

Supplementary information

Resveratrol accumulation and its involvement in stilbene synthetic pathway of Chinese wild grapes during berry development using quantitative proteome analysis

Ruimin Li^{a,b,c,†}, Xiaoqing Xie^{a,b,c,†}, Fuli Ma^{a,b,c,†}, Dan Wang^{a,b,c}, Lan Wang^{a,b,c}, Jianxia Zhang^{a,b,c}, Yan Xu^{a,b,c}, Xiping Wang^{a,b,c}, Chaohong Zhang^{a,b,c*}, Yuejin Wang^{a,b,c*}

^a College of Horticulture, Northwest A&F University, Yangling, Shaanxi, 712100, the People's Republic of China

^b Key Laboratory of Horticultural Plant Biology and Germplasm Innovation in Northwest China, Ministry of Agriculture, Yangling, Shaanxi 712100, the People's Republic of China

^c State Key Laboratory of Crop Stress Biology in Arid Areas, Northwest A&F University, Yangling, Shaanxi, 712100, the People's Republic of China

*Corresponding author: Chaohong Zhang

E-mail: zhangchaohong@nwsuaf.edu.cn

*Corresponding author: Yuejin Wang

E-mail: wangyj@nwsuaf.edu.cn

Tel: +86-29-87082522; Fax: +86-29-87082522

Supplementary Figures and Tables

Supplementary figure 1. Protein samples detected by SDS-PAGE gel. A1, A2, A3, three biological repeats of Green hard stage of *Vitis quinquangularis* accession Danfeng-2 and *V. vinifera* cv. Cabernet Sauvignon. B1, B2, B3, three biological repeats of Before Veraison stage of Danfeng-2. C1, C2, C3, three biological repeats of Veraison stage of Danfeng-2. D1, D2, D3, three biological repeats of Ripe stage of Danfeng-2. K1, K2, K3, three biological repeats of Green hard stage of Cabernet Sauvignon. L1, L2, L3, three biological repeats of Before Veraison stage of Cabernet Sauvignon. M1, M2, M3, three biological repeats of Veraison stage of Cabernet Sauvignon. N1, N2, N3, three biological repeats of Ripe stage of Cabernet Sauvignon.

Supplementary figure 2. Peptide fractionation using strong cation exchange. A,B,C represent three biological repeats of iTRAQ experiments.

Supplementary figure 3. Protein samples detected by Mass spectra (MALDI-TOF). A, Green hard stage of Danfeng-2. B, Before Veraison stage of Danfeng-2. C, Veraison stage of Danfeng-2. D, Ripe stage of Danfeng-2. E, Green hard stage of Cabernet Sauvignon. F, Before

Veraison stage of Cabernet Sauvignon. G, Veraison stage of Cabernet Sauvignon. H, Ripe stage of Cabernet Sauvignon.

Supplementary figure 4. Data repeatability of iTRAQ experiments of berry developmental stages of *Vitis quinquangularis* accession Danfeng-2 and *V. vinifera* cv. Cabernet Sauvignon. The Ratio at each development stage A) Green hard, B) Before veraison, C) Veraison, D) Ripe, of the three experiments between *Vitis quinquangularis* accession Danfeng-2 and *V. vinifera* cv. Cabernet Sauvignon are plotted in a correlation scatter diagram and the correlation coefficient R values were calculated. Three independent biological replicates are labeled as a, b, and c. 113, 114, 115, 116, 117, 118, 119, 121, samples number of different developmental stages of *Vitis quinquangularis* accession Danfeng-2 and *V. vinifera* cv. Cabernet Sauvignon (as indicated in Fig.1A).

Supplementary Table S1. Primers used in the present study.

Note: Primers were designed with Primer Premier 5.0 and used for qRT-PCR in Figure. 8 and Supplementary Table S6.

Supplementary Table S2. List of peptides identified and quantified in the iTRAQ experiments.

Note: Three independent biological replicates were labeled as a, b, and c. 113, 114, 115, 116, 117, 118, 119, 121, samples number of different developmental stages of Danfeng-2 and Cabernet Sauvignon (as indicated in Fig.1A).

Supplementary Table S3. List of proteins identified and quantified in the iTRAQ experiments.

Note: Three independent biological replicates were labeled as a, b, and c. 113, 114, 115, 116, 117, 118, 119, 121, samples number of different developmental stages of Danfeng-2 and Cabernet Sauvignon (as indicated in Fig.1A).

Supplementary Table S4. Differentially expressed proteins between Danfeng-2 and Cabernet Sauvignon at four developmental stages.

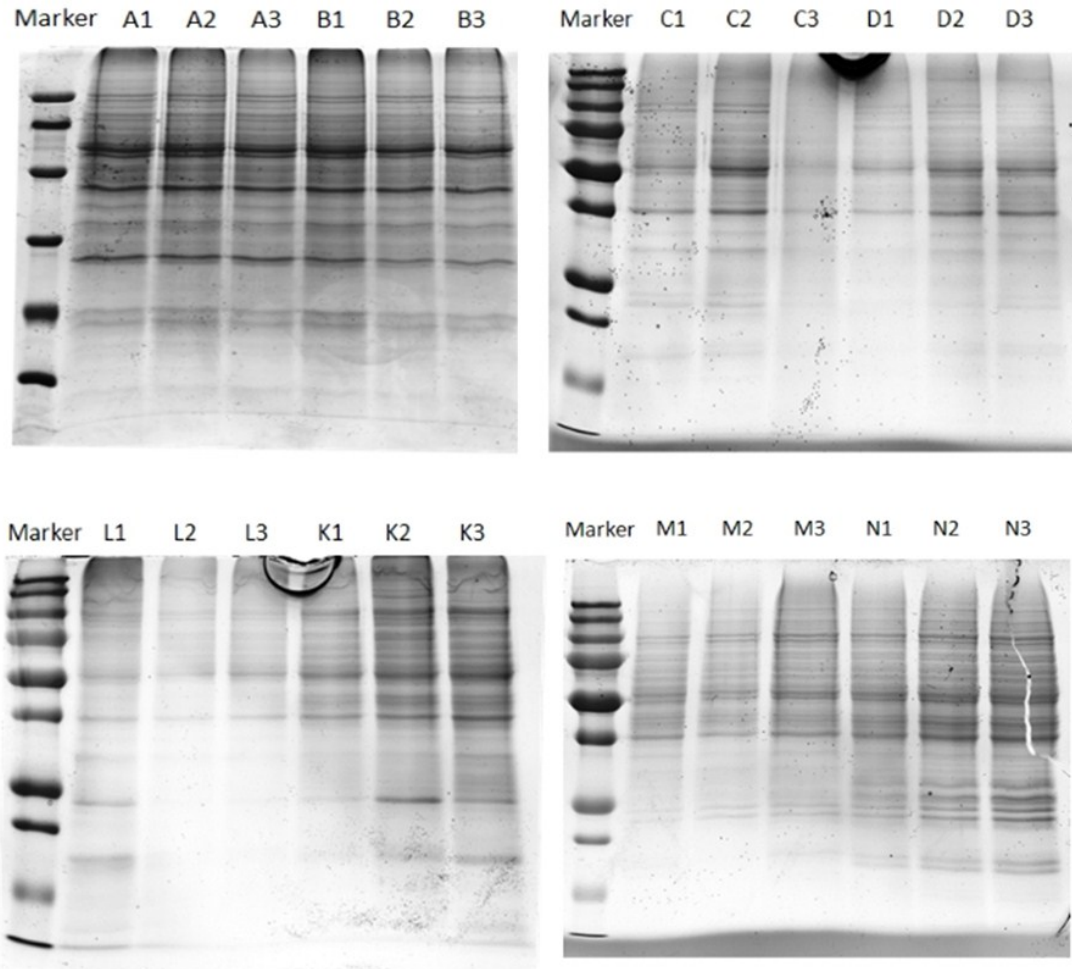
Note: *, significant differentially expressed proteins (p -value < 0.05). 'up' means up-regulated profile and 'down' means down-regulated profile in Danfeng-2. GH, green hard, BV, before veraison, V, veraison, and R, ripe. Three independent biological replicates were labeled as a, b, and c. 113, 114, 115, 116, 117, 118, 119, 121, samples number of different developmental stages of Danfeng-2 and Cabernet Sauvignon (as indicated in Fig.1A).

Supplementary Table S5 Enriched GO terms of differential expressed proteins between Danfeng-2 and Cabernet Sauvignon.

Note: Enriched GO terms were generated in agriGO with customized annotation as reference. *p-values* were converted with *Z*-score generated by z-test. FDR were generated as p-value with multiple test correction.

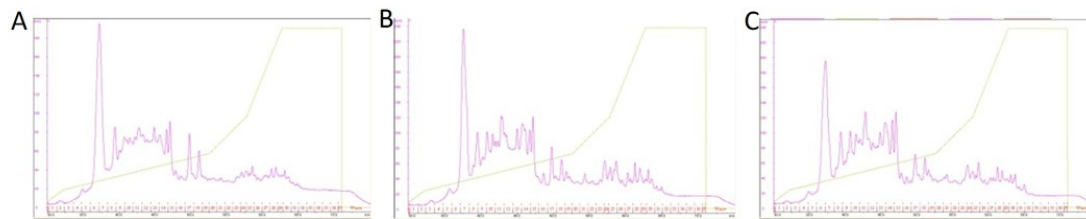
Supplementary Table S6. Comparison of protein and mRNA expression pattern of 15 candidate proteins (genes) at different developmental stages.

Note: RT-PCR data are log2 normalized $2^{-\Delta\Delta Ct}$ values. Relationships of proteins with qRT-PCR transcripts are indicated.

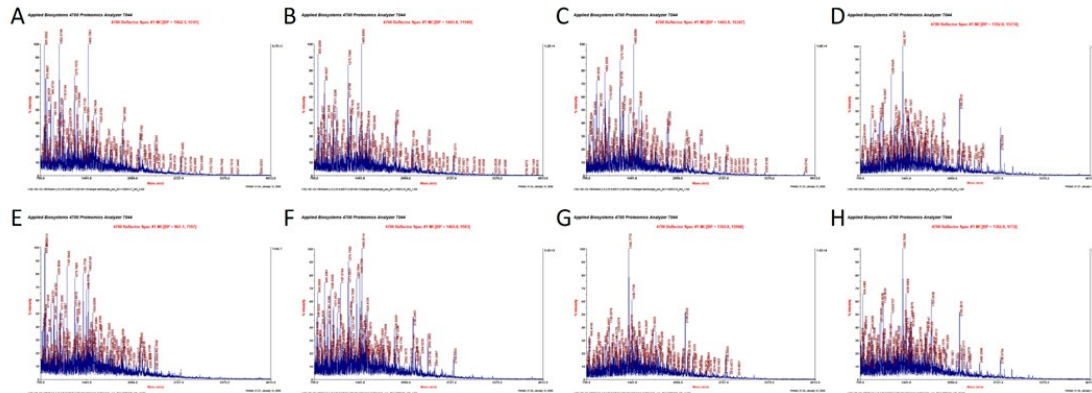


Supplementary figure 1. Protein samples detected by SDS-PAGE gel. A1, A2, A3, three biological repeats of Green hard stage of *Vitis*

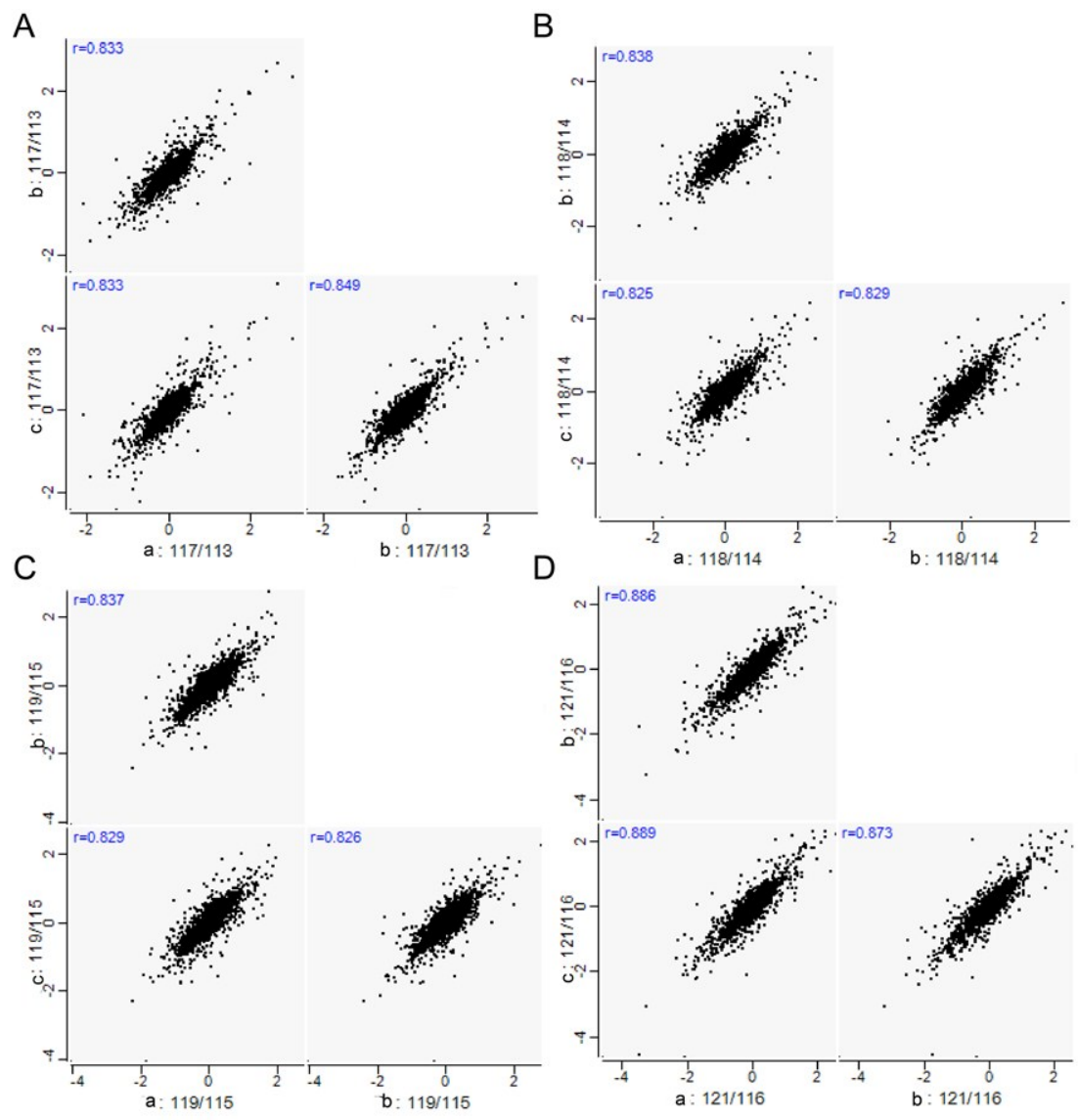
quinquangularis accession Danfeng-2 and *V. vinifera* cv. Cabernet Sauvignon. B1, B2, B3, three biological repeats of Before Veraison stage of Danfeng-2. C1, C2, C3, three biological repeats of Veraison stage of Danfeng-2. D1, D2, D3, three biological repeats of Ripe stage of Danfeng-2. K1, K2, K3, three biological repeats of Green hard stage of Cabernet Sauvignon. L1, L2, L3, three biological repeats of Before Veraison stage of Cabernet Sauvignon. M1, M2, M3, three biological repeats of Veraison stage of Cabernet Sauvignon. N1, N2, N3, three biological repeats of Ripe stage of Cabernet Sauvignon.



Supplementary figure 2. Peptide fractionation using strong cation exchange. A,B,C represent three biological repeats of iTRAQ experiments.



Supplementary figure 3. Protein samples detected by Mass spectra (MALDI-TOF). A, Green hard stage of Danfeng-2. B, Before Veraison stage of Danfeng-2. C, Veraison stage of Danfeng-2. D, Ripe stage of Danfeng-2. E, Green hard stage of Cabernet Sauvignon. F, Before Veraison stage of Cabernet Sauvignon. G, Veraison stage of Cabernet Sauvignon. H, Ripe stage of Cabernet Sauvignon.



Supplementary figure 4. Data repeatability of iTRAQ experiments of berry developmental stages of *Vitis quinquangularis* accession Danfeng-2 and *V. vinifera* cv. Cabernet Sauvignon. The Ratio at each development stage A) Green hard, B) Before veraison, C) Veraison, D) Ripe, of the three experiments between *Vitis quinquangularis* accession Danfeng-2 and *V. vinifera* cv. Cabernet Sauvignon are plotted in a correlation scatter diagram and the correlation coefficient R values were calculated. Three independent biological replicates are labeled as a, b, and c. 113, 114, 115, 116, 117, 118, 119, 121, samples number of different developmental stages of *Vitis quinquangularis* accession Danfeng-2 and *V. vinifera* cv. Cabernet Sauvignon (as indicated in Fig.1A).

Supplementary Table s1. Primers used in the present study

Gene Name_Forward or _Reverse Primer	Primer Sequence
UFGT_Forward	TAACACATTGTGGATGGAACATCAT
UFGT_Reverse	ACCTTCAATTCTCACTCCAATCTC
MYBA1_Forward	GAGGGTGATTTTCCATTTGAT
MYBA1_Reverse	CAAGAACAACTTTTGAACTTAAACAT
MYB14_Forward	TCTGAGGCCGGATATCAAAC
MYB14_Reverse	GGGACGCATCAAGAGAGTGT
MYB15_Forward	CAAGAATGAACAGATGGAGGAG
MYB15_Reverse	TCTGCGACTGCTGGGAAA
MYB5a_Forward	CTAGAACTGTCTGGGAACCT
MYB5a_Reverse	TGCAAGGATCCATTTACATAC
MYB5b_Forward	TGACAGCCGGTGTCTTTAAT
MYB5b_Reverse	AGCATACTAACACAACAACAACC
MYBPA1_Forward	AGATCAACTGGTTATGCTTGCT
MYBPA1_Reverse	AACACAAATGTACATCGCACAC
CHS_Forward	CATCACAAATAGCGAACACAAG
CHS_Reverse	CCTAGCATCCAGGGAAGC
STS_Forward	CAAGCCCTTTTTGGTGATG
STS_Reverse	CCACAAGTGAAAGGTGAGTCC
F35H1_Forward	TTCTTGAAAATGGGCACTAACA
F35H1_Reverse	CGCTCGCTGGCACAACCT
F35H2_Forward	TGCTGATGGAACGCCTG
F35H2_Reverse	CATTTGTCTGACTTTTTTGGG
F3H_Forward	TGTCTGGTGGCAAGAAAGG
F3H_Reverse	CAAGCATTGGTCAAAGCGT

LDOX_Forward	TGGAGTGGGGTGTGATGC
LDOX_Reverse	GGTGTCTTAGGCCAGATGGT
CHI1_Forward	GGAAGGGTAAATCTGGAAAGG
CHI1_Reverse	GCATGAAGTTGCAGGAAAATG
CHI2_Forward	GCTCCACCAACGACCTCTT
CHI2_Reverse	TCCTCCACAGTCTTGCCCT
DFR_Forward	GCGGAGACGCATCTGACT
DFR_Reverse	GCCCAACATCCCTTCAATA
C4H_Forward	ACCACCTGAACCTCTCCGA
C4H_Reverse	CGCCAATGCTCACCGTA
UBC32_Forward	CAAGAGTGGCTGACAGGATAG
UBC32_Reverse	CTTGATACAGGGCTGGGATTAG
LRR_Forward	GGCCAACCTGGTAAACAGAATA
LRR_Reverse	CGGAGGTTCTGCAGGTAAT
GRP_Forward	CTGTTGTTCTCATCCTGTCCTC
GRP_Reverse	CCCATCGTGCTTCTCATCTT
PIP2;3_Forward	CTGGAGTGACCATTGGGTATTT
PIP2;3_Reverse	AACAGCTCCAGCTCTCAATATG
USP_Forward	GTTCTTGGGAGCAGAGGTTTAG
USP_Reverse	TCACAACTGTAAGTGGACATGAG
RSGT_Forward	CTACCATGGCTTAGTCCCTTTC
RSGT_Reverse	AGCTGGCGATTTTCATCATACT
GAPDH_Forward	TTCTCGTTGAGGGCTATTCCA
GAPDH_Reverse	CCACAGACTTCATCGGTGACA

Note: Primers were designed with Primer Premier 5.0 and used for qRT-PCR in Figure. 8 and Supplementary Table S6.

Supplementary Table s5. Enriched GO terms of differential expressed proteins between Danfeng-2 and Cabernet Sauvignon

GO term	Ontology	Description	Number in input list	Number in BG/Ref	p-value	FDR
GO:0015979	P	photosynthesis	40	162	6.30E-35	1.50E-31
GO:0044237	P	cellular metabolic process	239	8722	2.90E-32	3.50E-29
GO:0009987	P	cellular process	283	11684	5.10E-31	4.10E-28
GO:0008152	P	metabolic process	266	10614	1.00E-30	6.10E-28
GO:0044262	P	cellular carbohydrate metabolic process	49	417	3.60E-29	1.80E-26
GO:0006082	P	organic acid metabolic process	62	860	7.40E-26	3.00E-23
GO:0034641	P	cellular nitrogen compound metabolic process	49	506	1.00E-25	3.50E-23
GO:0043436	P	oxoacid metabolic process	61	859	3.90E-25	1.10E-22
GO:0019752	P	carboxylic acid metabolic process	61	859	3.90E-25	1.10E-22
GO:0005975	P	carbohydrate metabolic process	61	866	5.90E-25	1.40E-22
GO:0042180	P	cellular ketone metabolic process	61	882	1.40E-24	3.20E-22
GO:000	P	alcohol metabolic process	37	270	2.30E	4.40E

6066								-24	-22
GO:000	P	cellular amino acid and derivative metabolic process	54	682	2.20E	4.40E			
6519								-24	-22
GO:000	P	monosaccharide metabolic process	30	168	6.70E	1.20E			
5996								-23	-20
GO:004	P	primary metabolic process	221	8995	1.40E	2.30E			
4238								-22	-20
GO:000	P	generation of precursor metabolites and energy	35	285	1.10E	1.60E			
6091								-21	-19
GO:004	P	cellular catabolic process	52	746	3.40E	4.90E			
4248								-21	-19
GO:003	P	cellular macromolecular complex assembly	28	200	6.00E	8.10E			
4622								-19	-17
GO:001	P	photosynthesis, light reaction	22	103	1.40E	1.70E			
9684								-18	-16
GO:006	P	macromolecular complex assembly	28	210	1.90E	2.30E			
5003								-18	-16
GO:004	P	cellular amine metabolic process	37	438	7.30E	8.40E			
4106								-18	-16
GO:003	P	cellular macromolecular complex subunit organization	28	224	8.80E	9.70E			
4621								-18	-16
GO:004	P	cellular component biogenesis	41	571	2.40E	2.60E			
4085								-17	-15
GO:004	P	macromolecular complex subunit organization	28	235	2.70E	2.80E			
3933								-17	-15
GO:000	P	amine metabolic process	39	521	4.10E	4.00E			

9308								-17	-15
GO:000	P	serine family amino acid metabolic process	17	54	4.60E	4.30E			
9069								-17	-15
GO:000	P	sulfur metabolic process	27	220	5.20E	4.70E			
6790								-17	-15
GO:001	P	hexose metabolic process	22	126	5.80E	5.10E			
9318								-17	-15
GO:000	P	cellular amino acid metabolic process	35	430	1.70E	1.40E			
6520								-16	-14
GO:002	P	cellular component assembly	28	265	4.50E	3.70E			
2607								-16	-14
GO:000	P	organelle organization	41	640	9.80E	7.70E			
6996								-16	-14
GO:000	P	catabolic process	59	1307	1.70E	1.30E			
9056								-15	-13
GO:000	P	glucose metabolic process	18	86	2.50E	1.90E			
6006								-15	-13
GO:004	P	carboxylic acid biosynthetic process	32	417	1.60E	1.10E			
6394								-14	-12
GO:001	P	organic acid biosynthetic process	32	417	1.60E	1.10E			
6053								-14	-12
GO:000	P	pyruvate metabolic process	12	25	3.40E	2.30E			
6090								-14	-12
GO:001	P	carbohydrate catabolic process	19	128	1.10E	7.10E			
6052								-13	-12
GO:000	P	cellular amino acid derivative metabolic process	27	315	1.60E	1.00E			

6575								-13	-11
GO:0000096	P	sulfur amino acid metabolic process	16	84	3.20E	2.00E		-13	-11
GO:0022613	P	ribonucleoprotein complex biogenesis	24	253	5.00E	3.00E		-13	-11
GO:0022618	P	ribonucleoprotein complex assembly	10	16	6.40E	3.80E		-13	-11
GO:0044271	P	cellular nitrogen compound biosynthetic process	29	394	7.20E	4.20E		-13	-11
GO:0000097	P	sulfur amino acid biosynthetic process	13	49	1.50E	8.20E		-12	-11
GO:0044272	P	sulfur compound biosynthetic process	17	115	2.30E	1.30E		-12	-10
GO:0008652	P	cellular amino acid biosynthetic process	21	202	2.90E	1.60E		-12	-10
GO:0009070	P	serine family amino acid biosynthetic process	11	29	3.10E	1.60E		-12	-10
GO:0009309	P	amine biosynthetic process	22	229	3.70E	1.90E		-12	-10
GO:0009058	P	biosynthetic process	127	5118	3.90E	2.00E		-12	-10
GO:0019748	P	secondary metabolic process	31	489	4.40E	2.20E		-12	-10
GO:0006725	P	cellular aromatic compound metabolic process	28	399	5.20E	2.50E		-12	-10
GO:004	P	cellular carbohydrate catabolic process	17	125	7.50E	3.60E			

4275								-12	-10
GO:003	P	monocarboxylic acid metabolic process	28	408	8.50E	4.00E			
2787								-12	-10
GO:001	P	cellular component organization	49	1179	8.70E	4.00E			
6043								-12	-10
GO:001	P	cysteine biosynthetic process	10	24	1.40E	6.30E			
9344								-11	-10
GO:005	P	nucleobase, nucleoside and nucleotide metabolic process	21	221	1.40E	6.30E			
5086								-11	-10
GO:000	P	cysteine metabolic process	10	24	1.40E	6.30E			
6534								-11	-10
GO:001	P	carbon fixation	9	16	1.90E	8.20E			
5977								-11	-10
GO:005	P	cofactor metabolic process	24	308	2.30E	9.90E			
1186								-11	-10
GO:004	P	heterocycle metabolic process	29	460	2.50E	1.00E			
6483								-11	-09
GO:000	P	cellular aldehyde metabolic process	10	27	3.70E	1.50E			
6081								-11	-09
GO:000	P	glucose catabolic process	14	83	4.20E	1.70E			
6007								-11	-09
GO:001	P	hexose catabolic process	14	84	4.80E	1.90E			
9320								-11	-09
GO:004	P	monosaccharide catabolic process	14	84	4.80E	1.90E			
6365								-11	-09
GO:003	P	cellular response to oxidative stress	8	11	5.80E	2.20E			

4599							-11	-09
GO:004	P	ribosome biogenesis	21	241	6.20E	2.30E	-11	-09
2254							-11	-09
GO:004	P	alcohol catabolic process	14	89	9.60E	3.50E	-11	-09
6164							-11	-09
GO:004	P	cellular macromolecule catabolic process	28	465	1.50E	5.40E	-10	-09
4265							-10	-09
GO:001	P	isopentenyl diphosphate biosynthetic process, mevalonate-independent pathway	8	13	1.50E	5.40E	-10	-09
9288							-10	-09
GO:001	P	glyceraldehyde-3-phosphate metabolic process	8	13	1.50E	5.40E	-10	-09
9682							-10	-09
GO:000	P	lipid biosynthetic process	27	439	2.00E	7.10E	-10	-09
8610							-10	-09
GO:005	P	localization	62	1922	3.40E	1.20E	-10	-08
1179							-10	-08
GO:005	P	establishment of localization in cell	29	525	4.60E	1.60E	-10	-08
1649							-10	-08
GO:005	P	establishment of localization	60	1851	5.70E	1.90E	-10	-08
1234							-10	-08
GO:005	P	cellular localization	30	569	6.60E	2.20E	-10	-08
1641							-10	-08
GO:000	P	flavonoid biosynthetic process	12	69	7.60E	2.40E	-10	-08
9813							-10	-08
GO:004	P	isopentenyl diphosphate metabolic process	8	17	7.70E	2.40E	-10	-08
6490							-10	-08
GO:000	P	isopentenyl diphosphate biosynthetic process	8	17	7.70E	2.40E	-10	-08

9240								-10	-08
GO:004	P	cellular biosynthetic process	116	4925	1.00E	3.20E			
4249								-09	-08
GO:003	P	cellular carbohydrate biosynthetic process	17	177	1.10E	3.30E			
4637								-09	-08
GO:000	P	coenzyme metabolic process	17	188	2.50E	7.50E			
6732								-09	-08
GO:000	P	flavonoid metabolic process	12	78	2.60E	7.90E			
9812								-09	-08
GO:001	P	carbohydrate biosynthetic process	20	277	3.70E	1.10E			
6051								-09	-07
GO:004	P	cellular lipid metabolic process	30	618	4.00E	1.20E			
4255								-09	-07
GO:004	P	cellular protein metabolic process	89	3487	4.00E	1.20E			
4267								-09	-07
GO:001	P	cellular homeostasis	16	174	5.90E	1.70E			
9725								-09	-07
GO:004	P	cellular polysaccharide metabolic process	14	127	6.40E	1.80E			
4264								-09	-07
GO:000	P	polysaccharide metabolic process	15	152	7.30E	2.00E			
5976								-09	-07
GO:000	P	nucleoside phosphate metabolic process	16	180	9.20E	2.50E			
6753								-09	-07
GO:000	P	nucleotide metabolic process	16	180	9.20E	2.50E			
9117								-09	-07
GO:004	P	glucan metabolic process	12	89	1.00E	2.70E			

4042								-08	-07
GO:001	P	rRNA metabolic process	13	110	1.00E	2.70E			
6072								-08	-07
GO:000	P	rRNA processing	13	110	1.00E	2.70E			
6364								-08	-07
GO:000	P	response to stress	66	2320	1.20E	3.00E			
6950								-08	-07
GO:004	P	homeostatic process	17	216	1.70E	4.40E			
2592								-08	-07
GO:000	P	protein folding	19	275	1.80E	4.50E			
6457								-08	-07
GO:000	P	transport	56	1846	2.10E	5.30E			
6810								-08	-07
GO:000	P	lipid metabolic process	34	841	2.90E	7.30E			
6629								-08	-07
GO:004	P	alcohol biosynthetic process	9	44	3.00E	7.40E			
6165								-08	-07
GO:000	P	glutathione metabolic process	6	10	3.70E	8.90E			
6749								-08	-07
GO:003	P	cellular response to reactive oxygen species	6	10	3.70E	8.90E			
4614								-08	-07
GO:004	P	cellular protein complex assembly	13	124	3.80E	9.20E			
3623								-08	-07
GO:003	P	macromolecule localization	24	462	4.50E	1.10E			
3036								-08	-06
GO:001	P	protein metabolic process	94	4009	7.50E	1.80E			

9538								-08	-06
GO:000	P	cellular glucan metabolic process	11	87	7.60E	1.80E			
6073								-08	-06
GO:000	P	post-embryonic morphogenesis	8	35	8.40E	1.90E			
9886								-08	-06
GO:000	P	protein complex assembly	13	134	8.80E	2.00E			
6461								-08	-06
GO:004	P	pigment metabolic process	13	134	8.80E	2.00E			
2440								-08	-06
GO:007	P	protein complex biogenesis	13	134	8.80E	2.00E			
0271								-08	-06
GO:000	P	isoprenoid biosynthetic process	13	135	9.50E	2.10E			
8299								-08	-06
GO:004	P	pigment biosynthetic process	12	112	1.00E	2.30E			
6148								-07	-06
GO:001	P	thylakoid membrane organization	7	23	1.00E	2.30E			
0027								-07	-06
GO:000	P	plastid membrane organization	7	23	1.00E	2.30E			
9668								-07	-06
GO:000	P	photosynthesis, light harvesting	7	26	2.10E	4.60E			
9765								-07	-06
GO:004	P	cellular amino acid derivative biosynthetic process	16	233	2.60E	5.40E			
2398								-07	-06
GO:004	P	hydrogen peroxide metabolic process	7	27	2.60E	5.60E			
2743								-07	-06
GO:001	P	aromatic compound biosynthetic process	16	237	3.20E	6.60E			

9438								-07	-06
GO:000	P	protein targeting	13	155	4.20E	8.70E			
6605								-07	-06
GO:004	P	intracellular transport	22	463	6.80E	1.40E			
6907								-07	-05
GO:000	P	peptide metabolic process	7	32	7.10E	1.50E			
6518								-07	-05
GO:000	P	phospholipid biosynthetic process	10	88	7.30E	1.50E			
8654								-07	-05
GO:000	P	isoprenoid metabolic process	13	168	9.80E	2.00E			
6720								-07	-05
GO:000	P	phenylpropanoid biosynthetic process	12	141	1.00E	2.00E			
9699								-06	-05
GO:003	P	regulation of protein modification process	5	10	1.10E	2.10E			
1399								-06	-05
GO:007	P	cellular response to hydrogen peroxide	5	10	1.10E	2.10E			
0301								-06	-05
GO:001	P	photosystem II assembly	5	10	1.10E	2.10E			
0207								-06	-05
GO:000	P	response to biotic stimulus	26	638	1.10E	2.10E			
9607								-06	-05
GO:003	P	ncRNA processing	13	170	1.10E	2.10E			
4470								-06	-05
GO:000	P	plastid organization	11	119	1.30E	2.60E			
9657								-06	-05
GO:000	P	protein localization	20	408	1.40E	2.60E			

8104								-06	-05
GO:000	P	glycine metabolic process	6	22	1.50E	2.80E			
6544								-06	-05
GO:000	P	phospholipid metabolic process	11	121	1.60E	2.90E			
6644								-06	-05
GO:000	P	glucan biosynthetic process	8	54	1.60E	2.90E			
9250								-06	-05
GO:004	P	carboxylic acid catabolic process	10	98	1.80E	3.20E			
6395								-06	-05
GO:001	P	organic acid catabolic process	10	98	1.80E	3.20E			
6054								-06	-05
GO:004	P	establishment of protein localization	19	381	2.00E	3.60E			
5184								-06	-05
GO:001	P	protein transport	19	381	2.00E	3.60E			
5031								-06	-05
GO:000	P	macromolecule catabolic process	33	982	2.50E	4.40E			
9057								-06	-05
GO:001	P	organophosphate metabolic process	11	130	3.00E	5.30E			
9637								-06	-05
GO:005	P	response to protein stimulus	5	14	3.90E	6.80E			
1789								-06	-05
GO:000	P	pentose-phosphate shunt	6	28	5.00E	8.70E			
6098								-06	-05
GO:001	P	proteasomal protein catabolic process	5	15	5.20E	8.90E			
0498								-06	-05
GO:004	P	cellular amide metabolic process	7	45	5.40E	9.20E			

3603								-06	-05
GO:000	P	NADPH regeneration	6	29	6.00E	0.000			
6740								-06	1
GO:000	P	oxygen and reactive oxygen species metabolic process	8	66	6.10E	0.000			
6800								-06	1
GO:000	P	phenylpropanoid metabolic process	12	175	8.10E	0.000			
9698								-06	14
GO:000	P	intracellular protein transport	16	311	8.80E	0.000			
6886								-06	15
GO:000	P	amine catabolic process	7	49	8.90E	0.000			
9310								-06	15
GO:004	P	cellular macromolecule metabolic process	125	6447	9.10E	0.000			
4260								-06	15
GO:000	P	NADP metabolic process	6	32	9.90E	0.000			
6739								-06	16
GO:004	P	cell redox homeostasis	8	72	1.10E	0.000			
5454								-05	18
GO:003	P	cellular protein localization	16	322	1.30E	0.000			
4613								-05	21
GO:000	P	polysaccharide catabolic process	5	19	1.40E	0.000			
0272								-05	22
GO:001	P	starch biosynthetic process	5	19	1.40E	0.000			
9252								-05	22
GO:003	P	cellular response to stress	18	399	1.40E	0.000			
3554								-05	22
GO:004	P	response to hydrogen peroxide	7	53	1.40E	0.000			

2542								-05	22
GO:000	P	toxin metabolic process	7	53	1.40E	0.000			
9404								-05	22
GO:000	P	toxin catabolic process	7	53	1.40E	0.000			
9407								-05	22
GO:000	P	fatty acid metabolic process	13	225	1.90E	0.000			
6631								-05	3
GO:007	P	divalent metal ion transport	5	21	2.10E	0.000			
0838								-05	31
GO:005	P	organelle localization	5	21	2.10E	0.000			
1640								-05	31
GO:004	P	heterocycle catabolic process	6	38	2.40E	0.000			
6700								-05	36
GO:000	P	oxidoreduction coenzyme metabolic process	7	58	2.40E	0.000			
6733								-05	36
GO:004	P	positive regulation of transcription, DNA-dependent	5	22	2.50E	0.000			
5893								-05	37
GO:007	P	cellular macromolecule localization	16	341	2.60E	0.000			
0727								-05	38
GO:000	P	nitrogen compound metabolic process	81	3826	3.00E	0.000			
6807								-05	44
GO:005	P	positive regulation of RNA metabolic process	5	23	3.00E	0.000			
1254								-05	44
GO:003	P	response to endoplasmic reticulum stress	5	23	3.00E	0.000			
4976								-05	44
GO:003	P	cellular cation homeostasis	8	84	3.10E	0.000			

0003								-05	44
GO:000	P	response to reactive oxygen species	8	85	3.30E	0.000			
0302								-05	48
GO:001	P	pentose metabolic process	6	41	3.50E	0.000			
9321								-05	49
GO:004	P	nicotinamide nucleotide metabolic process	6	41	3.50E	0.000			
6496								-05	49
GO:000	P	starch metabolic process	6	41	3.50E	0.000			
5982								-05	49
GO:000	P	nicotinamide metabolic process	6	41	3.50E	0.000			
6769								-05	49
GO:000	P	cellular biogenic amine metabolic process	7	62	3.60E	0.000			
6576								-05	5
GO:000	P	glutamine family amino acid metabolic process	6	42	3.90E	0.000			
9064								-05	54
GO:001	P	cellular membrane organization	9	114	3.90E	0.000			
6044								-05	54
GO:002	P	electron transport chain	8	88	4.20E	0.000			
2900								-05	57
GO:005	P	cation homeostasis	8	90	4.80E	0.000			
5080								-05	66
GO:004	P	cell wall macromolecule metabolic process	6	45	5.60E	0.000			
4036								-05	76
GO:003	P	cellular polysaccharide biosynthetic process	8	92	5.60E	0.000			
3692								-05	76
GO:000	P	aromatic amino acid family metabolic process	7	68	6.10E	0.000			

9072								-05	82
GO:001	P	pyridine nucleotide metabolic process	6	46	6.20E	0.000			
9362								-05	83
GO:000	P	protein modification process	39	1474	6.40E	0.000			
6464								-05	84
GO:003	P	ncRNA metabolic process	13	254	6.30E	0.000			
4660								-05	84
GO:000	P	nucleotide biosynthetic process	9	122	6.40E	0.000			
9165								-05	85
GO:000	P	cellular amino acid catabolic process	6	47	7.00E	0.000			
9063								-05	9
GO:003	P	regulation of cellular protein metabolic process	6	47	7.00E	0.000			
2268								-05	9
GO:000	P	cellular ion homeostasis	8	96	7.40E	0.000			
6873								-05	96
GO:005	P	cellular chemical homeostasis	8	97	7.90E	0.001			
5082								-05	
GO:005	P	cofactor biosynthetic process	11	191	8.60E	0.001			
1188								-05	1
GO:000	P	nucleoside metabolic process	6	50	9.50E	0.001			
9116								-05	2
GO:004	P	macromolecule metabolic process	130	7127	0.000	0.001			
3170								1	3
GO:000	P	positive regulation of biosynthetic process	7	76	0.000	0.001			
9891								12	4
GO:000	P	oligosaccharide metabolic process	6	52	0.000	0.001			

9311						12	4
GO:001	P	regulation of phosphate metabolic process	6	52	0.000	0.001	
9220					12	4	
GO:005	P	regulation of phosphorus metabolic process	6	52	0.000	0.001	
1174					12	4	
GO:005	P	ion homeostasis	8	103	0.000	0.001	
0801					12	4	
GO:003	P	positive regulation of cellular biosynthetic process	7	76	0.000	0.001	
1328					12	4	
GO:003	P	oxylipin biosynthetic process	5	32	0.000	0.001	
1408					12	5	
GO:005	P	regulation of protein metabolic process	6	54	0.000	0.001	
1246					14	7	
GO:005	P	oxidation reduction	11	203	0.000	0.001	
5114					14	7	
GO:006	P	regulation of biological quality	22	665	0.000	0.001	
5008					14	7	
GO:000	P	defense response	24	766	0.000	0.001	
6952					16	9	
GO:000	P	fatty acid biosynthetic process	9	140	0.000	0.002	
6633					17	1	
GO:000	P	ribonucleoside metabolic process	5	35	0.000	0.002	
9119					18	1	
GO:005	P	regulation of catalytic activity	9	141	0.000	0.002	
0790					18	1	
GO:000	P	glycolysis	6	57	0.000	0.002	

6096					18	2
GO:000	P	alkaloid metabolic process	6	57	0.000	0.002
9820					18	2
GO:000	P	polysaccharide biosynthetic process	8	112	0.000	0.002
0271					2	3
GO:000	P	RNA processing	17	453	0.000	0.002
6396					2	3
GO:001	P	proton transport	6	59	0.000	0.002
5992					22	5
GO:000	P	hydrogen transport	6	59	0.000	0.002
6818					22	5
GO:003	P	ion transmembrane transport	6	59	0.000	0.002
4220					22	5
GO:001	P	lipid catabolic process	7	85	0.000	0.002
6042					22	5
GO:000	P	response to oxidative stress	14	332	0.000	0.002
6979					24	7
GO:000	P	purine ribonucleoside triphosphate biosynthetic process	6	60	0.000	0.002
9206					24	7
GO:000	P	ribonucleoside triphosphate biosynthetic process	6	60	0.000	0.002
9201					24	7
GO:005	P	cellular response to stimulus	25	840	0.000	0.002
1716					25	8
GO:000	P	ribonucleoside triphosphate metabolic process	6	61	0.000	0.002
9199					26	9
GO:000	P	purine ribonucleoside triphosphate metabolic process	6	61	0.000	0.002

9205							26	9
GO:003							0.000	0.003
1407	P	oxylipin metabolic process	5	39			28	1
GO:000							0.000	0.003
9145	P	purine nucleoside triphosphate biosynthetic process	6	62			28	1
GO:000							0.000	0.003
9260	P	ribonucleotide biosynthetic process	7	89			29	2
GO:000							0.000	0.003
9142	P	nucleoside triphosphate biosynthetic process	6	63			3	3
GO:000							0.000	0.003
9144	P	purine nucleoside triphosphate metabolic process	6	63			3	3
GO:000							0.000	0.003
6164	P	purine nucleotide biosynthetic process	7	90			31	3
GO:000							0.000	0.003
6811	P	ion transport	16	427			31	3
GO:006							0.000	0.003
5009	P	regulation of molecular function	9	153			32	4
GO:003							0.000	0.003
1325	P	positive regulation of cellular metabolic process	7	91			33	5
GO:000							0.000	0.003
9893	P	positive regulation of metabolic process	7	92			35	7
GO:000							0.000	0.003
6163	P	purine nucleotide metabolic process	7	92			35	7
GO:000							0.000	0.003
9141	P	nucleoside triphosphate metabolic process	6	65			36	7
GO:001							0.000	0.003
	P	heterocycle biosynthetic process	8	123				

8130						36	8
GO:001	P	di-, tri-valent inorganic cation transport	5	43	0.000	0.004	
5674					42	4	
GO:001	P	vesicle-mediated transport	12	272	0.000	0.004	
6192					44	6	
GO:000	P	ribonucleotide metabolic process	7	96	0.000	0.004	
9259					44	6	
GO:004	P	macromolecule modification	39	1636	0.000	0.005	
3412					49		
GO:000	P	carbohydrate transport	5	45	0.000	0.005	
8643					51	2	
GO:000	P	photosynthetic electron transport chain	5	46	0.000	0.005	
9767					56	7	
GO:000	P	small GTPase mediated signal transduction	5	46	0.000	0.005	
7264					56	7	
GO:004	P	cellular metabolic compound salvage	6	73	0.000	0.006	
3094					63	3	
GO:000	P	chloroplast organization	6	73	0.000	0.006	
9658					63	3	
GO:004	P	chemical homeostasis	8	136	0.000	0.006	
8878					68	8	
GO:001	P	glycoside metabolic process	7	104	0.000	0.006	
6137					7	9	
GO:005	P	response to stimulus	78	4057	0.000	0.007	
0896					8	9	
GO:000	P	chromatin organization	9	175	0.000	0.008	

6325						81	
GO:000	P	purine ribonucleotide biosynthetic process	6	77	0.000	0.008	
9152						82	1
GO:005	P	chromosome organization	10	216	0.000	0.008	
1276						91	9
GO:004	P	post-translational protein modification	31	1248	0.000	0.009	
3687						97	5
GO:000	P	purine ribonucleotide metabolic process	6	80	0.000	0.009	
9150						99	6
GO:000	P	chromatin assembly or disassembly	6	82	0.001	0.011	
6333						1	
GO:001	P	monovalent inorganic cation transport	7	115	0.001	0.012	
5672						2	
GO:000	P	nucleosome assembly	5	56	0.001	0.012	
6334						3	
GO:003	P	nucleosome organization	5	56	0.001	0.012	
4728						3	
GO:001	P	protein import	6	86	0.001	0.013	
7038						4	
GO:000	P	ATP biosynthetic process	5	58	0.001	0.014	
6754						5	
GO:004	P	ATP metabolic process	5	59	0.001	0.015	
6034						6	
GO:000	P	porphyrin metabolic process	6	89	0.001	0.016	
6778						7	
GO:003	P	chromatin assembly	5	60	0.001	0.016	

1497						7	
GO:0065004	P	protein-DNA complex assembly	5	60	0.0017	0.016	
GO:0010035	P	response to inorganic substance	11	279	0.0018	0.017	
GO:0033013	P	tetrapyrrole metabolic process	6	93	0.002	0.019	
GO:0009314	P	response to radiation	18	613	0.0021	0.019	
GO:0010628	P	positive regulation of gene expression	5	63	0.0021	0.019	
GO:0045941	P	positive regulation of transcription	5	63	0.0021	0.019	
GO:0055085	P	transmembrane transport	10	244	0.0022	0.02	
GO:0006323	P	DNA packaging	5	64	0.0022	0.02	
GO:0006779	P	porphyrin biosynthetic process	5	65	0.0023	0.021	
GO:0015994	P	chlorophyll metabolic process	5	66	0.0025	0.022	
GO:0043413	P	macromolecule glycosylation	5	66	0.0025	0.022	
GO:0006486	P	protein amino acid glycosylation	5	66	0.0025	0.022	
GO:007	P	glycosylation	5	66	0.002	0.022	

0085							5	
GO:000	P	glycoprotein biosynthetic process	5	66	0.002	0.022		
9101					5			
GO:001	P	positive regulation of macromolecule biosynthetic process	5	69	0.003	0.026		
0557								
GO:004	P	positive regulation of nucleobase, nucleoside, nucleotide and nucleic acid metabolic process	5	69	0.003	0.026		
5935								
GO:005	P	positive regulation of nitrogen compound metabolic process	5	70	0.003	0.028		
1173					2			
GO:003	P	tetrapyrrole biosynthetic process	5	72	0.003	0.031		
3014					6			
GO:000	P	response to light stimulus	17	596	0.003	0.031		
9416					6			
GO:000	P	glycoprotein metabolic process	5	73	0.003	0.033		
9100					8			
GO:005	P	proteolysis involved in cellular protein catabolic process	11	309	0.003	0.033		
1603					8			
GO:007	P	cellular response to chemical stimulus	14	452	0.004	0.034		
0887								
GO:000	P	cation transport	12	357	0.004	0.034		
6812								
GO:004	P	cellular lipid catabolic process	5	74	0.004	0.034		
4242								
GO:005	P	defense response to fungus	6	108	0.004	0.035		
0832					1			
GO:004	P	cellular protein catabolic process	11	315	0.004	0.037		

4257							4	
GO:000	P	protein amino acid dephosphorylation	5	76	0.004	0.037		
6470					4			
GO:001	P	positive regulation of macromolecule metabolic process	5	76	0.004	0.037		
0604					4			
GO:001	P	root morphogenesis	6	114	0.005	0.044		
0015					3			
GO:000	P	microtubule-based process	6	114	0.005	0.044		
7017					3			
GO:003	P	protein localization in organelle	5	80	0.005	0.045		
3365					4			
GO:000	F	catalytic activity	291	9638	8.80E	5.90E		
3824					-52	-49		
GO:001	F	oxidoreductase activity	103	1463	2.50E	8.30E		
6491					-42	-40		
GO:004	F	metal ion binding	109	1997	2.40E	5.50E		
6872					-35	-33		
GO:004	F	ion binding	109	2087	9.90E	1.30E		
3167					-34	-31		
GO:004	F	cation binding	109	2087	9.90E	1.30E		
3169					-34	-31		
GO:004	F	tetrapyrrole binding	27	136	8.60E	9.60E		
6906					-22	-20		
GO:000	F	binding	239	11258	1.70E	1.60E		
5488					-16	-14		
GO:000	F	iron ion binding	22	161	5.70E	4.20E		

5506								-15	-13
GO:004								5.10E	4.20E
8037	F	cofactor binding		26	246			-15	-13
GO:001								2.60E	1.70E
9842	F	vitamin binding		14	54			-13	-11
GO:001								1.90E	1.10E
6168	F	chlorophyll binding		12	38			-12	-10
GO:007								4.00E	2.10E
0279	F	vitamin B6 binding		12	41			-12	-10
GO:003								4.00E	2.10E
0170	F	pyridoxal phosphate binding		12	41			-12	-10
GO:000								8.10E	3.90E
0166	F	nucleotide binding		73	2267			-12	-10
GO:001								1.10E	4.80E
7076	F	purine nucleotide binding		61	1713			-11	-10
GO:002								2.50E	1.10E
0037	F	heme binding		15	97			-11	-09
GO:003								3.90E	1.40E
2555	F	purine ribonucleotide binding		58	1631			-11	-09
GO:003								3.90E	1.40E
2553	F	ribonucleotide binding		58	1631			-11	-09
GO:004								6.30E	2.20E
6914	F	transition metal ion binding		55	1618			-10	-08
GO:001								6.90E	2.30E
6984	F	ribulose-bisphosphate carboxylase activity		7	9			-10	-08
GO:001								3.90E	1.20E
	F	carboxy-lyase activity		12	81				

6831							-09	-07
GO:005	F	iron-sulfur cluster binding	9	37	8.10E	2.30E	-09	-07
1536							-09	-07
GO:005	F	metal cluster binding	9	37	8.10E	2.30E	-09	-07
1540							-09	-07
GO:000	F	purine nucleoside binding	49	1465	9.50E	2.50E	-09	-07
1883							-09	-07
GO:000	F	nucleoside binding	49	1465	9.50E	2.50E	-09	-07
1882							-09	-07
GO:003	F	adenyl nucleotide binding	49	1465	9.50E	2.50E	-09	-07
0554							-09	-07
GO:000	F	structural molecule activity	30	659	1.60E	4.00E	-08	-07
5198							-08	-07
GO:003	F	UDP-glucosyltransferase activity	12	94	1.80E	4.20E	-08	-07
5251							-08	-07
GO:001	F	carbon-carbon lyase activity	14	141	2.20E	5.00E	-08	-07
6830							-08	-07
GO:003	F	adenyl ribonucleotide binding	46	1384	3.30E	7.40E	-08	-07
2559							-08	-07
GO:000	F	ATP binding	44	1377	1.90E	4.20E	-07	-06
5524							-07	-06
GO:001	F	lyase activity	22	430	2.10E	4.40E	-07	-06
6829							-07	-06
GO:001	F	isomerase activity	17	265	2.70E	5.40E	-07	-06
6853							-07	-06
GO:000	F	monooxygenase activity	12	127	3.60E	7.10E	-07	-06

4497								-07	-06
GO:000								5.00E	9.60E
5509	F	calcium ion binding		15	215			-07	-06
GO:004								7.00E	1.30E
6527	F	glucosyltransferase activity		12	136			-07	-05
GO:000								8.40E	1.50E
5507	F	copper ion binding		11	113			-07	-05
GO:001								1.00E	1.80E
6705	F	oxidoreductase activity, acting on paired donors, with incorporation or reduction of molecular oxygen		14	198			-06	-05
GO:001								1.70E	2.90E
6758	F	transferase activity, transferring hexosyl groups		18	340			-06	-05
GO:000								1.90E	3.20E
3735	F	structural constituent of ribosome		22	494			-06	-05
GO:001								2.10E	3.50E
6740	F	transferase activity		77	3321			-06	-05
GO:001								3.60E	5.70E
6679	F	oxidoreductase activity, acting on diphenols and related substances as donors		7	42			-06	-05
GO:005								3.70E	5.80E
0662	F	coenzyme binding		13	191			-06	-05
GO:001								6.00E	9.10E
6682	F	oxidoreductase activity, acting on diphenols and related substances as donors, oxygen as acceptor		6	29			-06	-05
GO:000								6.10E	9.10E
0287	F	magnesium ion binding		8	66			-06	-05
GO:005								8.40E	0.000
1213	F	dioxygenase activity		6	31			-06	12
GO:001								1.10E	0.000
	F	antioxidant activity		11	150				

6209								-05	15
GO:000								1.50E	0.000
8194	F	UDP-glycosyltransferase activity	13	219				-05	21
GO:001								1.70E	0.000
6765	F	transferase activity, transferring alkyl or aryl (other than methyl) groups	11	158				-05	23
GO:003								2.00E	0.000
1406	F	carboxylic acid binding	7	56				-05	26
GO:000								2.20E	0.000
4364	F	glutathione transferase activity	7	57				-05	28
GO:008								2.50E	0.000
0044	F	quercetin 7-O-glucosyltransferase activity	5	22				-05	32
GO:008								5.00E	0.000
0043	F	quercetin 3-O-glucosyltransferase activity	5	26				-05	63
GO:001								7.50E	0.000
6757	F	transferase activity, transferring glycosyl groups	20	544				-05	93
GO:001								0.000	0.002
9001	F	guanyl nucleotide binding	12	249				21	4
GO:003								0.000	0.002
2561	F	guanyl ribonucleotide binding	12	249				21	4
GO:000								0.000	0.002
5525	F	GTP binding	12	249				21	4
GO:001								0.000	0.005
6684	F	oxidoreductase activity, acting on peroxide as acceptor	8	127				45	1
GO:000								0.000	0.005
4601	F	peroxidase activity	8	127				45	1
GO:001								0.000	0.006
	F	protein disulfide oxidoreductase activity	5	46					

5035					56	2
GO:000					0.000	0.006
3924	F	GTPase activity	6	72	59	5
GO:001					0.000	0.009
6667	F	oxidoreductase activity, acting on sulfur group of donors	7	109	9	8
GO:001					0.001	0.014
6709	F	oxidoreductase activity, acting on paired donors, with incorporation or reduction of molecular oxygen, NADH or NADPH as one donor, and incorporation of one atom of oxygen	5	56	3	
GO:001					0.001	0.018
6787	F	hydrolase activity	67	3468	7	
GO:001					0.001	0.018
5036	F	disulfide oxidoreductase activity	5	60	7	
GO:000					0.002	0.025
4252	F	serine-type endopeptidase activity	5	66	5	
GO:004					0.002	0.028
2625	F	ATPase activity, coupled to transmembrane movement of ions	5	68	8	
GO:001					0.004	0.042
7171	F	serine hydrolase activity	8	186	4	
GO:000					0.004	0.042
8483	F	transaminase activity	5	76	4	
GO:000					0.004	0.042
8236	F	serine-type peptidase activity	8	186	4	
GO:001					0.004	0.044
6614	F	oxidoreductase activity, acting on CH-OH group of donors	8	188	7	
GO:001					0.004	0.044
6769	F	transferase activity, transferring nitrogenous groups	5	77	7	
GO:001	C	integral to membrane	99	395	6.40E	3.10E

6021							-87	-84
GO:004							1.10E	2.70E
4425	C	membrane part	129	1360			-67	-65
GO:003							1.20E	1.90E
1224	C	intrinsic to membrane	100	806			-61	-59
GO:001							3.60E	4.40E
6020	C	membrane	158	4068			-35	-33
GO:000							3.20E	3.20E
9579	C	thylakoid	44	376			-26	-24
GO:004							9.80E	8.00E
4422	C	organelle part	104	2562			-24	-22
GO:004							3.30E	2.30E
4446	C	intracellular organelle part	103	2561			-23	-21
GO:005							5.80E	3.20E
5044	C	symplast	17	19			-23	-21
GO:000							5.80E	3.20E
9506	C	plasmodesma	17	19			-23	-21
GO:000							1.90E	9.30E
5911	C	cell-cell junction	17	21			-22	-21
GO:003							3.00E	1.30E
4357	C	photosynthetic membrane	35	273			-22	-20
GO:000							3.80E	1.60E
9521	C	photosystem	22	66			-22	-20
GO:003							5.70E	2.10E
0054	C	cell junction	17	23			-22	-20
GO:000							4.00E	1.40E
	C	cytoplasm	176	6822				

5737								-19	-17
GO:000	C	intracellular	221	9671	1.30E	4.40E			
5622								-18	-17
GO:004	C	intracellular part	213	9302	8.00E	2.40E			
4424								-18	-16
GO:000	C	cell	294	15217	5.70E	1.60E			
5623								-16	-14
GO:000	C	photosystem II	15	45	1.60E	4.40E			
9523								-15	-14
GO:003	C	organelle membrane	46	842	4.40E	1.10E			
1090								-15	-13
GO:003	C	macromolecular complex	78	2180	7.30E	1.80E			
2991								-15	-13
GO:004	C	cell part	290	15217	9.60E	2.20E			
4464								-15	-13
GO:000	C	photosystem I	12	22	1.00E	2.30E			
9522								-14	-13
GO:004	C	thylakoid part	28	307	1.40E	2.90E			
4436								-14	-13
GO:004	C	plasma membrane part	23	222	2.90E	5.80E			
4459								-13	-12
GO:000	C	chloroplast thylakoid	25	290	1.20E	2.30E			
9534								-12	-11
GO:003	C	plastid thylakoid	25	293	1.40E	2.70E			
1976								-12	-11
GO:003	C	organelle subcompartment	25	295	1.60E	3.00E			

1984							-12	-11
GO:000	C	extracellular region	24	285	5.20E	9.10E		
5576							-12	-11
GO:004	C	cytoplasmic part	146	6289	7.30E	1.20E		
4444							-12	-10
GO:000	C	cytosol	42	912	1.40E	2.30E		
5829							-11	-10
GO:004	C	chloroplast part	37	746	3.30E	5.30E		
4434							-11	-10
GO:004	C	thylakoid membrane	21	244	7.70E	1.20E		
2651							-11	-09
GO:005	C	plastid thylakoid membrane	20	231	2.00E	2.80E		
5035							-10	-09
GO:000	C	chloroplast thylakoid membrane	20	231	2.00E	2.80E		
9535							-10	-09
GO:004	C	plastid part	37	867	1.80E	2.50E		
4435							-09	-08
GO:000	C	chloroplast envelope	20	265	1.80E	2.50E		
9941							-09	-08
GO:004	C	intracellular organelle	167	8149	2.10E	2.80E		
3229							-09	-08
GO:004	C	organelle	167	8155	2.30E	2.90E		
3226							-09	-08
GO:004	C	protein complex	49	1443	6.00E	7.50E		
3234							-09	-08
GO:000	C	plastid envelope	20	331	6.00E	7.40E		

9526								-08	-07
GO:004	C	intracellular non-membrane-bounded organelle	37	1040	1.60E	1.80E			
3232								-07	-06
GO:004	C	non-membrane-bounded organelle	37	1040	1.60E	1.80E			
3228								-07	-06
GO:000	C	vacuolar membrane	11	100	2.70E	3.10E			
5774								-07	-06
GO:003	C	envelope	26	595	3.10E	3.40E			
1975								-07	-06
GO:003	C	organelle envelope	26	595	3.10E	3.40E			
1967								-07	-06
GO:004	C	vacuolar part	11	104	3.90E	4.20E			
4437								-07	-06
GO:000	C	ribosome	24	524	4.00E	4.20E			
5840								-07	-06
GO:003	C	ribonucleoprotein complex	28	703	6.50E	6.60E			
0529								-07	-06
GO:000	C	oxygen evolving complex	6	21	1.20E	1.20E			
9654								-06	-05
GO:002	C	cytosolic ribosome	18	336	1.40E	1.40E			
2626								-06	-05
GO:004	C	apoplast	13	182	2.20E	2.10E			
8046								-06	-05
GO:000	C	chloroplast stroma	15	249	2.80E	2.60E			
9570								-06	-05
GO:004	C	cytosolic part	18	360	3.60E	3.30E			

4445							-06	-05
GO:002							2.10E	0.000
2625	C	cytosolic large ribosomal subunit	11	162			-05	19
GO:000							2.60E	0.000
9507	C	chloroplast	63	2740			-05	23
GO:003							3.40E	0.000
3279	C	ribosomal subunit	17	389			-05	3
GO:000							5.00E	0.000
9532	C	plastid stroma	15	322			-05	43
GO:000							9.60E	0.000
5773	C	vacuole	16	383			-05	81
GO:000							0.000	0.001
9536	C	plastid	63	2965			23	9
GO:000							0.000	0.002
5874	C	microtubule	5	38			25	
GO:004							0.000	0.002
4431	C	Golgi apparatus part	8	118			28	2
GO:001							0.000	0.002
5934	C	large ribosomal subunit	11	225			33	6
GO:000							0.000	0.003
5886	C	plasma membrane	36	1456			42	3
GO:004							0.000	0.004
3227	C	membrane-bounded organelle	133	7622			55	2
GO:004							0.000	0.005
3231	C	intracellular membrane-bounded organelle	132	7615			75	7
GO:000							0.002	0.016
	C	endoplasmic reticulum membrane	5	64				

5789							2	
GO:000	C	Golgi apparatus	11	293	0.002		0.019	
5794						6		
GO:004	C	nuclear envelope-endoplasmic reticulum network	5	67	0.002		0.019	
2175						7		
GO:000	C	chromatin	5	71	0.003		0.024	
0785						4		
GO:000	C	cell wall	13	403	0.003		0.027	
5618						9		
GO:003	C	intrinsic to plasma membrane	5	74	0.004		0.027	
1226								
GO:003	C	external encapsulating structure	13	407	0.004		0.028	
0312						2		
GO:004	C	endoplasmic reticulum part	5	75	0.004		0.028	
4432						2		
GO:000	C	endoplasmic reticulum	14	466	0.005		0.034	
5783						1		
GO:001	C	plastoglobule	5	81	0.005		0.037	
0287						7		

Note: Enriched GO terms were generated in agriGO with customized annotation as reference. p-values were converted with Z-score generated by z-test. FDR were generated as p-value with multiple test correction.

Supplementary Table s6. Comparison of protein and mRNA expression pattern of 15 candidate proteins (genes) at different developmental stages

Protein accession	Description	iTRAQ (8 × plex)								RT-PCR							
		Danfeng-2				Cabernet Sauvignon				Danfeng-2				Cabernet Sauvignon			
		Green	Before	Veraison	Ripe	Green	Before	Veraison	Ripe	Green	Before	Veraison	Ripe	Green	Before	Veraison	Ripe
hard	Veraison			hard	Veraison			hard	Veraison			hard	Veraison				
A5BGJ0	DFR	1.000	0.827	0.751	1.115	2.186	0.726	1.878	1.519	0.095	0.070	0.075	0.148	0.139	0.037	1.000	0.137
A5BMU2	CHI1	1.000	0.956	0.995	0.903	1.898	0.943	1.536	1.756	0.106	0.140	0.080	0.140	0.192	0.046	1.000	0.409
A5ANT9	CHI2	1.000	0.900	0.899	0.752	1.561	0.910	1.116	1.642	0.135	0.091	0.141	0.094	0.184	0.035	1.000	0.289
A2ICC9	LDOX	1.000	0.971	1.040	0.993	1.977	0.946	1.973	1.758	0.114	0.080	0.114	0.158	0.210	0.104	1.000	0.242
G4XGW2	CHS	1.000	0.825	0.810	0.706	1.827	0.733	3.971	2.818	0.020	0.007	0.006	0.003	0.113	0.001	1.000	0.248
Q2L7J4	F35'H1	1.000	1.125	0.756	1.012	1.759	1.057	0.993	1.972	0.020	0.004	0.020	0.002	0.068	0.003	1.000	0.086
F6HA89	F35'H2	1.000	0.928	1.120	1.298	1.909	1.324	1.300	2.962	1.029	0.915	0.494	0.651	0.565	0.534	0.333	1.128
A5BZR3	F3H	1.000	0.945	1.162	0.921	1.956	0.918	1.622	1.704	0.029	0.028	0.055	0.022	0.178	0.007	1.000	0.132
A5BRL4	C4H	1.000	0.954	1.046	0.904	1.230	0.939	1.360	1.786	0.047	0.056	0.325	0.138	0.144	0.061	1.000	0.428
A5BIH9	RSGT	1.000	0.815	1.113	1.994	0.997	0.875	0.889	0.938	0.402	0.416	0.581	2.564	1.286	0.211	0.148	0.037
A5BBF4	UBC32	1.000	0.947	1.029	1.334	0.985	1.011	1.662	1.320	0.764	0.580	0.488	0.954	0.278	0.361	0.590	1.000
A5BFQ1	LRR	1.000	0.987	0.973	0.835	1.013	0.781	1.997	1.609	0.528	0.502	0.798	0.272	1.173	0.649	1.893	0.245
A5AI47	GRP	1.000	0.760	1.667	7.442	1.657	1.177	0.965	4.355	0.171	0.047	1.738	0.250	0.000	0.007	0.068	1.000
A3FA68	PIP2;3	1.000	0.906	0.897	1.833	1.000	1.032	2.299	2.423	0.063	0.005	0.007	0.341	0.116	0.097	0.792	1.000
D7TA35	USP	1.000	1.117	1.003	1.437	1.059	1.124	1.160	0.903	1.368	1.553	1.125	1.013	1.286	0.657	1.587	0.602

Note: RT-PCR data are log₂ normalized 2^{-ΔΔCt} values. Relationships of proteins with qRT-PCR transcripts are indicated.