

Table S1 Sequences of qRT-PCR primers

Gene	Forward (5'→3')	Reverse (5'→3')
<i>BARX2</i>	GGGCTGTTCCGTCTCTGAC	CCTTCCCTGCGGGCATATC
<i>ACTIN</i>	GTCATTCCAAATATGAGATGCGT	GCATTACATAATTTACACGAAAGCA
<i>FOXA1</i>	GCAATACTCGCCTTACGGCT	TACACACCTTGGTAGTACGCC
<i>HK2</i>	GAGCCACCACTCACCCCTACT	CCAGGCATTGCGCAATGTG
<i>GPI</i>	TATTGTGTTACCAAGCTCACACC	TATTGTGTTACCAAGCTCACACC
<i>PFKL</i>	GGAGAAGCTGCGCGAGGTTTAC	ATTGTGCCAGCATCTTCAGCATGAG
<i>GAPDH</i>	ATTGTGCCAGCATCTTCAGCATGAG	CAAAGGTGGAGGAGTGGGTGTCCG
<i>ALDOA</i>	AGGCCATGCTTGCACTCAGAAGT	AGGGCCCAGGGCTTCAGCAGG
<i>ENO1</i>	GACTTGGCTGGCAACTCTG	GGTCATCGGGAGACTTGAA
<i>PKM2</i>	GCCCGTGAGGCAGAGGCTGC	TGGTGAGGACGATTATGGCCC
<i>LDHA</i>	ATGGCAACTCTAAAGGATCA	GCAACTTGCAGTTCGGGC
<i>GLUT1</i>	GGCCAAGAGTGTGCTAAAGAA	ACAGCGTTGATGCCAGACAG
<i>GLUT4</i>	TGGGCGGCATGATTCCTC	GCCAGGACATTGTTGACCAG
<i>PGK1</i>	ATGTCGCTTTCTAACAAGCTGA	GCGGAGGTTCTCCAGCA
<i>PGAM1</i>	GGAAACGTGTACTGATTGCAGCCC	TTCCATGGCTTTGCGCACCGTCT

qRT-PCR, quantitative real-time polymerase chain reaction.

Table S2 Sequences of siRNAs

Gene	Target sequence (5'→3')
<i>BARX2</i> (si1)	GAAGCAGAAGTATTTGTCA
<i>BARX2</i> (si2)	GGAACCGAAAGCACGTGAT
<i>FOXA1</i> (si1)	CACTGCAATACTCGCCTTA
<i>FOXA1</i> (si2)	TCCCGGTCAGCAACATGAA

Table S3 PCR primers

Region (gene)	Location	Forward (5'→3')	Reverse (5'→3')
<i>site1(HK2)</i>	-1693bp, -1704bp	GACAAGGGCAGGGAAGAGAAGA	TGCACGTCCTCAACCCTCCT
<i>site2(HK2)</i>	-1388bp, -1399bp	TTGCTGAGAGGCTAGATGGATTA	TGCCATGTTCTACTGAGGAGGA
<i>site3(HK2)</i>	-806bp, -817bp	TCGTGCGTGTCTTCCACTCTG	ACTTTCCTGGGACCTGCCTTAGA
<i>site1(BARX2)</i>	-1620bp, -1631bp	AGCCGCCTCTGCATGGAGAA	GCATTAGACAAGGCCCGCAAC
<i>site2(BARX2)</i>	-515bp, -529bp	CTCTGACCCTTTCCAACGAGGA	GGCGACAAGAGCGAGATTCTGA
<i>site3(BARX2)</i>	-1490bp, -1501bp	AATGCTAGGCTGTGACTTGGC	AGGCTGGTCTTGAACCTCTGAC

PCR, polymerase chain reaction.

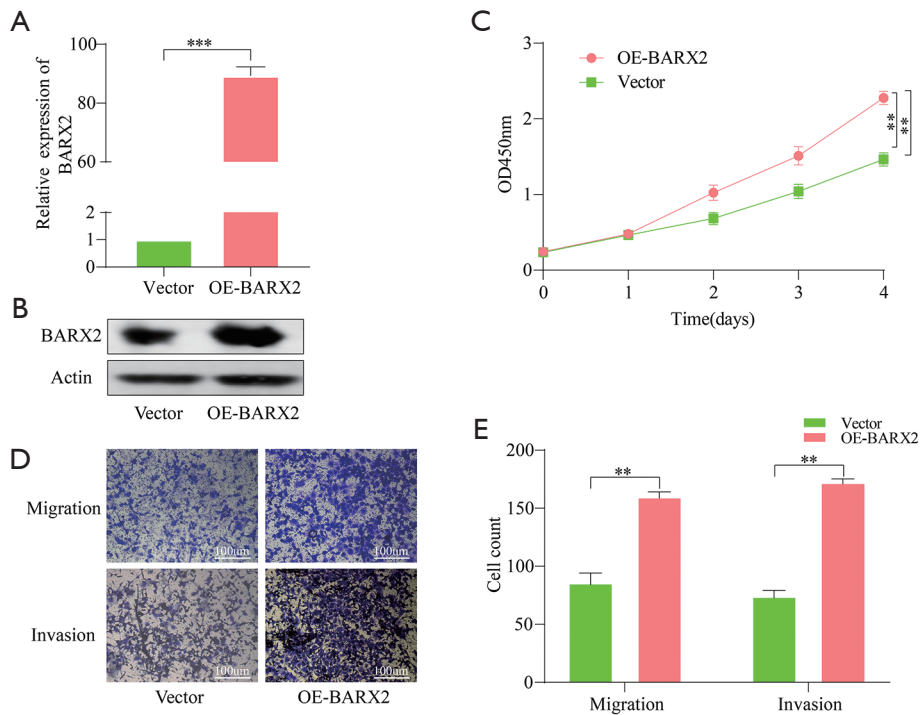


Figure S1 Overexpression of *BARX2* promoted proliferation and progression of A549 cells. (A,B). Overexpression of *BARX2* in A549 cells was validated by (A) qRT-PCR and (B) Western blotting. (C) CCK8 assays revealed that overexpression of *BARX2* promoted proliferation of A549 cells. (D,E) Transwell and Matrigel assays indicated that overexpression of *BARX2* promoted migration and invasion of A549 cells. After migration/invasion, the remaining cells on the top filter were washed off, and the filters were fixed in 4% methanol for 30 minutes. Filters were washed again in PBS before staining in 0.1% crystal violet for 30 min and then counted under the microscope. ** $P < 0.01$; *** $P < 0.001$. OE, overexpression; OD, optical density.

Table S4 *BARX2* LUAD GSEA Reactome

Description	Set	Enrichment score	NES	P value	Rank
Sulfur amino acid metabolism	10	-0.464	-1.802	0.020	2332
Diseases associated with glycosaminoglycan metabolism	30	0.355	1.641	0.030	3402
Heparan sulfate/heparin (HS-GAG) metabolism	34	0.335	1.597	0.041	2546
Selenoamino acid metabolism	65	-0.201	-2.129	0.045	6299
Glycosaminoglycan metabolism	77	0.261	1.509	0.046	2546

LUAD, lung adenocarcinoma; GSEA, Gene Set Enrichment Analysis; NES, normalized enrichment score; HS, heparan sulfate; GAG, glycosaminoglycans.

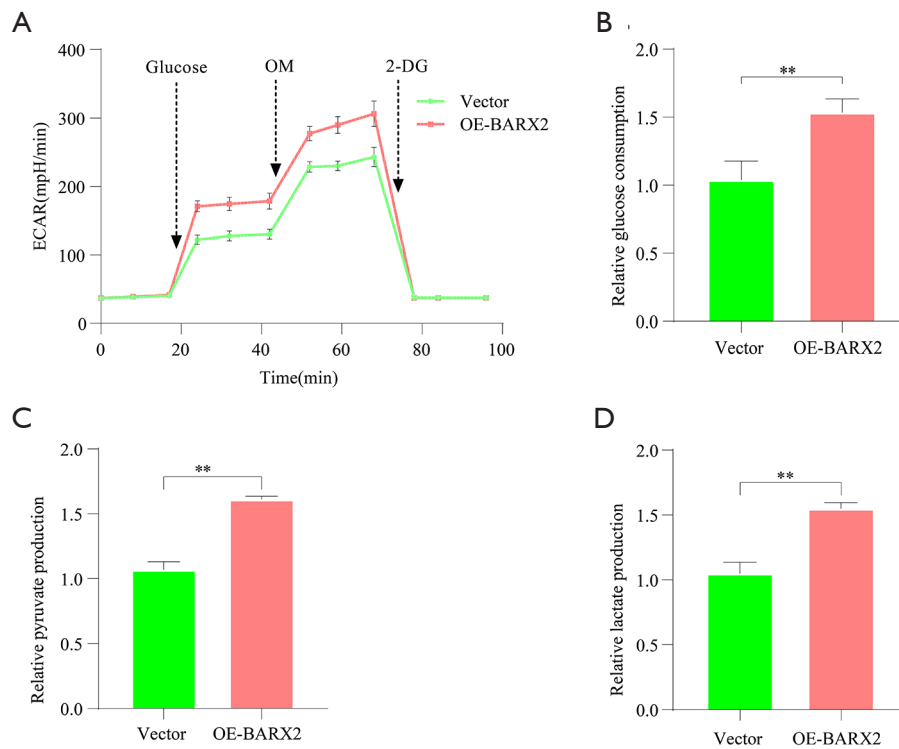


Figure S2 Overexpression of *BARX2* promoted the Warburg effect in A549 cells. (A) ECAR were measured by Seahorse XF in A549 cells after overexpression expression of *BARX2*. (B-D) Detection of (B) glucose consumption, (C) pyruvate production, and (D) lactate production in A549 cells after overexpression expression of *BARX2*. ** $P < 0.01$. OE, overexpression; ECAR, extracellular acidification rate; OM, oligomycin; 2-DG, 2-deoxy-glucose.

A

Matrix ID	Name	Score	Relative score	Sequence ID	Start	End	Strand
MA1471.1	BARX2	10.759	0.924323176424	NC_000002.12:74832126-74834125	603	614	-
MA1471.1	BARX2	9.30685	0.90149531146	NC_000002.12:74832126-74834125	602	613	+
Predicted sequence TATAATAATTTT							
MA1471.1	BARX2	6.97321	0.864811695429	NC_000002.12:74832126-74834125	26	37	-
MA1471.1	BARX2	6.92127	0.863995157411	NC_000002.12:74832126-74834125	297	308	+
Predicted sequence AAAAGCAGTTTG							
MA1471.1	BARX2	6.14421	0.851780172912	NC_000002.12:74832126-74834125	587	598	+
MA1471.1	BARX2	6.04621	0.850239758031	NC_000002.12:74832126-74834125	591	602	-
MA1471.1	BARX2	5.97022	0.849045222163	NC_000002.12:74832126-74834125	566	577	+
MA1471.1	BARX2	5.88926	0.847772506725	NC_000002.12:74832126-74834125	606	617	-
MA1471.1	BARX2	5.85091	0.847169632049	NC_000002.12:74832126-74834125	283	294	-
MA1471.1	BARX2	5.83968	0.846993184581	NC_000002.12:74832126-74834125	532	543	+

B

Matrix ID	Name	Score	Relative score	Sequence ID	Start	End	Strand	Predicted sequence
MA0148.1	FOXA1	11.153	0.909933400065	BARX2-promoter	385	395	-	TGTTTTCTTC
MA0148.2	FOXA1	11.1126	0.909824858351	BARX2-promoter	385	395	-	TGTTTTCTTC
MA0148.3	FOXA1	7.32982	0.873154356737	BARX2-promoter	1472	1486	-	ACATTGTTTATAAA
MA0148.2	FOXA1	7.85392	0.853925583843	BARX2-promoter	515	525	+	TATTTCTCAC
MA0148.1	FOXA1	7.89045	0.853268840335	BARX2-promoter	515	525	+	TATTTCTCAC
MA0148.4	FOXA1	9.0415	0.852950241651	BARX2-promoter	387	398	+	AAGAAAACAATT
MA0148.4	FOXA1	9.00937	0.852324437944	BARX2-promoter	1474	1485	+	TTATAACAATG
MA0148.2	FOXA1	7.7373	0.851925027617	BARX2-promoter	805	815	+	TATTTCTCTA
MA0148.1	FOXA1	7.79244	0.851566601006	BARX2-promoter	805	815	+	TATTTCTCTA

Figure S3 (A) Putative *BARX2* binding sites identified in the HK2 promoter with a calculated score of 10.759-5.83968 using Jaspar Database. (B) Putative *FOXA1* binding sites identified in the *BARX2* promoter with a calculated score of 11.153-7.32982 using Jaspar Database.