Figure 1 Receiver-operating characteristic (ROC) curves of the three miRNAs to discriminate papillary thyroid carcinoma patients from healthy controls. (A) miR-25-3p: AUC = 0.623, 95% CI: 0.542–0.704, *P* = 0.038; (B) miR-296-5p: AUC = 0.621, 95% CI: 0.540–0.703, *P* = 0.039; (C) miR-92a-3p: AUC = 0.702, 95% CI: 0.626–0.778, *P* = 0.037.

AUC: Areas under the curve; CI: Confidence interval.

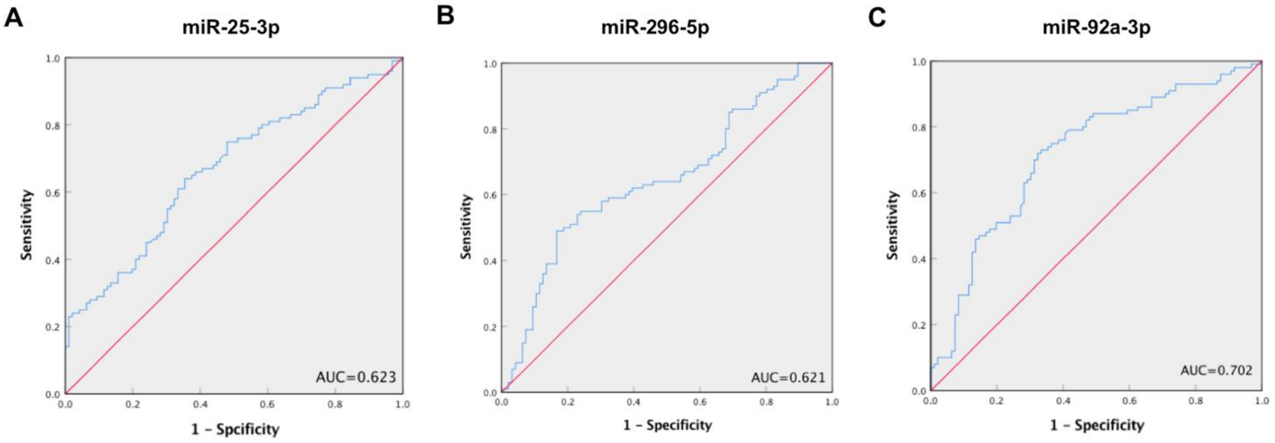

Figure 2. Comparison of the expression levels of the identified miRNAs between PTC patients and NGs. Horizontal line: Mean with 95% confidence interval. (A) miR-25-3p: $^{*}P$ = 0.007, Z = -2.636; (B) miR-296-5p: † P < 0.001, Z = -4.757; (C) miR-92a-3p: ‡ P = 0.001, Z = -3.295.

PTC: Papillary thyroid carcinoma; NG: Nodular goiter.

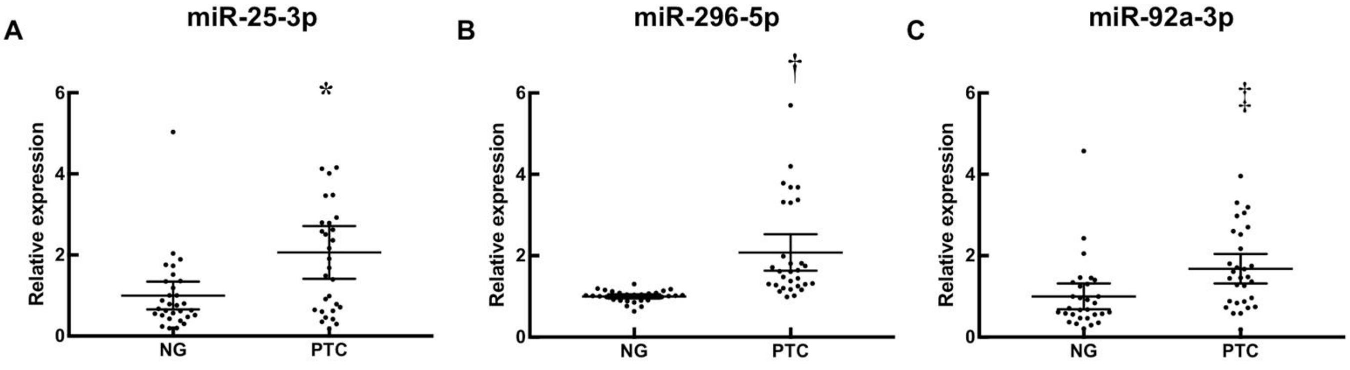

Figure 3 Receiver-operating characteristic (ROC) curve analysis of the three-miRNA panel to differentiate papillary thyroid carcinoma (PTC) patients from patients with nodular goiter (NG). AUC = 0.969, 95% confidence interval: 0.927–1.000, $P = 0.021$. AUC: Areas under the curve.

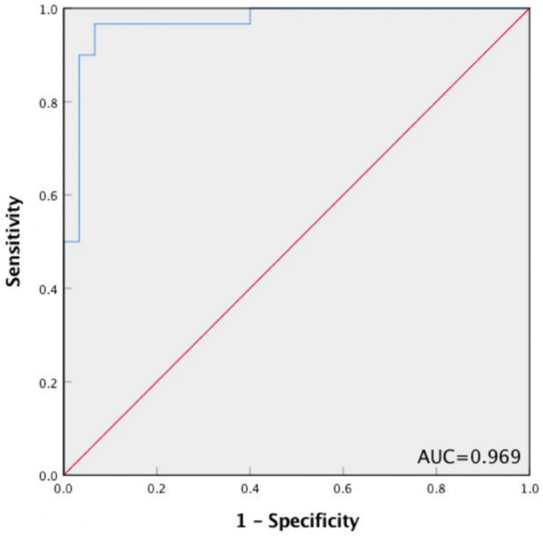

Figure 4 The Cancer Genome Atlas (TCGA) miRNA sequencing data of 59 pairs of tumor tissues and the matched normal tissues. (A) miR-25: $^{*}P < 0.001$, $Z = -4.286$; (B) miR-296: † $P < 0.001$, $Z = -3.527$; (C) miR-92a-1: ‡ $P = 0.251$, $Z = -0.095$; (D) miR-92a-2: § $P = 0.234$, $Z = -0.106$. RPKM: Reads Per Kilobase per Million.