

Figure S1. Relative levels of ABA and CKs in Arabidopsis plants after cold or dehydration treatments. ABA, abscisic acid; iPRPs, N6-(Δ^2 -isopentenyl) adenine ribotides; iPR, isopentenyladenosine; iP, isopentenyladenine; tZRP, trans-zeatin riboside-5'-phosphates; tZR, trans-zeatin riboside; tZ, trans-zeatin; cZRP, cis-zeatin 5'-phosphates; cZR, cis-zeatin riboside, cZ, cis-zeatin; C, cold; D, dehydration.

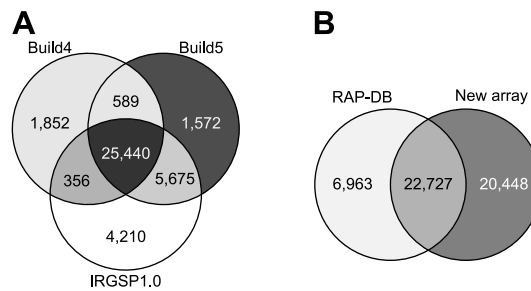


Figure S2. Rice genes identified in the rice annotation project database (RAP-DB) and included in our new oligonucleotide microarray. Rice genes in the RAP-DB (Ohyanagi et al., 2006) are classified as being supported by expression evidence (representative genes) or computationally predicted (predicted genes). A comparison of representative genes in IRGSP builds 4 and 5, as well as Os-Nipponbare-Reference-IRGSP-1.0 in RAP-DB, is represented in the Venn diagram. However, IRGSP build 4 was updated to build 5 with 7,247 genes added to, and 2,208 genes deleted from, the RAP-DB. When IRGSP build 5 was subsequently updated to Os-Nipponbare-Reference-IRGSP-1.0, 4,566 genes were added and 2,161 genes were deleted. Among the 4,566 new representative genes, 356 were re-annotated in RAP-DB. (a) Number of rice genes in RAP-DB (build4, build5, and IRGSP1.0). (b) Number of probes in RAP-DB (old microarray) and the new oligonucleotide microarray.

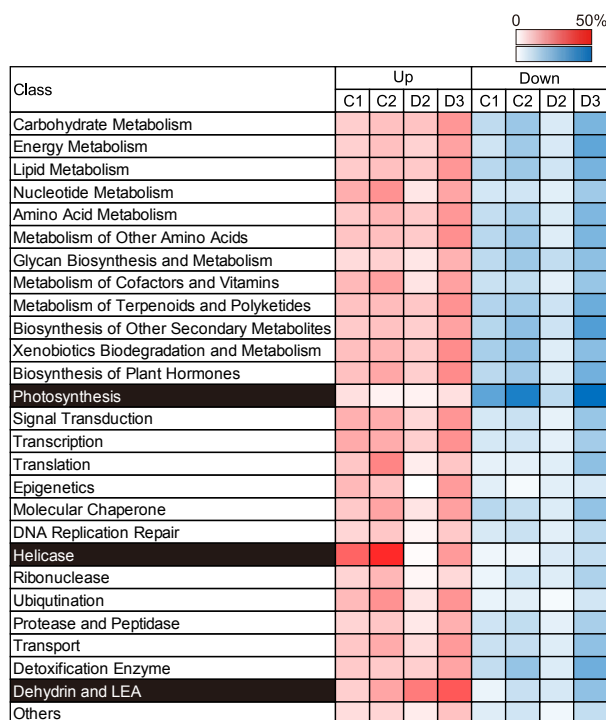


Figure S3. Molecular functions of cold-responsive and dehydration-responsive genes in rice plants. Abbreviations O and N denote old and new oligonucleotide microarray, respectively. Heat maps for 27 upregulated (up; red) or downregulated (down; blue) molecular functional classes, indicating the relative abundance (%) of transcripts in cold-treated (C1 and C2) and dehydration-treated (D2 and D3) plants.

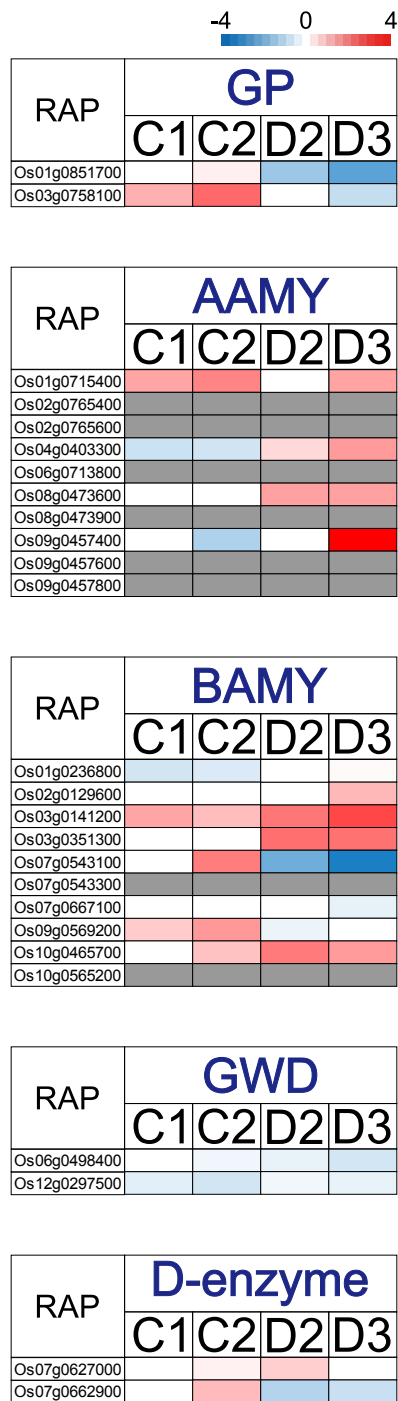


Figure S4. Effects of cold or dehydration on transcript levels of genes encoding starch degradation enzymes. Small grey square denotes the absence of a probe for that gene in the oligonucleotide microarray. GP, α -glucanphosphorylase; AAMY, α -amylase; BAMY, β -amylase; GWD, glucan water dikina

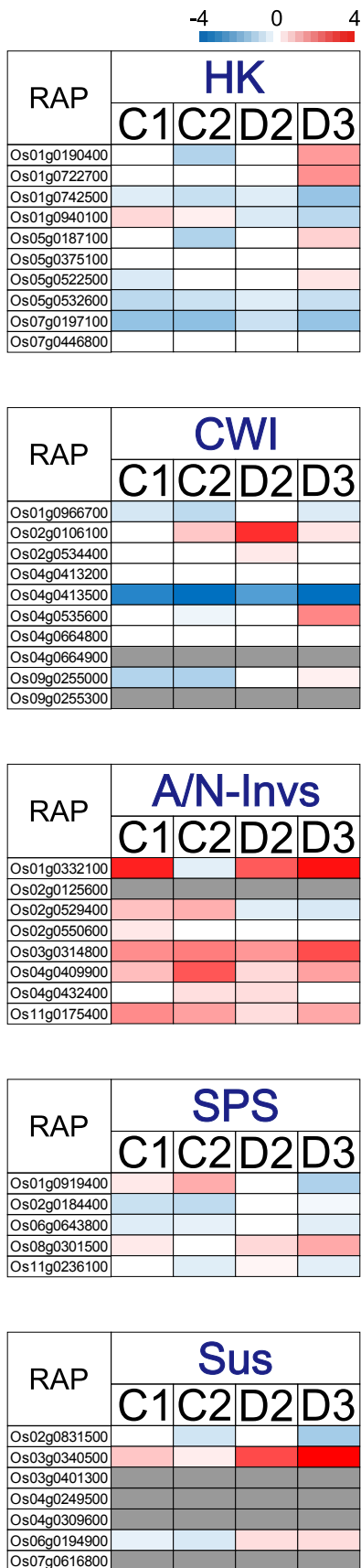


Figure S5. Effects of cold or dehydration on transcript levels of genes encoding sucrose metabolism enzymes. Small grey square denotes the absence of a probe for that gene in the oligonucleotide microarray. HK, hexokinase; SPS, sucrose phosphate synthase; Sus, sucrose synthase; A/N-invs, alkaline/neutral invertase; CWI, apoplastic invertase.

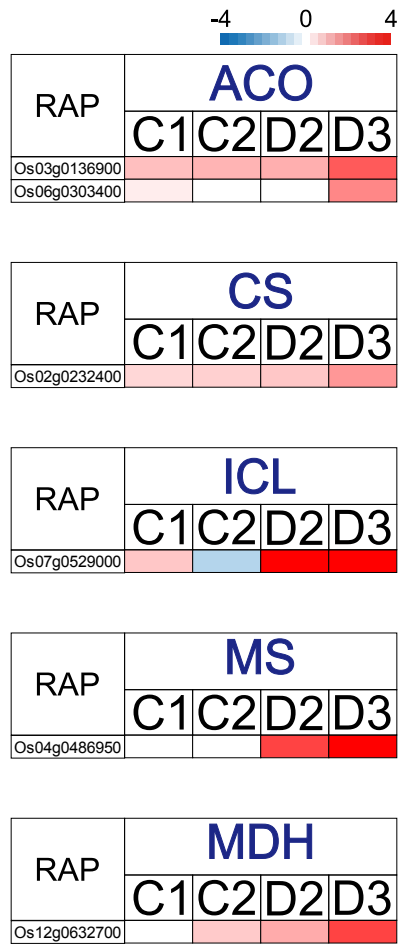


Figure S6. Effects of cold or dehydration on transcript levels of genes encoding glyoxylate cycle enzymes. ACO, aconitase hydratase; CS, citrate synthase; ICL, isocitrate lyase; MS, malate synthase; MDH, malate dehydrogenase.

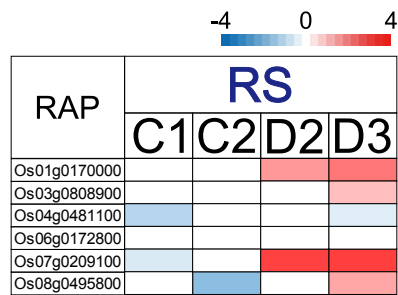


Figure S7. Effects of cold or dehydration on transcript levels of genes encoding raffinose biosynthesis enzymes. RS, raffinose synthase.

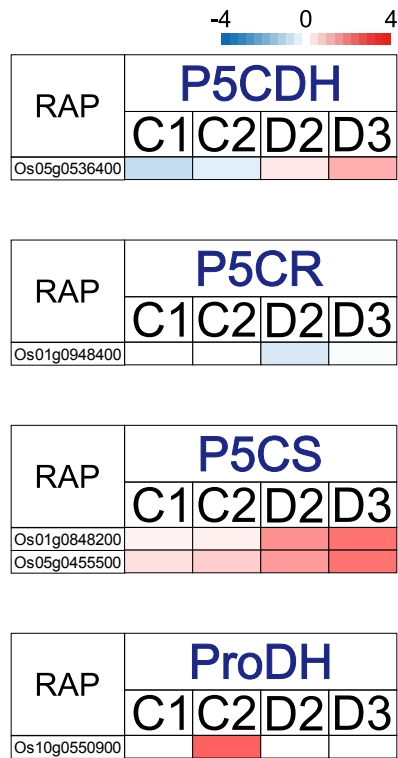


Figure S8. Effects of cold or dehydration on transcript levels of genes encoding proline metabolism enzymes. P5CDH, Δ^1 -pyrroline-5-carboxylate dehydrogenase; P5CS, Δ^1 -pyrroline-5-carboxylate synthetase; ProDH, proline dehydrogenase; P5CR, Δ^1 -pyrroline-5-carboxylate reductase.

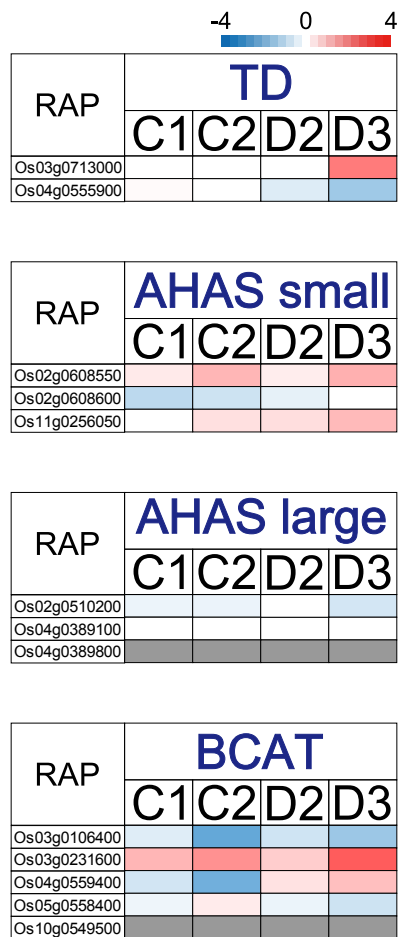


Figure S9. Effects of cold or dehydration on transcript levels of genes encoding enzymes related to BCAAs biosynthesis. Small grey square denotes the absence of a probe for that gene in the oligonucleotide microarray. AHAS, acetolactate synthase (small or large subunit); TD, threonine dehydratase; BCAT, branched-chain amino acid aminotransferase.

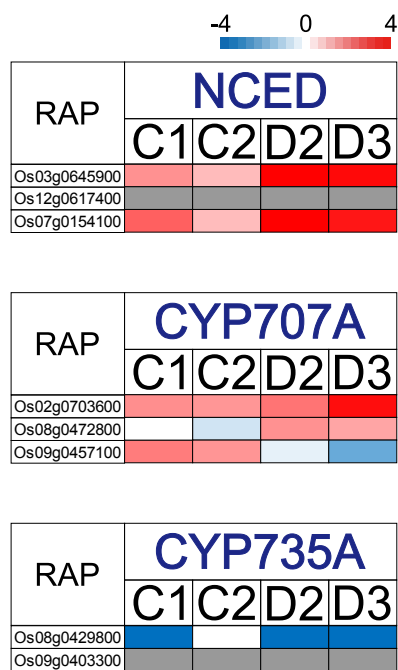


Figure S10. Effects of cold or dehydration on transcript levels of representative cold-responsive and dehydration-responsive genes involved in ABA and CK biosyntheses. Small grey square denotes the absence of a probe for that gene in the oligonucleotide microarray. NCED, 9-cis-epoxycarotenoid dioxygenase.

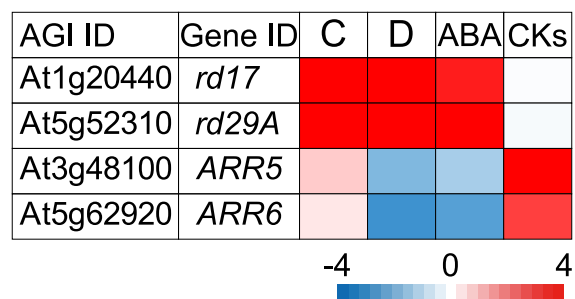


Figure S11. Transcript levels of genes encoding *rd17*, *rd29A* and ARR. Heat maps illustrate transcript levels of genes in cold-exposed, dehydration-exposed, ABA-treated, CKs-treated Arabidopsis plants.

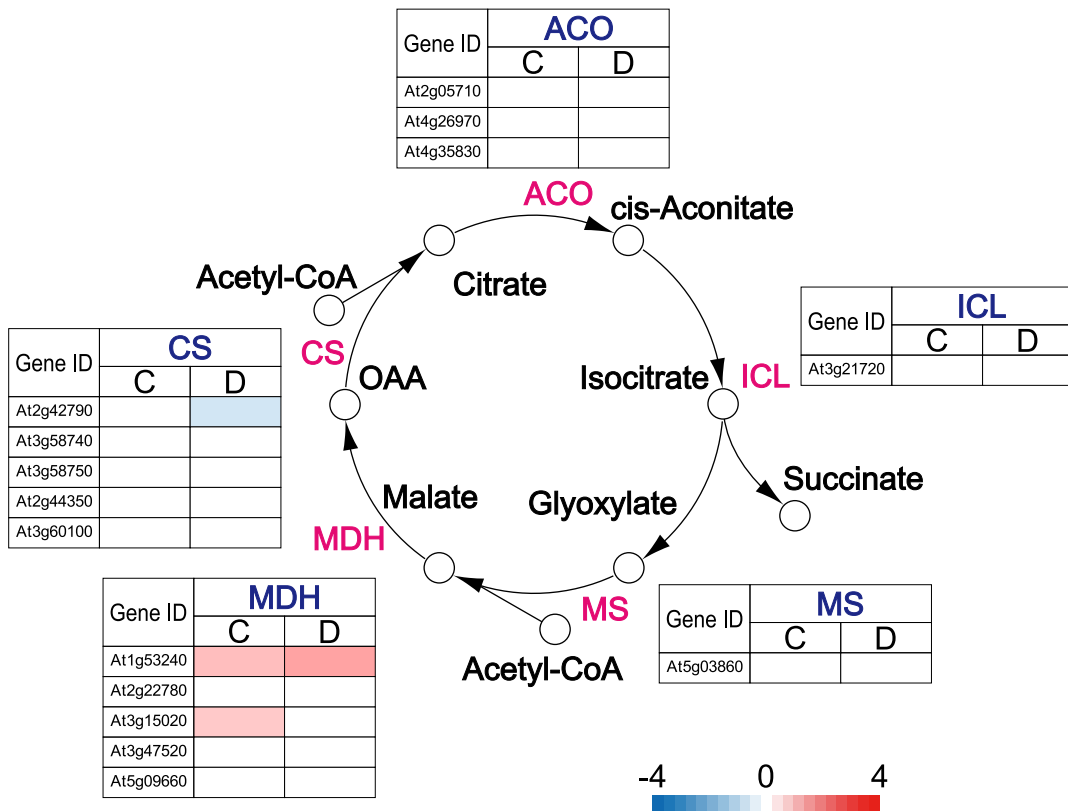


Figure S12. Glyoxylate cycle in Arabidopsis plants. Heat maps illustrate transcript levels of representative cold-responsive and dehydration-responsive genes. ACO, aconitase hydratase; ICL, isocitrate lyase; MS, malate synthase; MDH, malate dehydrogenase; CS, citrate synthase.

Gene ID	IPT	
	C	D
At1g68460	Blue	Red
At2g27760	Grey	Grey
At3g63110	Blue	Blue
At4g24650	Grey	Grey
At5g19040	Red	Grey
At1g25410	Grey	Grey
At3g23630	Red	Red
At3g19160	Grey	Grey
At5g20040	Blue	Blue

Gene ID	LOG	
	C	D
At2g28305	Grey	Grey
At2g35990	Grey	Grey
At2g37210	Red	Red
At3g53450	Red	Grey
At4g35190	Red	Red
At5g03270	Grey	Blue
At5g06300	Red	Red
At5g11950	Grey	Grey
At5g26140	Grey	Grey

Gene ID	CKX	
	C	D
At2g41510	Red	Blue
At2g19500	Grey	Grey
At5g56970	Grey	Grey
At4g29740	Grey	Blue
At1g75450	Blue	Grey
At3g63440	Blue	Blue
At5g21482	Blue	Grey

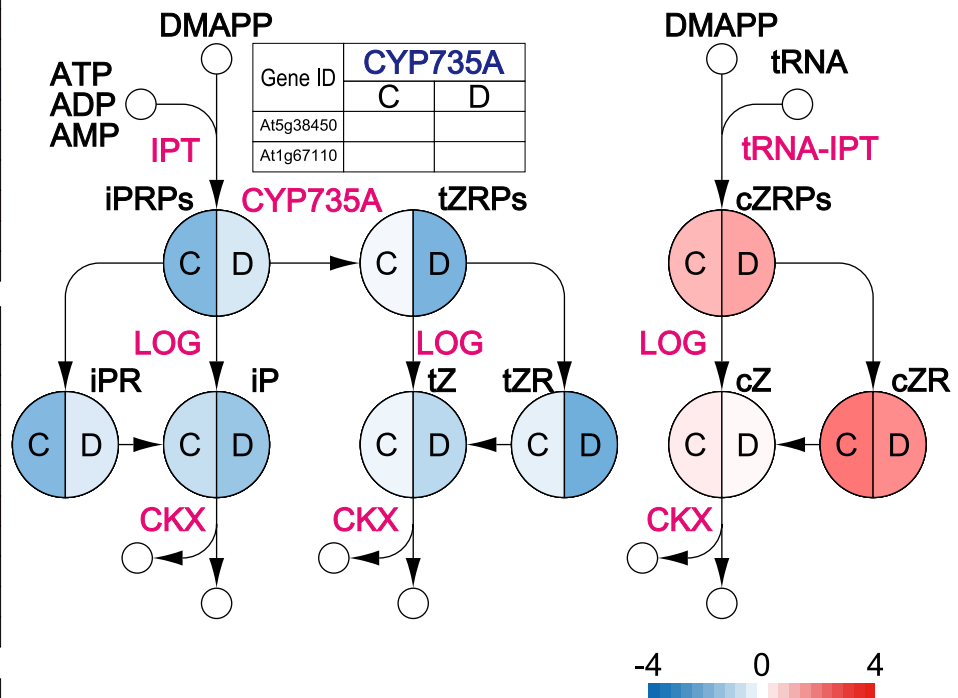


Figure S13. CK biosynthesis in Arabidopsis plants. The heat maps illustrate transcript levels of representative cold-responsive and dehydration-responsive genes. Small grey square denotes the absence of a probe in the oligonucleotide microarray for that gene. IPT, adenosine phosphate-isopentenyltransferase; LOG, cytokinin nucleoside 5'-monophosphate phosphoribohydrolase; CKX, cytokinin oxidase/dehydrogenase; tRN-IPT, tRNA isopentenyltransferase.