

Applications of Bayesian network models in predicting types of hematological malignancies

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Supplementary File 2: The BN structures obtained from subsampling

The following figures show BN structures learned using eigengenes in the MILE dataset for each of the 5 subsamples. Each BN is the consensus network obtained from the top third of 500 fitted networks. The nodes are colored similar to Fig. 2 in the paper.

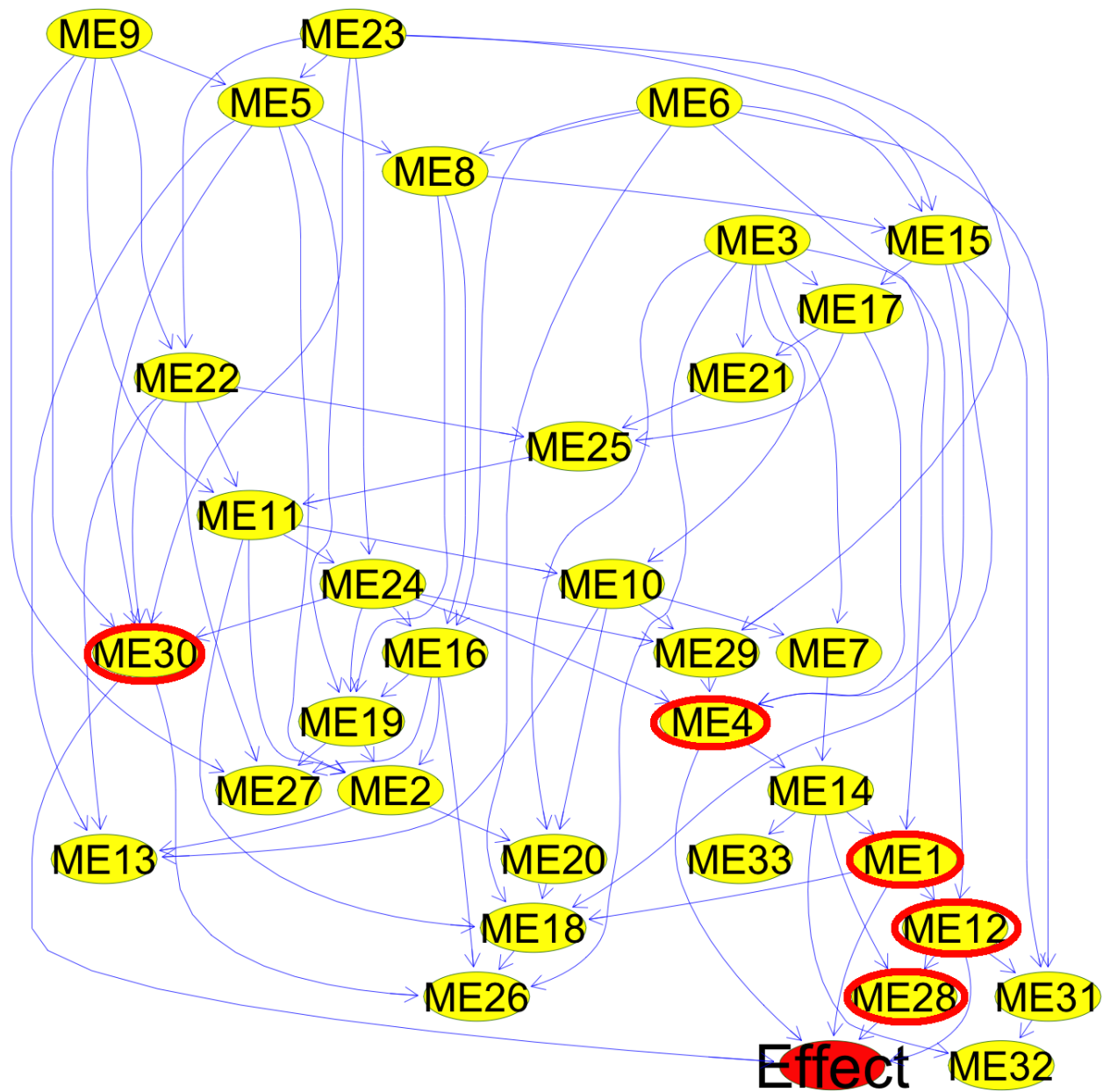


Figure 1

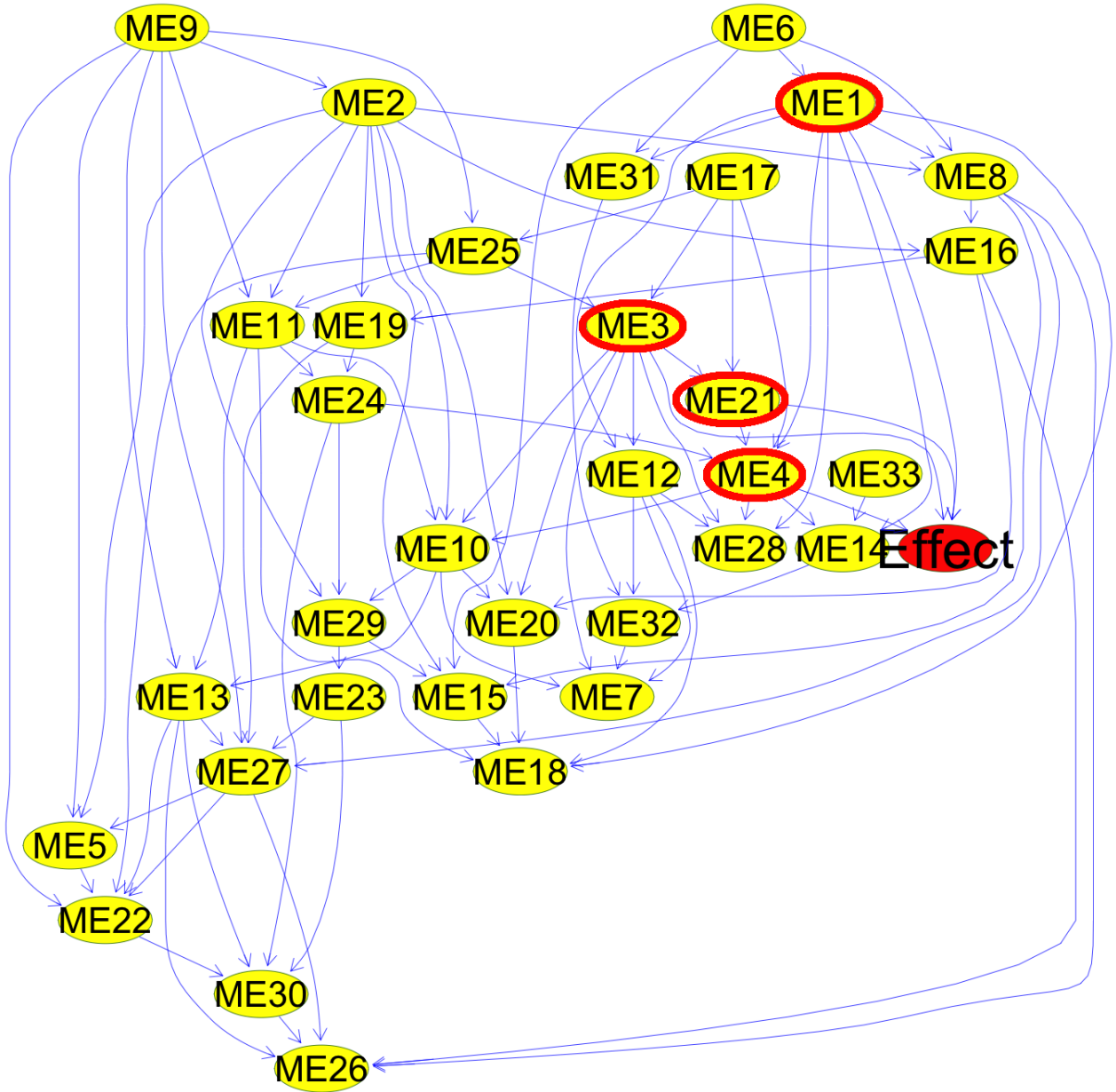


Figure 2

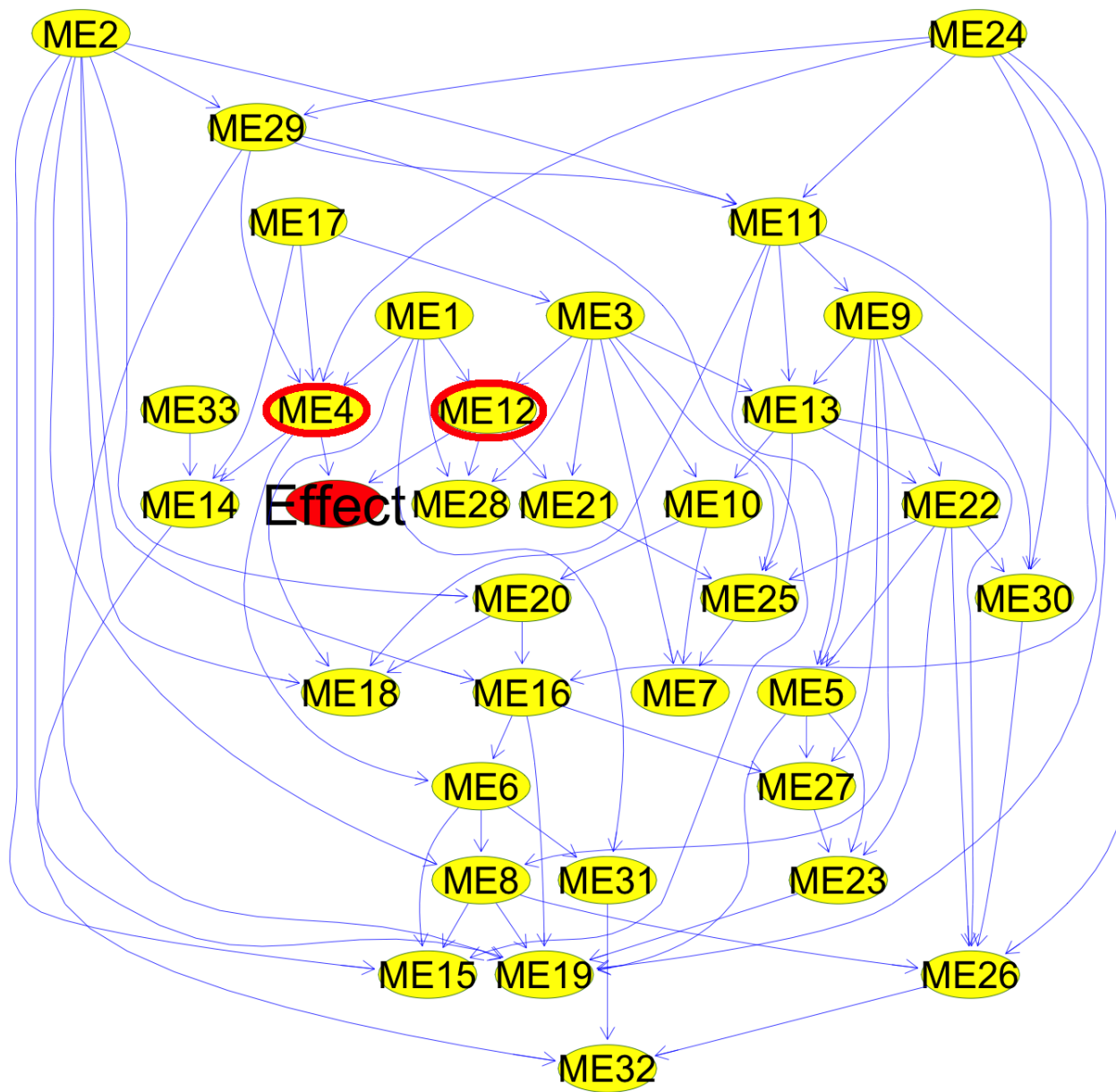


Figure 4

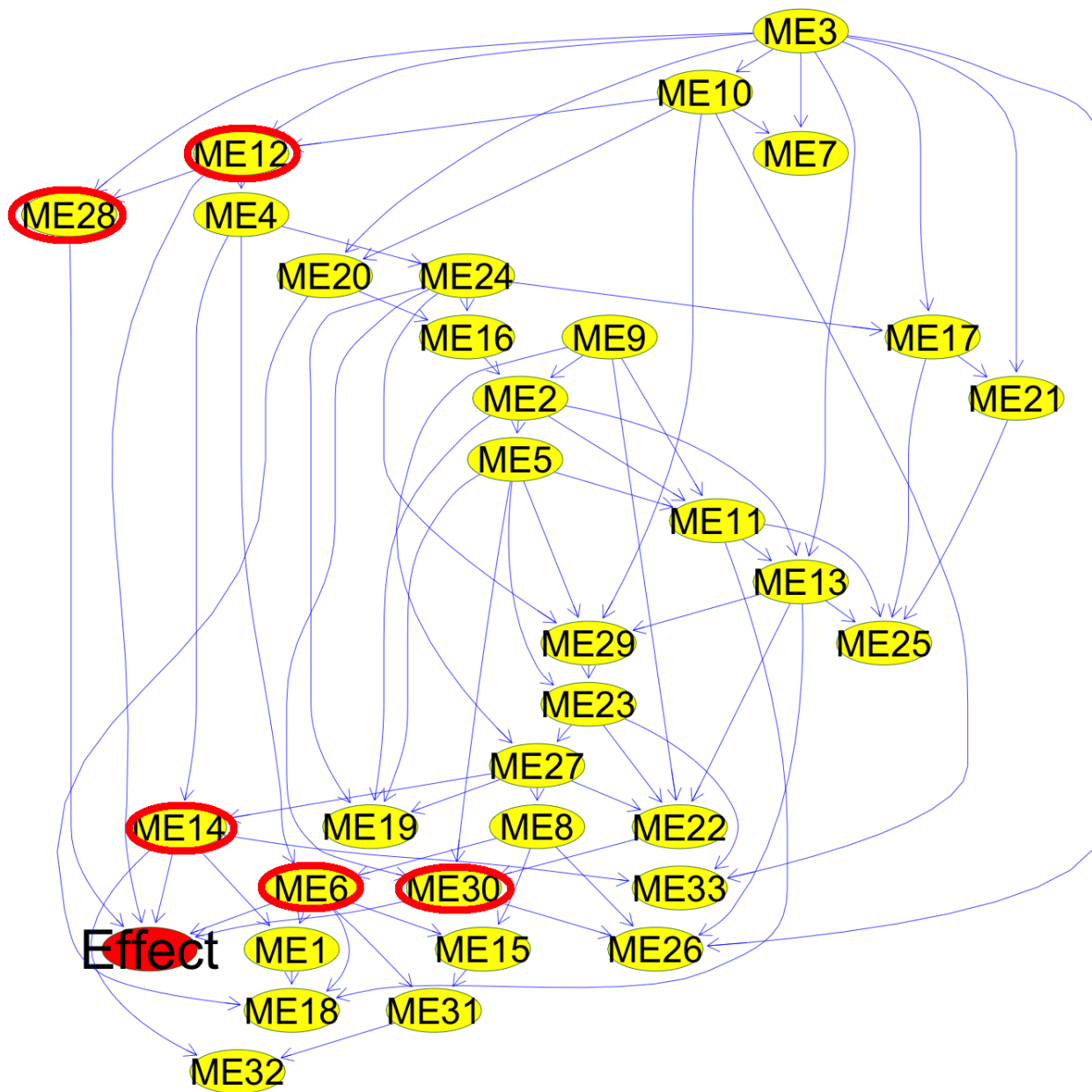


Figure 5