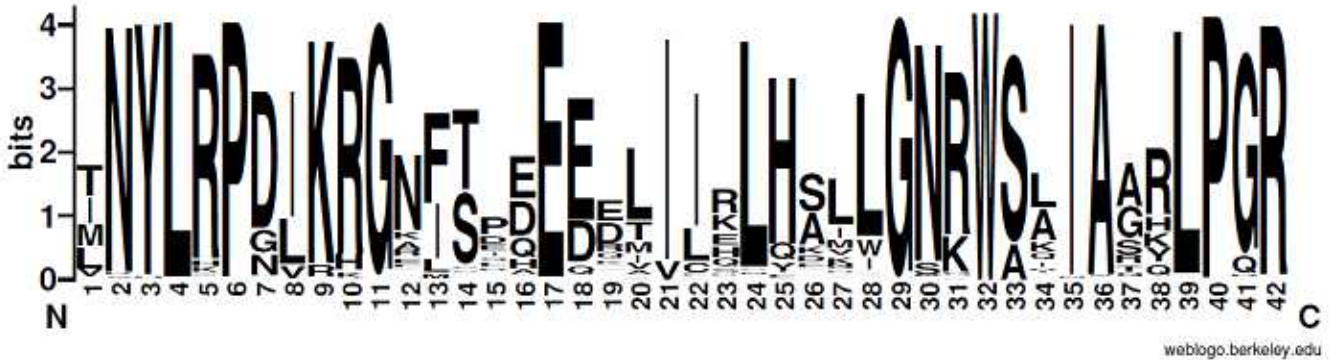
A

```
MYBdg FP1:            5′-GTGGRAAAAGTTGYAGRCTNAGWTGG-3′
N1:                 5′-CGGAATTCDKNAARAGYTGYAG-3′
N2:                 5′-CGGAATTCDKNAARAGYTGYCG-3′
N3:                 5′-CGGAATTCDKNAARTCNTGYAG-3′
N4:                 5′-CGGAATTCDKNAARTCNTGYCG-3′
N5:               5′-CCCGGGTGYGGNSSRTCNTG-3′
N6:              5′-GGAATTCTGYGGNAARAGYTG-3′
AnMYB FP:                    5′-AARAGCTGYAGAWTGAGRTGG-3′


MYBdg RP1:     5′-CCARTAATTYTTRATTTCRTTRTCWG-3′
C1:              5′-CGGAATTCTTNAYNGCRTTRTCNGT-3′
C2:              5′-CGGAATTCTTDATYTCRTTRTCNGT-3′
C3:              5′-CGGAATTCTTNAYNTKRTTRTCNGT-3′
AnMYB RP:      5′-CCAATARTTCTTNACRTCATT-3′
```

B



An extensive analysis of *R2R3-MYB* regulatory genes from *Fagus crenata*

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Supplementary Fig. S1
Nucleotide sequences of the forward primers (MYBdpFP1, N1~N6, and AnMYBFP) and the reverse primers (MYBdpRP1, N1~N3, and AnMYBRP) used for the PCR and RT-PCR experiments (A) and the sequence logos of the amplified partial R2R3-DBD based on the deduced 42-amino acid-long sequence of all the beech members as listed in Table S1 (B).