

Supplementary table S1. Correlation analysis of chlorophyll metabolism-related gene expression and chlorophyll content in three cultivars.

Gene name	Index	LJ-Correlation	LJ-P_value	BY-Correlation	BY-P_value	ZH-Correlation	ZH-P_value
<i>GLURS</i>	chl _a	0.593	0.320	-0.226	0.774	0.201	0.989
<i>GLURS</i>	chl _b	0.680	0.507	-0.284	0.716	0.665	0.933
<i>GLUTR</i>	chl _a	0.439	0.361	0.979	0.021	0.247	0.753
<i>GLUTR</i>	chl _b	0.357	0.643	0.951	0.049	0.544	0.456
<i>GSA-AM</i>	chl _a	0.569	0.331	-0.105	0.895	0.590	0.410
<i>GSA-AM</i>	chl _b	0.545	0.550	-0.219	0.781	-0.115	0.885
<i>PBGS</i>	chl _a	0.422	0.578	0.813	0.187	0.817	0.183
<i>PBGS</i>	chl _b	0.563	0.477	0.740	0.260	0.919	0.081
<i>PBGD</i>	chl _a	0.372	0.276	0.161	0.839	0.707	0.293
<i>PBGD</i>	chl _b	0.377	0.231	0.045	0.955	-0.113	0.887
<i>UROS</i>	chl _a	0.156	0.844	0.785	0.215	0.821	0.179
<i>UROS</i>	chl _b	0.353	0.647	0.707	0.293	0.965	0.035
<i>UROD</i>	chl _a	0.964	0.036	0.799	0.201	0.992	0.028
<i>UROD</i>	chl _b	0.970	0.053	0.732	0.268	0.658	0.342
<i>CPOX</i>	chl _a	0.795	0.020	0.775	0.225	0.951	0.055
<i>CPOX</i>	chl _b	0.669	0.003	0.698	0.302	0.491	0.509
<i>PPOX</i>	chl _a	0.425	0.575	0.631	0.369	0.989	0.011
<i>PPOX</i>	chl _b	0.465	0.535	0.552	0.448	0.797	0.203
<i>MgCh</i>	chl _a	0.320	0.680	0.846	0.154	0.968	0.032
<i>MgCh</i>	chl _b	0.046	0.954	0.783	0.217	0.596	0.404
<i>MgPMT</i>	chl _a	0.711	0.029	0.895	0.105	0.973	0.027
<i>MgPMT</i>	chl _b	0.893	0.011	0.841	0.159	0.649	0.351
<i>MgPEC</i>	chl _a	0.692	0.308	0.162	0.838	0.676	0.324

<i>MgPEC</i>	chlb	0.887	0.031	0.056	0.944	0.289	0.711
<i>DVR</i>	chla	0.389	0.611	0.588	0.412	0.913	0.049
<i>DVR</i>	chlb	0.611	0.389	0.497	0.503	0.393	0.607
<i>POR</i>	chla	0.118	0.882	0.313	0.687	0.915	0.085
<i>POR</i>	chlb	0.108	0.892	0.212	0.788	0.498	0.502
<i>CHLG</i>	chla	0.245	0.985	-0.624	0.764	0.988	0.001
<i>CHLG</i>	chlb	0.445	0.779	-0.612	0.879	0.668	0.332
<i>CAO</i>	chla	0.236	0.755	0.898	0.102	0.996	0.004
<i>CAO</i>	chlb	0.322	0.555	0.848	0.152	0.671	0.329
<i>NYC1</i>	chla	0.215	0.636	-0.634	0.366	0.493	0.507
<i>NYC1</i>	chlb	0.348	0.652	-0.633	0.367	0.654	0.346
<i>HCAR</i>	chla	0.527	0.473	0.963	0.037	0.076	0.924
<i>HCAR</i>	chlb	0.635	0.365	0.929	0.071	0.577	0.423
<i>CLH1</i>	chla	-0.174	0.773	0.970	0.030	-0.508	0.492
<i>CLH1</i>	chlb	-0.233	0.898	0.990	0.010	0.519	0.806
<i>CLH2</i>	chla	0.201	0.994	-0.063	0.937	0.480	0.520
<i>CLH2</i>	chlb	0.316	0.843	-0.159	0.841	0.740	0.260
<i>SGR</i>	chla	-0.123	0.826	0.866	0.134	0.534	0.466
<i>SGR</i>	chlb	-0.102	0.767	0.819	0.181	0.837	0.163
<i>PAO</i>	chla	-0.118	0.882	0.915	0.085	0.958	0.042
<i>PAO</i>	chlb	-0.239	0.761	0.900	0.100	0.765	0.235
<i>RCCR</i>	chla	0.683	0.417	0.415	0.585	0.990	0.210
<i>RCCR</i>	chlb	0.544	0.563	0.345	0.655	0.165	0.352

Supplementary table S2. Correlation analysis of carotenoids metabolism-related gene expression and carotenoids content.

Gene name	Index	LJ-Correlation	LJ-P_value	BY-Correlation	BY-P_value	ZH-Correlation	ZH-P_value
<i>DXS</i>	carotenoids	-0.252	0.748	0.904	0.096	0.086	0.137
<i>IPI</i>	carotenoids	0.145	0.855	0.161	0.839	-0.107	0.935
<i>GGPPS2</i>	carotenoids	0.321	0.786	-0.145	0.855	0.690	0.031
<i>PSY1</i>	carotenoids	0.249	0.751	0.545	0.455	0.430	0.697
<i>PDS</i>	carotenoids	0.375	0.625	0.705	0.295	-0.255	0.445
<i>Z-ISO</i>	carotenoids	0.638	0.617	-0.328	0.672	0.574	0.262
<i>ZDS</i>	carotenoids	0.238	0.762	0.605	0.040	0.335	0.966
<i>CRTISO</i>	carotenoids	-0.276	0.724	0.575	0.425	0.422	0.782
<i>LCYb1</i>	carotenoids	-0.687	0.313	0.828	0.172	0.207	0.926
<i>LCYb2</i>	carotenoids	0.008	0.221	0.105	0.949	-0.316	0.840
<i>CRTRB2</i>	carotenoids	-0.734	0.266	0.388	0.612	0.282	0.718
<i>BCH</i>	carotenoids	0.896	0.104	0.284	0.716	0.799	0.005
<i>VDE</i>	carotenoids	-0.073	0.927	-0.166	0.993	-0.486	0.142
<i>ZEP</i>	carotenoids	0.666	0.334	0.103	0.972	0.177	0.233
<i>NCED</i>	carotenoids	-0.757	0.243	-0.800	0.200	0.147	0.530
<i>NCED3</i>	carotenoids	0.190	0.810	0.222	0.778	-0.272	0.276
<i>CCD1</i>	carotenoids	0.727	0.273	0.296	0.704	0.007	0.259
<i>lcyE</i>	carotenoids	0.275	0.725	0.505	0.495	0.018	0.382
<i>CYP97A</i>	carotenoids	0.532	0.876	0.348	0.652	0.733	0.267
<i>CYP97C</i>	carotenoids	0.124	0.677	0.616	0.384	-0.283	0.165

Supplementary table S3. Gene-specific primer sequences used in the current study for RT-qPCR experiments.

Gene name	Gene ID	F (5'→3')	R (5'→3')
<i>GluRS</i>	CSS0015047	TCCACCAGGGAATCTGAGGA	CATATGAGGCATCAGCCCACT
<i>GluTR/hemA</i>	CSS0011743	ATCAGCAGGGCTAGACTCCC	GCTGATGTTCTGCCAAAGC
<i>GSAAM/hemL</i>	CSS0020466	GGTCACGCAGATGATGAGGT	CCATGGTAGCAACCCTCGAA
<i>PBGs/ALAD</i>	CSS0022256	ACTTAATAGGCGCCCTCGTC	TCAACACCTGTGGGAGACTT
<i>PBGD/hemC</i>	CSS0024885	TGGCCTTAGCAGGACTCAAAC	GTGCGACAAGAGCCATCCAA
<i>UROS/hemD</i>	CSS0036187	AATTGCTTGAGCTTCCCCT	GTACCAGCTCCGACTACACC
<i>UROD/hemE</i>	CSS0004968	AAGAGGTGAGGGTCCAGTT	GTGCGAGTTGTACCCCTTC
<i>CPOX/hemF</i>	CSS0041680	TGAAACCCCAAAAGATTCTCAGG	TCACACCATTCTTGAACCGAG
<i>PPOX/hemG</i>	CSS0022330	CACTCCGATGTAGCCCCAAA	AAAGCCTGCCCTGAGTTTCC
<i>MgCh</i>	CSS0016317	AGGAAAGCAGGTGGGAATGAG	CCACGGCTGTGTCTTTGAG
<i>MgPMT/CHLM</i>	CSS0004907	CATTACCCGCAAAACAAGGCA	GGCACAGCCTCAATCAACCT
<i>MgPEC</i>	CSS0045826	GAAGTGGTGCCAGGATGAGAA	TGCAGTTGTCCTGTTCTGCT
<i>DVR</i>	CSS0008645	GGGGAAGGCATTGACACCA	TCCTTCCCATAACTTGGCGTT
<i>POR</i>	CSS0041527	TGACTATCCATCGAAGCGCC	CTCGCATGTCCCCTAGGTTG
<i>CAO</i>	CSS0049616	CATCCGGCCTCCAAGGATAC	ATGGGAGCAAAATCCAGCGA
<i>CHLG</i>	CSS0018345	GCACCAGATAAGGCACCTGT	CCACTCCCCAAACCAATGGA
<i>NYC1</i>	CSS0034731	GGATGCGGGTTGTAAAGGGA	CGGCTTTCAGCCCAATTACG
<i>HCAR</i>	CSS0026751	AAACGGTCCAGACCCATTCC	ATGGACCACAGATTCGAGGC
<i>CLH1</i>	CSS0004684	CTAGCCCTTCCGGCCATAG	CAACGGGGTCAAGTCCTATT
<i>CLH2</i>	CSS0028283	AAGGAATGTTGCGAACCAGC	AACAAACCTCCTCATGGGCT
<i>SGR</i>	CSS0030812	AGATGCCAAAGCCATGCCAA	GAGTCCGATCCTGACCCGAT
<i>PAO</i>	CSS0024763	GTCGTATCACGGCTGGTCT	CAAATCGCGCTGAATCGTCA
<i>RCCR</i>	CSS0031276	AGCTTATCCAGAGCAGCCCA	GCGGACCAGAATAGCAGTAGG

<i>DXS</i>	CSS0018056	TGCAAAGGGCTTATGACCAG	AACCATGTGGAAGCTCGG
<i>IPI</i>	CSS0026150	TGTGAACCGGGATGAGTTGA	GGAGGGTCCCTTTTCCACAT
<i>GGPPS2</i>	CSS0007938	AGTCCATGCGCTACTCCCTC	TTCGTAGCTGTTGCGATGTG
<i>PSY1</i>	CSS0002725	AGGCAGGGCTTTCAGATGAG	TGGCGATACAACAACAGCGA
<i>PDS</i>	CSS0024321	GTGGCTGCGTGGAAGATGA	GTCAAATCGGCTGAACTCCC
<i>Z-ISO</i>	CSS0045415	ATGATGGTGTGCAGTTGTGG	GATTGTGTGAGCCAAGCACC
<i>ZDS</i>	CSS0031670	TTGCTCCAATGCGTGCTTAC	GTAGCACCTTCCATGCTGTCT
<i>CRTISO</i>	CSS0033902	AGGTGTTATTGCCGTTGCCT	TGCCAGTGTCTTAACCAACC
<i>LCYb1</i>	CSS0017943	TGCGCAACAAGTTTCAGAGG	AGTGGTCATCAACGAACACGA
<i>LCYb2</i>	CSS0031629	TTCAGAGGCAGGGCTTCTG	GCACCAGACCAGGTAGTGTC
<i>CRTRB2</i>	CSS0044082	GGTCTCTGTTTCGGAGCTGG	TGTCTGAATGGTGGAGCTGG
<i>BCH</i>	CSS0005162	CCTTGTTCTGGTCTCTGTT	ACTTCCTCAAGTTCCTTGGGTC
<i>VDE</i>	CSS0006565	CAGACGGTGGCTTCTTTACG	ACCATATCCATCCCATGCGTC
<i>ZEP</i>	CSS0031288	CTTGCCCTTGCCCTCAGTTT	AAGGCACCCGATACTGCTTG
<i>NCED</i>	CSS0033791	CCCTTCCATACGCCACCTTC	GCCGTCTTGGGTAGACGATG
<i>NCED3</i>	CSS0015210	TTGCACAGATTGAAGGCATTGT	ACCCAAACATGGCTTGATTTCC
<i>CCD1</i>	CSS0012422	CGGAGTGCCTGAATGGTGAG	TGCTCTCAGCATTTGCATGTTA
<i>LCYe</i>	CSS0031227	GACTACATCAAGCCGGTGG	GATCCGGTCCAATCAGTCCA
<i>CYP97A</i>	CSS0044082	GGTCTCTGTTTCGGAGCTGG	TGTCTGAATGGTGGAGCTGG
<i>CYP97C</i>	CSS0037493	AAGGGGCTTGTGTGCTGAGG	CGGACTATCAGTGGAAGGGAG
<i>GAPDH</i>	NA	GGAGCGAGATCCCTCCAAAAT	GGCTGTTGTCATACTTCTCATGG

GluRS - Glutamyl-tRNA synthetase 2. **GluTR/hemA** - Glutamyl-tRNA reductase 3. **GSAAM/hemL** - Glutamate-1-semialdehyde aminotransferase 4. **PBGS/ALAD** - Porphobilinogen synthase 5. **PBGD/hemC** - Porphobilinogen deaminase 6. **UROS/hemD** - Uroporphyrinogen III synthase 7. **UROD/hemE** - Uroporphyrinogen decarboxylase 8. **CPOX/hemF** - Coproporphyrinogen oxidase 9. **PPOX/hemG** - Protoporphyrinogen oxidase 10. **MgCh** - Magnesium chelatase 11. **MgPMT/CHLM** - Magnesium protoporphyrin IX monomethyl ester cyclase 12. **MgPEC** - Magnesium protoporphyrin IX ethyl ester cyclase 13. **DVR** - Dihydropteridine reductase 14. **POR** - Porphobilinogen oxidase 15. **CAO** - Chlorophyllide a oxygenase 16. **CHLG** - Chlorophyll a hydroxylase 17. **NYC1** - Non-yellow color 1 18. **HCAR** - Hydroxycarboxylic acid receptor 19. **CLH1** - Chlorophyllase 1 20. **CLH2** - Chlorophyllase 2 21. **SGR** - Stay green 22. **PAO** - Polyamine oxidase 23. **RCCR** - Red chlorophyll catabolite reductase 24. **DXS** - 1-deoxy-D-xylulose 5-phosphate synthase 25. **IPI** - Isopentenyl diphosphate isomerase 26. **GGPPS2** - Geranylgeranyl

pyrophosphate synthase 2 27. ****PSY1**** - Phytoene synthase 1 28. ****PDS**** - Phytoene desaturase 29. ****Z-ISO**** - Zeta-carotene isomerase 30. ****ZDS**** - Zeta-carotene desaturase 31. ****CRTISO**** - Carotenoid isomerase 32. ****LCYb1**** - Lycopene beta-cyclase 1 33. ****LCYb2**** - Lycopene beta-cyclase 2 34. ****CRTRB2**** - Carotenoid isomerase B2 35. ****BCH**** - Bacteriochlorophyll a hydroxylase 36. ****VDE**** - Violaxanthin de-epoxidase 37. ****ZEP**** - Zeaxanthin epoxidase 38. ****NCED**** - 9-cis-epoxycarotenoid dioxygenase 39. ****NCED3**** - 9-cis-epoxycarotenoid dioxygenase 3 40. ****CCD1**** - Carotenoid cleavage dioxygenase 1 41. ****LCYe**** - Lycopene epsilon-cyclase 42. ****CYP97A**** - Cytochrome P450 97A 43. ****CYP97C**** - Cytochrome P450 97C 44. ****GAPDH**** - Glyceraldehyde-3-phosphate dehydrogenase.

Supplementary table S4. Relative content of chlorophyll metabolism-related and carotenoids metabolism-related gene expression in three cultivars.

Gene name	LJ-15	SD	LJ-20	SD	LJ-25	SD	LJ-35	SD
<i>GluRS</i>	1.627	0.079	1.070	0.124	1.065	0.072	1.015	0.029
<i>GluTR</i>	0.285	0.037	0.972	0.041	1.023	0.160	0.797	0.072
<i>GSA-AM</i>	0.474	0.047	0.958	0.039	0.974	0.062	0.955	0.050
<i>PBGS</i>	0.330	0.040	0.784	0.094	0.980	0.076	2.136	0.019
<i>PBGD</i>	1.405	0.124	1.251	0.125	0.972	0.198	0.829	0.128
<i>UROS</i>	0.897	0.170	0.989	0.048	0.975	0.222	3.531	0.073
<i>UROS</i>	0.454	0.059	0.493	0.094	1.047	0.063	0.857	0.082
<i>CPOX</i>	0.453	0.077	0.818	0.115	0.915	0.167	0.993	0.128
<i>PPOX</i>	0.428	0.060	0.969	0.126	1.053	0.108	1.752	0.223
<i>Mgch</i>	0.253	0.038	1.395	0.077	1.110	0.082	1.061	0.124
<i>MgPMT</i>	0.695	0.111	0.535	0.128	1.049	0.120	1.136	0.073
<i>MgPEC</i>	0.769	0.146	0.618	0.111	1.042	0.108	1.115	0.131
<i>DVR</i>	0.663	0.106	0.404	0.057	1.039	0.199	2.145	0.026
<i>POR</i>	1.135	0.170	0.799	0.124	0.989	0.178	0.596	0.102
<i>CAO</i>	0.876	0.090	0.871	0.096	1.142	0.093	1.933	0.041
<i>CHLG</i>	1.097	0.154	1.120	0.101	0.963	0.072	1.906	0.168
<i>NYC1</i>	0.527	0.053	1.123	0.225	0.898	0.108	1.594	0.143
<i>HCAR</i>	0.456	0.091	0.683	0.109	1.193	0.029	1.650	0.032
<i>CLH1</i>	0.790	0.129	0.525	0.063	1.027	0.136	0.029	0.075
<i>CLH2</i>	1.210	0.092	1.750	0.150	0.983	0.124	4.114	0.032

<i>SGR</i>	0.942	0.183	2.064	0.035	0.981	0.074	2.194	0.049
<i>PAO</i>	0.772	0.093	2.062	0.066	1.030	0.148	1.979	0.194
<i>RCCR</i>	0.369	0.067	1.001	0.200	0.982	0.112	1.158	0.129
<i>DXS</i>	1.008	0.171	1.699	0.097	0.992	0.042	1.307	0.028
<i>IPI</i>	1.279	0.141	1.144	0.160	0.979	0.114	1.722	0.052
<i>GGPPS2</i>	1.226	0.110	0.672	0.067	0.962	0.104	84.298	0.146
<i>PSY1</i>	1.013	0.203	0.880	0.176	0.987	0.237	1.495	0.032
<i>PDS</i>	0.771	0.123	1.000	0.190	1.030	0.198	1.776	0.026
<i>Z-ISO</i>	0.339	0.037	1.348	0.202	1.086	0.143	2.400	0.018
<i>ZDS</i>	1.005	0.181	0.935	0.150	0.995	0.015	1.496	0.029
<i>CRTISO</i>	1.105	0.155	0.984	0.187	0.905	0.012	0.017	0.023
<i>LCYb1</i>	5.784	0.619	0.798	0.128	1.012	0.134	1.384	0.045
<i>LCYb2</i>	2.807	0.067	1.235	0.185	0.945	0.027	1.497	0.039
<i>CRTRB2</i>	2.324	0.130	1.058	0.265	0.943	0.147	0.931	0.021
<i>BCH</i>	0.712	0.092	0.894	0.116	1.045	0.339	0.981	0.044
<i>VDE</i>	1.314	0.112	0.718	0.122	0.976	0.109	1.405	0.029
<i>ZEP</i>	0.636	0.095	0.897	0.126	1.057	0.190	1.275	0.024
<i>NCED</i>	1.657	0.131	1.258	0.151	0.960	0.019	0.695	0.031
<i>NCED3</i>	1.315	0.158	0.638	0.108	0.977	0.141	5.785	0.194
<i>CCD1</i>	0.797	0.190	0.729	0.139	1.027	0.073	1.107	0.021
<i>LCYe</i>	0.965	0.070	0.804	0.088	1.036	0.113	2.047	0.134
<i>CYP97A</i>	1.234	0.084	0.668	0.087	1.043	0.009	1.864	0.074
<i>CYP97C</i>	0.702	0.154	0.874	0.071	1.028	0.151	0.488	0.036

Gene name	BY-15	SD	BY-20	SD	BY-25	SD	BY-35	SD
<i>GluRS</i>	0.450	0.083	1.659	0.028	1.013	0.112	0.709	0.106
<i>GluTR</i>	0.370	0.037	0.608	0.076	1.000	0.044	2.218	0.045
<i>MgPEC</i>	0.542	0.050	0.737	0.045	1.019	0.039	0.671	0.040
<i>PBGS</i>	0.153	0.087	0.623	0.019	0.977	0.091	1.333	0.094
<i>PBGD</i>	0.390	0.060	0.746	0.131	1.002	0.125	0.727	0.127
<i>UROS</i>	0.406	0.046	0.752	0.067	1.026	0.058	1.193	0.059
<i>UROD</i>	0.329	0.099	0.443	0.091	1.056	0.097	1.220	0.103
<i>CPOX</i>	0.300	0.107	0.564	0.152	1.116	0.112	1.176	0.124
<i>PPOX</i>	0.479	0.126	0.501	0.229	1.003	0.124	0.981	0.132
<i>Mgch</i>	0.094	0.009	0.366	0.129	0.918	0.072	1.431	0.073
<i>MgPMT</i>	0.280	0.010	0.477	0.077	0.870	0.126	1.523	0.139
<i>MgPEC</i>	0.133	0.016	0.294	0.137	0.847	0.124	0.516	0.119
<i>DVR</i>	0.215	0.056	0.399	0.027	1.001	0.059	0.920	0.053
<i>POR</i>	0.052	0.010	0.178	0.097	1.008	0.236	0.592	0.229
<i>CAO</i>	0.398	0.094	0.511	0.041	1.004	0.101	1.470	0.094
<i>CHLG</i>	0.674	0.106	0.882	0.175	0.848	0.105	0.881	0.100
<i>NYC1</i>	1.007	0.225	0.515	0.141	1.027	0.220	0.485	0.079
<i>HCAR</i>	0.493	0.083	0.959	0.032	1.016	0.098	1.898	0.100
<i>CLH1</i>	4.292	0.163	5.291	0.074	1.001	0.059	28.414	0.056
<i>CLH2</i>	0.684	0.160	1.049	0.032	1.003	0.148	0.850	0.150
<i>SGR</i>	0.526	0.034	0.491	0.048	1.322	0.034	1.345	0.035
<i>PAO</i>	0.415	0.072	2.002	0.190	1.005	0.060	3.637	0.051
<i>RCCR</i>	0.680	0.108	0.562	0.133	1.032	0.195	0.888	0.113
<i>DXS</i>	0.567	0.116	0.402	0.029	1.002	0.095	0.559	0.098
<i>IP1</i>	1.081	0.171	0.772	0.050	0.879	0.164	0.857	0.165

<i>GGPPS2</i>	0.099	0.058	2.786	0.140	1.000	0.070	0.974	0.067
<i>PSY1</i>	0.652	0.158	0.462	0.032	1.003	0.178	1.489	0.173
<i>PDS</i>	0.081	0.285	0.463	0.027	1.003	0.286	1.341	0.293
<i>Z-ISO</i>	0.684	0.195	0.925	0.020	0.867	0.207	0.490	0.197
<i>ZDS</i>	0.483	0.071	0.703	0.029	1.006	0.154	1.359	0.158
<i>CRTISO</i>	0.535	0.084	0.710	0.024	0.885	0.203	1.393	0.178
<i>LCYb1</i>	0.768	0.116	0.685	0.047	1.032	0.131	1.013	0.126
<i>LCYb2</i>	0.942	0.193	1.093	0.039	1.002	0.194	1.213	0.198
<i>CRTRB2</i>	0.726	0.273	0.701	0.022	1.157	0.272	1.708	0.275
<i>BCH</i>	1.056	0.099	0.749	0.043	1.107	0.113	1.192	0.110
<i>VDE</i>	1.078	0.121	0.741	0.029	1.002	0.125	0.343	0.044
<i>ZEP</i>	1.022	0.120	1.224	0.026	1.004	0.143	1.849	0.140
<i>NCED</i>	3.395	0.151	2.218	0.030	1.002	0.145	2.922	0.140
<i>NCED3</i>	0.365	0.053	1.356	0.176	1.002	0.115	0.977	0.106
<i>CCD1</i>	0.868	0.066	0.760	0.021	1.001	0.136	1.741	0.132
<i>LCYe</i>	0.390	0.089	0.738	0.127	1.004	0.088	1.613	0.124
<i>CYP97A</i>	0.809	0.099	0.667	0.073	1.010	0.085	0.359	0.044
<i>CYP97C</i>	0.681	0.027	0.391	0.037	1.074	0.282	0.322	0.086

Gene name	ZH-15	SD	ZH-20	SD	ZH-25	SD	ZH-35	SD
<i>GluRS</i>	0.490	0.079	1.352	0.029	0.958	0.106	1.791	0.126
<i>GluTR</i>	0.605	0.032	0.852	0.063	1.050	0.037	1.973	0.034
<i>MgPEC</i>	0.246	0.017	0.633	0.052	1.000	0.039	0.271	0.050
<i>PBGS</i>	0.442	0.040	0.171	0.019	1.006	0.091	1.101	0.078
<i>PBGD</i>	0.509	0.039	0.494	0.128	0.906	0.149	0.283	0.084
<i>UROS</i>	0.729	0.190	0.485	0.082	1.139	0.054	1.044	0.050
<i>UROD</i>	0.451	0.054	0.388	0.075	1.037	0.110	0.641	0.094
<i>CPOX</i>	0.384	0.078	0.409	0.130	1.092	0.116	0.534	0.083
<i>PPOX</i>	0.457	0.060	0.302	0.223	1.015	0.124	0.724	0.131
<i>Mgch</i>	0.209	0.038	0.243	0.125	0.944	0.073	0.544	0.085
<i>MgPMT</i>	0.379	0.113	0.384	0.074	0.906	0.130	0.677	0.103
<i>MgPEC</i>	0.575	0.154	0.815	0.138	0.840	0.131	0.905	0.121
<i>DVR</i>	0.228	0.090	0.276	0.022	0.996	0.062	0.324	0.047
<i>POR</i>	0.520	0.197	0.342	0.079	0.951	0.143	0.428	0.091
<i>CAO</i>	0.419	0.219	0.317	0.041	1.031	0.091	0.596	0.099
<i>CHLG</i>	0.530	0.154	0.493	0.068	0.868	0.103	0.722	0.105
<i>NYC1</i>	0.430	0.070	0.606	0.089	1.000	0.212	1.522	0.286
<i>HCAR</i>	1.322	0.093	0.875	0.033	1.064	0.125	6.049	0.113
<i>CLH1</i>	1.865	0.231	1.502	0.075	1.040	0.079	2.162	0.060
<i>CLH2</i>	0.683	0.093	0.676	0.033	1.197	0.157	1.442	0.191
<i>SGR</i>	0.712	0.178	0.546	0.047	1.271	0.031	1.454	0.034
<i>PAO</i>	0.611	0.095	0.576	0.200	0.920	0.057	0.863	0.082
<i>RCCR</i>	0.349	0.067	0.183	0.130	1.060	0.213	0.467	0.191
<i>DXS</i>	0.702	0.190	0.595	0.030	1.047	0.081	0.869	0.140
<i>IPI</i>	1.063	0.141	1.235	0.052	0.929	0.152	0.120	0.155

<i>GGPPS2</i>	0.990	0.094	0.889	0.124	0.963	0.073	0.453	0.051
<i>PSY1</i>	1.090	0.203	0.894	0.032	0.963	0.176	0.485	0.155
<i>PDS</i>	1.781	0.125	1.204	0.026	1.039	0.226	1.544	0.281
<i>Z-ISO</i>	0.558	0.037	0.577	0.018	0.856	0.203	0.912	0.201
<i>ZDS</i>	0.821	0.187	0.760	0.030	0.982	0.160	1.850	0.155
<i>CRTISO</i>	1.190	0.155	0.830	0.023	0.923	0.194	4.618	0.397
<i>LCYb1</i>	0.848	0.074	0.881	0.049	1.003	0.133	1.632	0.131
<i>LCYb2</i>	1.356	0.067	1.332	0.039	1.032	0.233	0.490	0.202
<i>CRTRB2</i>	0.531	0.131	2.028	0.021	1.322	0.272	0.621	0.277
<i>BCH</i>	0.206	0.081	0.052	0.038	1.202	0.121	0.153	0.092
<i>VDE</i>	0.702	0.116	0.683	0.030	0.980	0.114	0.877	0.121
<i>ZEP</i>	0.333	0.083	0.502	0.021	1.069	0.138	0.020	0.103
<i>NCED</i>	0.690	0.132	0.564	0.031	0.900	0.126	1.163	0.145
<i>NCED3</i>	1.954	0.140	1.624	0.172	0.990	0.113	1.310	0.095
<i>CCD1</i>	0.811	0.191	0.232	0.021	0.984	0.133	0.830	0.163
<i>LCYe</i>	0.742	0.070	0.691	0.134	0.984	0.091	1.023	0.092
<i>CYP97A</i>	1.165	0.084	1.228	0.074	0.985	0.076	1.023	0.095
<i>CYP97C</i>	0.207	0.055	0.182	0.036	1.131	0.278	0.708	0.186

SD, Standard Deviation, (each treatment shows the mean, n=3).