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***Research article***

**Five genes involved in circular RNA-associated competitive endogenous RNA network correlates with metastasis in papillary thyroid carcinoma**

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**Supplementary**



**Figure S1.** Results of the SVM-recursive feature elimination (RFE) algorithm. Distribution of the relationship between RMSE and the number of circRNAs. The horizontal axis represents the number of circRNAs included in the model, and the vertical axis represents the RMSE corresponding to the number of circRNAs.

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**Figure S2.** Expression correlation between miRNAs and mRNAs. Pearson correlation analysis showed a significant negative correlation between the expression of miR-7-5p and its targets LPAR5, MFGE8, and TIMP1 in both the GSE104006 and GSE151181 datasets.

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**Figure S3.** Association between the expression of key mRNAs and clinical features. Box plots showing the expression differences of key mRNAs between groups divided by age, sex, pathologic T stage, tumor stage, and tumor location.

**Table S1.** The 37 key circRNAs screened using the SVM-recursive feature elimination (RFE) algorithm.

|  |  |  |
| --- | --- | --- |
|  | x |  |
| 1 | hsa\_circ\_0002111 | 1 |
| 2 | hsa\_circ\_0032704 | 2 |
| 3 | hsa\_circ\_0060055 | 3 |
| 4 | hsa\_circ\_0008016 | 4 |
| 5 | hsa\_circ\_0005273 | 5 |
| 6 | hsa\_circ\_0000644 | 6 |
| 7 | hsa\_circ\_0069104 | 7 |
| 8 | hsa\_circ\_0016404 | 8 |
| 9 | hsa\_circ\_0003141 | 9 |
| 10 | hsa\_circ\_0030428 | 10 |
| 11 | hsa\_circ\_0000228 | 11 |
| 12 | hsa\_circ\_0092283 | 12 |
| 13 | hsa\_circ\_0017639 | 13 |
| 14 | hsa\_circ\_0004053 | 14 |
| 15 | hsa\_circ\_0082182 | 15 |
| 16 | hsa\_circ\_0028602 | 16 |
| 17 | hsa\_circ\_0014879 | 17 |
| 18 | hsa\_circ\_0091710 | 18 |
| 19 | hsa\_circ\_0038718 | 19 |
| 20 | hsa\_circ\_0006608 | 20 |
| 21 | hsa\_circ\_0004458 | 21 |
| 22 | hsa\_circ\_0001806 | 22 |
| 23 | hsa\_circ\_0006896 | 23 |
| 24 | hsa\_circ\_0021549 | 24 |
| 25 | hsa\_circ\_0021553 | 25 |
| 26 | hsa\_circ\_0004789 | 26 |
| 27 | hsa\_circ\_0028198 | 27 |
| 28 | hsa\_circ\_0004315 | 28 |
| 29 | hsa\_circ\_0084443 | 29 |
| 30 | hsa\_circ\_0088494 | 30 |
| 31 | hsa\_circ\_0079557 | 31 |
| 32 | hsa\_circ\_0003528 | 32 |
| 33 | hsa\_circ\_0065214 | 33 |
| 34 | hsa\_circ\_0029426 | 34 |
| 35 | hsa\_circ\_0001955 | 35 |
| 36 | hsa\_circ\_0089131 | 36 |
| 37 | hsa\_circ\_0012077 | 37 |

**Table S2.** Pearson correlation analysis for the miRNAs and mRNAs in the ceRNA network.

|  |  |  |  |
| --- | --- | --- | --- |
| miRNA | mRNA | r | p-value |
| GSE104006 dataset |  |  |  |
| hsa-miR-199a-5p | APOA2 | 0.126956522 | 0.552903032 |
| hsa-miR-199a-5p | CCL20 | 0.136521739 | 0.523099349 |
| hsa-miR-199b-5p | APOA2 | −0.01826087 | 0.933558598 |
| hsa-miR-199b-5p | CCL20 | 0.100869565 | 0.637963022 |
| hsa-miR-7-5p | APOA2 | 0.033913043 | 0.875565759 |
| hsa-miR-7-5p | LPAR5 | −0.506956522 | 0.012440445 |
| hsa-miR-7-5p | MFGE8 | −0.63826087 | 0.001030663 |
| hsa-miR-7-5p | TIMP1 | −0.430434783 | 0.036906565 |
| GSE151181 dataset |  |  |  |
| hsa-miR-199a-5p | APOA2 | 0.031336725 | 0.83402097 |
| hsa-miR-199a-5p | CCL20 | 0.082446809 | 0.580572246 |
| hsa-miR-199b-5p | APOA2 | −0.03873728 | 0.795518727 |
| hsa-miR-199b-5p | CCL20 | −0.073543016 | 0.622219627 |
| hsa-miR-7-5p | APOA2 | −0.216697502 | 0.143166389 |
| hsa-miR-7-5p | LPAR5 | −0.526595745 | 0.000179005 |
| hsa-miR-7-5p | MFGE8 | −0.375925069 | 0.009601295 |
| hsa-miR-7-5p | TIMP1 | −0.544981499 | 9.70E−05 |

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