            | 0.022   |
| LOC18770251  | XM_007202669.2 | XP_007202731.1    | <i>multiprotein-bridging factor 1c</i>   | 2.57            | 0.019   |
| LOC18786863  | XM_007218228.2 | XP_007218290.1    | <i>enoyl-CoA delta isomerase 1, peroxisomal</i>                                      | 2.55            | 0.020   |
| LOC18772307  | XM_007205984.2 | XP_007206046.1    | <i>zinc finger A20 and AN1 domain-containing stress-associated protein 3</i>         | 2.55            | 0.014   |
| LOC18766507  | XM_007199633.2 | XP_007199695.2    | <i>calcium-transporting ATPase 12, plasma membrane-type</i>                          | 2.54            | 0.023   |
| LOC18787090  | XM_007218734.2 | XP_007218796.1    | <i>glycine-rich RNA-binding protein RZ1C, transcript variant X1</i>                  | 2.53            | 0.016   |
| LOC18769680  | XM_007204563.2 | XP_007204625.1    | <i>wall-associated receptor kinase-like 14</i>                                       | 2.52            | 0.010   |
| LOC18780279  | XM_007211916.2 | XP_007211978.1    | <i>ethylene-responsive transcription factor 3</i>                                    | 2.52            | 0.015   |
| LOC18767780  | XM_007200991.2 | XP_007201053.1    | <i>alcohol dehydrogenase 1</i>   | 2.51            | 0.024   |
| LOC18767388  | XM_007201305.2 | XP_007201367.1    | <i>cinnamyl alcohol dehydrogenase 1</i>  | 2.45            | 0.026   |
| LOC18770307  | XM_020568329.1 | XP_020423918.1    | <i>polygalacturonase ADPG2</i>   | 2.44            | 0.011   |
| LOC18778952  | XM_007213821.2 | XP_007213883.1    | <i>bifunctional riboflavin kinase/FMN phosphatase</i>                                | 2.43            | 0.030   |
| LOC18786375  | XM_007220153.2 | XP_007220215.1    | <i>L-type lectin-domain containing receptor kinase S.4</i>                           | 2.43            | 0.029   |
| LOC18773417  | XM_020565931.1 | XP_020421520.1    | <i>4-alpha-glucanotransferase, chloroplastic/amyloplastic, transcript variant X2</i> | 2.42            | 0.012   |
| LOC18768018  | XM_007200293.2 | XP_007200355.1    | <i>UDP-galactose transporter 2</i>   | 2.42            | 0.012   |
| LOC18781646  | XM_007215020.2 | XP_007215082.1    | <i>17.4 kDa class III heat shock protein</i>   | 2.40            | 0.036   |
| LOC18766098  | XM_007198776.2 | XP_007198838.1    | <i>E3 ubiquitin-protein ligase RMA1H1</i>  | 2.37            | 0.035   |
| LOC18772229  | XM_020566279.1 | XP_020421868.1    | <i>alkaline/neutral invertase E, chloroplastic, transcript variant X2</i>            | 2.34            | 0.033   |
| LOC109946804 | XM_020555654.1 | XP_020411243.1    | <i>glycine-rich protein 2-like</i>   | 2.34            | 0.036   |

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| Gene_id               | mRNA accession | Protein accession | Gene descriptions   | Log fold change | p value |
|-----------------------|----------------|-------------------|---|-----------------|---------|
| LOC18791585           | XM_020569234.1 | XP_020424823.1    | <i>probable protein phosphatase 2C 59</i>                                       | 2.34            | 0.030   |
| LOC18770835           | XM_007202017.2 | XP_007202079.1    | <i>phosphoserine aminotransferase 1, chloroplastic</i>                          | 2.30            | 0.030   |
| LOC18785040           | XM_020558370.1 | XP_020413959.1    | <i>L-type lectin-domain containing receptor kinase VIII.2</i>                   | 2.29            | 0.032   |
| LOC18768133           | XM_020569850.1 | XP_020425439.1    | <i>patellin-6</i>   | 2.28            | 0.037   |
| LOC18777090           | XM_007209028.2 | XP_007209090.1    | <i>beta-amylase 3, chloroplastic</i>  | 2.26            | 0.032   |
| LOC18768033           | XM_007201220.2 | XP_007201282.1    | <i>universal stress protein PHOS34</i>  | 2.21            | 0.037   |
| LOC18776383           | XM_007209540.2 | XP_007209602.1    | <i>heat shock 22 kDa protein, mitochondrial</i>                                 | 2.21            | 0.042   |
| LOC109946242          | XM_020565479.1 | XP_020421068.1    | <i>probable histone H2B.1</i>   | 2.21            | 0.022   |
| LOC18769662           | XM_007202310.2 | XP_007202372.1    | <i>heat stress transcription factor B-1</i>                                     | 2.20            | 0.042   |
| LOC18789842           | XM_007222319.2 | XP_007222381.1    | <i>UDP-glucuronate 4-epimerase 1</i>  | 2.19            | 0.037   |
| LOC18767607           | XM_007201272.2 | XP_007201334.1    | <i>SKP1-interacting partner 15</i>  | 2.13            | 0.045   |
| LOC18769952           | XM_007202265.2 | XP_007202327.1    | <i>F-box protein SKIP1</i>  | 2.12            | 0.047   |
| LOC18774456           | XM_007205974.2 | XP_007206036.1    | <i>60S ribosomal protein L12</i>  | 2.10            | 0.029   |
| LOC18784867           | XM_007220189.2 | XP_007220251.1    | <i>golgin candidate 4</i>   | 2.08            | 0.036   |
| LOC18767471           | XM_007200989.2 | XP_007201051.1    | <i>BTB/POZ and MATH domain-containing protein 2</i>                             | 2.02            | 0.034   |
| LOC18784947           | XM_007220253.2 | XP_007220315.2    | <i>glucan endo-1,3-beta-glucosidase</i>   | 2.02            | 0.039   |
| LOC18788282           | XM_007225331.2 | XP_007225393.1    | <i>putative calcium-transporting ATPase 13, plasma membrane-type</i>            | 2.02            | 0.034   |
| LOC18785734           | XM_007218126.2 | XP_007218188.1    | <i>F-box/kelch-repeat protein SKIP4</i>   | 2.01            | 0.035   |
| LOC18786278           | XM_020557544.1 | XP_020413133.1    | <i>protein TRANSPARENT TESTA GLABRA 1, transcript variant X1</i>                | 2.01            | 0.039   |
| LOC18767346           | XM_007200378.2 | XP_007200440.2    | <i>epoxide hydrolase A</i>  | 2.00            | 0.043   |
| LOC18766155           | XM_007201165.2 | XP_007201227.1    | <i>RPM1-interacting protein 4</i>   | 2.00            | 0.047   |
| <b>Down-regulated</b> |                |                   |   |                 |         |
| LOC18783695           | XM_007215345.2 | XP_007215407.1    | <i>phytoene synthase 2, chloroplastic</i>                                       | -4.58           | 0.003   |
| LOC18782475           | XM_020559547.1 | XP_020415136.1    | <i>ABC transporter I family member 11, chloroplastic, transcript variant X2</i> | -4.09           | 0.029   |
| LOC18785488           | XM_007218726.2 | XP_007218788.1    | <i>phosphoglucan phosphatase LSF2, chloroplastic</i>                            | -3.72           | 0.008   |

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| Gene_id      | mRNA accession | Protein accession | Gene descriptions   | Log fold change | p value |
|--------------|----------------|-------------------|---|-----------------|---------|
| LOC18790537  | XM_007222967.2 | XP_007223029.1    | <i>caffeoylshikimate esterase</i>   | -3.64           | 0.009   |
| LOC18768052  | XM_020570437.1 | XP_020426026.1    | <i>probable ethylene response sensor 1, transcript variant X2</i>             | -3.37           | 0.006   |
| LOC18771959  | XM_007208512.2 | XP_007208574.2    | <i>fasciclin-like arabinogalactan protein 4</i>                               | -3.36           | 0.016   |
| LOC18783832  | XM_007217106.2 | XP_007217168.1    | <i>phosphoglucan phosphatase LSF1, chloroplastic, transcript variant X1</i>   | -3.36           | 0.017   |
| LOC18769772  | XM_020567700.1 | XP_020423289.1    | <i>B3 domain-containing transcription factor VRN1, transcript variant X2</i>  | -3.30           | 0.037   |
| LOC109946232 | XM_007209634.2 | XP_007209696.1    | <i>probable phospholipid hydroperoxide glutathione peroxidase</i>             | -2.84           | 0.011   |
| LOC18776292  | XM_020563447.1 | XP_020419036.1    | <i>methanol O-anthraniloyltransferase</i>                                     | -2.77           | 0.039   |
| LOC18784624  | XM_007220161.2 | XP_007220223.1    | <i>beta-amylase 7</i>   | -2.71           | 0.044   |
| LOC18771811  | XM_007201984.2 | XP_007202046.1    | <i>lycopene beta cyclase, chloroplastic/chromoplastic</i>                     | -2.70           | 0.009   |
| LOC18781009  | XM_007211705.2 | XP_007211767.1    | <i>ycf3-interacting protein 1, chloroplastic</i>                              | -2.70           | 0.046   |
| LOC18770198  | XM_020568695.1 | XP_020424284.1    | <i>cold-regulated 413 plasma membrane protein 2, transcript variant X2</i>    | -2.65           | 0.046   |
| LOC18776549  | XM_020564416.1 | XP_020420005.1    | <i>ethylene-responsive transcription factor ERF118, transcript variant X1</i> | -2.65           | 0.047   |
| LOC18777969  | XM_007209427.2 | XP_007209489.1    | <i>bidirectional sugar transporter SWEET4</i>                                 | -2.56           | 0.020   |
| LOC18786335  | XM_007218842.2 | XP_007218904.1    | <i>beta-galactosidase</i>   | -2.52           | 0.008   |
| LOC18769184  | XM_007203569.2 | XP_007203631.1    | <i>DELLA protein DWARF8</i>   | -2.49           | 0.024   |
| LOC18786577  | XR_002270240.1 |                   | <i>pyruvate kinase 1, cytosolic</i>   | -2.46           | 0.033   |
| LOC18767724  | XM_007201691.2 | XP_007201753.1    | <i>ETO1-like protein 1, transcript variant X1</i>                             | -2.34           | 0.038   |
| LOC18782183  | XM_007215315.2 | XP_007215377.1    | <i>protein farnesyltransferase subunit beta</i>                               | -2.24           | 0.043   |
| LOC18786310  | XM_007220464.2 | XP_007220526.1    | <i>NADP-dependent D-sorbitol-6-phosphate dehydrogenase</i>                    | -2.16           | 0.045   |
| LOC18785044  | XM_007218342.2 | XP_007218404.1    | <i>soluble inorganic pyrophosphatase 1</i>                                    | -2.16           | 0.046   |
| LOC18766941  | XM_007201311.2 | XP_007201373.1    | <i>probable 2-oxoglutarate-dependent dioxygenase At5g05600</i>                | -2.11           | 0.049   |
| LOC18779016  | XM_020561850.1 | XP_020417439.1    | <i>starch synthase 3, chloroplastic/amyloplastic, transcript variant X2</i>   | -2.01           | 0.039   |
| LOC18781818  | XM_007215454.2 | XP_007215516.1    | <i>pyrophosphate--fructose 6-phosphate 1-phosphotransferase subunit beta</i>  | -2.01           | 0.040   |



**Table S3.** List of exclusively expressed and identified DEGs in the comparison of control vs. CS with control vs. CO<sub>2</sub> + CS ‘Madoka’ peach fruit after 12 days storage.

| Gene_id             | mRNA_accession | Protein accession | Gene descriptions  | Log fold change | p value |
|---------------------|----------------|-------------------|--|-----------------|---------|
| <b>Up-regulated</b> |                |                   |  |                 |         |
| LOC18777938         | XM_007210330.2 | XP_007210392.1    | disease resistance protein RPM1                                      | 5.00            | 0.047   |
| LOC18778873         | XM_020562922.1 | XP_020418511.1    | E3 ubiquitin-protein ligase RMA1H1                                   | 4.29            | 0.006   |
| LOC109949277        | XM_020564500.1 | XP_020420089.1    | zinc finger MYM-type protein 1-like, transcript variant X1           | 3.79            | 0.046   |
| LOC18792502         | XM_007223052.2 | XP_007223114.2    | beta-amylase 1, chloroplastic  | 3.54            | 0.038   |
| LOC109946750        | XM_020555453.1 | XP_020411042.1    | MDIS1-interacting receptor like kinase 2-like                        | 3.51            | 0.015   |
| LOC18781808         | XM_007215851.2 | XP_007215913.1    | 26.5 kDa heat shock protein, mitochondrial                           | 3.38            | 0.020   |
| LOC18785140         | XM_007218771.2 | XP_007218833.1    | ethylene-responsive transcription factor 2                           | 3.33            | 0.005   |
| LOC18792321         | XM_007222045.2 | XP_007222107.1    | probable xyloglucan endotransglucosylase /hydrolase protein 23       | 3.32            | 0.048   |
| LOC18784769         | XM_007218307.2 | XP_007218369.1    | homeobox-leucine zipper protein ATHB-12                              | 3.27            | 0.005   |
| LOC18782384         | XM_007215690.2 | XP_007215752.1    | Xyloglucan endotransglucosylase/hydrolase protein 9                  | 3.22            | 0.008   |
| LOC18781249         | XM_007213862.2 | XP_007213924.2    | non-specific phospholipase C2  | 3.18            | 0.024   |
| LOC18792450         | XM_020554466.1 | XP_020410055.1    | putative disease resistance protein At1g50180, transcript variant X2 | 3.14            | 0.015   |
| LOC18786254         | XM_007220340.2 | XP_007220402.1    | probable protein phosphatase 2C 25                                   | 2.99            | 0.033   |
| LOC109950746        | XM_020570777.1 | XP_020426366.1    | phosphopantothenoylcysteine decarboxylase subunit VHS3               | 2.92            | 0.041   |
| LOC109948313        | XM_020560949.1 | XP_020416538.1    | prostatic spermine-binding protein-like                              | 2.90            | 0.038   |
| LOC18766151         | XM_020553614.1 | XP_020409203.1    | CCG-binding protein 1  | 2.88            | 0.006   |
| LOC18782080         | XM_007214780.2 | XP_007214842.1    | chaperone protein dnaJ 8, chloroplastic                              | 2.79            | 0.009   |
| LOC109946468        | XM_020554385.1 | XP_020409974.1    | G-type lectin S-receptor-like serine/threonine-protein kinase SD2-5  | 2.79            | 0.039   |
| LOC18783132         | XM_020559174.1 | XP_020414763.1    | Probable receptor-like serine/threonine-protein kinase LRK10L-1.4    | 2.78            | 0.021   |
| LOC18767054         | XM_007200310.2 | XP_007200372.1    | nitronate monooxygenase  | 2.71            | 0.046   |
| LOC18766098         | XM_007198776.2 | XP_007198838.1    | E3 ubiquitin-protein ligase RMA1H1                                   | 2.65            | 0.017   |
| LOC18785778         | XM_007219774.2 | XP_007219836.2    | glycerol-3-phosphate dehydrogenase [NAD(+)] 2, chloroplastic         | 2.61            | 0.047   |
| LOC18772963         | XM_007207282.2 | XP_007207344.1    | probable aquaporin PIP2-5  | 2.58            | 0.047   |

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| Gene_id     | mRNA_accession | Protein accession | Gene descriptions  | Log fold change | p value |
|-------------|----------------|-------------------|--|-----------------|---------|
| LOC18785553 | XM_007217962.2 | XP_007218024.1    | UDP-glucuronate 4-epimerase 3                                | 2.46            | 0.021   |
| LOC18766119 | XM_007198838.2 | XP_007198900.1    | transcriptional regulator DEF1, transcript variant X2        | 2.46            | 0.016   |
| LOC18791459 | XM_020562849.1 | XP_020418438.1    | disease resistance protein RGA2, transcript variant X1       | 2.45            | 0.013   |
| LOC18770307 | XM_020568329.1 | XP_020423918.1    | polygalacturonase ADPG2                                      | 2.44            | 0.011   |
| LOC18780582 | XM_007211964.2 | XP_007212026.1    | probable polygalacturonase                                   | 2.36            | 0.032   |
| LOC18772623 | XM_007208228.2 | XP_007208290.1    | WRKY transcription factor WRKY24                             | 2.34            | 0.036   |
| LOC18766055 | XM_007198843.2 | XP_007198905.2    | callose synthase 12  | 2.29            | 0.019   |
| LOC18776744 | XM_007210319.2 | XP_007210381.1    | chaperone protein ClpB1                                      | 2.28            | 0.019   |
| LOC18776384 | XM_020564475.1 | XP_020420064.1    | heat stress transcription factor B-2b, transcript variant X2 | 2.28            | 0.035   |
| LOC18768018 | XM_007200293.2 | XP_007200355.1    | UDP-galactose transporter 2                                  | 2.28            | 0.019   |
| LOC18785165 | XM_007218813.2 | XP_007218875.1    | CDPK-related kinase 4  | 2.25            | 0.033   |
| LOC18785268 | XM_007219503.2 | XP_007219565.2    | ethylene-responsive transcription factor ERF106              | 2.25            | 0.043   |
| LOC18766507 | XM_007199633.2 | XP_007199695.2    | calcium-transporting ATPase 12, plasma membrane-type         | 2.24            | 0.043   |
| LOC18769333 | XM_007202197.2 | XP_007202259.1    | fructose-bisphosphate aldolase, cytoplasmic isozyme          | 2.24            | 0.019   |
| LOC18778646 | XM_020563201.1 | XP_020418790.1    | 50S ribosomal protein L34, chloroplastic                     | 2.20            | 0.044   |
| LOC18766383 | XM_007199596.2 | XP_007199658.1    | serine/threonine-protein kinase STY46, transcript variant X1 | 2.20            | 0.023   |
| LOC18777605 | XM_007209252.2 | XP_007209314.1    | ethylene-responsive transcription factor 5                   | 2.20            | 0.022   |
| LOC18783057 | XM_007217136.2 | XP_007217198.1    | non-specific lipid-transfer protein 2                        | 2.16            | 0.024   |
| LOC18785293 | XM_007218710.2 | XP_007218772.1    | probable aquaporin PIP2-5                                    | 2.14            | 0.041   |
| LOC18781811 | XM_007215725.2 | XP_007215787.2    | biotin carboxyl carrier protein of acetyl-CoA carboxylase    | 2.13            | 0.025   |
| LOC18776564 | XM_007209454.2 | XP_007209516.1    | bax inhibitor 1  | 2.12            | 0.047   |
| LOC18793488 | XM_007222228.2 | XP_007222290.1    | probable beta-1,4-xylosyltransferase IRX9H                   | 2.07            | 0.028   |
| LOC18786093 | XM_007220350.2 | XP_007220412.2    | putative lipase ROG1   | 2.06            | 0.036   |
| LOC18772322 | XM_007205075.2 | XP_007205137.1    | WRKY transcription factor 44, transcript variant X3          | 2.05            | 0.029   |
| LOC18788001 | XM_007221428.2 | XP_007221490.1    | probable WRKY transcription factor 23                        | 2.00            | 0.041   |

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| Gene_id               | mRNA_accession | Protein accession | Gene descriptions  | Log fold change | p value |
|-----------------------|----------------|-------------------|--|-----------------|---------|
| LOC18772307           | XM_007205984.2 | XP_007206046.1    | <i>zinc finger A20 and AN1 domain-containing stress-associated protein 3</i> | 2.00            | 0.048   |
| <b>Down-regulated</b> |                |                   |  |                 |         |
| LOC18777021           | XM_007209293.2 | XP_007209355.1    | <i>magnesium protoporphyrin IX methyltransferase, chloroplastic</i>          | -4.77           | 0.049   |
| LOC18789892           | XM_007222098.2 | XP_007222160.1    | <i>probable pectate lyase 8</i>  | -4.63           | 0.033   |
| LOC18787444           | XM_020557608.1 | XP_020413197.1    | <i>glyoxylate/hydroxypyruvate reductase HPR3, transcript variant X3</i>      | -3.29           | 0.012   |
| LOC18771700           | XM_007202680.2 | XP_007202742.1    | <i>protein RALF-like 34</i>  | -3.28           | 0.016   |
| LOC18769359           | XM_007202057.2 | XP_007202119.1    | <i>calcium uniporter protein 2, mitochondrial</i>                            | -3.27           | 0.002   |
| LOC18790537           | XM_007222967.2 | XP_007223029.1    | <i>caffeoylshikimate esterase</i>  | -3.23           | 0.016   |
| LOC18786520           | XM_007218309.2 | XP_007218371.1    | <i>chalcone--flavonone isomerase</i>   | -3.13           | 0.020   |
| LOC18781009           | XM_007211705.2 | XP_007211767.1    | <i>ycf3-interacting protein 1, chloroplastic</i>                             | -3.08           | 0.028   |
| LOC18782204           | XM_007215934.2 | XP_007215996.1    | <i>30S ribosomal protein 3, chloroplastic</i>                                | -3.08           | 0.026   |
| LOC18768052           | XM_020570437.1 | XP_020426026.1    | <i>probable ethylene response sensor 1, transcript variant X2</i>            | -3.06           | 0.009   |
| LOC18786646           | XM_007220912.2 | XP_007220974.1    | <i>binding partner of ACD11 1</i>  | -3.04           | 0.005   |
| LOC18768521           | XM_007199673.2 | XP_007199735.1    | <i>U-box domain-containing protein 15</i>                                    | -3.01           | 0.036   |
| LOC18788573           | XM_007222706.2 | XP_007222768.1    | <i>homogentisate phytyltransferase 1, chloroplastic</i>                      | -3.00           | 0.029   |
| LOC18782078           | XM_007214887.2 | XP_007214949.1    | <i>receptor protein kinase TMK1</i>  | -2.98           | 0.035   |
| LOC18786236           | XM_020558363.1 | XP_020413952.1    | <i>protein IQ-DOMAIN 1, transcript variant X2</i>                            | -2.94           | 0.028   |
| LOC18788709           | XM_007226933.2 | XP_007226995.1    | <i>subtilisin-like protease SBT1.7</i>                                       | -2.80           | 0.014   |
| LOC109948334          | XM_020561096.1 | XP_020416685.1    | <i>7-deoxyloganetin glucosyltransferase-like</i>                             | -2.79           | 0.043   |
| LOC18766941           | XM_007201311.2 | XP_007201373.1    | <i>probable 2-oxoglutarate-dependent dioxygenase At5g05600</i>               | -2.79           | 0.012   |
| LOC18784565           | XM_007218152.2 | XP_007218214.2    | <i>probable membrane-associated kinase regulator 6</i>                       | -2.76           | 0.041   |
| LOC18782183           | XM_007215315.2 | XP_007215377.1    | <i>protein farnesyltransferase subunit beta</i>                              | -2.73           | 0.017   |
| LOC109948390          | XM_020561186.1 | XP_020416775.1    | <i>thioredoxin-like protein CXXS1</i>  | -2.68           | 0.049   |
| LOC18784663           | XM_020556720.1 | XP_020412309.1    | <i>probable prolyl 4-hydroxylase 12, transcript variant X1</i>               | -2.64           | 0.045   |
| LOC18784624           | XM_007220161.2 | XP_007220223.1    | <i>beta-amylase 7</i>  | -2.61           | 0.049   |

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| Gene_id     | mRNA_accession | Protein accession | Gene descriptions  | Log fold change | p value |
|-------------|----------------|-------------------|--|-----------------|---------|
| LOC18788499 | XM_007225093.2 | XP_007225155.1    | <i>two-component response regulator ARR2, transcript variant X2</i>      | -2.61           | 0.011   |
| LOC18783524 | XM_007215463.2 | XP_007215525.1    | <i>probable fructokinase-6, chloroplastic</i>                            | -2.57           | 0.017   |
| LOC18767462 | XM_007201294.2 | XP_007201356.2    | <i>ADP-ribosylation factor-like protein 2</i>                            | -2.57           | 0.045   |
| LOC18784309 | XM_020560648.1 | XP_020416237.1    | <i>phytoene synthase 2, chloroplastic</i>                                | -2.49           | 0.024   |
| LOC18793939 | XM_020555471.1 | XP_020411060.1    | <i>serine/threonine-protein kinase CTR1, transcript variant X2</i>       | -2.49           | 0.044   |
| LOC18767253 | XM_007200562.2 | XP_007200624.2    | <i>pathogenesis-related protein 1</i>                                    | -2.38           | 0.029   |
| LOC18782207 | XM_020558899.1 | XP_020414488.1    | <i>WRKY transcription factor 1, transcript variant X1</i>                | -2.33           | 0.026   |
| LOC18782906 | XM_007215833.2 | XP_007215895.1    | <i>membrane-associated progesterone-binding protein 4</i>                | -2.28           | 0.034   |
| LOC18782125 | XM_020560215.1 | XP_020415804.1    | <i>protein phosphatase 2C 16, transcript variant X2</i>                  | -2.26           | 0.038   |
| LOC18790012 | XM_007225054.2 | XP_007225116.1    | <i>EIN3-binding F-box protein 1</i>                                      | -2.26           | 0.043   |
| LOC18766258 | XM_007201027.2 | XP_007201089.1    | <i>homoserine kinase</i>   | -2.21           | 0.043   |
| LOC18770881 | XM_007203554.2 | XP_007203616.1    | <i>4-coumarate--CoA ligase-like 7</i>                                    | -2.15           | 0.046   |
| LOC18786577 | XR_002270240.1 |                   | <i>pyruvate kinase 1, cytosolic</i>                                      | -2.13           | 0.030   |
| LOC18783169 | XM_007215295.2 | XP_007215357.1    | <i>COBRA-like protein 1</i>  | -2.11           | 0.032   |
| LOC18767451 | XM_007199766.2 | XP_007199828.1    | <i>4-hydroxy-3-methylbut-2-enyl diphosphate reductase, chloroplastic</i> | -2.05           | 0.033   |