

| Table S1. Differentially expressed proteins of the strawberry ( <i>Fragaria × ananassa</i> Duch. ‘Benihoppe’) proteome at five developmental stages. Different letters followed means indicated significantly different in the same row, <i>P</i> < 0.05. |                                                                     |                               |                      |                    |           |                                         |       |        |        |       |
|-----------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|---------------------------------------------------------------------|-------------------------------|----------------------|--------------------|-----------|-----------------------------------------|-------|--------|--------|-------|
| No. <sup>a</sup>                                                                                                                                                                                                                                          | Protein name                                                        | Accession number <sup>b</sup> | MW [Da] <sup>c</sup> | Score <sup>d</sup> | #Peptides | Protein Relative abundance <sup>e</sup> |       |        |        |       |
|                                                                                                                                                                                                                                                           |                                                                     |                               |                      |                    |           | SG                                      | BG    | WF     | TU     | RF    |
| 1                                                                                                                                                                                                                                                         | alcohol acyltransferase                                             | gi 10121328                   | 52048.20             | 143                | 10        | 0d                                      | 1.11c | 1.65c  | 2.47b  | 5.53a |
| 2                                                                                                                                                                                                                                                         | pyruvate decarboxylase                                              | gi 10121330                   | 67197.97             | 628                | 30        | 0e                                      | 0.24d | 1.03c  | 1.49b  | 3.04a |
| 3                                                                                                                                                                                                                                                         | pyruvate decarboxylase                                              | gi 17225598                   | 67388.31             | 641                | 32        | 0d                                      | 0.55c | 0.79c  | 1.27b  | 2.95a |
| 4                                                                                                                                                                                                                                                         | UDP-glucosyltransferase                                             | gi 28628183                   | 63479.89             | 238                | 16        | 0e                                      | 0.21d | 0.62c  | 1.50b  | 2.52a |
| 5                                                                                                                                                                                                                                                         | 11S globulin precursor isoform 3B                                   | gi 118340975                  | 56780.38             | 127                | 13        | 0d                                      | 0.36c | 0.74b  | 1.41a  | 1.42a |
| 6                                                                                                                                                                                                                                                         | putative N-terminal acetyltransferase                               | gi 6730746                    | 81031.78             | 52                 | 2         | 0d                                      | 0.39c | 0.63b  | 1.56a  | 1.45a |
| 7                                                                                                                                                                                                                                                         | biotin carboxylase subunit                                          | gi 870726                     | 59564.13             | 172                | 6         | 0e                                      | 0.34d | 0.94c  | 1.48b  | 1.83a |
| 8                                                                                                                                                                                                                                                         | thioredoxin H3                                                      | gi 33621084                   | 14036.79             | 98                 | 6         | 0e                                      | 0.44d | 0.74c  | 1.09b  | 2.03a |
| 9                                                                                                                                                                                                                                                         | enolase                                                             | gi 238814974                  | 49121.07             | 339                | 7         | 0d                                      | 0.96c | 1.25b  | 1.18b  | 1.61a |
| 10                                                                                                                                                                                                                                                        | short-chain dehydrogenase reductase                                 | gi 134304897                  | 39959.81             | 35                 | 2         | 0d                                      | 0.35c | 1.38b  | 2.24a  | 2.01a |
| 11                                                                                                                                                                                                                                                        | hsp70-interacting protein                                           | gi 15232329                   | 41289.03             | 53                 | 2         | 0e                                      | 0.52d | 0.83c  | 1.88b  | 2.37a |
| 12                                                                                                                                                                                                                                                        | precursor of carboxylase h-protein 4, glycine decarboxylase complex | gi 224138868                  | 17965.77             | 67                 | 2         | 0e                                      | 0.37d | 0.95c  | 1.83b  | 2.13a |
| 13                                                                                                                                                                                                                                                        | GTP-binding protein                                                 | gi 7643796                    | 46106.61             | 76                 | 5         | 0e                                      | 0.32d | 1.06c  | 1.84b  | 2.16a |
| 14                                                                                                                                                                                                                                                        | Fra a 2 allergen                                                    | gi 260600660                  | 18079.02             | 164                | 11        | 0d                                      | 0.38c | 0.72b  | 2.01a  | 1.98a |
| 15                                                                                                                                                                                                                                                        | cytochrome b-c1 complex subunit 7                                   | gi 225430198                  | 15018.79             | 101                | 4         | 0e                                      | 0.78d | 1.25c  | 1.93b  | 2.44a |
| 16                                                                                                                                                                                                                                                        | TUDOR protein with multiple SNe domains                             | gi 114144940                  | 111360.36            | 65                 | 6         | 0e                                      | 1.06d | 1.83b  | 1.64c  | 2.44a |
| 17                                                                                                                                                                                                                                                        | late embryogenesis abundant hydroxyproline-rich glycoprotein        | gi 15227542                   | 26361.17             | 23                 | 2         | 0e                                      | 1.18d | 1.86c  | 2.01b  | 2.45a |
| 18                                                                                                                                                                                                                                                        | G6PD1                                                               | gi 149938954                  | 60466.65             | 56                 | 2         | 0e                                      | 0.79d | 1.80c  | 2.44b  | 2.91a |
| 19                                                                                                                                                                                                                                                        | potassium channel beta subunit 1                                    | gi 15219795                   | 37332.96             | 87                 | 6         | 0e                                      | 0.99d | 1.85c  | 2.36b  | 2.64a |
| 20                                                                                                                                                                                                                                                        | adenosine kinase isoform 1T-like protein                            | gi 82400168                   | 38621.11             | 499                | 7         | 0e                                      | 0.72d | 1.72c  | 2.01b  | 2.74a |
| 21                                                                                                                                                                                                                                                        | synptobrevin-related protein                                        | gi 33347409                   | 22758.86             | 99                 | 6         | 0d                                      | 1.28c | 1.52b  | 2.33a  | 2.58a |
| 22                                                                                                                                                                                                                                                        | chloroplast carbonic anhydrase                                      | gi 62865755                   | 19698.86             | 283                | 3         | 0e                                      | 1.18d | 1.65c  | 3.58a  | 2.49b |
| 23                                                                                                                                                                                                                                                        | UDP-glucose:hydroxycinnamate 1-O-glucosyltransferase                | gi 165994472                  | 55176.08             | 50                 | 2         | 0e                                      | 1.11d | 1.93c  | 2.28b  | 3.94a |
| 24                                                                                                                                                                                                                                                        | O-methyltransferase                                                 | gi 6760443                    | 41335.80             | 776                | 26        | 0d                                      | 0.91c | 1.86bc | 2.18b  | 4.31a |
| 25                                                                                                                                                                                                                                                        | anthocyanidin synthase                                              | gi 51872683                   | 44306.31             | 338                | 19        | 0e                                      | 0.81d | 1.43c  | 1.96b  | 3.86a |
| 26                                                                                                                                                                                                                                                        | anthocyanidin synthase                                              | gi 51872681                   | 44254.21             | 426                | 21        | 0e                                      | 0.64d | 1.12c  | 2.46b  | 3.44a |
| 27                                                                                                                                                                                                                                                        | quinoneoxidoreductase                                               | gi 29468088                   | 35288.00             | 817                | 51        | 0e                                      | 0.26d | 1.38c  | 1.95b  | 4.71a |
| 28                                                                                                                                                                                                                                                        | annexin                                                             | gi 211906452                  | 36962.45             | 43                 | 3         | 0e                                      | 0.25d | 0.55c  | 1.02b  | 5.04a |
| 29                                                                                                                                                                                                                                                        | cytosolic aldolase                                                  | gi 10645188                   | 39801.97             | 897                | 32        | 0d                                      | 0.30c | 0.76a  | 0.64ab | 0.84a |
| 30                                                                                                                                                                                                                                                        | glyceraldehyde 3-phosphate dehydrogenase                            | gi 16226113                   | 14122.94             | 78                 | 2         | 0e                                      | 0.27d | 0.56c  | 0.79b  | 1.06a |
| 31                                                                                                                                                                                                                                                        | serine carboxipeptidase                                             | gi 6850918                    | 41256.92             | 59                 | 4         | 0d                                      | 0.26c | 0.62b  | 0.68b  | 0.98a |
| 32                                                                                                                                                                                                                                                        | pectinesterase 3-like                                               | gi 225441977                  | 68470.78             | 496                | 23        | 0d                                      | 0.27c | 0.56b  | 0.71a  | 0.73a |
| 33                                                                                                                                                                                                                                                        | Aconitatehydratase, cytoplasmic                                     | gi 3121731                    | 68583.68             | 229                | 5         | 0e                                      | 0.25d | 0.48c  | 0.61b  | 0.75a |
| 34                                                                                                                                                                                                                                                        | pectin methylesterase isoform 1                                     | gi 62288364                   | 24884.99             | 528                | 25        | 0e                                      | 0.27d | 0.47c  | 0.68b  | 0.90a |
| 35                                                                                                                                                                                                                                                        | nutrient reservoir, putative                                        | gi 255570801                  | 53389.02             | 96                 | 3         | 0e                                      | 0.34d | 0.42c  | 0.82a  | 0.72b |
| 36                                                                                                                                                                                                                                                        | nucleoside diphosphate kinase                                       | gi 47026989                   | 18154.51             | 633                | 20        | 0d                                      | 0.28c | 0.48bc | 0.81a  | 0.62b |
| 37                                                                                                                                                                                                                                                        | pyruvate kinase, cytosolic isozyme-like                             | gi 225441044                  | 59061.08             | 174                | 9         | 0d                                      | 0.26c | 0.39bc | 0.46b  | 0.78a |
| 38                                                                                                                                                                                                                                                        | clathrin heavy chain, putative                                      | gi 255574808                  | 197803.76            | 273                | 21        | 0e                                      | 0.17d | 0.34c  | 0.45b  | 0.62a |
| 39                                                                                                                                                                                                                                                        | cytosolic ascorbate peroxidase                                      | gi 5257552                    | 28023.85             | 255                | 13        | 0e                                      | 0.38d | 0.57b  | 0.46c  | 0.62a |
| 40                                                                                                                                                                                                                                                        | heat shock protein 70                                               | gi 6911549                    | 75908.37             | 1127               | 18        | 0d                                      | 0.18c | 0.52a  | 0.39b  | 0.56a |
| 41                                                                                                                                                                                                                                                        | ascorbate peroxidase                                                | gi 15808779                   | 28433.42             | 71                 | 4         | 0e                                      | 0.21d | 0.75b  | 0.48c  | 1.62a |

|    |                                                               |              |           |      |    |    |        |        |        |        |
|----|---------------------------------------------------------------|--------------|-----------|------|----|----|--------|--------|--------|--------|
| 42 | proton P-ATPase                                               | gi 64460298  | 107161.19 | 57   | 5  | 0d | 0.22c  | 0.57b  | 0.50b  | 1.64a  |
| 43 | uridylyate kinase                                             | gi 192910870 | 23450.97  | 76   | 4  | 0e | 0.19d  | 0.57b  | 0.26c  | 1.17a  |
| 44 | 14-3-3 protein, putative                                      | gi 255545912 | 29225.16  | 306  | 33 | 0e | 0.23d  | 0.62b  | 0.35c  | 1.15a  |
| 45 | cystatin CPI-1                                                | gi 70907497  | 27169.49  | 254  | 5  | 0d | 0.17c  | 0.47b  | 0.47b  | 1.13a  |
| 46 | uncharacterized protein LOC100258445                          | gi 225450055 | 40967.19  | 67   | 6  | 0d | 0.39c  | 0.41c  | 0.86b  | 1.21a  |
| 47 | cell wall invertase                                           | gi 4205113   | 46555.50  | 159  | 4  | 0e | 0.35d  | 0.48c  | 0.76b  | 1.23a  |
| 48 | Ribosomal protein S5/Elongation factor G/III/V family protein | gi 238479752 | 93889.68  | 304  | 12 | 0d | 0.33c  | 0.63b  | 0.68b  | 1.36a  |
| 49 | actin                                                         | gi 113367104 | 14471.89  | 400  | 11 | 0d | 0.40c  | 0.93b  | 0.91b  | 0.95a  |
| 50 | Heat shock 70 kDa protein                                     | gi 123601    | 73086.97  | 1102 | 19 | 0e | 0.39d  | 0.73c  | 0.88b  | 0.95a  |
| 51 | oligomycin sensitivity conferring protein                     | gi 23507246  | 26255.84  | 56   | 4  | 0d | 0.23c  | 0.47b  | 1.25a  | 1.29a  |
| 52 | temperature-induced lipocalin                                 | gi 77744891  | 21898.88  | 48   | 2  | 0e | 0.39d  | 0.59c  | 1.14ab | 1.21a  |
| 53 | 26S proteasome subunit 4-like                                 | gi 77745479  | 51240.89  | 80   | 5  | 0d | 0.09c  | 0.57b  | 1.18a  | 1.06a  |
| 54 | putative alpha-glucosidase                                    | gi 9049411   | 104345.70 | 49   | 2  | 0e | 0.41d  | 0.62c  | 1.19a  | 0.91b  |
| 55 | peroxiredoxin                                                 | gi 211906454 | 17720.99  | 373  | 5  | 0e | 0.02c  | 0.19b  | -0.04d | 0.24a  |
| 56 | transaldolase isoform 1                                       | gi 225425280 | 49224.17  | 297  | 6  | 0d | -0.22c | 0.13a  | -0.02b | 0.15a  |
| 57 | d-3-phosphoglycerate dehydrogenase, putative                  | gi 255555301 | 64472.46  | 196  | 11 | 0e | -0.13d | 0.08b  | -0.01c | 0.24a  |
| 58 | linoleate 13S-lipoxygenase 2-1                                | gi 225450227 | 104384.78 | 134  | 6  | 0d | 0.16b  | 0.30a  | -0.01c | 0.31a  |
| 59 | actin                                                         | gi 4691448   | 10543.05  | 399  | 8  | 0e | 0.04c  | 0.19b  | -0.12d | 0.42a  |
| 60 | 20S proteasome beta subunit PBG1                              | gi 3421123   | 28097.82  | 298  | 4  | 0d | 0b     | 0.22a  | -0.32c | 0.23a  |
| 61 | transaldolase                                                 | gi 217795376 | 49072.01  | 165  | 7  | 0d | 0.13c  | 0.19b  | 0.11c  | 0.25a  |
| 62 | phospholipase D alpha                                         | gi 58891689  | 93417.08  | 532  | 24 | 0e | 0.11d  | 0.13c  | 0.19b  | 0.29a  |
| 63 | phosphate carrier protein, mitochondrial                      | gi 225456463 | 40338.80  | 111  | 8  | 0d | 0.05c  | 0.18b  | 0.33a  | 0.35a  |
| 64 | protein argonaute 1-lik                                       | gi 225464279 | 122517.55 | 68   | 4  | 0d | 0.07c  | 0.21bc | 0.29b  | 0.43a  |
| 65 | heat shock 70kD protein                                       | gi 3023068   | 15613.10  | 1044 | 18 | 0e | 0.05d  | 0.18c  | 0.26b  | 0.44a  |
| 66 | proteasome subunit beta type, putative                        | gi 255552111 | 22749.27  | 124  | 8  | 0e | 0.04d  | 0.17c  | 0.31a  | 0.24b  |
| 67 | heat shock protein 70                                         | gi 6911551   | 73542.79  | 1641 | 35 | 0e | 0.06d  | 0.22b  | 0.14c  | 0.55a  |
| 68 | heat shock protein 70                                         | gi 254558248 | 72920.86  | 869  | 9  | 0d | 0.17c  | 0.34b  | 0.30bc | 0.41a  |
| 69 | T5E21.1                                                       | gi 7527721   | 64464.83  | 82   | 2  | 0c | 0.29b  | 0.31b  | 0.28b  | 0.53a  |
| 70 | acyl carrier protein                                          | gi 2465010   | 15276.53  | 124  | 4  | 0d | 0.19b  | 0.17b  | -0.49c | 0.45a  |
| 71 | 14-3-3 family protein                                         | gi 55375985  | 30442.78  | 622  | 37 | 0d | 0.21bc | 0.29b  | -0.02c | 0.73a  |
| 72 | ADP-ribosylation factor 1-like protein                        | gi 77999251  | 21019.57  | 358  | 12 | 0e | 0.29c  | 0.48b  | -0.26d | 0.61a  |
| 73 | proteasome subunit alpha type-6 isoform 1                     | gi 225442079 | 27963.59  | 170  | 7  | 0d | -0.20c | -0.12b | -0.19c | 0a     |
| 74 | ER-binding protein                                            | gi 57639078  | 75991.26  | 906  | 22 | 0d | -0.21c | -0.10b | -0.24c | 0.03a  |
| 75 | phosphoenolpyruvate carboxylase                               | gi 294864784 | 34311.46  | 49   | 4  | 0d | -0.12c | -0.07b | -0.11c | 0.06a  |
| 76 | receptor for activated protein kinase C, putative             | gi 255577354 | 36969.56  | 224  | 7  | 0a | -0.10b | -0.13b | -0.33c | -0.12  |
| 77 | 60S ribosomal protein L21                                     | gi 3885884   | 19336.58  | 71   | 2  | 0a | 0.07a  | -0.04b | -0.41d | -0.21c |
| 78 | prohibitin, putative                                          | gi 255553601 | 32637.05  | 137  | 4  | 0b | 0.11a  | -0.10c | -0.08c | -0.13d |
| 79 | Tubulin beta-6 chain                                          | gi 54036489  | 51628.78  | 340  | 16 | 0b | 0b     | 0.28a  | -0.05b | -0.21c |
| 80 | potassium channel beta, putative                              | gi 255554204 | 37301.97  | 88   | 5  | 0d | 0.61a  | 0.13c  | 0.45b  | 0.03d  |
| 81 | ATP synthase beta chain                                       | gi 49182408  | 40597.61  | 292  | 12 | 0e | 0.38c  | 0.57b  | 0.71a  | 0.16d  |
| 82 | aquaporin                                                     | gi 82568687  | 30532.60  | 42   | 2  | 0d | 0.52c  | 0.99b  | 1.66a  | -0.23e |
| 83 | heat shock protein 70                                         | gi 1143427   | 77428.62  | 313  | 10 | 0a | 0a     | -0.77b | -0.73b | -1.03c |
| 84 | tubulin beta-1 chain                                          | gi 225434722 | 51290.03  | 656  | 24 | 0a | -0.20b | -0.55c | -0.80d | -0.90e |
| 85 | dihydrolipoamide S-acetyltransferase                          | gi 9279589   | 46130.85  | 120  | 2  | 0a | -0.21b | -0.56c | -0.60c | -1.11d |
| 86 | cyprosin                                                      | gi 556819    | 56779.90  | 48   | 2  | 0a | -0.22b | -0.61c | -0.85d | -1.32e |
| 87 | major storage protein                                         | gi 54306591  | 17334.94  | 186  | 10 | 0a | -0.43b | -0.86d | -0.57c | -1.13e |

|     |                                                                               |              |          |      |    |    |        |        |         |        |
|-----|-------------------------------------------------------------------------------|--------------|----------|------|----|----|--------|--------|---------|--------|
| 88  | methionine synthase                                                           | gi 115361539 | 86630.12 | 587  | 23 | 0a | -0.30b | -0.65c | -1.11e  | -0.92d |
| 89  | beta-tubulin 13                                                               | gi 166343833 | 51638.06 | 461  | 16 | 0a | -0.10b | -0.35c | -0.69d  | -0.80e |
| 90  | elongation factor 1-alpha                                                     | gi 226530753 | 50911.78 | 775  | 53 | 0a | -0.11b | -0.41c | -0.67d  | -0.82e |
| 91  | 60S ribosomal protein L8                                                      | gi 225447408 | 28859.01 | 200  | 9  | 0a | 0a     | -0.43b | -0.61c  | -0.70d |
| 92  | enolase                                                                       | gi 225455555 | 49654.75 | 446  | 10 | 0a | -0.11b | -0.40c | -0.64d  | -0.71e |
| 93  | 3-isopropylmalate dehydratase, putative                                       | gi 255574875 | 57620.17 | 63   | 2  | 0a | -0.12b | -0.27c | -0.71d  | -0.82e |
| 94  | 5-methyltetrahydropteroyltriglutamate-homocysteinemethyltransferase, putative | gi 255569484 | 86466.10 | 1272 | 48 | 0a | -0.10b | -0.27c | -0.52d  | -0.84e |
| 95  | methionine synthase                                                           | gi 219522337 | 86085.84 | 535  | 21 | 0a | -0.13b | -0.43c | -0.84e  | -0.71d |
| 96  | Beta-tubulin                                                                  | gi 5668671   | 50528.23 | 756  | 27 | 0a | -0.13b | -0.49c | -0.74d  | -0.80d |
| 97  | GDP-D-mannose-3',5'-epimerase                                                 | gi 223469963 | 43838.21 | 314  | 14 | 0a | -0.34b | -0.44c | -0.63d  | -0.80e |
| 98  | cytosolic glyceraldehyde-3-phosphodehydrogenase                               | gi 77416993  | 7156.11  | 161  | 8  | 0a | -0.37b | -0.55c | -0.69d  | -0.74d |
| 99  | cytoplasmic Cu/Zn-superoxide dismutase                                        | gi 95106179  | 15746.65 | 199  | 20 | 0a | -0.10b | -0.43c | -0.58d  | -0.53d |
| 100 | ribosomal protein S19                                                         | gi 445612    | 16297.98 | 131  | 5  | 0a | -0.13b | -0.24c | -0.87d  | -0.86d |
| 101 | elongation factor 1-alpha                                                     | gi 209922600 | 51367.00 | 838  | 54 | 0a | -0.12b | -0.18c | -0.37d  | -0.41e |
| 102 | Tubulin beta-2 chain                                                          | gi 464851    | 47178.96 | 895  | 25 | 0a | -0.10b | -0.18c | -0.49d  | -0.50d |
| 103 | similar to ribosomal protein S26                                              | gi 3885515   | 14946.51 | 79   | 2  | 0a | -0.15b | -0.21c | -0.42d  | -0.60e |
| 104 | harpin binding protein 1                                                      | gi 38679311  | 31724.11 | 36   | 2  | 0a | -0.10b | -0.11b | -0.16bc | -0.42c |
| 105 | 2,3-bisphosphoglycerate-independent phosphoglyceratemutase                    | gi 3914394   | 62579.23 | 64   | 4  | 0a | -0.32b | -0.41c | -0.32b  | -0.81d |
| 106 | 40S ribosomal protein S16                                                     | gi 6984222   | 16987.95 | 154  | 14 | 0a | -0.21b | -0.43d | -0.32c  | -0.62e |
| 107 | ATP synthase beta subunit                                                     | gi 7706846   | 52611.50 | 337  | 17 | 0a | -0.21b | -0.38d | -0.28c  | -0.51e |
| 108 | putative mitochondrial NAD-dependent malate dehydrogenase                     | gi 21388552  | 37160.17 | 527  | 14 | 0a | 0a     | -0.25b | -0.72c  | -0.30b |
| 109 | leaf catalase                                                                 | gi 3202032   | 58022.58 | 123  | 6  | 0a | -0.10b | -0.43d | -0.82e  | -0.20c |
| 110 | putative multispinning membrane protein                                       | gi 4115377   | 77434.75 | 44   | 3  | 0a | -0.16b | -0.16b | -1.08d  | -0.22c |
| 111 | putative selenium binding protein                                             | gi 21693595  | 17424.70 | 39   | 3  | 0a | 0a     | -0.26b | -0.25b  | -1.40c |
| 112 | serine hydroxymethyltransferase                                               | gi 134142065 | 53631.69 | 549  | 21 | 0a | -0.20b | -0.57c | -1.42d  | -1.41d |
| 113 | actin                                                                         | gi 157060284 | 25129.89 | 221  | 13 | 0a | -0.63b | -0.91c | -1.27d  | -1.40e |
| 114 | beta tubulin like protein                                                     | gi 78210840  | 45390.73 | 625  | 26 | 0a | -0.64b | -1.05c | -1.28d  | -1.62e |
| 115 | 1-Cys peroxiredoxin                                                           | gi 54306593  | 10065.71 | 198  | 3  | 0a | -0.34b | -0.86c | -1.31d  | -2.22e |
| 116 | RAD23 protein                                                                 | gi 5640111   | 41904.84 | 69   | 3  | 0a | -0.32b | -0.77c | -1.22d  | -1.90e |
| 117 | putative phosphoglucomutase                                                   | gi 15220668  | 64946.97 | 185  | 11 | 0a | -0.41b | -1.83d | -1.89d  | -1.41c |
| 118 | non-specific lipid transfer protein precursor                                 | gi 67937775  | 12513.94 | 103  | 5  | 0a | -0.40b | -2.05d | -1.31c  | -1.40c |
| 119 | chlorophyll a-b binding protein 40, chloroplastic                             | gi 225446831 | 29153.39 | 80   | 5  | 0a | -0.52b | -1.65d | -0.96c  | -2.10e |
| 120 | ribulose-1,5-bisphosphate carboxylase/oxygenase small subunit                 | gi 116672873 | 20485.35 | 46   | 2  | 0a | -0.53b | -0.89c | -1.37d  | -2.71e |
| 121 | 2-cys peroxiredoxin                                                           | gi 269980509 | 29339.63 | 161  | 4  | 0a | -0.51b | -1.51c | -1.78d  | -2.73e |
| 122 | Triosephosphateisomerase, chloroplastic;                                      | gi 13431949  | 34535.36 | 103  | 10 | 0a | -1.56b | -1.83c | -2.28e  | -2.11d |
| 123 | putative NAD dependent malic enzyme                                           | gi 148807201 | 26539.36 | 138  | 3  | 0a | -0.92b | -2.23d | -2.05c  | -2.32d |
| 124 | aspartyl protease family protein                                              | gi 15232503  | 46665.41 | 61   | 4  | 0a | -0.52b | -1.83c | -1.79c  | -2.19d |
| 125 | methionine synthase                                                           | gi 71000469  | 90032.14 | 431  | 26 | 0a | -0.70b | -1.67c | -2.06d  | -2.10d |
| 126 | elongation factor 1-alpha                                                     | gi 148524155 | 49629.91 | 419  | 39 | 0a | -0.82b | -1.42c | -2.33e  | -1.81d |
| 127 | Fra a 1 allergen                                                              | gi 74197562  | 18391.20 | 632  | 23 | 0a | -0.41b | -2.24c | -2.33c  | -2.82d |
| 128 | Major strawberry allergen Fra a 1-B                                           | gi 90185678  | 18419.23 | 651  | 23 | 0a | -0.82b | -2.05c | -2.26d  | -2.61e |
| 129 | Major strawberry allergen Fra a 1-C                                           | gi 90185686  | 18348.19 | 594  | 20 | 0a | -0.95b | -2.02c | -2.31d  | -2.60e |
| 130 | methionine synthase                                                           | gi 151347486 | 86452.04 | 1447 | 44 | 0a | -1.50b | -1.79c | -2.13d  | -2.22e |
| 131 | malate dehydrogenase, cytoplasmic                                             | gi 162464321 | 36518.84 | 1675 | 30 | 0a | -1.93b | -2.19c | -2.39d  | -2.60e |
| 132 | isoflavonereductase related protein                                           | gi 3243234   | 34475.04 | 92   | 2  | 0a | -0.85b | -1.64c | -2.62d  | -3.21e |

|     |                                                               |              |          |      |    |    |        |        |        |        |
|-----|---------------------------------------------------------------|--------------|----------|------|----|----|--------|--------|--------|--------|
| 133 | Pectinesterase-3 precursor, putative                          | gi 255550271 | 65621.11 | 97   | 8  | 0a | -0.32b | -2.06c | -3.67d | -2.12c |
| 134 | ribulose-1,5-bisphosphate carboxylase/oxygenase large subunit | gi 17154560  | 50134.90 | 183  | 20 | 0a | -1.34b | -2.62c | -3.06d | -3.75e |
| 135 | ribulose-1,5-bisphosphate carboxylase/oxygenase               | gi 22859628  | 48066.58 | 140  | 12 | 0a | -0.99b | -2.75c | -3.25d | -4.10e |
| 136 | malate dehydrogenase                                          | gi 259414628 | 44350.30 | 296  | 10 | 0a | -1.03b | -3.03c | -3.68e | -3.52d |
| 137 | S-adenosylmethionine synthase 2                               | gi 75309777  | 44094.15 | 522  | 24 | 0a | -0.92b | -2.97c | -3.84d | -4.23e |
| 138 | putative quinoneoxidoreductase                                | gi 15808674  | 37312.13 | 2048 | 63 | 0e | 0.77d  | 1.87c  | 2.76b  | 5.21a  |
| 139 | phenylalanine ammonia-lyase                                   | gi 39777534  | 79365.62 | 100  | 6  | 0e | 0.75d  | 2.36c  | 2.77b  | 5.62a  |
| 140 | aldo/ketoreductase                                            | gi 53988164  | 37035.99 | 215  | 15 | 0e | 1.11d  | 1.88c  | 2.99b  | 4.67a  |
| 141 | alcohol acyltransferase                                       | gi 254771939 | 51772.08 | 95   | 7  | 0e | 1.13d  | 2.40c  | 3.39b  | 6.21a  |
| 142 | UDP glucose:flavonoid-3-O-glucosyltransferase                 | gi 46370000  | 51676.80 | 513  | 14 | 0e | 0.41d  | 1.68c  | 3.57b  | 5.75a  |
| 143 | flavanone 3-hydroxylase                                       | gi 51493451  | 42413.72 | 606  | 34 | 0e | 0.83d  | 3.04c  | 4.34b  | 6.18a  |

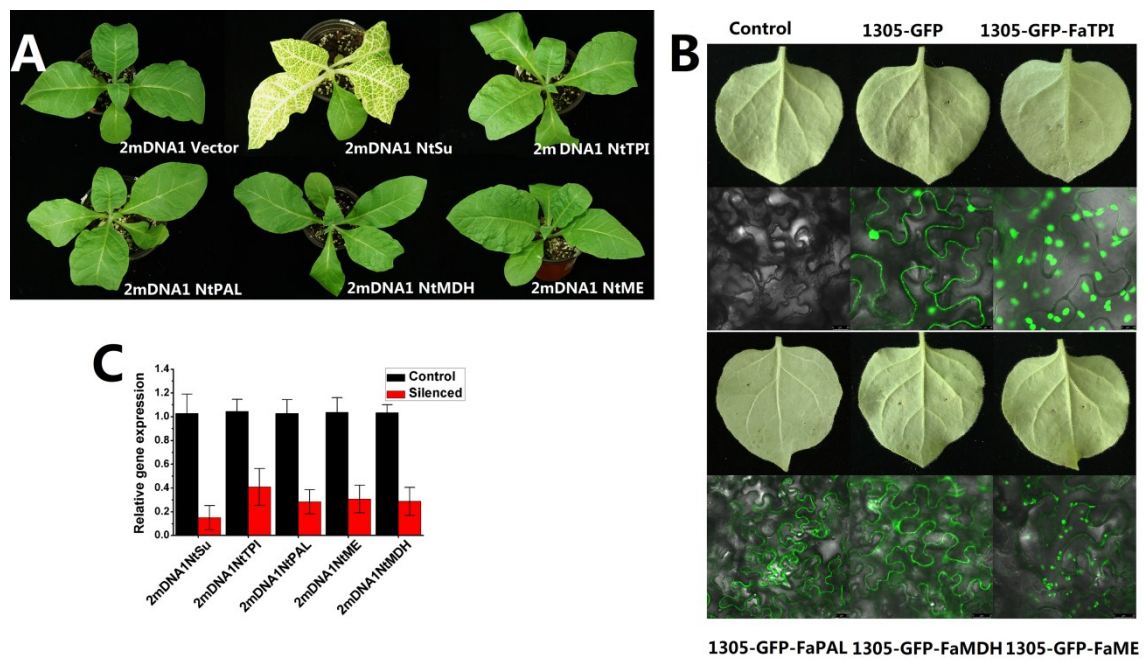
a :Protein no. and order correspond to the hierarchical clustering analysis in Figure 6; b: Accession numbers from theNCBI Viridiplantae database; c: Experimental mass (Da) of identified proteins; d: Mascot score reported after searching against the NCBI Viridiplantae database; e: Relative abundances of normalized protein expression; values are expressed as the mean of three replications (n=3). Different letters followed means indicated significantly different in the same row,  $P < 0.05$ .

**Table S2.** Primers used for RT-PCR analysis in strawberry fruit.

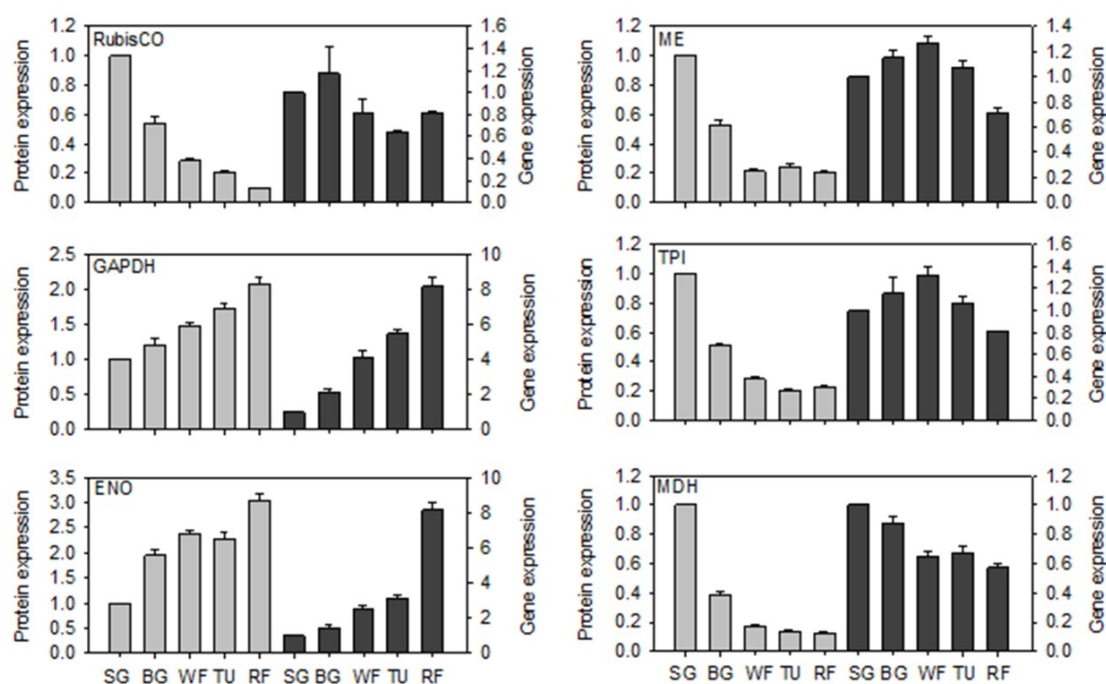
| Gene    | Forward (5'–3')       | Reverse (5'–3')       | Product length |
|---------|-----------------------|-----------------------|----------------|
| PDC     | GCAAAACCGAGAACCACGAC  | GTGACGCCGATTTGAACGAG  | 145            |
| ME      | AGAGACGTGTACGGTGAGGA  | AAGACCACGCAAGTAGTGGG  | 159            |
| RubisCO | ATGCGTTGGAGAGACCGTTT  | AAGTAGACCGTTGTCTCGGC  | 237            |
| TPI     | GGCACTCTGAACGGAGACAT  | GGCCACCTTACCAGTTCCAA  | 248            |
| GAPDH   | TGTCGGAAGGTTCTGCCTG   | AGGTGGCCTTCTTCTCAAGTC | 116            |
| MDH     | CCAGTTCGCGTTCTCGTTAC  | TCAATGCCTCAGCAGCGAAT  | 142            |
| ENO     | GAGAGATGGCGGTTTCGGATT | TGTTCCGTTGGGTCCCTTTC  | 105            |
| AAT     | TTTCTCAAGTCCTGGGGTGC  | ACTGACTCGCTCTTCGCTTC  | 227            |
| QR      | GGTCGGAAGCCAAGTAACCA  | TCTGCCAAAGACCCAAACCT  | 102            |
| OMT     | CAACCTCTTCGCCATGCAAC  | GGTTCTTGGTCGGAAGCTGA  | 155            |
| MetS    | AACCCTTCGGGACGTTTTGT  | TGTATGCACCACTTCGGTCC  | 157            |
| APX     | CACACAAGGAACGGTCTGGA  | AACAAGAGGGCGGAAGACAG  | 161            |
| PrxR2   | AAATTGCTACTCCGGCGAAC  | ACCCTTTTGGGAAGGAAGGT  | 128            |
| TRX     | CTGTCTCATCGCTCCGTCG   | TCCTCTTGTTGTTGGGAGCC  | 109            |
| IFR     | GGCCACCCGACTTATGTTCT  | AGATGAGCGCCTTGCTTCTT  | 101            |
| PAL     | CATTGACGATCCTTGACGCG  | GCCCTAACGCTCTCAACCTC  | 183            |
| F3H     | TTTCTACCCGAAATGCCCCG  | TCACCACGAAAGCTCCTTCC  | 170            |
| ANS     | TATCAACCACGGCATCTCCG  | GGCCTGGTCATTGGCATACT  | 109            |
| AKR     | TGACAGCAACCCAAATCCCA  | GCAGTGTCGAAGTGTCCGTA  | 163            |
| UFGT    | TACCCGTTTTTGAGGAGGGC  | AGGACCAACAGCCTTGATCG  | 144            |
| Fraa1   | TGGTATCAGCTCCTCACGGA  | AGTTGTATTGCTGGGGTGG   | 168            |
| Fraa2   | CGTCATCCCACCAAGAT     | CGCCTCCGTCTCCTTCAATG  | 116            |
| nsLTP1  | CTTTGGTCGCTCTCTTGTC   | CCGCGCTGTTAAGGGATCTA  | 162            |

**Table S3.** Primers used for vectors construction and RT-PCR analysis in tobacco plants.

|                                                          | Gene          | Accession number | Primers | Sequence(5'-3')                    | Restriction site |
|----------------------------------------------------------|---------------|------------------|---------|------------------------------------|------------------|
| Primers used for 2mDNA1-derivated vectors construction   | NtTPI         | 107760622        | -F      | CGCGGATCCCCACAGTTCTCTGGCCTCCGTAA   | BamHI            |
|                                                          |               |                  | -R      | CTAGTCTAGACCAGTCCAACAATTTTGGGC     | XbaI             |
|                                                          | NtPAL         | 107792668        | -F      | CGCGGATCCTCTGAGGAATGCAGTCAAGA      | BamHI            |
|                                                          |               |                  | -R      | CTAGTCTAGATTGCAGGGTTCCCATTTTCC     | XbaI             |
|                                                          | NtMDH         | 107773752        | -F      | CGCGGATCCCTCGAGAAGCATGCAGCTTC      | BamHI            |
|                                                          |               |                  | -R      | CTAGTCTAGACTCTGCTGCACAGTAGTTATG    | XbaI             |
|                                                          | NtME          | 107804419        | -F      | CGCGGATCCATCAGTCCATCACCCCTTGG      | BamHI            |
|                                                          |               |                  | -R      | CTAGTCTAGACCTGAAGATGCTGCCATATT     | XbaI             |
| Primers used for 1305-GFP-derivated vectors construction | TPI           | AF257322         | -F      | TCCCCCGGGATGGCGGTGGCCTCCACATCTCTCG | SmaI             |
|                                                          |               |                  | -R      | CGCGGATCCAGCAGCAACTTTCTTGGATGTTACA | BamHI            |
|                                                          | PAL           | 101292546        | -F      | TCCCCCGGGATGGCGCTTAACGGAACGGAA '   | SmaI             |
|                                                          |               |                  | -R      | CGCGGATCCAGATATGGGCAGGGGGGCACCATT  | BamHI            |
|                                                          | MDH           | 101301095        | -F      | TCCCCCGGGATGGCCAAAGAACCAGTTCGCGT   | SmaI             |
|                                                          |               |                  | -R      | CGCGGATCCATTGATGCAAGTGTATGCCAAGGCC | BamHI            |
|                                                          | ME            | 101305570        | -F      | CTAGTCTAGAATGGACACCATGATCTCGTGAATA | XbaI             |
|                                                          |               |                  | -R      | TCCCCCGGGCTTGAAACTTCGGTAGTTAGGG    | SmaI             |
| Primers used for qRT-PCR in tobacco plants               | NtTPI         | 107760622        | -F      | TCGGAGAGGAGACATGTAAT               |                  |
|                                                          |               |                  | -R      | GGCTCATATGCAATGACAAC               |                  |
|                                                          | NtPAL         | 107792668        | -F      | TTGGTGCTACTTCACATAGG               |                  |
|                                                          |               |                  | -R      | AATCTGATGCCAGAATATCC               |                  |
|                                                          | NtMDH         | 107773752        | -F      | CTTCTTAAGGGTGTTGTTGC               |                  |
|                                                          |               |                  | -R      | AACCAACACCTTGACAGTTAG              |                  |
|                                                          | NtGAPDH       | 107780142        | -F      | TCTTGAGGTGTTGGCATGGT               |                  |
|                                                          |               |                  | -R      | GTTGCGATCGGAGACGACTT               |                  |
|                                                          | NtFBA         | 107797422        | -F      | TTGTGACAGCTCCAGGACTT               |                  |
|                                                          |               |                  | -R      | AGGCAAGACCATCAAGACCT               |                  |
|                                                          | NtRubisco     | 800513           | -F      | ATGGACTTACCAGCCTTGAT               |                  |
|                                                          |               |                  | -R      | CGCAGATCTTCCAGACGTAG               |                  |
|                                                          | NtME          | 107804419        | -F      | GGAGGCTGGAACAGGTATAG               |                  |
|                                                          |               |                  | -R      | TGACAGCATTCACCAGTTCT               |                  |
|                                                          | NtPEPC        | 107798381        | -F      | AACGGTCCAAGAATGTTATG               |                  |
|                                                          |               |                  | -R      | CTTTTCAACTTTTGTCGTCG               |                  |
|                                                          | NtCHI         | 107779699        | -F      | GCTCAGAGGAGTTGGCTAAT               |                  |
|                                                          |               |                  | -R      | TCTCTGCATCGGTGTAGGTT               |                  |
|                                                          | NtCHS         | AF311783         | -F      | GGTACTCCGGATGGCTAAGG               |                  |
|                                                          |               |                  | -R      | CCTCTCGACCTCTGGAATTG               |                  |
|                                                          | EF-1 $\alpha$ | AF120093         | -F      | TGAGATGCACCACGAAGCTC               |                  |
|                                                          |               |                  | -R      | CCAACATTGTCACCAGGAAGTG             |                  |

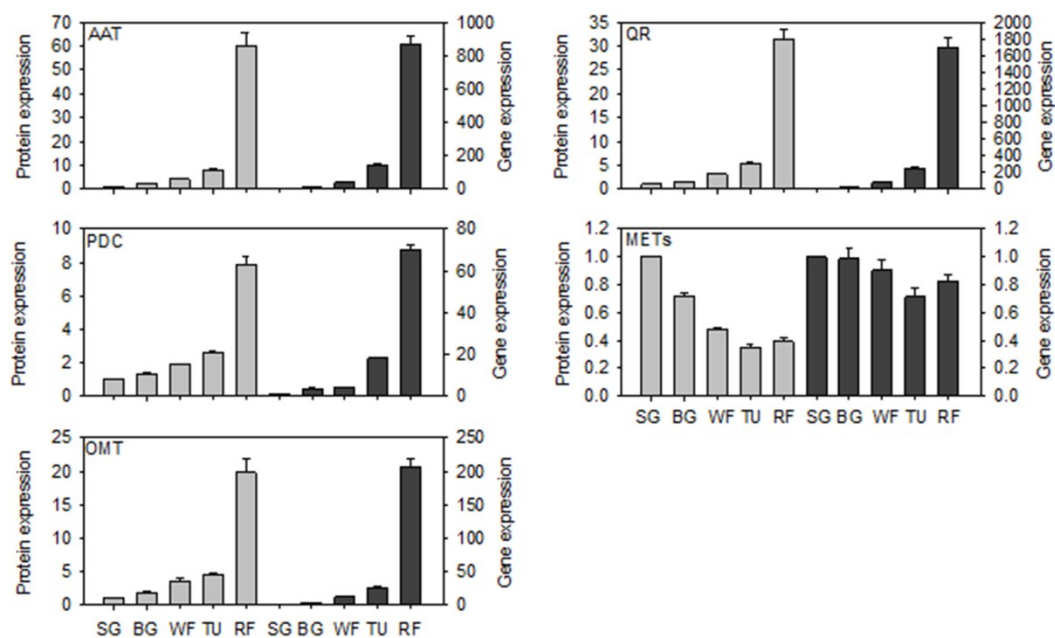


**Figure S1.** Transient expression assay of target genes in tobacco plants. The VIGS induced gene silencing was performed with 2mDNA1 and Pbinplus-Y35-1.9A. The overexpression of target genes was driven by pCAMBIA1305 with a CaMV 35S promoter. (A) Phenotype of 2mDNA1 empty or derived clones infected tobacco plants; (B) Phenotype and fluorescent pictures of tobacco leaves infected by 1305-GFP derived clones; (C) Silencing efficiency analysis in 2mDNA1 derived clones infected tobacco plants.

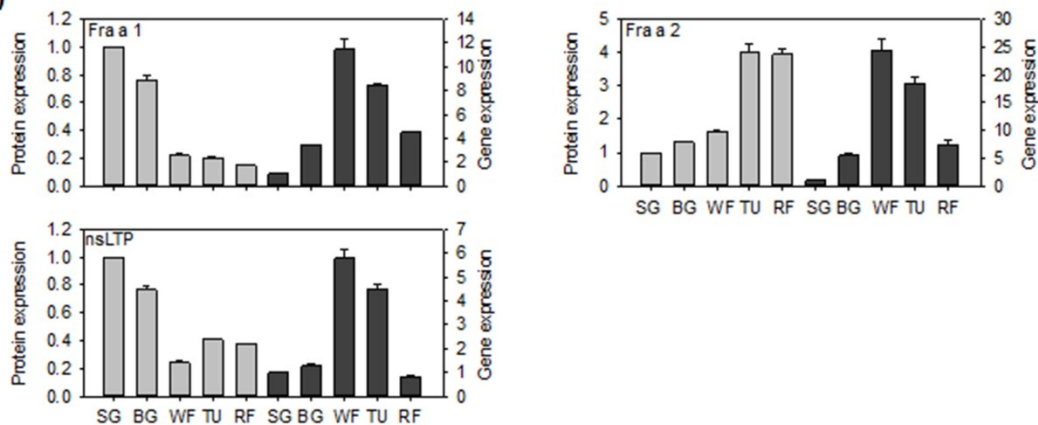


**Figure. S2** Relative expression of detected proteins and encoding genes involved in the carbohydrate and energy metabolism of strawberry (*Fragaria × ananassa* Duch. 'Benihoppe') at five developmental stages.

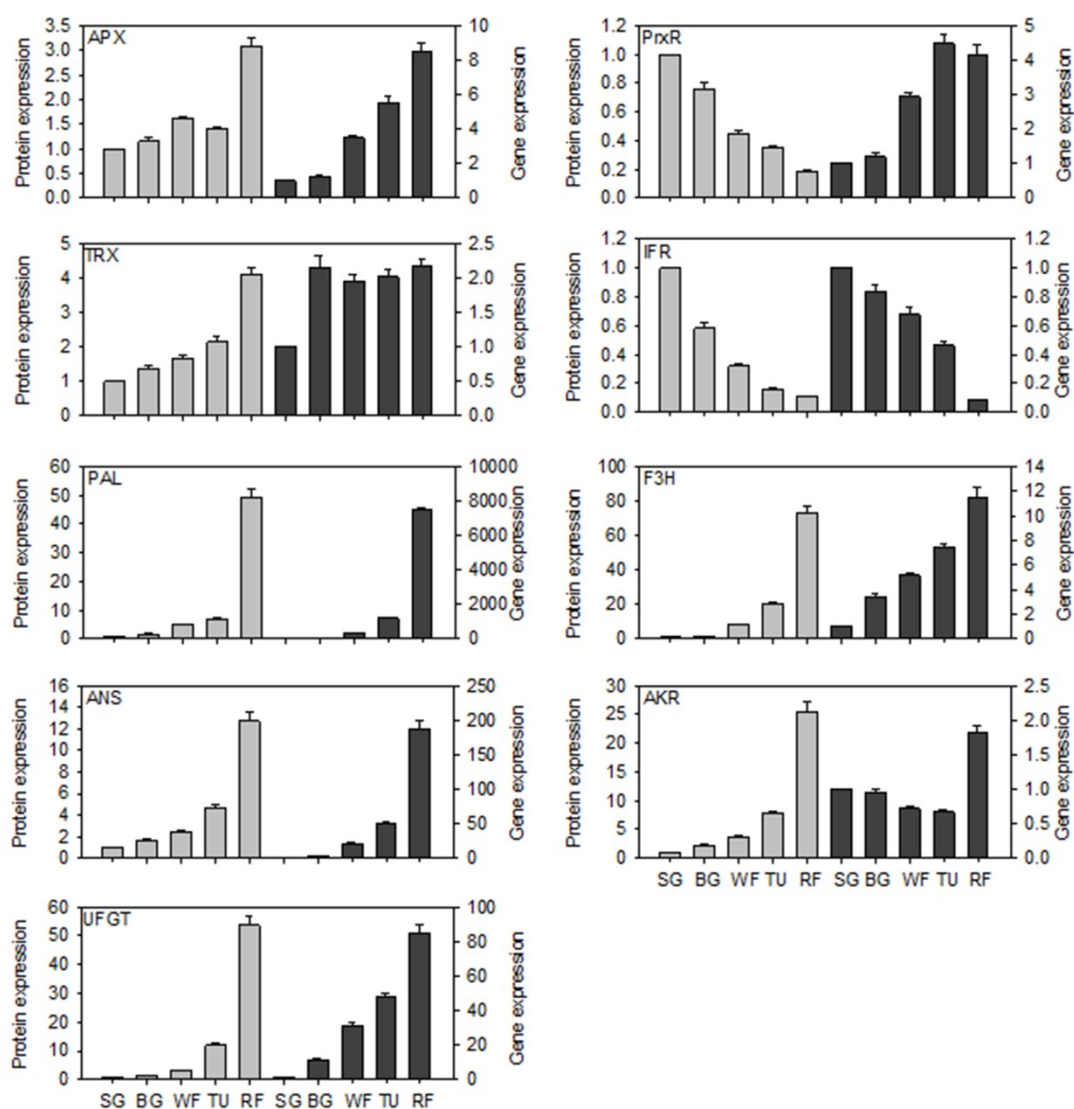
(A)



(B)



**Figure. S3** Relative expression of detected proteins and encoding genes involved in the volatile biosynthesis and allergens of strawberry (*Fragaria × ananassa* Duch. 'Benihoppe') at five developmental stages.



**Figure. S4** Relative expression of detected proteins and encoding genes involved in the flavonoids biosynthesis and defense metabolism of strawberry (*Fragaria x ananassa* Duch. 'Benihoppe') at five developmental stages.