



Prediction of Key Gene Functions Associated with Chronic Hepatitis B Utilizing Network-Based Gene Function Inference Method

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ABSTRACT The objective of this paper was to reveal key gene functions associated with chronic hepatitis B (CHB) patients utilizing network-based guilt by association (GBA) method. Firstly, differentially expressed genes (DEGs) and gene ontology (GO) annotation data were prepared. Subsequently, a co-expression matrix for DEGs was constructed based on Spearman correlation coefficient (SCC) method. And then prediction of optimal gene functions were conducted through extended GBA algorithm. Finally, key gene functions were selected according to the area under the receiver operating characteristics curve (AUC) index. Results of predictions showed that 241 GO terms had a good classification performance with AUC > 0.5. In particular, AUC for 8 ones was more than 0.7 and defined as key gene functions. The results might provide potential biomarkers for early detection and treatment of CHB patients, and give great insights to revealing molecular mechanism underlying this progression.