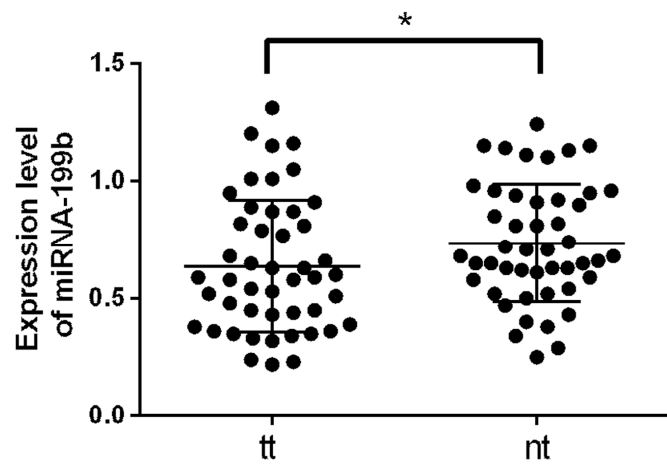
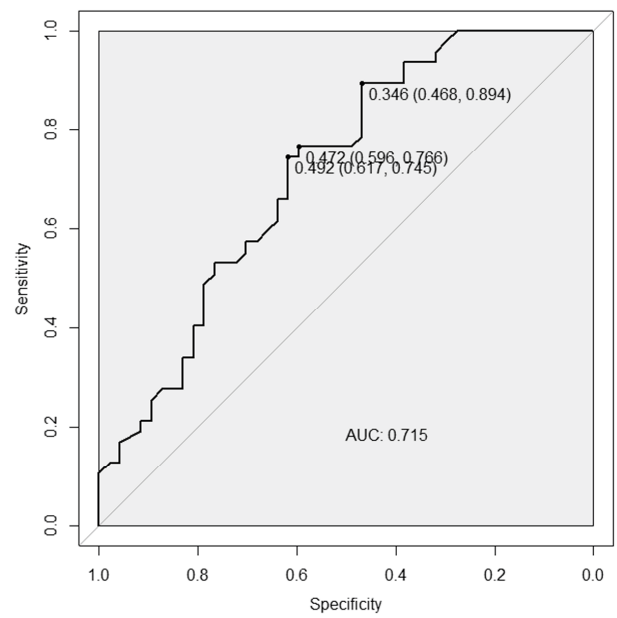
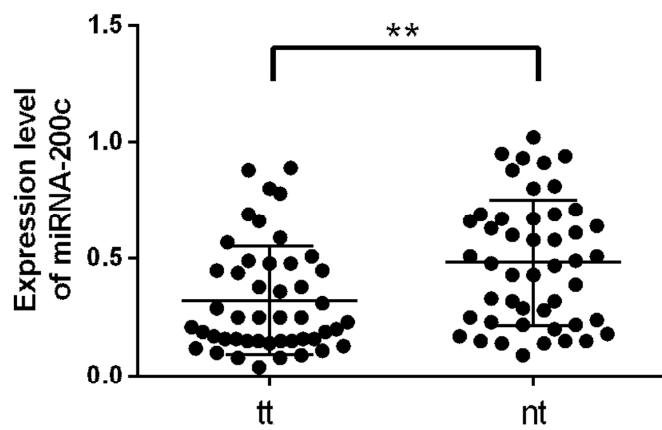
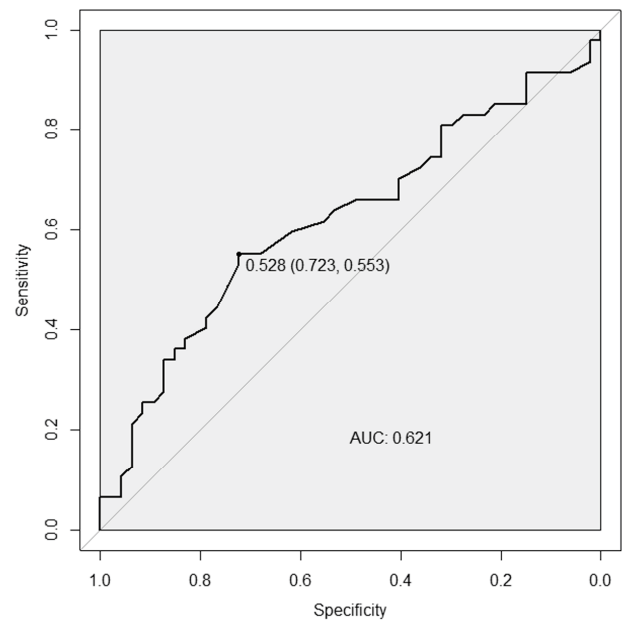


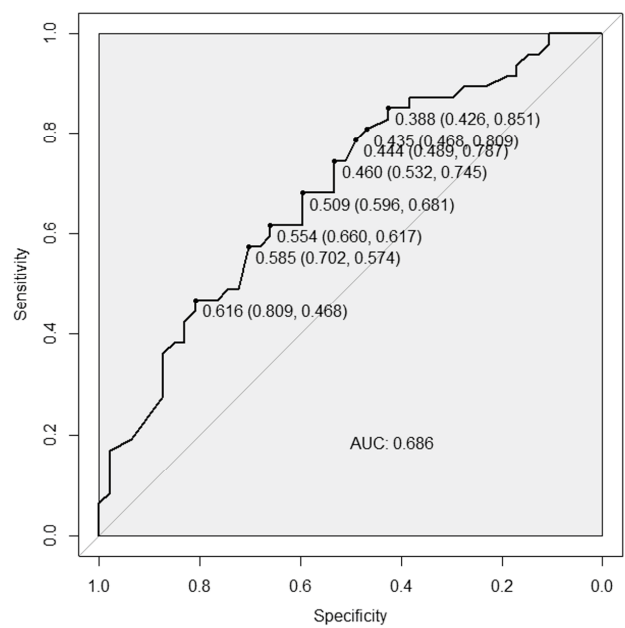
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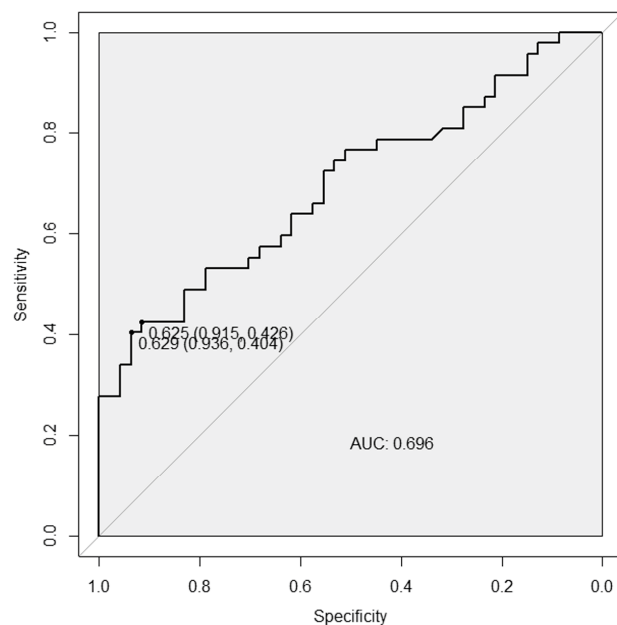
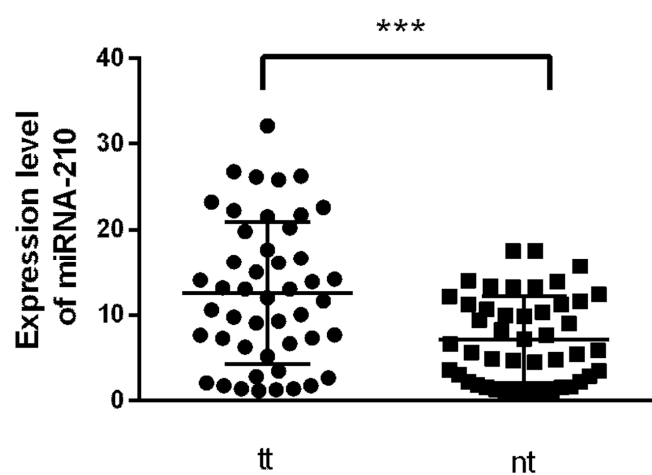


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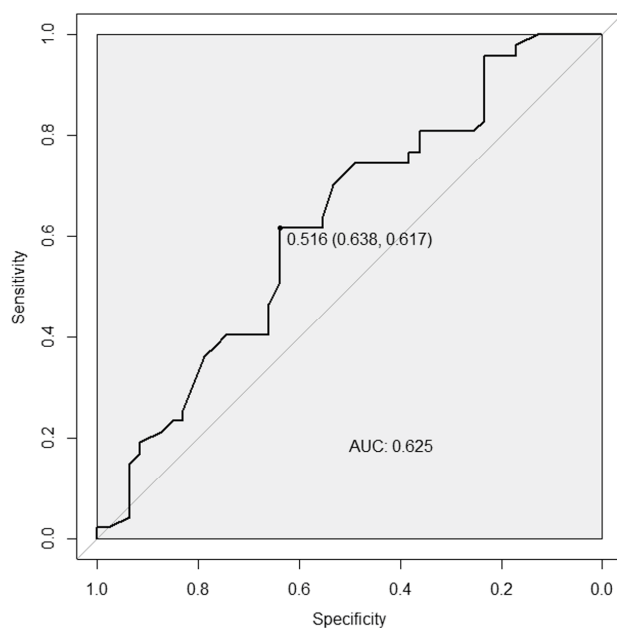
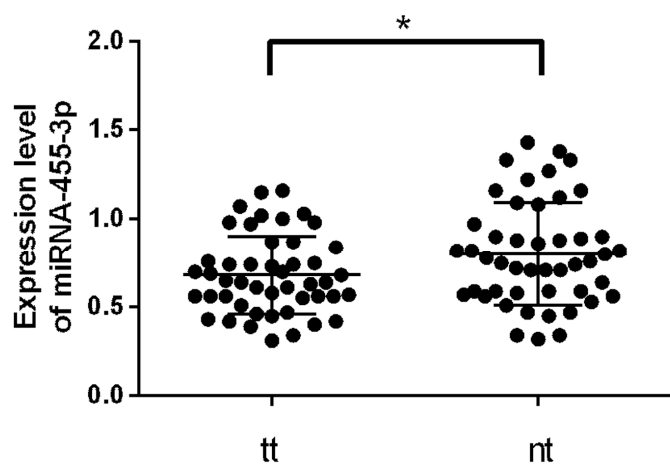


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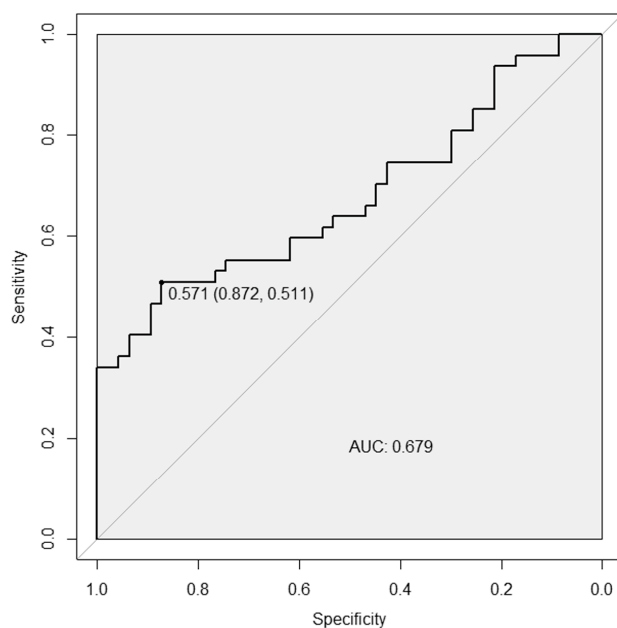
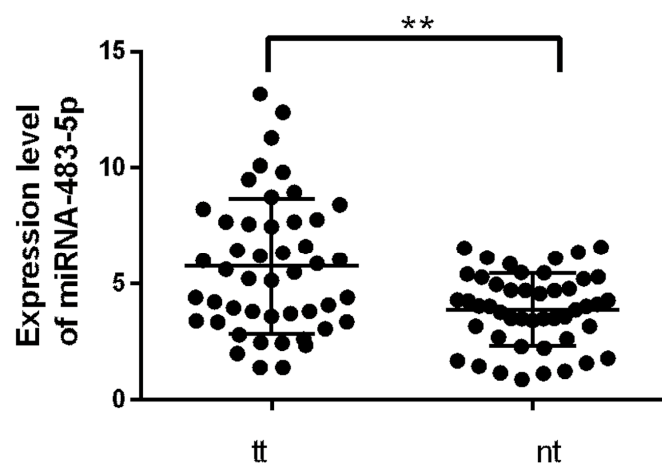




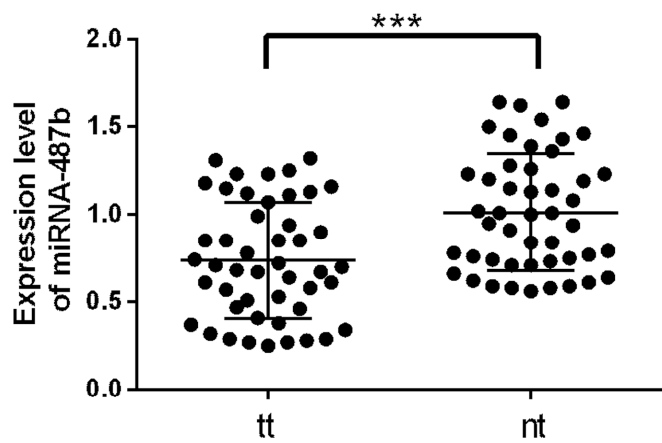
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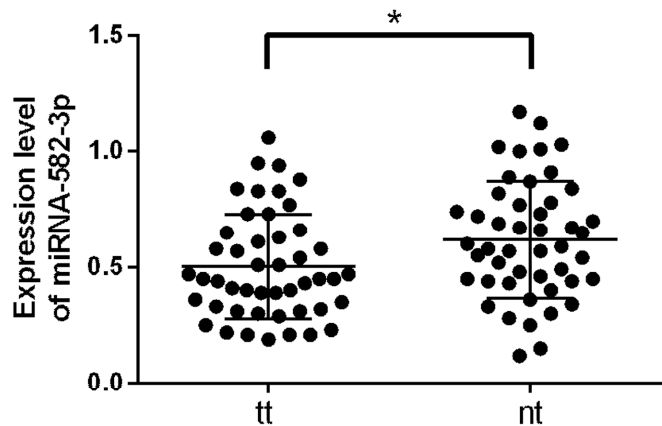
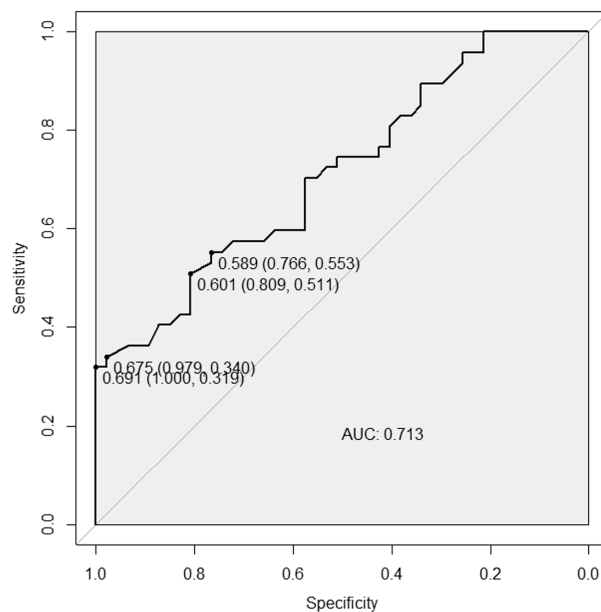
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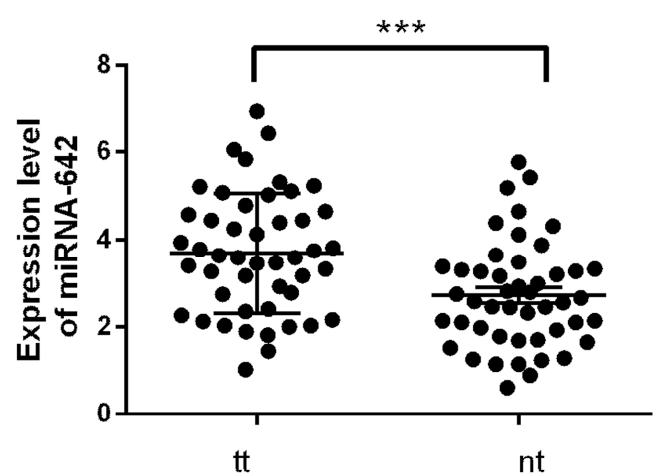
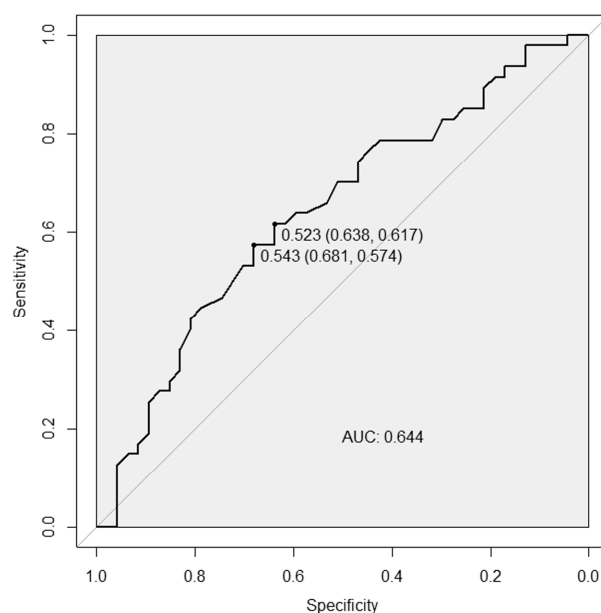
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g



h



i

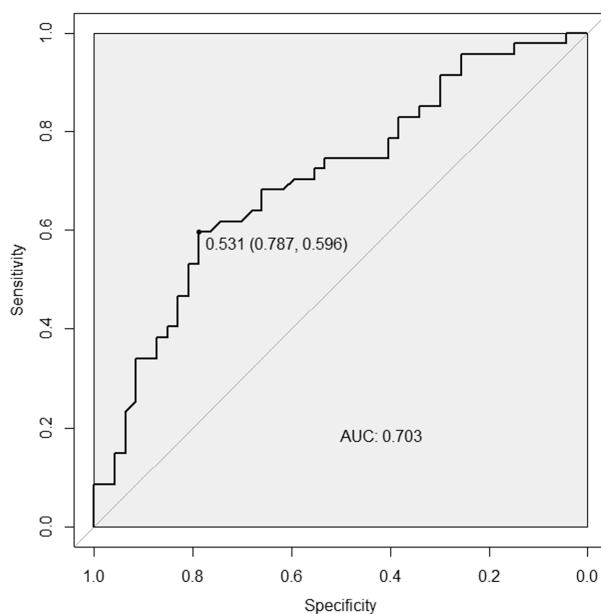


Figure S1: MicroRNAs from validation analysis with significant differences. The scatter plots show (a) miRNA-18a, (b) miRNA-199b, (c) miRNA-200c, (d) miRNA-210, (e) miRNA-455-3p, (f) miRNA-483-5p, (g) miRNA-487b, (h) miRNA-582-3p and (i) miRNA-642 expression level analysis performed using Mann–Whitney U test. The line plots present ROC-curve analysis of each miRNAs discrimination power to distinguish tumor and normal tissues. tt—ccRCC tumor tissue; nt—normal renal tissue; AUC—area under the curve; p -value: ***— $p < 0.0001$, **— $p < 0.001$, *— $p < 0.01$.

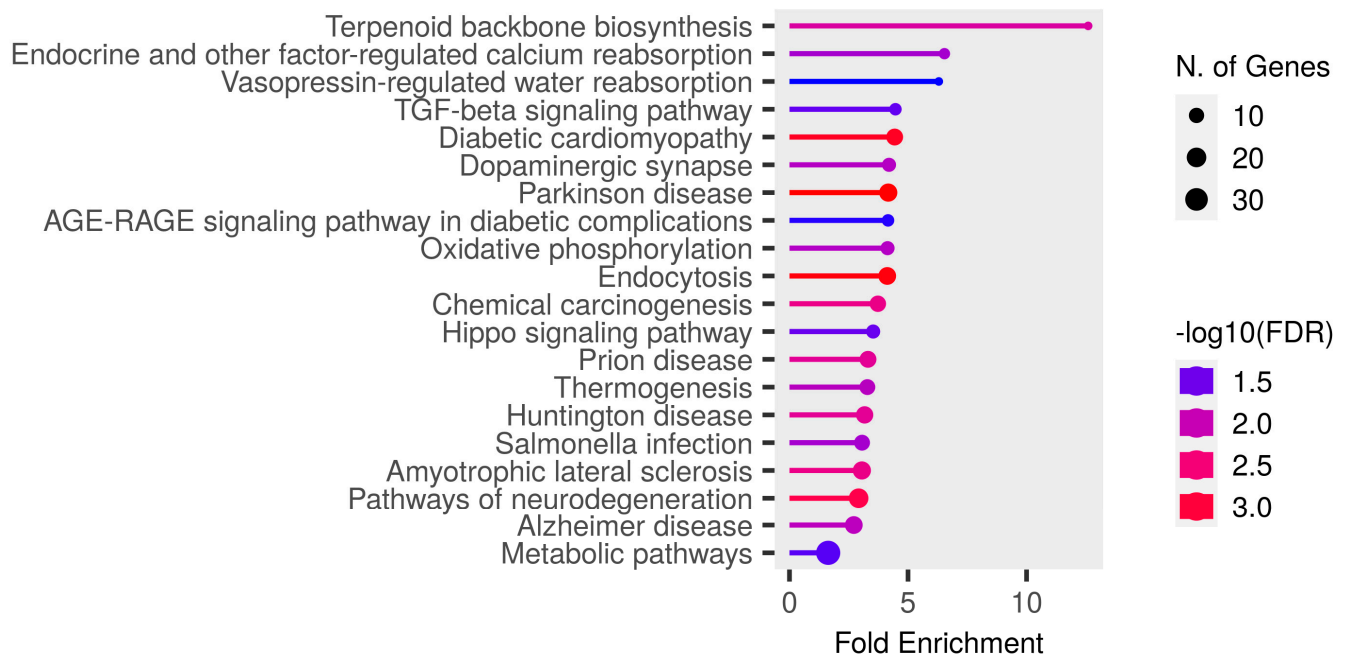


Figure S2: The results of enrichment of miRNA-18a targets.

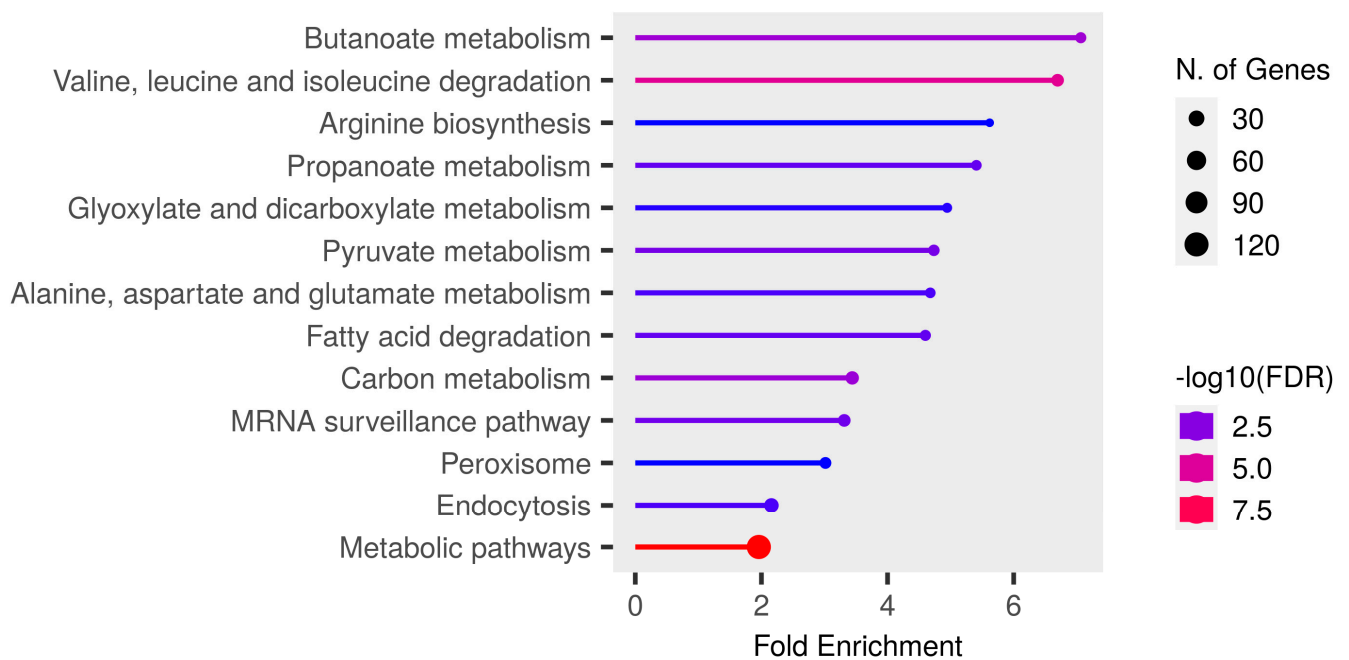


Figure S3: The results of enrichment of miRNA-210 targets.

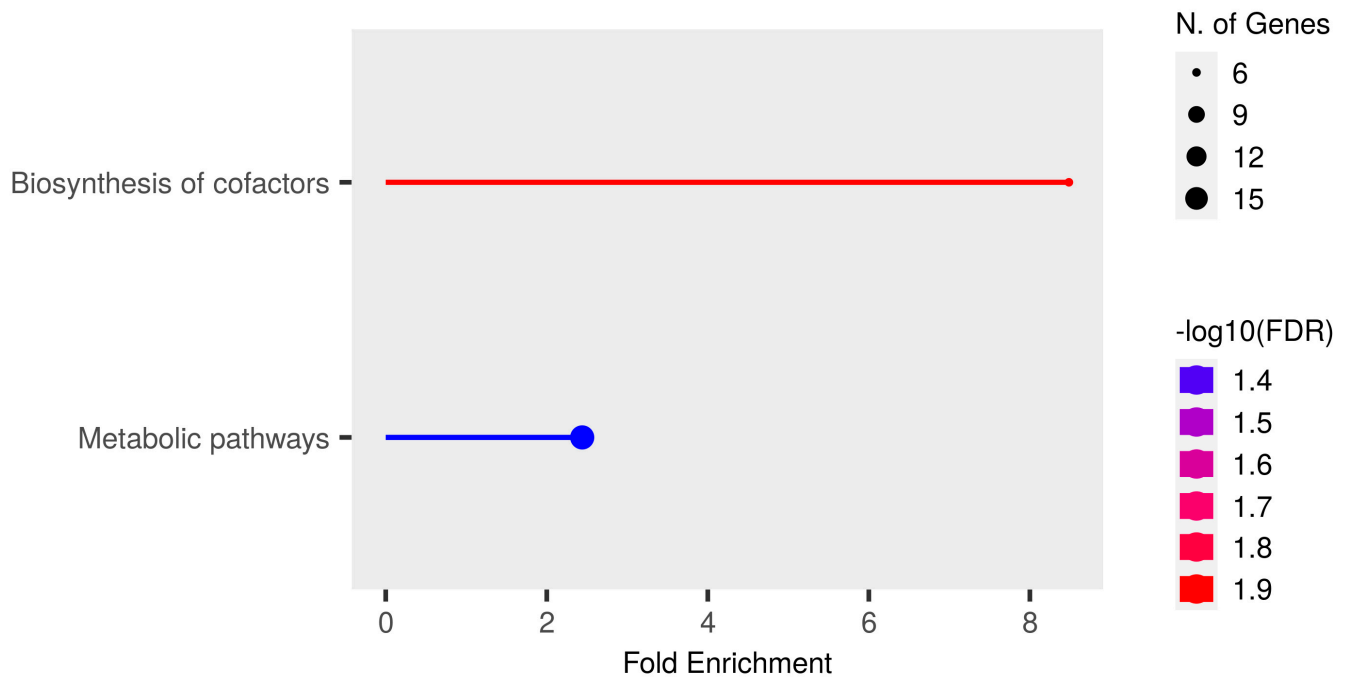


Figure S4: The results of enrichment of miRNA-642 targets.

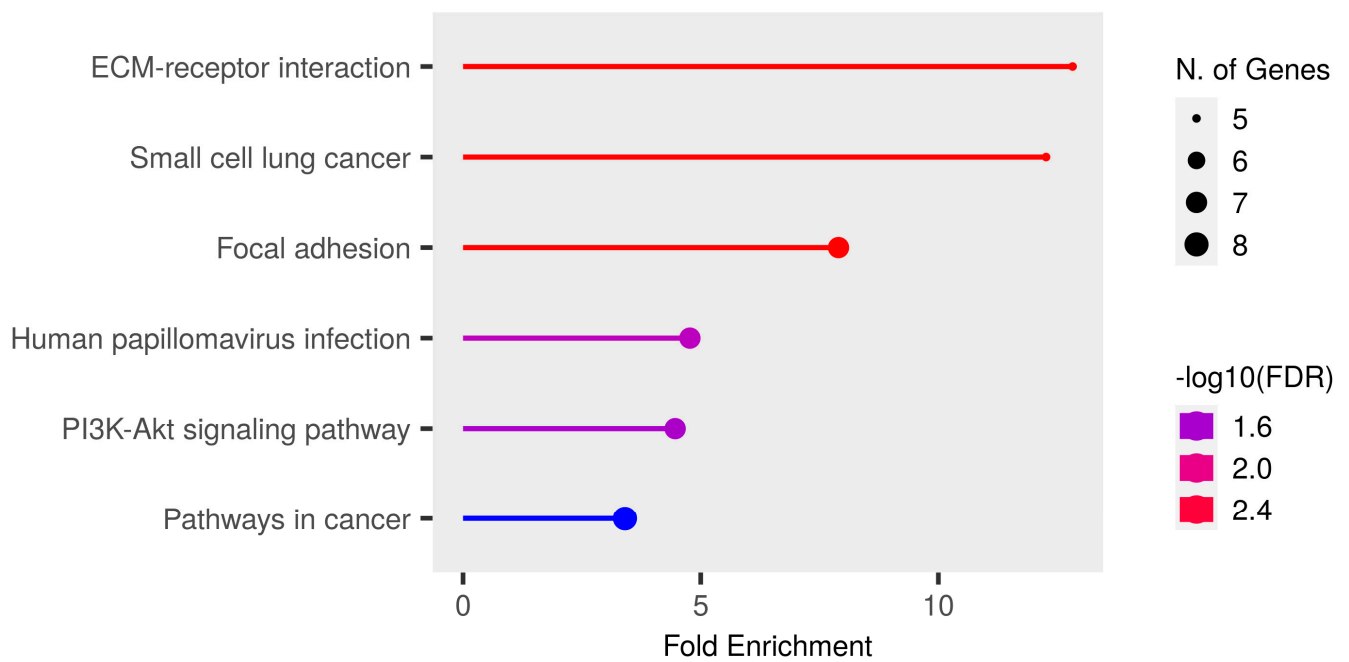


Figure S5: The results of enrichment of miRNA-199b targets.

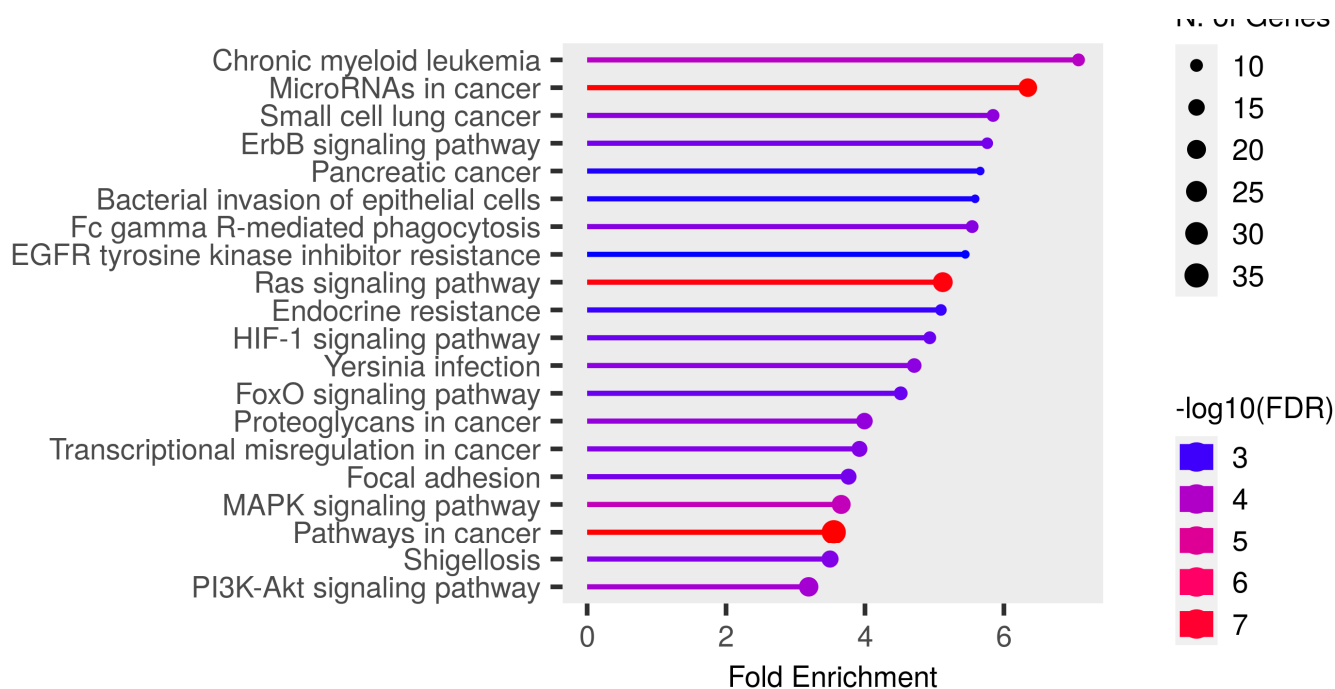


Figure S6: The results of enrichment of miRNA-200c targets.

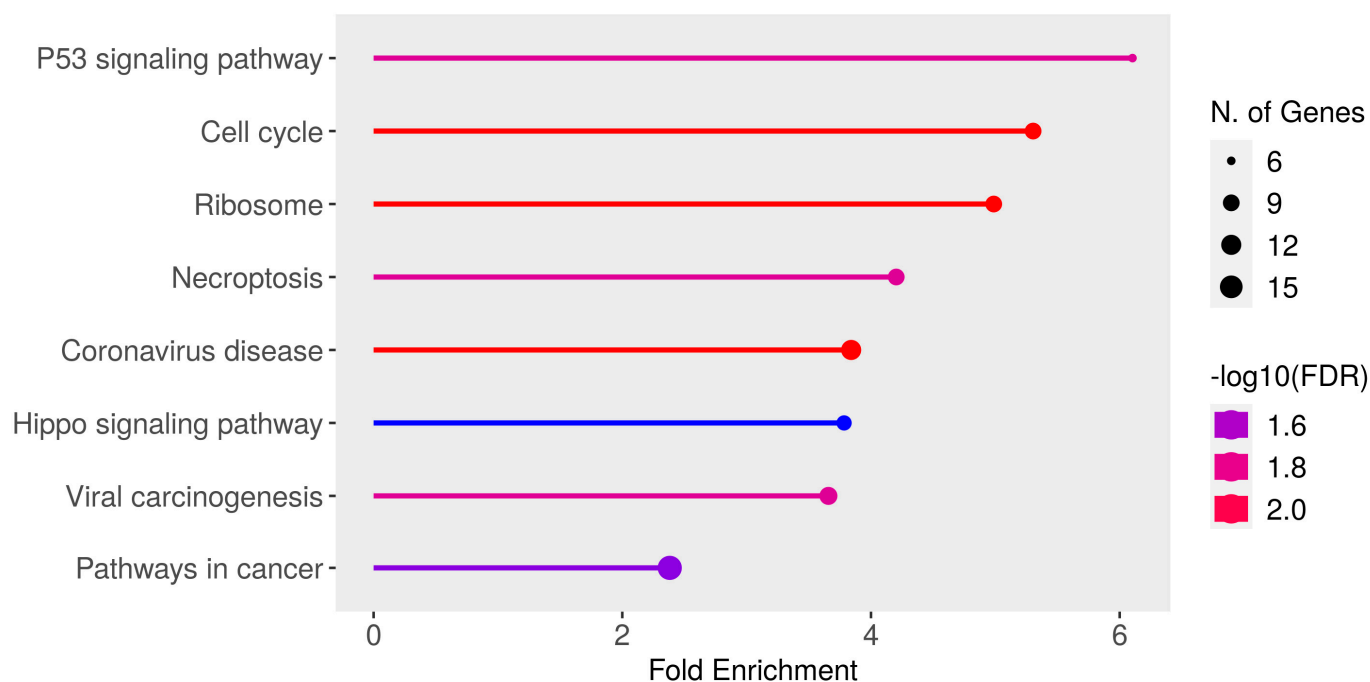


Figure S7: The results of enrichment of miRNA-455 targets.

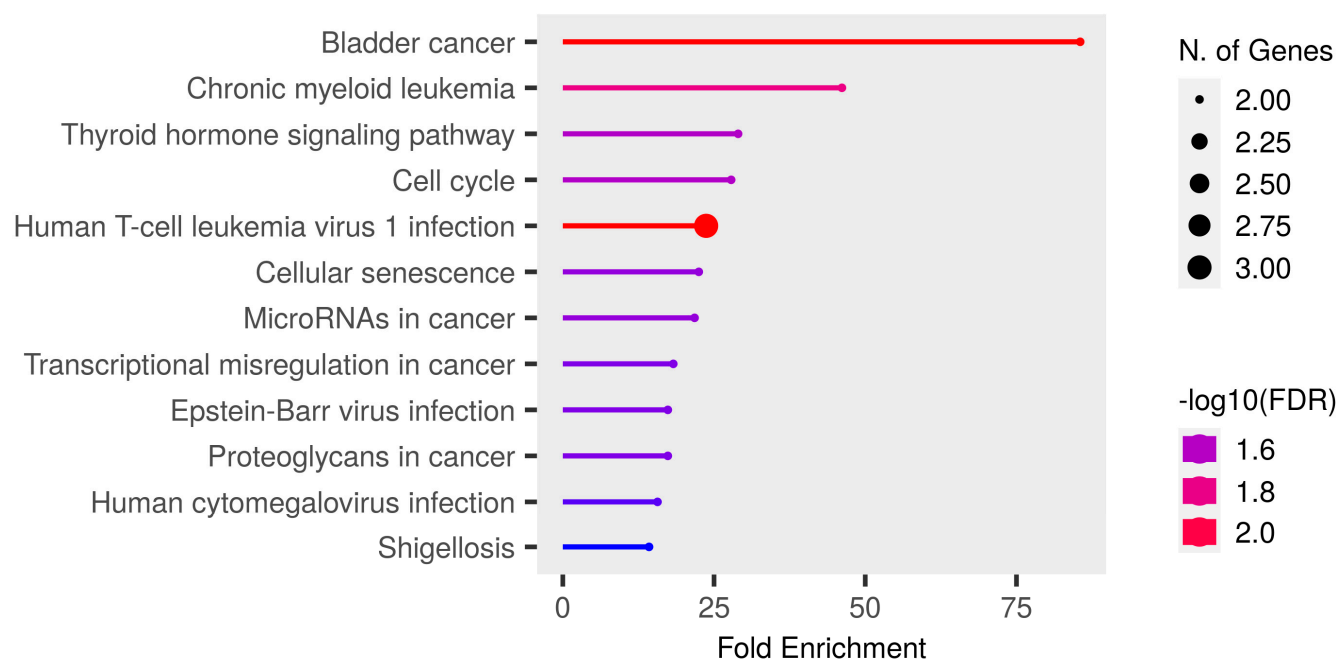


Figure S8: The results of enrichment of miRNA-487-3p targets.

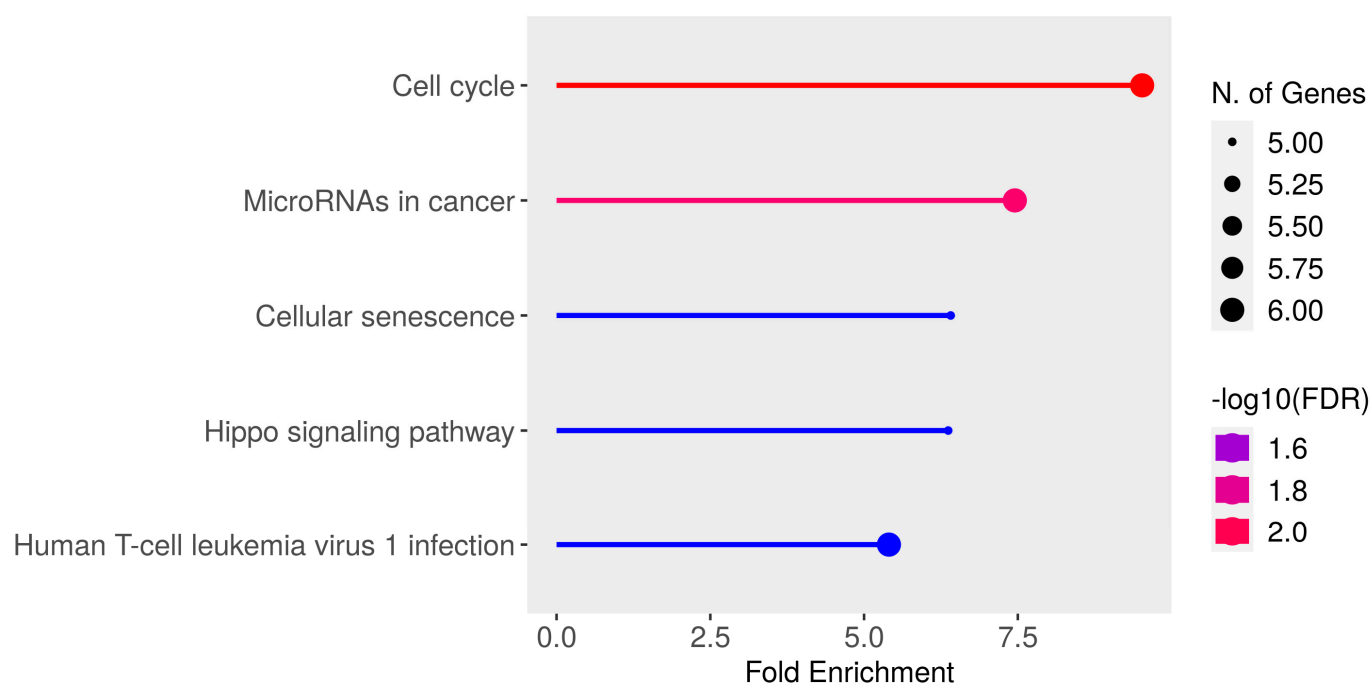


Figure S9: The results of enrichment of miRNA-582-3p targets