

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

(Bessho-Uehara et al. 2016)



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



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.





В

rae2/OsEPFL1	1	ATGAGGACGGCGGCCACGCCGCCTCTCGCCGCCGCCGCCGCCGCCGCGCGCG	70
RAE2	1		70
rae2/OsEPFL1	71	TGCTGCTCGCCTCCGCCTCC <mark>GCCTCCCAGCCTCC</mark> AGGCTCCTCCTCGCCGTCTTCTTCCCCTGGTTGG	140
RAE2	71	TGCTGCTCGCCTCCGCCTCC <mark></mark> AGGCTCCCTCCTCCTCGCCGTCTTCTTCCCCTGGTTGG	128
rae2/OsEPFL1	141	TGGCGAGGTGGCGGTGGCGGTGGTGGCTGGGGAGGAGGAGGAGGAGGTGCGGCTGGGGTCGAGCCCGCCGAGC	210
RAE2	129	TGGCGAGGTGGCGGTGGCGGTGGTGGCTGGGGAGGAGGAGGAGGAGGAGGTGCGGCTGGGGTCGAGCCCGCCGAGC	198
rae2/OsEPFL1	211	TGCTACAGCAAGTGCTACGGGTGCAGCCCGTGCGTGCGGGTGCAGGTGCCCACCTTGTCCGCCCCGTCCG	280
RAE2	199	TGCTACAGCAAGTGCTACGGGTGCAGCCCGTGCGTGCGGGTGCCGGGTGCCCACCTTGTCCGCCCCGTCCG	268
rae2/OsEPFL1	281	TCCCCGCCGCCGCGCGCGCGCACGACGCCGCCGCCGCTCGTGGCGACGTTCACCAACTACAAGCCGCTA	350
RAE2	269	TCCCCGCCGCCGCCGCCGCCGCCGCCGCCGCTCGTGGCGACGTTCACCAACTACAAGCCGCTA	336
rae2/OsEPFL1	351	G	351
RAE2	337	GGTGGAAGTGCCAGTGCCGCGACCGCCTGTTCGACCCCTGA	378

С

rae2/OsEPFL1	1	MRTAATPPLAAAAAAVAAVFLSALLLASAS <mark>ASAS</mark> RLPPPRRLLPLVGGEVAVAVVAGEEEKVRLGSSPPS	70
RAE2	1	MRTAATPPLAAAAAAAVAAVFLSALLLASAS <mark></mark> RLPPPRRLLPLVGGEVAVAVVAGEEEKVRLGSSPPS	66
rae2/OsEPFL1	71	CYSKCYGCSPCVAVQVPTLSAPSVPAAAAPRTTPRRSWRRSPTTSR	116
RAE2	67	CYSKCYGCSPCVAVQVPTLSAPSVPAAAAAHDAAPLVATFTNYKPLGWKCQCRDRLFDP	125

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.

(Bessho- Uehara et al. 2016)



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 .





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

(Bessho-Uehara et al. 2016)

Α



В

0.	sativa	1	MQTYVIVFDGLPASPSGLLATVVTSFQLLYVLSPIQVIVVQIDESFVGVIKQLPGVLAVIPDVLHKVHTT	70
0.	glaberrima	1	MQTYVIVFDGLPASPSGLLATVVTSFQLLYVLSPIQVIVVQIDESFVGVIKQLPGVLAVIPDVLHKVHTT	70
0.	sativa	71	RSWDFLELERNGAATGAWKDAAKYG /DAIIGNVDTGVWPESASFKDDGYSVPSRWRGKCITGNDTTFKCN	140
0.	glaberrima	71	RSWDFLELERNGAATGAWKDAAKYG /DAIIGNVDTGVWPESASFKDDGYSVPSRWRGKCITGNDTTFKCN	140
0.	sativa	141	NKLIG <mark>A</mark> GFFNLGFLASGLLQGKPPSQAAELYTPRDYIGHGTHTLSTAGGGFVPDASVFGHGKGTAKGGSP	210
0.	glaberrima	141	NKLIG <mark>T</mark> GFFNLGFLASGLLQGKPPSQAAELYTPRDYIGHGTHTLSTAGGGFVPDASVFGHGKGTAKGGSP	210
0.	sativa	211	LAR <mark>V</mark> AAYKACYAEGCSSSDILAAMVTAVEDGVNVLSLSVGGPADDYLSDPIAIGAFYAVQKGV <mark>I</mark> VVCSAS	280
0.	glaberrima	211	LAR <mark>L</mark> AAYKACYAEGCSSSDILAAMVTAVEDGVNVLSLSVGGPADDYLSDPIAIGAFYAVQKGV <mark>T</mark> VVCSAS	280
0.	sativa	281	NSGPQPGSVTNVAPWILTVGASTMDRDFPAYVTFGGVTSSMTIKGQSLSNSTLPQGQRYAMINAKNANAA	350
0.	glaberrima	281	NSGPQPGSVTNVAPWILTVGASTMDRDFPAYVTFGGVTSSMTIKGQSLSNSTLPQGQRYAMINAKNANAA	350
0.	sativa	351	NVPSENSTLCFPGSLDSDKVRGKIVVCTRGVNARVEKGLVVKQAGGVGMVLCN <mark>Y</mark> AGNGEDVIADPHLIAA	420
0.	glaberrima	351	NVPSENSTLCFPGSLDSDKVRGKIVVCTRGVNARVEKGLVVKQAGGVGMVLCN <mark>G</mark> AGNGEDVIADPHLIAA	420
0.	sativa	421	AHVSYSQCINLFNYLGSTDNPVGYITASDARLGVKPAPVMAAFSSRGPNPITPQILKPDITAPGVSVIAA	490
0.	glaberrima	421	AHVSYSQCINLFNYLGSTDNPVGYITASDARLGVKPAPVMAAFSSRGPNPITPQILKPDITAPGVSVIAA	490
0.	sativa	491	YSEAVSPTELSFDDRRVPYNIMSGTSMSCPHVSGIVGLIKTKYPDWTPAMIKSAIMTTAITGDNDSGKIR	560
0.	glaberrima	491	YSEAVSPTELSFDDRRVPYNIMSGTSMSCPHVSGIVGLIKTKYPDWTPAMIKSAIMTTAITGDNDSGKIR	560
0.	sativa	561	DETGAAATPFAYGSGHVRSVQALDPGLVYDTTSADYADFLCALRPTQN <mark></mark> PLPLPVFGDDGKPRACSQGA	628
0.	glaberrima	561	DETGAAATPFAYGSGHVRSVQALDPGLVYDTTSADYADFLCALRPTQN <mark>PL</mark> PLPLPVFGDDGKPRACSQGA	630
0.	sativa	629	QYGRPEDLNYPSIAVPCLSGSATVRRRVKNVGAAPCRYAVSVTEALAGVKVTVYPPELSFESYGEEREFT	698
0.	glaberrima	631	QYGRPEDLNYPSIAVPCLSGSATVRRRVKNVGAAPCRYAVSVTEALAGVKVTVYPPELSFESYGEEREFT	700
0.	sativa	699	VRLEVQDAAAAANYVFGSIEWSEESESDPDRKHRVRSPIVAKTTCG	744
0.	glaberrima	701	VRLEVQDAAAAANYVFGSIEWSEESESDPDRKHRVRSPIVAKTTCG	746

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