

Table S1 SiRNA, miRNA mimics, and inhibitors sequences used in this research.

SiRNA, mimics and inhibitors	Sequences
siRNA control	TTCTCCGAACGTGTCACGT
<i>hsa_circ_0000235</i> siRNA-1	CGUCACCCUGCAUCCUCCATT
<i>hsa_circ_0000235</i> siRNA-2	CAUCGUCACCCUGCAUCCUTT
<i>MCT4</i> siRNA	TCCTGGGCTTCATTGACATCT
mimics-NC	UCACAACCUCCUAGAAAGAGUAGA
<i>hsa-miR-326</i> mimics	Sense(5'-3') CCUCUGGGCCCUUCCUCCAG
	Antisense(5'-3') CUGGAGGAAGGGCCCAGAGG
<i>hsa-miR-330-5p</i> mimics	Sense(5'-3') UCUCUGGGCCUGUGUCUUAGGC
	Antisense(5'-3') GCCUAAGACACAGGCCCCAGAGA
<i>hsa-miR-335</i> mimics	Sense(5'-3') UCAAGAGCAAUAACGAAAAAUGU
	Antisense(5'-3') ACAUUUUUCGUUAUUGCUCUUGA
<i>hsa-miR-502-5p</i> mimics	Sense(5'-3') AUCCUUGCUAUCUGGGUGCUA
	Antisense(5'-3') UAGCACCCAGAUAGCAAGGAU
<i>hsa-miR-873</i> mimics	Sense(5'-3') GCAGGAACUUGUGAGUCUCCU
	Antisense(5'-3') AGGAGACUCACAAGUCCUGC
<i>hsa-miR-330-5p</i> inhibitor	GCCUAAGACACAGGCCCCAGAGA

Table S2 Primers for qRT-PCR.

Gene Symbol	Forward Primer	Reverse Primer
<i>hsa_circ_0000235</i>	TCGAAATCCGAAGTGCCACC	GGAGGATGCAGGGTGACG
<i>MCT4</i>	ACTCCGTCTACCTCTTCAGC	ATGGCACTGGAGAACTTGTG
<i>GAPDH</i>	GGAGCGAGATCCCTCCAAAAT	GGCTGTTGTCATACTTCTCATGG
<i>CBLL1</i>	TGTGCAGCGAATTGAGCAGT	GCACGGGTAACAGGTTTTCCA
<i>CTDSP1</i>	AGACCCAGTCCAATACCTG	GACGCTTCAACACGTAGACCT
<i>TOMM40</i>	TCGGGGAGTCCAAC TACCAC	TGAGCGTTGAGACTGCCAC
<i>ENG</i>	GGCCAGCATTGTCTCACTTC	CGGCACACTTTGTCTGGATC
<i>HARS2</i>	TCCCTCCGCTATGACCTTACT	GCCACACCTTTCCAACATGAT
<i>LITAF</i>	ATGTCGGTTCCAGGACCTTAC	TACGAAGGAGGATTCATGCCC
<i>PAK4</i>	GGACATCAAGAGCGACTCGAT	CGACCAGCGACTTCCTTCG
<i>NOP2</i>	CCCAGTCCCTATTTAATGCTCCT	CGTGGTTCACCATACCATCTTCT
<i>PRR11</i>	AAAGATGGACCCATGCAGATAAC	TGCTTTCGGCGATGGTATAAG
<i>RAPGEF3</i>	GACCGGAAGTACCACCTTAGG	AGATTCCCACAACCTTGGCTCC
<i>SF3B4</i>	GGAAGATGCTGACTATGCCATT	TGTTGTGAGCTGATGCTTTGTT
<i>SLC37A4</i>	CTCCACAGTACCTGTCTTTGC	ACCCACAGGTAAGGGGACAG
<i>ENO1</i>	GCCGTGAACGAGAAGTCTTG	ACGCCTGAAGAGACTCGGT
<i>G6PD</i>	AACATCGCCTGCGTTATCCTC	ACGTCCCGGATGATCCCAA
<i>CPNE1</i>	CACTGCGTGACCTTGGTTCA	CTCCCACATCCTGTAAAAGGAC
<i>FAM129B</i>	CTGACGGAGTTCCTCCAGTTC	GAGGTTCCCCGAGAAGACGAT
<i>G6PC3</i>	CGAGGCGCTACAGAACCAG	CACTCGGTGATGAGGCTGAT
<i>GRINA</i>	CTCACCCCAGCATGGAAACTA	CAAGGTCAGCACTAGGAACAC
<i>SNRPA</i>	CTTTCTGAGAATCCACCGAATCA	CCAGACGGACCTCCTTGAAG
<i>β-actin</i>	AATCTGGCACCACACCTTCTAC	ATAGCACAGCCTGGATAGCAAC
<i>CCNY</i>	TAGCACAGTCAGTCAACCAAAC	TGGTGGCACTTCGGATTTTCG
<i>U6</i>	CGCTTCGGCAGCACATATACTA	TCACGAATTTGCGTGTCATCCT
<i>ALDOA</i>	ATGCCCTACCAATATCCAGCA	GCTCCAGTGGACTCATCTG

Table S3 Specific upstream primers for miRNAs used in qPCR assays.

miRNA	Sequences
<i>hsa-miR-326</i>	CTCTGGGCCCTTCCTCCAG
<i>hsa-miR-330-5p</i>	TCTCTGGGCCTGTGTCTTAG
<i>hsa-miR-335</i>	TCAAGAGCAATAACGAAAAATGT
<i>hsa-miR-502-5p</i>	ATCCTTGCTATCTGGGTGCTA
<i>hsa-miR-873</i>	GTGCAGGAACTTGTGAGTCT

Table S4 Sequences of the FISH and pulldown probes used in this study.

Gene name	Probe (5'-3')
<i>hsa_circ_0000235</i>	5'CY3 - TTTGTCCTGGAGGATGCAGGGTGACGATGGC
<i>hsa-miR-330-5p</i>	5'CY5 - GCCTAAGACACAGGCCAGAGA
<i>hsa-miR-330-5p</i> pulldown	UCUCUGGGCCUGUGUCUUAGGC - 3'Biotin
<i>hsa-miR-330-5p</i> mut pulldown	UGCCUGUGUCUUAGGC - 3'Biotin

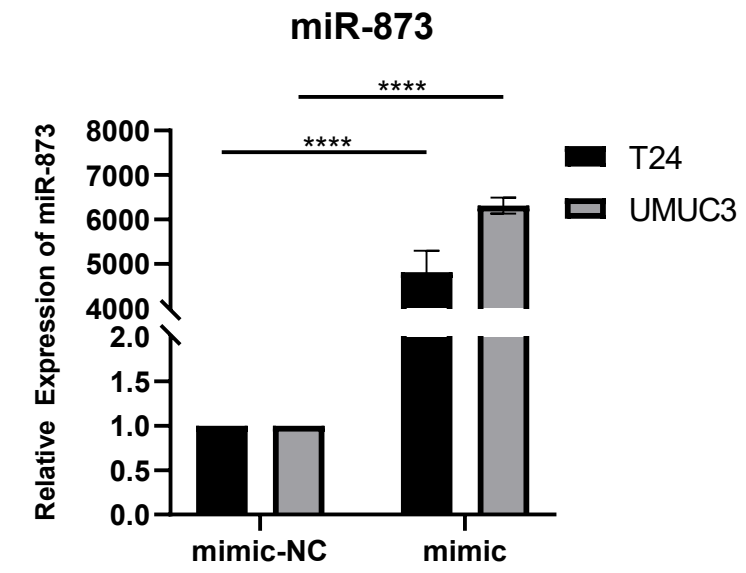
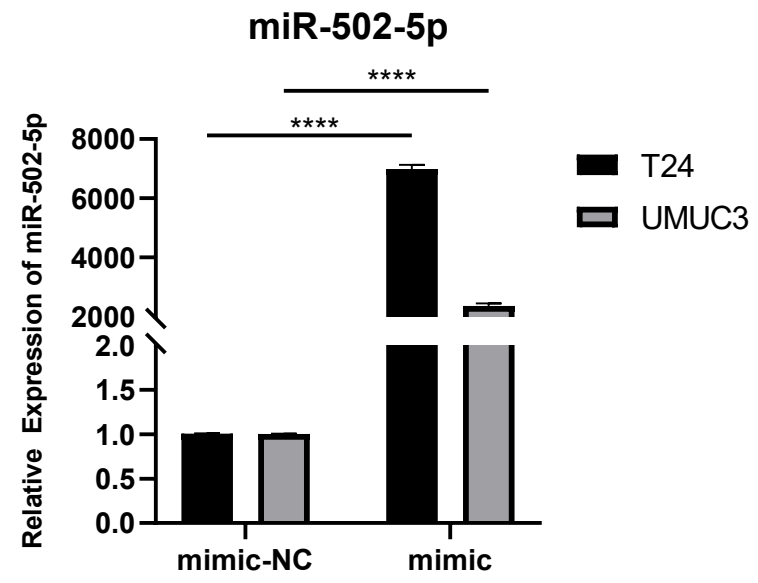
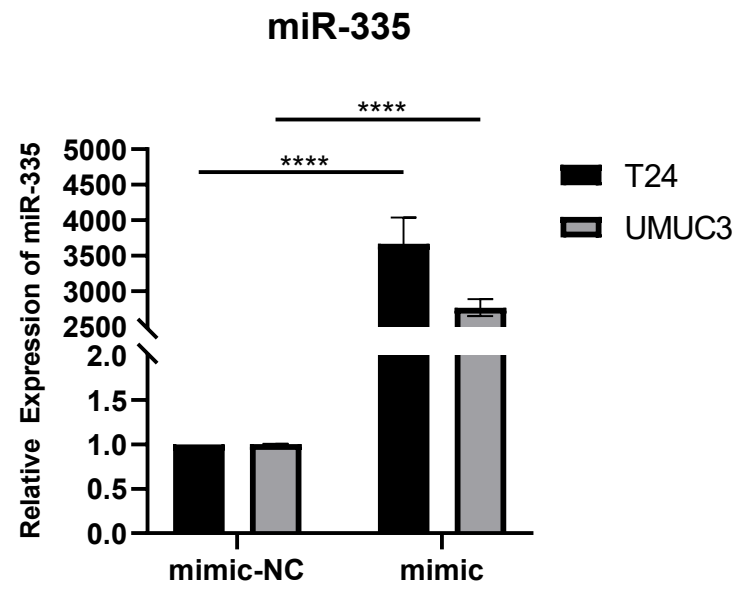
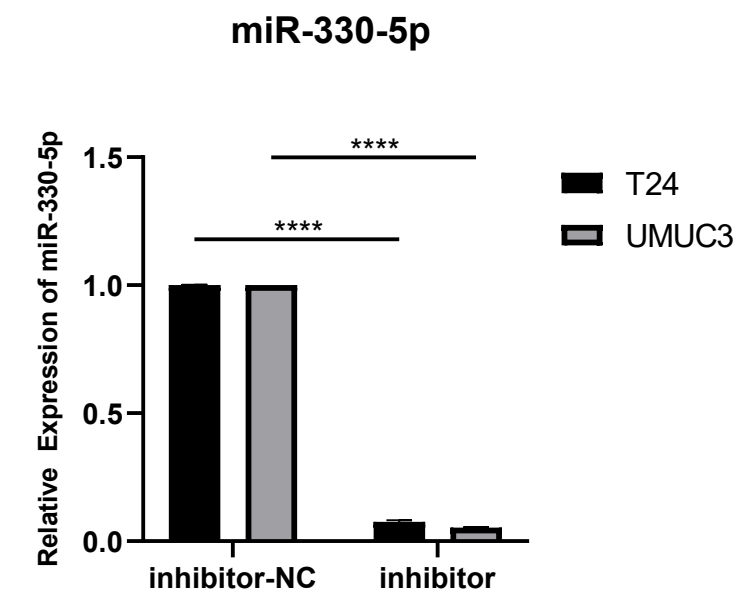
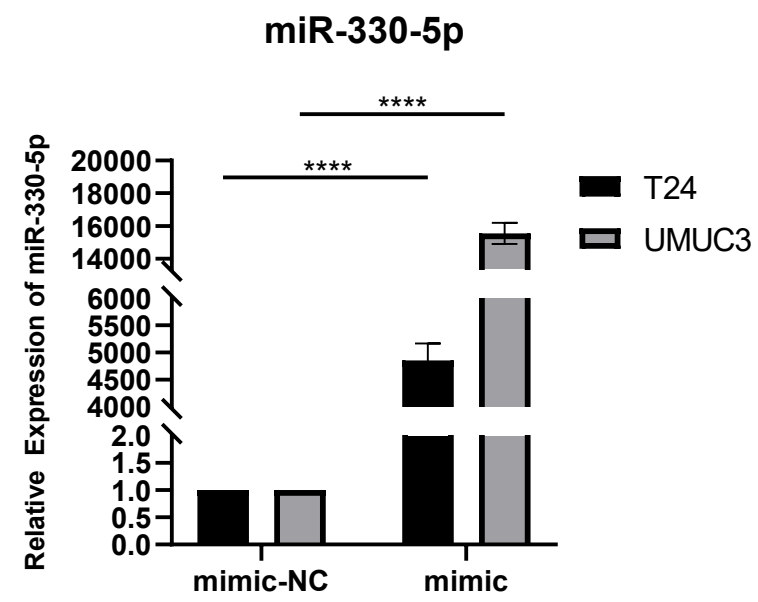
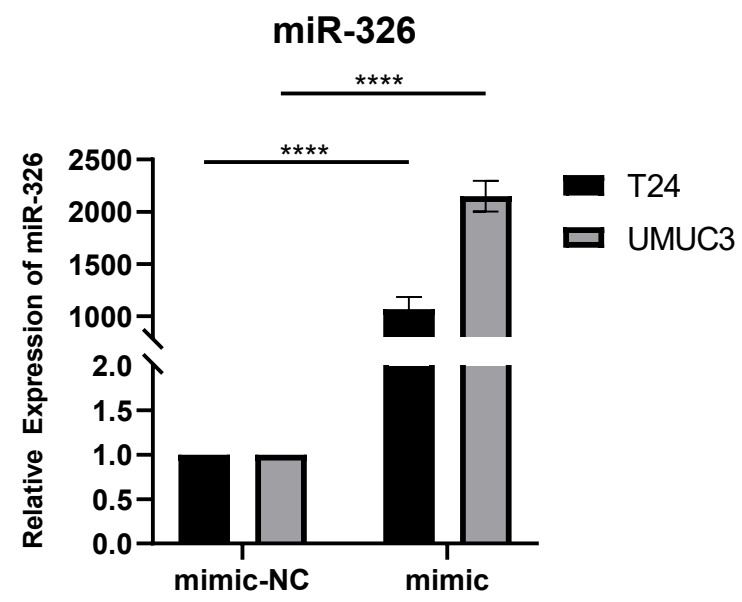
Table S5 Predicted miRNA-circ235 interaction by Circinteractome.

Circ-MiRNA Prediction											
Circ-Mirbase ID	CircRNA (Top) - miRNA (Bottom) Pairing	Site Type	CircRNA Start	CircRNA End	3' pairing	local AU	position	TA	SPS	context+ score	context+ score percentile
hsa_circ_0000235 (5' ... 3')	AGCUGACGGCUGAAUGUGCCAUC 	7mer-m8	299	305	0.003	0.019	-0.06	-0.007	-0.036	-0.201	94
hsa-miR-183 (3' ... 5')	UCACUUAAGAUGGUCACGGUAU										
hsa_circ_0000235 (5' ... 3')	UUAUGACAAACACAACCCAGAGC 										
hsa-miR-326 (3' ... 5')	GACCUCCUCCCCGGGUCUCC	7mer-m8	231	237	0.012	-0.027	-0.051	0.026	-0.066	-0.226	94
hsa_circ_0000235 (5' ... 3')	UUAUGACAAACACAA-CCCAGAGC 										
hsa-miR-330-5p (3' ... 5')	CGGAUUCUGUGUCCGGGUCUCU										
hsa_circ_0000235 (5' ... 3')	ACAAUAAAUGUGUCGCUCUUGC 	7mer-m8	106	112	0.003	-0.032	-0.047	0.005	-0.018	-0.209	96
hsa-miR-335 (3' ... 5')	UGUAAAAAGCAAUAACGAGAACU										
hsa_circ_0000235 (5' ... 3')	CCUCCAGGACAAAUAGCAAGGAA 										
hsa-miR-502-5p (3' ... 5')	AUCGUGGGUCUAUCGUUCCUA	8mer-1a	19	26	0.003	-0.054	-0.109	0.01	-0.063	-0.46	99
hsa_circ_0000235 (5' ... 3')	CAACCAAACCUCAAGUAUACAAU 										
hsa-miR-568 (3' ... 5')	CACACAU AUGUAAAUAUGUA										
hsa_circ_0000235 (5' ... 3')	GAUGAAAUCUUCACCCUCUUUC 	7mer-m8	187	193	0.012	0.015	-0.044	0.022	0.021	-0.094	93

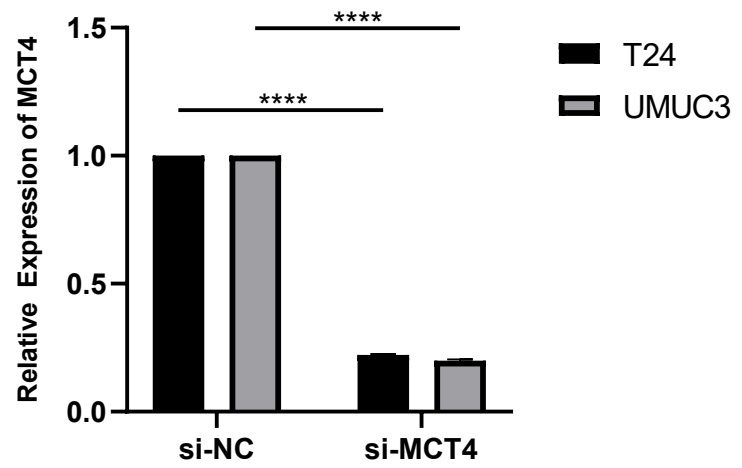
hsa-miR-583 (3' ... 5')	CAUUACCCUGGAAGGAGAAAC											
hsa_circ_0000235 (5' ... 3')	AUAGCACAGUCAGUCAACCAAAC											
		7mer-1a	74	80	0.004	0.01	-0.042	0.008	0.027	-0.067	85	
hsa-miR-659 (3' ... 5')	ACCCUGGGAGGGACUUGGUUC											
hsa_circ_0000235 (5' ... 3')	GACAAACACAACCCAGAGCAGAA											
		7mer-1a	235	241	0.001	0.026	-0.042	0.011	-0.052	-0.13	82	
hsa-miR-767-3p (3' ... 5')	UCUUUGGUACCCCAUACUCGUCU											
hsa_circ_0000235 (5' ... 3')	UAGCAAGGAAAUACAGUCCUGC											
		7mer-m8	32	38	0.012	-0.021	-0.057	0.02	-0.018	-0.184	95	
hsa-miR-873 (3' ... 5')	UCCUCUGAGUGUUCAAGGACG											

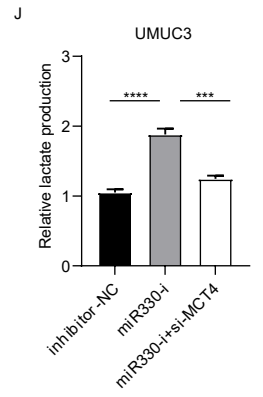
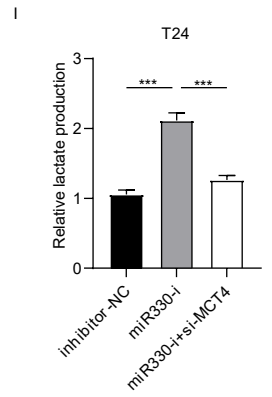
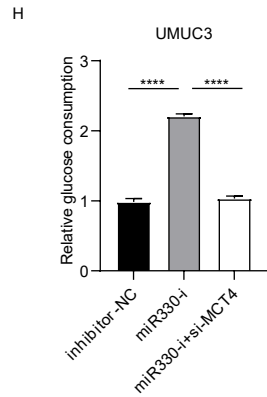
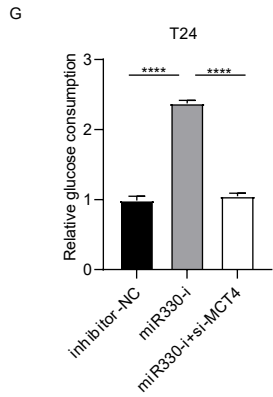
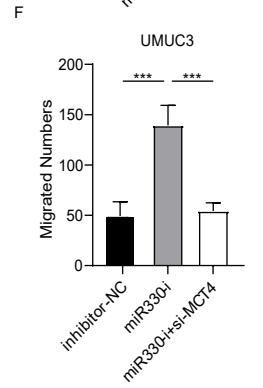
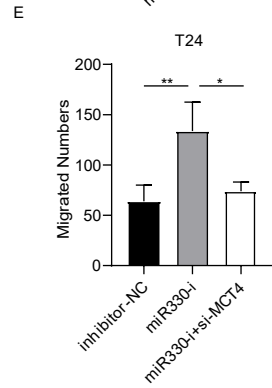
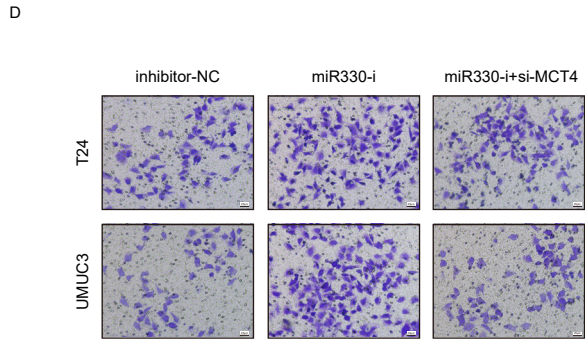
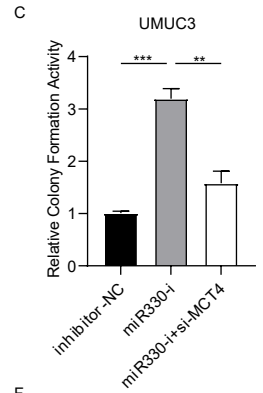
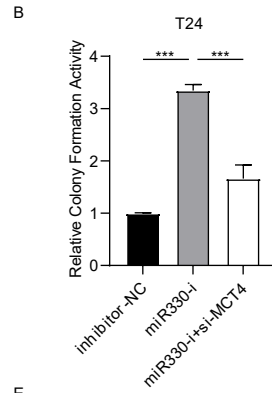
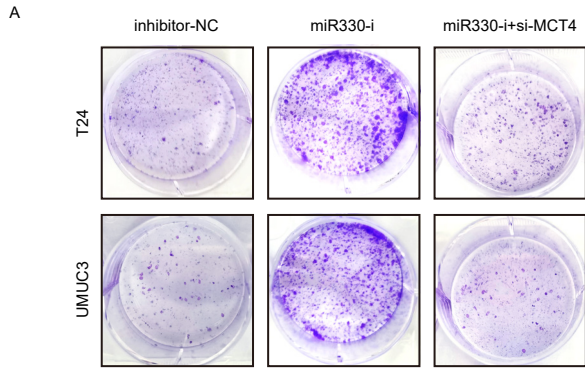
MiRNAs with potential interactions with has_circ_0000235 were predicted using the Circinteractome tool. Only miRNAs with scores higher than 90 were considered for further confirmation in the subsequent step.

A



B





circ235

vector

circ235+sh-MCT4

