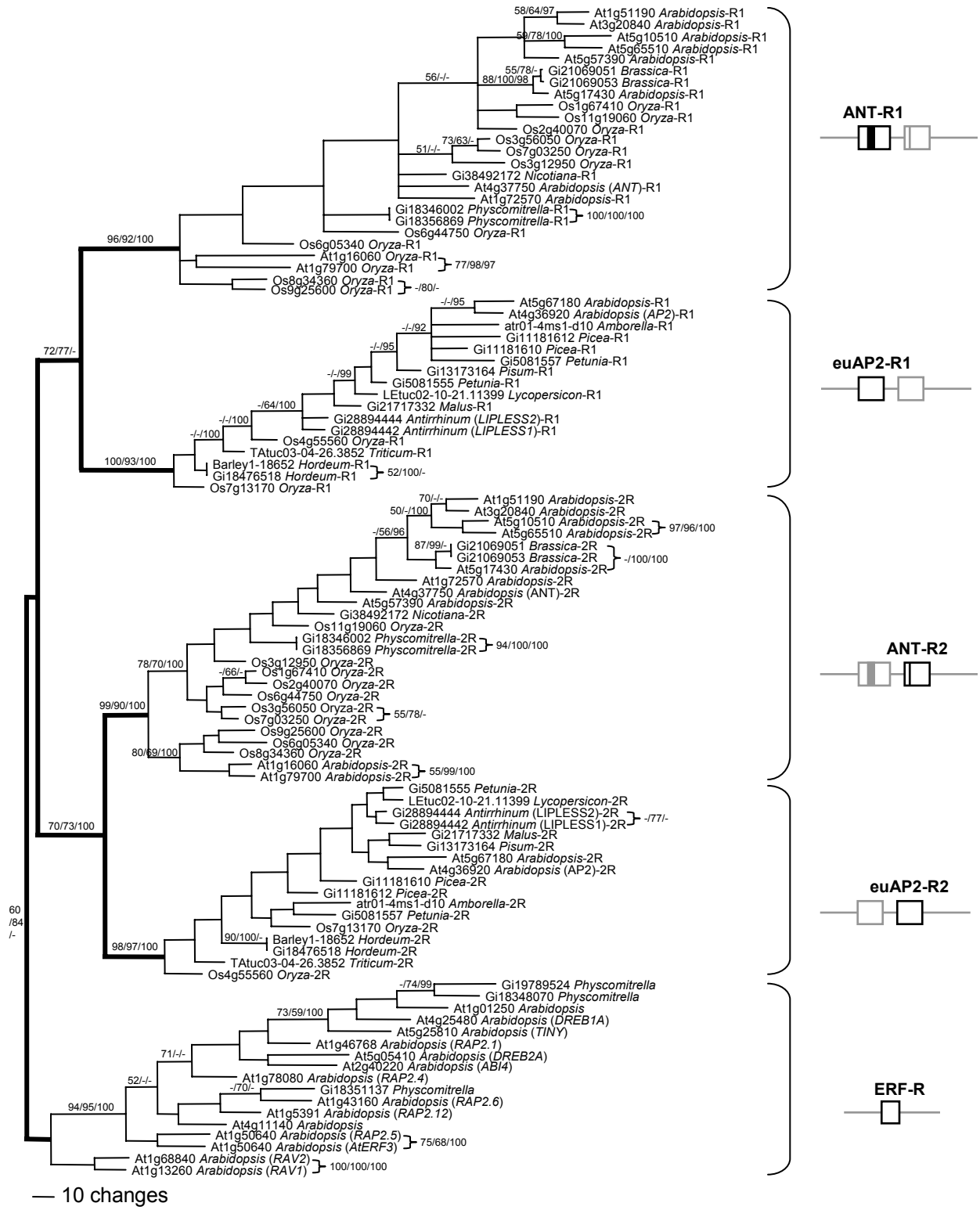
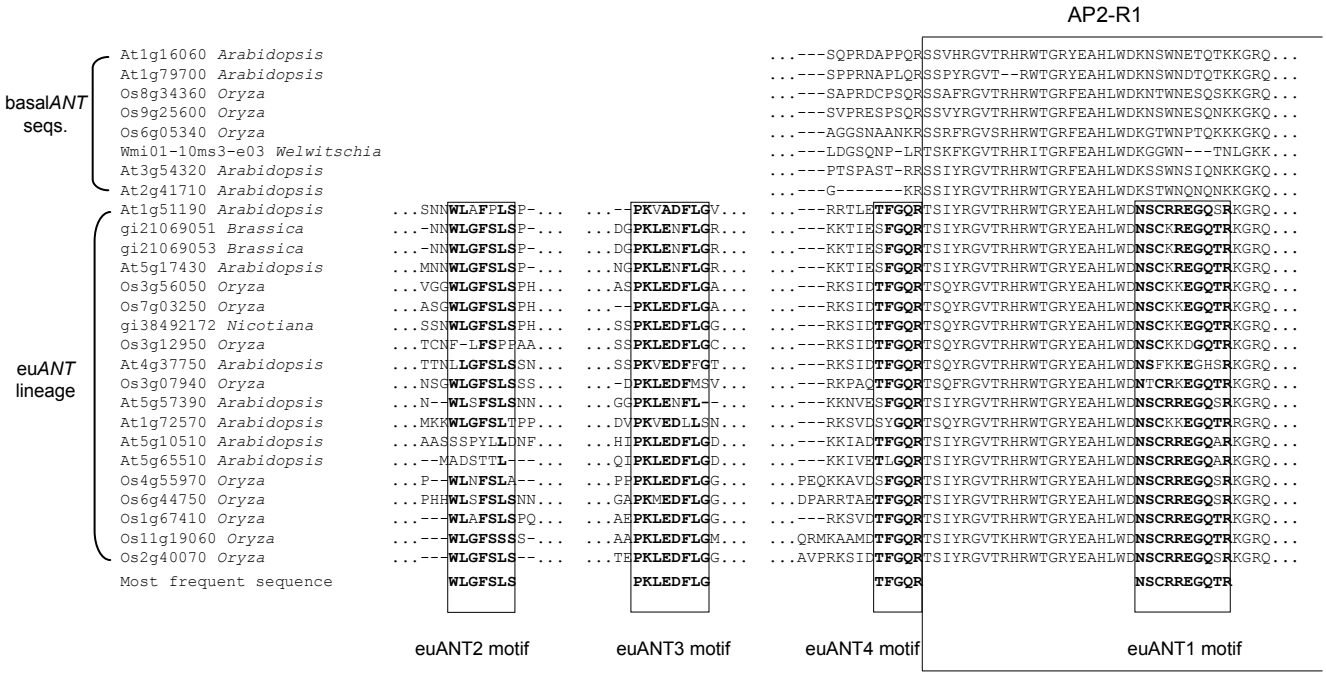
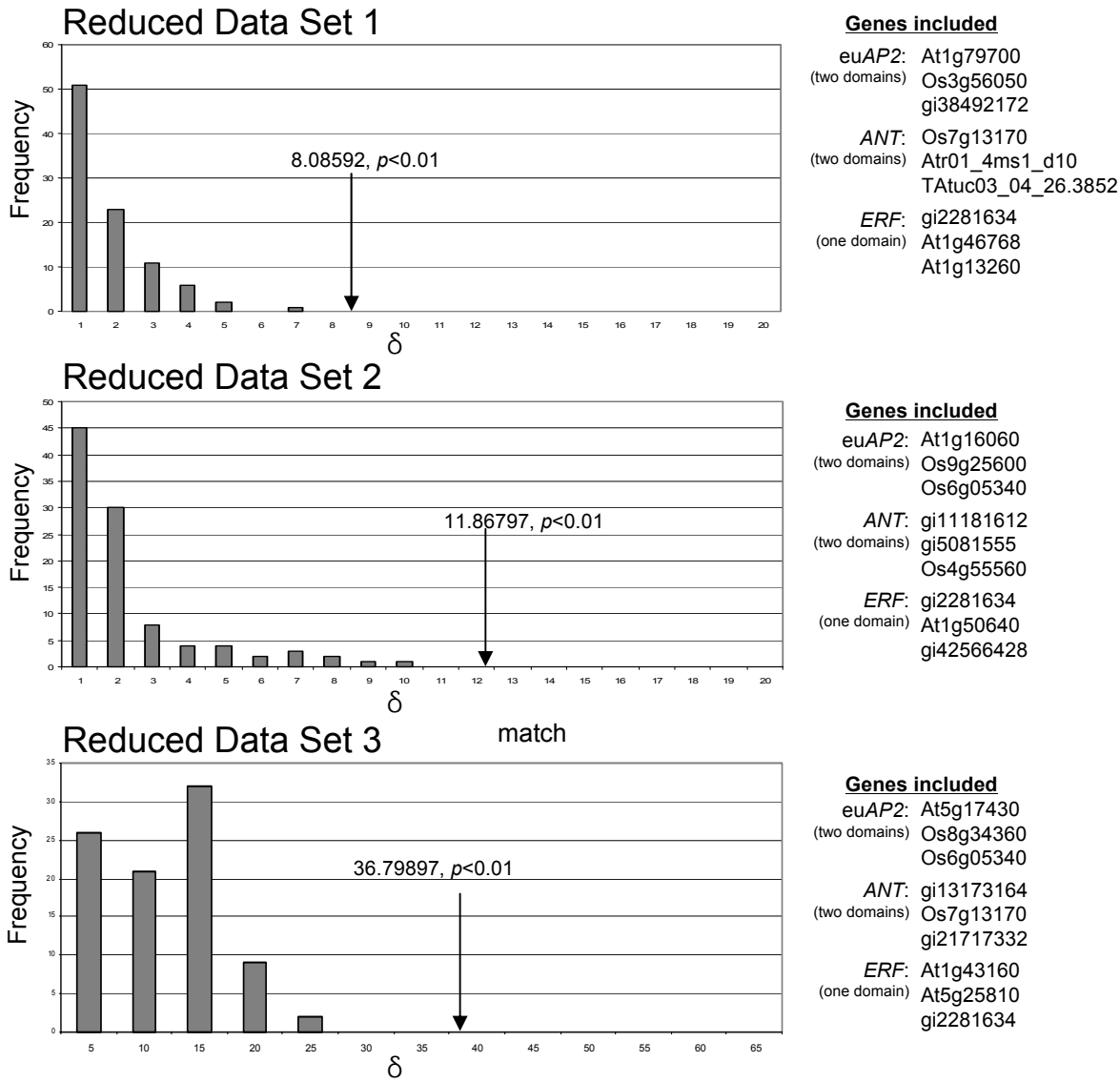


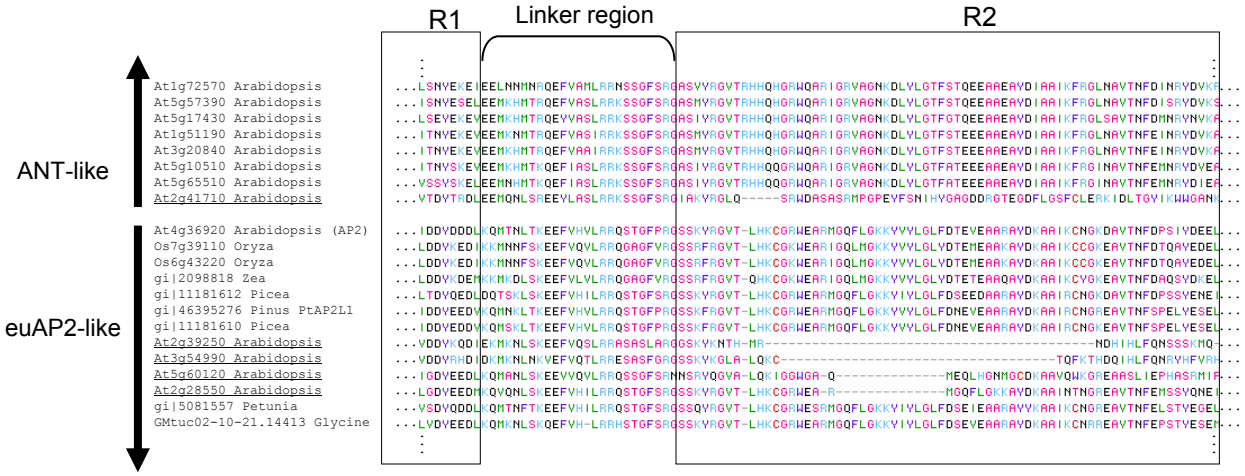
Supplementary material 3. Strict consensus of 31 most parsimonious trees using DNA sequences of R1 and R2 domains in each lineage of *AP2*-like gene family (length=2960, CI=0.16, and RI=0.64), shown as a phylogram (full tree of Fig. 6). Numbers above the branches are bootstrap values of aa analysis DNA data analyses (>50%) and posterior probabilities in the Bayesian analysis (>90). The posterior probabilities are multiplied by 100. The relationships among domains are indicated as thick lines.



Supplementary material 4. Motif regions in sequences of the *ANT* lineage. The most frequent amino acid at each site is highlighted in bold.



Supplementary material 5. Results of the likelihood ratio test with the parametric bootstrap, showing the distribution of δ (the likelihood ratio test statistic), which is the difference between –ln likelihood scores of the optimal trees supporting Model B and Model A for simulated data assuming that hypothesis B is correct. The observed value for the actual data (represented by the arrow) is shown in relation to the distribution. If the observed value is much greater than the values found in the distribution, the null hypothesis (Model B) is rejected. The observed values are significantly different from the values in the distribution (p<0.01).



Supplementary material 6. A part of alignment of *AP2*-like genes, which showed five *Arabidopsis* sequences having uncertain R2 domain (see text).