

Supplementary Figure S1. Genomic and transcriptional situation of *OsPCS1* locus (Os06g0102300/LOC_Os06g01260). Original images were captured from the RAP-DB database showing transcript abundance of *OsPCS1* in various rice tissues and callus. A, Transcript abundance in the region starting from TSS2 (predicted secondary transcript starting site specific to *OsPCS1b/1c*, Fig. 1A) and the flanking *OsPCS1*s common region separated by an orange line. In all tested tissues, the expression level is much lower in the

OsPCS1b/1c specific region than in the *OsPCS1* common region, suggesting higher expression of *OsPCS1full* and/or *OsPCS1a*. B, Transcript abundance in the 11 bp-region after the alternative splicing site (SS) specific to *OsPCS1a/1c* (Fig. 1A) and the flanking *OsPCS1*s common region separated by an orange line. The expression level is much lower in the *OsPCS1a/1c* specific region than in the *OsPCS1* common region. Taken together, these results suggest that *OsPCS1full* is a major variant with higher expression levels in various rice tissues.

AtPCS1 AtPCS2 OsPCS2 OsPCS1a OsPCS1c OsPCS1full OsPCS1b	1 1 1 1 1	
AtPCS1 AtPCS2 OsPCS2 OsPCS1a OsPCS1c OsPCS1full OsPCS1b	86 85 101 87 1 87 1	SMEDCCEPJEVVKEKCHSECKVVCHALCSGAKVEAFRT SOSJUDDERKFVVKCTSSENCHMASTYHEGVFKORGYCHFSPIGGYNAERDMALTADVARFX SMEDCCEPJEIVKEKCHSECKVVCLAHSSGAKVEAFRTNOSTIDDERKFVVKCTSSENCHMASTYHEGVFKORGYCHFSPIGGYNAERDMALTADVARFX SMEDCCHDEIVKDKCISEGKVVCLAHSSGAKVEAFRTNOSTIDDERKFVVKCSSSENCHMASTYHEGVFKORGYCHFSPIGGYNAERDMALTADVARFX SMEDCCHDEIVKAEGTOFFAKUACHAHGAGANVRSFRADOSTIHDERHHAVRSASSODCHF4ASYHERVFKOTGCHFSPIGGYHAGDALTADVARFX SMEDCCEPJAKVAEGTOFFAKUACHAHGAGANVRSFRADOSTIHDFRHHAVRSASSODCHF4ASYHERVPFKOTGCHFSPIGGYHAGODALTADVARFX SMEDCCEPJAKVAEGTOFFAKUACHAHGAGANVRSFRADOSTIHDFRHHAVRSASSODCHF4ASYHERVPFKOTGCHFSPIGGYHAGODALTADVARFX SMEDCCEPJAKVAEGTOFFAKUACHAHGAGANVRSFRADOSTIHDFRHHAVRSASSODCHF4ASYHERVPFKOTGCHFSPIGGYHAGODALTADVARFX
AtPCS1 AtPCS2 OsPCS2 OsPCS1a OsPCS1c OsPCS1full OsPCS1b	186 185 201 187 12 187 12	YPPHWVPLKULWEANDS IDOSWCKRRGFMLISRPHREPCULYTLSCKDESNIE IAKYLKEDVPRUVSSOHUDSVEKIISVVPKSLPSNPNOFIRIUABIR YPPHWVPLKULMDANDS IDOSWCKRRGFMLISRPHREPCULYTLSCKDESNIEJTAKYLKEDVPRUVSSOHUDSVEKIISVVPKSLPSNPNOFIRIUABIR YPPHWPLDLWEANNTDDATGLRGFMLISRPHREPLUHRAVVN YPPHWVPLPLLWEANNTDDATGLRGFMLISRFTAAPSULYTVLCR YPPHWVPLPLLWEANNTTDDATGLRGFMLISRFTAAPSULYTVSCRDESNKSMAKYCMEOVPDILKDESVDWVPLUGSRUWSIPANAGHLIKVIEV YPPHWPLPLLWEANNTTDDATGLRGFMLISRFTAAPSULYTVSCRDESNKSMAKYCMEOVPDILKDESVDWVPLUGSRUWSIPANAGHLIKVIEV YPPHWPLPLLWEANNTTDDATGLRGFMLISRFTAAPSULYTVSCRDESNKSMAKYCMEOVPDILKDESVDWVPALUSRUVSIPANAGHLIKVIEV
AtPCS1 AtPCS2 OsPCS2 OsPCS1a OsPCS1c	286 285	ITEDSNONINIALERSKARAROLVIRKEVNERHERHARIKKINKFLETVGYEDELLYAATAKACCOCHEILSCEFSKELCCHERCVLCIKGPDDSE LTEDVNONINISEERSTIKKINOELLKOVOELKARHUDKFLESV-YEDNLFYVAARUYCDGDEILSC-YESDESCCKELCVLCIKGLCEEK
OsPCS1full OsPCS1b	287 112	ġġġġġġġġġġġġġġġġġġġġġġġġġġġġġġġġġġġġġġ
AtPCS1 AtPCS2 OsPCS2 OsPCS1a	375 373	GHWWHGVVWRDGHEGKWDLMVBSTOTESCECGPEATYÐAGNDVFHAMAAAMPBOHUSCHKUDQAMMHEMKOMISMASMAPTIMQEEVMEHAROMOLL VHVVA
OSPCS1C OSPCS1full OSPCS1b	387 212	ĸŀŧvwłġtawsgyliegsudmałejistletsvcasassaevvkwesktoliliumaaahissłivcakderiakaeposiałeta imhodakreinelaktomaty kt <u>vwr</u> gtawsgyliegsudmilejistletsvcasassaevvk yes ktoliliumaaahisstivcakderiakaeposiałeto imhodiakreinelaktoma v
AtPCS1 AtPCS2 OsPCS2 OsPCS1a OsPCS1c	469 437	RROGINKEEUDIAAPAY KROGINKEDEELSAPA-
OsPCS1full OsPCS1b	487 312	RSCHIEEYGDPVPQSH- RSCHIEEYGDPVPQSH-

Supplementary Figure S2. Alignment of rice and Arabidopsis PCS amino acid sequences.



Supplementary Figure S3. Expression analyses of *OsPCS* transgenes in the Arabidopsis transgenic plants by RT-PCR.



Supplementary Figure S4. As and Cd sensitivity assay of the Arabidopsis plants harboring *OsPCS* transgenes. Primary root lengths were measured after 12 d cultivation on the agar plates containing As(III) (A to D) or Cd (E to H). A and E, *cad1-3/OsPCS1full*. B and F, *cad1-3/OsPCS1a*. C and G, *cad1-3/OsPCS1b*. D and H, *cad1-3/OsPCS2*. Data represent means with SD of two independent experiments (n = 13 - 25). Asterisks indicate significant differences from *cad1-3* within each treatment (* p<0.05, ** p<0.01, *** p<0.001; *t*-test).



Supplementary Figure S5. GSH concentrations in roots of Col-0, *cad1-3* and *cad1-3* transgenic plants with *OsPCS* exposed to As(III) (A) or Cd (B). 7 d old seedlings were transferred from the control medium to the medium containing 5μ M As(III) or 5μ M Cd and grown for 7 d before harvest. Data represent means with SD of two independent experiments (n = 3 - 4). Means sharing the same lowercase (PC2) and uppercase (PC3) letter are not significantly different (*p*<0.05, Tukey's HSD).



Supplementary Figure S6. Characterization of *OsPCS1* mutant rice. A, Insertion sites of T-DNA and *Tos17* in Os06g0102300 (*OsPCS1full*). Black and blue boxes represent untranslated regions and coding regions, respectively. B and C, *OsPCS1* expression analyses in the wild-type and mutant plants by RT-PCR (B) and quantitative real-time PCR (C). D, PCs concentrations in the rice roots exposed to 10µM Cd for 3 d. C and D, Data represent means with SD of at least three biological replicates. Asterisks indicate significant differences from each wild-type line (* p<0.05, ** p<0.01, *** p<0.001; *t*-test).



Supplementary Figure S7. As and Cd sensitivity assay of the *Tos17* insertion rice. A to C, the wild-type NB and *Tos17* mutant of *OsPCS1* (NG5045) were hydroponically grown for 2 weeks without As(III) or Cd addition and then grown further for 3 weeks with or without 5 μ M As(III) or 1 μ M Cd. A, Phenotypes of the NB and NG5045 after cultivation. A white bar = 10cm. B and C, Fresh weight of shoot (B) and root (C) after cultivation. Data represent means with SD of two independent experiments (n = 6 - 10). Asterisks indicate significant differences from the wild-type NB (** p<0.01, *** p<0.001; t-test).



Supplementary Figure S8. As and Cd accumulation in the hydroponically grown *OsPCS1* mutant rice and the respective wild-type plants. A to F, The wild-type and *OsPCS1* mutant rice were hydroponically grown for 2 weeks without As(III) or Cd addition and then grown further for 3 weeks with or without 5 μ M As(III) or 1 μ M Cd. A, As concentration in shoot. B, Cd concentration in shoot. C, As concentration in root. D, Cd concentration in root. E, As distribution ratio. E, Cd distribution ratio. Data represent means with SD of two independent experiments (n = 6 - 8). Asterisks indicate significant differences between each wild-type and mutant pair (* p<0.05, ** p<0.01; t-test).



Supplemental Figure S9. As concentrations in *OsPCS1* mutant rice and the respective wild-type plants grown under intermittent water conditions. The wild-type and *OsPCS1* mutant rice were grown in pots until grain ripening. After harvest, element concentrations in leaf blade and brown rice were measured by ICP-MS. A and B, As concentrations in flag leaf blade (A) and grain (B). Data represent means with SD of two independent experiments (n = 11 - 12).



1 alternative SS for long variant

Supplementary Figure S10. Genomic and transcriptional situation of *OsPCS2* locus (Os05g0415200/LOC_Os05g34290). Original image was captured from the RAP-DB database showing transcript abundance of *OsPCS2* in roots and shoots. Decrease of transcript abundance after a possible alternative splicing site indicated with an orange line is much evident in shoot, suggesting the long variant is dominant in shoot. In root such remarkable decrease is not observed, suggesting the short variant is dominant in root.

Supplemental Table S1 List of primers used in the study

Primer set for	Primer name	Primer sequence (5' to 3')
Cloning of OsPCS1 cDNA	OsPCS1fuil/a 5'UTR Fwd OsPCS1b/c 5'UTR Fwd OsPCS1 3'UTR Rev	TCGAGTGCAAGAAGAGGAAAGC CATTGCATTGCATTTCAGAC CTTTTGCAAGGACACCAGCC
Cloning of OsPCS2 cDNA	OsPCS2 Fwd OsPCS2 3'UTR Rev	ATGGCGTCTAAACCAAGCAG CCAGCATTGGGAGGAAGATG
Plasmid construction for Arabidopsis transform	aProAtPCS1 HindIII Fwd ProAtPCS1 KpnI Rev OsPCS1full/a KpnI Fwd OsPCS1full/b Pacl Rev OsPCS1b/c KpnI Fwd OsPCS1a/c Pacl Rev sGFP KpnI Fwd sGFP Pacl Rev	ccCAAGCTTCTCATGTTTATTGAAC ggggtaccTTTTCACTGCTTGTTTTGGT ggggtaccATGGCAGCGATGGCATCCCT ccttaattaaTTAATGGGATTGTGGCACAG ggggtaccATGGCGCTTATCCTGGATGTC ccttaattaaCTACACTCTCATCCTTAAGAAG ggggtaccATGGTGAGCAAGGGCGAGG ccttaattaaTTACTTGTACAGCTCGTCCATGCC
Plasmid construction for yeast transformation	OsPCS1full/a XhoI Fwd OsPCS1b/c XhoI Fwd OsPCS2 Xho1 Fwd OsPCS1full Notl Rev OsPCS1a Notl Rev OsPCS1b Notl Rev OsPCS1c Notl Rev OsPCS2 Notl Rev	ccgctcgagATGGCAGCGATGGCATCCCT ccgctcgagATGGCGCTTATCCTGGATGT ccgctcgagATGGCGTCTAAACCAAGCAG ataagaatgcggccgccATGGGATTGTGGCACAG ataagaatgcggccgccACTCTCATCCTTAAGAAGATCG ataagaatgcggccgccACTGGGATTGTGGCACAGGAT ataagaatgcggccgccACTCTCATCCTTAAGAAGATC ataagaatgcggccgccACTCTCATCCTTAAGAAGATC ataagaatgcggccgccACTTTACCACTGCACGGATC
RT-PCR of Arabidopsis transgenic plants	OsPCS1 common Fwd OsPCS1 common Rev OsPCS2 Fwd OsPCS2 Rev AtEF1a Fwd AtEF1a Rev	TTCAAATACCCTCCTCACTGG CACTGTGTAGAGCAATGAAGGAG TCGCTTCAAATACCCTCCTC TGAGATAAGCATGAACCCCCC AGCACGCTCTTCTTGCTTTC AACGCCTGTCAATCTTGGTC
Genotyping of Tos17 mutant rice	Tos17 OsPCS1 Fwd Tos17 OsPCS1 Rev Tos17 LB	TGCTCCCTACTCCCTAGCAA TGTGGCACAGGATCTCCATA ATTGTTAGGTTGCAAGTTAGTTAAGA
Genotyping of T-DNA mutant rice	T-DNA OsPCS1 Fwd T-DNA OsPCS1 Rev POSTECH T-DNA RB	GCAAGTCCGTGATACTGAGC GGATTAATACAACAAACCTCTCG GCACCGTGGTAGTAAGAATGG
RT-PCR of OsPCS1	OsPCS1full/a Fwd OsPCS1 3'UTR Rev	GACTTCCGCCACCATCTC CTTTTGCAAGGACACCAGCC
Real-time PCR of OsPCSs	OsPCS1full/a Fwd OsPCS1b/c Fwd OsPCS1full/b Rev OsPCS1a/c Rev OsPCS2 Fwd OsPCS2 Rev	GACTTCCGCCACCATCTC CATTGCATTGCATTTCAGAC CATCTCTGCAACTCACTGTG GCAACTCTGCACAAAAGCAC ATGGCGTCTAAACCAAGCAG CGGAGACGAGGCTGAAGAAC
Real-time PCR and RT-PCR of OsUBQ5	OsUBQ5 Fwd OsUBQ5 Rev	GAAGGAGGAGGAAATCGAAC CTTCACAGAGGTGATGCTAAGG

Lowercase sequences indicate additional sequences for restriction enzyme digestion.

Element concentration (mg kg ⁻¹ DW)	As	0.73± 0.03
	Cd	0.015± 0.001
	Fe	26.9± 2.2
	Mn	53.3± 2.4
	Cu	2.06± 0.10
	Zn	3.99 ± 0.08
рН (H ₂ O)		4.83± 0.03

Data represent mean with SD of 4 replicates.