

a >PbLHY coding sequence

ATGGACACAAACTCATCTGGAGAAGACCTTTCAAGGCACGAAAGCCTTACGATTACCAAGCAACGAGAGCGATGGACAGAGGAGGCATAATAGGTTCTTGATGCCTGAAGCTCTATGGCGAGCAGCGATTGAAGAACATATTGGAAAGAAGACTGCTGTGAGATCAGGAGTCATGCTCAGAAGTTCTTCAAAGCTGGAGAAGGGAGCACACAATAAGGTGTTCAATGGACAATCAATTGACATAGATATCCCGCCTCACGTCCAAGAGGAAACCAAGCAATCCTTACCTCGAAAGTCTAGTTCAGCTGCCAGCATTGACCAATCCGATGTGGAGCAAGGATGAAAACCTTATCAGCATCTCTCACACTGTCACAGTAAAGTAGTGGATTGGAAAGAACACCACCTCATGAGAGACCTACTGAAGAAGAAAATCGAAAATGGAAAAGAAAATCCGGATGAAATTGCTCAGAAGCCTTACTTGCTCAGAACATAATTGTTCTCTGATTCTACTGCAAACAAAATCTACCTACACAGGTGGTCTGAGAACGCTTGCACTTTCAGGAGTTGCTCCTCGTAAAGAGGTAATAAGTCAAGATGTAACAACACTGAATCTTATGTTACTATTGAACTTAATGAAATCAGAAATATGAAGAAAATGATGCCAAAAGATAGTCAAGTTAATGGCACAAGTGGAGCCTCAGTGTCAAGGAAACACTAATGCTCTCATAAGAAGTGGTCAAGGTGAGAACGAGATGATTGAATTGTCATTGCCAACAGATGGGATGCAAAGCACTCAGAACTACCCAAGGAATGTTCTGTACATGACTGGATGGTAGCGTAGGCGTGTAACTCAAACACTACACCTGCAGATATGTCATTCCCTGACTCCGGTTCCATCTATGGGGAAGGTTCATGGACGCCAACCTGTTGCAAACTCCAGCGGCTACTACTACTGAACATGAAAGTAATGCAAGATCTACTATTACCAATCGTTTCAAGCTTTCCACCTCCCTACACCAATTGTCAGGAACTACCAATCATTCCACCAATTCTCAGCCTTATGTCGTCTCTGCTCACAAACCTGAGCTTCCACCGCTGAGCCCATGCTGGGCTAGCTTGCAAGCCACATTGGCCTTATGCAAAATGTTGAAAATACGGAAGACTCCTCTGCATGCTCTGCTGGAGGTTCCACCGAACTCCCTCCAAAGTAGGCCAACATTGCTGCCACTGTAGCTGTCAACTGCATGGTAGCTGGGGGGTCCGTAGTGAATACTGATCAAGAGTCTCGCAGTGTAGACAGAGAGAGGGAGAATTCTCTTCAAACTCTTCTGCAGGAGTCAACAATTGGAGCGGAACACTTGGAACTGTGGATGCTCAGCATTAGCTCACAATCACCACAGGTCACTCAGACTGTGATAATGGAGGTTGAGAGCCTAATACAGAATTGAAAGTCTGTGATGAGAAGGCTGAGCATCAACTGCTCGAGTTAATGATTGAGACAATGCAAAGAGTAGAAAACAGGTTGACCTTCTCGTGTGGCTCCAAACACCTTCCGGCAGTGAAGTAGAGACAGATGCATTAGAGAACATGAGAAAGGAGCAGAACAGAACCTAAAGAACCAAAGAACCTGAGCTTCAAAATCTTCAAGCGCTTACCGCAGAGGTTCTCAGGTTAATGAGCATCAGGAGTCAGAACACCAGCAATCAAATTCTGACAAGAAAGATAGAGATGCTCAGGAGTGTGATCTGCTTCAAGGAGGAGAAAGTGTGTCACCAGCACAAGGCAGCAACACAGAACAGGCTACTGACACTAGGACTTAGCCAAGGGAAACTCAAGGCCGCCAACAGGATTCAAACCTTACAAGAGGTTGCTCCGTAGAGGCCAACAGAACCGGGTGGCCAATGCCAGCAGCACTGCGAAGAGAACAGTGGCCGAAGAGGTTACGCTTAGAAGGGGGAAAGCTCAAC

b

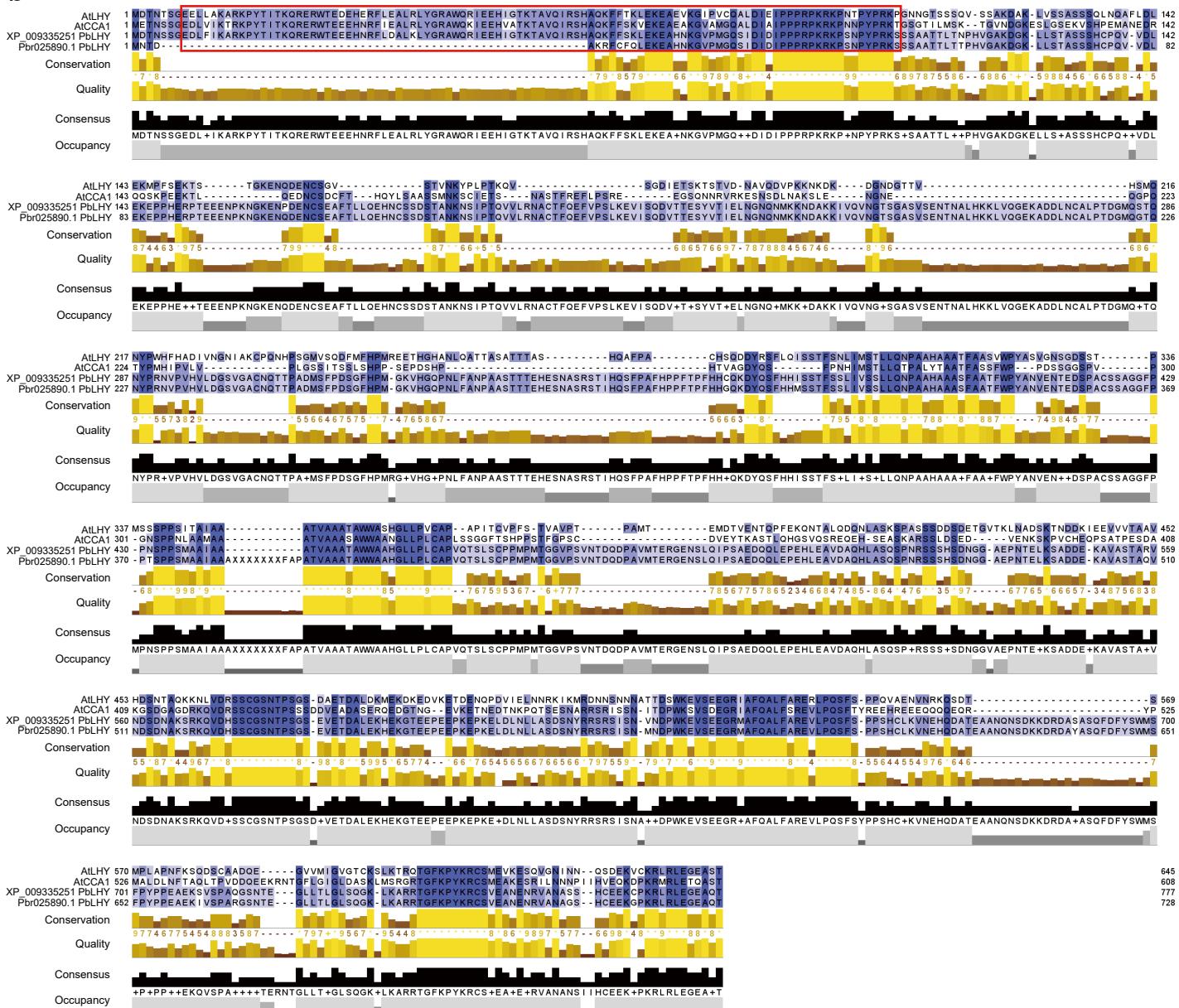


Fig. S1 (a) Coding sequence of *PbLHY*. (b) Alignment of *PbLHY* and *AtCCA1/AtLHY* protein sequences. The red box indicates the MYB domain. The blue backgrounds correspond to the percent identity of the multiple alignment.

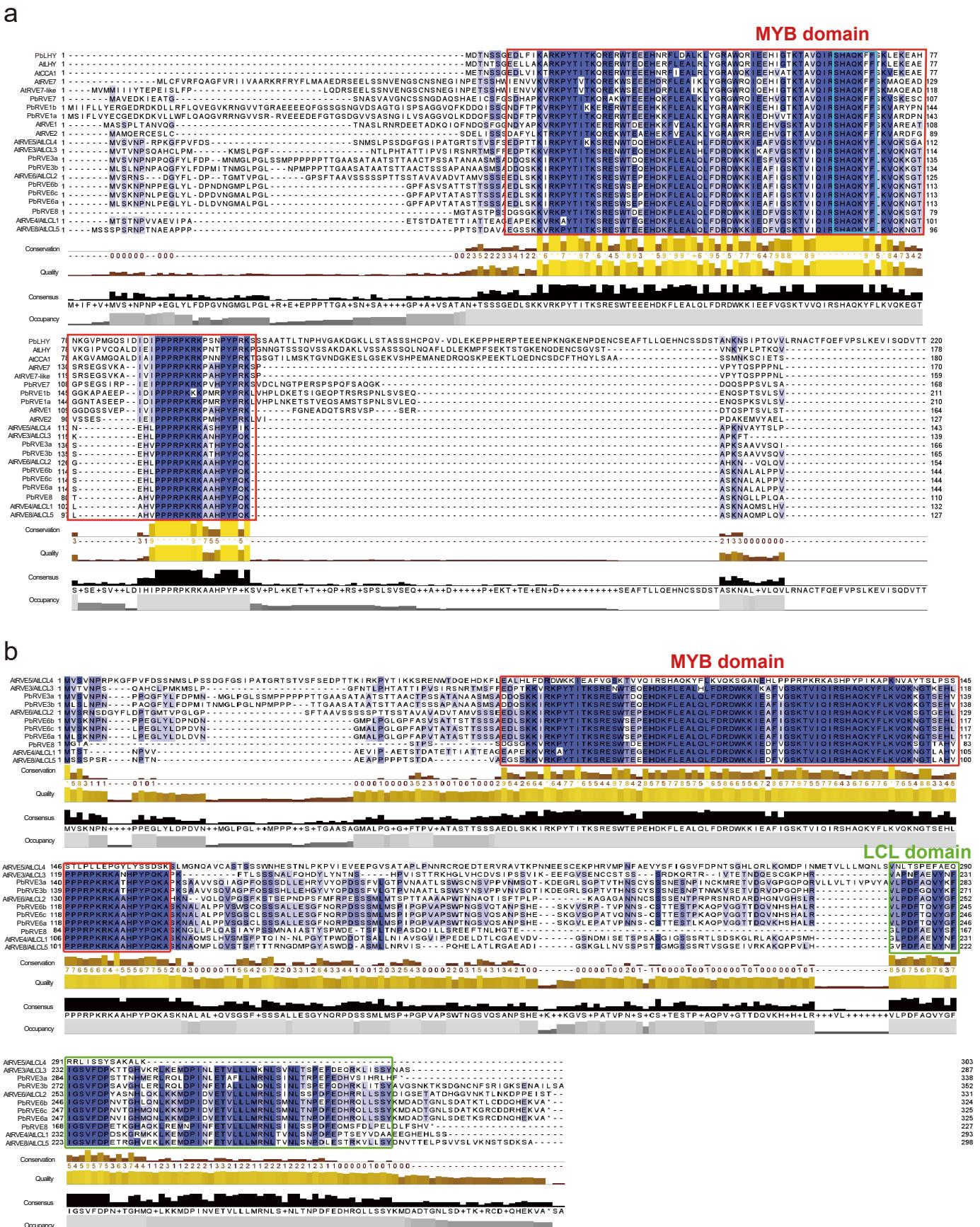


Fig. S2 Alignment of conserved domains from PbRVE proteins. (a) Alignment of MYB domains from ten PbRVEs and eleven AtRVEs. Red box indicates MYB domain, and blue box indicates SHAQK(Y/F)F sequence. (b) Alignment of LCL domains from subfamily II members. The red box indicates the MYB domain. The green box indicates the LCL domain. The blue backgrounds correspond to the percent identity of the multiple alignment.

		E-value	Sites	Width
Motif 1		3.8e-835	21	50
Motif 2		3.9e-329	11	50
Motif 3		3.7e-311	21	29
Motif 4		2.8E-74	21	15
Motif 5		3E-64	6	50
Motif 6		4.2E-44	4	50
Motif 7		6.5E-44	10	17
Motif 8		2.6E-29	7	50
Motif 9		1.6E-30	8	29
Motif 10		5E-25	3	29

Fig. S3 The motif details of ten conserved domains identified in RVE proteins and the logos of these domains created using the MEME. Amino acids are expressed in the standard single letter code. The size of the letters at each position represents their frequency.