

A

B

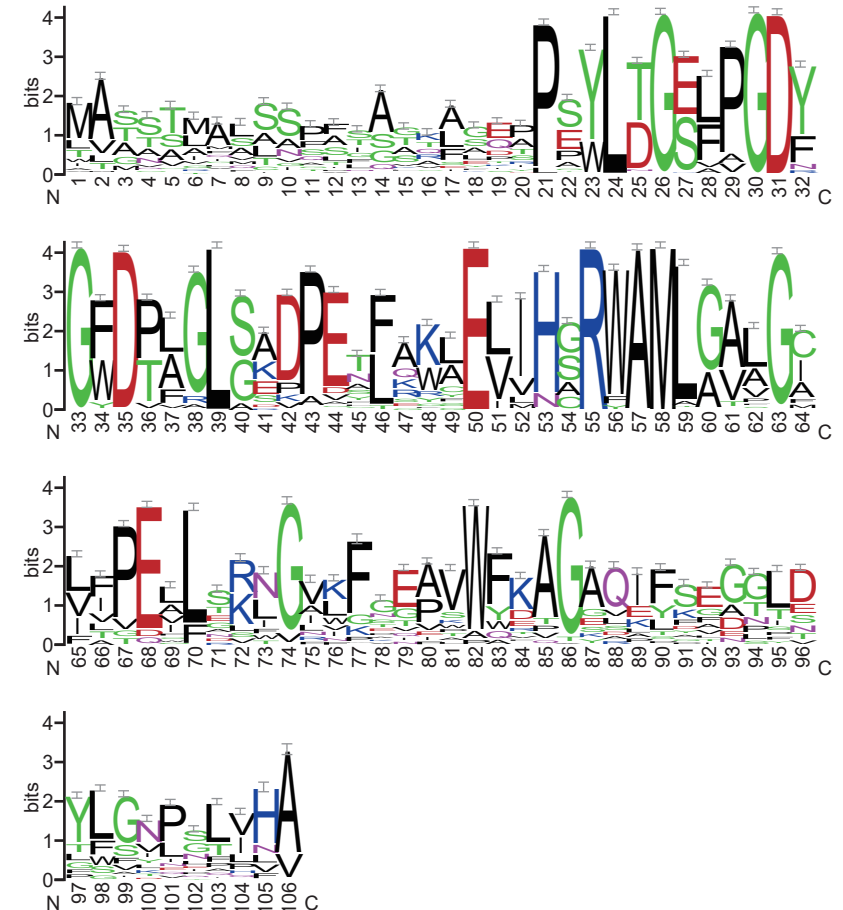


Fig.S1 Multiple sequence alignment of the LHCB domain. Multiple sequence analysis of LHCB gene in pear and peach (A). Sequence markers of repeated sequences are based on full-length alignment of all Arabidopsis LHCB domains. Multiple comparison analysis of 290 LHCB domains was performed using ClustalW. The bit fraction indicates the content of the information at each position in the sequence(B).