

## Supplementary Material

### **Proteomics analyses revealed the reduction of carbon- and nitrogen-metabolism and ginsenoside biosynthesis in the red-skin disorder of *Panax ginseng***

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### **File S1. Supplementary Tables**

Supplementary Table 1

Supplementary Table 2

Supplemental table 1

Spot no. <sup>a</sup>	Protein	Organism	Accession No. <sup>b</sup>	Pep. Count <sup>c</sup>	Score	Theor. Mr (kDa) <sup>d</sup>	Theor. pI <sup>e</sup>	Exp. Mr (kDa) <sup>f</sup>	Exp. pI <sup>g</sup>	RSD/Healthy ginseng <sup>h</sup>
P1	Ketol-acid reductoisomerase	<i>Zea mays</i>	gi 195627844	11	209	63.05	6.18	95.5	5.72	down
P2	Glutamine synthetase cytosolic isozyme	<i>Lotus japonicus</i>	gi 12643762	12	102	39.15	5.49	43.65	5.9	up
P3	Cytosolic glutamine synthetase	<i>Helianthus annuus</i>	gi 2209149	8	175	17.25	6.51	44.67	5.42	up
P4	Cysteine synthase	<i>Arabidopsis thaliana</i>	gi 330255224	7	124	41.66	8.14	35.48	6.12	up
P5	Cysteine synthase	<i>Sesamum indicum</i>	gi 158263556	11	239	34.33	5.62	38.02	5.12	up
P6	arginase	<i>Arabidopsis lyrata</i> subsp. <i>lyrata</i>	gi 297813247	12	266	37.28	6.11	43.65	5.2	up
P7	Glutamate-1-semialdehyde 2,1-aminomutase, chloroplastic (GSA)	<i>Nicotiana tabacum</i>	gi 399785	9	164	50.88	6.43	50.12	5.4	up
P8	Ribonuclease-like storage protein	<i>Panax ginseng</i>	gi 51701931	7	81	27.34	5.87	22.39	5.15	down
P9	Ribonuclease-like storage protein	<i>Panax ginseng</i>	gi 51701931	13	251	27.34	5.87	26.3	6.58	down
P10	Ribonuclease-like storage protein	<i>Panax ginseng</i>	gi 51701931	9	108	27.34	5.87	26.92	6.22	up
P11	Ribonuclease-like storage protein	<i>Panax ginseng</i>	gi 51701931	5	351	27.32	5.87	10.72	7.22	up
P12	Ribonuclease-like storage protein	<i>Panax ginseng</i>	gi 51701931	9	501	27.32	5.87	25.12	6.3	down
P13	Ribonuclease-like storage protein	<i>Panax ginseng</i>	gi 51701931	8	118	27.32	5.87	26.92	6.7	down
P14	Ribonuclease-like storage protein	<i>Panax ginseng</i>	gi 51701931	10	209	27.32	5.87	23.99	7.5	down
P15	Ribonuclease-like storage protein;	<i>Panax ginseng</i>	gi 51701931	5	111	27.32	5.87	13.8	7	up
P16	Ribonuclease-like storage protein	<i>Panax ginseng</i>	gi 51701931	6	325	27.32	5.87	25.12	4.35	up

## Supplemental table 1 (cont.)

P17	Isoflavone reductase homolog Bet v 6.0101	Betula pendula	gi 4731376	13	225	33.15	7.82	36.3	6.2	up
P18	Isoflavone reductase-like protein CJP-6	Cryptomeria japonica	gi 19847822	6	86	33.57	6.25	33.88	6.4	up
P19	Isoflavone reductase homolog Bet v 6.0101	Betula pendula	gi 4731376	10	190	33.15	7.82	37.15	6.6	up
P20	Allergenic isoflavone reductase-like protein Bet v 6.0102	Betula pendula	gi 10764491	5	127	34.19	6.73	36.31	6.7	up
P21	Isoflavone reductase homolog Bet v 6.0101	Betula pendula	gi 4731376	6	79	33.15	7.82	38.02	5.3	up
P22	Spermidine synthase	Panax ginseng	gi 251831262	7	157	36.39	5.02	38.02	4.9	up
P23	Pterocarpan reductase molecular	Lotus japonicus	gi 116077986	5	157	33.99	5.94	38.02	5.8	up
P24	chaperone Hsp90-1	Nicotiana benthamiana	gi 38154482	13	250	80.05	4.94	35.48	4.31	up
P25	Predicted protein	Populus trichocarpa	gi 222850363	23	315	73.26	5.56	69.18	5.28	down
P26	Predicted protein	Populus trichocarpa	gi 224122096	7	86	45.27	4.94	47.86	4.8	up
P27	hypothetical protein	Vitis vinifera	gi 147862790	11	268	24.3	7.03	33.11	6.6	up
P28	predicted protein	Populus trichocarpa	gi 224106660	11	87	27.34	6.61	30.2	6.2	up
P29	20S proteasome subunit alpha-1 V-type proton	Gossypium hirsutum	gi 211906468	10	246	27.28	5.92	28.18	6.1	down
P30	ATPase subunit B 2	Hordeum vulgare	gi 2493132	22	218	53.73	5.12	56.23	4.82	up
P31	ATP synthase subunit beta, mitochondrial	Oryza sativa subsp. japonica	gi 84028177	17	318	58.93	5.95	57.54	4.9	up
P32	ATP synthase subunit beta	Sorghum bicolor	gi 4388533	23	828	49.14	5.25	56.23	5.38	up
P33	ATP synthase subunit beta	Ostreococcus tauri	gi 308800050	11	166	57.07	5.43	53.7	4.62	down
P34	ATP synthase subunit beta	Sorghum bicolor	gi 4388533	19	458	49.14	5.25	58.88	4.99	up
P35	ATP synthase subunit beta	Oryza sativa subsp. japonica (Rice)	gi 56784991	19	544	45.91	5.33	56.23	5.24	up
P36	Cytochrome P450 family protein	Oryza sativa (japonica cultivar-group)	gi 108862162	28	76	177.58	8.62	17.37	8.6	up

## Supplemental table 1 (cont.)

P37	RuBisCO large subunit-binding protein subunit beta, chloroplastic	<i>Pisum sativum</i>	gi 2506277	14	186	62.98	5.85	54.95	4.95	up
P38	ATP synthase subunit beta	<i>Zea mays</i>	gi 226493589	26	860	58.98	5.9	56.23	5.49	up
P39	F1 ATPase a-subunit	<i>Panax ginseng</i>	gi 2645893	12	190	54.89	5.93	56.23	6.4	up
P40	F1 ATPase a-subunit	<i>Panax ginseng</i>	gi 2645893	20	334	54.89	5.93	56.23	6.5	up
P41	ATP synthase subunit beta	<i>Vitis vinifera</i>	gi 225456079	17	751	59.14	5.9	56.23	5.1	down
P42	Phosphorylase	<i>Ricinus communis</i>	gi 255570250	15	132	111.02	6.13	56.23	4.54	up
P43	Enolase 1	<i>Hevea brasiliensis</i>	gi 14423688	10	182	47.83	5.57	57.54	4.89	up
P44	Pyruvate dehydrogenase E1 beta subunit isoform 2	<i>Zea mays</i>	gi 3851001	10	128	40.03	5.66	42.66	5.06	up
P45	Malate dehydrogenase	<i>Ricinus communis</i>	gi 255585546	11	96	35.66	6.4	39.81	4.92	up
P46	6-phosphogluconate dehydrogenase	<i>Cucumis sativus</i>	gi 193735602	8	79	34.51	8.27	46.77	5.38	up
P47	Enolase	<i>Brassica campestris</i>	gi 34597330	10	122	47.38	5.46	50.12	5.85	down
P48	Fructose-bisphosphate aldolase	<i>Codonopsis lanceolata</i>	gi 82941449	11	238	38.16	6.47	34.67	5	down
P49	Enolase 1	<i>Hevea brasiliensis</i>	gi 14423688	11	199	47.83	5.57	60.26	4.94	up
P50	Enolase 1	<i>Hevea brasiliensis</i>	gi 14423688	11	106	47.83	5.57	56.23	4.68	down
P51	Enolase 1	<i>Hevea brasiliensis</i>	gi 14423688	9	199	47.83	5.57	60.26	5.01	up
P52	Enolase 1	<i>Hevea brasiliensis</i>	gi 14423688	9	80	47.83	5.57	58.88	4.7	down
P53	Enolase	<i>Brassica napus</i>	gi 34597332	7	88	47.38	5.78	54.95	5	up
P53	Putative heat shock 70 KD protein, mitochondrial	<i>Oryza sativa</i> subsp. japonica	gi 27476086	17	240	70.45	5.45	54.95	5	down
P54	Pyruvate dehydrogenase E1 beta subunit isoform 3	<i>Zea mays</i>	gi 3851003	9	106	39.96	5.46	56.23	5.18	up
P55	UDP-glucose pyrophosphorylase	<i>Bambusa oldhamii</i>	gi 224814363	12	107	51.73	5.43	56.23	6.6	up
P56	Enolase 1	<i>Hevea brasiliensis</i>	gi 9581744	9	111	47.83	5.75	63.1	5.68	up
P57	Cofactor-independent phosphoglycerate mutase	<i>Apium graveolens</i>	gi 6706331	11	327	60.93	5.26	66.07	6	up

## Supplemental table 1 (cont.)

P58	Putative aconitase	Prunus avium	gi 34851120	18	207	98.88	6.01	79.43	6.4	up
P59	Phosphofructokinase, putative	Ricinus communis	gi 255554757	11	79	60.11	6.09	60.26	6.35	up
P60	Phosphoglycerate kinase	Zea mays	gi 28172917	8	105	31.63	5.01	43.65	6.9	up
P61	6-phosphogluconate dehydrogenase, decarboxylating	Pinus pinaster	gi 310689613	10	190	53.2	6.74	50.12	5.97	up
P62	Pyruvate dehydrogenase E1 beta subunit isoform 3	Zea mays	gi 3851003	11	115	39.96	5.46	25.12	4.7	up
p63	beta-amylase	Ipomoea batatas	gi 217940	8	91	56.01	5.18	66.07	4.78	up
P64	unknown	Panax ginseng	gi 89475528	10	449	17.5	7.96	36.31	7.2	down
P65	Enolase 1	Hevea brasiliensis	gi 14423688	8	245	47.8	5.57	56.23	5.1	up
P66	isocitrate dehydrogenase NADP-specific	Cucumis sativus	gi 19171610	10	411	46.15	6	52.48	6.6	up
P67	isocitrate dehydrogenase, putative	Ricinus communis	gi 255575226	13	462	46.23	6.29	52.48	6.7	up
P68	beta-amylase	Ipomoea batatas	gi 217940	8	86	56.01	5.18	64.57	4.7	up
P69	beta-amylase	Ipomoea batatas	gi 217940	10	107	56.01	5.18	64.57	4.85	up
P70	beta-amylase	Ipomoea batatas	gi 217940	11	119	56.01	5.18	75.86	4.7	down
P71	hydrolase, putative	Ricinus communis	gi 255542026	6	132	68.76	6.57	69.18	6.8	up
P72	ACT1	Actinidia deliciosa	gi 149938964	20	378	41.64	5.31	50.12	5.1	down
P73	Actin	Isatis tinctoria	gi 58013197	16	155	41.82	5.31	47.86	5.19	up
P74	Heat shock 70 kDa protein 7, chloroplastic	Arabidopsis thaliana	gi 332008487	21	631	77	5.17	74.13	4.62	up
P75	Heat shock 70 kDa protein 7, chloroplastic	Arabidopsis thaliana	gi 24030296	14	467	77	5.17	69.18	4.51	up
P76	Chaperone DnaK	Medicago truncatula	gi 92870233	19	365	75.76	5.19	70.79	4.6	up
P77	Heat shock protein 70	Zea mays	gi 59799993	15	206	40.98	4.77	46.77	4.58	up
P78	High molecular weight heat shock protein	Malus x domestica	gi 6969976	28	359	71.22	5.16	46.77	4.61	up
P79	14-3-3 protein 9	Solanum lycopersicum	gi 26454611	14	105	29.43	4.74	31.62	4.6	up
P80	class 1 chitinase	Panax ginseng	gi 225593665	5	103	34.9	8.57	34.67	7.4	up

## Supplemental table 1 (cont.)

P81	class 1 chitinase	Panax ginseng	gi 225593665	3	94	34.9	8.57	20.42	7.15	up
P82	14-3-3 protein 2		gi 26454607	10	167	28.86	4.72	37.15	4.28	up
P83	class 1 chitinase	Panax ginseng	gi 225593665	2	105	34.9	8.57	31.62	7.4	up
P84	Calreticulin-2	Arabidopsis thaliana	gi 1009712	11	83	48.16	4.37	61.66	4.3	down
P86	dehydrin 1	Panax ginseng	gi 94962317	5	311	20.56	7.88	26.92	6.5	down
P87	Aldehyde dehydrogenase, putative	Ricinus communis	gi 255568744	9	110	41.95	5.87	60.26	6.42	up
P88	Annexin	Gossypium hirsutum	gi 15214410	11	120	35.82	6.41	33.88	6.9	up
P89	Uv excision repair protein rad23, putative	Ricinus communis	gi 255576447	8	102	42.65	4.61	53.7	4.5	up
P90	unnamed protein product	Vitis vinifera	gi 297737829	12	154	41.95	4.71	52.48	4.5	up
P91	Putative uncharacterized protein	Oryza sativa subsp. japonica	gi 222640948	29	80	166.34	7.31	39.81	5.8	up
P92	Aldo/keto reductase, putative	Ricinus communis	gi 223543702	8	212	39.18	5.7	38.9	6.59	up
P93	aldo/keto reductase, putative	Ricinus communis	gi 255552045	9	269	39.15	5.69	26.92	7	up
P94	Cytosolic glutathione reductase	Malus pumila	gi 326367526	4	135	29.35	6.06	54.95	5.9	down
P95	Catalase	Raphanus sativus	gi 7302765	16	281	56.72	6.63	47.86	6.8	up
P96	Catalase	Helianthus annuus	gi 1168785	11	144	56.75	6.6	44.67	6.74	up
P97	Catalase 1	Jatropha curcas	gi 212171838	13	107	57.3	6.68	44.67	6.61	up
P98	Superoxide dismutase	Digitalis lanata	gi 9929159	5	105	24.76	8.07	24.55	7	up
P99	Superoxide dismutase	Zantedeschia aethiopica	gi 3719457	5	98	26.28	6.71	24.55	6.8	up
P10 0	Biotin carboxylase	Camellia oleifera	gi 239759398	21	334	58.51	6.88	52.48	6.3	up
P10 1	Elongation factor 1-delta 1	Zea mays	gi 226505926	7	85	24.82	4.39	36.31	4.24	up
P10 2	Putative polyprotein	Oryza sativa Japonica Group	gi 46981311	32	77	165.11	9.14	31.62	4	up
P10 3	Putative uncharacterized protein	Vitis vinifera	gi 297746431	25	81	100.47	5.12	46.77	4.85	up
P10 4	putative reverse transcriptase	Oryza sativa Japonica Group	gi 30017567	22	75	93.82	9.05	36.31	6.4	up
P10 5	putative kinesin heavy chain	Arabidopsis thaliana	gi 4056495	24	73	115.67	5.95	17.78	9.7	up
P10 6	Putative uncharacterized protein	Oryza sativa subsp. indica	gi 125555658	22	75	54.87	6.03	34.67	6.73	up

## Supplemental table 1 (cont.)

P10 7	flagellar associated protein	Chlamydomo nas reinhardtii	gi 159479852	14	73	49.7	9.3	21.38	7.55	up
P10 8	hypothetical protein OsI_10115	Oryza sativa Indica Group	gi 218192137	36	75	28.98	4.93	33.88	8.4	up
P10 9	hypothetical protein CHLREDRAFT 192775	Chlamydomo nas reinhardtii	gi 159479330	39	73	435.77	4.87	22.39	4.15	up
P11 0	hypothetical protein OsI_02313	Oryza sativa Indica group	gi 125526309	15	74	42.61	9.82	25.12	7.2	up
P11 1	unknown	Picea sitchensis	gi 148905774	10	169	17.18	6.32	12.3	7.15	up
P11 2	predicted protein	Micromonas pusilla CCMP1545	gi 226459791	46	77	271	9.85	37.15	4.42	up
P11 3	P5CDH1 hypothetical protein	Actinidia chinensis	gi 149938952	12	230	62.01	6.36	64.57	6.02	up
P11 4	VOLCADRAFT 90264 hypothetical protein	Volvox	gi 300264746	25	74	154.19	4.97	17.37	6.86	up
P11 5	hypothetical protein OsI_33626 hypothetical protein	Oryza sativa Indica Group	gi 125531967	33	91	226.19	4.83	47.86	4.9	down
P11 6	VOLCADRAFT 118298	Volvox carteri f. nagariensis	gi 300261549	55	72	683.08	5.26	45.71	5	down

Supplemental table 2

No. <sup>a</sup>	Protein name and Species	Protein accession	Molecular weight (Da)	Isoelectric point	score	Reliability	Protein abundance ratio <sup>b</sup>	RSD/Healthy ginseng <sup>c</sup>
iT1	glutamate decarboxylase [Panax ginseng]	28419245 4 gb ADB82905.1	61352.53	5.69	3.53	62.65	3.01	up
iT2	Set domain protein, putative OS=Ricinus communis GN=RCOM_0542660 PE=3 SV=1	tr B9SKN2 B9SKN2_RICCO	100861.94	5.46	22.72	71.65	2.93	up
iT3	Predicted protein OS=Hordeum vulgare var. distichum PE=2 SV=1	tr F2DVQ0 F2DVQ0_HORVD	37733.31	8.39	27.09	88.77	1.90	up
iT4	Putative uncharacterized protein OS=Medicago truncatula PE=2 SV=1	tr B7FL89 B7FL89_MEDTR	55601.93	6.23	22.66	71.46	0.31	down
iT5	putative glycosyltransferase, partial [Aralia elata]	6 gb AFO67252.1	18486.07	9.02	10.79	91.21	2.42	up
iT6	putative cytochrome P450 monooxygenase, partial [Aralia elata]	39778928 8 gb AFO67233.1	21514.06	9.70	6.18	75.06	2.29	up
iT7	Predicted protein OS=Physcomitrella patens subsp. patens GN=PHYPADRAFT_191594 PE=4 SV=1	tr A9T4Q1 A9T4Q1_PHYPA	48134.17	8.26	21.63	65.28	2.29	up
iT8	squalene epoxidase 2 [Eleutherococcus senticosus]	34405018 6 gb AEM89290.1	62741.16	8.86	7.62	82.67	0.62	down
iT9	squalene synthase [Panax ginseng]	27030361 0 gb ACZ71037.1	51268.70	6.07	32.14	99.71	0.60	down
iT10	squalene epoxidase [Panax notoginseng]	92122627  gb ABE73759.1	62695.22	8.63	12.68	97.27	0.20	down
iT11	squalene epoxidase [Eleutherococcus senticosus]	33946181 9 gb AEJ79818.1	64832.44	8.98	12.68	97.57	0.20	down
iT12	Casein kinase, putative OS=Ricinus communis GN=RCOM_1047520 PE=4 SV=1	tr B9RK86 B9RK86_RICCO	54287.31	9.59	23.71	78.07	3.85	up
iT13	Midasin OS=Arabidopsis thaliana GN=Atlg67120 PE=3 SV=1	tr F4HRR8 F4HRR8_ARATH	656451.44	5.15	26.26	86.20	3.24	up



## Supplemental table 2 (cont.)

iT14	Chaperone clpb, putative OS= <i>Ricinus communis</i> GN=RCOM_0921740 PE=3 SV=1	tr B9RNX 1 B9RNX 1_RICCO	118936.50	6.34	23.63	77.15	0.59	down
iT15	40S ribosomal protein SA OS= <i>Oryza brachyantha</i> GN=OB03G29840 PE=3 SV=1	tr J3LPK8  J3LPK8_ ORYBR	34897.74	4.96	27.18	89.91	0.38	down
iT16	F5O11.10 OS= <i>Arabidopsis thaliana</i> GN=At1g12380 PE=4 SV=1	tr Q9LNA 8 Q9LNA 8_ARAT H	104194.90	8.96	29.08	93.28	0.36	down
iT17	Predicted protein OS= <i>Hordeum vulgare</i> var. <i>distichum</i> PE=2 SV=1	tr F2EHY 9 F2EHY9 _HORVD	58149.27	5.49	22.47	70.80	0.35	down
iT18	NADH dehydrogenase subunit F [ <i>Oplopanax</i> <i>elatus</i> ]	12410916 7 gb ABM 91059.1	79659.39	8.93	5.40	72.09	0.00	down
iT19	ribulose-1,5-bisphosphate carboxylase/oxygenase large subunit, partial (chloroplast) [ <i>Panax</i> sp. ShS-2012]	39235849 6 gb AFM 73456.1	18117.51	4.86	7.97	84.22	29.04	up
iT20	ribulose-1,5-bisphosphate carboxylase/oxygenase large subunit, partial (chloroplast) [ <i>Polyscias</i> <i>guilfoylei</i> ]	1293020 g b AAB011 29.1	55992.14	6.10	10.04	89.09	23.13	up
iT21	cytochrome P450 [ <i>Panax</i> <i>notoginseng</i> ]	33207110 0 gb AED 99869.1	60044.73	8.96	5.10	70.44	9.89	up
iT22	ribulose-1,5-bisphosphate carboxylase/oxygenase large subunit, partial (chloroplast) [ <i>Billardiera</i> <i>heterophylla</i> ]	1293040 g b AAA989 56.1	56102.43	6.09	11.62	96.03	4.89	up
iT23	photosystem II subunit D1, partial (chloroplast) [ <i>Polyscias fruticosa</i> ]	34510562 9 gb AEN 71627.1	3186.57	5.11	4.87	69.97	4.65	up
iT24	ribulose-1,5-bisphosphate carboxylase/oxygenase large subunit [ <i>Osmoxylon</i> <i>sessiliflorum</i> ]	29101090 6 gb ADD 71819.1	51414.56	6.09	13.29	98.18	3.53	up
iT25	Protein ycf2 OS= <i>Oenothera biennis</i> GN=ycf2-A PE=3 SV=1	sp B0Z503  YCF2_O ENBI	293446.31	5.07	26.22	85.50	3.53	up

## Supplemental table 2 (cont.)

iT26	ycf1 gene product (chloroplast) [Sesamum indicum]	33742222 0 ref YP_0 04935725. 11	242064.03	9.73	6.40	76.50	3.18	up
iT27	ATP synthase beta subunit [Schefflera delavayi]	30567165 3 gb ADM 63136.1  33742222U	55510.39	5.08	6.77	80.43	2.79	up
iT28	ycf1 protein (chloroplast) [Eleutherococcus senticosus]	2 ref YP_0 04935611. 11	253856.45	9.74	4.83	69.76	2.20	up
iT29	ribulose 1,5-bisphosphate carboxylase [Sanicula gregaria]	295091 gb  AAA9946 0.1	55765.32	5.85	5.99	73.52	2.02	up
iT30	Ribulose bisphosphate carboxylase large chain (Fragment) OS=Ulva pertusa GN=rbcL PE=3 SV=1	tr B0YH5 6 B0YH56 _ULVPE	35392.27	7.59	23.16	75.21	1.71	up
iT31	cytochrome P450 [Panax notoginseng]	33207110 2 gb AED 99870.1	59858.60	7.61	7.42	82.10	0.70	down
iT32	ribulose-1,5-bisphosphate carboxylase/oxygenase large subunit [Schefflera elegantissima]	75758101  gb ABA28 206.1	55002.44	6.18	3.42	62.39	0.69	down
iT33	cytochrome P450 CYP73A100 [Panax ginseng]	37350180 0 gb AEY 75219.1	64422.34	8.18	11.70	96.21	0.69	down
iT34	cytochrome P450 [Panax notoginseng]	33207109 4 gb AED 99866.1	63265.66	6.03	8.24	84.78	0.64	down
iT35	Kinesin-like protein 1 OS=Arabidopsis thaliana GN=KP1 PE=3 SV=1	tr F4J373  F4J373_A RATH	131161.69	8.68	25.86	85.30	0.62	down
iT36	ribulose-1,5-bisphosphate carboxylase/oxygenase large subunit, partial (chloroplast) [Panax quinquefolius]	1293022 g b AAB011 30.1	56571.03	6.00	4.32	64.90	0.61	down
iT37	ABC transporter A family member 7 OS=Arabidopsis thaliana GN=ABCA7 PE=1 SV=2	sp Q9STT 5 AB7A_ ARATH	113194.06	9.03	21.47	63.99	0.60	down
iT38	photosystem I assembly protein Ycf4 (chloroplast) [Eleutherococcus senticosus]	34744821 8 gb AEO 92630.1	22264.95	9.57	12.11	96.42	0.56	down

## Supplemental table 2 (cont.)

iT39	Putative uncharacterized protein At3g27700 (Fragment) OS=Arabidopsis thaliana GN=At3g27700 PE=2 SV=1	tr C0SVD1 C0SVD1_ARATH	107669.17	6.40	21.14	62.48	0.54	down
iT40	photosystem II cp47 protein [Aralia spinosa]	30567181 7 gb ADM63241.1	56748.23	6.13	6.85	80.48	0.48	down
iT41	Cytochrome b6-f complex iron-sulfur subunit [Panax ginseng]	89475526  gb ABD73295.1	21372.01	5.76	6.32	75.40	0.37	down
iT42	RecName: Full=Cytochrome b559 subunit alpha; AltName: Full=PSII reaction center subunit V	60390363  sp Q68RY9.3 PSBE_PANGI	9588.85	4.83	3.29	61.43	0.33	down
iT43	Heparanase-like protein OS=Medicago truncatula GN=MTR_4g116040 PE=4 SV=1	tr G7JGK8 G7JGK8_MEDTR	40291.17	8.96	21.15	62.48	0.00	down
iT44	Predicted protein OS=Hordeum vulgare var. distichum PE=2 SV=1	tr F2E0B6 F2E0B6_HORVD	103386.73	6.49	25.77	85.20	0.00	down
iT45	UDP-glucosyl transferase 85A2 OS=Arabidopsis thaliana GN=UGT85A2 PE=3 SV=1	tr F4I1C6 F4I1C6_A_RATH	56796.23	5.36	23.42	76.36	16.56	up
iT46	Sucrose synthase OS=Populus trichocarpa GN=SuS3 PE=2 SV=1	tr B9GSC7 B9GSC7_POPTR	99652.20	5.90	21.55	64.96	3.74	up
iT47	Galactosyltransferase B1 OS=Triticum aestivum GN=GALT-B2 PE=2 SV=1	tr I6QFY9 I6QFY9_WHEAT	57125.56	6.76	20.65	70.06	2.85	up
iT48	LG27/30-like gene OS=Arabidopsis thaliana GN=T22A6.260 PE=2 SV=1	tr Q9STV1 Q9STV1_ARATH	79614.68	5.04	30.31	96.16	2.55	up
iT49	Uncharacterized protein OS=Oryza glaberrima PE=3 SV=1	tr I1QA66 I1QA66_ORYGL	34290.95	9.53	26.28	91.77	2.25	up
iT50	Xylosidase OS=Arabidopsis thaliana GN=At5g49360 PE=2 SV=1	tr Q0WQK4 Q0WQK4_ARATH	35835.76	9.15	27.50	91.17	0.64	down
iT51	short-chain alcohol dehydrogenase [Panax ginseng]	21981607 5 gb ACL37155.1	32019.21	6.85	6.66	80.12	0.50	down

## Supplemental table 2 (cont.)

iT52	RecName: Full=Aralin B chain	47115652  sp P83573 .1 ARALB _ARAE	3264.82	8.91	6.10	74.71	0.00	down
iT53	beta-tubulin 1 [Alternaria panax]	35326100 5 gb AEQ 77138.1	16616.36	9.86	6.01	74.71	1.95	up
iT54	Profilin OS=Olea europaea PE=2 SV=1	tr A4KA5 4 A4KA54 _OLEEU	15306.74	5.24	20.96	61.61	0.67	down
iT55	Cyclin-like F-box; FBD OS=Medicago truncatula GN=MtrDRAFT_AC174468g15v1 PE=4 SV=1	tr A2Q6E5  A2Q6E5_ MEDTR	42943.96	9.31	21.64	65.28	1.93	up
iT56	DNA-directed RNA polymerase subunit beta OS=Nicotiana sylvestris GN=rpoB PE=3 SV=1	sp Q3C1G 7 RPOB_ NICSY	127821.00	8.35	24.10	78.71	0.52	down
iT57	Pleiotropic drug resistance protein OS=Medicago truncatula GN=MTR_7g098780 PE=4 SV=1	tr G7KYG 0 G7KYG 0_MEDT R	172985.73	8.61	24.53	79.92	3.88	up
iT58	Disease resistance protein RPP1-like protein R7 OS=Arabidopsis thaliana PE=4 SV=1	tr B7U887  B7U887_ ARATH	139641.80	6.33	39.48	99.61	0.69	down
iT59	Pathogenesis-related protein B OS=Petroselinum crispum GN=PCPR1-3 PE=2 SV=1	sp P19418  PR13_PE TCR	18535.96	4.85	29.46	94.05	0.67	down
iT60	PR10-3, partial [Panax ginseng]	32149595 4 gb ADW 93868.1	18428.89	4.76	92.08	100.00	0.57	down
iT61	Putative citrus disease resistance protein Pt9 (Fragment) OS=Citrus maxima x Citrus trifoliata PE=4 SV=1	tr Q8H1Z9  Q8H1Z9_ 9ROSI	21812.36	8.77	26.52	87.41	0.42	down
iT62	Late embryogenesis abundant protein D-29 OS=Gossypium hirsutum PE=3 SV=1	sp P13940  LEA29_G OSHI	39899.98	5.80	37.66	99.53	0.00	down
iT63	Uncharacterized protein OS=Oryza brachyantha GN=OB06G29210 PE=4 SV=1	tr J3MFX7  J3MFX7_ ORYBR	163080.48	8.16	29.31	93.97	5.32	up
iT64	calcium-dependent protein kinase 1 [Panax ginseng]	26763189 0 gb ACY 78680.1	67492.08	6.19	7.86	84.18	4.66	up

## Supplemental table 2 (cont.)

	calcium-dependent	14875147						
iT65	protein kinase 1 [Panax ginseng]	1 gb ABR_10296.1	13963.29	5.92	7.86	84.18	2.61	up
iT66	NBS-LRR-like protein OS= <i>Oryza sativa</i> subsp. japonica GN=YR14 PE=2 SV=1	tr Q8LL83 Q8LL83_ORYSJ	115122.94	6.28	25.14	82.03	2.48	up
iT67	Kinase, putative OS= <i>Ricinus communis</i> GN=RCOM_0478410 PE=4 SV=1	tr B9T4K8 B9T4K8_RICCO	68885.49	8.60	20.96	61.70	0.51	down
iT68	calcium-dependent protein kinase 2ds isoform 2d-3b [Panax ginseng]	195970503 gb ACG_60719.1	9800.17	4.75	9.23	87.64	0.36	down
iT69	Stress-related protein 1 OS= <i>Capsicum annuum</i> GN=SRP1 PE=2 SV=1	tr D7PF27 D7PF27_CAPAN	28382.51	9.27	25.31	82.55	0.35	down
iT70	Salt overly sensitive 2-like protein (Fragment) OS= <i>Triticum aestivum</i> PE=2 SV=1	tr H9BRR7 H9BRR7_WHEAT	22008.27	4.94	21.83	67.35	0.16	down
iT71	Auxin response factor OS= <i>Medicago truncatula</i> GN=MTR_5g090170 PE=4 SV=1	tr G7KCZ2 G7KCZ2_MEDTR	115743.31	6.44	30.19	96.02	0.48	down
iT72	catalase-1 precursor [Panax ginseng]	162951424 gb ABY_21704.1	60045.68	6.68	3.00	61.34	3.74	up
iT73	Cu/Zn superoxide dismutase [Eleutherococcus senticosus]	384503186 gb AFH9_6953.1	15872.97	5.29	6.60	79.51	40.49	up
iT74	Putative oxidoreductase protein OS= <i>Gossypioides kirkii</i> PE=4 SV=1	tr B2ZAP1 B2ZAP1_9ROSI	49236.23	8.36	45.09	99.65	0.33	down
iT75	At5g48440 OS= <i>Arabidopsis thaliana</i> GN=At5g48440 PE=2 SV=1	tr Q9LV69 Q9LV69_ARATH	53374.93	6.33	32.61	97.86	0.23	down
iT76	accD gene product (chloroplast) [ <i>Sesamum indicum</i> ]	0 ref YP_004935675.1	61202.26	5.04	5.56	72.28	0.00	down
iT77	UDP-glucose:sterol 3-O-glucosyltransferase [Panax ginseng]	24459979 dbj BAC2_2617.1	71990.47	6.01	8.08	84.43	4.54	up
iT78	Predicted protein OS= <i>Hordeum vulgare</i> var. distichum PE=2 SV=1	tr F2E1D3 F2E1D3_HORVD	97606.71	7.04	26.53	87.41	0.42	down

## Supplemental table 2 (cont.)

iT79	maturase, partial (chloroplast) [Pimpinella saxifraga]	2281205 g b AAB662 86.1	45202.14	9.46	8.64	85.16	0.00	down
iT80	Putative polyprotein OS=Oryza sativa subsp. japonica GN=OSJNBa0028C16.7 PE=4 SV=1	tr Q8W2R 5 Q8W2R 5_ORYSJ	98130.19	9.71	25.56	84.31	42.93	up
iT81	PHYTOCHROME C (Fragment) OS=Pennisetum americanum GN=PHYC6bF1 PE=4 SV=1	tr G9M1E 0 G9M1E 0_PENA M	13898.30	6.31	25.36	83.17	23.46	up
iT82	hypothetical protein [Hydrocotyle rotundifolia]	3288410 e mb CAA1 1334.1	34913.60	9.81	3.44	62.57	18.72	up
iT83	reverse transcriptase [Panax ginseng]	15676638 3 gb ABU 94829.1	10624.67	5.77	2.54	61.08	4.89	up
iT84	maturase, partial (chloroplast) [Fatsia japonica]	2281247 g b AAB640 61.1	45207.78	9.38	5.86	73.52	4.89	up
iT85	ribosomal protein S4 [Panax ginseng]	51235315  gb AAT98 511.1	25603.38	10.67	10.30	89.22	3.06	up
iT86	ribosomal protein L32 (chloroplast) [Eleutherococcus senticosus]	34744825 5 gb AEO 92667.1	7878.75	12.20	11.33	94.11	1.99	up
iT87	maturase, partial (chloroplast) [Eryngium bourgatii]	2281165 g b AAB662 67.1	44830.49	9.59	6.50	78.46	1.65	up
iT88	ribosomal protein S3 [Hedera helix]	30274877 4 gb ADL6 3867.1	62724.03	10.43	5.81	72.79	0.71	down
iT89	Putative retroelement integrase OS=Arabidopsis thaliana GN=At2g06890 PE=2 SV=1	tr Q8S8M 1 Q8S8M1 _ARATH	154689.02	8.38	20.72	60.18	0.69	down
iT90	maturase, partial (chloroplast) [Centella erecta]	2281237 g b AAB640 56.1	45209.09	9.55	8.99	87.41	0.64	down
iT91	L.esculentum protein with leucine zipper OS=Medicago truncatula GN=MTR_3g036750 PE=4 SV=1	tr G7K5S0  G7K5S0_ MEDTR	113747.00	6.45	31.92	97.61	0.53	down
iT92	maturase [Tetraplasandra hawaiensis]	2281225 g b AAB662 96.1	45063.21	9.35	5.29	71.51	0.53	down

## Supplemental table 2 (cont.)

iT93	Maturase K (Fragment) OS=Echinodorus inpai GN=matK PE=3 SV=1	tr A8QLC1  A8QLC1_9LILI	55586.35	9.42	30.19	95.99	0.48	down
iT94	Copia-type polyprotein OS=Glycine max PE=4 SV=1	tr C0JJ2  C0JJ2_S OYBN	133543.08	8.52	21.61	65.20	0.33	down
iT95	maturase, partial (chloroplast) [Aralidium pinnatifidum]	2281231 g b AAB640 53.1	44325.65	9.81	11.30	91.83	0.21	down
iT96	Predicted protein OS=Physcomitrella patens subsp. patens GN=PHYPADRAFT_65 173 PE=4 SV=1	tr A9RES6  A9RES6_ PHYPA	78463.06	6.43	22.27	69.92	0.03	down
iT97	Uncharacterized protein OS=Glycine max PE=4 SV=1	tr K7LV86  K7LV86_ SOYBN	123548.42	5.76	29.75	95.44	2.20	up
iT98	En/Spm-like transposon protein, putative OS=Arabidopsis thaliana GN=T2H7.5 PE=4 SV=1	tr Q9C6Z6  Q9C6Z6_ ARATH	48961.16	5.44	23.07	73.76	6.02	up
iT99	Coatomer subunit beta-2 OS=Medicago truncatula GN=MTR_4g132130 PE=4 SV=1	tr G7JJ75  G7JJ75_ MEDTR	10928.24	9.52	21.83	67.13	0.16	down
iT100	Putative protein phosphatase 2C-like protein 44 OS=Arabidopsis thaliana GN=At3g23360 PE=5 SV=1	sp Q9LW60  P2C44_ ARATH	32763.35	7.01	22.17	69.16	0.00	down
iT101	alpha-copaene synthase [Eleutherococcus trifoliatus]	30213538 3 gb ADK 94034.1	69377.93	5.55	4.55	65.46	55.40	up
iT102	Uncharacterized protein OS=Cedrus deodara GN=ycf1 PE=4 SV=1	tr E1CBQ5  E1CBQ5_ CEDDE	233487.34	9.05	24.08	78.41	26.62	up
iT103	Pentatricopeptide repeat- containing protein At3g62540, mitochondrial OS=Arabidopsis thaliana GN=At3g62540 PE=2 SV=1	sp Q3EAF8  PP294_ ARATH	74658.46	7.83	20.60	69.99	9.21	up
iT104	Uncharacterized protein OS=Oryza brachyantha GN=OB12G26570 PE=4 SV=1	tr J3NF99  J3NF99_ ORYBR	14416.01	8.56	21.17	62.82	6.53	up
iT105	Osusogusoo protein OS=Oryza sativa subsp. japonica GN=P0545E05.6 PE=4 SV=1	tr Q5Z4V4  Q5Z4V4_ ORYSJ	79205.13	8.24	25.99	85.50	2.83	up

## Supplemental table 2 (cont.)

iT106	At5g43870	tr Q9LKC						
	OS=Arabidopsis thaliana	2 Q9LKC2	53513.54	9.44	32.84	98.40	0.67	down
	GN=At5g43870 PE=2 SV=1	_ARATH						
iT107	Os02g0822500 protein	tr Q6KA0						
	OS=Oryza sativa subsp.	1 Q6KA01	100704.78	8.91	22.30	70.06	0.25	down
	japonica GN=OJ1119_A01.22-1 PE=2 SV=1	_ORYSJ						
iT108	Protein AFR, putative	tr B9S0Z8						
	OS=Ricinus communis	B9S0Z8_	56631.67	8.83	21.83	67.43	0.16	down
	GN=RCOM_0632280 PE=4 SV=1	RICCO						