(A) *OsPCS1*

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Genome      161>TTTTGCCGCAATGGCGTCTAAACCAAGCAGCCGAGCGGAAAGCAACCAGGCGGCGGCGGCGGTGCCGTCGCTGTACGGGC>240
CB646798      1>~~~~~~~~~~ATGGCGTCTAAACCAAGCAGCCGAGCGGAAAGCAACCAGGCGGCGGCGGCGGTGCCGTCGCTGTACGGGC>70
OsPCS1#1    161>TTTTGCCGCAATGGCGTCTAAACCAAGCAGCCGAGCGGAAAGCAACCAGGCGGCGGCGGCGGTGCCGTCGCTGTACGGGC>240
OsPCS1#2      1>~~~~~~~~~~ATGGCGTCTAAACCAAGCAGCCGAGCGGAAAGCAACCAGGCGGCGGCGGCGGTGCCGTCGCTGTACGGGC>70
OsPCS1#3      1>~~~~~~~~~~ATGGCGTCTAAACCAAGCAGCCGAGCGGAAAGCAACCAGGCGGCGGCGGCGGTGCCGTCGCTGTACGGGC>70
OsPCS1#4      1>~~~~~~~~~~ATGGCGTCTAAACCAAGCAGCCGAGCGGAAAGCAACCAGGCGGCGGCGGCGGTGCCGTCGCTGTACGGGC>70
                        *         *         *         *         *         *         *         *
                        *         *         *         *         *         *         *         *
Genome      641>GGATTGCCATCTCGTCGCCTCCTACCACCGGAAGCTTCTCGGCCAGGTTGCTGCCTGCTCGTCCGCACCTCTCTCGGAAC>720
CB646798    471>GGATTGCCATCTCGTCGCCTCCTACCACCGGAAGCTTCTCGGCCAG---------------------------------->516
OsPCS1#1    641>GGATTGCCATCTCGTCGCCTCCTACCACCGGAAGCTTCTCGGCCAG---------------------------------->686
OsPCS1#2    471>GGATTGCCATCTCGTCGCCTCCTACCACCGGAAGCTTCTCGGCCAG---------------------------------->516
OsPCS1#3    471>GGATTGCCATCTCGTCGCCTCCTACCACCGGAAGCTTCTCGGCCAG---------------------------------->516
OsPCS1#4    471>GGATTGCCATCTCGTCGCCTCCTACCACCGGAAGCTTCTCGGCCAG---------------------------------->516
                        *         *         *         *         *         *         *         *
Genome      721>TCGAATTCGACGATTTCTGTTTGCTGTTCGTTCTGAACGAATGATGTTTGTTTGGATTCGATGCAGACTGGAACAGGGCA>800
CB646798    517>------------------------------------------------------------------ACTGGAACAGGGCA>530
OsPCS1#1    687>------------------------------------------------------------------ACTGGAACAGGGCA>700
OsPCS1#2    517>------------------------------------------------------------------ACTGGAACAGGGCA>530
OsPCS1#3    517>------------------------------------------------------------------ACTGGAACAGGGCA>530
OsPCS1#4    517>------------------------------------------------------------------ACTGGAACAGGGCA>530
                        *         *         *         *         *         *         *         *
                        *         *         *         *         *         *         *         *
Genome      881>ATTGGATTCCGCTGCCGCTTCTTTGGGAAGCCATGAACACGATTGATGAAGCAACTGGGCTTCTCAGGGGGTATATATTC>960
CB646798    611>ATTGGATTCCGCTGCCGCTTCTTTGGGAAGCCATGAACACGATTGATGAAGCAACTGGGCTTCTCAGGGG---------->680
OsPCS1#1    781>ATTGGATTCCGCTGCCGCTTCTTTGGGAAGCCATGAACACGATTGATGAAGCAACTGGGCTTCTCAGGGG---------->850
OsPCS1#2    611>ATTGGATTCCGCTGCCGCTTCTTTGGGAAGCCATGAACACGATTGATGAAGCAACTGGGCTTCTCAGGGG---------->680
OsPCS1#3    611>ATTGGATTCCGCTGCCGCTTCTTTGGGAAGCCATGAACACGATTGATGAAGCAACTGGGCTTCTCAGGGG---------->680
OsPCS1#4    611>ATTGGATTCCGCTGCCGCTTCTTTGGGAAGCCATGAACACGATTGATGAAGCAACTGGGCTTCTCAGGGG---------->680
                        *         *         *         *         *         *         *         *
                        *         *         *         *         *         *         *         *
Genome     1761>GTTTAACATGTCGGCATCTTCATATTTGGTAGGTTCATGCTTATCTCAAGGAATACTGAAGCTCCTTTATTGATCCGTGC>1840
CB646798    681>--------------------------------GTTCATGCTTATCTCNAGGAATACTGAAGCTCCTTTATTGATCCGTGC>728
OsPCS1#1    851>--------------------------------GTTCATGCTTATCTCAAGGAATACTGAAGCTCCTTTATTGATCCGTGC>898
OsPCS1#2    681>--------------------------------GTTCATGCTTATCTCAAGGAATACTGAAGCTCCTTTATTGATCCGTGC>728
OsPCS1#3    680>-------------------------------------------------------------------------------->680
OsPCS1#4    681>--------------------------------GTTCATGCTTATCTCAAGGAATACTGAAGCTCCTTTATTGATCCGTGC>728
                        *         *         *         *         *         *         *         *
Genome     1841>AGTGGTAAATTAACATGCCAATGCTTGGTGAATCAAATATGTAAGTGTCAAGTGTCACCCTTGATCTATTTTTTTCTCAT>1920
CB646798    729>AGTG---------------------------------------------------------------------------->732
OsPCS1#1    899>AGTG---------------------------------------------------------------------------->902
OsPCS1#2    729>AGTG---------------------------------------------------------------------------->732
OsPCS1#3    681>--TGGTAAATTAACATGCCAATGCTTGGTGAATCAAATAT---------------------------------------->718
OsPCS1#4    729>AGTGGTAAATTAACATGCCAATGCTTGGTGAATCAAATAT---------------------------------------->768
                        *         *         *         *         *         *         *         *
Genome     1921>TCCTTTCAATGCTATGCAGAATTGCAGGGATGAAAGCTGGCAAAGCATGGCAAAGTATTGCATAGAAGTTGTCCCAAATC>2000
CB646798    733>-------------------AATTGCAGGGATGAAAGCTGGCAAAGCATGGCAAAGTATTGCA~~~~~~~~~~~~~~~~~~>775
CK083842      8>---------------------------------------------------------------AGAAGTTGTCCCAAATC>24
OsPCS1#1    903>-------------------AATTGCAGGGATGAAAGCTGGCAAAGCATGGCAAAGTATTGCATAGAAGTTGTCCCAAATC>963
OsPCS1#2    733>-------------------AATTGCAGGGATGAAAGCTGGCAAAGCATGGCAAAGTATTGCATAGAAGTTGTCCCAAATC>793
OsPCS1#3    718>-------------------------------------------------------------------------------->718
OsPCS1#4    768>-------------------------------------------------------------------------------->768
                        *         *         *         *         *         *         *         *
Genome     2001>TTTTGAGGGATAACAGCGTAGACAATGTCCTAACAATTCTTTCCCGTTTAGTGAATCATCTTCCTCCCAATGCTGGAAAT>2080
CK083842     25>TTTTGAGGGATAACAGCGTAGACAATGTCCTAACAATTCTTTCCCGTTTAGTGAATCATCTTCCTCCCAATGCTGGAAAT>104
OsPCS1#1    964>TTTTGAGGGATAACAGCGTAGACAATGTCCTAACAATTCTTTCCCGTTTAGTGAATCATCTTCCTCCCAATGCTGGAAAT>1043
OsPCS1#2    794>TTTTGAGGGATAACAGCGTAGACAATGTCCTAACAATTCTTTCCCGTTTAGTGAATCATCTTCCTCCCAATGCTGGAAAT>873
OsPCS1#3    719>---------------------------------------------------TGAATCATCTTCCTCCCAATGCTGGAAAT>747
OsPCS1#4    769>---------------------------------------------------TGAATCATCTTCCTCCCAATGCTGGAAAT>797
                        *         *         *         *         *         *         *         *
                        *         *         *         *         *         *         *         *
Genome     2161>CCTGAAGGTCATTTTAATTTTCCATTTCTGTTGTTGGGTCAGTTTTGTTTCCTCTGTTCAACCAGTTAATGTTGTATGTT>2240
CK083842    185>CCTGAAG------------------------------------------------------------------------->191
OsPCS1#1   1124>CCTGAAG------------------------------------------------------------------------->1130
OsPCS1#2    954>CCTGAAG------------------------------------------------------------------------->960
OsPCS1#3    828>CCTGAAG------------------------------------------------------------------------->834
OsPCS1#4    878>CCTGAAG------------------------------------------------------------------------->884
                        *         *         *         *         *         *         *         *
Genome     2241>CGCTTGCAGGAAAAGGTCCTACAGCAAATCCGTGATACTAAGCTTTTTCAGCTGGTCCACAAACTGCAATGTTCTAAGCA>2320
CK083842    192>---------GAAAAGATCCTACAGCAAATCCGTGATACTAGGCTTTTTCAGCTGGTCCACAAACTGCAATGTTCTAAGCA>262
CB646799    794<-----------------------GCAAATCCGTGATACTAAGCTTTT-CAGCTGGTCCACAAACTGCAATGTTCTAAGCA<739
OsPCS1#1   1131>---------GAAAAGGTCCTACAGCAAATCCGTGATACTAAGCTTTTTCAGCTGGTCCACAAACTGCAATGTTCTAAGCA>1201
OsPCS1#2    961>---------GAAAAGGTCCTACAGCAAATCCGTGATACTAAGCTTTTTCAGCTGGTCCACAAACTGCAATGTTCTAAGCA>1031
OsPCS1#3    835>---------GAAAAGGTCCTACAGCAAATCCGTGATACTAAGCTTTTTCAGCTGGTCCACAAACTGCAATGTTCTAAGCA>905
OsPCS1#4    885>---------GAAAAGGTCCTACAGCAAATCCGTGATACTAAGCTTTTTCAGCTGGTCCACAAACTGCAATGTTCTAAGCA>955
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Genome     2321>GCCCTGTTGTAGTTGCTCGTCTTTAACGGACGAAGATTCCATTTCCCAGATTGCAGCCAGTGTGTGCTGTGAAGCAACCG>2400
CK083842    263>GCCCTGTTTTAGTTGCTCGTCTTTAACGGACGAAGATTCCATTTCCCAGATTGCAGCCAGTGTGTGCTGTGAAGCAACCG>342
CB646799    738<GCCCTGTTGTAGTTGCTCGTCTTTAACGGACGAAGATTCCATTTCCCAGATTGCAGCCAGTGTGTGCTGTGAAGCAACCG<659
OsPCS1#1   1202>GCCCTGTTGTAGTTGCTCGTCTTTAACGGACGAAGATTCCATTTCCCAGATTGCAGCCAGTGTGTGCTGTGAAGCAACCG>1281
OsPCS1#2   1032>GCCCTGTTGTAGTTGCTCGTCTTTAACGGACGAAGATTCCATTTCCCAGATTGCAGCCAGTGTGTGCTGTGAAGCAACCG>1111
OsPCS1#3    906>GCCCTGTTGTAGTTGCTCGTCTTTAACGGACGAAGATTCCATTTCCCAGATTGCAGCCAGTGTGTGCTGTGAAGCAACCG>985
OsPCS1#4    956>GCCCTGTTGTAGTTGCTCGTCTTTAACGGACGAAGATTCCATTTCCCAGATTGCAGCCAGTGTGTGCTGTGAAGCAACCG>1035
                     *         *         *         *         *         *         *         *
                     *         *         *         *         *         *         *         *

Genome     2481>GAGGGGCTTAAAAATGTCATTACAGGCAAAGTGGTATCTGAAGGCAATGGACATGTTGATAAGCTTTCACCGATATCCTC>2560
CK083842    423>GAGGGGCTTAAAAATGGCATTACAGGCAAAGTGGTATCTGAAGGCAATGGACATGTTGATAAGCTTTCACCGATATCCTC>502
CB646799    578<GAGGGGCTTAAAAATGTCATTACAGGCAAAGTGGTATCTGAAGGCAATGGACATGTTGATAAGCTTTCACCGATATCCTC<499
OsPCS1#1   1362>GAGGGGCTTAAAAATGTCATTACAGGCAAAGTGGTATCTGAAGGCAATGGACATGTTGATAAGCTTTCACCGATATCCTC>1441
OsPCS1#2   1192>GAGGGGCTTAAAAATGTCATTACAGGCAAAGTGGTATCTGAAGGCAATGGACATGTTGATAAGCTTTCACCGATATCCTC>1271
OsPCS1#3   1066>GAGGGGCTTAAAAATGTCATTACAGGCAAAGTGGTATCTGAAGGCAATGGACATGTTGATAAGCTTTCACCGATATCCTC>1145
OsPCS1#4   1116>GAGGGGCTTAAAAATGTCATTACAGGCAAAGTGGTATCTGAAGGCAATGGACATGTTGATAAGCTTTCACCGATATCCTC>1195
                     *         *         *         *         *         *         *         *

Genome     2561>GACTGAAACATGCTTCTGCAATTCAACTCTGAGCAATGAAA-CTGTC-AATTATCCATCAAACACAGAC-ATTCTAACTG>2637
CK083842    503>GACTGAAACATGCTTCTGCAATTCAACTCTGAGCAATGAAA-CTGTC-AATTATCCATCAAACACAGAC-ATTCTAACTG>579
CB646799    498<GACTGAAACATGCTTCTGCAATTCAACTCTGAGCAATGAAA-CTGTC-AATTATCCATCAAACACAGAC-ATTCTAACTG<422
C96924       32>-----AAACATGCTTCTGCAATNCACCTCTGAGCACTGAAACCTGTCAAATTATCCATCAAACACAGACCANTCTAACTG>106
OsPCS1#1   1442>GACTGAAACATGCTTCTGCAATTCAACTCTGAGCAATGAAA-CTGTC-AATTATCCATCAAACACAGAC-ATTCTAACTG>1518
OsPCS1#2   1272>GACTGAAACATGCTTCTGCAATTCAACTCTGAGCAATGAAA-CTGTC-AATTATCCATCAAACACAGAC-ATTCTAACTG>1348
OsPCS1#3   1146>GACTGAAACATGCTTCTGCAATTCAACTCTGAGCAATGAAA-CTGTC-AATTATCCATCAAACACAGAC-ATTCTAACTG>1222
OsPCS1#4   1196>GACTGAAACATGCTTCTGCAATTCAACTCTGAGCAATGAAA-CTGTC-AATTATCCATCAAACACAGAC-ATTCTAACTG>1272
                     *         *         *         *         *         *         *         *

Genome     2638>TTCTATTACTGTCGTTACATCCTAGCACATGGTTGTGCATTGAAGATGAGAAGTTGAAAGCTGAATTTCAGAGCCTTGTT>2717
CK083842    580>TTCTATTACTG~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~>590
CB646799    421<TTCTATTACTGTCGTTACATCCTAGCACATGGTTGTGCATTGAAGATGAGAAGTTGAAAGCTGAATTTCAGAGCCTTGTT<342
C96924      107>TTCTATTACTGTCGTTACATCCTAGCACATGGTTGTGCATTGAAGATGAGAAGTTGAAAGCTGAATTTCAGAGCCTTGTT>186
OsPCS1#1   1519>TTCTATTACTGTCGTTACATCCTAGCACATGGTTGTGCATTGAAGATGAGAAGTTGAAAGCTGAATTTCAGAGCCTTGTT>1598
OsPCS1#2   1349>TTCTATTACTGTCGTTACATCCTAGCACATGGTTGTGCATTGAAGATGAGAAGTTGAAAGCTGAATTTCAGAGCCTTGTT>1428
OsPCS1#3   1223>TTCTATTACTGTCGTTACATCCTAGCACATGGTTGTGCATTGAAGATGAGAAGTTGAAAGCTGAATTTCAGAGCCTTGTT>1302
OsPCS1#4   1273>TTCTATTACTGTCGTTACATCCTAGCACATGGTTGTGCATTGAAGATGAGAAGTTGAAAGCTGAATTTCAGAGCCTTGTT>1352
                     *         *         *         *         *         *         *         *

Genome     2718>TCTACGGACGATCTTCCTGATCCTCTTAAACTGGAGGTGTGCTGTCTCACTCCTAGAACCTTGCATTGATTGTTTACCTT>2797
CB646799    341<TCTACGGACGATCTTCCTGATCCTCTTAAACTGGAG--------------------------------------------<306
C96924      187>TCTACGGACGATCTTCCTGATCCTCTTAAACTGGAG-------------------------------------------->222
OsPCS1#1   1599>TCTACGGACGATCTTCCTGATCCTCTTAAACTGGAG-------------------------------------------->1634
OsPCS1#2   1429>TCTACGGACGATCTTCCTGATCCTCTTAAACTGGAGGTGTGCTGTCTCACTCCTAGAACCTTGCATTGA~~~~~~~~~~~>1497
OsPCS1#3   1303>TCTACGGACGATCTTCCTGATCCTCTTAAACTGGAGGTGTGCTGTCTCACTCCTAGAACCTTGCATTGA~~~~~~~~~~~>1371
OsPCS1#4   1353>TCTACGGACGATCTTCCTGATCCTCTTAAACTGGAGGTGTGCTGTCTCACTCCTAGAACCTTGCATTGA~~~~~~~~~~~>1421
                     *         *         *         *         *         *         *         *
                     *         *         *         *         *         *         *         *

Genome     3358>TCTATTCTAAGTAGAGCTACTATTTATATTGACAGATATTGCACCTAAGGAGGCAGCTCCGTTATCTGAAGGCTTGTAGA>3437
CB646799    305<-----------------------------------ATATTGCACCTAAGGAGGCAGCTCCGTTATCTGAAGGCTTGTAGA<261
C96924      223>-----------------------------------ATATTGCACCTAAGGAGGCAGCTCCGTTATCTGAAGGCTTGTAGA>267
OsPCS1#1   1635>-----------------------------------ATATTGCACCTAAGGAGGCAGCTCCGTTATCTGAAGGCTTGTAGA>1679
                     *         *         *         *         *         *         *         *

Genome     3438>GAAAAGGAGGCATATGAAGATACTTGGCCACAACCTTGGGAACAATGCTAACATGGCAACCCACTCACTTAATAATGAAT>3517
CB646799    260<GAAAAGGAGGCATATGAAGATACTTGGCCACAACCTTGGGAACAATGCTAACATGGCAACCCACTCACTTAATAATGAAT<181
C96924      268>GAAAAGGAGGCATATGAAGATACTTGGCCACAACCTTGGGAACAATGCTAACATGGCAACCCACTCACTTAATAATGAAT>347
OsPCS1#1   1680>GAAAAGGAGGCATATGAAGATACTTGGCCACAACCTTGGGAACAATGCTAACATGGCAACCCACTCACTTAATAATGAAT>1759
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(B) *OsPCS2*

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                     *       *        *       *        *       *        *       *
Genome    81>AGAGAAGCACGCATCCGATCGCCGGCGACGACCGAATCTGTGCCGGGCGGCAGGAAGGAGAGCGGCGATGGCAGCGATGG>160
OsPCS2#1  81>AGAGAAGCACGCATCCGATCGCCGGCGACGACCGAATCTGTGCCGGGCGGCAGGAAGGAGAGCGGCGATGGCAGCGATGG>160
OsPCS2#2  81>AGAGAAGCACGCATCCGATCGCCGGCGACGACCGAATCTGTGCCGGGCGGCAGGAAGGAGAGCGGCGATGGCAGCGATGG>160
AK071958   0>~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~>0
OsPCS2#3   1>~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~ATGGCAGCGATGG>13
                     *       *        *       *        *       *        *       *

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Genome    561>CTCTGCCTCCTCCCAGGACTGCCATCTCATCGCATCCTACCACAGGAAGCCTTTCAAACAGGTTGTTTTTGTTAATCCTT>640
OsPCS2#1  561>CTCTGCCTCCTCCCAGGACTGCCATCTCATCGCATCCTACCACAGGAAGCCTTTCAAACAG------------------->621
OsPCS2#2  561>CTCTGCCTCCTCCCAGGACTGCCATCTCATCGCATCCTACCACAGGAAGCCTTTCAAACAG------------------->621
AK071958    0>~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~>0
OsPCS2#3  414>CTCTGCCTCCTCCCAGGACTGCCATCTCATCGCATCCTACCACAGGAAGCCTTTCAAACAG------------------->474
                     *       *        *       *        *       *        *       *
Genome    641>CTCTTCTTCATTTCAAGGTCTTAATAACCAACCAATTTATCATTGCATTGCATTTCAGACTGGAACCGGCCATTTCTCTC>720
OsPCS2#1  622>----------------------------------------------------------ACTGGAACCGGCCATTTCTCTC>643
OsPCS2#2  622>----------------------------------------------------------ACTGGAACCGGCCATTTCTCTC>643
AK071958    1>~~~~~~~~~ATTTCAAGGTCTTAATAACCAACCAATTTATCATTGCATTGCATTTCAGACTGGAACCGGCCATTTCTCTC>71
OsPCS2#3  475>----------------------------------------------------------ACTGGAACCGGCCATTTCTCTC>496
                     *       *        *       *        *       *        *       *

                     *       *        *       *        *       *        *       *
Genome    801>CCACTCCCACTGCTTTGGGAAGCCATGAATACAACTGATGACGCAACTGGTCTACTCAGGGGGTCTCTTCTCTACCCATC>880
OsPCS2#1  724>CCACTCCCACTGCTTTGGGAAGCCATGAATACAACTGATGACGCAACTGGTCTACTCAGGGG------------------>785
OsPCS2#2  724>CCACTCCCACTGCTTTGGGAAGCCATGAATACAACTGATGACGCAACTGGTCTACTCAGGGG------------------>785
AK071958  152>CCACTCCCACTGCTTTGGGAAGCCATGAATACAACTGATGACGCAACTGGTCTACTCAGGGG------------------>213
OsPCS2#3  577>CCACTCCCACTGCTTTGGGAAGCCATGAATACAACTGATGACGCAACTGGTCTACTCAGGGG------------------>638
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Genome    4721>CCATCTTGATATTTGAAGGTTCATGCTTATCTCAAGGCACACTGCAGCTCCTTCATTGCTCTACACAGTGGTAAACATGC>4800
OsPCS2#1   786>------------------GTTCATGCTTATCTCAAGGCACACTGCAGCTCCTTCATTGCTCTACACAGTG---------->837
OsPCS2#2   786>------------------GTTCATGCTTATCTCAAGGCACACTGCAGCTCCTTCATTGCTCTACACAGTG---------->837
AK071958   214>------------------GTTCATGCTTATCTCAAGGCACACTGCAGCTCCTTCATTGCTCTACACAGTG---------->265
OsPCS2#3   639>------------------GTTCATGCTTATCTCAAGGCACACTGCAGCTCCTTCATTGCTCTACACA------------->687
                     *       *        *       *        *       *        *       *
Genome    4801>CAATGCTTGGTATATCGAATTCAAGTGGGTACATTGATATAATTTCCTTTATATCATTCCTTTAGCTTTTGTGCAGAGTT>4880
OsPCS2#1   838>----------------------------------------------------------------------------AGTT>841
OsPCS2#2   838>-----------------------------------------------------------------CTTTTGTGCAGAGTT>852
AK071958   266>----------------------------------------------------------------------------AGTT>269
OsPCS2#3   688>-----------------------------------------------------------------CTTTTGTGCAGAGTT>702
                     *       *        *       *        *       *        *       *
Genome    4881>GCAGAGATGAAAGCTGGAAAAGCATGGCGAAGTATTGCATGGAAGATGTACCCGATCTTCTTAAGGATGAGAGTGTAGAC>4960
OsPCS2#1   842>GCAGAGATGAAAGCTGGAAAAGCATGGCGAAGTATTGCATGGAAGATGTACCCGATCTTCTTAAGGATGAGAGTGTAGAC>921
OsPCS2#2   853>GCAGAGATGAAAGCTGGAAAAGCATGGCGAAGTATTGCATGGAAGATGTACCCGATCTTCTTAAGGATGAGAGTGTAGAC>932
AK071958   270>GCAGAGATGAAAGCTGGAAAAGCATGGCGAAGTATTGCATGGAAGATGTACCCGATCTTCTTAAGGATGAGAGTGTAGAC>349
OsPCS2#3   703>GCAGAGATGAAAGCTGGAAAAGCATGGCGAAGTATTGCATGGAAGATGTACCCGATCTTCTTAAGGATGAGAGTGTAGAC>782
                     *       *        *       *        *       *        *       *

                     *       *        *       *        *       *        *       *
Genome    5041>TAGGAGACAAGAGGAAGGAGGATCAGGATTAAGCAAAGAGGAGGAAGAAAGGCTTATTTTGAAGGTCATCTTCAACCTTT>5120
OsPCS2#1  1002>TAGGAGACAAGAGGAAGGAGGATCAGGATTAAGCAAAGAGGAGGAAGAAAGGCTTATTTTGAAG---------------->1065
OsPCS2#2  1013>TAGGAGACAAGAGGAAGGAGGATCAGGATTAAGCAAAGAGGAGGAAGAAAGGCTTATTTTGAAG---------------->1076
AK071958   430>TAGGAGACAAGAGGAAGGAGGATCAGGATTAAGCAAAGAGGAGGAAGAAAGGCTTATTTTGAAG---------------->493
OsPCS2#3   863>TAGGAGACAAGAGGAAGGAGGATCAGGATTAAGCAAAGAGGAGGAAGAAAGGCTTATTTTGAAG---------------->926
                     *       *        *       *        *       *        *       *
Genome    5121>TCTTTTCAATCTGGGATTCTGGATCAGAATTTTCTTTTTGTCTCTTTTAACACACCTTACACTGTGTGCACTTGCAGGAA>5200
OsPCS2#1  1066>-----------------------------------------------------------------------------GAA>1068
OsPCS2#2  1077>-----------------------------------------------------------------------------GAA>1079
AK071958   494>-----------------------------------------------------------------------------GAA>496
OsPCS2#3   927>-----------------------------------------------------------------------------GAA>929
                     *       *        *       *        *       *        *       *

                     *       *        *       *        *       *        *       *
Genome    5681>CTTCATGATGATCTTAAACGAGAGGTTTGTTGTATTAATCCAAACATCCCTTGCTCCCTACTCCCTAGCAAGATTTGTTT>5760
OsPCS2#1  1549>CTTCATGATGATCTTAAACGAGAG-------------------------------------------------------->1572
OsPCS2#2  1560>CTTCATGATGATCTTAAACGAGAG-------------------------------------------------------->1583
AK071958   977>CTTCATGATGATCTTAAACGAGAG-------------------------------------------------------->1000
OsPCS2#3  1410>CTTCATGATGATCTTAAACGAGAG-------------------------------------------------------->1433
                     *       *        *       *        *       *        *       *

                     *       *        *       *        *       *        *       *
Genome    6481>AAAAACATTTGTTGCACTAGTTTAGAATAACATTTTGTCTGTTGACACAGATATTGCATCTAAGACGGCAACTCCATTAT>6560
OsPCS2#1  1573>--------------------------------------------------ATATTGCATCTAAGACGGCAACTCCATTAT>1602
OsPCS2#2  1584>--------------------------------------------------ATATTGCATCTAAGACGGCAACTCCATTAT>1613
AK071958  1001>--------------------------------------------------ATATTGCATCTAAGACGGCAACTCCATTAT>1030
OsPCS2#3  1434>--------------------------------------------------ATATTGCATCTAAGACGGCAACTCCATTAT>1463
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Genome      6561>GTGAGGTCCTGTAAAGAGGAGGAATATGGAGATCCTGTGCCACAATCCCATTAACAATGATGCAAATCGCGCAGTTGGTT>6640
OsPCS2#1    1603>GTGAGGTCCTGTAAAGAGGAGGAATATGGAGATCCTGTGCCACAATCCCATTAACAATGATGCAAATCGCGCAGTTGGTT>1682
OsPCS2#2    1614>GTGAGGTCCTGTAAAGAGGAGGAATATGGAGATCCTGTGCCACAATCCCATTAACAATGATGCAAATCGCGCAGTTGGTT>1693
AK071958    1031>GTGAGGTCCTGTAAAGAGGAGGAATATGGAGATCCTGTGCCACAATCCCATTAACAATGATGCAAATCGCGCAGTTGGTT>1110
OsPCS2#3    1464>GTGAGGTCCTGTAAAGAGGAGGAATATGGAGATCCTGTGCCACAATCCCATTAA~~~~~~~~~~~~~~~~~~~~~~~~~~>1517
                       *         *         *         *         *         *         *         *
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Supplementary Fig. S1 Alignment of *OsPCS* sequences among genomic sequence, transcripts, and ESTs. (A) *OsPCS1* genomic sequence, ESTs (CB646798, CK083842, CB646799 and C96924) and transcript sequences (*OsPCS1*#1–4) were compared. *OsPCS1*#4 is the transcript sequence on the RAP-DB (AF439787). **(B)** *OsPCS2* genomic sequence and transcript sequences (*OsPCS2*#1–3) were compared. *OsPCS2*#2 (AK071754) and AK071958 are the transcript sequences on the RAP-DB. White boxes show the start codon and the stop codon. Gray boxes show the splice donor sites (GT) and the splice acceptor sites (AG). Black boxes show the site different from genomic sequence.

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OsPCS1  MASKPSSRAESNQAAAAVPSLYGRALPSPPAVEFASAEGRRLFAEALQGGTMQGFFSLVSVFQTQSEPAFCGLATLAVVLNALRIDPGRR  90
OsPCS2  --------------MAAMASLYRRVLPSPPAVEFASEEGKRLFSEALESGTLQGFFNLISVFQTQSEPAFCGLASLSVVLNALAIDPGRQ  76
TaPCS1  ---------------MEVASLYRRVLPSPPAVEFASAEGKRLFAEALQGGTMEGFFNLISYFQTQSEPAFCGLASLSVVLNALAIDPGRP  75
AtPCS1  ---------------MAMASLYRRSLPSPPAIDFSSAEGKLIFNEALQKGTMEGFFRLISYFQTQSEPAYCGLASLSVVLNALSIDPGRK  75
AtPCS2  ---------------MSMASLYRRSL-SPPAIDFASFEGKQIFNEALQKGTMEGFFGLISYFQTQSEPAFCGLASLSMVLNSLSIDPGRK  74

OsPCS1  WKGPWRWFDESMLDCCEHLDTVRAEGITFGKVACLAHCSGADVRTFRAAQATLADLRRHLLRCASSQDCHLVASYHRKLLGQTGTGHFSP  180
OsPCS2  WKGPWRWFDESMLDCCEPLDKVKAEGITFAKLACLAHCAGANVRSFRADQSTIHDFRHHLVRSASSQDCHLIASYHRKPFKQTGTGHFSP  166
TaPCS1  WKGPWRWFDESMLDCCEPLHKVKAEGITFGKVVCLAHCAGARVQSFRADQTTIHDFRAHLTRCASSQDCHLISSYHRSPFKQTGTGHFSP  165
AtPCS1  WKGPWRWFDESMLDCCEPLEVVKEKGISFGKVVCLAHCSGAKVEAFRTSQSTIDDFRKFVVKCTSSENCHMISTYHRGVFKQTGTGHFSP  165
AtPCS2  WKGPWRWFDESMLECCEPLEIVKDKGISFGKVVCLAHSSGAKVEAFRTNQSTIDDFRKYVVKCSTSDNCHMISTYHRQVLKQTGTGHFSP  164

OsPCS1  IGGYHAGQDMALILDVARFKYPPHWIPLPLLWEAMNTIDEATGLLRGFMLISRNTEAPLLIRAVNCRDESWQSMAKYCIEVVPNLLRDNS  270
OsPCS2  IGGYHAGQDMALILDVARFKYPPHWVPLPLLWEAMNTTDDATGLLRGFMLISRHTAAPSLLYTVSCRDESWKSMAKYCMEDVPDLLKDES  256
TaPCS1  IGGYHAEKDMALILDVARFKYPPHWVPLTLLWDAMNTTDEATGLLRGFMLVSRRSSAPSLLYTVSCGHGSWKSMAKYCVEDVPNLLKDES  255
AtPCS1  IGGYNAERDMALILDVARFKYPPHWVPLKLLWEAMDSIDQSTGKRRGFMLISRPHREPGLLYTLSCKDESWIEIAKYLKEDVPRLVSSQH  255
AtPCS2  IGGYNAERDMALILDVARFKYPPHWVPLKLLWDAMDSIDQSTGRRRGFMLISRPHREPGLLYTLSCKDESWISIAKYLKEDVPRLVSSQH  254

OsPCS1  VDNVLTILSRLVNHLPPNAGNFIKWVIEVRRQEEGGSSPSKEANEMPFLKEKVLQQIRDTKLFQLVHKLQCSKQPCCSCSSLTDEDSISQ  360
OsPCS2  VDNVPALLSRLVKSLPANAGNLIKWVIEVRRQEEGGSGLSKEEEERLILKEMILQQVRDTELFRLVRELQFTKQPCCSCSYSSDDDSFTR  346
TaPCS1  LDNVTTLLSRLVESLPANAGDLIKCVIEVRRKEEGESSLSKEEKERLFLKEKVLQQIRDTDLFRVVHELQYPKGLCGSCSSSSDEDSLAE  345
AtPCS1  VDSVEKIISVVFKSLPSNFNQFIRWVAEIRITEDSNQNLSAEEKSRLKLKQLVLKEVHETELFKHINKFLSTVG---------YEDSLTY  336
AtPCS2  VDTIERILYVVFKSLPANFNQFIKWMAEIRRTEDVNQNLSSEEKSRLKLKQELLKQVQETKLFKHVDKFLSSV----------YEDNLPY  334

OsPCS1  IAASVCCEATALLSGNLSSRDGLFFSETCSGCTQVNDEGLKNVITGKVVSEGN-GHVDKLSPISSTETCFCNSTLSNETVNYPSNTDILT  449
OsPCS2  IAASVCCQGAALLTGNLSSKDGFCCRETCFKCVQVDGDGPKTVVTGTAVSGVNEQSVDMLLPISTLETSVCNSNSSNEVVKYPSRTDILT  436
TaPCS1  IAATVCCQGAAFLSGNLVSRDGFCCRETCIKCIEANGDGLKTVISGTVVSKGNEQAVDLLLPTSSSKTSLCNSNLKSKIVKYPSSTDVLT  435
AtPCS1  AAAKACCQGAEILSG--SPSKEFCCRETCVKCIKGPDDSEGTVVTGVVVRDGNEQKVDLLVPSTQTECECGPE------ATYPAGNDVFT  418
AtPCS2  VAAKVYCDGDEILSG--YESDESCCKETCVKCIKGLGEEKVTVVA------------------------------------YPSGNDVFT  386

OsPCS1  VLLLSLHPSTWLCIEDEKLKAEFQSLVSTDDLPDPLKLEILHLRRQLRYLKACREKEAYEDTWPQPWEQC  519
OsPCS2  VLLLALHPSTWVGIKDERLKAEFQSLISTDILHDDLKREILHLRRQLHYVRSCKE-EEYGDPVPQSH---  502
TaPCS1  VLLLVLQPNTWLGIKDENVKAEFQSLVSTDNLPDLLKQEILHLRRQLHYLAGCKGQEACQEP-PSP----  500
AtPCS1  ALLLALPPQTWSGIKDQALMHEMKQLISMASLPTLLQEEVLHLRRQLQLLKRCQENKEEDDLAAPAY---  485
AtPCS2  ALLLALPPQTWSGIKDQSLLQEMKQLISMVSHPTLLQQEVLHLRRQLEMLKRCQENKEDEELSAPA----  452
```

Supplementary Fig. S2 Alignment of predicted amino acid sequences of PC synthase from rice, *Arabidopsis*, and wheat. Black boxes show identical amino acid residues. Gray boxes show similar amino acid residues. Alignment was conducted by ClustalW in the DNA Data Bank of Japan (DDBJ). Accession number of the sequences is as following. AtPCS1: AAD50593, AtPCS2: AAK94671, TaPCS1: AAD50592.

```
OsPCS1             1 ------------------------------------------------AC      2
                                                                     |.
OsPCS2             1 GCATCTAAGACGGCAACTCCATTATGTGAGGTCCTGTAAAGAGGAGGAAT     50

OsPCS1             3 ATGG-------------CAA-CCCACTCACTTAATAATGAATTTCGCTGT     38
                     ||||             ||| ||||.|.||  |||.|||.|..||||
OsPCS2            51 ATGGAGATCCTGTGCCACAATCCCATTAAC--AATGATGCAAATCGC---     95

OsPCS1            39 TCACTGGGCCTTTGGTTGCTGGCTTAACCTTACTGGAAATTGACGCGAAA     88
                            ||..||||||         |||   |||||    ||.||.|||
OsPCS2            96 -------GCAGTTGGTT---------ACC---CTGGA----GATGCAAAA    122

OsPCS1            89 AGAAAAGGTTAGGATGTTAGGAGAGGAGGTGAAAA------------TAT    126
                     |.||..||||           ||||||||    ||            |||
OsPCS2           123 AAAAGGGGTT-----------AGAGGAGG----AACTACATACTCCGTAT    157

OsPCS1           127 TACCTCCTTTTCAAATAAGGACTATATAAACAATTTTCTGATAATAATGA    176
                     |||||...||||.|.|.|||||             ||||.||
OsPCS2           158 TACCTTTGTTTCGAGTGAGGAC-------------TTCTCAT--------    186

OsPCS1           177 TGTTTT--GGCAATTGGC--AAGTACTTTGCAACCGTGAAG-TATCTTTC    221
                       ||||  |.||..||.|  .|| ||   |.|.|||||.|| .||.||
OsPCS2           187 --TTTTGAGACACCTGACCTGAG-AC---GGATCCGTGTAGACATGTT--    228

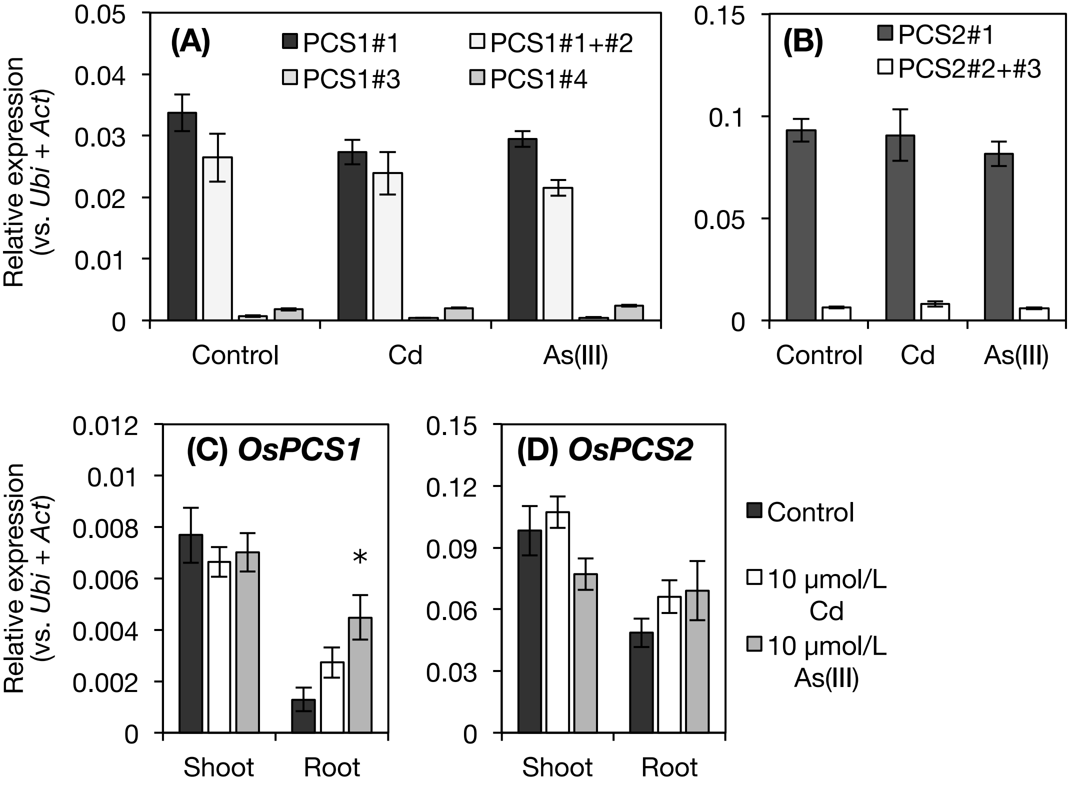
OsPCS1           222 CTTGCTTAATTTCTCTTTTGTT--TTTCCCTTGTACTTCTGATAGTTCCA    269
                     |.||.|.|   ||.|.|.||.|  ||||.|||||        ||||..||
OsPCS2           229 CATGTTCA---TCACCTGTGGTCGTTTCTCTTGT--------TAGTGACA    267

OsPCS1           270 --TGTACTTTATTCCCTCTAATTAATGGATAAGCACACTTAGCT------    311
                       || ||            ||.||..||..|.||||||   |||
OsPCS2           268 ACTG-AC------------AACTAGCGGGGAGGCACAC---GCTAATTGT    301

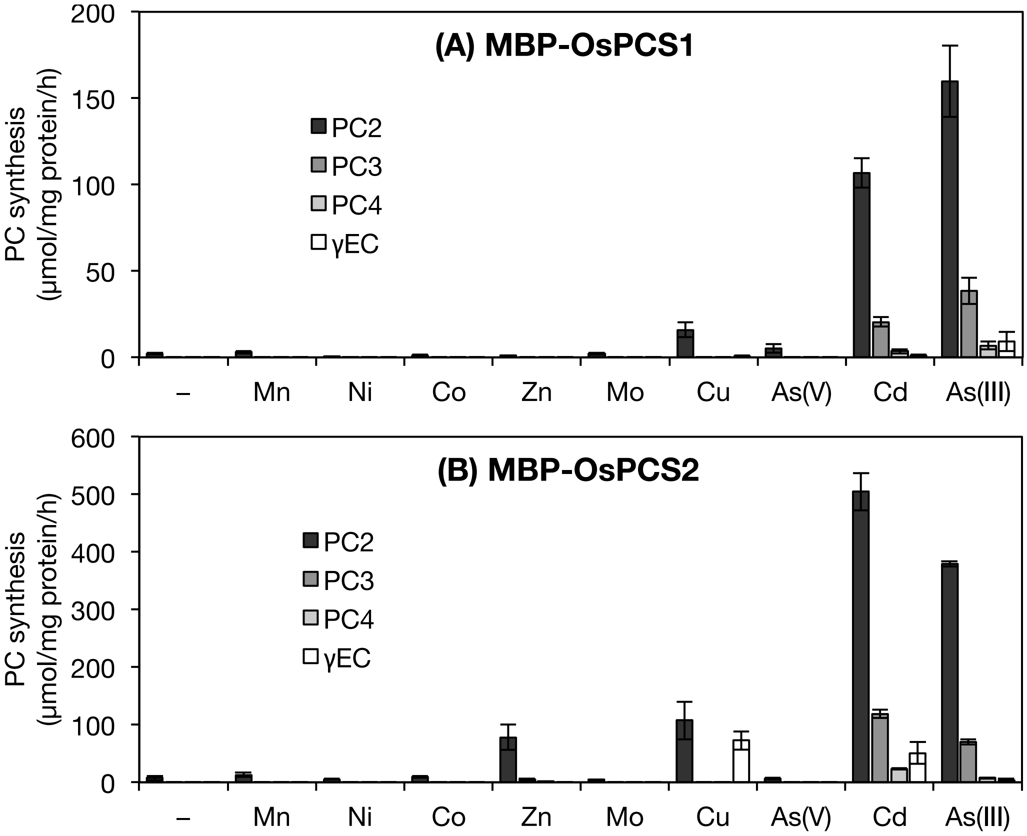
OsPCS1           312 --------CGTCCT------------    317
                             .|||||
OsPCS2           302 GCGGCTGGTGTCCTTGCAAAAGTTTC    327
```

Supplementary Fig. S3 Alignment of RNAi trigger sequences of 3′-UTR in *OsPCS1* and *OsPCS2*.

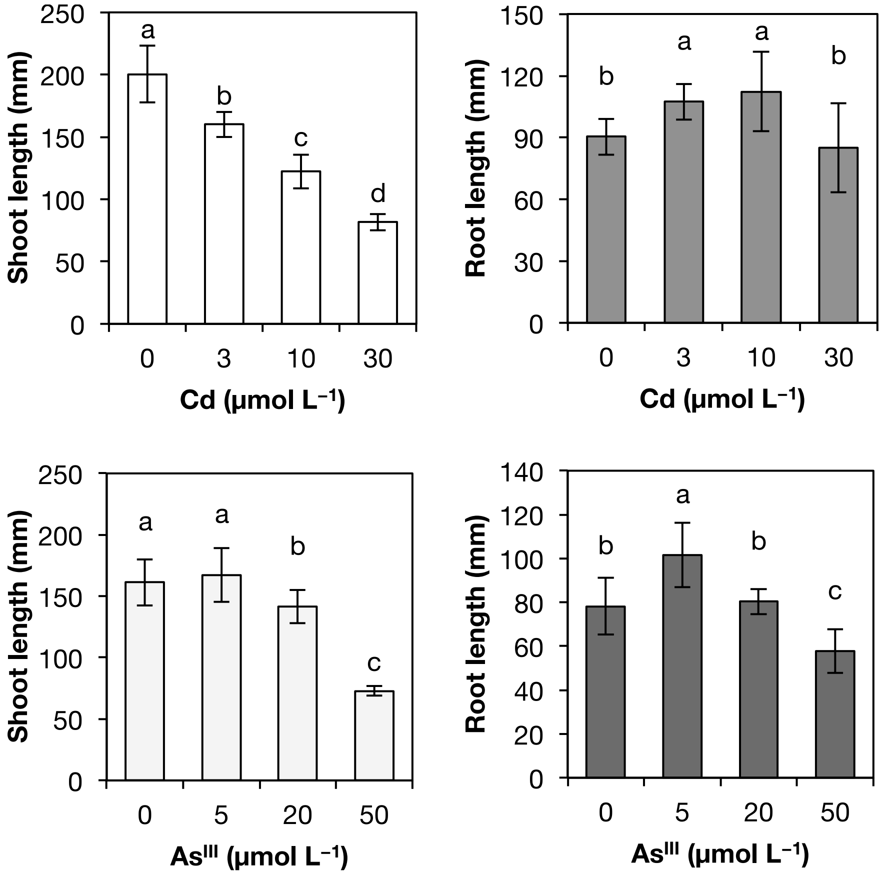
A segment of 317 bp or 327 bp in the 3′ untranslated region specific to *OsPCS1* or *OsPCS2*, respectively, was used for the RNAi trigger. Global alignment of two nucleotide sequences was conducted by the EMBOSS Needle. Nucleotide sequence identity is 39.9%.



Supplementary Fig. S4 Expression levels of *OsPCS*. (A, B) Relative expression of *OsPCS1* and *OsPCS2* transcriptional variants in shoots under control conditions and heavy metal toxicity. Specific primers for each transcript were used. **(C, D)** Total expression levels of *OsPCS1* and *OsPCS2*. Common primers to all of the variants were used. The expression level was analyzed by quantitative RT-PCR in 10-day-old seedlings hydroponically grown under control, Cd stress (10 μmol L^{-1} $CdSO_4$), or As(III) stress (10 μmol L^{-1} $NaAsO_2$) condition. *Ubiquitin* and *Actin* were used as internal standards. Values are expressed as means ± SE (n = 4). An asterisk (*) shows a significant difference from the control ($p < 0.05$, Dunnett test).

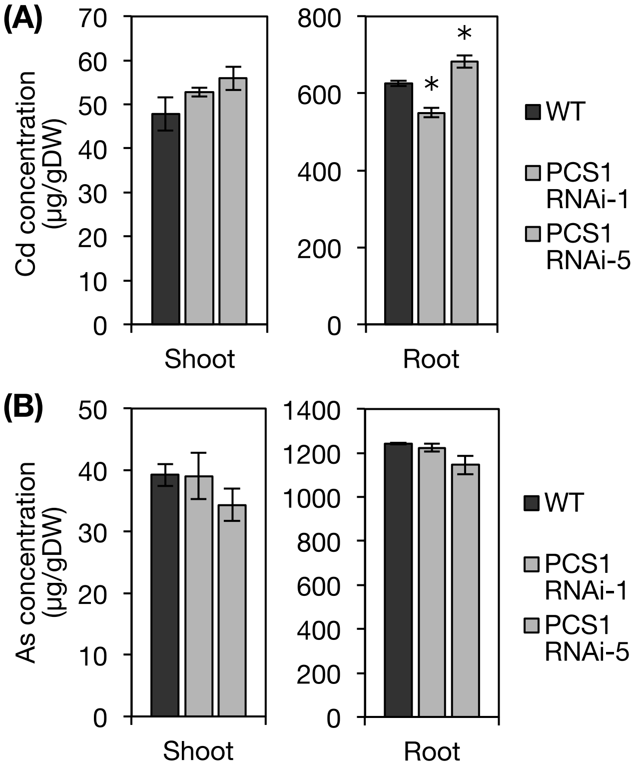


Supplementary Fig. S5 Activation of MBP-OsPCS by various heavy metals/metalloids. PC synthesis catalyzed by **(A)** OsPCS1 and **(B)** OsPCS2 in the presence of different heavy metals/metalloids. Purified MBP-OsPCS1 (15 µg mL^{-1}) or MBP-OsPCS2 (5 µg mL^{-1}) was incubated for 1 h in the reaction medium containing 10 mmol L^{-1} GSH, 200 mmol L^{-1} HEPES-KOH buffer (pH8.0), and 50 µmol L^{-1} of the metal ion indicated. The reaction was stopped by the addition of TFA at a final concentration of 1% (v/v). PC_{2-4} and γEC were derivatized with monobromobimane and quantified by HPLC-fluorescent detection. Values are expressed as means ± SE from three independent experiments.



Supplementary Fig. S6 Growth of WT plants under Cd or As(III) stress.

Shoot and root lengths of WT plants under Cd or As(III) stress. WT plants (cv. Nipponbare) were hydroponically grown in the culture solution containing 3, 10, or 30 µmol L^{-1} Cd or 5, 20, or 50 µmol L^{-1} As(III) and the control culture solution for 10 days. Values are expressed as means ± SD (Cd: $n \geq 14$, As: $n \geq 10$). Different letters show a significant difference ($p < 0.05$, Tukey test).



Supplementary Fig. S7 Cd and As concentrations in *OsPCS1* RNAi plants. **(A)** Cd concentration in shoots (left) and roots (right). **(B)** As concentration in shoots (left) and roots (right). WT and *OsPCS1* RNAi plants were hydroponically grown in a culture solution containing 10 µmol L^{-1} Cd or 20 µmol L^{-1} As(III) for 10 days. Each plant was separated into shoots and roots and oven-dried. After digestion with HNO_3 and $HClO_4$, Cd concentration was analyzed by atomic absorption spectroscopy and As concentration was analyzed by inductively coupled plasma atomic emission spectroscopy. Values are expressed as means ± SE (n = 4). An asterisk (*) shows a significant difference from WT plants ($p < 0.05$, Dunnett test).

Supplementary Table S1 Identity and similarity of predicted amino acid sequences of PC synthase from rice, *Arabidopsis*, and wheat.

Identity	OsPCS1	OsPCS2	AtPCS1	AtPCS2	TaPCS1
OsPCS1	-	69.6%	49.2%	46.9%	67.5%
OsPCS2	69.6%	-	56.5%	52.5%	76.3%
Similarity					
OsPCS1	-	80.4%	65.8%	62.5%	77.9%
OsPCS2	80.4%	-	71.2%	67.7%	86.7%

Global alignment of two protein sequences was conducted by EMBOSS Needle. Accession number of the sequences is as following. AtPCS1: AAD50593, AtPCS2: AAK94671, TaPCS1: AAD50592.

Supplementary Table S2 The concentration of thiol peptides in rice plants treated with BSO.

		Thiol peptides (nmol g^{-1}DW)						
−BSO		GSH	PC_2	PC_3	PC_4	hmGSH	γECE	γEC
Shoot	Control	48.0	-	-	-	25.3	-	-
	Cd	119	-	-	-	118	28.4	33.4
	As(III)	156	-	-	-	160	79.0	50.8
Root	Control	240	-	-	-	161	-	-
	Cd	188	50.4	53.8	5.80	790	221	208
	As(III)	444	532	203	11.0	1310	1260	1230
+BSO		GSH	PC_2	PC_3	PC_4	hmGSH	γECE	γEC
Shoot	Control	10.5	-	-	-	-	-	-
	Cd	8.84	-	-	-	-	-	-
	As(III)	21.1	-	-	-	6.24	4.96	12.2
Root	Control	7.04	-	-	-	-	-	-
	Cd	10.6	-	-	-	-	-	-
	As(III)	38.1	-	-	-	-	21.1	65.3

The 7-day-old seedlings of Nipponbare were transferred to a culture solution containing 10 μmol L^{-1} Cd or As(III) either alone or in combination with 0.5 mmol L^{-1} BSO. Controls without toxic metals were also tested. At 7 days after transfer, the concentration of thiol peptides in the shoots and roots was determined for a bulked sample of each treatment.

Supplementary Table S3 The sequences of primer used in this study.

For sequence analysis	
PCS1.seq1F	5′-CCAGACTGGAACAGGGCATT-3′
PCS1.seq2F	5′-GCCCTACCCTATCCAGCCTA-3′
PCS1.seqR	5′-AGGACGAGCTAAGTGTGCTT-3′
PCS1-2.3.R	5′-TCAATGCAAGGTTCTAGGAGTGAG-3′
PCS2.seqF	5′-AAGCAAGACGCGTCAAATCT-3′
PCS2.seq1R	5′-GAAACTTTTGCAAGGACACCA-3′
PCS2.seq2R	5′-TTTGACAACCTCGTTGCTTG-3′
For expression analysis	
PCS1-1.ex-F	5′-AACTGGAGATATTGCACCTAAGGA-3′
PCS1-1.ex-R	5′-GCCCAGTGAACAGCGAAA-3′
PCS1-1.2.ex-F	5′-GCATGGCAAAGTATTGCATAGAAG-3′
PCS1-1.2.ex-R	5′-TCCAGCATTGGGAGGAAGA-3′
PCS1-3.ex-F	5′-GGCTTCTCAGGGGTGGTAAA-3′
PCS1-4.ex-F	5′-CTTTATTGATCCGTGCAGTGGTA-3′
PCS1-3.4.ex-R	5′-ATCCTCCTTCCTCTTGTCTCCTAAC-3′
PCS2-1.ex-F	5′-CATTGCTCTACACAGTGAGTTGC-3′
PCS2-1.ex-R	5′-ATTTCACTAAGCGGGACAGAAG-3′
PCS2-2.ex-F	5′-TTTGGGAAGCCATGAATACAAC-3′
PCS2-2.ex-R	5′-TTTCATCTCTGCAACTCTGCAC-3′
Ubiquitin. F	5′-AGAAGGAGTCCACCCTCCACC-3′
Ubiquitin. R	5′-GCATCCAGCACAGTAAAACACG-3′
Actin1. F	5′-ATCCTTGTATGCTAGCGGTCGA-3′
Actin1. R	5′-ATCCAACCGGAGGATAGCATG-3′
PCS1.total.ex-F	5′-TCGCTTCAAATACCCTCCTCA-3′
PCS1.total.ex-R	5′-TCACTGCACGGATCAATAAAGG-3′
PCS2.total.ex-F	5′-CTTTGGGAAGCCATGAATACAAC-3′
PCS2.total.ex-R	5′-TTCCAGCTTTCATCTCTGCAAC-3′
For recombinant protein analysis	
PCS1.proF	5′-**ATG**GCGTCTAAACCAAGCAGC-3′
PCS1-1.proR	5′-ACTGCCTGCAGG**TTA**GCATTGTTCCCAAGGTTG-3′
PCS2.proF	5′-**ATG**GCAGCGATGGCATCCCT-3′
PCS2-1.proR	5′-GAGTCCTGCAGG**TTA**ATGGGATTGTGGCACAG-3′
For RNAi trigger	
PCS1.RNAi.F	5′-CACCACATGGCAACCCACTCACTT-3′
PCS2.RNAi.F	5′-CACCGCATCTAAGACGGCAACTCC-3′
PCS2.RNAi.R	5′-GAAACTTTTGCAAGGACACCA-3′