

Fig. S1. Positional cloning and complementation test of *RAE2*.

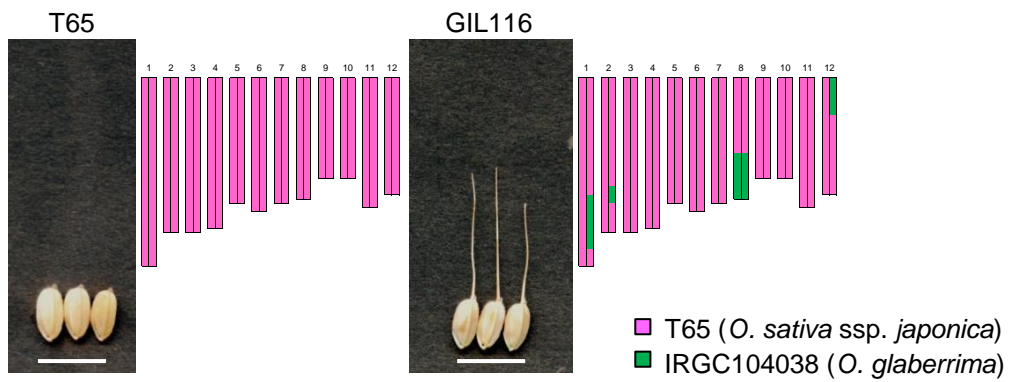
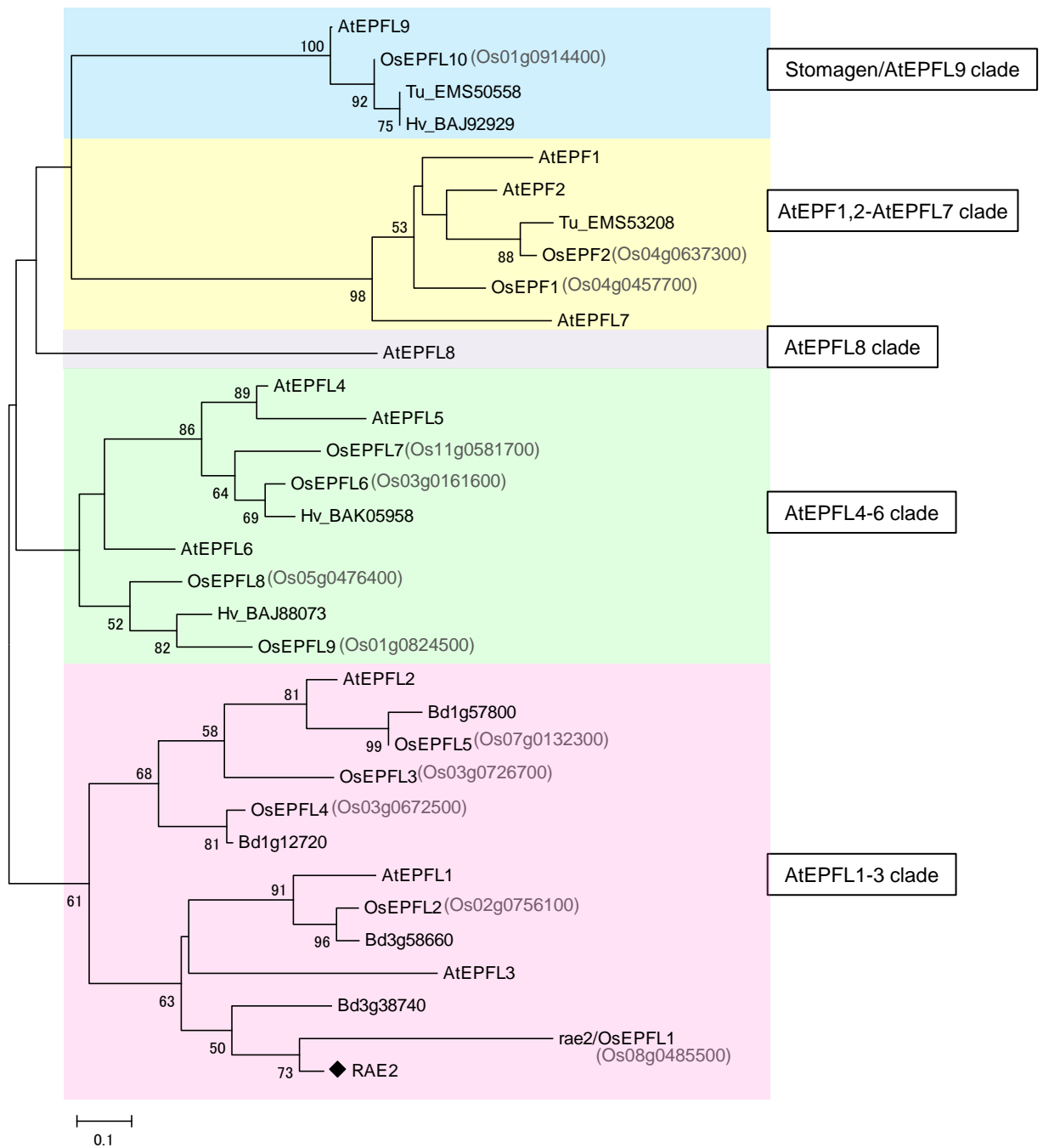


Fig. S2. Seed phenotype and graphical genotype of Taichung65 (T65) and the chromosome segment substitution line, GIL116.

A



B

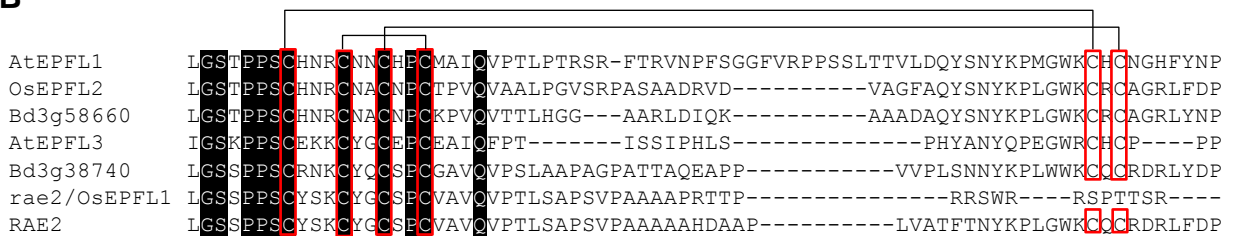


Fig. S3. Phylogenetic tree of EPF/EPFL family genes and comparison of the sequences in cysteine-rich region.

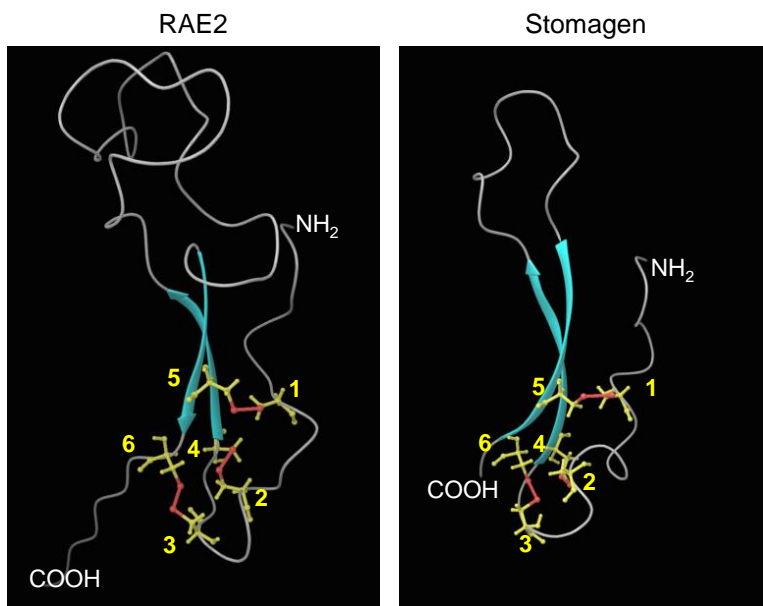


Fig. S4. Predicted 3-D structure of RAE2 and Stomagen.

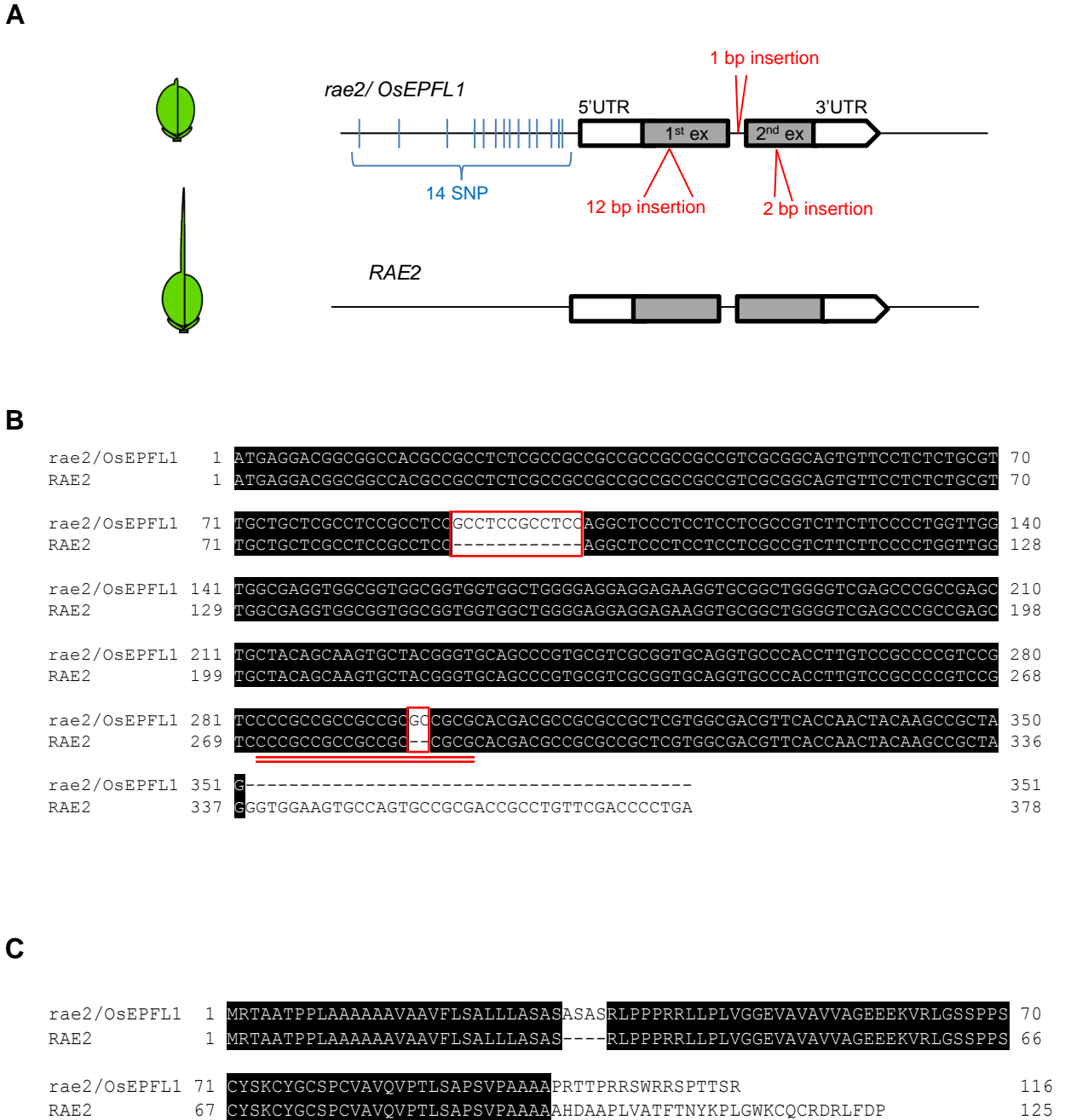


Fig. S5. RAE2 sequence comparison between *O. sativa* ssp. *japonica* cv. Koshihikari and *O. glaberrima* IRGC104038.

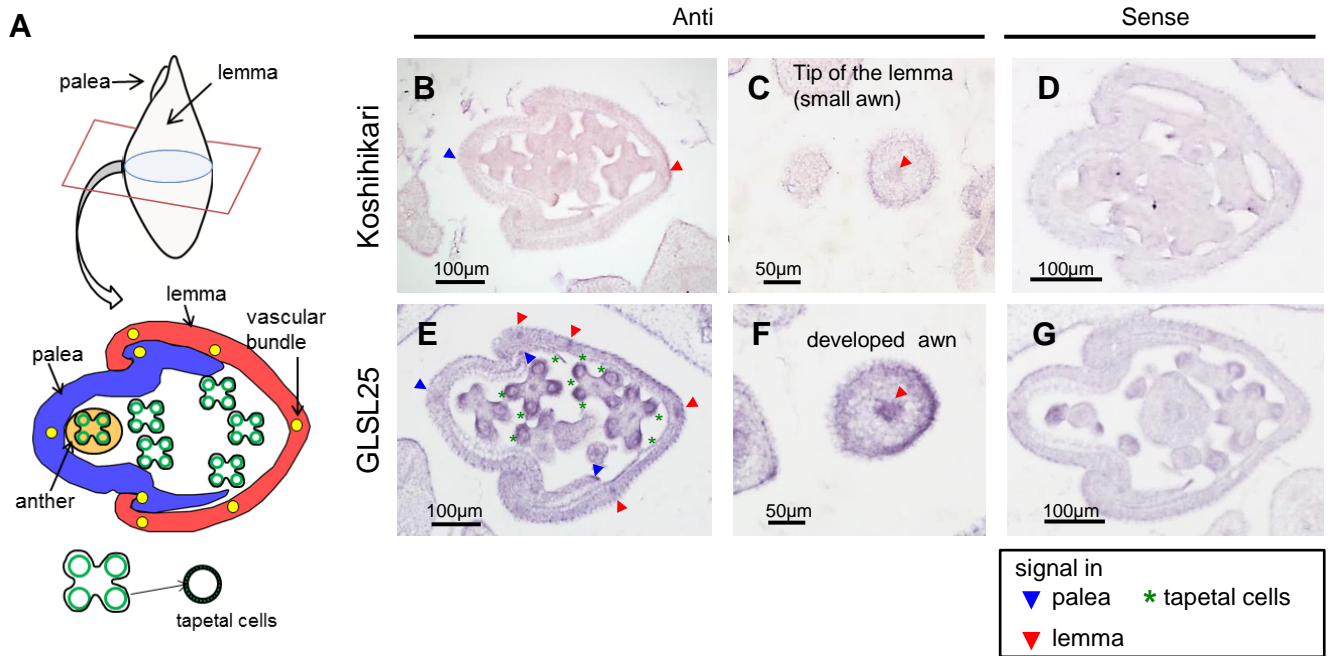


Fig. S6. Tissue-specific expression of RAE2 during awn development.

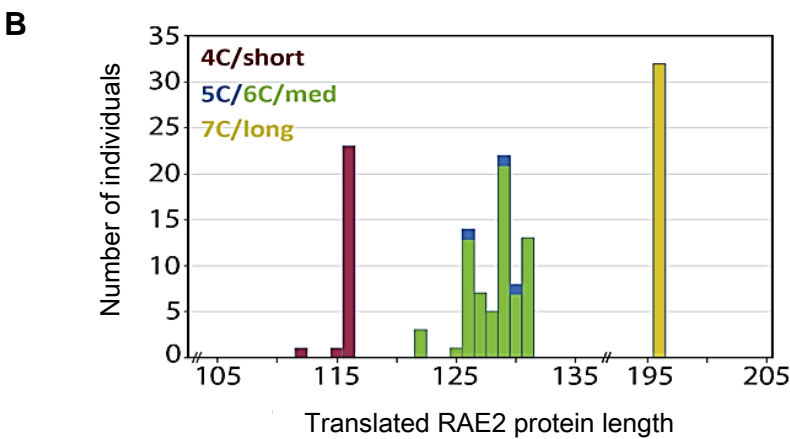
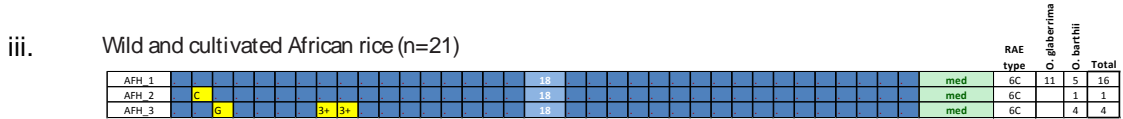
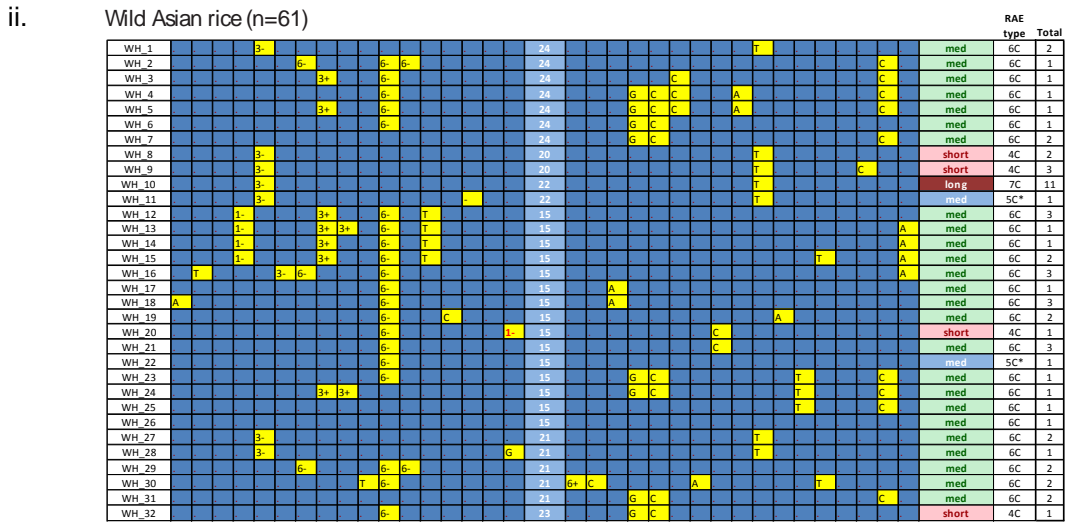
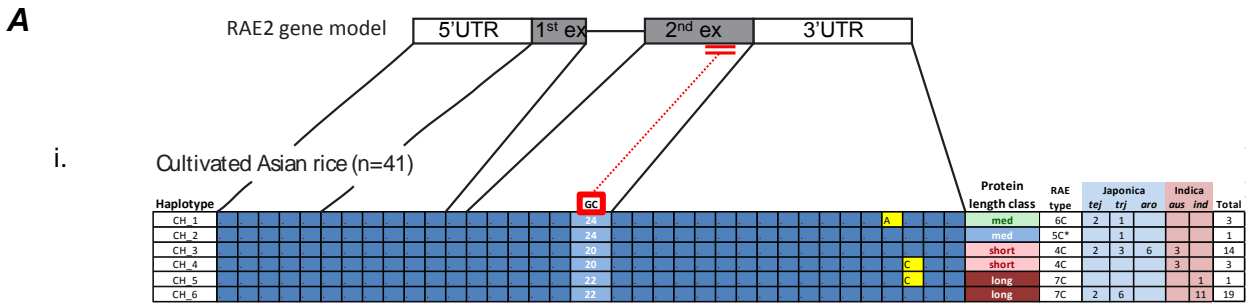


Fig. S7. RAE2 diversity and distribution across Asian and African rice accessions.

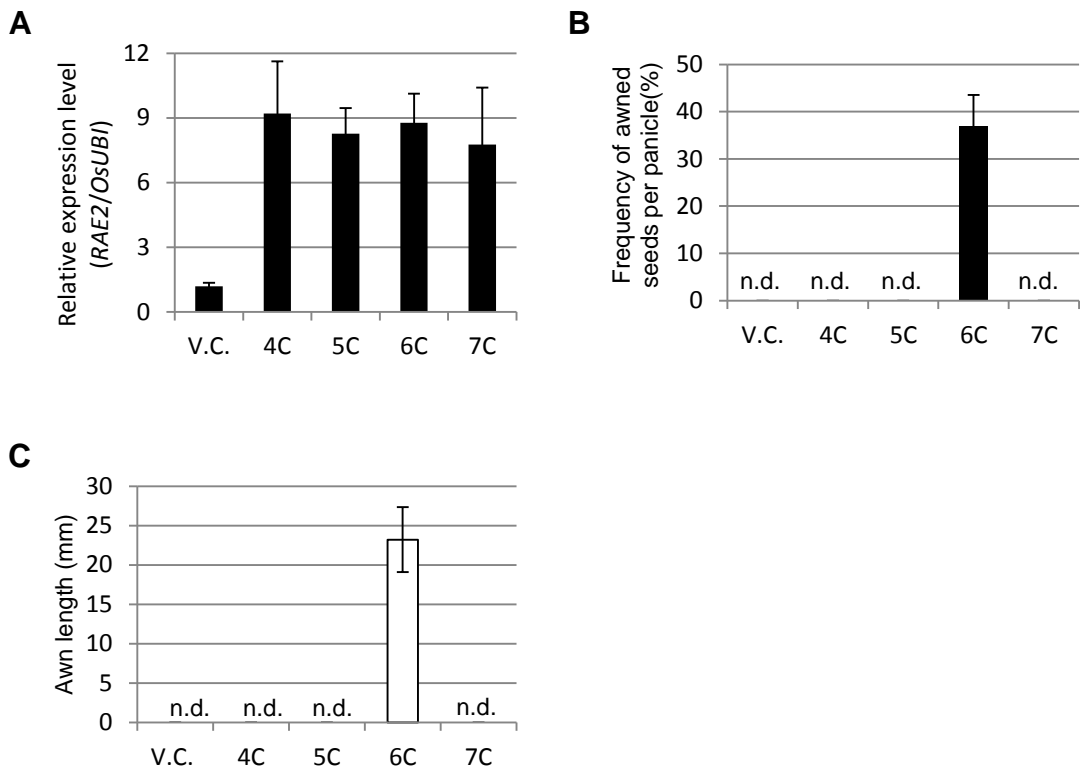


Fig. S8. Different types of RAE2 and definition of each function for awn elongation.

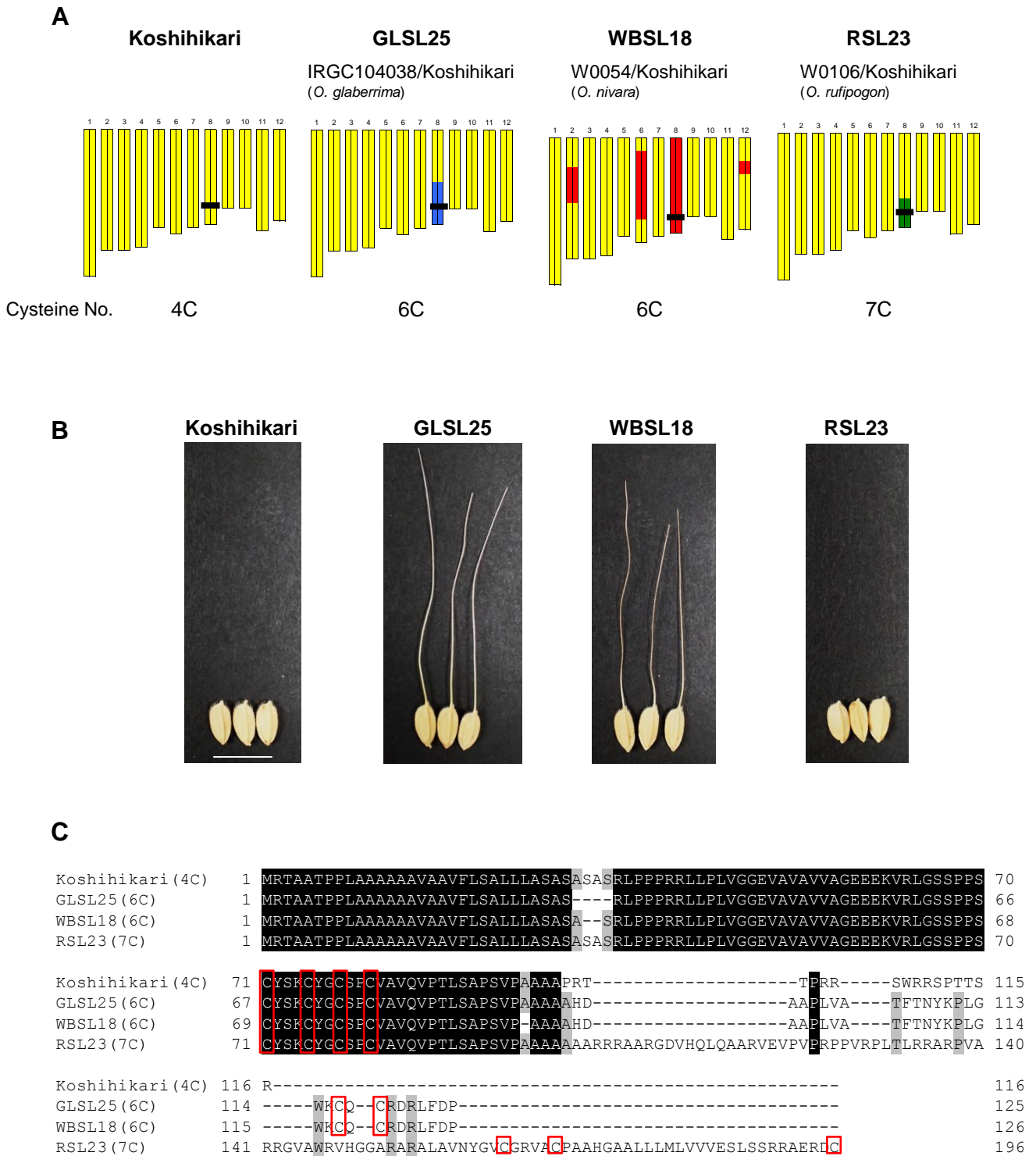


Fig. S9. Awn phenotypes of CSSLs and the number of RAE2 cysteine residues.

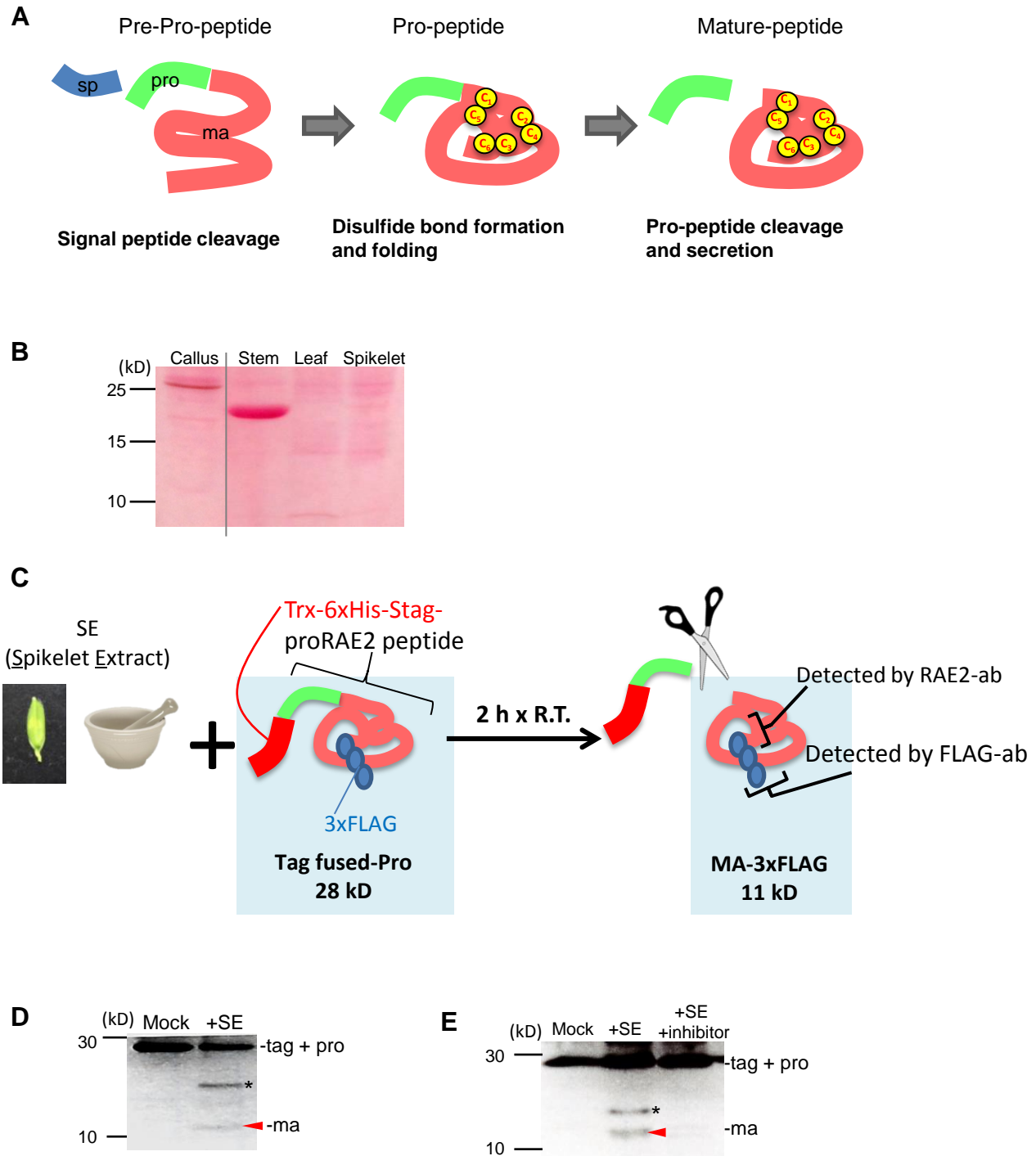


Fig. S10. The RAE2 maturation process occurs specifically in the spikelet.

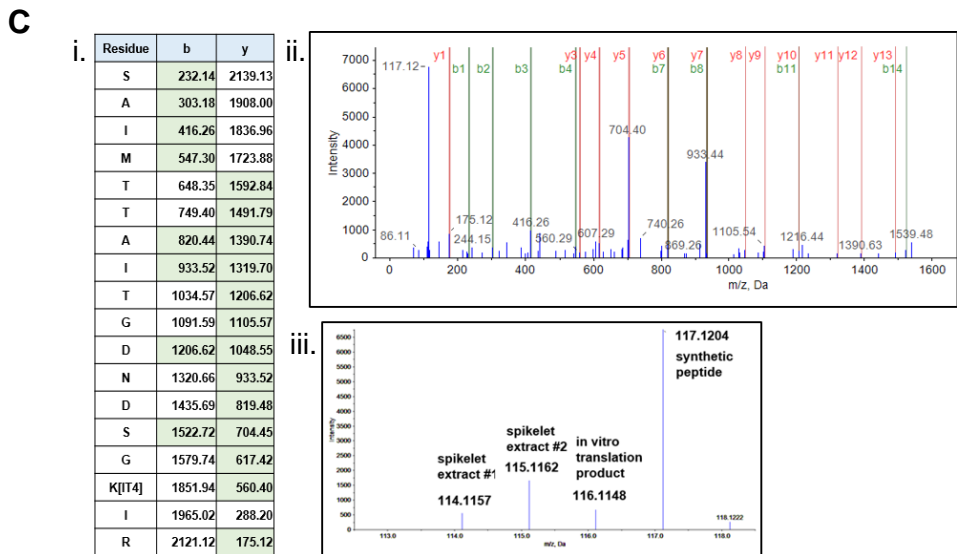
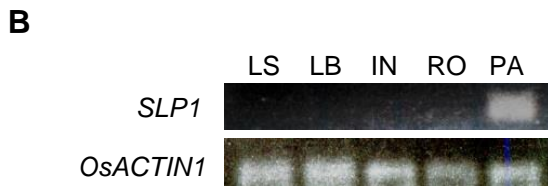
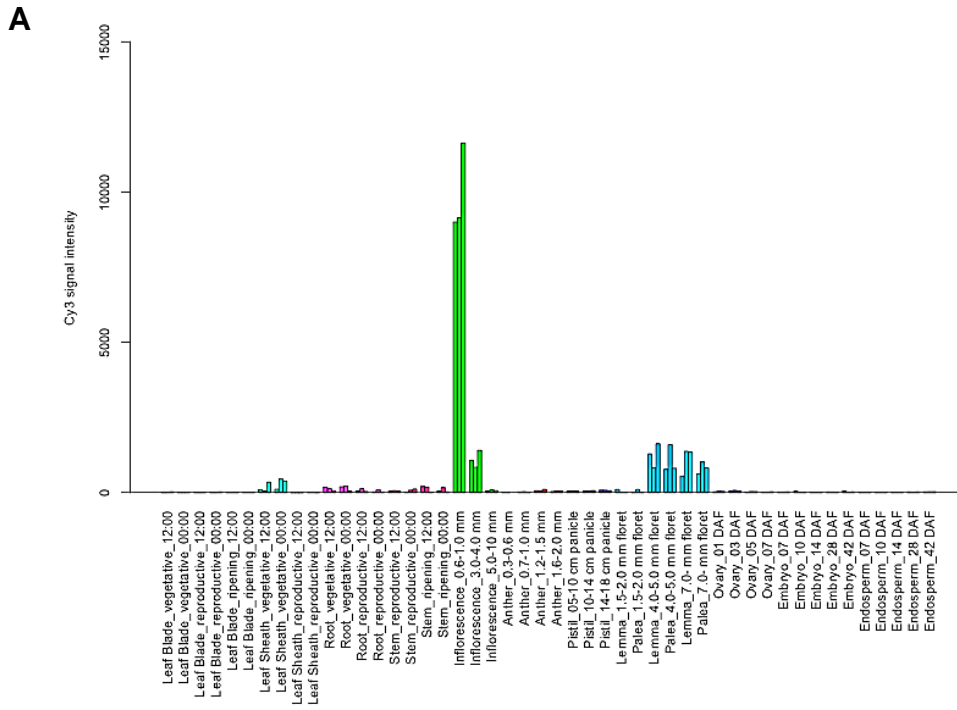
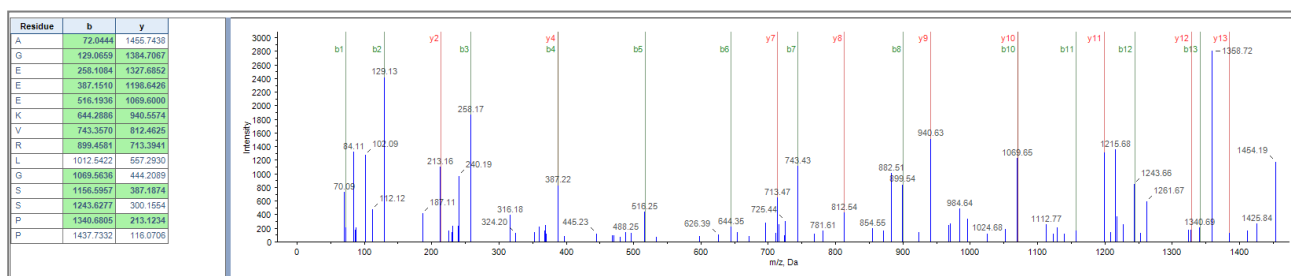


Fig. S11. Specific expression pattern of SLP1 .

A



B

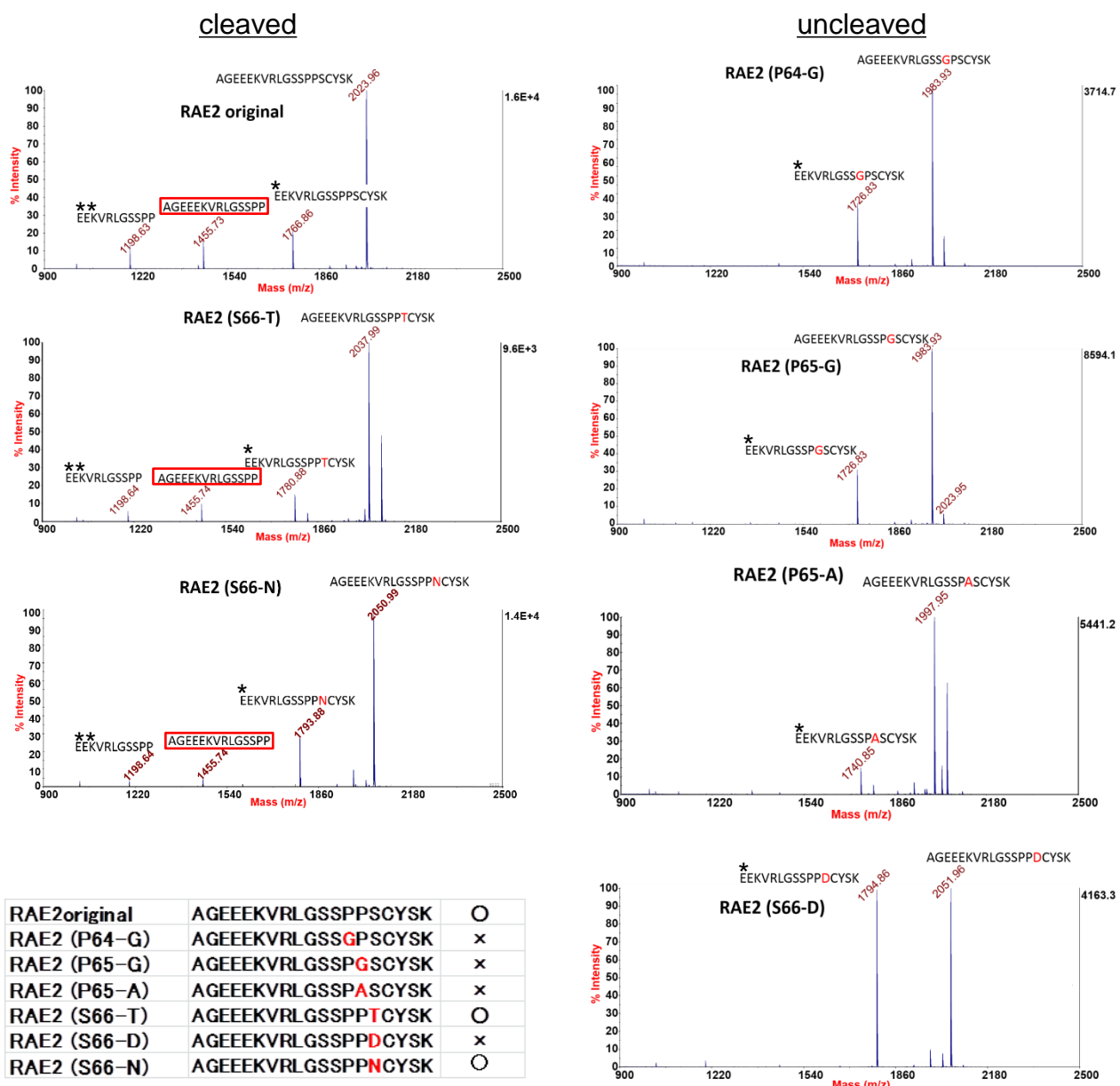
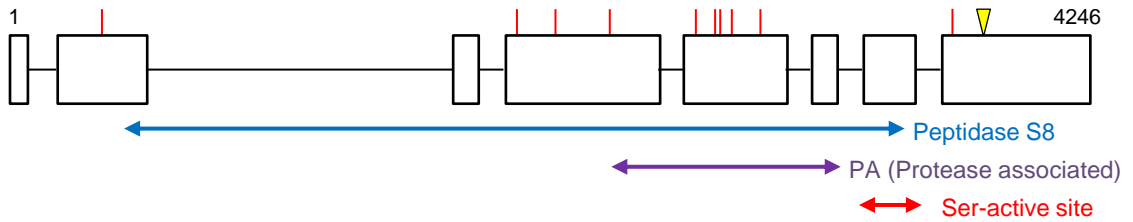


Fig. S12. Detection of the cleavage site of RAE2 by *in vitro* processing assay.

A



B

O. sativa	1	MQTYVIVFDGLPASPSGLLATVVTFSQLLYVLSPIQVIVVQIDESFVGVKQLPGVLAVIPDVLHKVHTT	70
O. glaberrima	1	MQTYVIVFDGLPASPSGLLATVVTFSQLLYVLSPIQVIVVQIDESFVGVKQLPGVLAVIPDVLHKVHTT	70
O. sativa	71	RSWDFLELERNGAATGAWKDAAKYG/DAIIGNVDTGVWPESASFKDDGYSVPSRWRGKCITGNDTTFKCN	140
O. glaberrima	71	RSWDFLELERNGAATGAWKDAAKYG/DAIIGNVDTGVWPESASFKDDGYSVPSRWRGKCITGNDTTFKCN	140
O. sativa	141	NKLI GAGFFNLGFLASGLLQ GKPPSQA AE LYTPRDYIGHGHTLSTAGGGFVPDASVFGHGKTAKGGSP	210
O. glaberrima	141	NKLI GAGFFNLGFLASGLLQ GKPPSQA AE LYTPRDYIGHGHTLSTAGGGFVPDASVFGHGKTAKGGSP	210
O. sativa	211	LARVAAYKACYAEGCSSSDILAAMVTAVEDG VNVLSLSVGGPADDYLSDP IAI GAFYAVQKGVIVVCSAS	280
O. glaberrima	211	LARVAAYKACYAEGCSSSDILAAMVTAVEDG VNVLSLSVGGPADDYLSDP IAI GAFYAVQKGVIVVCSAS	280
O. sativa	281	NSGPQPGSVTNVAPWILTVGASTMDRDFPAYVTFGGVTSSMTIKGQSLSNSTLPQGQRYAMINAKNANAA	350
O. glaberrima	281	NSGPQPGSVTNVAPWILTVGASTMDRDFPAYVTFGGVTSSMTIKGQSLSNSTLPQGQRYAMINAKNANAA	350
O. sativa	351	NVPSENSTLCFPGSLDSKVRGKIVVCTRGVNARVEKGLVVKQAGGVGMVLCN YAGNGEDVIADPHLIAA	420
O. glaberrima	351	NVPSENSTLCFPGSLDSKVRGKIVVCTRGVNARVEKGLVVKQAGGVGMVLCN YAGNGEDVIADPHLIAA	420
O. sativa	421	AHVSYSQCINLFN YLGSTDN PVGYITASDARLG V K P A P V M A A F S S R G P N P I T P Q I L K P D I T A P G V S V I A A	490
O. glaberrima	421	AHVSYSQCINLFN YLGSTDN PVGYITASDARLG V K P A P V M A A F S S R G P N P I T P Q I L K P D I T A P G V S V I A A	490
O. sativa	491	YSEAVSPTELSFDDRRVPY N I M S G T S M S C P H V S G I V G L I K T K Y P D W T P A M I K S A I M T T A I T G D N D S G K I R	560
O. glaberrima	491	YSEAVSPTELSFDDRRVPY N I M S G T S M S C P H V S G I V G L I K T K Y P D W T P A M I K S A I M T T A I T G D N D S G K I R	560
O. sativa	561	DETGA A A T P F A Y G S G H V R S V Q A L D P G L V Y D T T S A D Y A D F L C A L R P T Q N -- P L P L P V F G D D G K P R A C S Q G A	628
O. glaberrima	561	DETGA A A T P F A Y G S G H V R S V Q A L D P G L V Y D T T S A D Y A D F L C A L R P T Q N P L P L P V F G D D G K P R A C S Q G A	630
O. sativa	629	QYGRPEDLNYP S I A V P C L S G S A T V R R R V K N V G A A P C R Y A V S V T E A L A G V K V T V Y P P E L S F E S Y G E E R E F T	698
O. glaberrima	631	QYGRPEDLNYP S I A V P C L S G S A T V R R R V K N V G A A P C R Y A V S V T E A L A G V K V T V Y P P E L S F E S Y G E E R E F T	700
O. sativa	699	VRLEVQDAAAAAANYVFGSIEWSESESDPDRKHRVRSPIVAKTTCG	744
O. glaberrima	701	VRLEVQDAAAAAANYVFGSIEWSESESDPDRKHRVRSPIVAKTTCG	746

Fig. S13. Sequence and amino acid structure of SLP1.