

Supplementary Figure S1 Part of alignments of amino acid sequences of OsCESA4 with similar sequences in other CESA family members of rice and Arabidopsis (**a**) and in different species (**b**).

Dark and gray backgrounds showed the identical and similar residues, respectively. A red arrow indicates the missense mutation P507S in mutant *Bc19*, which is strictly conserved and is only one residue away from the R588G mutation in mutant *Bc6* (black arrow, Kotake et al. 2011).

Accession numbers for these sequences are as follows: *Oryza sativa* OsCESA4

(LOC_Os01g54620, Q5JN63.1), OsCESA1 (LOC_Os05g08370, Q6AT26.1), OsCESA2

(LOC_Os03g59340, Q84M43.1), OsCESA3 (LOC_Os07g24190, Q69V23.1), OsCESA5

(LOC_Os03g62090, Q851L8.1), OsCESA6 (LOC_Os03g62090, Q6YVM4.1), OsCESA7

(LOC_Os10g32980, Q9AV71.1), OsCESA8 (LOC_Os07g10770, Q84ZN6.1), and OsCESA9

(LOC_Os09g25490, Q69P51.1); *Arabidopsis thaliana* AtCESA1 (At4g32410, NP_194967.1),

AtCESA2 (At4g39350, NP_195645.1), AtCESA3 (At5g05170, NP_196136.1), AtCESA4

(At5g44030, Q84JA6.1), AtCESA5 (At5g09870, Q8L778.2), AtCESA6 (At5g64740, Q94JQ6.2),

AtCESA7 (At5g17420, NP_197244.1), AtCESA8 (At4g18780, NP_567564.1), and AtCESA9

(At2g21770, Q9SJ22.1); *Zea mays* (DAA36974.1); *Hordeum vulgare* (AAR29965.1); *Aegilops*

tauschii (EMT23140.1); *Brachypodium distachyon* (XP_003569818.1); *Eucalyptus camaldulensis*

(AEK31215.1); *Populus tomentosa* (AEE60894.1); *Setaria italica* (XP_004969957.1); *Sorghum*

bicolor (XP_002456361.1); and *Triticum aestivum* (CBH32503.1).

Zinc finger

OscESA4 MMESEG.....VPPCAACGDDAHA.....ACRACSYVALCKACLDEDDAECRTTCARGCGGEYGA 52
AtCESA8 MMESEK.....SPICNTCCGEEIGAKSNCEFFVACHCECSFFLCKACLDEDDAECRTTCARGCGGNPY 58
OscESA7 MDTASVTGGEHKK.....EKTQVCGEEVAAREDCKPFVACAECCGFFVCKPQVVEYERSLGTCCPCGNTYRKR 69
AtCESA4 MEFNPTMASFDDDEHRHSSF.....SAKIKVCGDEVKDDDDGQTFVACHVQVYVYVCKPQVVEYERSNGKCCPCGNTLYKR 74
OscESA9 MEASAGLVAGSHNRNELVIRGHEEPKPLRALSGQVCEICGDEVEGRITVDGLFVACNECCGFFVCKPQVVEYERRGTQNPCCKTRYKR 88
AtCESA7 MEASAGLVAGSHNRNELVVITHNEEPKPLKNLDGQVCEICGDDQITGLTVEGLFVACNECCGFFVCKPQVVEYERRGTQNPCCKTRYKR 88

OscESA4 P.DPAHGGCAVVEEVEESHPEAAGVVRERT.....MASQLSDHQDEGVHARTMSTHA.....RTISSVS 112
AtCESA8 ..DENVFDVDTKTSKTQSIVP.....TQTNNTS.QDSGIHAR.....HISTVS 99
OscESA7 HKGCPRVCEDEDDGGMDDFEEFQIKSPTKQ.....KPPHEPVNFDVYSENSEQ.....PAQKWR 125
AtCESA4 HKGSPKIAICDEENN.PDDSDDELNIKRYRQDG.....SSIHQ.NFAYGSENGDYN.....SKQQR 128
OscESA9 LKGSPRVCEDEDED.IDDLEHEFNIDDEKQKQLQDDQDGMQNSHITeamLHGKMSYGRGDDGDGNSTPLPPIITGARSVPVSGEFP 175
AtCESA7 LRGSPRVCEDEDED.IDDLEHEFNIEHEQDK.....HKHSAEAMLYGKMSYGRGPEDDENG..RFPPVIAGG...HSGEFP 159

OscESA4 VGSELNDESCKPIWKNRVESWKEKK.....KEKKASAKK...AAKAQAPPVEEQIMDEKDLTD..AYEPLSRITPI 180
AtCESA8 TIDSELNDEYCNPIWKNRVESWKKDKK.....KSKKKKKDKKATK...AEQDQAQVPTQQHMEIMPNTESGATDVLVSVVPI 175
OscESA7 PGGPALSSFTCSVAGKDLQEREMEGM.....EWKDRIDKWKTKQEKRGKLNRRDSDDDDDKNDDEYMLLAEARQPLWRKVP 204
AtCESA4 PNGRAFSS.TCSVLGKDFEAERDGYTDA.....EWKERVDKWKARQEKRLVTKGEQTNEDKEDDEEYLDABARQPLWRKVP 206
OscESA9 ISNSHGHEGFSSSLHKKRHPYPVSEPGSAKWEKKEVSWKERMDDWKSQ.....GIVAGGAPDDDY..DADVPLNDEARQPLSRKVP 258
AtCESA7 VGGYGNCEHC..LHKRVHPYPSSAEGS.....EGGWRERMDDWKLQH...GNLG...PEPDD..DPEMGLIDBARQPLSRKVP 229

OscESA4 SKNKLTPYRAVILMLRVLVGLFHHYRITNPVYSAFGLWMTSVICEIFWGF SWILDQFPKWCPINRETYVDRILRIARG.DGEDSLGAPV 267
AtCESA8 PRTKITSYRIVILMLRVLVGLFHHYRITNPVYSAYGLWMTSVICEIFWGF SWILDQFPKWCPINRETYVDRILRIARFERGEQSLAAV 263
OscESA7 PSSKLNPRYIVILMLRVLVGLFHHYRITNPVYSAYGLWMTSVICEIFWGF SWILDQFPKWCPINRETYVDRILRIARFERGEQSLAAV 292
AtCESA4 SSKLNPRYIVILMLRVLVGLFHHYRITNPVYSAYGLWMTSVICEIFWGF SWILDQFPKWCPINRETYVDRILRIARFERGEQSLAAV 294
OscESA9 ASSKLNPRYIVILMLRVLVGLFHHYRITNPVYSAYGLWMTSVICEIFWGF SWILDQFPKWCPINRETYVDRILRIARFERGEQSLAAV 346
AtCESA7 ASSKLNPRYIVILMLRVLVGLFHHYRITNPVYSAYGLWMTSVICEIFWGF SWILDQFPKWCPINRETYVDRILRIARFERGEQSLAAV 317

OscESA4 DFFVSTVDPLKEPPLITANTVLSILAVDYPVEKISCYVSDDGASMLIFESLSETAEAFARRWVFPCKKYSIEPRAPPEFYFSOKIDYLD 355
AtCESA8 DFFVSTVDPLKEPPLITANTVLSILAVDYPVEKISCYVSDDGASMLIFESLSETAEAFARRWVFPCKKYSIEPRAPPEFYFSOKIDYLRD 351
OscESA7 DFFVSTVDPLKEPPLITANTVLSILAVDYPVEKISCYVSDDGASMLIFESLSETAEAFARRWVFPCKKYSIEPRAPPEFYFSOKIDYLD 350
AtCESA4 DFFVSTVDPLKEPPLITANTVLSILAVDYPVEKISCYVSDDGASMLIFESLSETAEAFARRWVFPCKKYSIEPRAPPEFYFSOKIDYLD 382
OscESA9 DFFVSTVDPLKEPPLITANTVLSILAVDYPVEKISCYVSDDGASMLIFESLSETAEAFARRWVFPCKKYSIEPRAPPEFYFSOKIDYLD 434
AtCESA7 DFFVSTVDPLKEPPLITANTVLSILAVDYPVEKISCYVSDDGASMLIFESLSETAEAFARRWVFPCKKYSIEPRAPPEFYFSOKIDYLD 405

P-PCR

OscESA4 KIHFSFVKERRAMKRYEYEFKVRINALVAKAQRTPBEGWIMQDGTTPWPGNTRDHPGMIQVFLGEGARDFDGNELPRLVYVSRKRP 443
AtCESA8 KIHFSFVKERRAMKRYEYEFKVRINALVAKAQRTPBEGWIMQDGTTPWPGNTRDHPGMIQVFLGEGARDFDGNELPRLVYVSRKRP 439
OscESA7 KIHFSFVKERRAMKRYEYEFKVRINALVAKAQRTPBEGWIMQDGTTPWPGNTRDHPGMIQVFLGEGARDFDGNELPRLVYVSRKRP 468
AtCESA4 KIHFSFVKERRAMKRYEYEFKVRINALVAKAQRTPBEGWIMQDGTTPWPGNTRDHPGMIQVFLGEGARDFDGNELPRLVYVSRKRP 470
OscESA9 KIHFSFVKERRAMKRYEYEFKVRINALVAKAQRTPBEGWIMQDGTTPWPGNTRDHPGMIQVFLGEGARDFDGNELPRLVYVSRKRP 522
AtCESA7 KIHFSFVKERRAMKRYEYEFKVRINALVAKAQRTPBEGWIMQDGTTPWPGNTRDHPGMIQVFLGEGARDFDGNELPRLVYVSRKRP 493

OscESA4 GYQHKKAGAMNLRVSAVLTNAPFLNLDGDHYVNNKSAIREAMCFMMDPQVGRVVCYVQFPQRFDFGIDRSDRYANRNIVFFDINM 531
AtCESA8 GYQHKKAGAMNLRVSAVLTNAPFLNLDGDHYVNNKSAIREAMCFMMDPQVGRVVCYVQFPQRFDFGIDRSDRYANRNIVFFDINM 527
OscESA7 GYQHKKAGAMNLRVSAVLTNAPFLNLDGDHYVNNKSAIREAMCFMMDPQVGRVVCYVQFPQRFDFGIDRSDRYANRNIVFFDINM 556
AtCESA4 GYQHKKAGAMNLRVSAVLTNAPFLNLDGDHYVNNKSAIREAMCFMMDPQVGRVVCYVQFPQRFDFGIDRSDRYANRNIVFFDINM 558
OscESA9 GYQHKKAGAMNLRVSAVLTNAPFLNLDGDHYVNNKSAIREAMCFMMDPQVGRVVCYVQFPQRFDFGIDRSDRYANRNIVFFDINM 610
AtCESA7 GYQHKKAGAMNLRVSAVLTNAPFLNLDGDHYVNNKSAIREAMCFMMDPQVGRVVCYVQFPQRFDFGIDRSDRYANRNIVFFDINM 581

C-SR

OscESA4 KGLDGLQGPVYVGTGCFYRQALYGYPPSLP.ALKPKSSVCSW..CCCCPKKKAEKSEKEMHRD..... 593
AtCESA8 KGLDGLQGPVYVGTGCFYRQALYGYPPSKPRILPQSSSSS...CCCLTKKKQPQDPAEITYKD..... 588
OscESA7 KGLDGLQGPVYVGTGCFYRQALYGYDPPRPE.KRKPMTCDPWSWCCCCCGGGRKGRKSHKKNKGGGGGEGGLDEPRRGLLGFYK 643
AtCESA4 KGLDGLQGPVYVGTGCFYRQALYGYPPVSE.KRKPMTCDPWSWCCCCCGGNRHKSDSSKK.....KSGIKSLFS 631
OscESA9 KGLDGLQGPVYVGTGCFYRQALYGYPPKGP.KRKPMTV...CDCCPCFGR...KRRK..... 662
AtCESA7 KGLDGLQGPVYVGTGCFYRQALYGYPPKGP.KRKPMTS...CCGCPCFGR...KNNK..... 635

OscESA4 ..SRREDLESAIFNLREIDN.....YDEYERSMLISQMSFEKSFGLSSVFLBSTLMENGGVFE..SANFSTLI 657
AtCESA8 ..AKREEDLDAIFNLGLDNL.....YDEYDRSMLISQTSFBRFGSTVFLBSTLMENGGVFE..SVNFTLI 652
OscESA7 KRKSKDKLGGGAASLAGGKGYRKHQRGFELEEIEEGLEGVYDELESSLMSQKSFERRFGSPVFLASTVEDGGLQGAADAAAL 731
AtCESA4 KLKHKTKKSDDKTMSYSRKRSTTEAIFDLEDIEEGLEGVYDELESSLMSQKSFERRFGSPVFLASTVEDGGLQGAADAAAL 717
OscESA9 ..HGKDGPEVAADGG.....MDSKEMLSQMNFEKRGSAAFVSTLMBEGGVFP..SSSPAAAL 722
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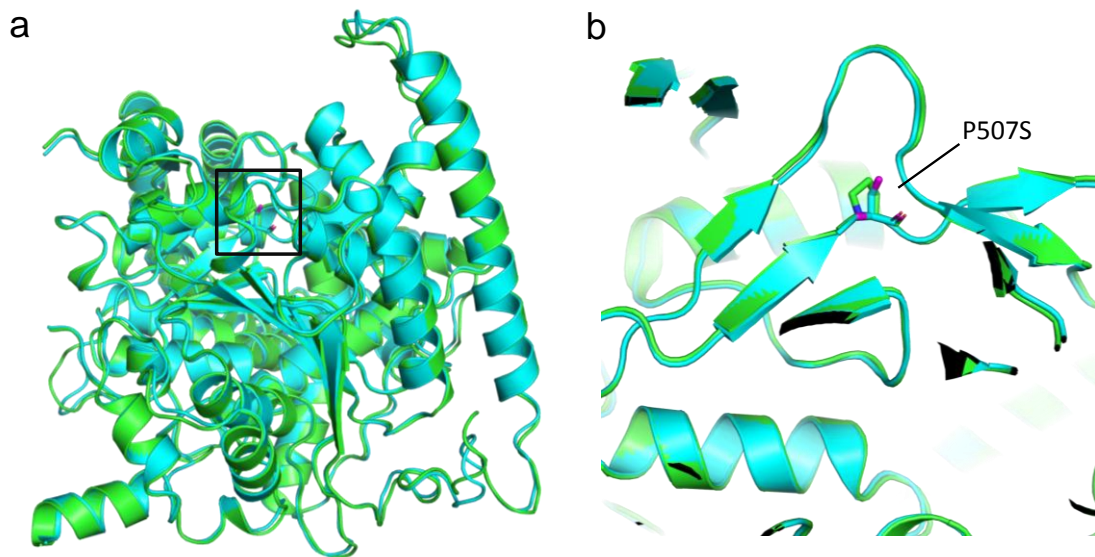
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OscESA7 KEATHVISCYGEKTEWCKEIGWIYGSVTEIDLTGFKMHCGRWRSIYCMPIRPAFAAFKGSAPINLSDRLQVLRWALGSVEIFLSRHCP 819
AtCESA4 KEATHVISCYGEKTEWCKEIGWIYGSVTEIDLTGFKMHCGRWRSIYCMPIRPAFKGSAPINLSDRLQVLRWALGSVEIFLSRHCP 805
OscESA9 KEATHVISCYGEKTEWCKEIGWIYGSVTEIDLTGFKMHCGRWRSIYCMPIRPAFAAFKGSAPINLSDRLQVLRWALGSVEIFLSRHCP 810
AtCESA7 KEATHVISCYGEKTEWCKEIGWIYGSVTEIDLTGFKMHCGRWRSIYCMPIRPAFKGSAPINLSDRLQVLRWALGSVEIFLSRHCP 783

OscESA4 WYGYGGRKLVLRSLYNTIVYPPFTSPLIAYCCLPAICLLTGKFIPTLSNAITWFLGLFSTIATVLELRWSGVLGTEWWRNE 833
AtCESA8 WYGCSSGRLKLVLRSLYNTIVYPPFTSPLIAYCCLPAICLLTGKFIPTLSNLASMLFLGLFSTIATVLELRWSGVLGTEWWRNE 828
OscESA7 WYAYG.GRLKVLREYANTIVYPPFTSPLIAYCCLPAICLLTGKFIPTLNNLASIWFIALFSTIATVLELRWSGVLGTEWWRNE 906
AtCESA4 WYAWG.GRLKVLREYANTIVYPPFTSPLIAYCCLPAICLLTGKFIPTLNNFASLWFLAFSTIATVLELRWSGVLGTEWWRNE 892
OscESA9 WYGYKNGRLKVLREYANTIVYPPFTSPLIAYCCLPAICLLTGKFIPTLSTFASLFFIALFSTIATVLELRWSGVLGTEWWRNE 898
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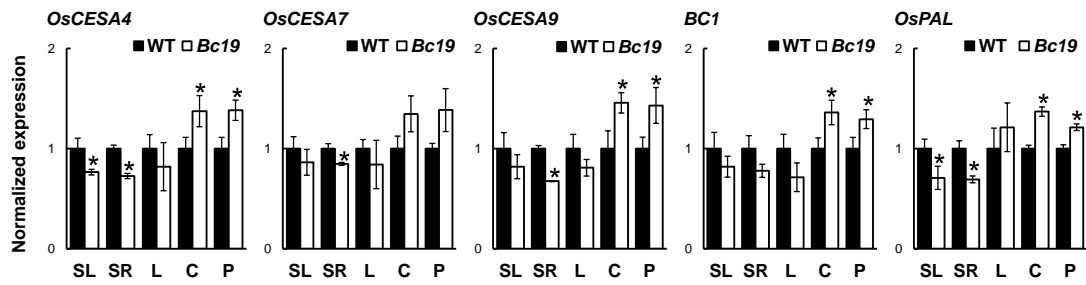
OscESA4 QFWVIGGSAHLFAVQCGLKMLAGLDNFTVTSKAT..DDTEFGELYVFKWTTLLIPPTSLIILNIVGVVAGSDAANNGYESWGPI 919
AtCESA8 QFWVIGGSAHLFAVQCGLKMLAGLDNFTVTSKATA..DDLTEFGELYVFKWTTLLIPPTSLIILNIVGVVAGSDAANNGYEAWGPI 914
OscESA7 QFWVIGGSAHLFAVQCGLKMLAGLDNFTVTSKAAADETDAFEGELYVFKWTTLLIPPTSLIILNIVGVVAGSDAANNGYESWGPI 994
AtCESA4 QFWVIGGSAHLFAVQCGLKMLAGLDNFTVTSKGADEADFDGLYVFKWTTLLIPPTSLIILNIVGVVAGSDAANNGYESWGPI 980
OscESA9 QFWVIGGSAHLFAVQCGLKMLAGLDNFTVTSKATGEDDEDEALYVFKWTTLLIPPTSLIILNIVGVVAGSDAANNGYEAWGPI 986
AtCESA7 QFWVIGGSAHLFAVQCGLKMLAGLDNFTVTSKAT..DDDDTEFGELYVFKWTTLLIPPTSLIILNIVGVVAGSDAANNGYESWGPI 957

OscESA4 FGKVPFAFWVILHLYPFLKGLMGRQNRTPITVILWSILLASVLSLWVRIDPFIKSGSETTTTNS.CANFD 988
AtCESA8 FGKVPFAFWVILHLYPFLKGLMGRQNRTPITVILWSILLASVLSLWVRIDPFIKSGIDTTSLSLNCLLID 984
OscESA7 FGKVPFAFWVILHLYPFLKGLMGRQNRTPITVILWSILLASVLSLWVRIDPFIKPKGVPVKP..CGVS 1062
AtCESA4 FGKVPFAFWVILHLYPFLKGLMGRQNRTPITVILWSILLASVLSLWVRIDPFLPKQTGPLLQK..CGVD 1048
OscESA9 FGKVPFAFWVILHLYPFLKGLMGRQNRTPITVILWSILLASVLSLWVRIDPFIKARGPDVRQ..CGTN 1054
AtCESA7 FGKVPFAFWVILHLYPFLKGLMGRQNRTPITVILWSILLASVLSLWVRIDPFLKTKGPDTSK..CGIN 1025

Supplementary Figure S2 Alignment of amino acid sequences of three main kinds of CESAs in rice and Arabidopsis. Dark and gray backgrounds showed the identical and similar residues, respectively. The Zink finger domain, Plant-Conserved Region (P-CR) and Class-Specific Region (C-SR) are overlined in blue, green, and yellow, respectively, and inverted triangles point out the D,D,D,QXXRW motif. A red arrow indicates the missense mutation P507S in mutant *Bc19*, which is strictly conserved and is only one residue away from the R588G mutation in mutant *Bc6* (black arrow, Kotake et al. 2011). GenBank accession numbers for these sequences are as Supplementary Fig. S1.



Supplementary Figure S3 Predicted three dimensional (3D) structures of OsCESA4 and Bc19 (OsCESA4^{P507S}) proteins. **a** Alignment of the wild type OsCESA4 (green) and the P507S mutated Bc19 (OsCESA4^{P507S}, blue). **b** The magnified section of **a**, showing the P507S mutation between two β -pleated sheets (thick arrow).



Supplementary Figure S4 Comparison of *OsCESAs*, *BC1* and *OsPAL* mRNAs between WT and *Bc19* mutant. Total RNA was isolated from seedling leaves (SL), seedling roots (SR), leaves and culms from plants two weeks after heading (L and C), young panicles (P). The rice *Actin1* was used as a control. Values represent averages of three independent replicates. Vertical bars show standard errors. The expression data of WT were all set to 1.0 and those of *Bc19* were adjusted accordingly. Asterisks signify statistically significant differences compared to WT at $P < 0.05$.