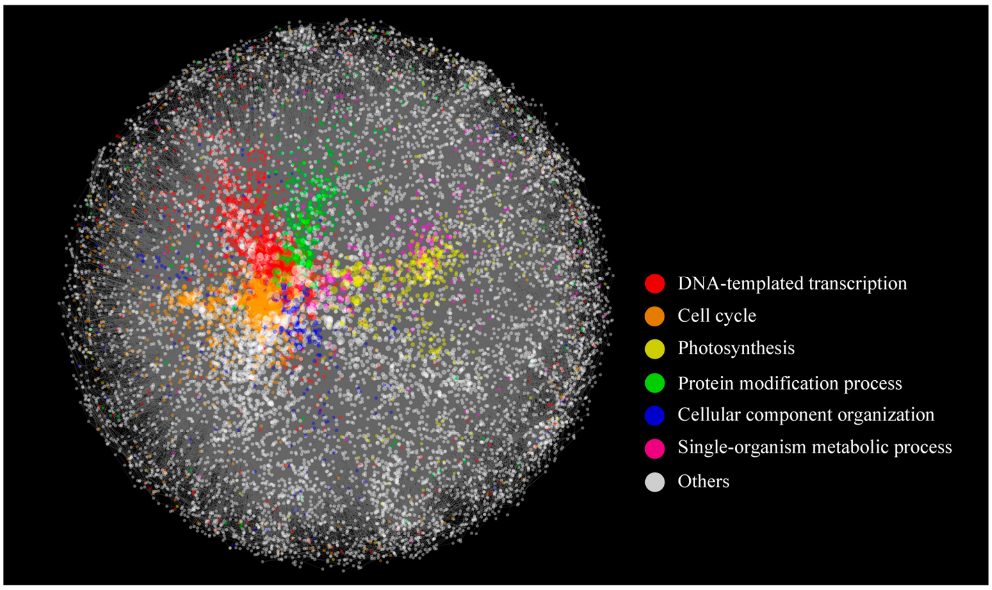

Figure S1. Global view of AraPPINet with the top six assigned modules containing at least 200 node proteins.

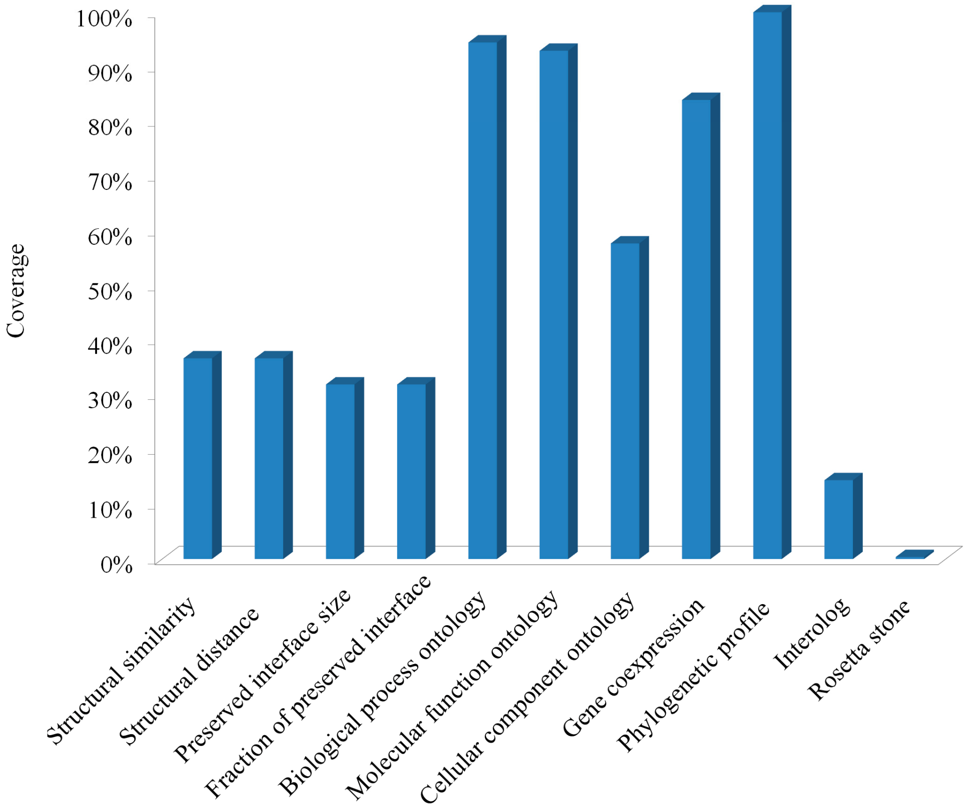

Figure S2. Coverage of features for interactions in AraPPINet.

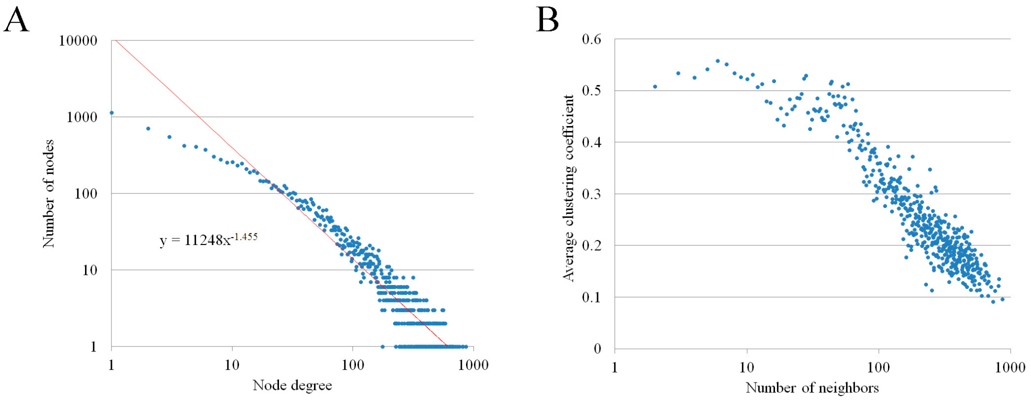

Figure S3. Topological properties of AraPPINet. A) Degree distribution of the node proteins. B) Average clustering coefficient of proteins with the same degree.

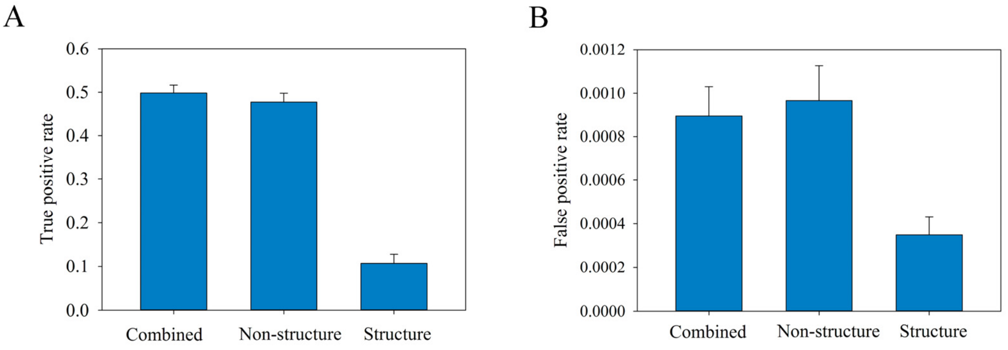

Figure S4. Comparisons of performance for methods using different sources of information. A) True positive rates of the methods from three different data sources. B) False positive rate of the methods from three different data sources. Error bars represent the standard error of the mean.

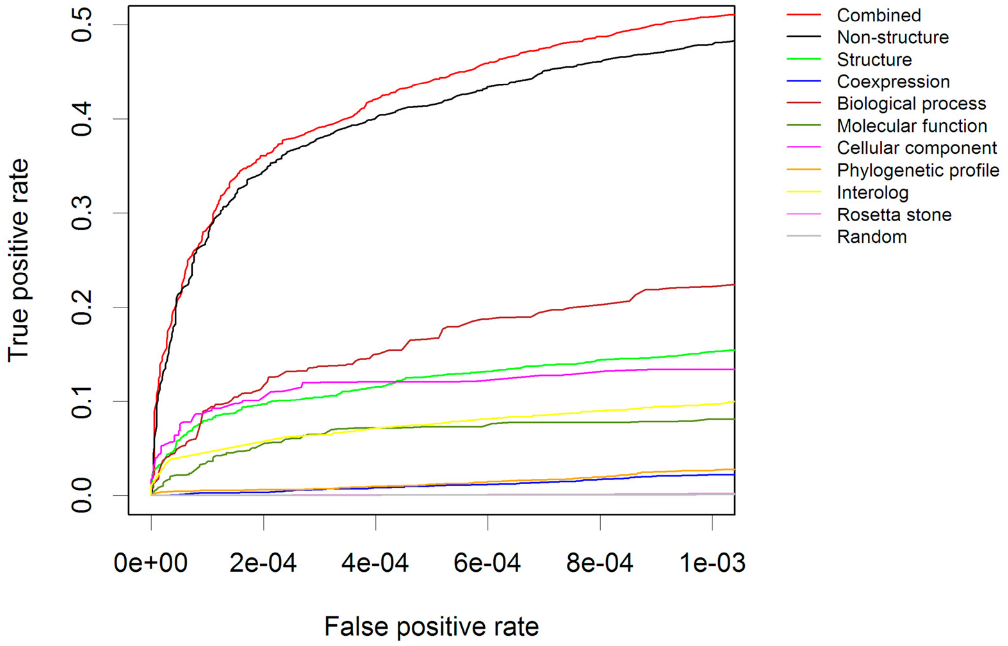

Figure S5. Partial ROC curves for PPIs predicted based on different sources of information.

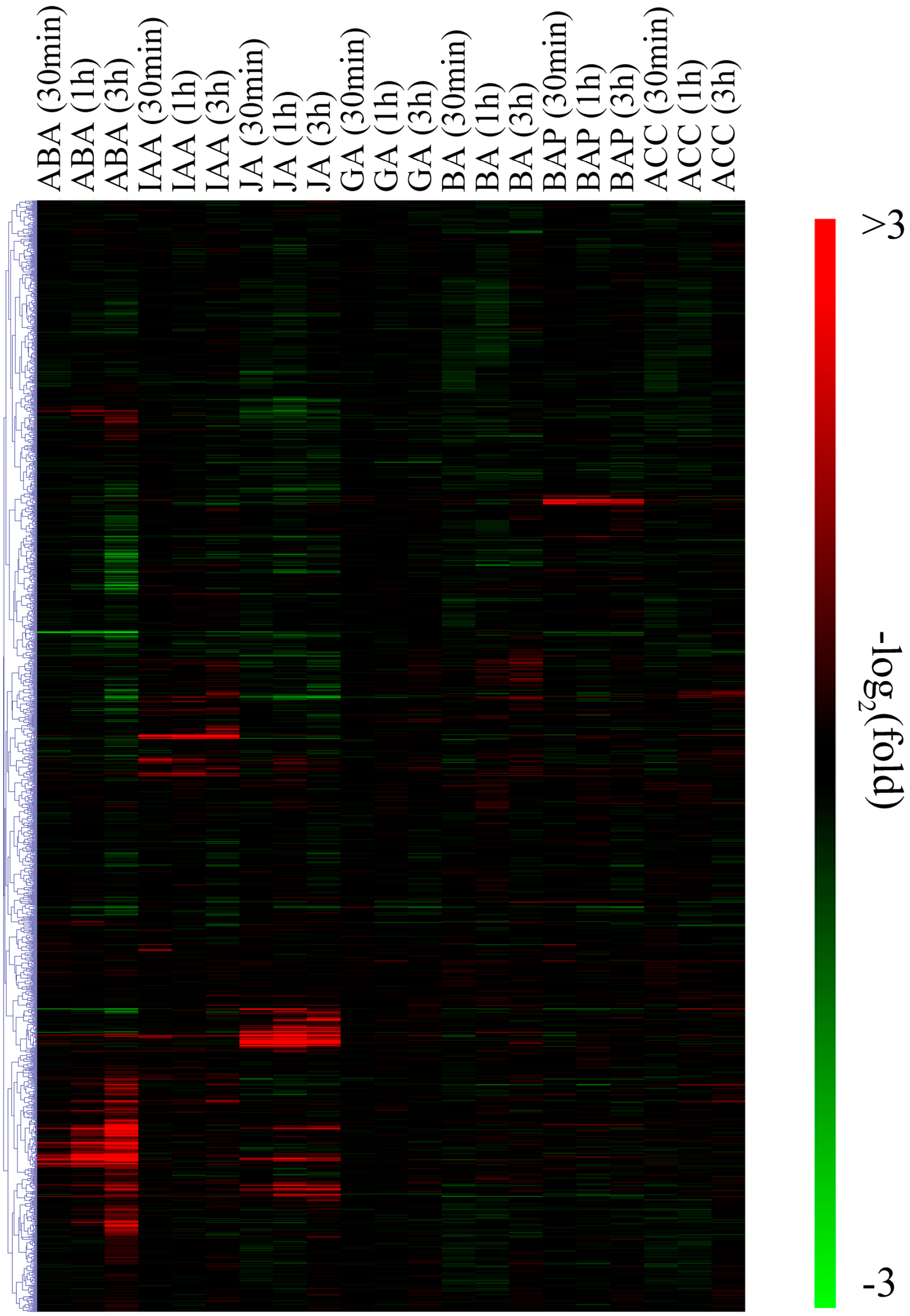

Figure S6. Heatmap of genes within the ABA signaling network in response to plant hormones at different times.