CXCL12 methylation-mediated epigenetic regulation of gene expression in papillary thyroid carcinoma

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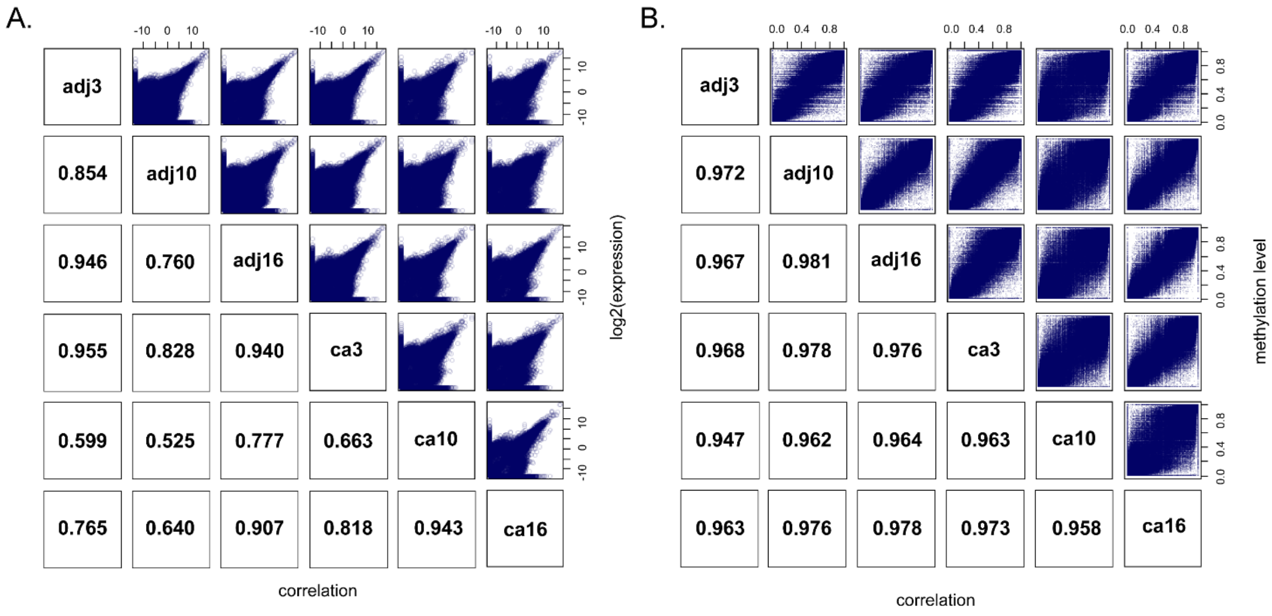
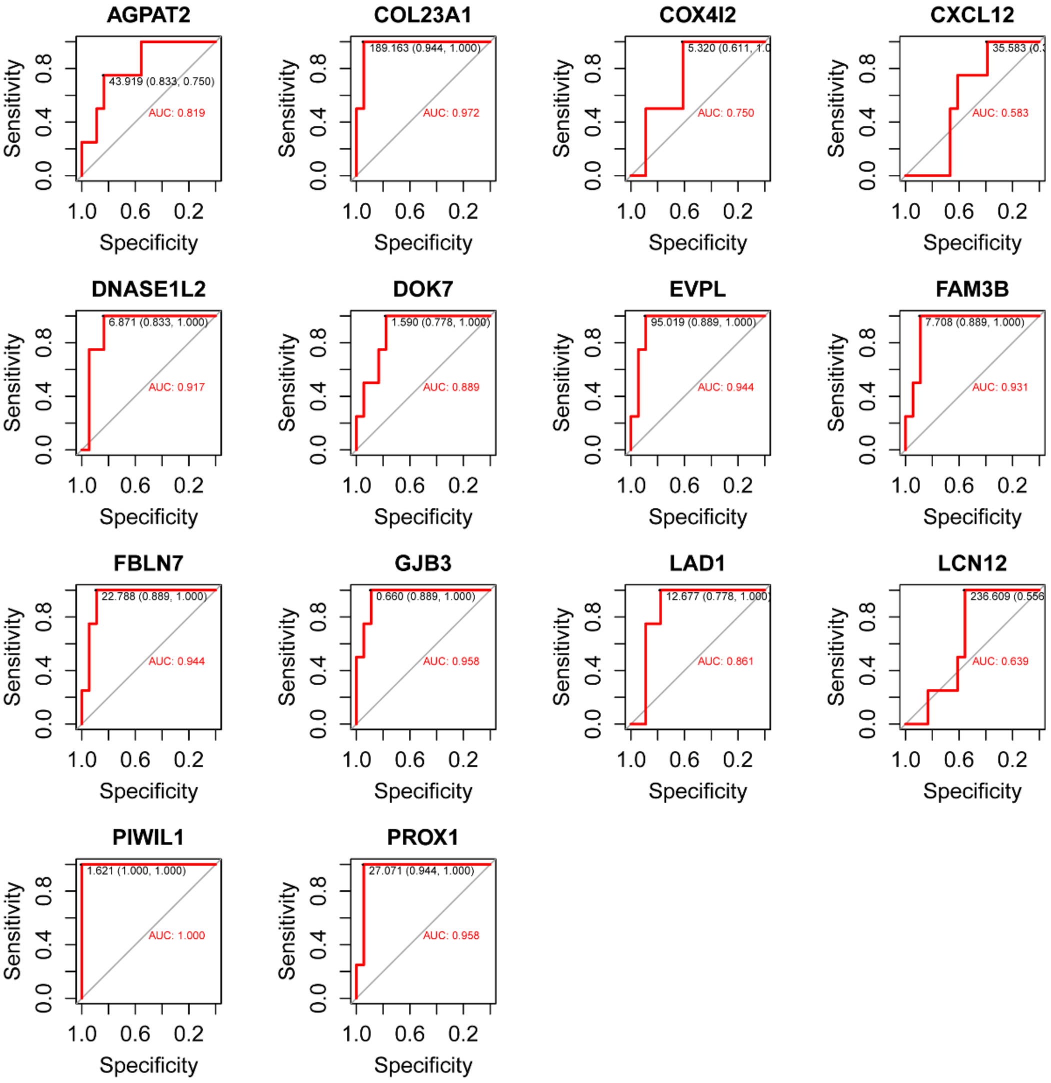
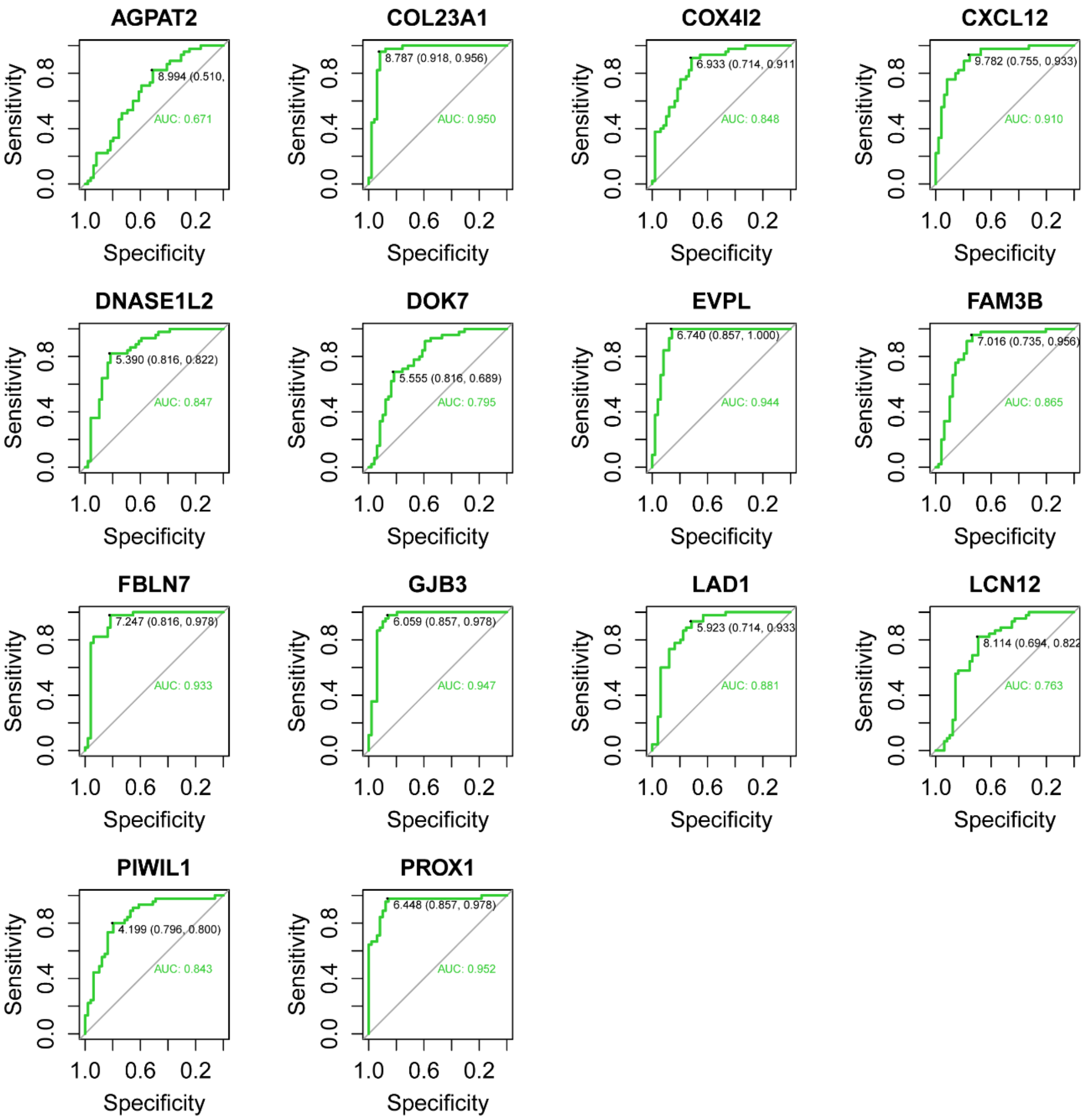
Supplementary Figures



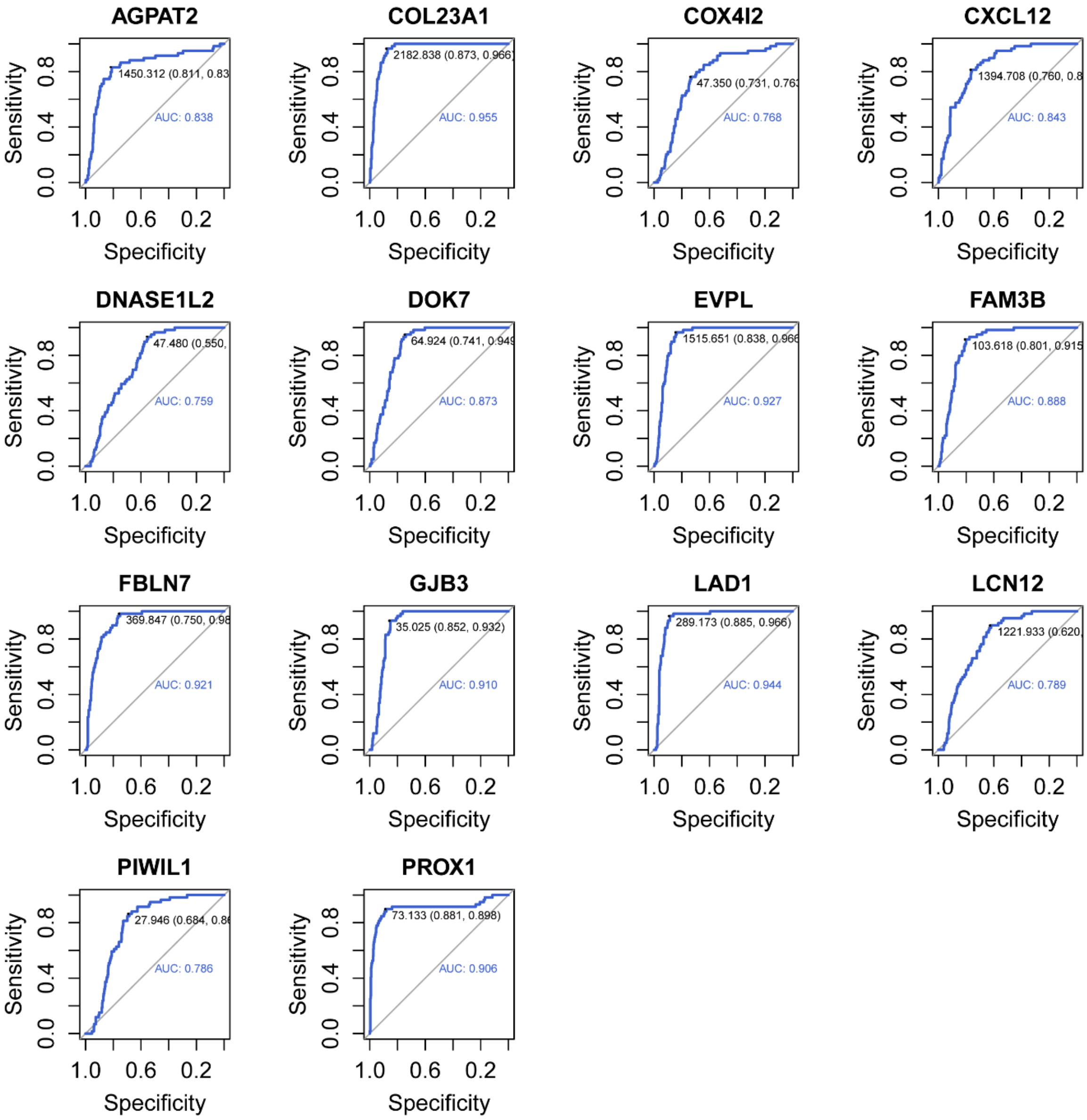
Supplementary Figure S1. The correlation of transcript expression and DNA methylation between six samples. “adj” represented the normal samples and “ca” represented the cancer samples. “3”, “10, and ”16” represented the number of the patients. The Pearson correlation coefficients of all transcripts were calculated to evaluate the correlation between each two samples.



Supplementary Figure S2.The ROC curves of the gene expression of 14 biomarkers using the data from GSE64912.



Supplementary Figure S3. The ROC curves of the gene expression of 14 biomarkers using the data from GSE33630.



Supplementary Figure S4. The ROC curves of the gene expression of 14 biomarkers using the data from TCGA RNA-seqV2.