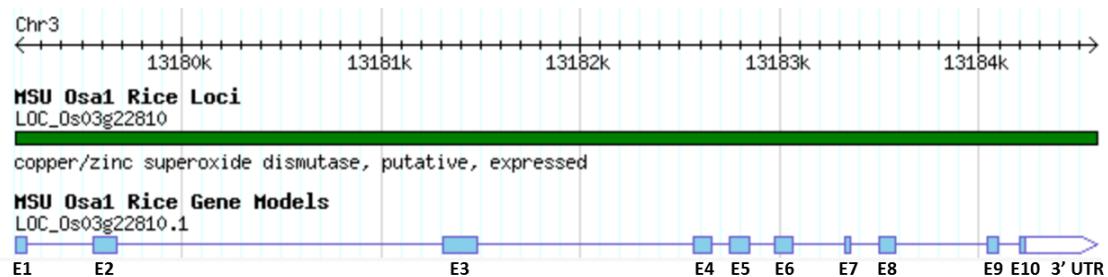
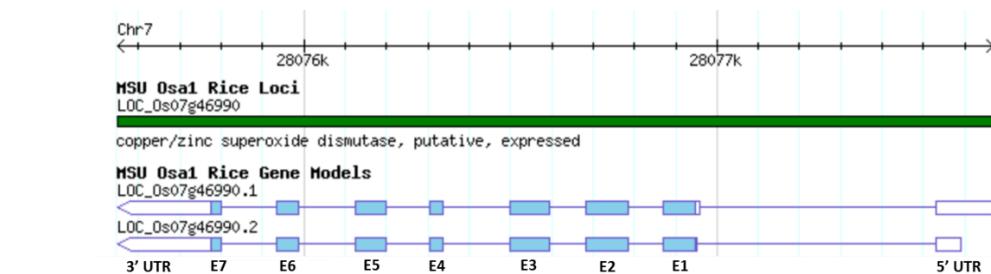


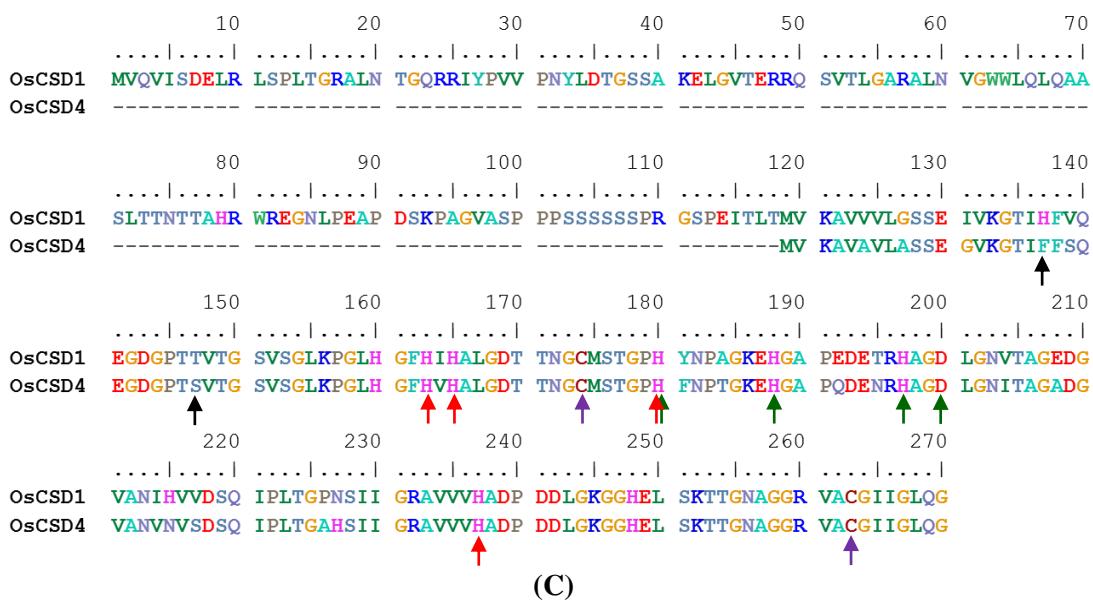
Supplementary Figure 1: Predicted gene structure organization of *loci* encoding two rice cytosolic CuZn Superoxide dismutase (*CSD*) genes as per Rice Genome Annotation Project database (<http://rice.uga.edu>). (A) LOC\_Os03g22810 (*OsCSD1*), (B) LOC\_Os07g46990 (*OsCSD4*). Regions corresponding to the exons/coding regions (blue boxes, indicated by ‘E’), introns (connecting lines), and UTRs (white boxes) are indicated. Scale on the top indicates the chromosomal coordinates. (C) Sequence alignment of the RGAP predicted amino acid sequences of OsCSD1 and OsCSD4. Predicted OsCSD1 is 270 AA long, while OsCSD4 is 152 AA long (length variation: 118 AA). Important residues are indicated by different coloured arrows: co-ordination with Cu<sup>2+</sup> (red) and co-ordination with Zn<sup>2+</sup> (green), intra-subunit disulfide bond (purple), variations at subunit interaction interface (black).



(A)

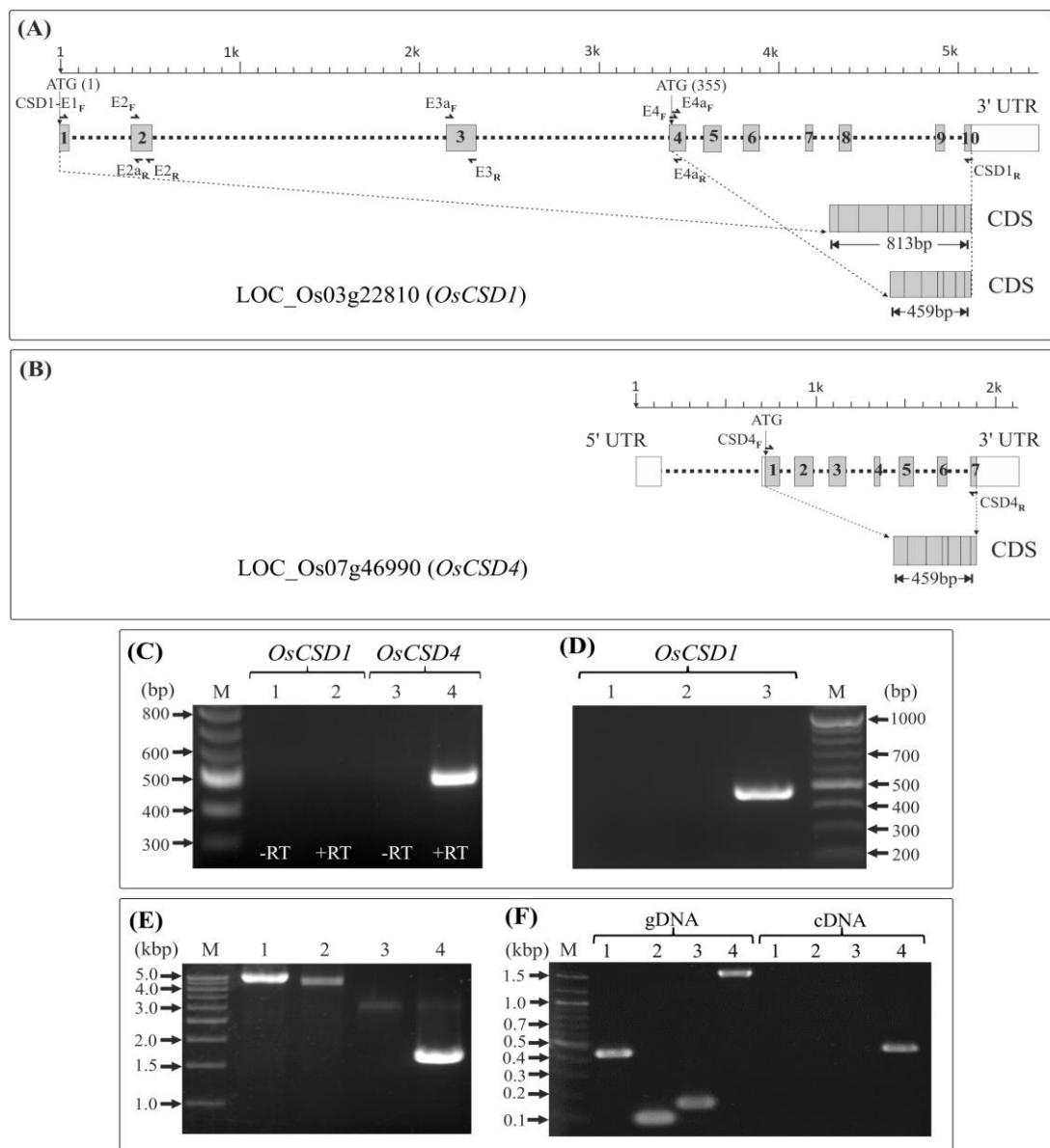


(B)



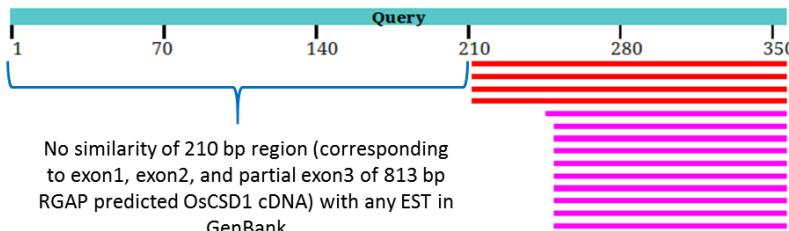
(C)

Supplementary Figure 2: Schematic representation of RGAP-predicted gene structures (exon-intron-UTR organization) of rice cytosolic *CSD* genes: (A) of LOC\_Os03g22810 (*OsCSD1*) and (B) LOC\_Os07g46990 (*OsCSD4*). Exons (grey boxes), introns (thick dashed line), UTRs (white boxes), and start codons (ATG) in the *OsCSD1* (w.r.t. cDNA) and *OsCSD4* genes are shown along with length of the coding region. Positions of various forward and reverse oligonucleotide primers used for PCR amplification of FL-cDNAs (RGAP predicted) and individual exons are also shown. (C-F): PCR amplification of *OsCSD1* and *OsCSD4* FL-cDNA, and validation of exon organization of RGAP predicted *OsCSD1* gene. (C) FL-cDNA amplification of *OsCSD1* (primers: CSD1-E1<sub>F</sub> + CSD1<sub>R</sub>) and *OsCSD4* (primers: CSD4<sub>F</sub> and CSD4<sub>R</sub>) in '+RT' (with reverse transcriptase) and '-RT' control (without reverse transcriptase) samples. (D) PCR amplification of different *OsCSD1* cDNA regions, exon1-10 (lane 1, primers: CSD1-E1<sub>F</sub> + CSD1<sub>R</sub>), exon1-4 (lane 2, primers: CSD1-E1<sub>F</sub> + CSD-E4a<sub>R</sub>) and exon4-10 (lane 3, primers: CSD1-E4a<sub>F</sub> + CSD1<sub>R</sub>). (E) PCR amplification of *OsCSD1* regions using genomic DNA template and different primers: CSD1-E1<sub>F</sub> + CSD1<sub>R</sub> (lane 1), CSD1-E2<sub>F</sub> + CSD1<sub>R</sub> (lane 2), CSD1-E3a<sub>F</sub> + CSD1<sub>R</sub> (lane 3), CSD1-E4<sub>F</sub> + CSD1<sub>R</sub> (lane 4). (F) PCR amplification of *OsCSD1* exon/exon-combinations with genomic DNA (left panel) or cDNA templates (right panel), and different primers: CSD1-E1<sub>F</sub> + CSD1-E2a<sub>R</sub> (lane 1); CSD1-E2<sub>F</sub> + CSD1-E2r (lane 2); CSD1-E3af + CSD1-3<sub>R</sub> (lane 3); CSD1-E4<sub>F</sub> + CSD1<sub>R</sub> (lane 4). Lane M indicates DNA markers, 100 bp ladder (Figure B, D, F) and 500 bp ladder (Figure E).



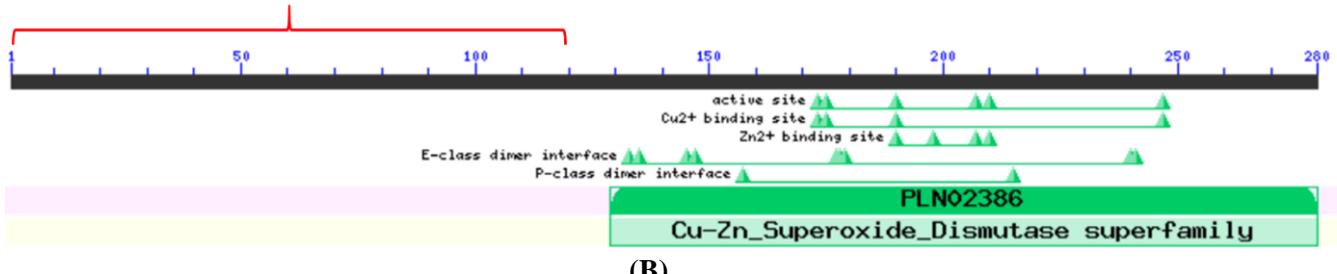
Supplementary Figure 3: Database search analysis of cDNA region (and encoded amino acid sequence) of the region corresponding to exon1, exon2, exon3, and exon4 (till ATG at 355) of the RGAP predicted *OsCSD1* gene structure. (A) Top hits obtained in ‘Blastn’ search of the *OsCSD1* 1-354 bp cDNA region. No similarity observed in region 1-210 bp with any available EST. (B) Results of conserved domain analysis (at CDD-Blast, NCBI) of RGAP predicted *OsCSD1* protein sequence (length: 270 AA). No conserved domains detected in the N-terminal 118 AA region of *OsCSD1*. (C) Schematic representation of location of SAGE Tags and microarray probes (Affymetrix and Agilent) along the length of RGAP predicted *OsCSD1* gene structure. No Tags/probes are designed/utilized in exon1-exon4 region.

### Schematic representation of distribution of top 20 Blast hits



(A)

No conserved domains detected in N-Ter 118 amino acid region encoded by exon1, exon2, exon3 and partial exon4 region predicted at RGAP database



(B)

LOC\_Os03g22810  
copper/zinc superoxide dismutase, putative, expressed

MSU Osal Rice Gene Models

SAGE Tags

Affymetrix GeneChip Rice Genome Array

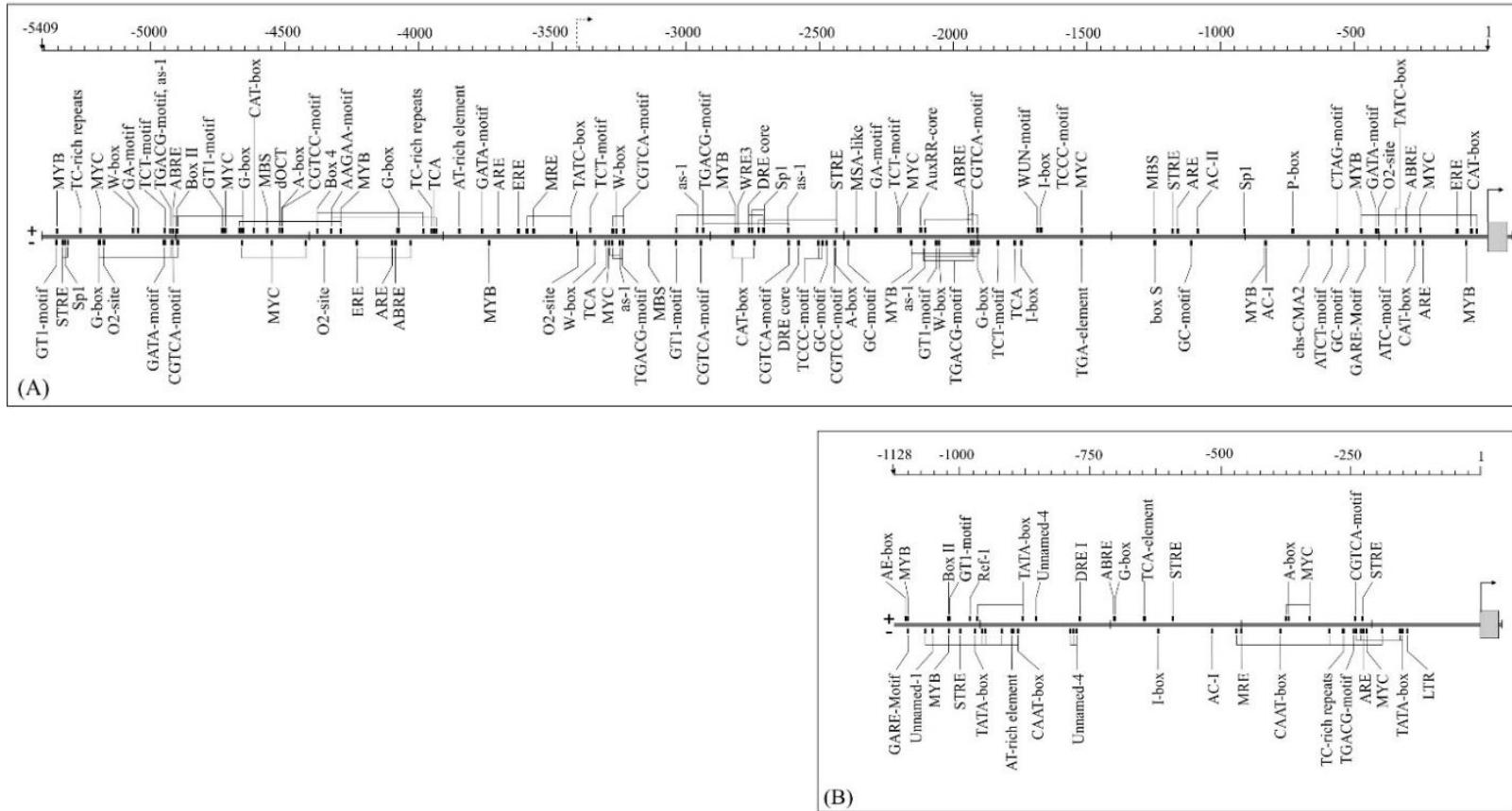
Agilent Rice Oligo Microarray

No probes used in exon 1-4 region for transcript analysis, in different approaches

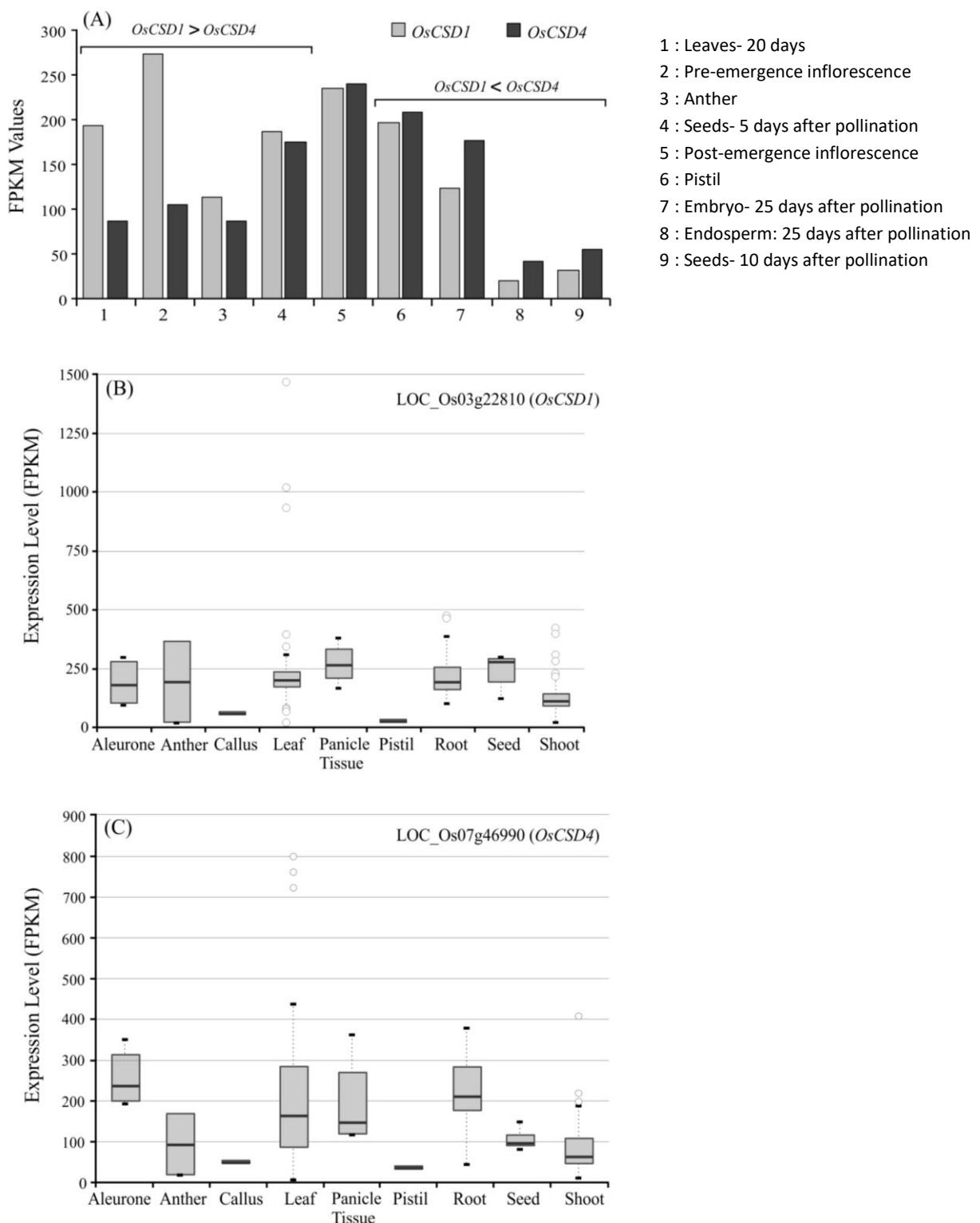
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CATGGAAAATTGATAAAGTT  
CATGCCAGAGA  
probe:Rice:Os.186.1.S1\_at:889:1021 probe:Rice:Os.186.1.  
probe:Rice:Os.186.1.S1\_at:465:1667 probe:Rice:Os.186.1.  
probe:Rice:Os.186.1.S1\_at:925:341 probe:Rice:Os.186.1.  
probe:Rice:Os.186.1.S1\_at:6:643 probe:Rice:Os.186.1.  
probe:Rice:Os.186.1.S1\_at:552:711 probe:Rice:Os.186.1.  
probe:Rice:Os.186.1.S1\_at:552:711 probe:Rice:Os.186.1.  
probe:Rice:Os.186.1.S1\_at:470:43 probe:Rice:  
AR10117\_AK0616

(C)

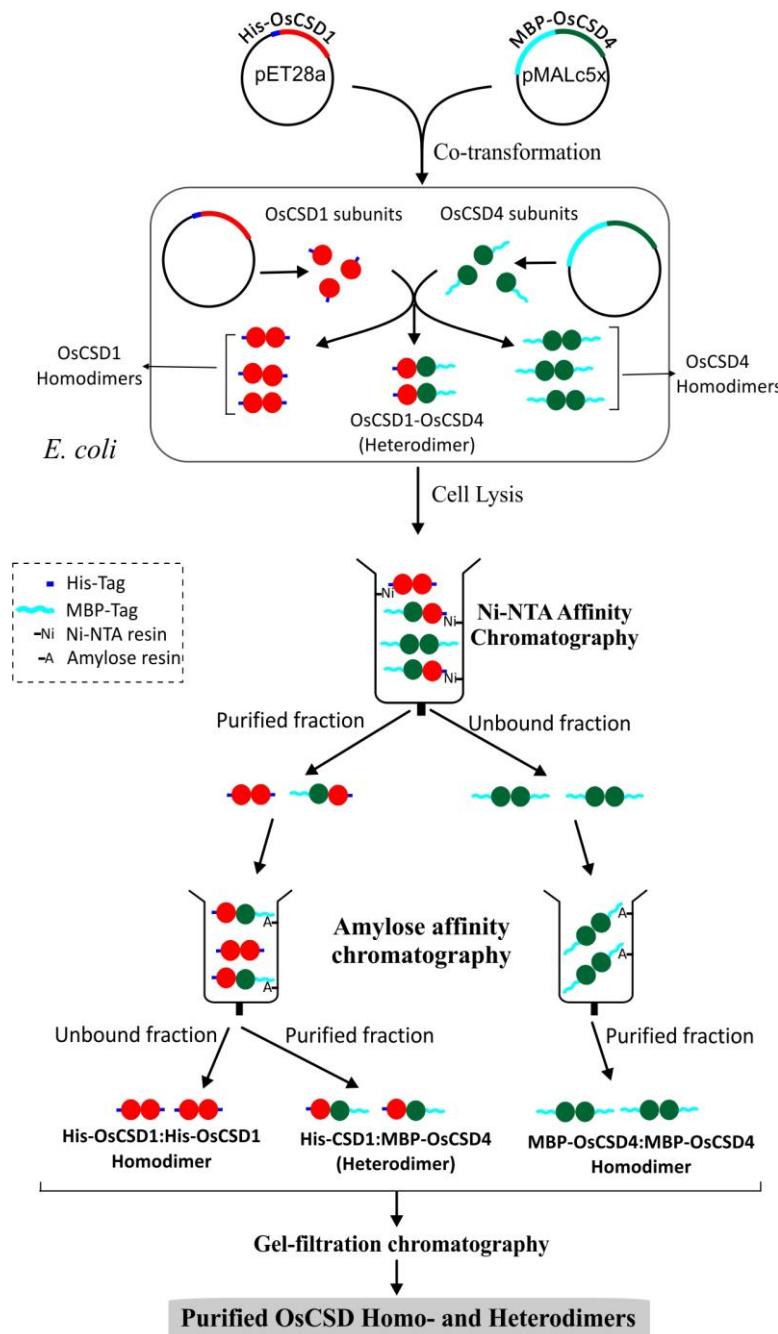
Supplementary Figure 4: Locations of relative positions of the cis- regulatory elements in the upstream region of rice cytosolic CSD genes, (A) *OsCSD1* and (B) *OsCSD4*. Analysis of *cis*-elements was carried at PlantCARE database (<http://bioinformatics.psb.ugent.be/webtools/plantcare/html>). Scale at the top is indicative of relative positions of *cis*-elements relative to the translation start site (+1), and '+' and '-' indicates the plus and minus strands, respectively. Positions of common promoter elements (TATA, CAAT etc.) and unnamed motifs are not indicated.



Supplementary Figure 5: Relative transcript levels of two rice cytosolic CSDs, *OsCSD1* and *OsCSD4*: (A) Transcript levels of *OsCSD1* and *OsCSD4* in different rice tissues/developmental stages as per RGAP database (<http://rice.uga.edu>). (B-C) Expression level of *OsCSD1* and *OsCSD4* transcripts in different tissues/developmental stages as per rice expression database (RED, <http://expression.ic4.org>). FPKM: Fragments per kilo base per million mapped reads.



Supplementary Figure 6: Schematic representation of approach for co-expression and isolation of homodimeric and heterodimeric subunit configurations of OsCSD1 and OsCSD4. His-tagged OsCSD1 (cloned in pET28 plasmid, kanamycin selection marker) and MBP-tagged OsCSD4/OsCSD1 (cloned in pMAL-c5x, ampicillin selection marker) were co-transformed in *E. coli* SHuffle T7 Express host and over-expressed. Cells were lysed and homodimers (His-OsCSD1:OsCSD1, MBP-OsCSD4:MBP-OsCSD4) and heterodimer (His-OsCSD1:MBP-OsCSD4) subunit configurations were isolated and purified by combination of affinity (Ni-NTA and Amylose based) and gel-filtration purification methods. For convenience different colour codes are used for the two affinity tags (His: dark blue; MBP: light blue-green) and OsCSDs (OsCSD1: red; OsCSD4: green).



Supplementary Figure 7: Multiple sequence alignment (MSA) of 92 cytosolic CuZn SODs (monocots: 1-43, dicots: 44-92) retrieved from the PLAZA web resource for monocot ([https://bioinformatics.psb.ugent.be/plaza/versions/plaza\\_v4\\_5\\_monocots/](https://bioinformatics.psb.ugent.be/plaza/versions/plaza_v4_5_monocots/)) and dicots ([https://bioinformatics.psb.ugent.be/plaza/versions/plaza\\_v4\\_5\\_dicots/](https://bioinformatics.psb.ugent.be/plaza/versions/plaza_v4_5_dicots/)). MSA was carried out using ClustalX software (Thompson et al., 1997) using default gap opening and gap extension penalties, followed by alignment editing by BioEdit Software (Hall, 1999). The name of the species is followed by genomic location (chromosome/linkage group/scaffold etc.) in the parenthesis. For convenience, the duplicated sequences (due to block/tandem duplication) in a genome are arranged next each other. Regions (#1- #15) with length variations are indicated below the alignment. (Note: *C. sim*, *C. simplicifolius*; *H. bra*, *H. brasiliensis*; *T. has*, *T. hassleriana*).

## **Monocots**

→ ← #2 → ← #3 → ← #4 → ← #5 → ← #6







— #12 —→

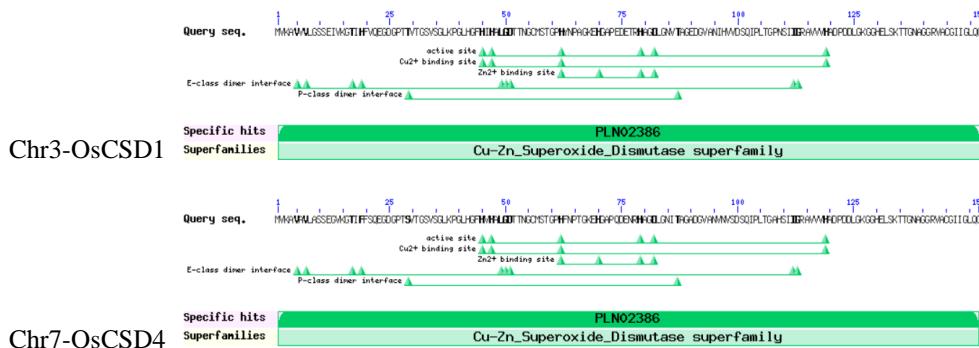
←

#13

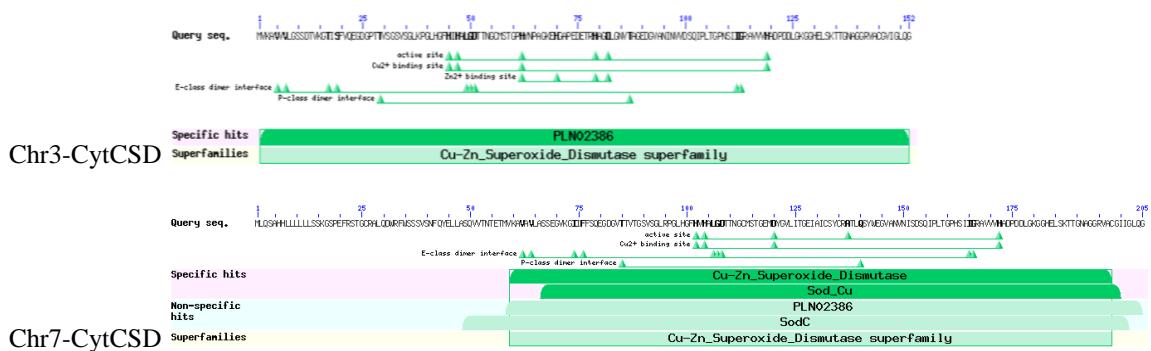
	430	440	450	460	470
<i>O. sativa</i> (Chr3-CSD1)		-LQG-			
<i>O. sativa</i> (Chr7-CSD4)		-LQG-			
<i>O. brachyantha</i> (Chr3-CSD)		-LQG-			
<i>O. brachyantha</i> (Chr7-CSD)		-LQG-			
<i>S. italica</i> (Chr2-CSD)		-LQG-			
<i>S. italica</i> (Chr9-CSD)		-LQG-			
<i>S. bicolor</i> (Chr1-CSD)		-LQG-			
<i>S. bicolor</i> (Chr2-CSD)		-LQG-			
<i>E. guineensis</i> (Chr5-CSD)		-LQA-			
<i>E. guineensis</i> (Chr14-CSD)		-LQA-			
<i>O. thomaeum</i> (001-CSDa)		-LQG-			
<i>O. thomaeum</i> (001-CSDb)		-LQG-			
<i>O. thomaeum</i> (027-CSD)		-LQG-			
<i>Z. mays</i> (B73)(Chr7-CSD)		-RSEH LRMLLFHFPC IGNTI			
<i>Z. mays</i> (B73)(Chr9-CSD)		-LGGA			
<i>Z. mays</i> (PH207)(Chr1-CSD)		-LQG-			
<i>Z. mays</i> (PH207)(Chr7-CSD)		-RSEH LRMLLFHFPC IGNTI			
<i>Z. mays</i> (PH207)(Chr9-CSD)		-LQG-			
<i>C. americanus</i> (Chr5-CSD)	SFFDKLLHLL	IALCYCFCQGS	LDFRAEAESV R-		
<i>C. americanus</i> (Chr7-CSD)		-RQG-			
<i>A. comosus</i> (LG4-CSD)					
<i>A. comosus</i> (LG14-CSD)	AQGSARLVPD	TEESKAKNNN	LLILWNYHCW KTKAYA		
<i>M. acuminata</i> (Chr8-CSD)		-LQE-			
<i>T. aestivum</i> (Ch2A-CSD)		-LQG-			
<i>T. aestivum</i> (Ch2D-CSD)		-LQG-			
<i>S. spontaneum</i> (Chr1B-CSD)		-LQG-			
<i>S. spontaneum</i> (Chr1C-CSD)		-LQG-			
<i>S. spontaneum</i> (Chr1D-CSD)		-LQG-			
<i>S. spontaneum</i> (Chr2C-CSD)		-YSK-			
<i>A. officinalis</i> (V102-CSD)		-LQA-			
<i>A. officinalis</i> (V108-CSD)		-LQA-			
<i>A. officinalis</i> (V103-CSD)		IKAS SPKLTTILYKI	IYIFYLPGNF KLFV-		
<i>Z. japonica</i> (Sca0001-CSD)		-LQG-			
<i>Z. japonica</i> (Sca0003.1-CSD)		-IKEQ T			
<i>H. vulgare</i> (Chr2-CSD)		-LQG-			
<i>H. vulgare</i> (Chr5-CSD)					
<i>H. vulgare</i> (Chr5-CSDb)					
<i>C. sim</i> (Sca247-CSD)		-YLH-		TCDAC	
<i>C. sim</i> (Sca212-CSD)		-TLYR MLFFSYFVLL		TWELHSS	
<i>B. distachyon</i> -CSD		-LQG-			
<i>S. polyrhiza</i> -CSD		-LQA-			
<i>P. glaucum</i> -CSD		-LQG-			
<i>Z. marina</i> -CSD		-LKG-			
<i>D. carota</i> (Chr1-CSD)		-LQG-			
<i>D. carota</i> (Chr9-CSD)		-LQG-			
<i>M. esculanta</i> (Chr8-CSD)		-LQG-			
<i>M. esculanta</i> (Chr9-CSD)		-LQG-			
<i>E. guttata</i> (Sca7-CSD)		-IQG-			
<i>E. guttata</i> (Sca14-CSD)		-LQG-			
<i>C. cajan</i> (LG03-CSDa)		-L-			
<i>C. cajan</i> (LG03-CSDb)		-LQG-			
<i>C. cajan</i> (SC130189-CSD)					
<i>H. bra</i> (NW018746327.1-CSD)		-LQG-			
<i>H. bra</i> (NW018745806.1-CSD)		-LQE-			
<i>H. bra</i> (NW018746407.1-CSD)		-LQG-			
<i>E. grandis</i> (Chr2-CSD)		-LQG-			
<i>E. grandis</i> (Chr8-CSD)		-SMGM ISVSSVFRDE	LPQSTT		
<i>C. melo</i> (Sca3-CSD)		-LQE-			
<i>C. melo</i> (Sca25-CSD)		WSAR LRFVAFVAVS	IEALNPNAI		
<i>C. clementina</i> (Sca5-CSDa)		-LQA-			
<i>C. clementina</i> (Sca5-CSDb)		-IQLN			
<i>B. oleracea</i> (Chr5-CSD)		-LQG-			
<i>B. oleracea</i> (Chr8-CSD)		-LQG-			
<i>A. chinensis</i> (Chr3-CSD)		FHDV YVLFWHRPPL	LLPNCLVL		
<i>A. chinensis</i> (Chr29-CSD)		-LQG-			
<i>V. vinifera</i> (Chr14-CSDa)		-LQG-			
<i>V. vinifera</i> (Chr14-CSDb)		-LQG-			
<i>M. domestica</i> (Bb4037-CSD)		-SARD ELEHYAMDME	FQLSVLSSCK FEGNRASNWF		
<i>M. domestica</i> (Bb6170-CSD)		-VCKD ELEHQAKRHG	VSVKCM -K FL		
<i>T. has</i> (NW_010961290.1-CSD)		-LQG-			
<i>T. has</i> (NW_010966881.1-CSD)		-LQG-			
<i>G. max</i> (Chr3-CSD)		-LQG-			
<i>G. max</i> (Chr19-CSD)		-LQG-			
<i>B. rapa</i> (Chr6-CSD)		-LQG-			
<i>B. rapa</i> (Chr9-CSD)		-LQG-			
<i>N. nucifera</i> (MSc13-CSD)		-LQG-			
<i>N. nucifera</i> (MSc9-CSD)		-LQG-			
<i>C. canephora</i> (Chr2-CSD)		-LQG-			
<i>C. canephora</i> (Chr3-CSD)		-LQG-			
<i>P. trichocarpa</i> (Chr5-CSD)		-LQG-			
<i>P. trichocarpa</i> (Chr13-CSD)		-LQG-			
<i>A. thaliana</i> -CSD		-LQG-			
<i>P. axilleris</i> -CSD		-LQG-			
<i>P. bretschneideri</i> -CSD		-LQG-			
<i>S. lycopersicum</i> -CSD		-LQG-			
<i>M. truncatula</i> -CSD		-LQG-			
<i>V. radiata</i> -CSD		-LQG-			
<i>P. atrosanguinea</i> -CSD		-LQG-			
<i>C. limon</i> -CSD		-LQG-			
<i>C. annum</i> -CSD		-LQG-			
<i>C. aromatica</i> -CSD		-LQG-			
<i>A. trichopoda</i> -CSD		-LQG-			

Supplementary Figure 8: Analysis of domains/important features of the proteins encoded by CuZn SOD (CSD) genes originated due to block/tandem chromosomal duplication events in monocot plant genomes. The duplication events were analyzed at Monocots PLAZA 4.5 database (Bel et al., 2018), while the analysis of conserved domains was carried out at Conserved Domain Database (CDD, <https://www.ncbi.nlm.nih.gov/structure/cdd/>). Following designation for genes is used below for different SOD isoforms; CytCSD: cytosolic CuZn SOD, ChlCSD: chloroplastic CuZn SOD and PerCSD: peroxisomal CuZn SOD. The designation used to indicate genomic locations (chromosome, scaffold, linkage group etc.) are as per the PLAZA database (Chr: chromosome, Sca: Scaffold, MSc: Megasccaffold, LG: Linkage groups etc. Domains, and important amino acids are indicated.

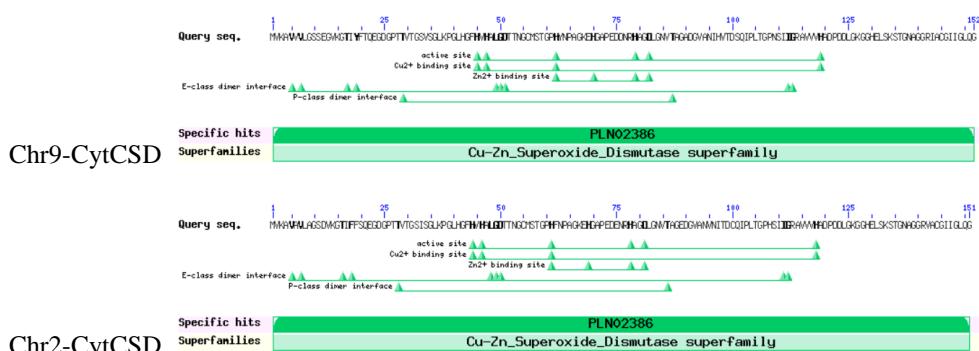
- A) *Oryza sativa*: Domain analysis of two cytosolic CSDs (CytCSDs: OsCSD1, OsCSD4) originated in due to a block duplication event between Chr3 and Chr7



- B) *Oryza brachyantha*: Domain analysis of two cytosolic CSDs (CytCSDs) originated due to a block duplication event between Chr3 and Chr7



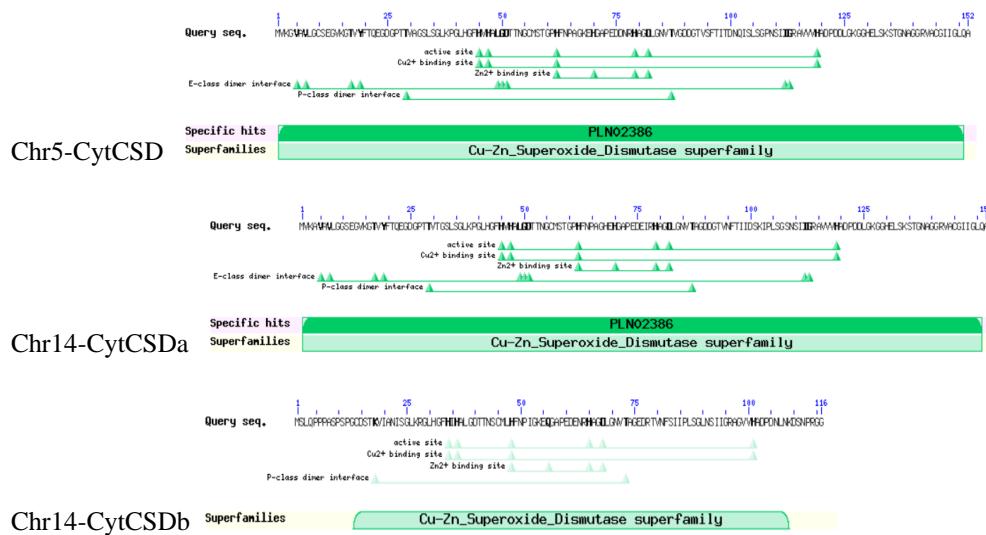
- C) *Setaria italica*: Domain analysis of two cytosolic CSDs (CytCSDs) originated due to a block duplication event between Chr9 and Chr2.



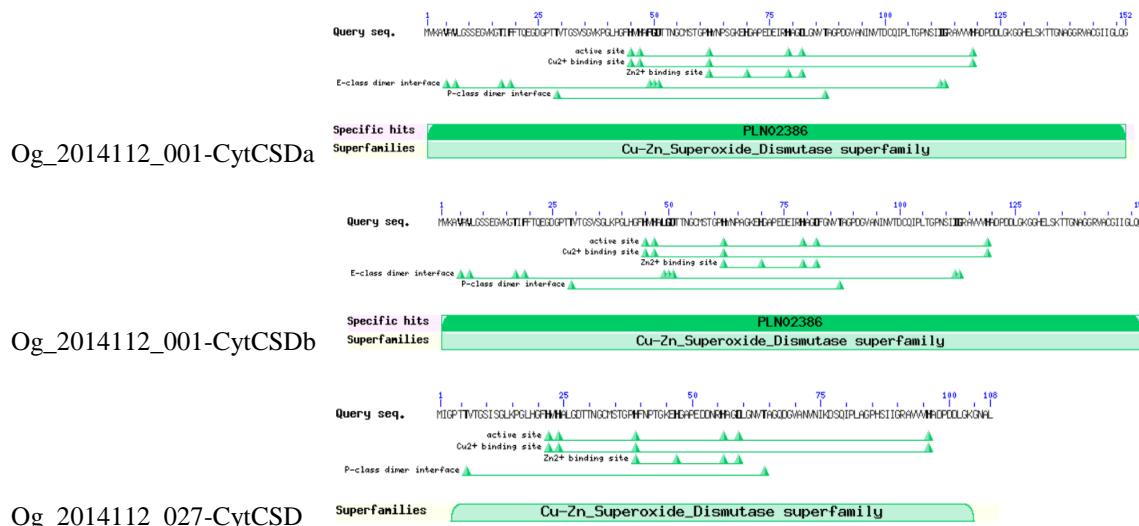
D) *Sorghum bicolor*: Domain analysis of two cytosolic CSDs (CytCSDs) originated due to a block duplication event between Chr1 and Chr2.



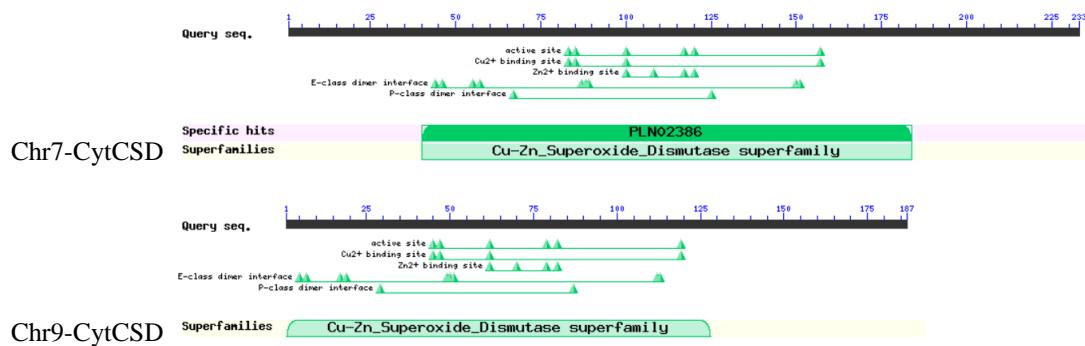
E) *Elaeis guineensis*: Domain analysis of three cytosolic CSDs (CytCSDs) originated due to two block duplication between Chr5 and Chr14.



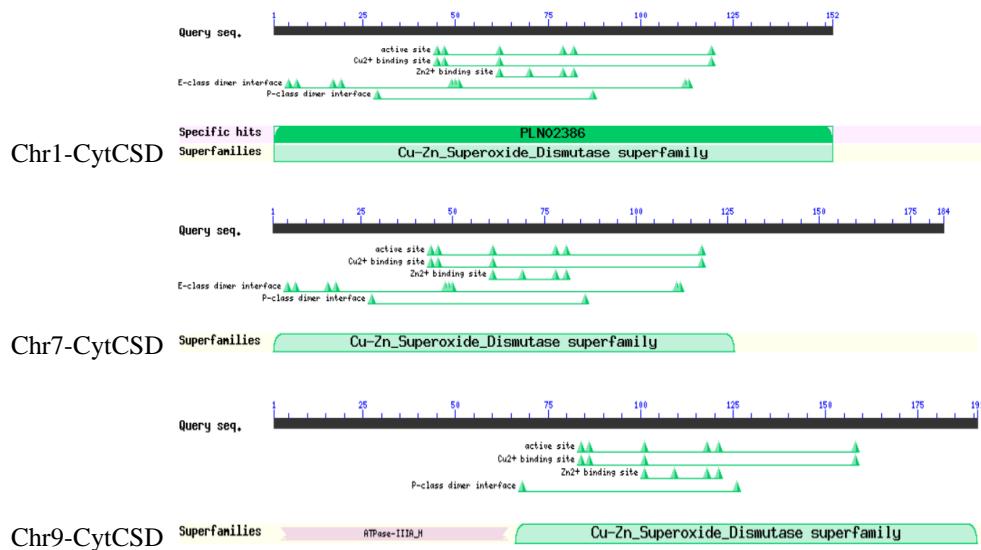
F) *Oropetium thomaeum*: Domain analysis of three cytosolic CSDs (CytCSDs) originated due to a block duplication event between chromosome Og\_2014112\_001 and Og\_2014112\_027, and a tandem duplication event (gene ids: Oropetium\_20150105\_01325 and Oropetium\_20150105\_01319) within chromosome Og\_2014112\_001



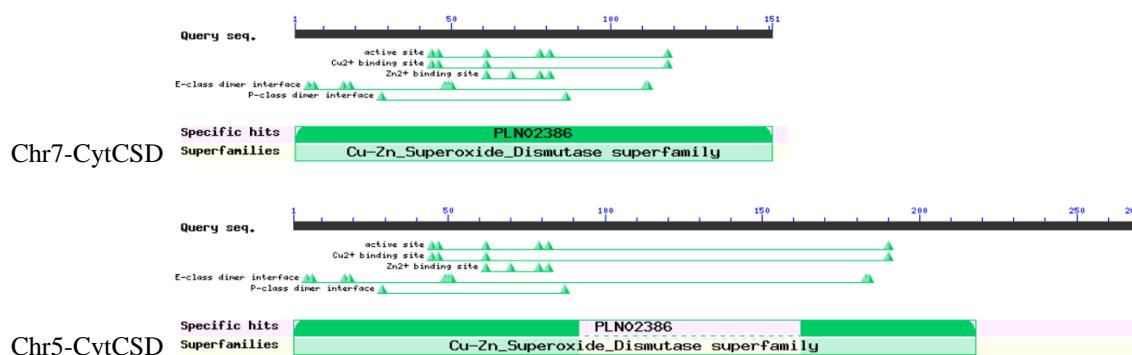
G) *Zea mays* (**B73**): Domain analysis of two cytosolic CSDs (CytCSDs) originated due to a block duplication event between Chr7 and Chr9.



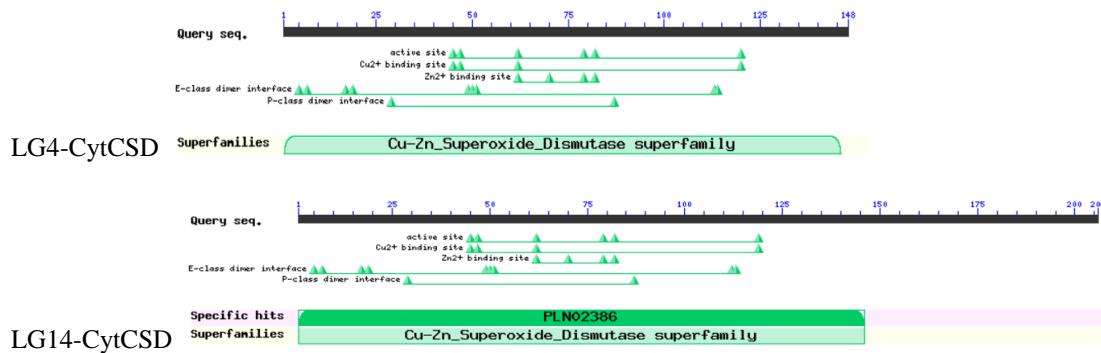
H) *Zea mays* (**PH207**): Domain analysis of three cytosolic CSDs (CytCSDs) originated due to two block duplication events (between Chr1 and Chr9; Chr7 and Chr9).



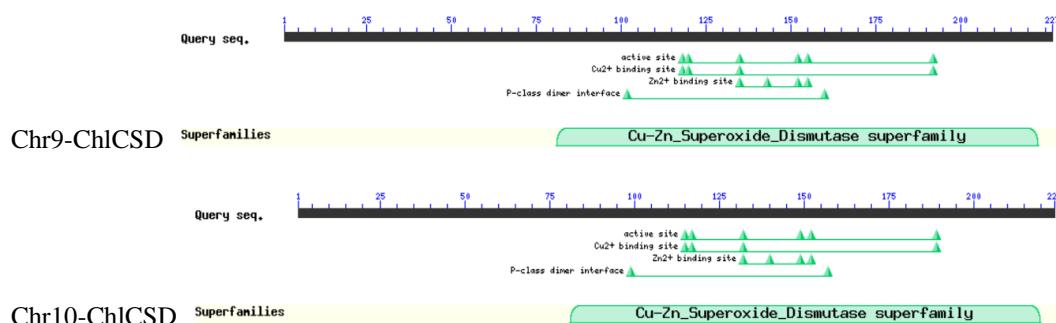
I) *Cenchrus americanus*: Domain analysis of two cytosolic CSDs (CytCSDs) originated due to a block duplication event between Chr7 and Chr5.



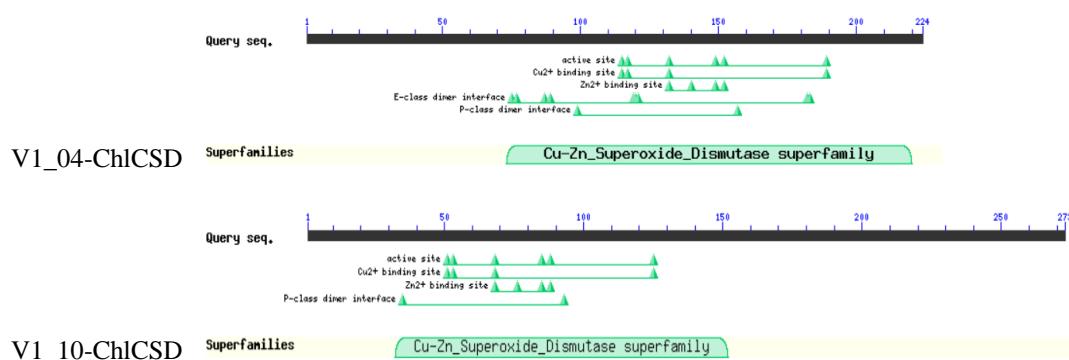
J) *Ananas comosus*: Domain analysis of two cytosolic CSDs (CytCSDs) originated due to a block duplication event between LG4 and LG14.



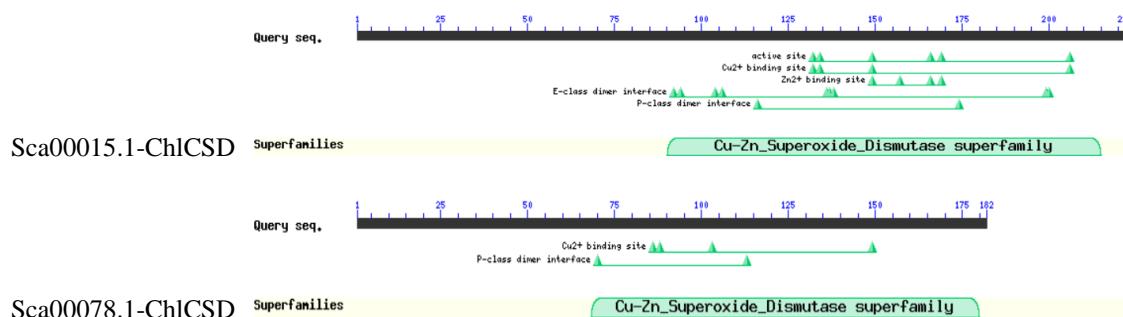
- K) *Musa acuminata*: Domain analysis of two chloroplastic CSDs (ChlCSDs) originated due to a block duplication between Sca00015.1 and Sca00078.1.



- L) *Asparagus officinalis*: Domain analysis of two chloroplastic CSDs (ChlCSDs) originated due to a block duplication between chromosome number V1\_04 and V1\_10.

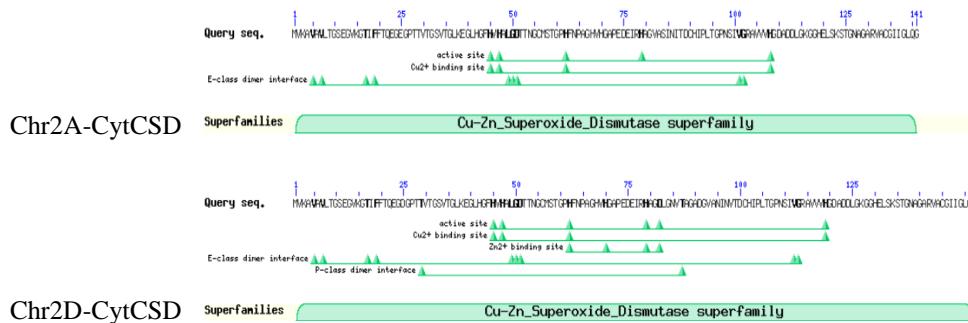


- M) *Zoysia japonica* ssp. *nagirizaki*: Domain analysis of two chloroplastic CSDs (ChlCSDs) originated due to a block duplication event between chromosome number Sca00015.1 and Sca00078.1.

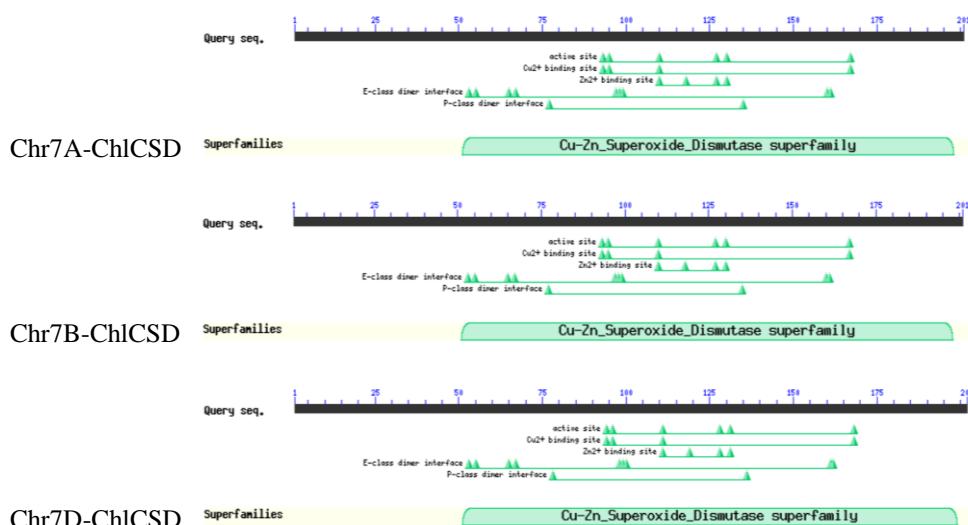


N) *Triticum aestivum*:

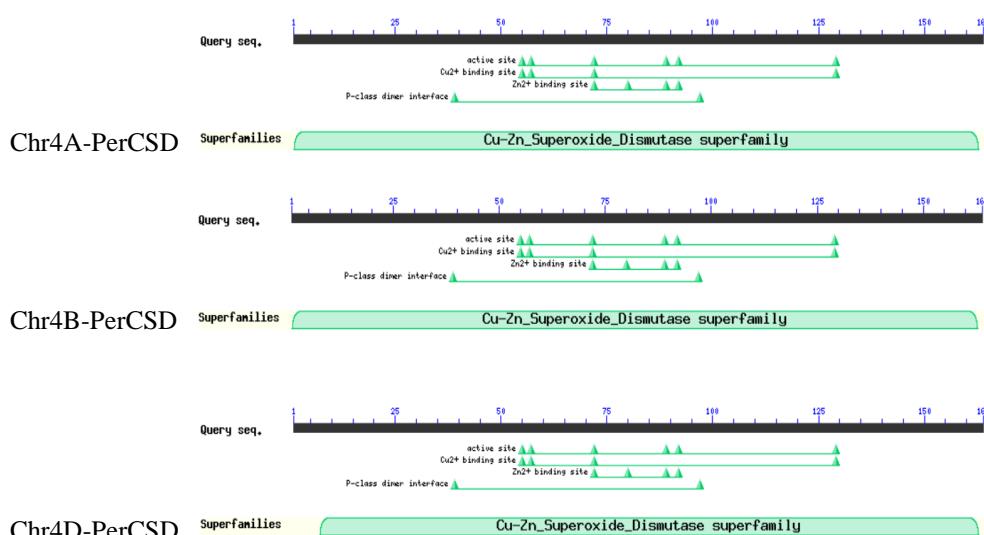
- i) Domain analysis of two cytosolic CSDs (CytCSDs) originated due to a block duplication between chromosome Chr2A and Chr2D.



- ii) Domain analysis of three chloroplastic CSDs (ChlCSDs) originated due to block duplication events between chromosome Chr7A, Chr7B and Chr7D.

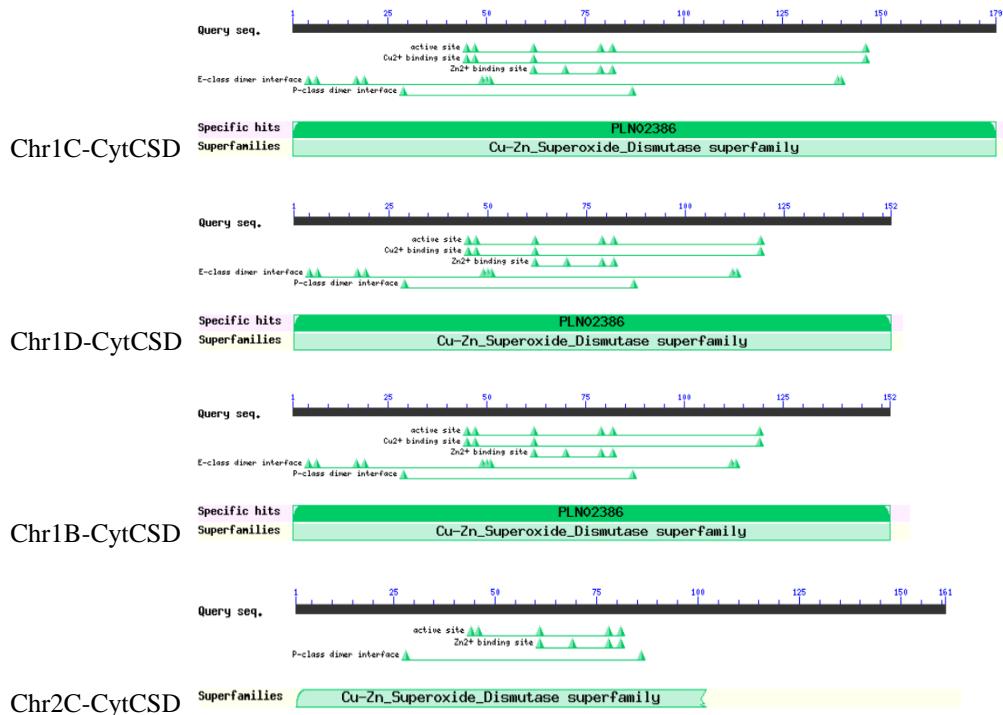


- iii) Domain analysis of three peroxisomal CSDs (PerCSDs) due to block duplication events between chromosome Chr4A, Chr4B and Chr4D.

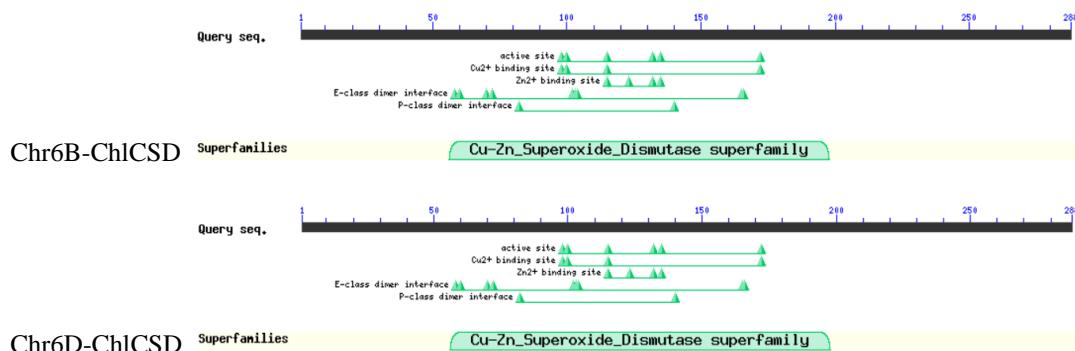


O) *Saccharum spontaneum*:

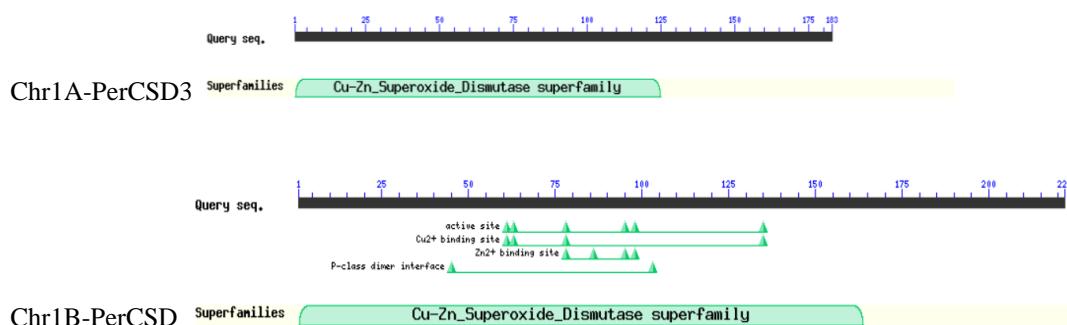
- i) Domain analysis of four cytosolic CSDs (CytCSDs) originated due to block duplication events involving four chromosomes (Chr1B, IC, ID, and 2C).

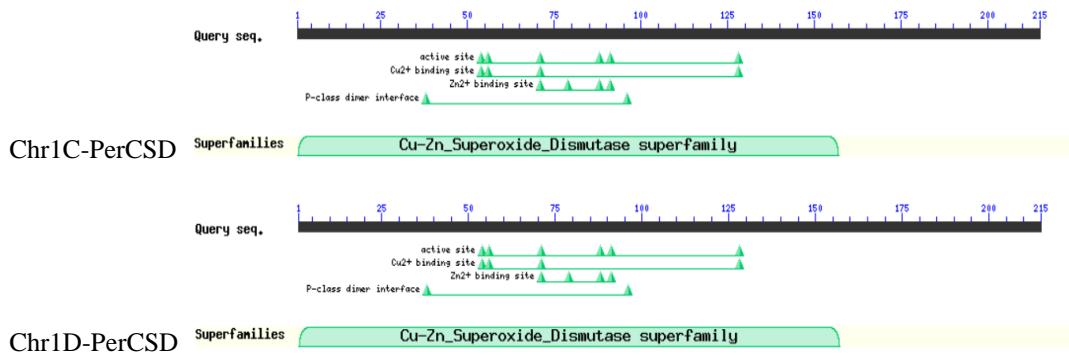


- ii) Domain analysis of two chloroplastic CSDs (ChlCSDs) originated due to a block duplication involving events between Chr6B and Chr6D.

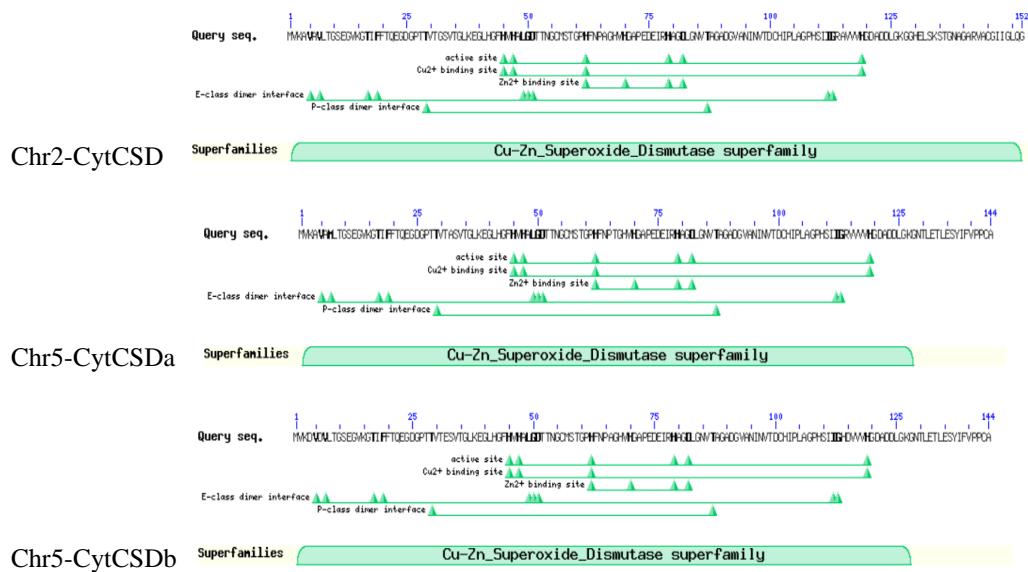


- iii) Domain analysis of four peroxisomal CSDs (PerCSDs) originated due to block duplication events involving four chromosomes (Chr1A, 1B, 1C, and 1D).



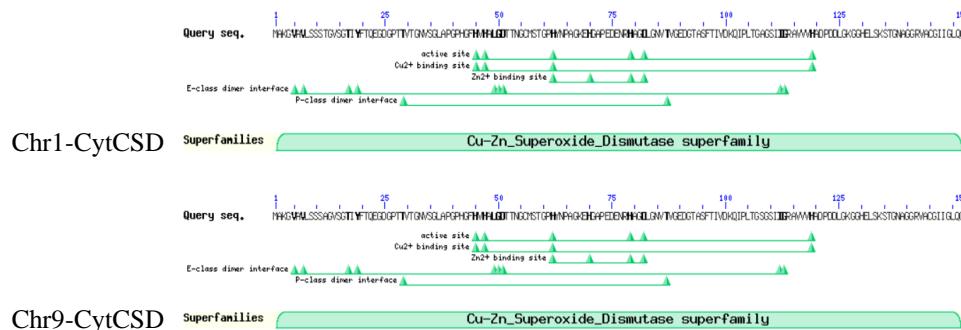


P) *Hordeum vulgare*: Domain analysis of three cytosolic CSDs (CytCSD) present in the genome. No block/tandem duplication events predicted



Supplementary Figure 9: Analysis of domains/important features of the proteins encoded by CuZn SOD (CSD) genes originated due to block/tandem chromosomal duplication events in dicot plant genomes. The duplication events were analyzed at Monocots PLAZA 4.5 database (Bel et al., 2018), while the analysis of conserved domains was carried out at Conserved Domain Database (CDD, <https://www.ncbi.nlm.nih.gov/structure/cdd/>). Following designation for genes is used below for different SOD isoforms; CytCSD: cytosolic CuZn SOD, ChlCSD: chloroplastic CuZn SOD and PerCSD: peroxisomal CuZn SOD. The designation used to indicate genomic locations (chromosome, scaffold, linkage group etc.) are as per the PLAZA database (Chr: chromosome, Sca: Scaffold, MSc: Megascaffold, LG: Linkage groups etc. Domains, and important amino acids are indicated.

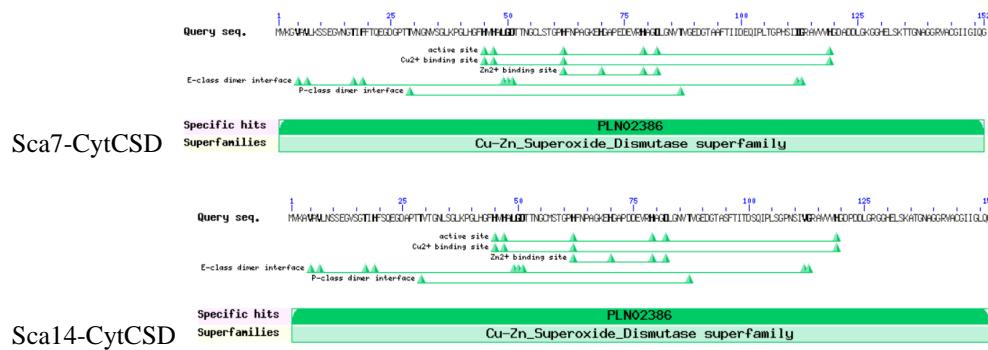
**A) *Daucus carota*:** Domain analysis of two cytosolic CSDs (CytCSDs) originated in due to a block duplication event between Chr1 and Chr9.



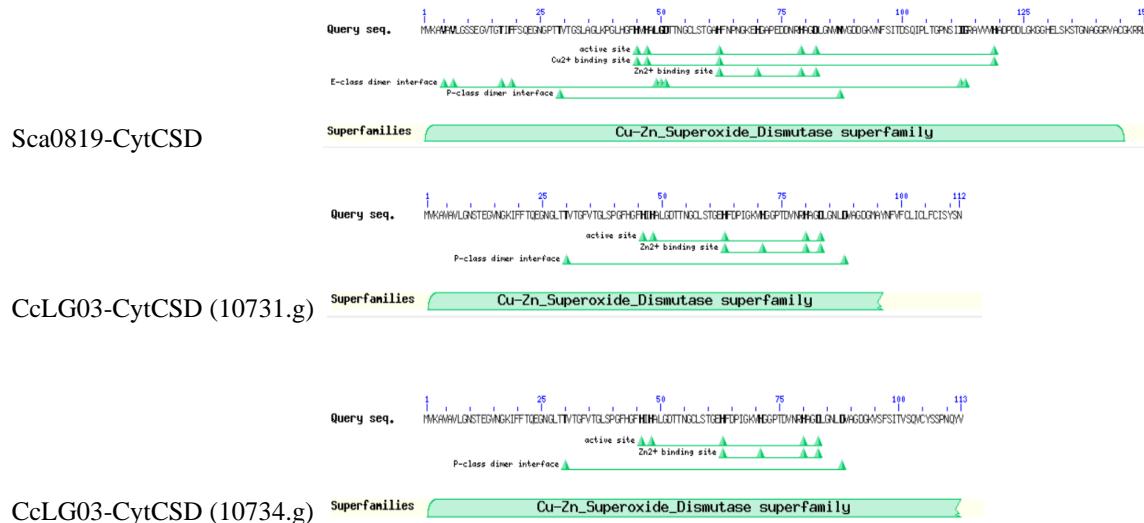
**B) *Manihot esculanta*:** Domain analysis of two cytosolic CSDs (CytCSDs) originated due to a block duplication event between chromosomes Chr8 and Chr9.



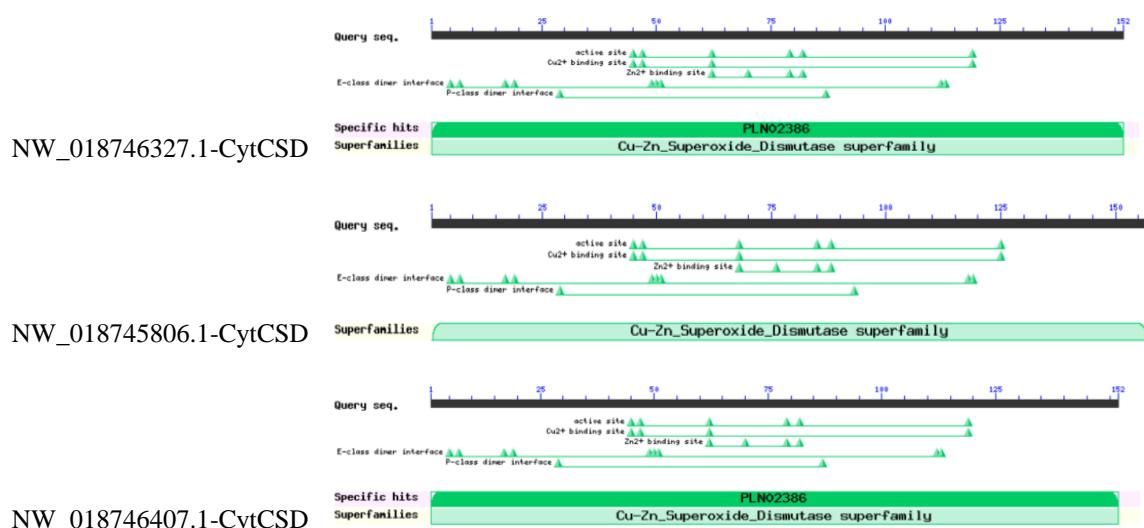
**C) *Erythranthe guttata*:** Domain analysis of two cytosolic CSDs (CytCSDs) originated in due to a block duplication event between chromosome Sca7 and Sca14.



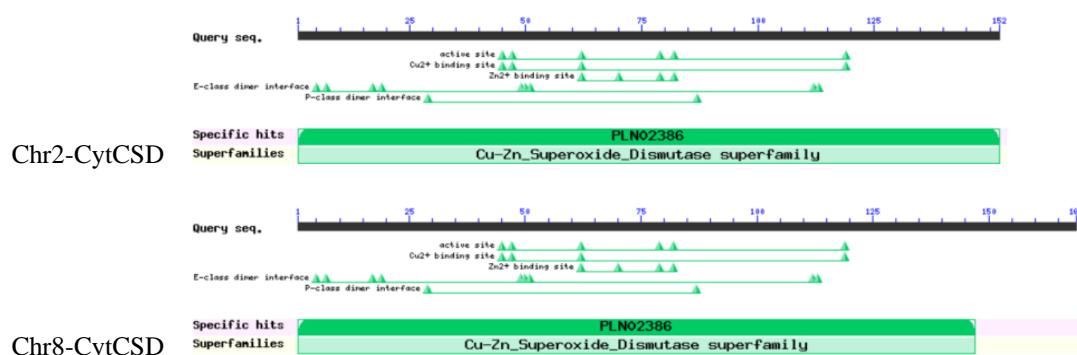
D) *Cajanus cajan*: Domain analysis of two cytosolic CSDs (CytCSDs) originated in due to a tandem duplication event within chromosome CcLG03 (gene ids: 10731.g and 10734.g). Another CytCSD on chromosome Sca0819 (gene id: g.4037.5) does not show evidence of any duplication event.



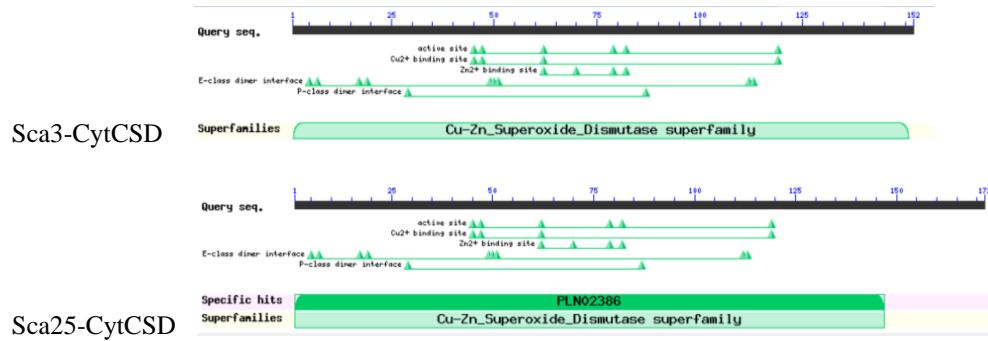
E) *Hevea brasiliensis*: Domain analysis of three cytosolic CSDs (CytCSDs) originated due to a block duplication events between chromosomes NW\_018746327.1, NW\_018745806.1 and NW\_018746407.1



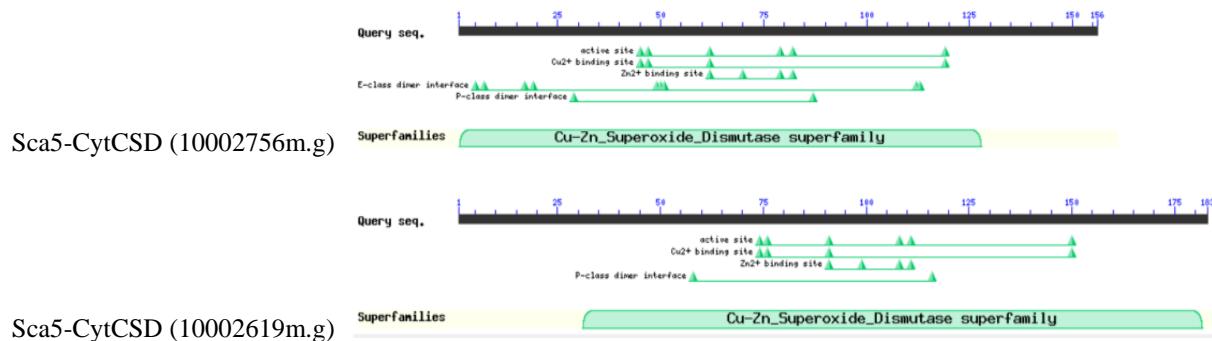
F) *Eucalyptus grandis*: Domain analysis of two cytosolic CSDs (CytCSDs) originated in due to a block duplication event between chromosome Chr2 and Chr8.



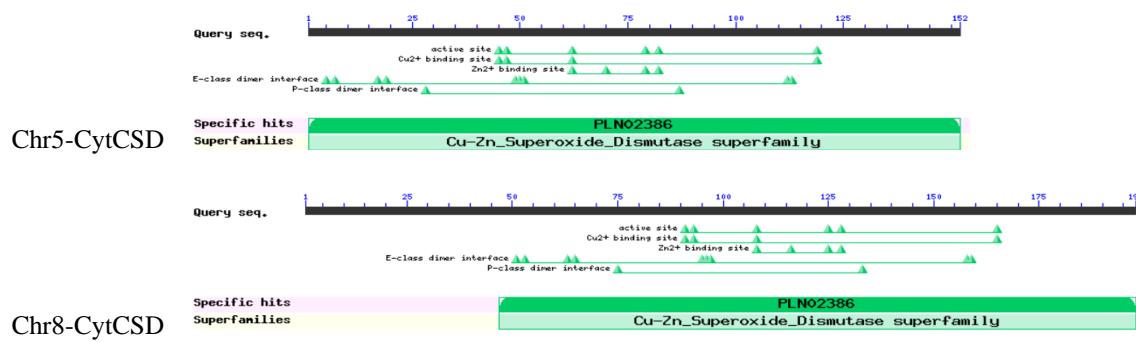
G) *Cucumis melo*: Domain analysis of two cytosolic CSDs (CytCSDs) originated due to a block duplication between chromosomes Sca3and Sca25.



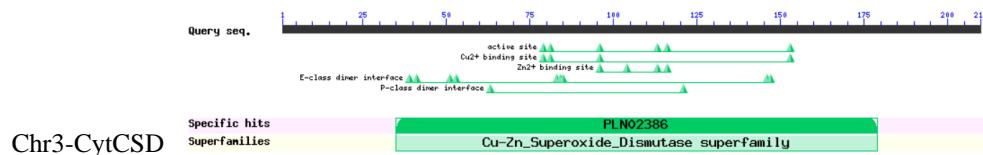
H) *Citrus clementina*: Domain analysis of two cytosolic CSDs (CytCSDs) originated due to a tandem duplication event (gene ids: Ciclev10002756m.g and Ciclev10002619m.g) within chromosome Sca5.

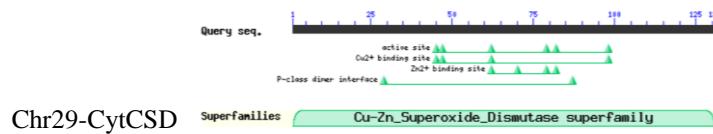


I) *Brassica oleracea*: Domain analysis of two cytosolic CSDs (CytCSDs) originated due to a block duplication event between Chr5 and Chr8.

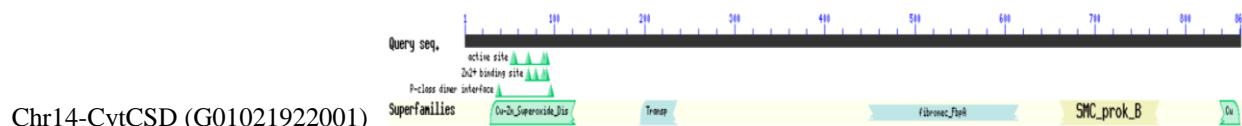
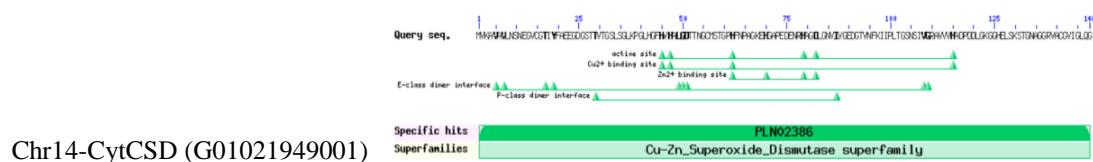
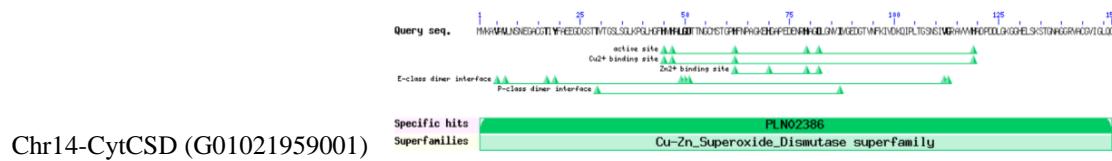


J) *Actinidia chinensis*: Domain analysis of two cytosolic CSDs (CytCSDs) originated in due to a tandem duplication event between Chr3 and Chr29.

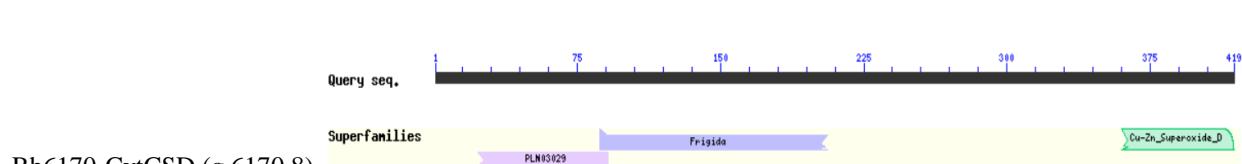
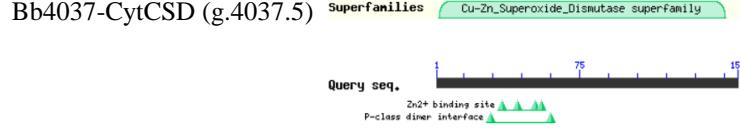
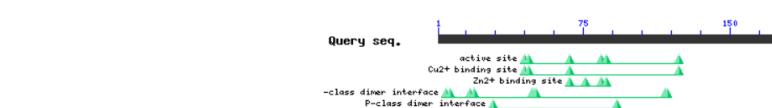




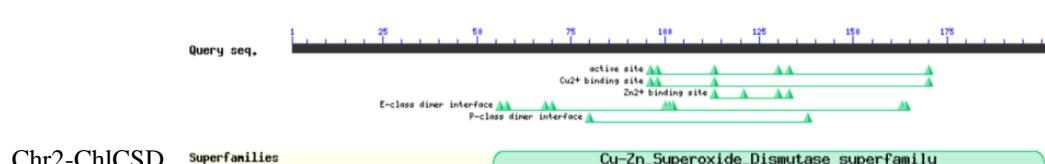
K) *Vitis vinifera*: Domain analysis of three cytosolic CSDs (CytCSDs) originated due to tandem duplication events (gene ids: GSVIVG01021922001, GSVIVG01021949001 and GSVIVG01021959001) within chromosome Chr14.

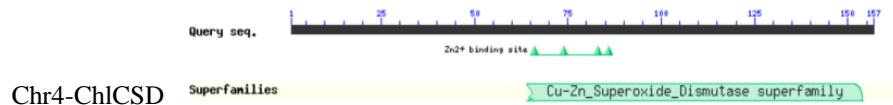


L) *Malus domestica*: Domain analysis of two cytosolic CSDs (CytCSDs) originated in due to a tandem duplication event within chromosome backbone Bb6170 (gene ids: g.6170.7 and g.6170.8). Another CytCSD on chromosome backbone Bb4037 (gene id: g.4037.5) shows no indication of any duplication event.

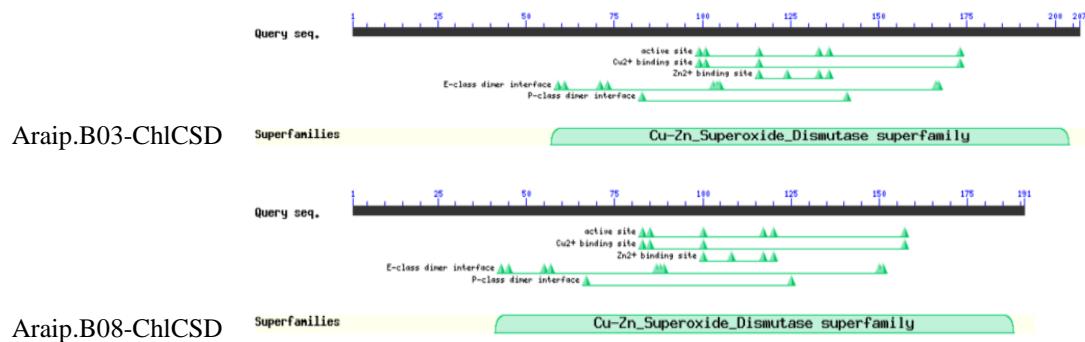


M) *Vigna radiata var. radiata*: Domain analysis of two chloroplastic CSDs (ChlCSD) originated due to a block duplication between chromosome Chr2 and Chr4.



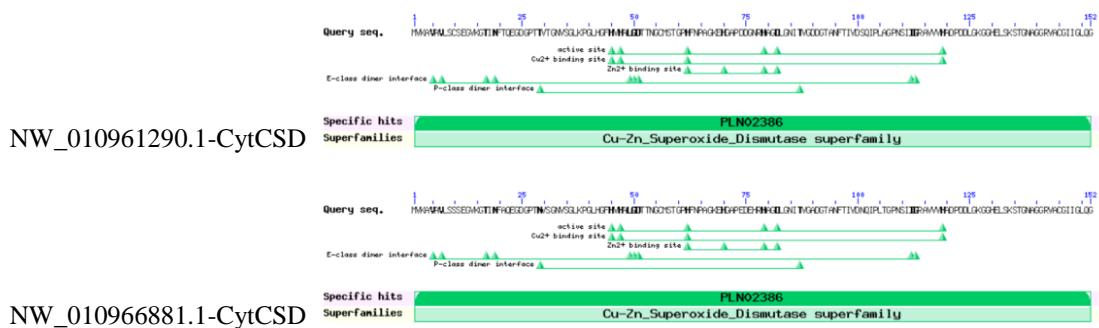


N) *Arachis ipaensis*: Domain analysis of two chloroplastic CSDs (ChlCSDs) originated due to a block duplication event between chromosome Araip.B03 and Araip.B08.

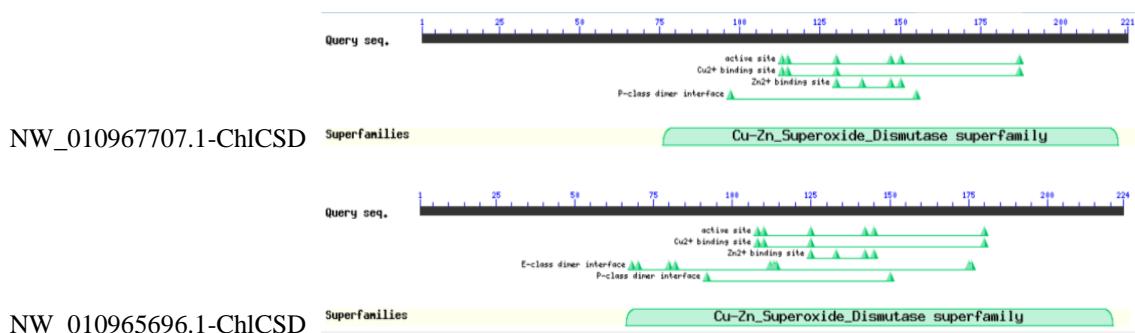


O) *Tarenaya hassleriana*:

- i) Domain analysis of two cytosolic CSDs (CytCSD) originated due to a block duplication event between chromosome NW\_010961290.1 and NW\_010966881.1.

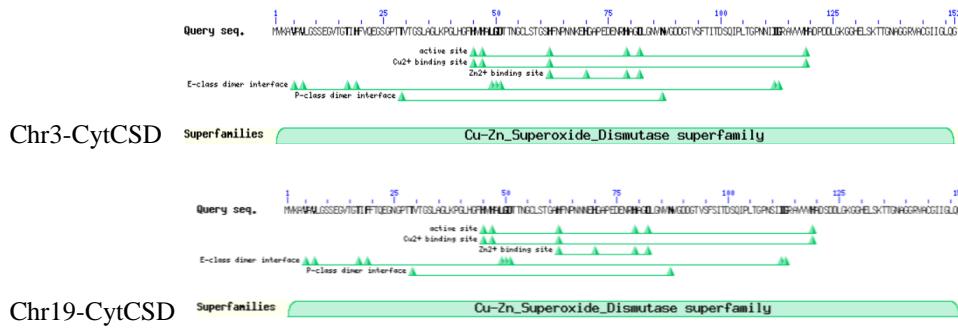


- ii) Domain analysis of two chloroplastic CSDs (ChlCSDs) originated due to a block duplication event between chromosome NW\_010967707.1 and NW\_010965696.1.

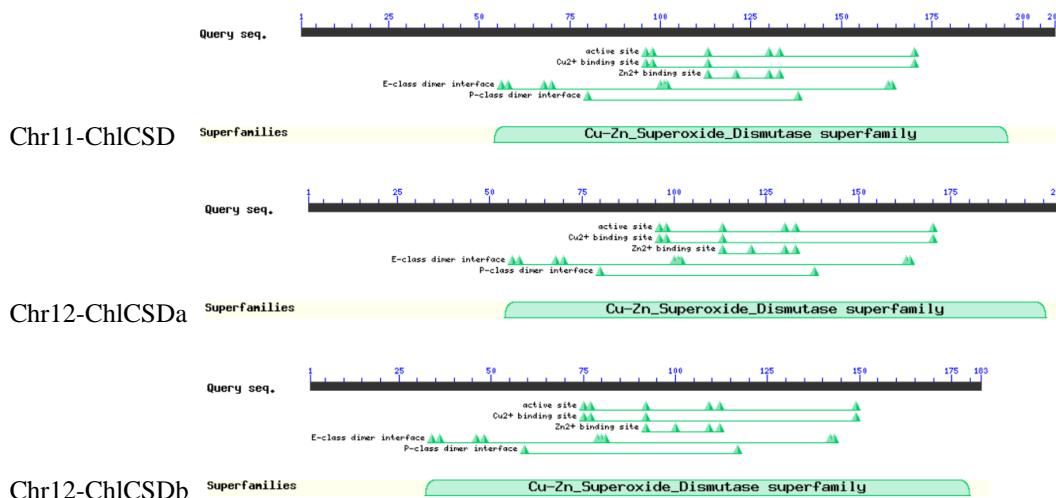


P) *Glycine max*:

- i) Domain analysis of two cytosolic CSDs (CytCSD) originated due to a block duplication event between Chromosome Chr3 and Chr19.

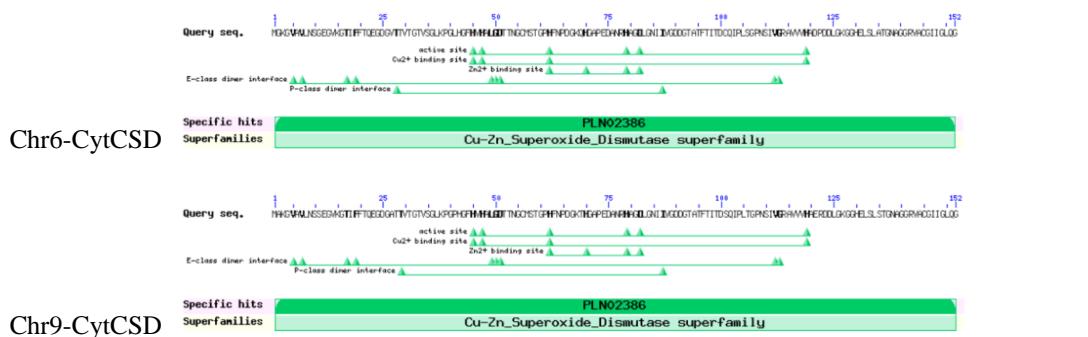


- ii) Domain analysis of three chloroplastic CSDs (ChlCSDs) originated due to two block duplication events between Chromosome Chr11 and Chr12.

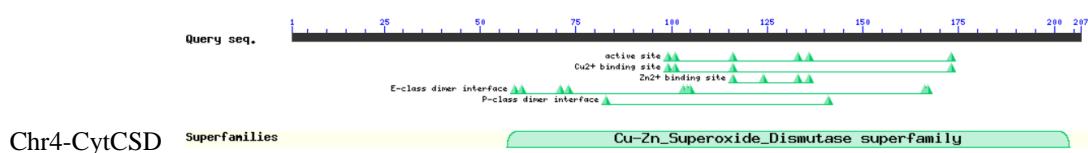


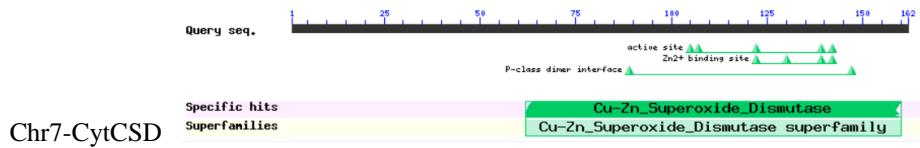
#### Q) *Brassica rapa*:

- i) Domain analysis of two cytosolic CSDs (CytCSDs) originated due to a block duplication event between chromosome Chr6 and Chr9



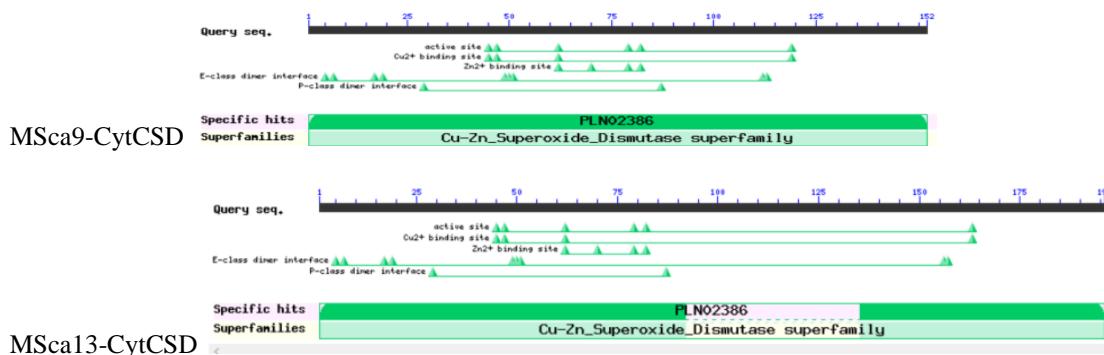
- ii) *Brassica rapa*: Domain analysis of two chloroplastic CSDs (ChlCSDs) originated due to a block duplication event between chromosome Chr4 and Chr7



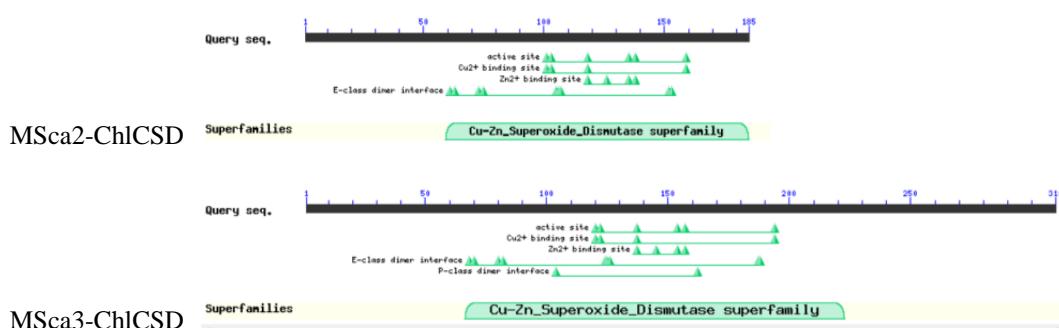


#### R) *Nelumbo nucifera*:

- i) Domain analysis of two cytosolic CSDs (CytCSDs) originated due to a block duplication event between chromosome MSc9 and MSc13.

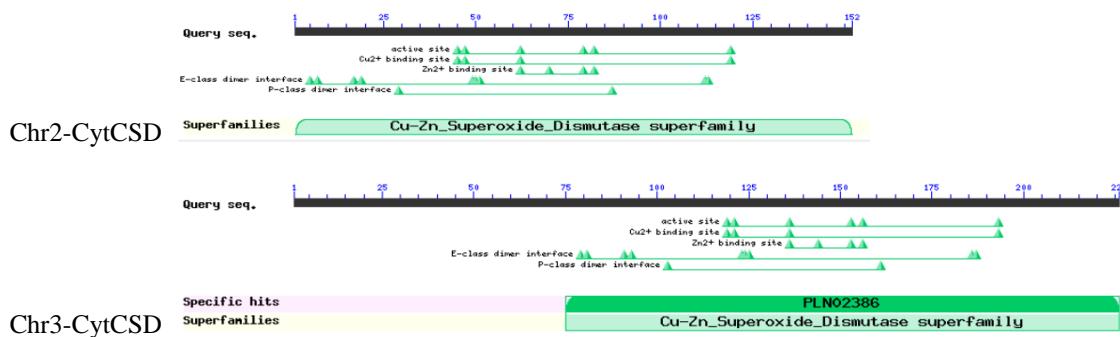


- ii) *Nelumbo nucifera*: Domain analysis of two chloroplastic CSDs (ChlCSDs) originated due to a block duplication event between chromosome MSc2 and MSc3.

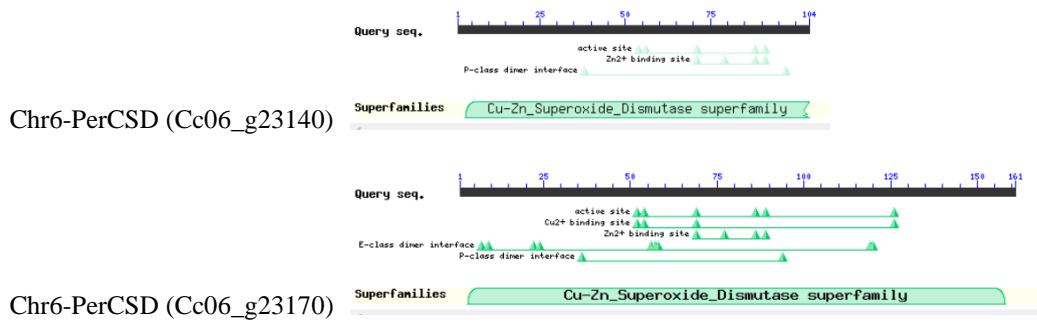


#### S) *Coffea canephora*:

- i) Domain analysis of two cytosolic CSDs (CytCSDs) originated due to a block duplication between Chromosome Chr2 and Chr3.

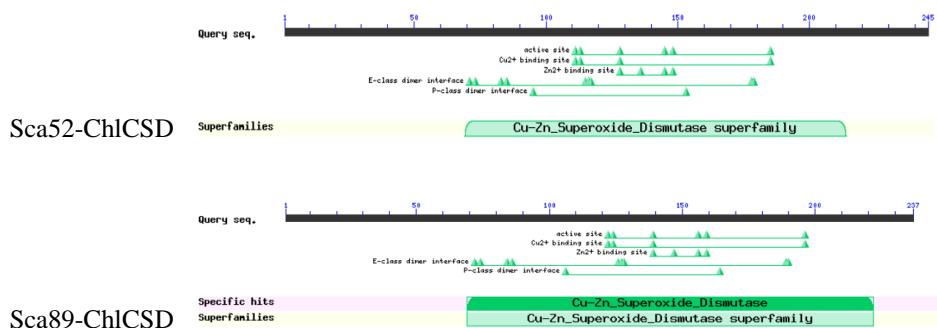


- ii) *Coffea canephora*: Domain analysis of two peroxisomal CSDs (PerCSD) originated due to a tandem duplication event (gene ids: Cc06\_g23140 and Cc06\_g23170) within chromosome Chr6.

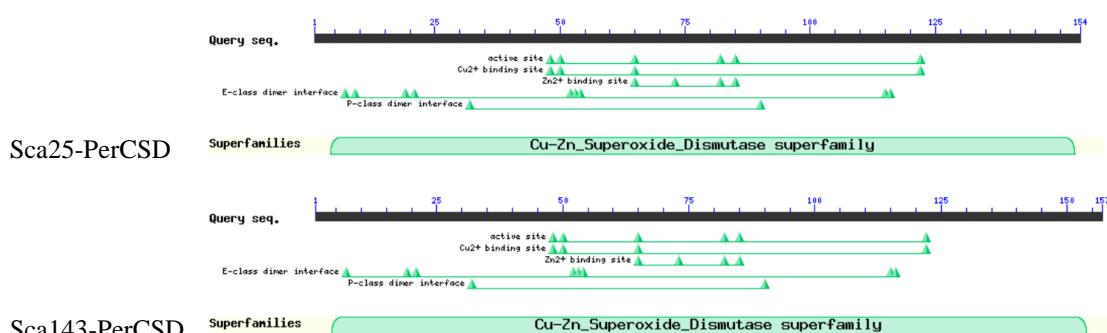


#### T) *Pyrus bretschneideri*:

- i) Domain analysis of two chloroplastic CSDs (ChlCSD) originated due to a block duplication between chromosome Sca52 and Sca89

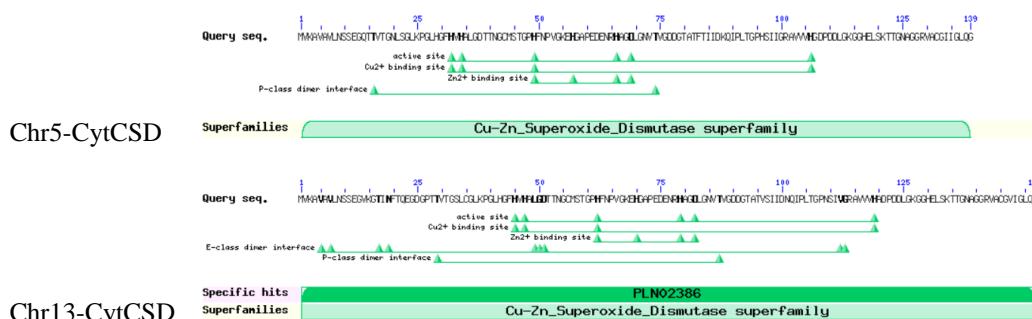


- ii) *Pyrus bretschneideri*: Domain analysis of two peroxisomal CSDs (PerCSD) originated due to a block duplication between chromosome Sca25 and Sca143

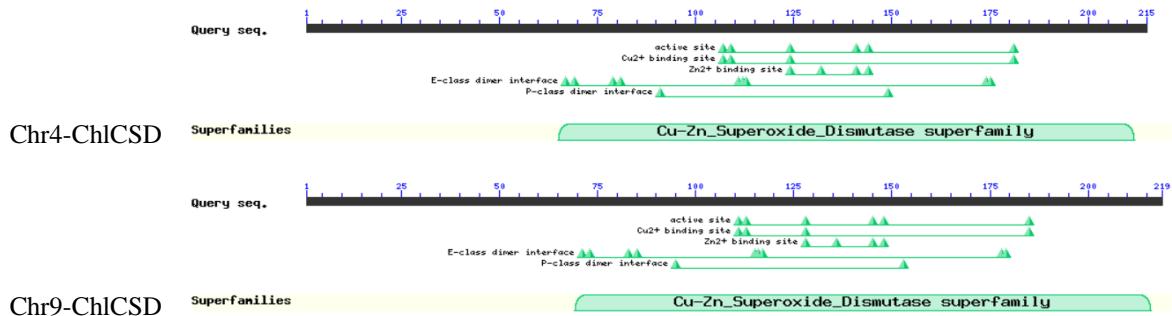


#### U) *Populus trichocarpa*:

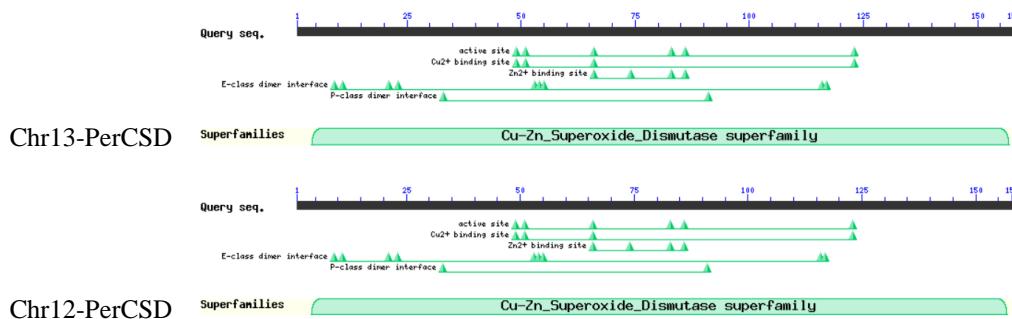
- i) Domain analysis of two cytosolic CSDs (CytCSD) originated due to a block duplication event between chromosome Chr5 and Chr13



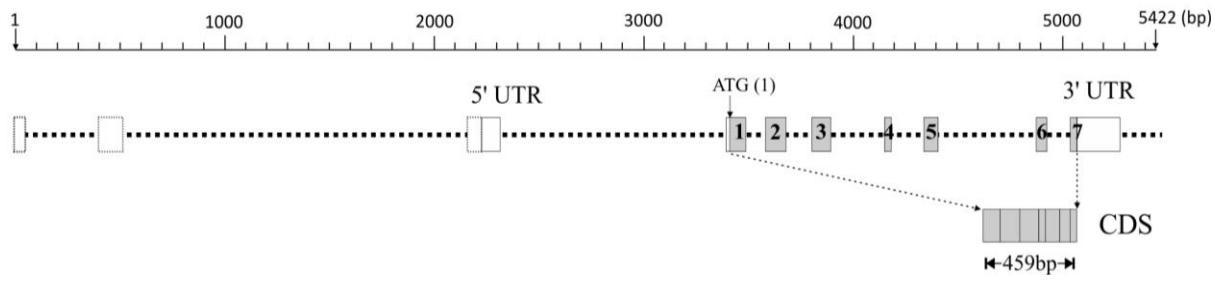
ii) *Populus trichocarpa*: Domain analysis of two chloroplastic CSDs (ChlCSD) originated due to a block duplication event between chromosome Chr4 and Chr9



iii) *Populus trichocarpa*: Domain analysis of two peroxisomal CSDs (PerCSD) originated due to a block duplication event between chromosome Chr13 and Chr19



Supplementary Figure 10: Schematic representation of organization of *OsCSD1* gene structure (locus designation: Os03g351300) as per Rice Annotation Project Database (<https://rapdb.dna.affrc.go.jp>). Scale on the top shows the relative location of exons (grey boxes), introns (dotted line), UTRs (white boxes) across the length of the gene (w.r.t. RGAP predicted *OsCSD1* gene). The position of the ‘ATG’ (in the is shown by a vertical arrow and the exons corresponding to the length of the coding sequence (CDS, 459 bp) is also shown below the gene. For comparison, RGAP predicted exon1, 2 and 3 (not predicted in RAP-DB) are also shown by white boxes with dotted boundary line.



Locus Os03g351500 (*OsCSD1*)