

**Supplemental Table S4.** Down-regulated gene by the overexpression of *CRCT* analyzed by microarray.

Top 50 of down-regulated genes showing average signal intensity of Cyanine-3 and Cyanine-5 above 10 and  $P < 0.05$  are listed. Ratio of change and signal average are expressed as means of four replicates.

Rank	Description	RAP-DB	Ratio of change	Signal av.	P-value
1	(No Hit)	Os03g0323700	0.09	27.95	0.000
2	Peptidase S10, serine carboxypeptidase family protein.	Os11g0461000	0.12	61.85	0.004
3	Pectinesterase family protein.	Os03g0399000	0.13	25.22	0.000
4	Heat shock protein 26.	Os03g0245800	0.14	453.61	0.037
5	ADP-glucose pyrophosphorylase large subunit 1 (AGPL1).	Os05g0580000	0.18	7855.33	0.000
6	Cytochrome P450 family protein.	Os10g0524700	0.21	178.49	0.000
7	CO <sub>2</sub> Responsive CCT Protein (CRCT)	Os05g0595300	0.22	1562.09	0.000
8	Hypothetical protein.	Os12g0117700	0.25	23.68	0.036
9	Ankyrin repeat containing protein.	Os05g0124000	0.25	11.83	0.026
10	Retrotransposon gag protein family protein.	Os08g0315200	0.26	12.16	0.002
11	Hypothetical protein.	Os11g0294300	0.28	10.10	0.000
12	Plastidial $\alpha$ -glucan phosphorylase 1 (Pho1).	Os03g0758100	0.30	7151.93	0.000
13	Hypothetical protein.	Os02g0452900	0.31	11.48	0.003
14	TPR-like domain containing protein.	Os08g0481000	0.31	23.78	0.001
15	Anthocyaninless2.	Os08g0136100	0.33	10.58	0.000
16	Terpene synthase-like domain containing protein.	Os04g0344100	0.33	228.65	0.018
17	Caffeic acid O-methyltransferase (EC 2.1.1.6).	Os04g0175600	0.35	535.17	0.004
18	Zn-finger, CCHC type domain containing protein.	Os06g0583500	0.36	106.39	0.000
19	Hypothetical protein.	Os10g0146300	0.36	10.42	0.003
20	Conserved hypothetical protein.	Os01g0339500	0.36	20.40	0.001
21	Conserved hypothetical protein.	Os09g0256700	0.36	34.58	0.005
22	Granule-bound starch synthase II (GBSSII).	Os07g0412100	0.37	363.17	0.002
23	Hypothetical protein.	Os11g0626700	0.37	33.04	0.010
24	Zn-finger, CCHC type domain containing protein.	Os02g0552700	0.37	174.30	0.003
25	Starch-branching enzyme I (BEI).	Os06g0726400	0.37	3188.19	0.000
26	S-adenosyl-L-methionine: beta-alanine N-methyltransferase	Os04g0176200	0.37	18.04	0.000
27	Hypothetical protein.	Os11g0692700	0.38	14.47	0.002
28	Non-protein coding transcript, unclassifiable transcript.	Os01g0261000	0.38	10.06	0.001

29	Conserved hypothetical protein.	Os01g0507400	0.38	15.80	0.001
30	Conserved hypothetical protein.	Os10g0445700	0.38	11.62	0.007
31	ADP-glucose pyrophosphorylase small subunit I (AGPS1).	Os09g0298200	0.39	11693.51	0.000
32	Hypothetical protein.	Os06g0322400	0.40	21.54	0.009
33	Peptidase C1A, papain family protein.	Os09g0381400	0.40	10.53	0.001
34	Transferase family protein.	Os02g0484600	0.40	10.13	0.005
35	Transposase, IS4 family protein.	Os10g0143400	0.41	313.31	0.001
36	Cellular retinaldehyde-binding/triple function, N-terminal domain containing protein.	Os07g0456500	0.41	11.32	0.021
37	Autophagy protein Apg6 family protein.	Os03g0258500	0.41	30.62	0.008
38	Pectate lyase/Amb allergen family protein.	Os06g0584000	0.42	10.53	0.001
39	OsPK4.	Os01g0206300	0.42	10.04	0.008
40	Lipase, class 3 family protein.	Os01g0900400	0.42	20.02	0.010
41	Hypothetical protein.	Os08g0233500	0.42	10.77	0.003
42	Hypothetical protein.	Os04g0489900	0.42	139.56	0.000
43	Phospholipase D nu-2 (Fragment).	Os02g0120200	0.42	10.37	0.004
44	Cold acclimation protein COR413-TM1.	Os05g0566800	0.42	1970.85	0.002
45	Hypothetical protein.	Os12g0406000	0.43	229.87	0.002
46	Conserved hypothetical protein.	Os02g0253700	0.43	13.04	0.012
47	Starch debranching enzyme (PUL).	Os04g0164900	0.43	64.29	0.000
48	Heat shock protein DnaJ family protein.	Os08g0374400	0.44	18.58	0.004
49	Caffeic acid 3-O-methyltransferase	Os04g0176100	0.44	195.11	0.010
50	miRNA	osa-miR535	0.44	10.48	0.012