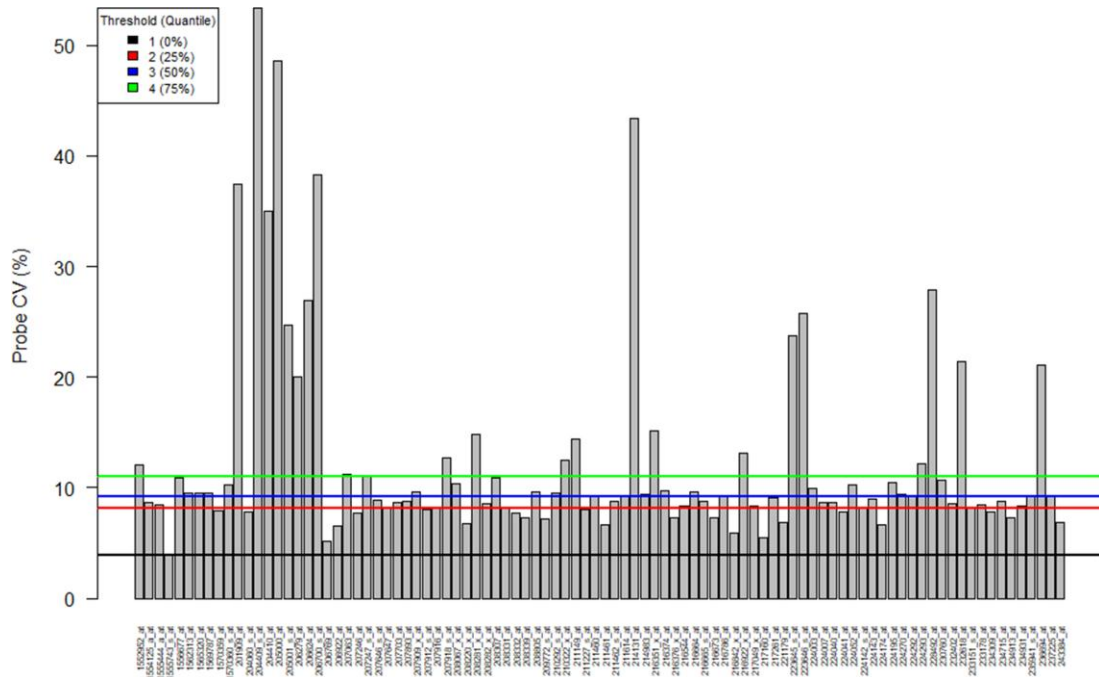
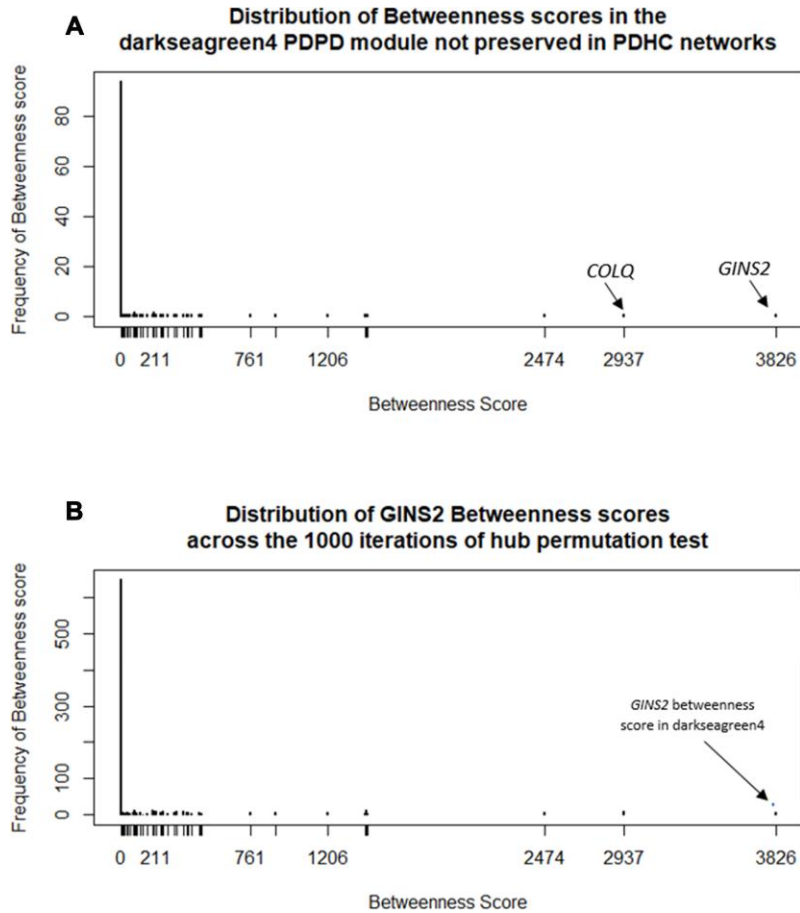


## SUPPLEMENTARY FIGURES



**Supplementary Figure 1. The probe variation plot used to determine which genes to use in massIR R package [53]. A threshold of 4 was selected as it encompassed the genes with the highest variation and ignores genes with low variation that may be useful in classifying samples.**



**Supplementary Figure 2.** (A) The distribution of betweenness scores for each gene in the darkseagreen4 module. Many genes have a betweenness score of 0 indicating they do not act as hubs in regard to betweenness in this module. After the hub permutation test, one gene was found to be significant (GINS2, Pvalue = 0.005). (B) The distribution of betweenness scores for GINS2 over the 1000 iterations of the hub permutation test. The betweenness score of GINS2 in the original darkseagreen4 module network is highlighted.