

RESEARCH ARTICLE

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# Genome-wide analysis of the AP2/ERF transcription factor superfamily in Chinese cabbage (*Brassica rapa* ssp. *pekinensis*)

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## Abstract

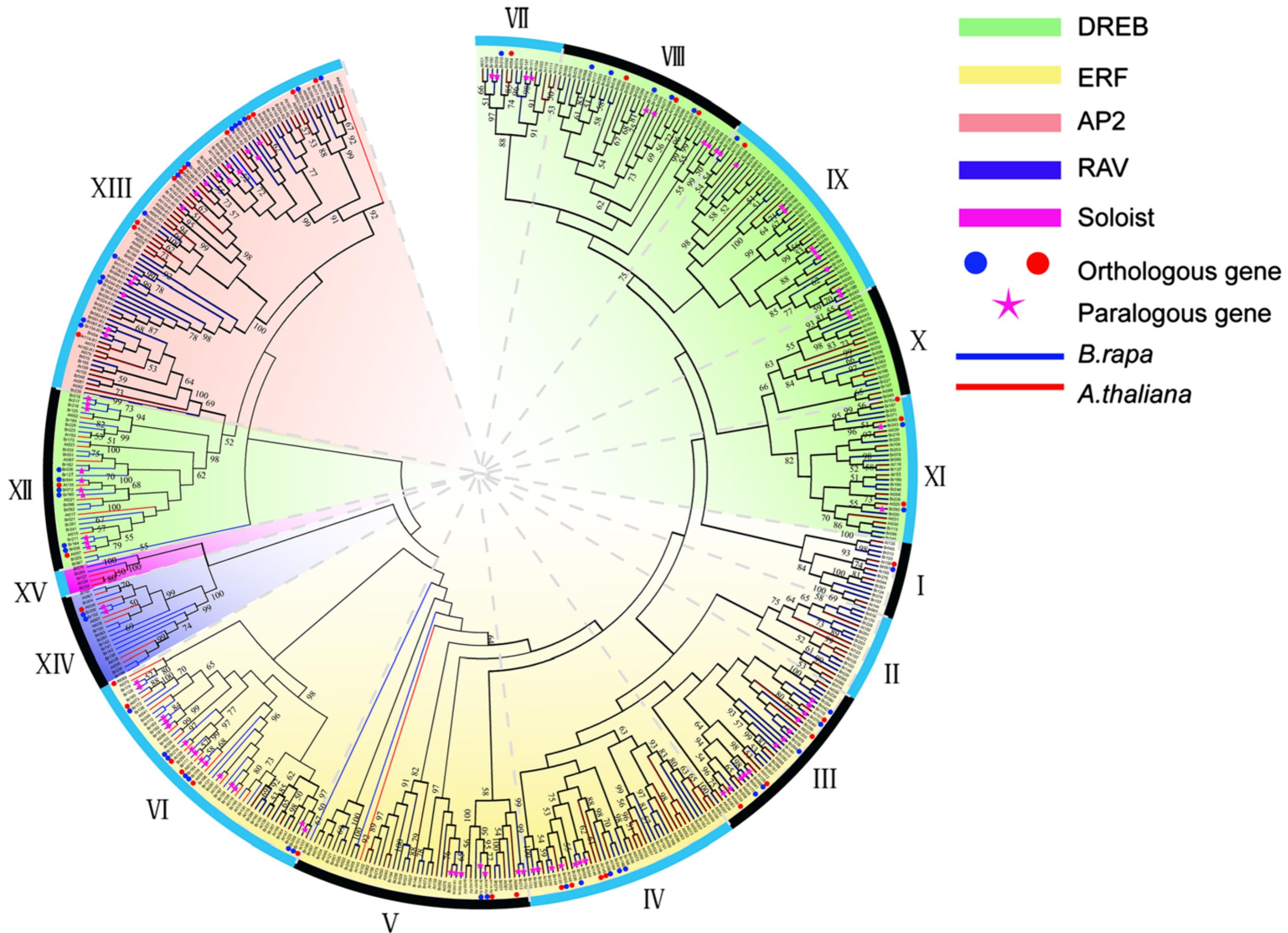
**Background:** Chinese cabbage (*Brassica rapa* ssp. *pekinensis*) is a member of one of the most important leaf vegetables grown worldwide, which has experienced thousands of years in cultivation and artificial selection. The entire Chinese cabbage genome sequence, and more than forty thousand proteins have been obtained to date. The genome has undergone triplication events since its divergence from *Arabidopsis thaliana* (13 to 17 Mya), however a high degree of sequence similarity and conserved genome structure remain between the two species. *Arabidopsis* is therefore a viable reference species for comparative genomics studies. Variation in the number of members in gene families due to genome triplication may contribute to the broad range of phenotypic plasticity, and increased tolerance to environmental extremes observed in *Brassica* species. Transcription factors are important regulators involved in plant developmental and physiological processes. The AP2/ERF proteins, one of the most important families of transcriptional regulators, play a crucial role in plant growth, and in response to biotic and abiotic stressors. Our analysis will provide resources for understanding the tolerance mechanisms in *Brassica rapa* ssp. *pekinensis*.

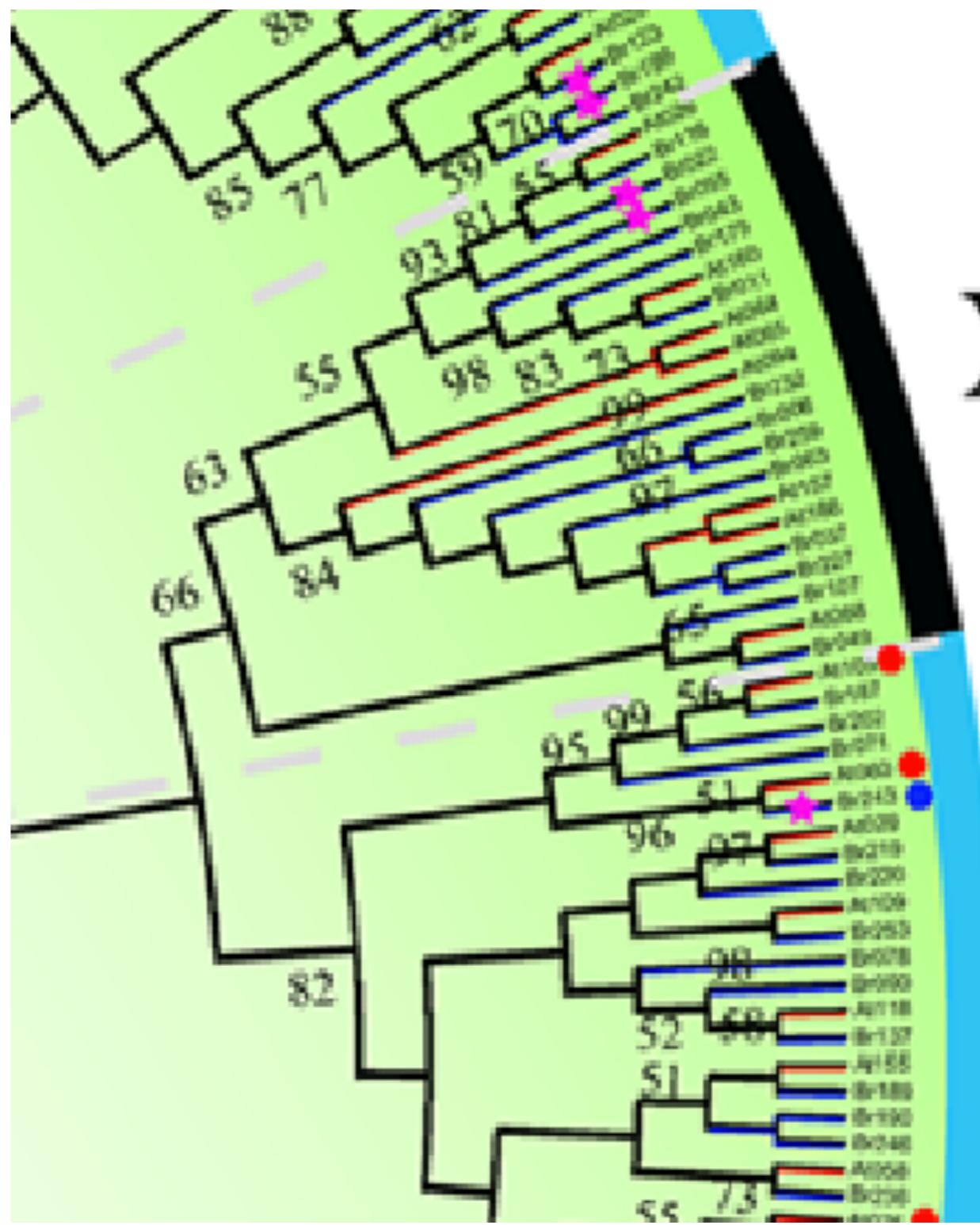
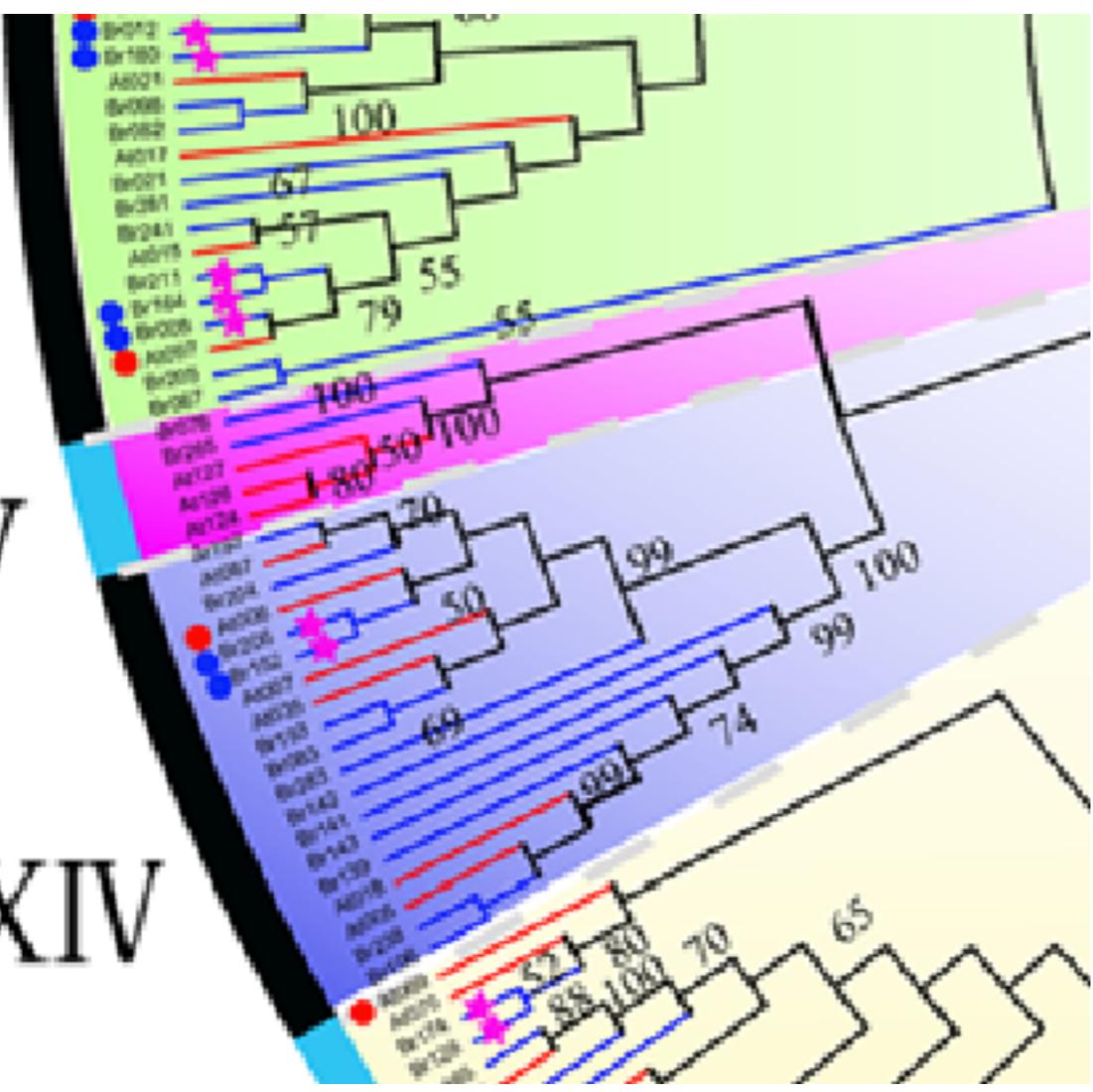
**Results:** In the present study, 291 putative AP2/ERF transcription factor proteins were identified from the Chinese cabbage genome database, and compared with proteins from 15 additional species. The Chinese cabbage AP2/ERF superfamily was classified into four families, including AP2, ERF, RAV, and Soloist. The ERF family was further divided into DREB and ERF subfamilies. The AP2/ERF superfamily was subsequently divided into 15 groups. The identification, classification, phylogenetic reconstruction, conserved motifs, chromosome distribution, functional annotation, expression patterns, and interaction networks of the AP2/ERF transcription factor superfamily were predicted and analyzed. Distribution mapping results showed AP2/ERF superfamily genes were localized on the 10 Chinese cabbage chromosomes. AP2/ERF transcription factor expression levels exhibited differences among six tissue types based on expressed sequence tags (ESTs). In the AP2/ERF superfamily, 214 orthologous genes were identified between Chinese cabbage and *Arabidopsis*. Orthologous gene interaction networks were constructed, and included seven CBF and four AP2 genes, primarily involved in cold regulatory pathways and ovule development, respectively.

**Conclusions:** The evolution of the AP2/ERF transcription factor superfamily in Chinese cabbage resulted from genome triplication and tandem duplications. A comprehensive analysis of the physiological functions and biological roles of AP2/ERF superfamily genes in Chinese cabbage is required to fully elucidate AP2/ERF, which provides us with rich resources and opportunities to understand crop stress tolerance mechanisms.

**Keywords:** Chinese cabbage, AP2/ERF, Stress tolerance, Gene expression, Interaction network, Protein annotation

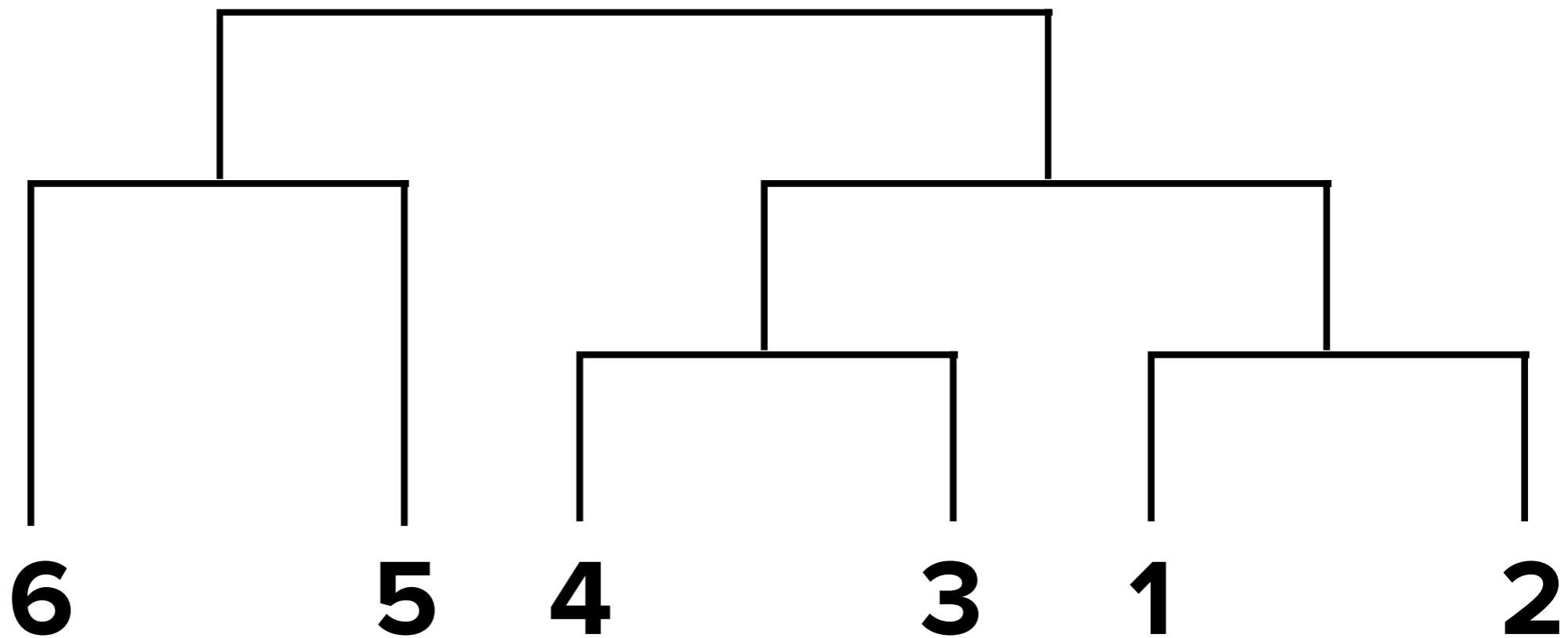
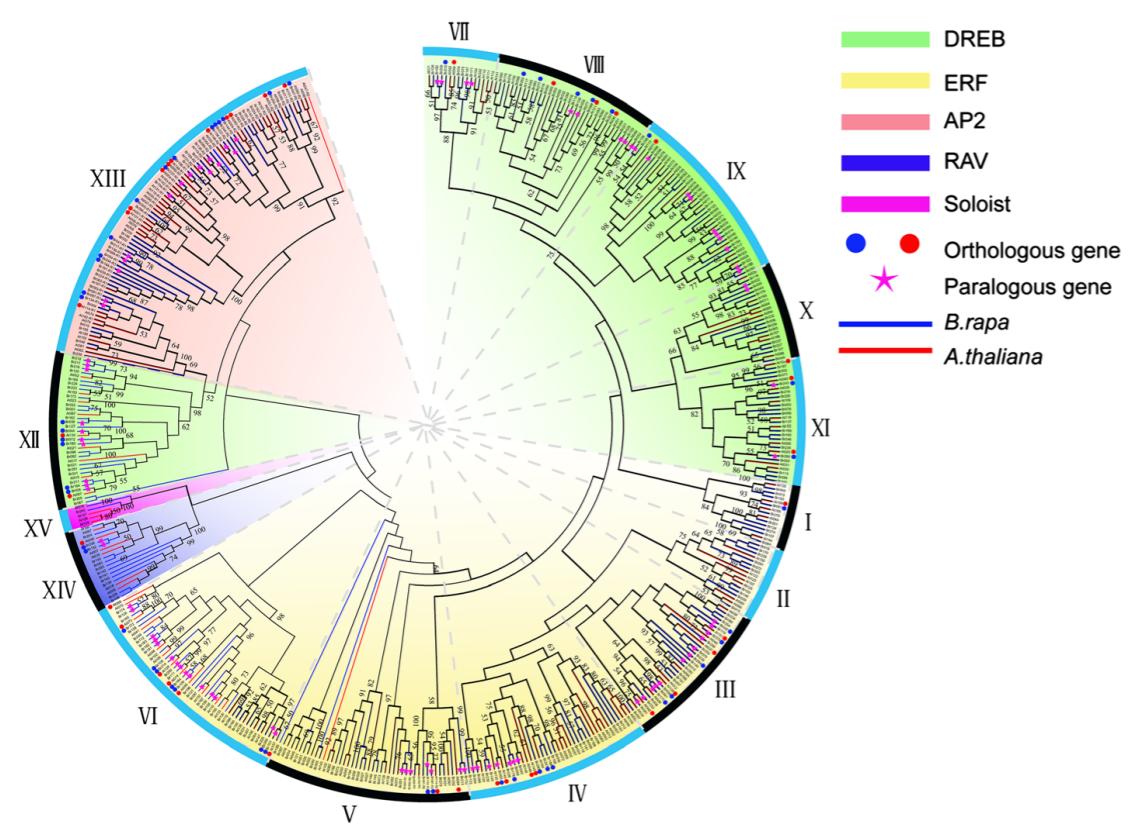
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X

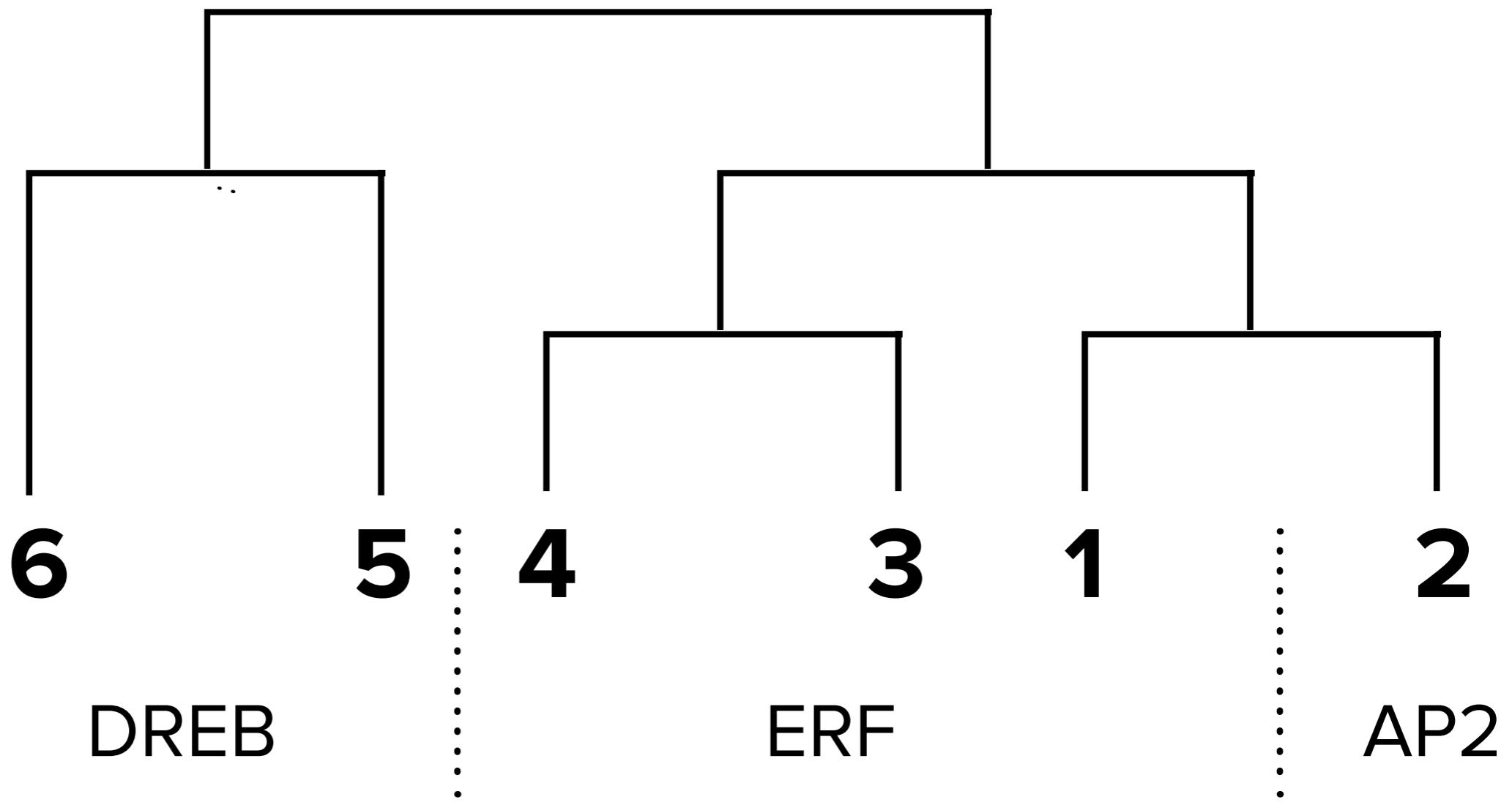
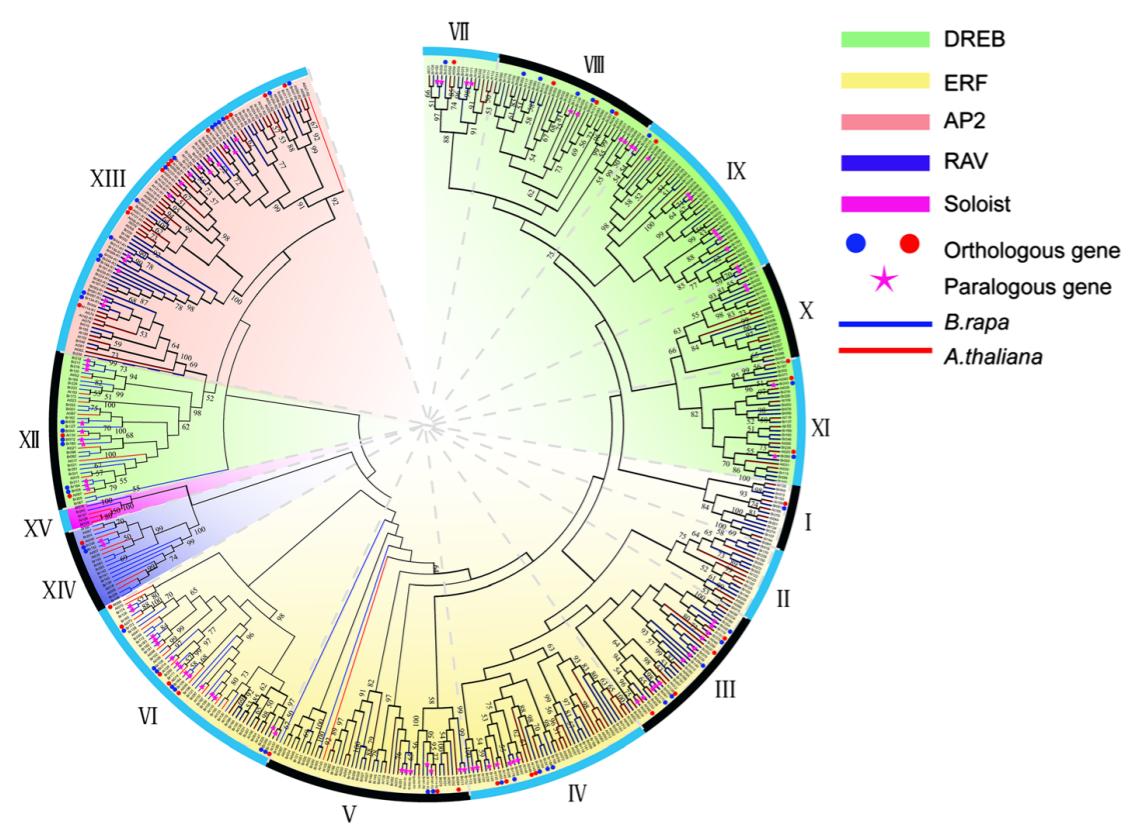
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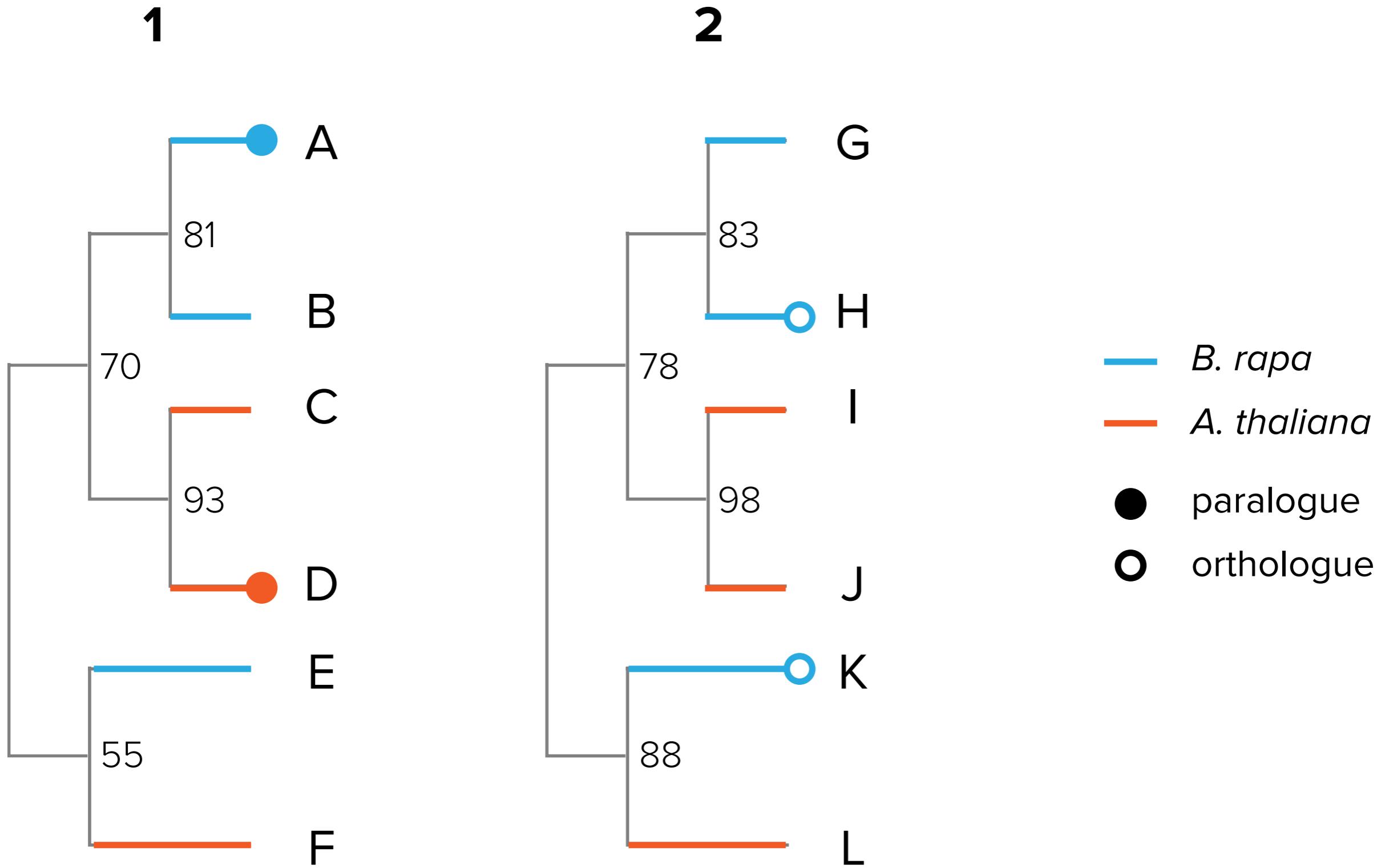


DREB

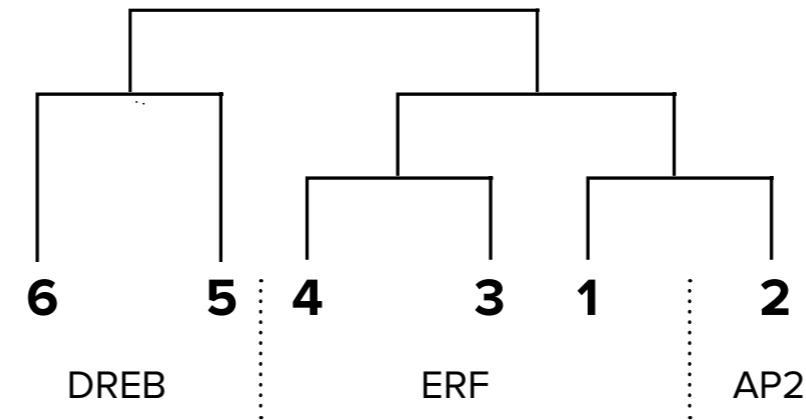
ERF

AP2

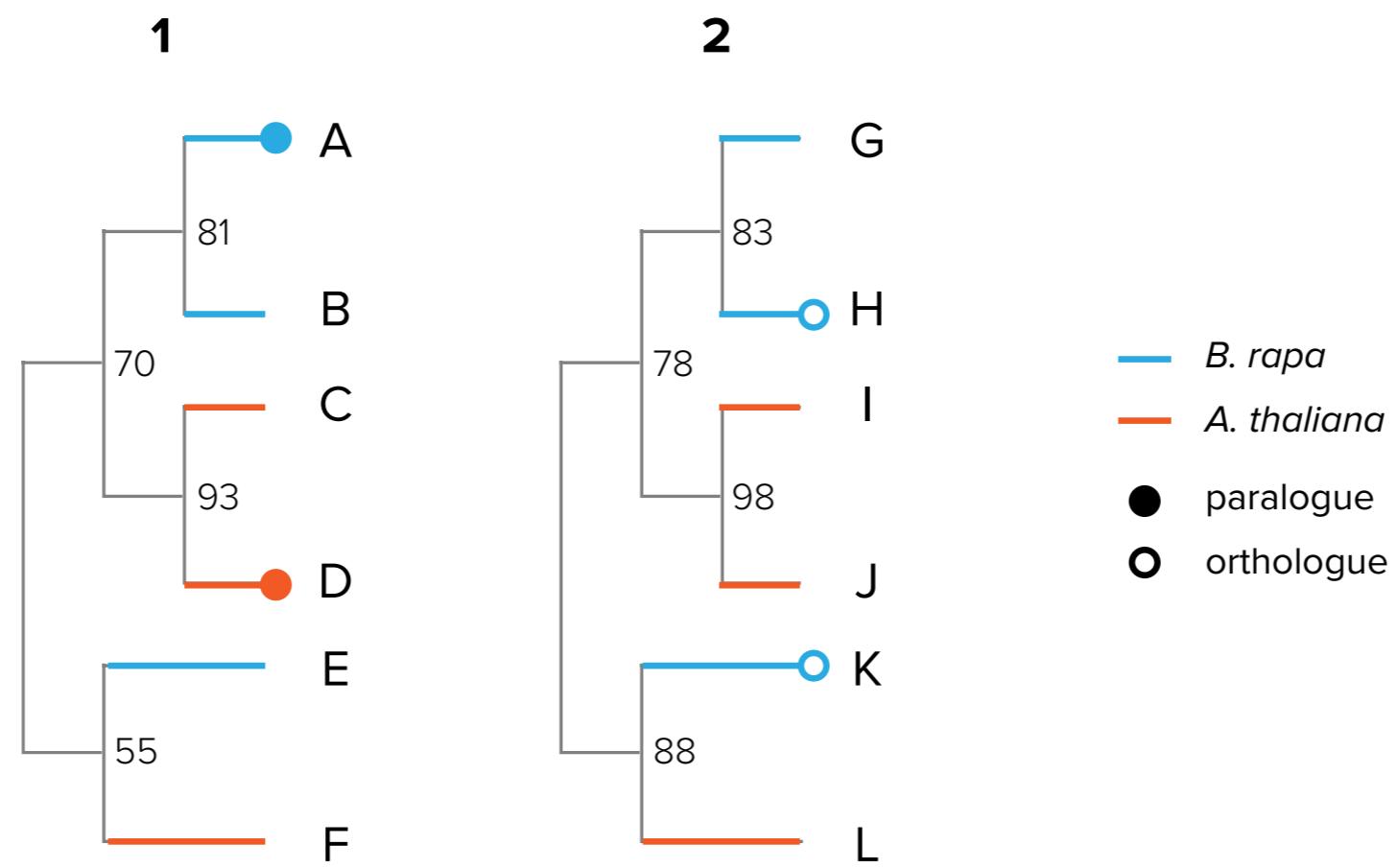


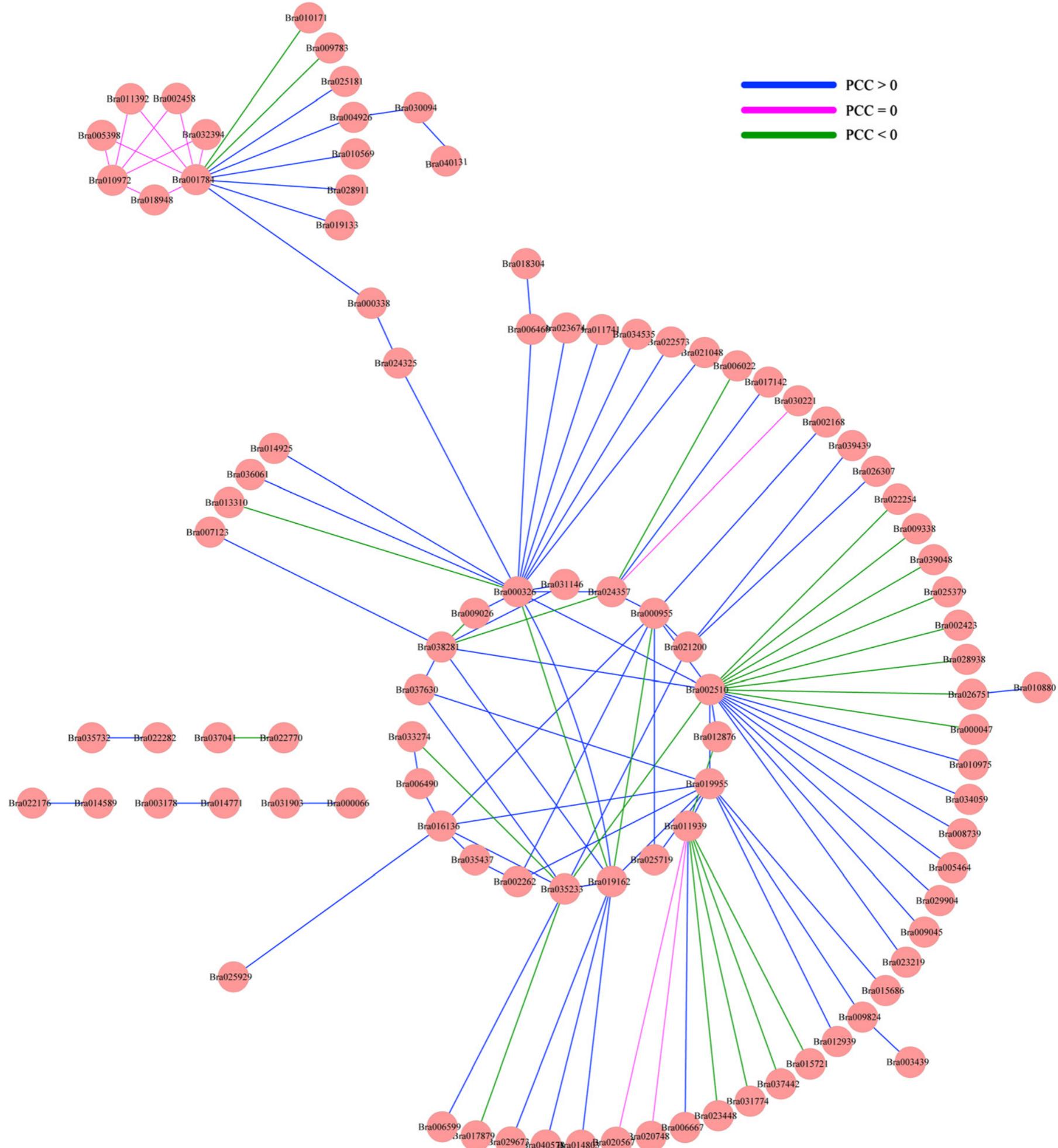


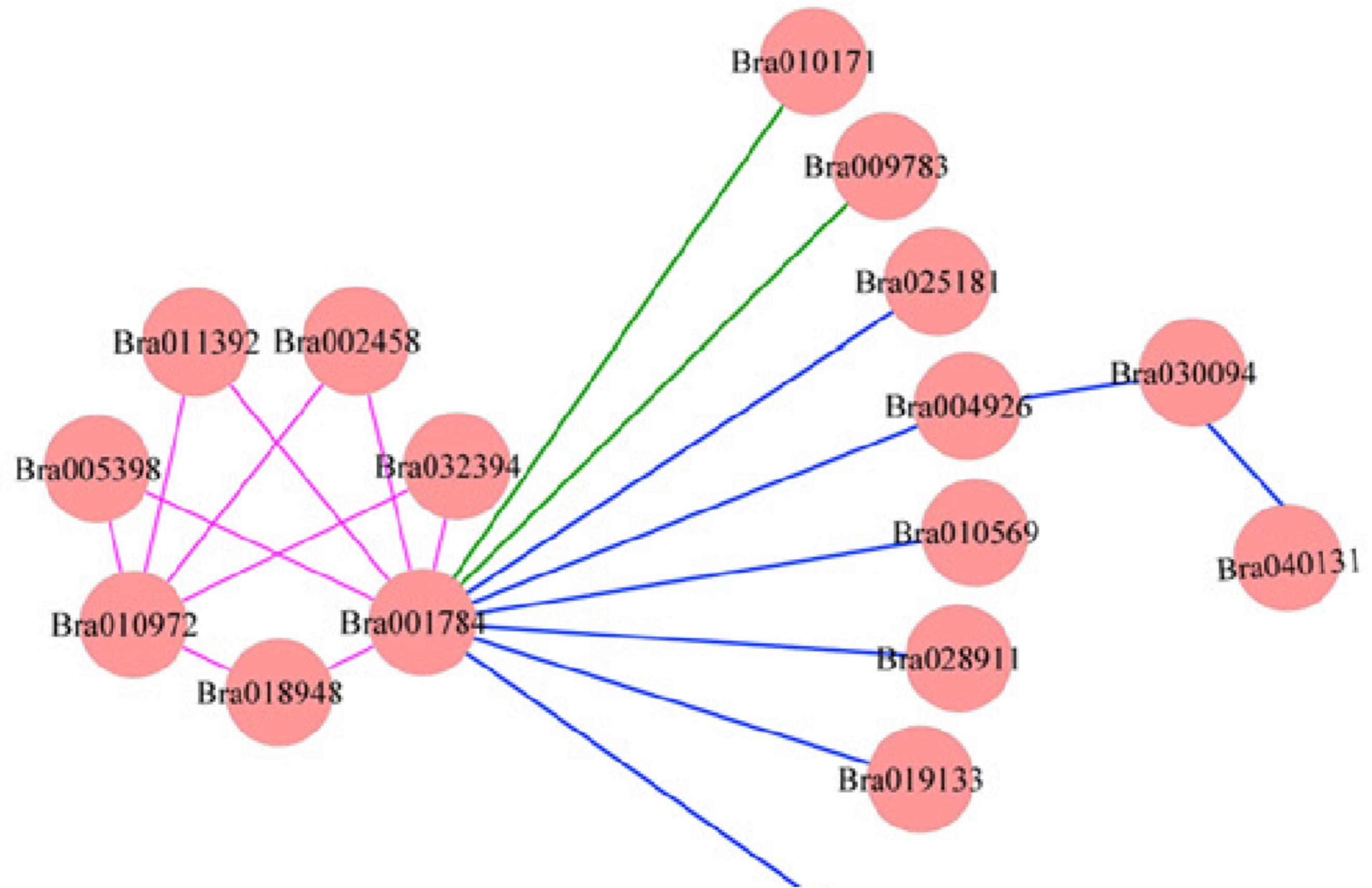
## OVERVIEW



## DETAIL









$r > 0$

$r = 0$

$r < 0$

$r > 0$  —

$r = 0$  —

$r < 0$  —

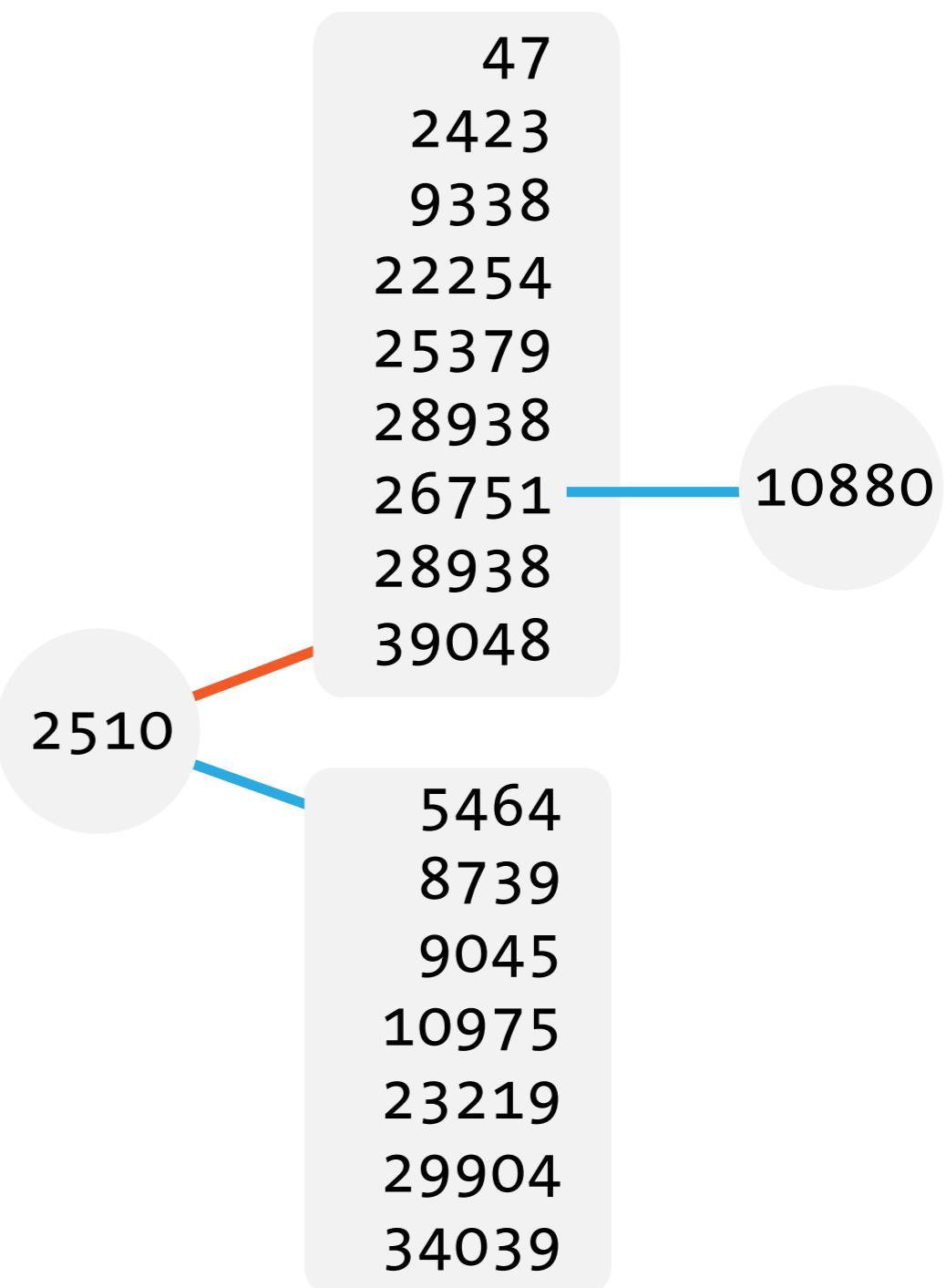
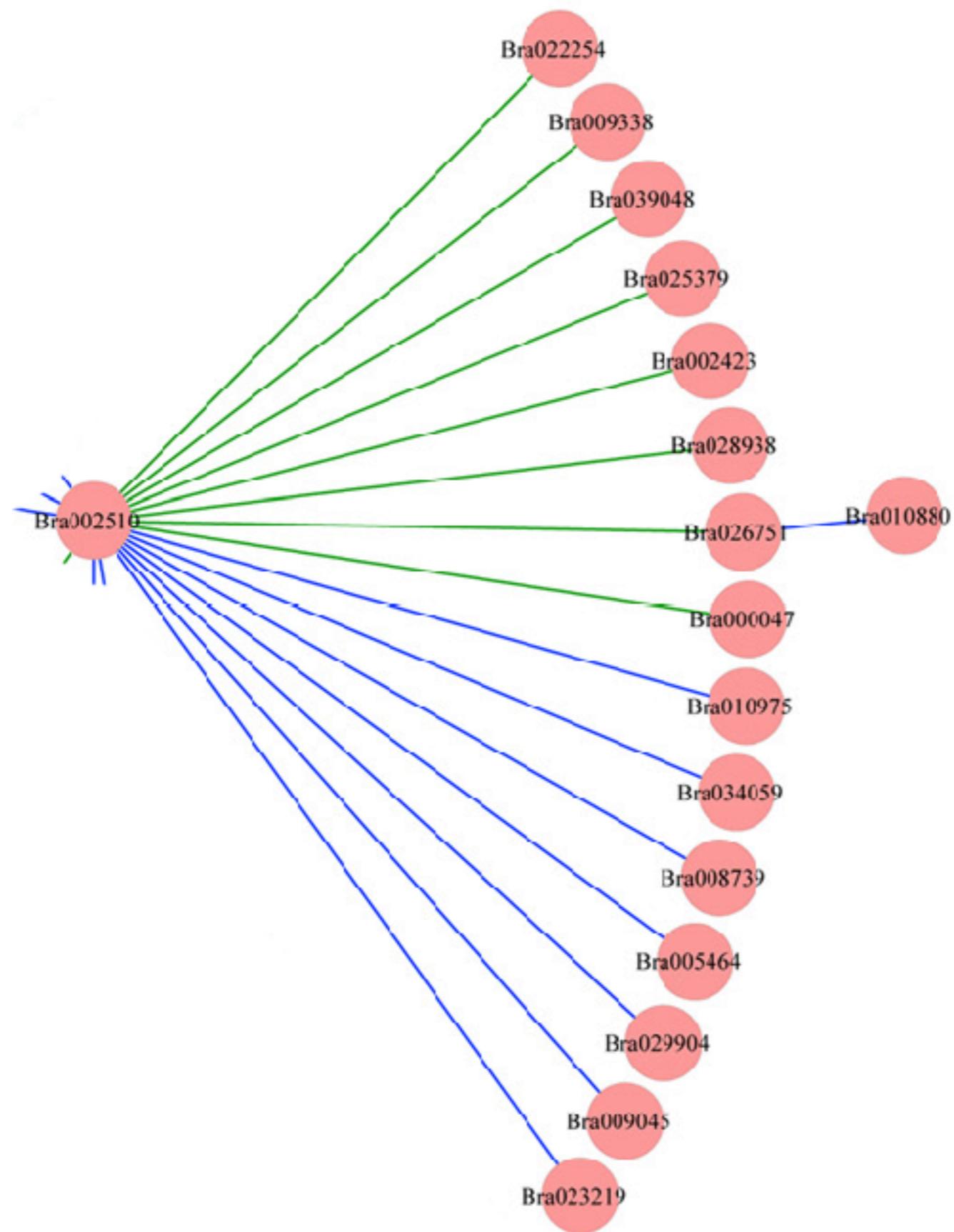
$r > 0$  —

$r = 0$  —

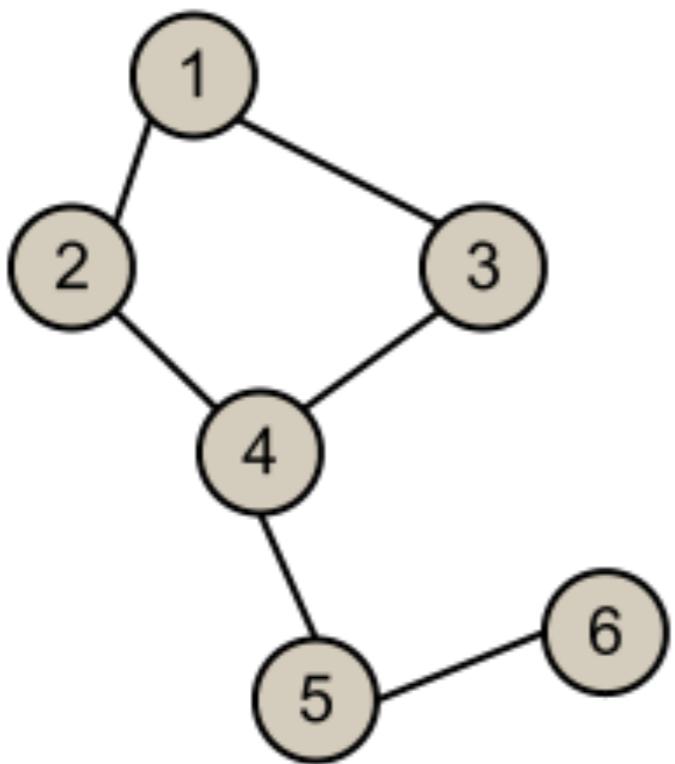
$r < 0$  —

Bra005464

5464



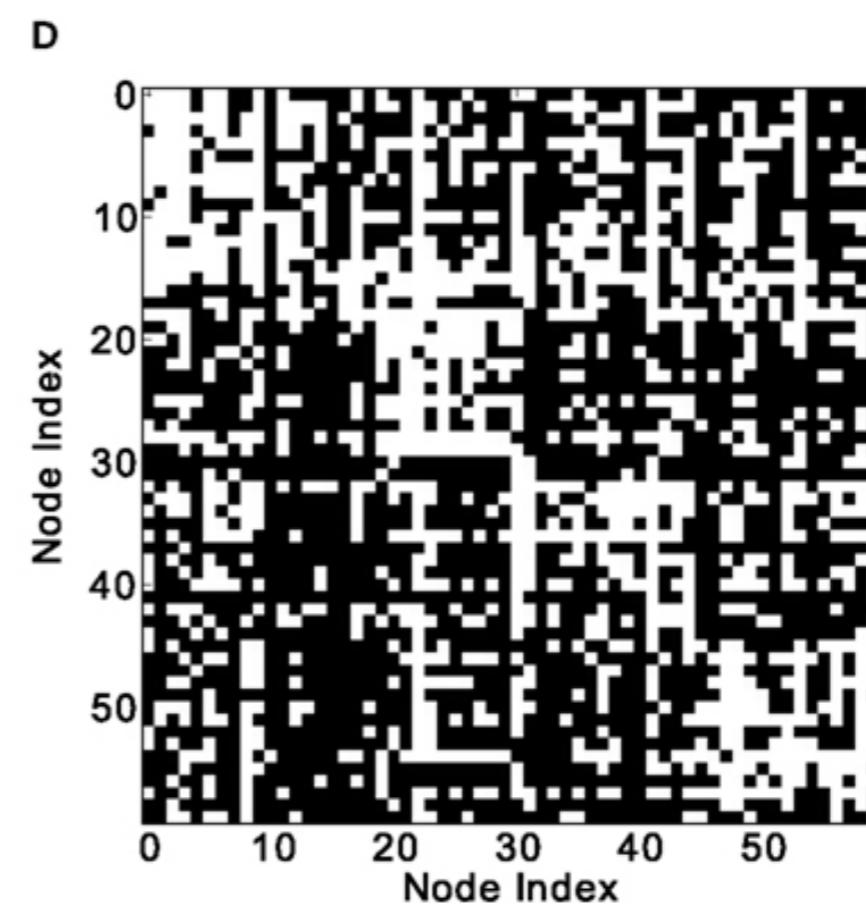
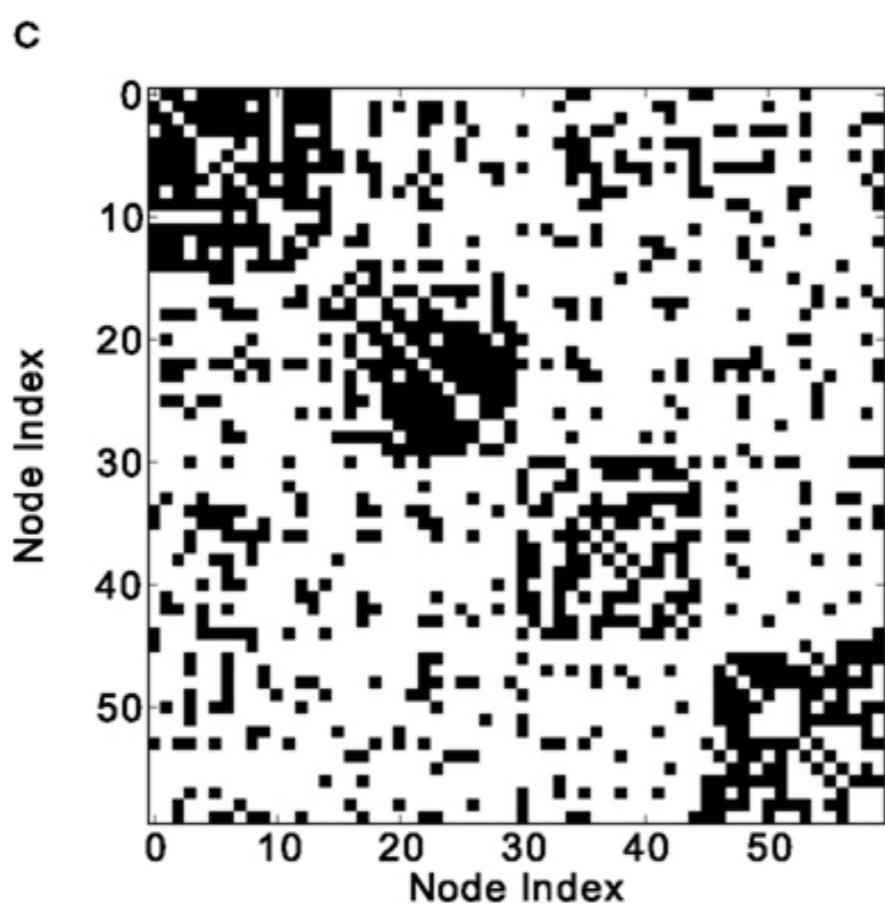
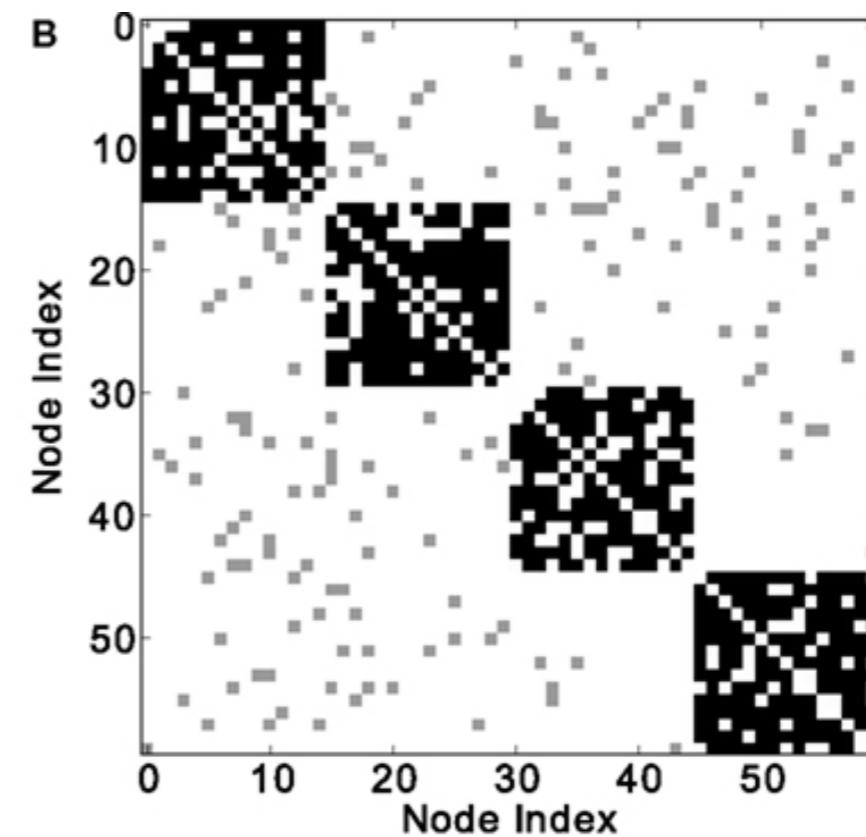
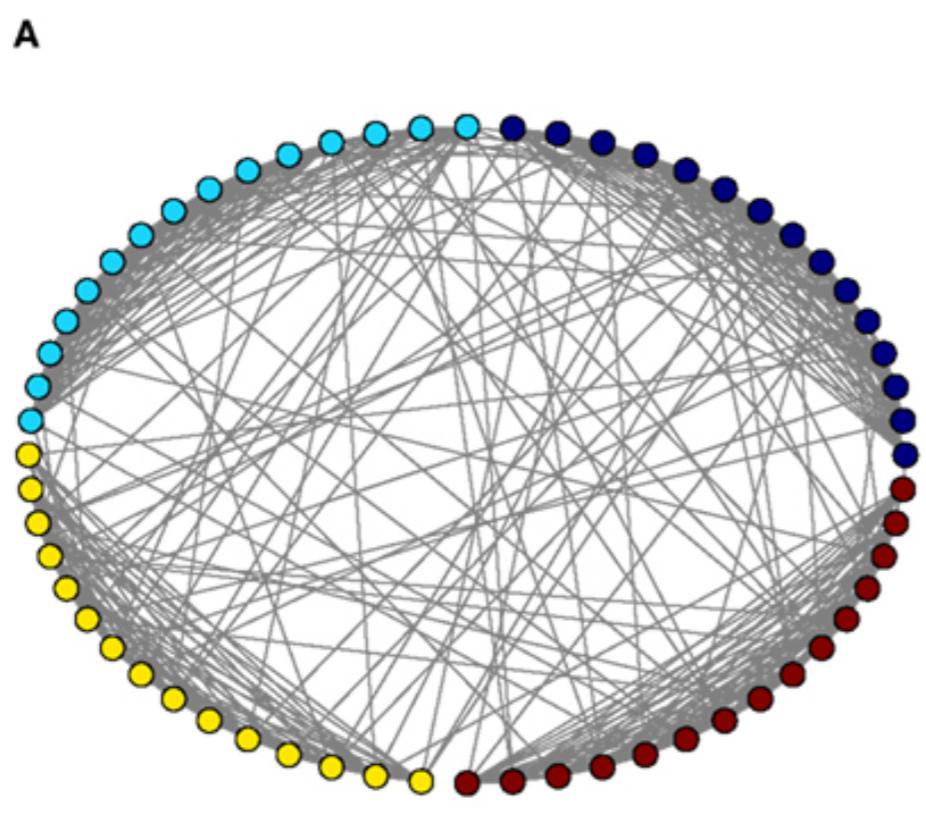
## Undirected Graph & Adjacency Matrix

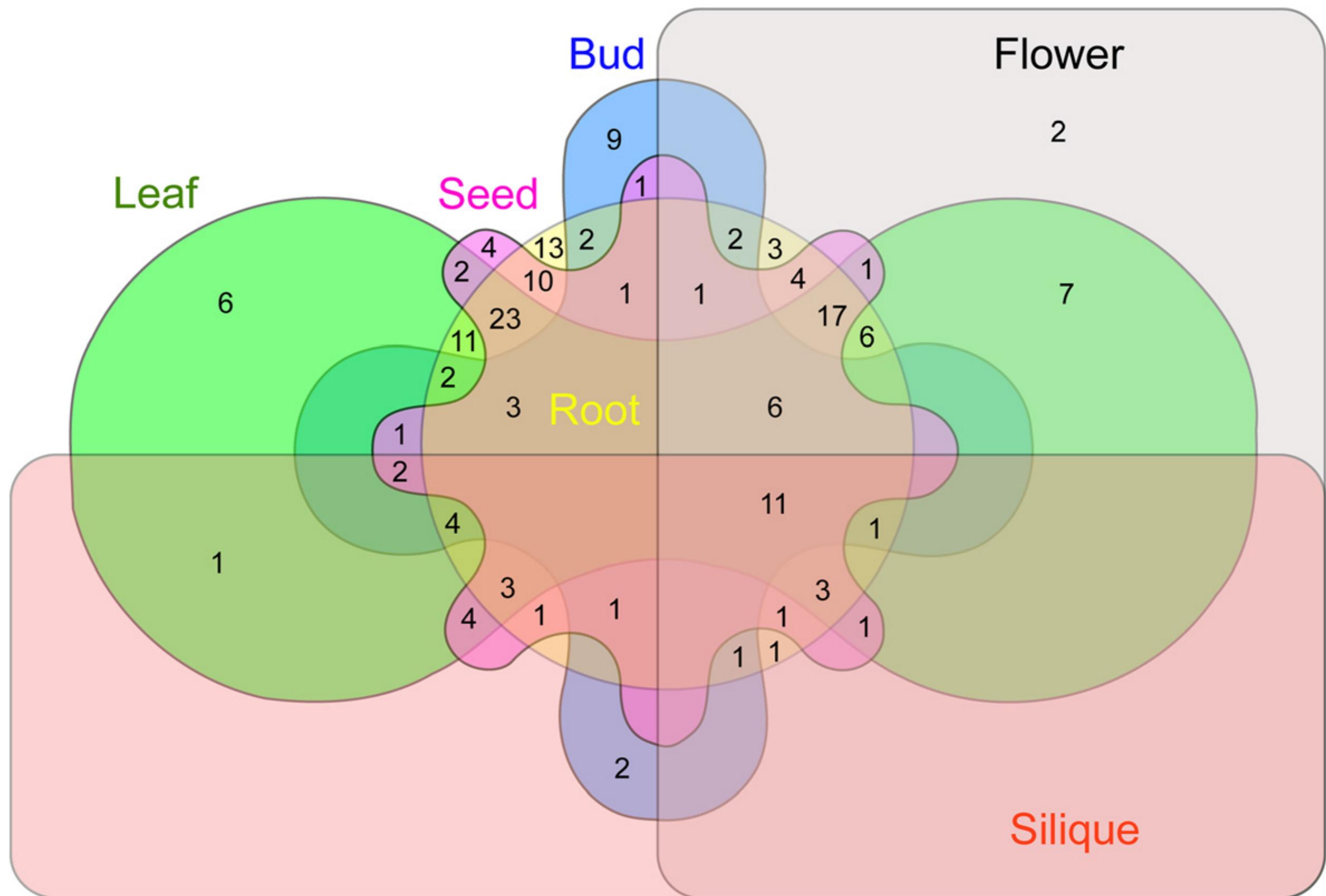


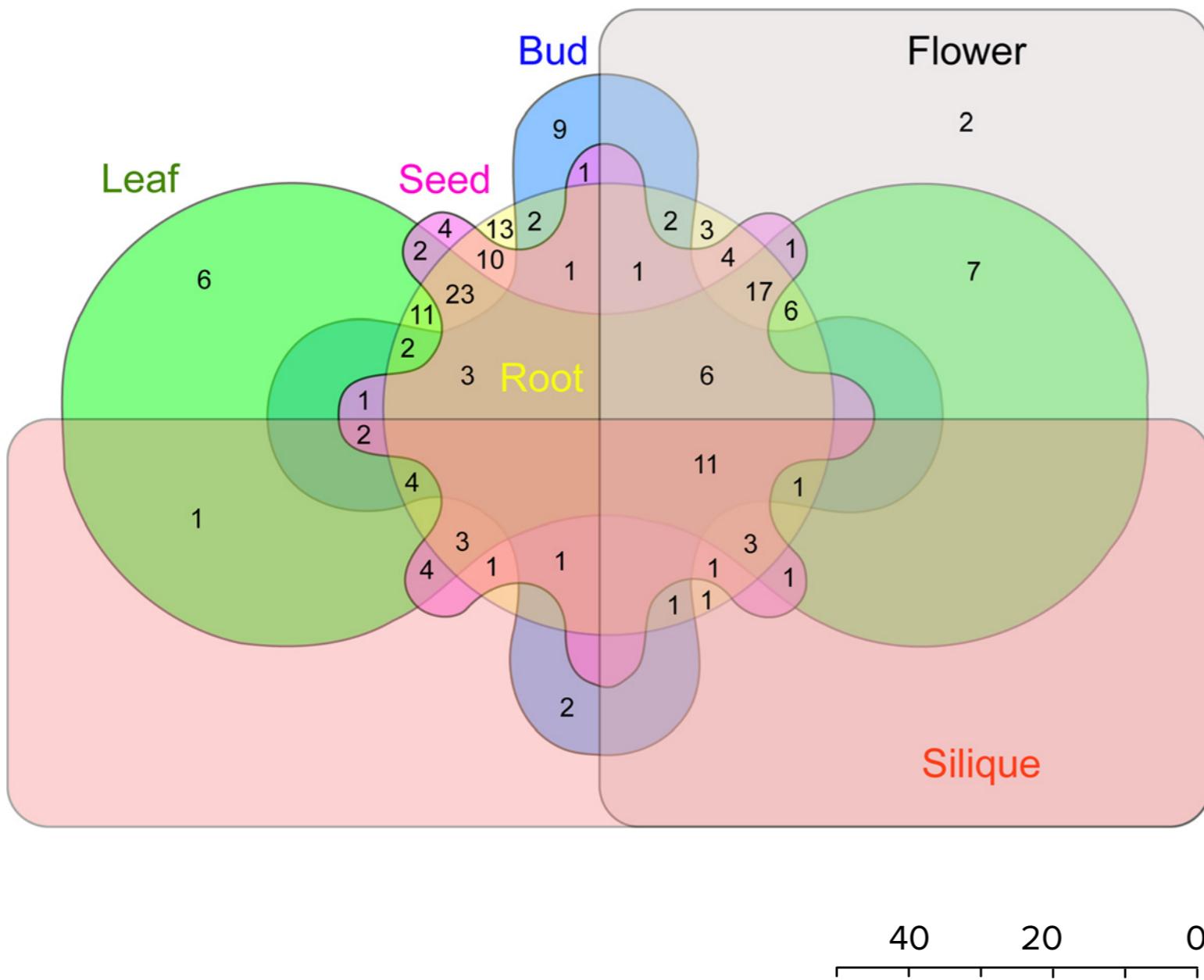
Undirected Graph

	1	2	3	4	5	6
1	0	1	1	0	0	0
2	1	0	0	1	0	0
3	1	0	0	1	0	0
4	0	1	1	0	1	0
5	0	0	0	1	0	1
6	0	0	0	0	1	0

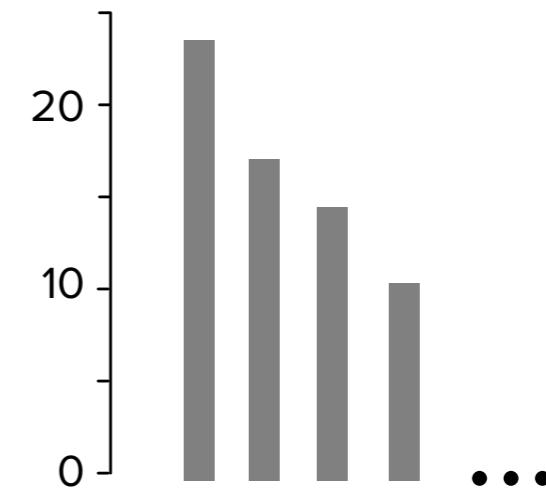
Adjacency Matrix







40 20 0



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