

**Table S1** The primers used for the PCR validation

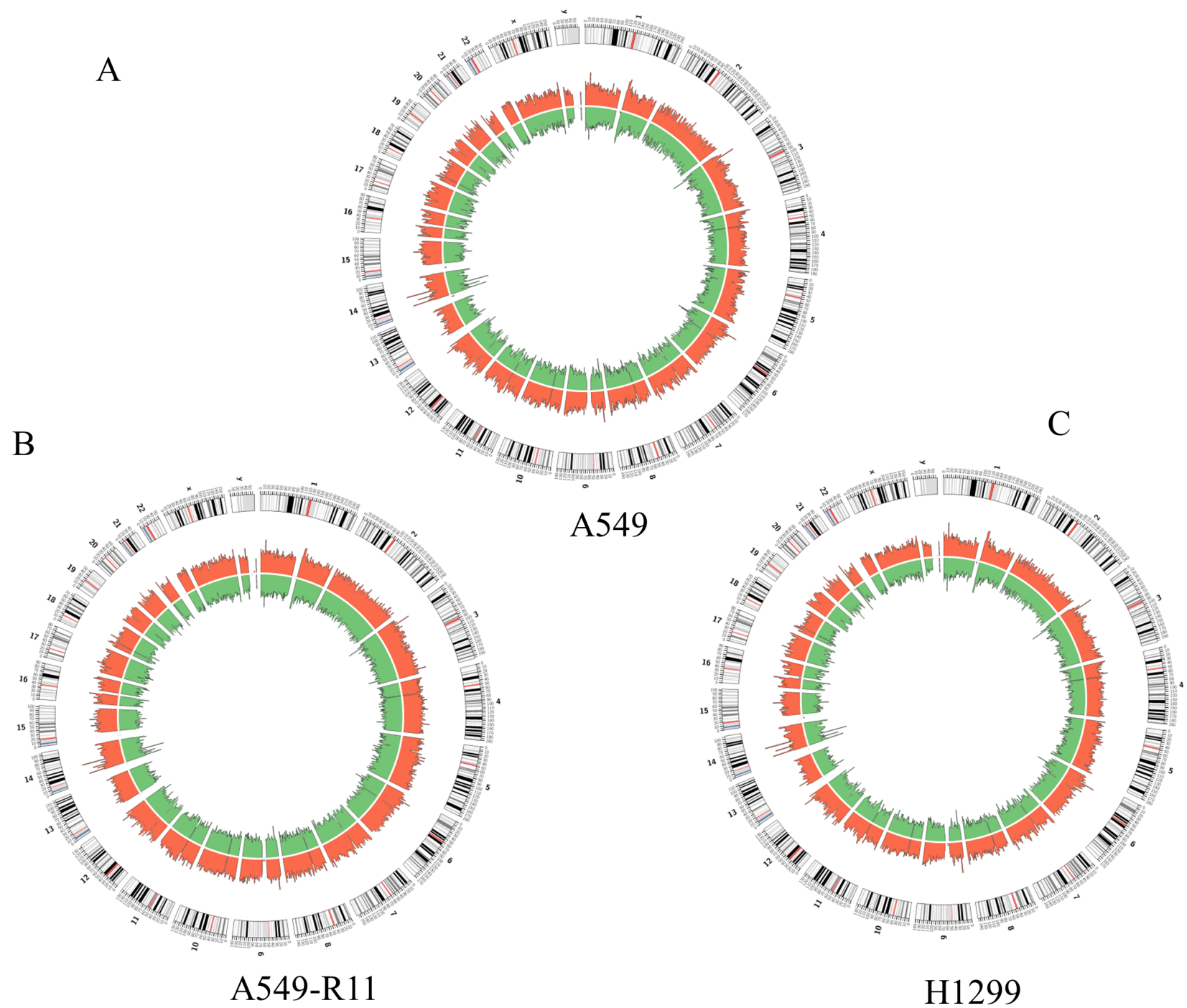
Gene	Forward and reverse primers	Length (bp)
<i>hsa_circ_0109301</i>	F: 5'-ATGGTGAAGAATCCCCAGTTAT-3'; R: 5'-GGCCACATCCCTAAATGTCAA-3'	125
<i>hsa_circ_0000586</i>	F: 5'-GACGACATTGAAGCTAGCCG-3'; R: 5'-GCCAAACTTCTGAGGAGCTG-3'	89
<i>hsa_circ_0008012</i>	F: 5'-GGACTACCTGGTGCCTCTAG-3'; R: 5'-TGGATCATCTTCTGCCATTCTG-3'	79
<i>hsa_circ_0008543</i>	F: 5'-TTGATGACCTGTCTGGAGCAA-3'; R: 5'-AATGTCAACACTCCCTGGGT-3'	100
<i>hsa_circ_0008749</i>	F: 5'-TGTGGGAATGCATGAAAGG-3'; R: 5'-ATTCAGTTGCCCGCCATTC-3'	79
<i>hsa_circ_0030389</i>	F: 5'-GCCTCTGGTGTAGCTGGAAT-3'; R: 5'-TCATAGCGTAGAGAGTTTCCCA-3'	87
<i>hsa_circ_0001944</i>	F: 5'-TCTGTTCCCAATACAAGAAGACTC-3'; R: 5'-AGGCTGAGGCAGGAGAATAG-3'	207
<i>hsa_circ_0044833</i>	F: 5'-TGACTIONCAGTGATGACGCAG-3'; R: 5'-GCAGTTTCCGCAGATCCATC-3'	79
<i>hsa_circ_0007161</i>	F: 5'-TTCCAGTGGATGCCCATCAG-3'; R: 5'-CACCTCCTTCTTCAAGAAACTT-3'	144
<i>hsa_circ_0002945</i>	F: 5'-CTGGAGGTGGCTTGGACTC-3'; R: 5'-TATGGGCTTCGCAGGAGAAA-3'	102
<i>chr19:15280897-15281636</i>	F: 5'-AACATGGCCAAGGGTGAGAG-3'; R: 5'-CAGAGCCGGTTGTCAATCTC-3'	119
<i>hsa_circ_0009158</i>	F: 5'-TGTGGAAGAACAGCAGGAAG-3'; R: 5'-CTCCCTCAACATGTTCTGCG-3'	205
<i>hsa_circ_0007781</i>	F: 5'-CGCAGCCAATGATAGACCAC-3'; R: 5'-TGTCTCCCCACATTCTCCTG-3'	138
<i>hsa_circ_0046534</i>	F: 5'-CGCAGCCAATGATAGACCAC-3'; R: 5'-TGTCTCCCCACATTCTCCTG-3'	212
<i>hsa_circ_0084606</i>	F: 5'-TGTGGAAGAACAGCAGGAAG-3'; R: 5'-CTCCCTCAACATGTTCTGCG-3'	247
<i>chr11:27412641-27434407</i>	F: 5'-GGCCTTGTCTGGGTGAAAG-3'; R: 5'-CCCGCCAATTGTAGCTCTTC-3'	188
<i>hsa_circ_0035277</i>	F: 5'-ATATACCCGAAACAGCCT-3'; R: 5'-ACTTGTGGCTTTACTGTGGC-3'	135
<i>hsa_circ_0080085</i>	F: 5'-TGCTGGACCCAACACAAATG-3'; R: 5'-ACGATCAGGGGTAACAGCT-3'	179
<i>hsa_circ_0037955</i>	F: 5'-TTTGTTCCTTAGCCAGCC-3'; R: 5'-TGGGGAATGTCACATGGAGA-3'	135
<i>hsa_circ_0087232</i>	F: 5'-CCGGATGATGATGGCAAGAC-3'; R: 5'-TCCGATCTTGGCGTTGAAAG-3'	162
<i>GAPDH</i>	F: 5'-TCTCTGCTCCTCTGTTCTGA-3'; R: 5'-GCGCCCAATACGACCAAATC-3'	122

**Table S2** Differentially expressed miRNAs correlated with patient survival significantly

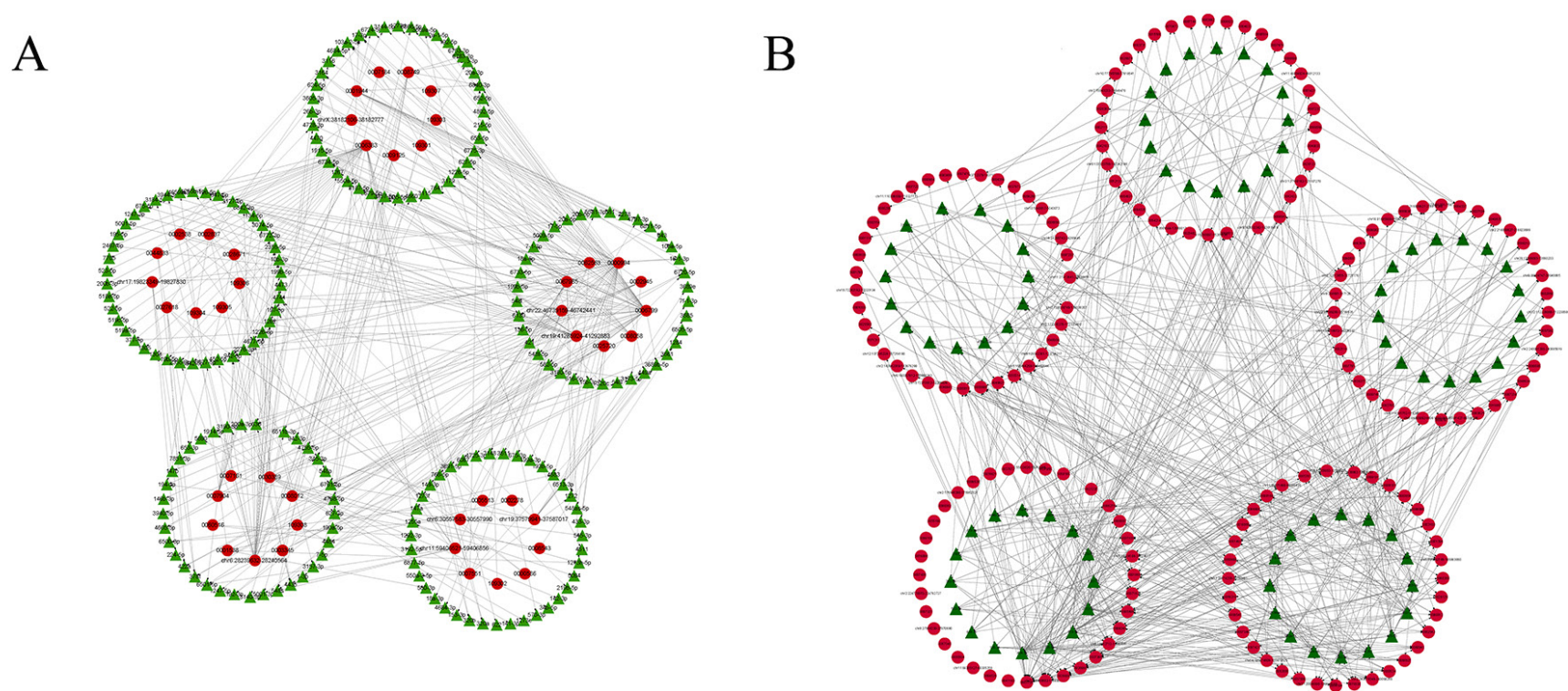
miRNA ID	log <sub>2</sub> (fold change)	Prognosis
hsa-miR-429	-10.7698	Low expression suggests poor prognosis
hsa-miR-200a-5p	-8.6713	Low expression suggests poor prognosis
hsa-miR-1468-5p	-8.2368	Low expression suggests poor prognosis
hsa-miR-34a-3p	-7.0553	Low expression suggests poor prognosis
hsa-miR-142-5p	-6.2915	Low expression suggests poor prognosis
hsa-miR-34b-5p	-6.1633	Low expression suggests poor prognosis
hsa-miR-299-5p	-5.4152	Low expression suggests poor prognosis
hsa-miR-146b-3p	-2.0371	Low expression suggests poor prognosis
hsa-miR-365a-5p	-1.9874	Low expression suggests poor prognosis
hsa-miR-16-1-3p	-1.643	Low expression suggests poor prognosis
hsa-miR-99a-3p	-1.6329	Low expression suggests poor prognosis
hsa-miR-449a	-1.3207	Low expression suggests poor prognosis
hsa-miR-146a-5p	-1.2417	Low expression suggests poor prognosis
hsa-miR-548v	-1.0741	Low expression suggests poor prognosis
hsa-miR-199b-5p	-1.0611	Low expression suggests poor prognosis
hsa-miR-424-3p	1.1499	High expression suggests poor prognosis
hsa-miR-584-5p	1.96	High expression suggests poor prognosis

**Table S3** MiRNA-targeted mRNAs

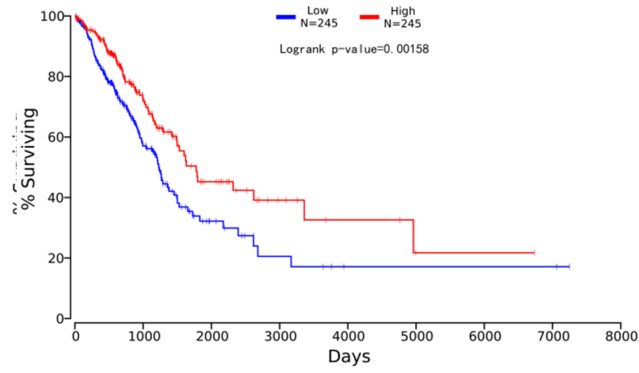
Gene	$\log_2$ (fold change)	P value
<i>FOXL2NB</i>	-3.67726	0.000451
<i>ANXA1</i>	-1.8883	1.43E-06
<i>ATP6V1E2</i>	-1.54805	0.000401
<i>SCN9A</i>	-1.4202	0.000901
<i>PLPP3</i>	-1.34197	0.000419
<i>B4GAT1</i>	1.250781	0.00056
<i>ITGA3</i>	1.397485	0.000117
<i>NETO2</i>	1.489256	0.000706
<i>ARSJ</i>	1.703083	1.1E-05
<i>PIM2</i>	1.763272	3.35E-05
<i>SOX4</i>	1.970212	2.18E-08
<i>XK</i>	1.971835	0.000176
<i>SH3TC2</i>	2.115496	0.000213
<i>S1PR3</i>	2.169896	1.16E-07
<i>RTN4RL1</i>	2.255763	0.000819
<i>TMEM59L</i>	2.350886	0.000305
<i>COL5A2</i>	2.369889	1.69E-07
<i>TPPP</i>	2.634742	6.37E-08
<i>SLC16A7</i>	2.853034	0.000584
<i>RASL10B</i>	2.992356	3.41E-05
<i>FBN2</i>	3.032016	7.88E-05
<i>LMNA</i>	3.116185	0.000892
<i>RNF144B</i>	3.499924	0.000761
<i>TOX</i>	4.876351	0.000226
<i>SHC4</i>	5.190201	8.22E-07
<i>RPS6KL1</i>	5.307752	3.5E-16
<i>DLL1</i>	5.931623	5.98E-08
<i>PXDN</i>	7.197225	8.9E-17
<i>STK32A</i>	7.264389	9.36E-06
<i>SEMA3F</i>	7.390137	1.37E-09
<i>PCDH7</i>	7.673314	4.07E-11
<i>ZNF736</i>	8.052809	1.49E-27



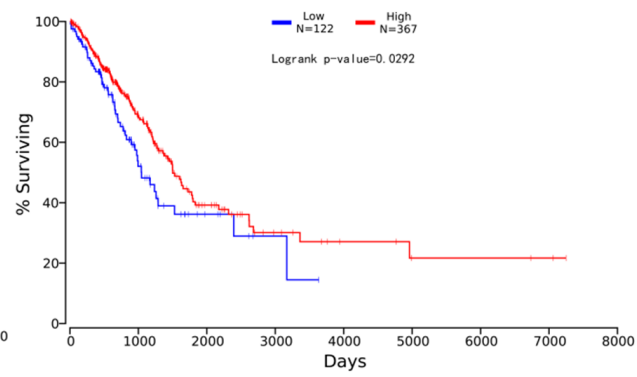
**Figure S1** The distribution of the circRNAs and mRNAs on the chromosomes in A549 (A), A549-R11 (B) and H1299 (C) cells.



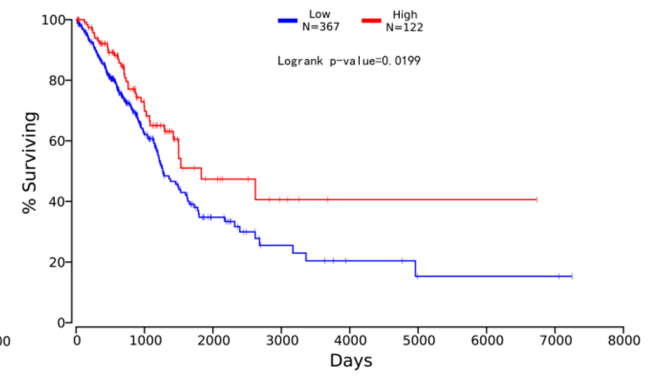
**Figure S2** The circRNA-miRNA interaction networks predicted by the miRanda, RNA hybrid and TargetScan databases. Red symbols represent up-regulated expressions, whereas green ones represent down-regulated expressions. Triangular and oval nodes represent miRNAs and circRNAs, respectively.



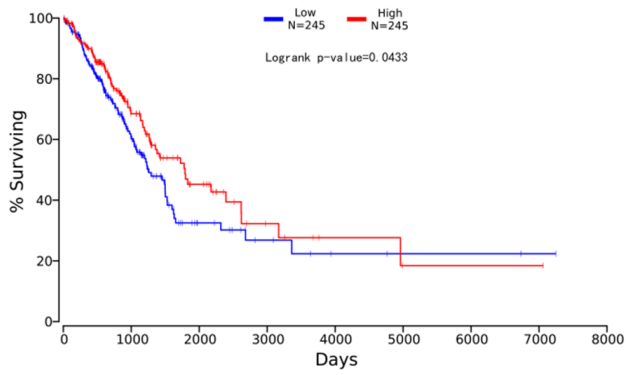
hsa-miR-16-1-3p



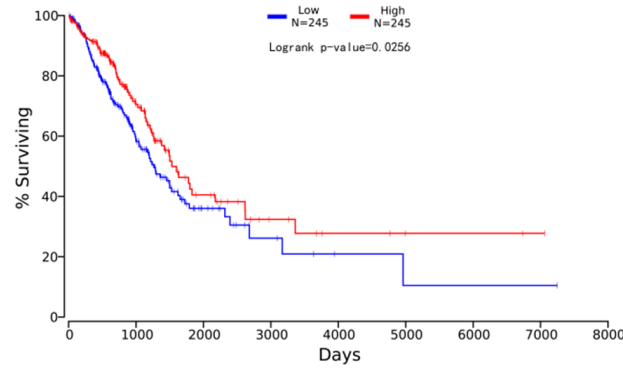
hsa-miR-34b-5p



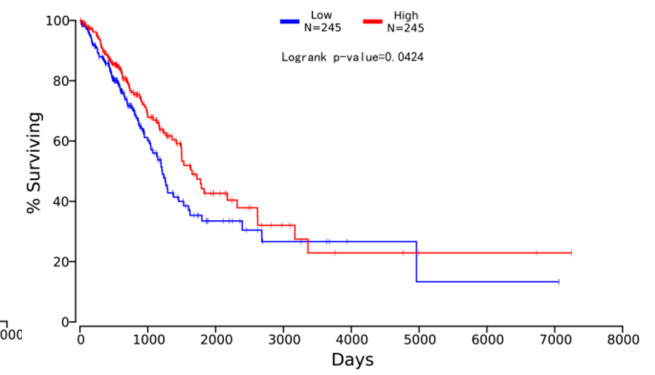
hsa-miR-142-3p



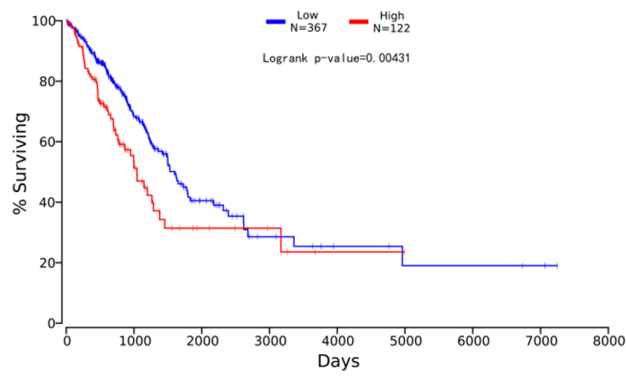
hsa-miR-146b-3p



hsa-miR-199b-5p

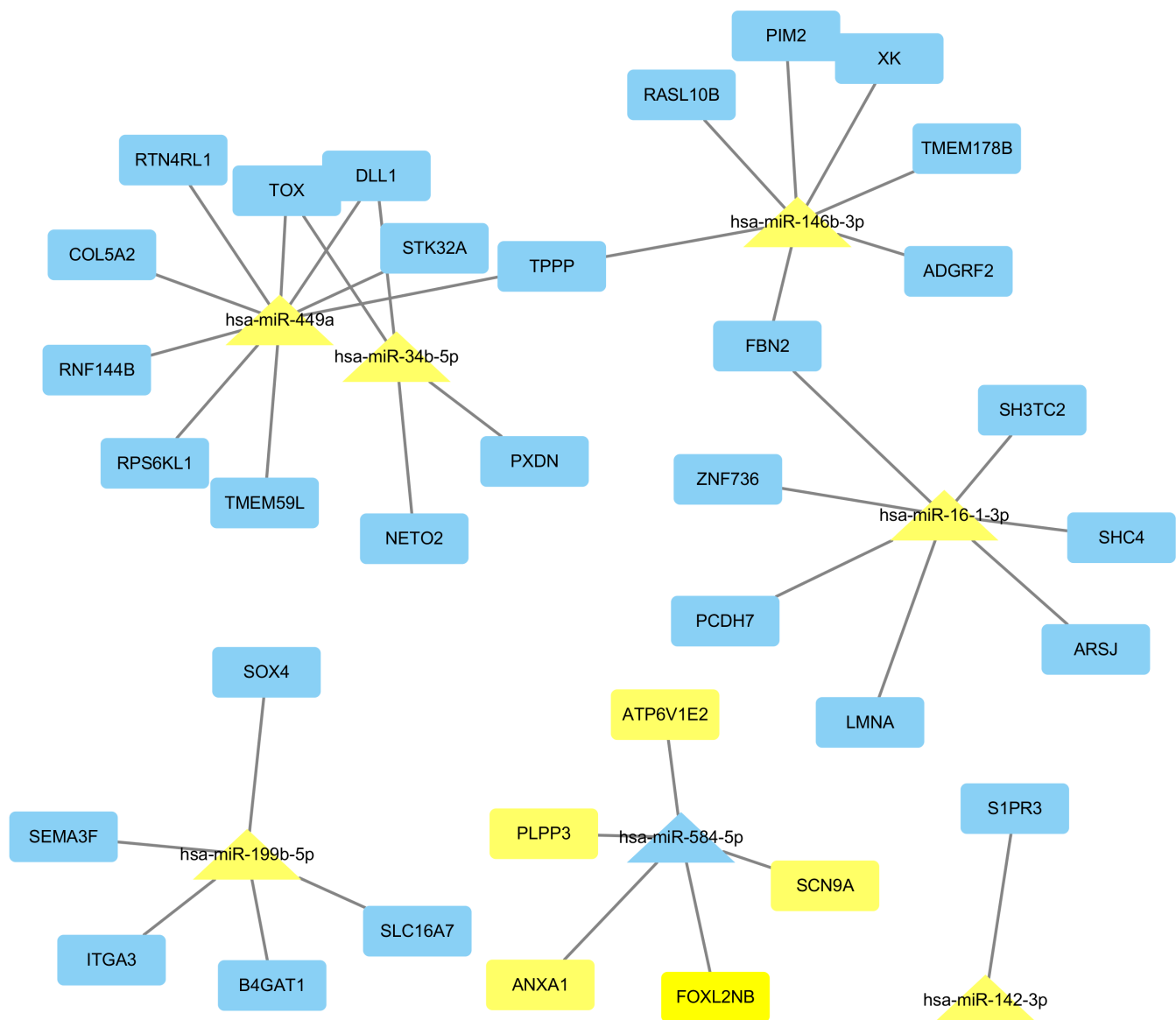


hsa-miR-449a

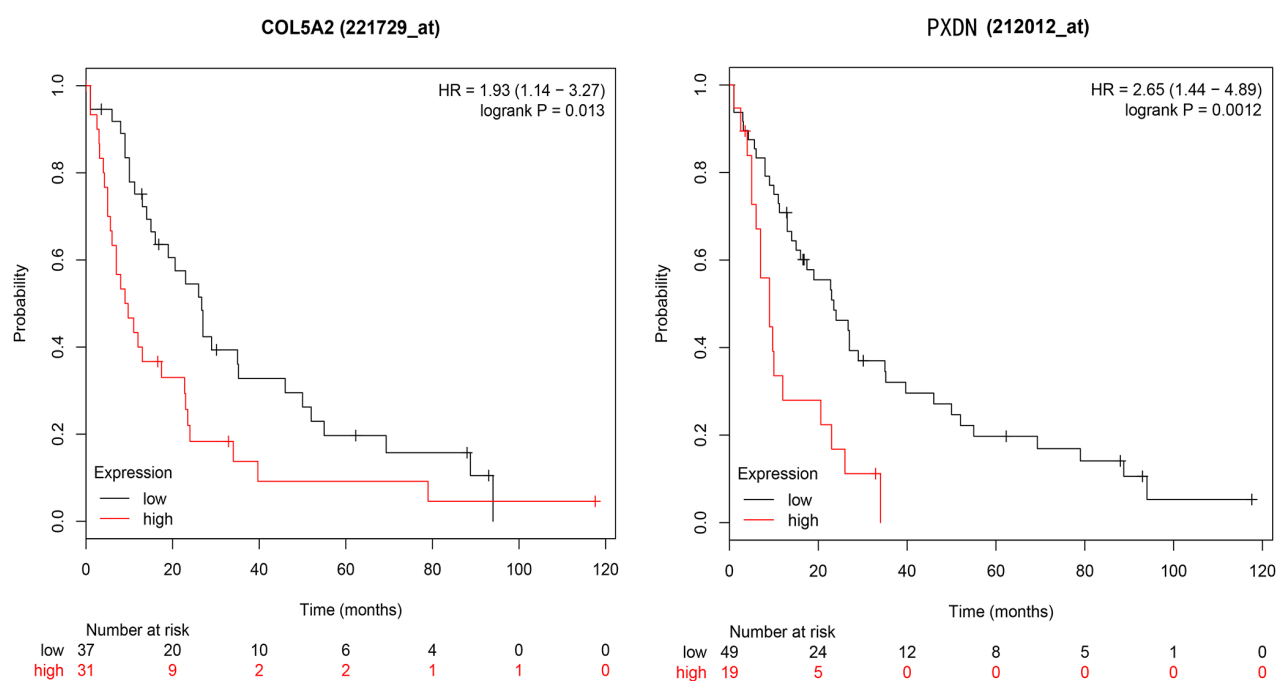


hsa-miR-584-5p

**Figure S3** The significant correlation of the differentially expressed miRNAs with the survival of patients. (A) The low expression suggests poor prognosis. (B) The high expression suggests poor prognosis.  $P < 0.05$ .



**Figure S4** The predicted miRNA-mRNA interactions. Blue symbols represent up-regulated expressions, whereas yellow symbols represent down-regulated expression. Triangular and quadrilateral nodes represent miRNAs and circRNAs, respectively.



**Figure S4** The predicted miRNA-mRNA interactions. Blue symbols represent up-regulated expressions, whereas yellow symbols represent down-regulated expression. Triangular and quadrilateral nodes represent miRNAs and circRNAs, respectively.