

Supplemental figures and tables

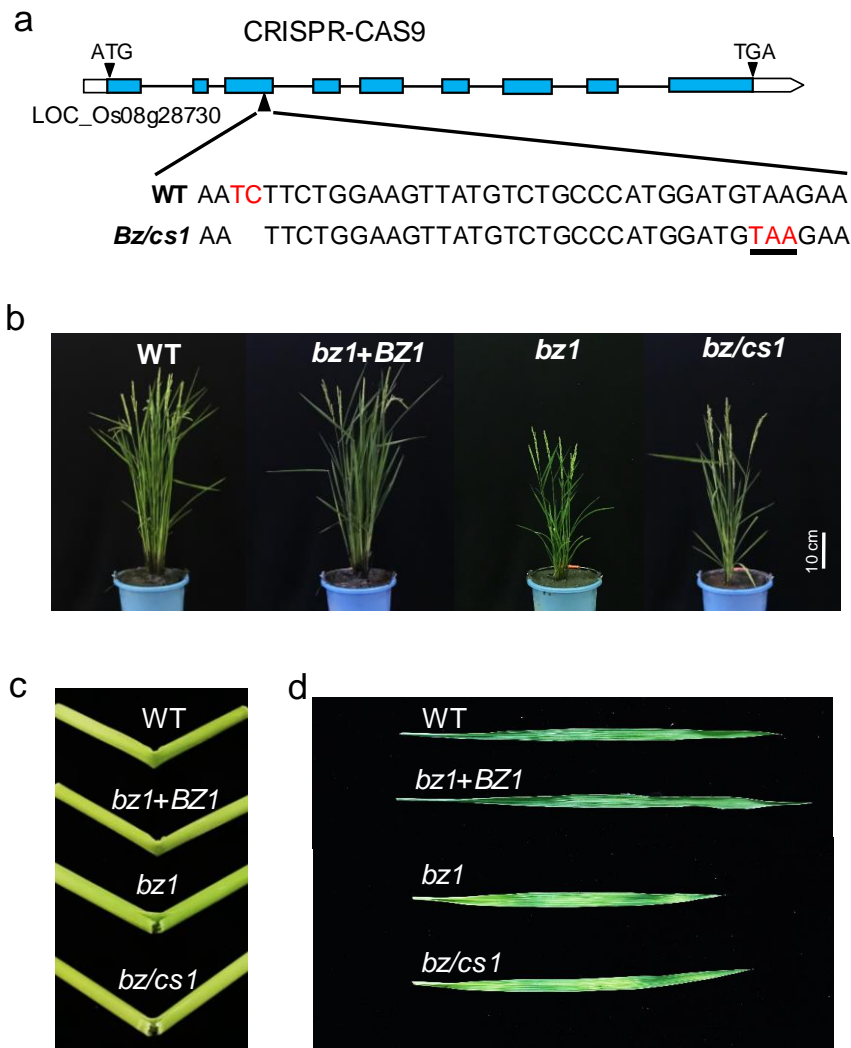


Figure S1. The *BZ1* gene is confirmed to be response for the brittle culm and zebra leaf phenotypes. **a**, The transgenic plants *bz/cs1* generated by CRISPR/Cas9 approach had two base pairs deletion in the third exon of LOC_Os08g28730. The arrowhead indicates two base pairs deletion (showing in red letters) in the third exon inducing a premature translational stop codon (underlined). **b–d**, The complementary lines showed restored phenotypes as wild-type (**b**) whereas the *bz/cs1* displayed brittle culm (**c**) and zebra leaf phenotypes (**d**) as similar as *bz1*.

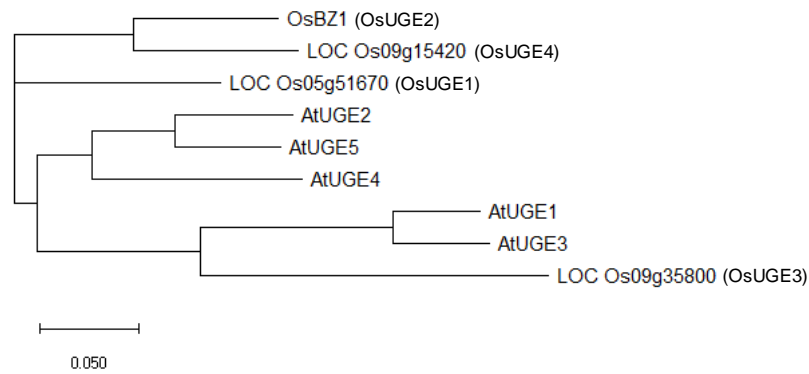


Figure S2. Phylogeny of UGE isoforms in rice and *Arabidopsis* based on maximum likelihood.

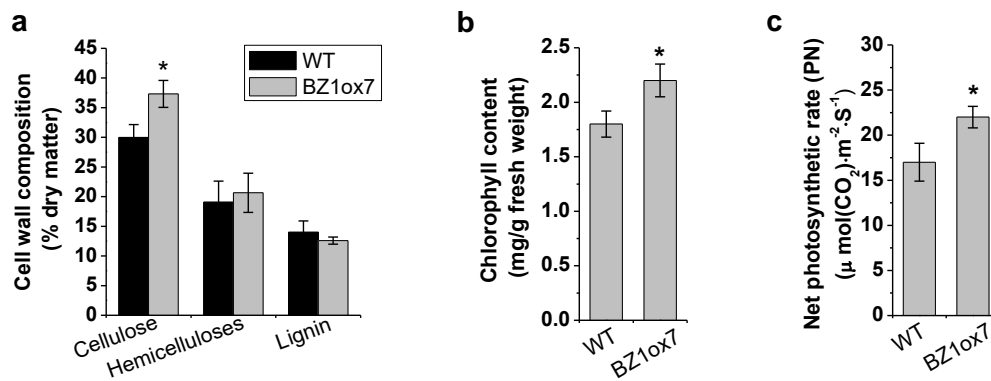


Figure S3. Comparison of cell wall composition (a), chlorophyll content (b) and photosynthetic efficiency (c) between WT and BZ1ox7 transgenic line * indicates significant differences between WT and *bz1* by *t*-test at $P < 0.05$.

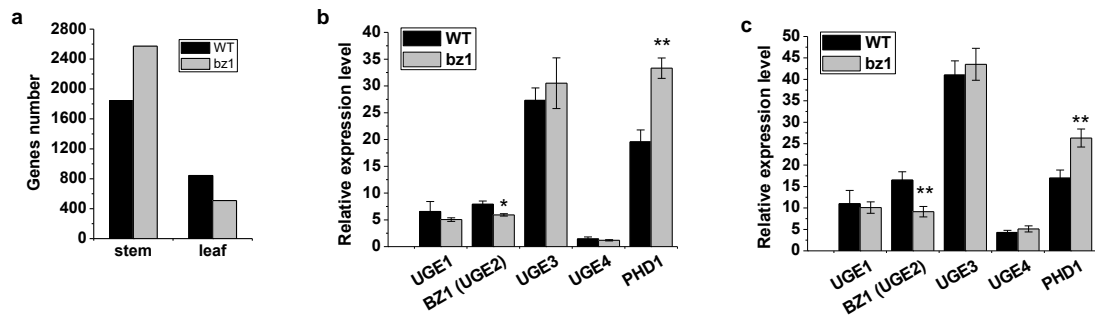


Figure S4. a, Number of genes that are upregulated and downregulated in stem and leaf of *bz1* compared with those in the WT. b, Relative expression level of *UGEs* and *PHD1* based on RNA-Sequencing analysis. c, Relative expression level of *UGEs* and *PHD1* based on qRT-PCR assay.

Table S1. Comparison of expression levels of putative AGPs biosynthesis-related genes between WT and *bz1* plants by stem RNA-Sequencing analysis.

Name	Locus	RPKM		log ₂ Ratio	<i>p</i>	FDR	change
		WT	<i>bz1</i>				
<i>AGP1</i>	LOC_Os08g37630	11.51	3.28	-1.62	0.00	0.01	down
<i>AGP2</i>	LOC_Os01g71170	98.80	48.70	-0.85	0.00	0.01	down
<i>AGP3</i>	LOC_Os03g08940	103.99	77.57	-0.19	0.76	0.86	
<i>AGP12</i>	LOC_Os01g02010	132.41	194.44	0.74	0.01	0.03	up
<i>AGP14</i>	LOC_Os01g37950	448.79	261.87	-0.59	0.03	0.09	down
<i>AGP17</i>	LOC_Os01g55220	35.09	3.39	-3.18	0.00	0.00	down
<i>AGP19</i>	LOC_Os01g57040	24.39	29.73	0.50	0.12	0.25	
<i>AGP20</i>	LOC_Os02g16500	278.33	115.58	-1.07	0.00	0.00	down
<i>AGP21</i>	LOC_Os02g48710	614.19	1155.84	1.10	0.00	0.00	up
<i>AGP23</i>	LOC_Os05g12580	285.37	162.80	-0.60	0.09	0.20	
<i>AGP24</i>	LOC_Os06g21400	48.10	197.49	2.30	0.03	0.10	up
<i>AGP26</i>	LOC_Os06g30920	22.95	21.04	0.09	0.78	0.87	
<i>AGP27</i>	LOC_Os07g38630	44.06	47.76	0.35	0.42	0.59	
<i>AGP29</i>	LOC_Os01g42210	1.77	0.83	-0.90	0.04	0.12	down
<i>AGP31</i>	LOC_Os03g63540	26.13	30.61	0.42	0.14	0.28	
<i>LLA1</i>	LOC_Os03g26820	26.43	17.41	-0.42	0.14	0.28	
<i>LLA6</i>	LOC_Os07g07790	0.59	2.22	2.07	0.01	0.05	up
<i>LLA7</i>	LOC_Os07g43290	15.56	10.96	-0.33	0.27	0.44	
<i>FLA1</i>	LOC_Os04g48490	10.48	1.17	-3.00	0.00	0.00	down
<i>FLA2</i>	LOC_Os03g03600	33.55	47.08	0.67	0.01	0.05	up
<i>FLA3</i>	LOC_Os08g23180	93.72	116.95	0.51	0.06	0.15	
<i>FLA4</i>	LOC_Os08g38270	63.22	77.08	0.50	0.11	0.24	
<i>FLA5</i>	LOC_Os08g39270	67.26	28.85	-1.04	0.00	0.00	down
<i>FLA6</i>	LOC_Os05g48900	254.09	327.34	0.56	0.04	0.11	up
<i>FLA7</i>	LOC_Os01g47780	354.01	372.81	0.27	0.31	0.49	
<i>FLA8</i>	LOC_Os01g06580	150.68	208.37	0.65	0.02	0.06	up
<i>FLA9</i>	LOC_Os05g07060	180.56	259.12	0.69	0.01	0.04	up
<i>FLA10</i>	LOC_Os09g30010	3.41	1.33	-1.17	0.00	0.02	down
<i>FLA11</i>	LOC_Os09g07350	158.94	296.77	1.09	0.00	0.00	up
<i>FLA12</i>	LOC_Os01g62380	7.90	4.93	-0.50	0.10	0.22	
<i>FLA15</i>	LOC_Os02g20560	4.13	12.81	1.82	0.00	0.00	down
<i>FLA16</i>	LOC_Os07g06680	301.56	464.02	0.81	0.00	0.02	up
<i>FLA17</i>	LOC_Os03g57490	0.77	0.68	0.04	0.93	0.96	
<i>FLA21</i>	LOC_Os02g49420	2.23	0.19	-3.37	0.00	0.00	down
<i>FLA24</i>	LOC_Os03g57460	100.11	175.04	1.02	0.01	0.03	
<i>FLA26</i>	LOC_Os05g38500	4.90	5.16	0.26	0.41	0.59	
<i>FLA27</i>	LOC_Os09g30486	78.36	96.39	0.49	0.07	0.17	
<i>ELA2</i>	LOC_Os02g06670	4.73	3.36	-0.32	0.36	0.53	

Table S2. Comparison of expression levels of leaf color associated genes between WT and *bz1* plants by leaf RNA-Sequencing analysis.

Gene	Locus	WT	<i>bz1</i>	logFC	P Value	FDR	Change
<i>DI; RGA1; D89</i>	LOC_Os05g26890	62.91	75.88	0.27	0.11	0.35	
<i>Spl11</i>	LOC_Os12g38210	19.83	18.05	-0.14	0.43	0.71	
<i>sp15; SF3b3; OsSL5</i>	LOC_Os07g10390	7.11	6.70	-0.09	0.62	0.84	
<i>Se5; OsHY1; OsHO1; ygl2; grc1</i>	LOC_Os06g40080	167.01	159.34	-0.06	0.71	0.88	
<i>OsDVR</i>	LOC_Os03g22780	68.84	83.87	0.29	0.08	0.28	
<i>YGL1; ygl80</i>	LOC_Os05g28200	80.51	118.72	0.56	0.00	0.03	Up
<i>OsChH</i>	LOC_Os03g20700	323.51	594.44	0.88	0.00	0.00	Up
<i>OsCAO1; PGL</i>	LOC_Os10g41780	44.14	80.68	0.87	0.00	0.01	Up
<i>NAL9; VYL; ClpP</i>	LOC_Os03g29810	41.60	55.31	0.41	0.02	0.12	
<i>Chl1; OsChLD; ygl3; Ygl7; ygl98</i>	LOC_Os03g59640	156.92	236.01	0.59	0.00	0.01	Up
<i>Ch9; OsChH</i>	LOC_Os03g36540	210.19	316.47	0.59	0.00	0.01	Up
<i>NYC1</i>	LOC_Os01g12710	434.41	300.22	-0.53	0.00	0.01	Down
<i>SGR</i>	LOC_Os09g36200	1.40	2.31	0.72	0.03	0.14	
<i>v2</i>	LOC_Os03g20460	12.16	13.91	0.19	0.35	0.64	
<i>OsCRTISO; ZEBRA2; PHS3; ZL2; MHZ5</i>	LOC_Os11g36440	40.23	42.59	0.08	0.63	0.84	
<i>NOL</i>	LOC_Os03g45194	13.52	33.08	1.28	0.00	0.00	Up
<i>OsDOS</i>	LOC_Os01g09620	12.17	7.01	-0.80	0.00	0.00	Down
<i>OsGluRS; Cde1(t)</i>	LOC_Os02g02860	28.12	48.28	0.77	0.00	0.01	Up
<i>OsHAP3A</i>	LOC_Os01g61810	9.75	9.20	-0.08	0.69	0.87	
<i>OsHAP3B</i>	LOC_Os05g38820	9.25	9.93	0.10	0.61	0.83	
<i>NYC3</i>	LOC_Os06g24730	6.80	7.55	0.15	0.39	0.68	
<i>OsMADS26</i>	LOC_Os08g02070	3.22	17.99	2.47	0.00	0.00	Up
<i>RNRL1; V3</i>	LOC_Os06g07210	2.59	2.65	0.03	0.91	0.97	
<i>RNRS1; Sr1</i>	LOC_Os06g14620	5.44	5.95	0.13	0.73	0.89	
<i>OsPHR2</i>	LOC_Os07g25710	17.64	17.19	-0.04	0.82	0.94	
<i>OsFRDL1</i>	LOC_Os03g11734	0.83	0.68	-0.28	0.37	0.66	
<i>OsSPX1</i>	LOC_Os06g40120	32.54	24.29	-0.42	0.25	0.54	
<i>SPP</i>	LOC_Os06g41990	226.97	224.20	-0.02	0.91	0.97	
<i>DTH8; Ghd8; OsHAP3H; LHDI; EF8</i>	LOC_Os08g07740	8.58	6.71	-0.35	0.10	0.32	
<i>OsLSD1; OsLOL1</i>	LOC_Os08g06280	38.03	33.36	-0.19	0.25	0.54	
<i>SPL3; OsEDR1; OsACDR1; OsMAPKKK1</i>	LOC_Os03g06410	14.58	16.82	0.20	0.23	0.51	
<i>β-OsLcY; zebra324</i>	LOC_Os02g09750	73.82	66.24	-0.15	0.41	0.69	
<i>RLN1; LLM1</i>	LOC_Os04g52130	165.23	250.86	0.60	0.00	0.03	
<i>etl1</i>	LOC_Os11g01210	69.25	43.88	-0.65	0.00	0.03	
<i>etl2</i>	LOC_Os12g01210	186.70	129.89	-0.52	0.02	0.10	
<i>OsAPX2; APXb</i>	LOC_Os07g49400	208.22	117.78	-0.82	0.01	0.08	
<i>OsWRKY53</i>	LOC_Os05g27730	47.34	72.62	0.61	0.00	0.05	Up
<i>WSL12; OsNDPK2</i>	LOC_Os12g36194	23.57	45.04	0.93	0.00	0.03	Up
<i>RLS1</i>	LOC_Os02g10900	2.61	6.02	1.20	0.00	0.00	Up
<i>OsABC1-2</i>	LOC_Os02g36570	121.91	144.37	0.24	0.12	0.37	
<i>CHR729; CRL6</i>	LOC_Os07g31450	14.61	14.74	0.01	0.95	0.98	
<i>OsNUS1; V1</i>	LOC_Os03g45400	106.32	109.78	0.04	0.78	0.92	
<i>YSA</i>	LOC_Os03g40020	18.08	15.27	-0.25	0.13	0.38	
<i>OsHPL3; cea62</i>	LOC_Os02g02000	39.07	51.38	0.39	0.09	0.31	
<i>MPR25</i>	LOC_Os04g51350	13.63	18.07	0.40	0.02	0.11	
<i>YLC1; OsV5A</i>	LOC_Os09g21250	18.17	32.06	0.81	0.00	0.02	Up
<i>OsPORB; FGL; PGL10</i>	LOC_Os10g35370	184.67	258.38	0.48	0.01	0.07	
<i>Cgal</i>	LOC_Os02g12790	9.81	13.39	0.44	0.05	0.21	
<i>PAPST1</i>	LOC_Os01g16040	22.93	31.30	0.44	0.01	0.07	
<i>WSL</i>	LOC_Os01g37870	21.42	26.35	0.29	0.08	0.28	
<i>OsHO2; OsYLC2</i>	LOC_Os03g27770	34.88	61.14	0.80	0.00	0.01	Up
<i>HYR</i>	LOC_Os03g02650	0.78	0.93	0.22	0.58	0.81	
<i>AM1</i>	LOC_Os04g58620	52.91	56.46	0.10	0.55	0.79	
<i>OsPPR1</i>	LOC_Os09g24680	1.42	1.03	-0.46	0.11	0.35	
<i>OsPDF1B</i>	LOC_Os01g45070	59.02	57.06	-0.05	0.76	0.90	
<i>SPL29; UAP1</i>	LOC_Os08g10600	6.25	6.93	0.15	0.44	0.72	
<i>SPL33</i>	LOC_Os01g02720	11.81	11.37	-0.05	0.76	0.91	
<i>WLP1</i>	LOC_Os01g54540	339.98	568.88	0.74	0.00	0.01	Up
<i>OsRH34</i>	LOC_Os03g36930	9.04	13.56	0.58	0.00	0.03	Up
<i>OsV5B</i>	LOC_Os08g32130	2.91	2.66	-0.13	0.63	0.84	
<i>OsCUL3a</i>	LOC_Os02g51180	5.51	5.39	-0.03	0.88	0.96	
<i>LYL1</i>	LOC_Os02g51080	740.99	830.74	0.17	0.35	0.64	
<i>AL2; CRS1</i>	LOC_Os09g19850	41.61	51.25	0.30	0.06	0.25	
<i>ASL2; RPL21c</i>	LOC_Os02g15900	330.28	616.38	0.89	0.00	0.01	Up
<i>LLB</i>	LOC_Os07g14350	18.66	27.94	0.58	0.00	0.01	Up
<i>YGL138(t)</i>	LOC_Os11g05552	56.33	80.27	0.51	0.00	0.03	Up
<i>OsCYO1</i>	LOC_Os09g28480	13.43	11.46	-0.23	0.18	0.45	
<i>RLS3</i>	LOC_Os03g38990	24.46	27.32	0.16	0.35	0.64	
<i>OsNaPRT1; LT S1</i>	LOC_Os03g62110	22.93	16.73	-0.45	0.01	0.07	
<i>BGL11(t)</i>	LOC_Os11g38040	2.80	2.43	-0.20	0.49	0.76	
<i>TCDS</i>	LOC_Os05g34040	17.90	25.16	0.49	0.01	0.08	
<i>YSS1</i>	LOC_Os04g59570	214.49	241.29	0.17	0.29	0.58	
<i>GIC</i>	LOC_Os04g57920	3.57	2.23	-0.67	0.01	0.06	
<i>Fd-GOGAT1; lc7; ABC1; spl23</i>	LOC_Os07g46460	628.62	669.76	0.09	0.56	0.80	
<i>LMR; LRD6-6</i>	LOC_Os06g03940	12.14	13.58	0.16	0.37	0.66	
<i>OsGATA12</i>	LOC_Os03g61570	9.32	8.42	-0.14	0.46	0.74	
<i>OsFdc2</i>	LOC_Os03g48040	205.38	216.38	0.07	0.64	0.85	
<i>OsPAP1/OspTAC3; WSL3</i>	LOC_Os10g32540	48.94	79.35	0.69	0.00	0.02	Up
<i>OsAld-Y; ygd1-1</i>	LOC_Os06g40640	289.66	187.83	-0.62	0.00	0.04	Down
<i>TCDD10</i>	LOC_Os10g28600	81.80	98.94	0.27	0.09	0.30	
<i>WSP1</i>	LOC_Os04g51280	331.01	354.71	0.10	0.53	0.78	
<i>YGL8</i>	LOC_Os01g17170	356.29	600.84	0.75	0.00	0.01	Up
<i>YLI</i>	LOC_Os02g05890	53.18	96.68	0.86	0.00	0.00	
<i>OsDG2</i>	LOC_Os02g39340	20.21	28.89	0.51	0.01	0.05	
<i>OsValRS2; WP1</i>	LOC_Os07g06940	31.45	50.24	0.67	0.00	0.02	Up
<i>ALI</i>	LOC_Os03g31150	61.89	81.98	0.40	0.01	0.08	
<i>GRY79</i>	LOC_Os02g33610	191.54	189.43	-0.02	0.91	0.97	
<i>OsABC18</i>	LOC_Os11g29850	7.89	8.68	0.14	0.48	0.75	

Table S3. Significant alterations of genes involved in photosynthesis pathway in comparison of *bz1* leaf RNA-Sequencing data to that of the WT.

Accession	WT	<i>bz1</i>	Log2 Ratio	P	FDR	Description
LOC_Os01g57962	3.58	1.69	-1.08	0.04	0.18	photosystem I P700 chlorophyll a apoprotein A2, putative, expressed
LOC_Os01g57964	2.36	1.01	-1.22	0.02	0.12	photosystem I P700 chlorophyll a apoprotein A1, putative, expressed
LOC_Os03g55874	4.99	1.99	-1.32	0.03	0.17	ATP synthase subunit beta, putative, expressed
LOC_Os04g16748	166.12	69.50	-1.26	0.00	0.03	ATP synthase B chain, putative, expressed
LOC_Os04g16740	71.11	31.80	-1.17	0.00	0.04	ATP synthase subunit alpha, putative, expressed
LOC_Os04g16872	8.81	3.69	-1.25	0.02	0.12	photosystem II D2 protein, putative, expressed
LOC_Os05g01675	8.30	3.41	-1.29	0.03	0.15	photosystem I P700 chlorophyll a apoprotein A1, putative, expressed
LOC_Os06g02980	1.35	0.44	-1.60	0.00	0.03	ATP synthase F1, epsilon subunit family protein, expressed
LOC_Os06g39756	3.74	1.06	-1.78	0.00	0.04	ATP synthase epsilon chain, putative, expressed
LOC_Os07g05360	1.16	0.34	-1.77	0.00	0.03	photosystem II 10 kDa polypeptide, chloroplast precursor, putative, expressed
LOC_Os07g22498	32.34	15.45	-1.07	0.00	0.04	photosystem I iron-sulfur center, putative, expressed
LOC_Os10g21230	11.36	4.83	-1.22	0.04	0.18	ATP synthase C chain, putative, expressed
LOC_Os10g21238	6.49	2.49	-1.38	0.02	0.13	ATP synthase B chain, putative, expressed
LOC_Os10g21240	16.66	7.25	-1.20	0.00	0.02	ATP synthase, putative, expressed
LOC_Os10g21250	1.81	0.73	-1.29	0.02	0.11	photosystem I P700 chlorophyll a apoprotein A1, putative, expressed
LOC_Os10g21266	2.89	1.04	-1.46	0.01	0.08	ATP synthase subunit beta, putative, expressed
LOC_Os10g21406	13.92	5.60	-1.32	0.00	0.03	photosystem I iron-sulfur center, putative, expressed
LOC_Os10g38229	3.08	1.14	-1.44	0.01	0.06	photosystem I P700 chlorophyll a apoprotein A1, putative, expressed
LOC_Os10g38272	88.32	32.73	-1.44	0.00	0.01	ATP synthase B chain, putative, expressed
LOC_Os10g39880	9.09	2.70	-1.73	0.05	0.20	photosynthetic reaction center protein, putative, expressed
LOC_Os10g41689	1.72	0.53	-1.69	0.01	0.07	photosystem II D2 protein, putative, expressed

Table S4. Primers used for qRT-PCR analysis

Gene	Locus	Annotation	Forward primers	Reverse primers
<i>Actin1</i>	LOC_Os03g50885	Actin	ACCATTGGTGCTGAGCGTTT	CGCAGCTTCCATTCCATGAA
<i>UGE1</i>	LOC_Os05g51670	UDP-Glu/Gal epimerase 1	TGGAACCGACTACAACACCA	CAGCAAATACAAGCGGGATT
<i>BZ1 (UGE2)</i>	LOC_Os08g28730	UDP-Glu/Gal epimerase 2	CTAAAAGCTGTGGCGAAAG	TGCCATATGGATTGTTTGGGA
<i>UGE3</i>	LOC_Os09g35800	UDP-Glu/Gal epimerase 3	CCCAACAACCTTCTCCGTA	AAGCCACACAACCAATGTCA
<i>UGE4</i>	LOC_Os09g15420	UDP-Glu/Gal epimerase 4	CGTTCATTTTGTGGTCTGA	ACGGCAAATCTCCTCTGCTA
<i>AGP1</i>	LOC_Os08g37630	Arabinogalactan protein 1	TGGCCATGGCCGCGCTCTT	AAACCGGGGAGGCGCTCGT
<i>AGP2</i>	LOC_Os01g71170	Arabinogalactan protein 2	TTCCTCCTCGTACTCGTGCT	GGAGCAGCGCATTATGT
<i>AGP14</i>	LOC_Os01g37950	Arabinogalactan protein 14	ATGGCCAGGTTCTCCGCA	AAATACACAGATCCCAAACC
<i>AGP17</i>	LOC_Os01g55220	Arabinogalactan protein 17	AAGGCCCTGGCTCTCCTCT	GAAGCCAGGAGCGAGAC
<i>AGP20</i>	LOC_Os02g16500	Arabinogalactan protein 20	CTCGTCGTGGCATCTTC	GGGAGAAGAAGCATCCAGTG
<i>AGP29</i>	LOC_Os01g42210	Arabinogalactan protein 29	GCCTTGTTGGCATCAATT	TGGCAGTGACTTGAGGTCTG
<i>FLA1</i>	LOC_Os04g48490	Fasciclin-like AGP1	AAGAAGCTGCACTCCCTCAG	CCTCAAGAACGGAGAGGTTG
<i>FLA5</i>	LOC_Os08g39270	Fasciclin-like AGP5	GAATCCAAAGCAGCCATGAT	GTCCGTTCTCCAGGAGGT
<i>FLA10</i>	LOC_Os09g30010	Fasciclin-like AGP10	GTTCTGCCCAGGTACAAGA	GTTCTGCACCGTGAAGTTGT
<i>FLA21</i>	LOC_Os02g49420	Fasciclin-like AGP21	CCCTACAACATCTCCGTGCT	TTCTTCTGCCACCATCTCC
<i>DVR</i>	LOC_Os03g22780	Divinyl-reductase	CCGTCCTTACCTACAGCAT	CGATGGGGAGGATCTTGTT
<i>YGL1</i>	LOC_Os05g28200	Prenyltransferase	TTGGGCACTGTTGTAGCAG	CAATGTAGCTGCACCAAGA
<i>CAO1</i>	LOC_Os10g41780	Chlorophyllide a oxygenase	GCTGCTTACCGGATGTCTC	ACAACCGATACCGGATACCA
<i>ClpP</i>	LOC_Os03g29810	Clp protease	GATCAAGCCCAAAGTTGGAA	CCAAGTTTGCCCAAGTAAA
<i>ChlD</i>	LOC_Os03g59640	Magnesium-chelatase subunit chlD	AAAGAATGGCTCGAAAAGCA	GCCACCACATGGTAGCTTCT
<i>ChlH</i>	LOC_Os03g20700	Magnesium-chelatase subunit chlH	TGGAGCAGCTCTGCACTAGA	TTGGAGGACGGAGTAGATGG
<i>ChlI</i>	LOC_Os03g36540	Magnesium-chelatase subunit chlI	ATGGAACACCGTGGAGAGAG	GCTGGAGCTTGCTTTGTTCC
<i>SGR</i>	LOC_Os09g36200	Senescence-inducible chloroplast stay-green protein 1	AGGGGTGGTACAACAAGCTG	GCTCCTTGCGGAAGATGTAG
<i>V1</i>	LOC_Os03g45400	Antitermination NusB domain	TTTAGTGGCTGTTGCCAGTG	TCCATTGATTACCCGAGGAG
<i>V2</i>	LOC_Os03g20460	Guanylate kinase	AAGGAGCAGCAACCTTGAGA	GCGTTTCACCTCTCTCTGG
<i>NOL</i>	LOC_Os03g45194	Oxidoreductase	TGGTGCAACGAAGAGAAGTG	ACGAGATAATCCGCAACCAC
<i>GluRS</i>	LOC_Os02g02860	Glutamyl-tRNA synthetase	ATTTGGCACTTCTTGTTGG	AATGCCTGTCTCTCCATC