

Table S1 The sequences of siRNAs

Name	Sequence (5'→3')
siBHLHE40-1 sense	CAUGUGAAAGCACUAACAACTT
siBHLHE40-1 antisense	GUUUGUUAGUGCUUUCACAUGTT
siBHLHE40-2 sense	UGCCCACAUGUACCAAGUGUATT
siBHLHE40-2 antisense	UACACUUGGUACAUGUGGGCATT
siBHLHE40-3 sense	GCCCUGCAGAGUGGUUUACAATT
siBHLHE40-3 antisense	UUGUAAACCACUCUGCAGGGCTT
siTLR3-1 sense	CCUGAGCUGUCAAGCCACUACCUUUTT
siTLR3-1 antisense	AAAGGUAGUGGCUUGACAGCUCAGGTT
siTLR3-2 sense	GGAGAUUCCAGAUUUAUAATT
siTLR3-2 antisense	UUUAUAUCUGGAAUCUCCTT
siTLR3-3 sense	GCACCUUAACAUGGAAGUAATT
siTLR3-3 antisense	UUAUCUCCAUGUUAAGGUGCTT

siRNAs, small interfering RNAs.

Table S2 Primers used for the qRT-PCR analysis

Target gene	Sequence	
	Forward primer (5'→3')	Reverse primer (5'→3')
BHLHE40	GAAAGGATCGGCGCAATTAA	CATCATCCGAAAGCTGCATC
TLR3	TTGCCTTGTATCTACTTTTGGGG	TCAACACTGTTATGTTTGTGGGT
β-Actin	TCATGAAGTGTGACGTGGACAT	CTCAGGAGGAGCAATGATCTTG

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

Table S3 ChIP primer sequences are presented

Binding site	Sequence	
	Forward primer (5'→3')	Reverse primer (5'→3')
S1	CAATGCAAACCTGAATTTGCCTGGAC	ACCAACCTGGGCAACGTG
S2	AGTGAAGTTTTCTGACATCCCAA	ACTGGGCTCAGGGCTACATG

ChIP, chromatin immunoprecipitation.

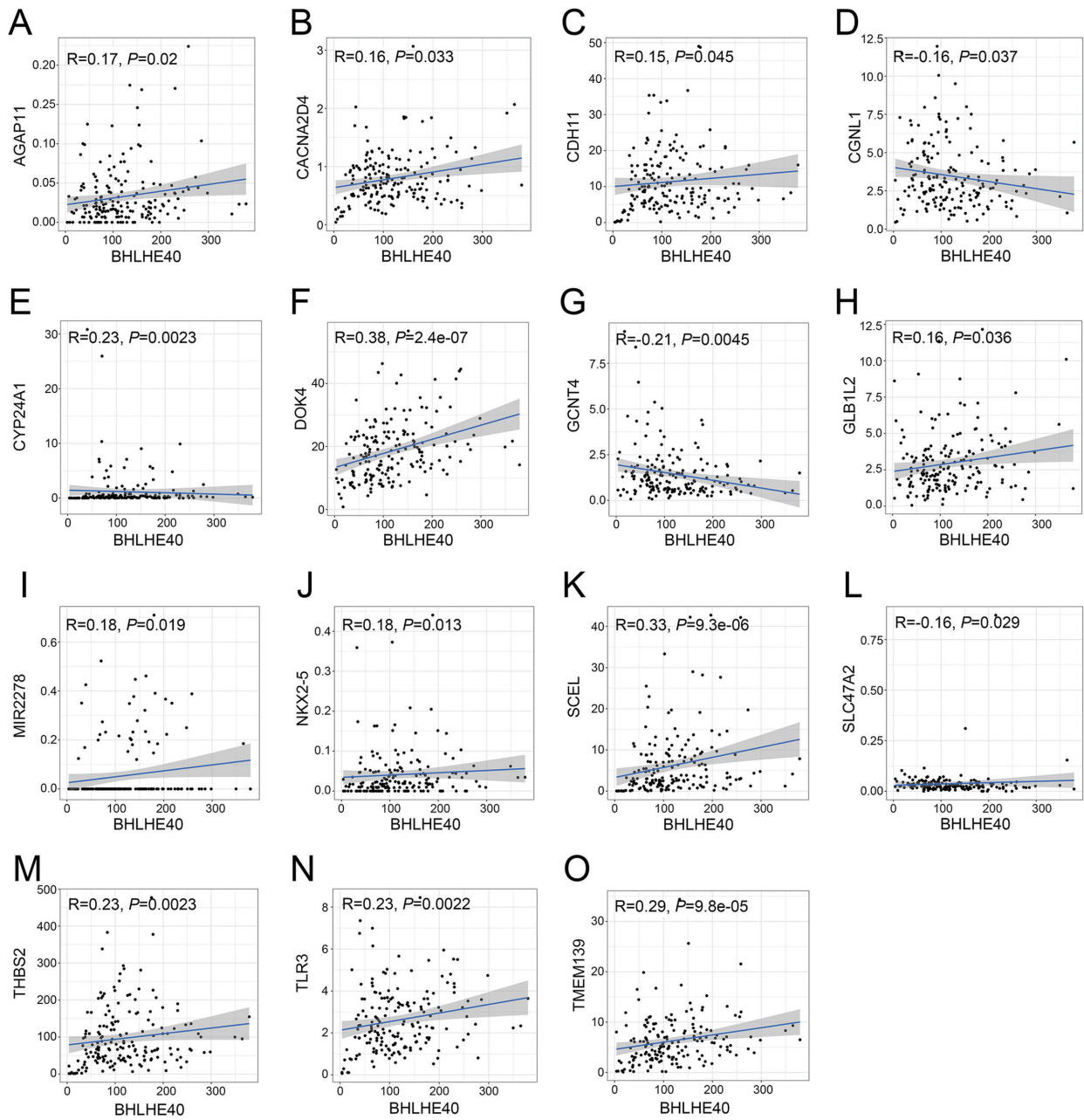


Figure S1 15 genes correlated with *BHLHE40* in the TCGA training set. TCGA, The Cancer Genome Atlas.

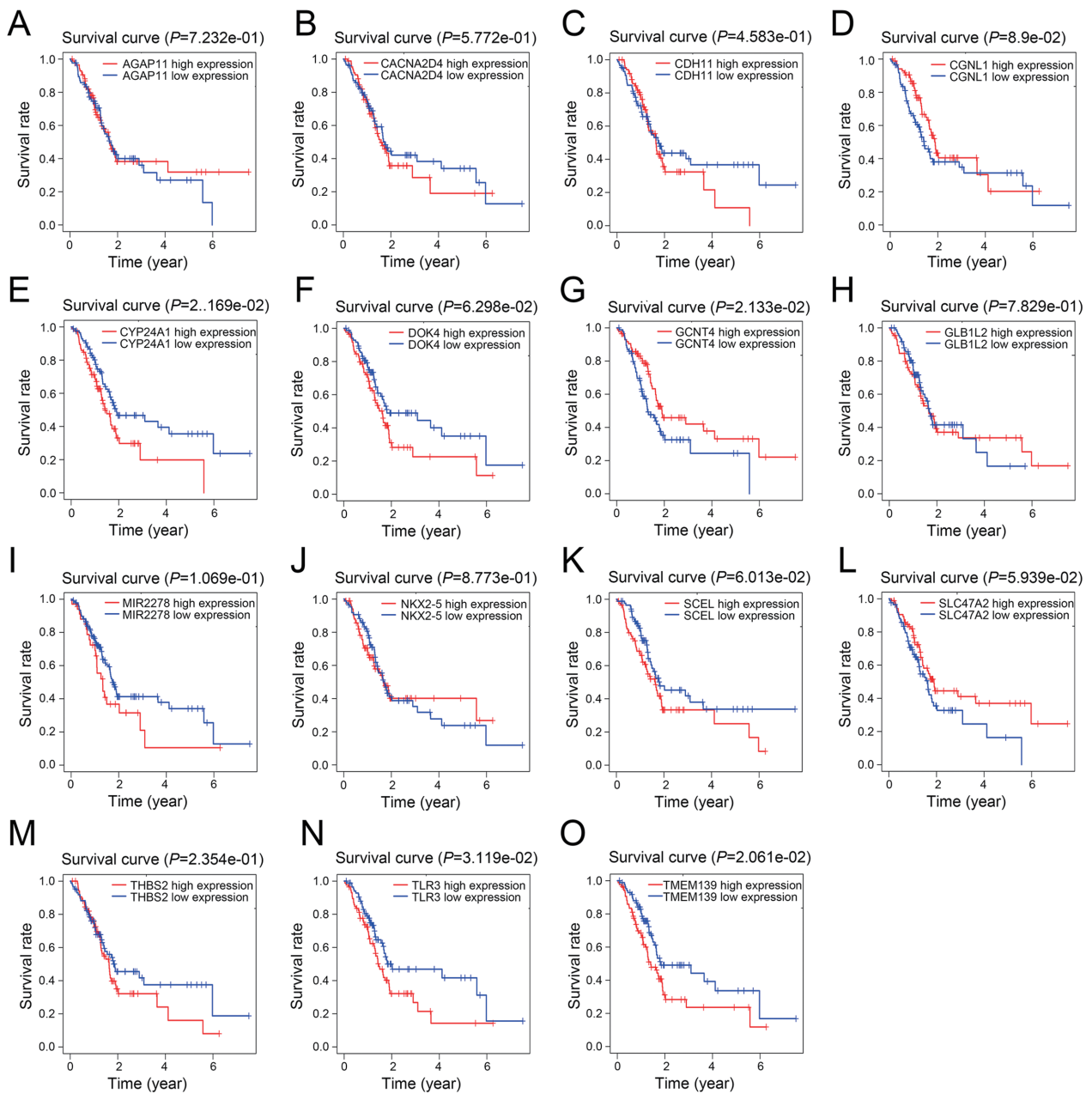


Figure S2 The KM survival curves of 15 genes. KM, Kaplan–Meier.

A CYP24A1

Matrix ID	Name	Score	Relative score	Sequence ID	Start	End	Strand	Predicted sequence
MA0464.2	MA0464.2.BHLHE40	3.6567006	0.8086477398915903	hg38_knownGene_ENST00000216862.8	1304	1313	+	tttacgtgca
MA0464.2	MA0464.2.BHLHE40	3.5735972	0.807267164311251	hg38_knownGene_ENST00000216862.8	832	841	-	attacgtgtc
MA0464.2	MA0464.2.BHLHE40	3.1592686	0.8003840309284996	hg38_knownGene_ENST00000216862.8	1788	1797	+	ctcccgcgcc

B GCNT4

Matrix ID	Name	Score	Relative score	Sequence ID	Start	End	Strand	Predicted sequence
MA0464.2	MA0464.2.BHLHE40	8.314361	0.8860242401066183	hg38_knownGene_ENST00000652361.2	1317	1326	-	ggccccgtgac
MA0464.2	MA0464.2.BHLHE40	8.00434	0.8808739506633737	hg38_knownGene_ENST00000652361.2	1317	1326	+	gtcacgggcc
MA0464.2	MA0464.2.BHLHE40	6.3500767	0.8533920993519108	hg38_knownGene_ENST00000652361.2	848	857	+	cgcacgtcac
MA0464.2	MA0464.2.BHLHE40	5.1984615	0.8342606150436587	hg38_knownGene_ENST00000652361.2	1594	1603	-	cccacgagcc
MA0464.2	MA0464.2.BHLHE40	5.0548964	0.8318756039002583	hg38_knownGene_ENST00000652361.2	853	862	-	ccccctgac
MA0464.2	MA0464.2.BHLHE40	3.900839	0.8127035492594978	hg38_knownGene_ENST00000652361.2	848	857	-	gtgacgtgcg
MA0464.2	MA0464.2.BHLHE40	3.240371	0.8017313636307034	hg38_knownGene_ENST00000652361.2	1577	1586	+	cccaagtgcc

C TLR3

Matrix ID	Name	Score	Relative score	Sequence ID	Start	End	Strand	Predicted sequence
MA0464.2	MA0464.2.BHLHE40	6.7578855	0.8601669210766743	hg38_knownGene_ENST00000296795.8	923	932	-	agtactgtac
MA0464.2	MA0464.2.BHLHE40	5.8901772	0.8457519092265093	hg38_knownGene_ENST00000296795.8	26	35	+	ctcaagtgat
MA0464.2	MA0464.2.BHLHE40	4.9893675	0.8307869897492056	hg38_knownGene_ENST00000296795.8	923	932	+	gtcacgtact
MA0464.2	MA0464.2.BHLHE40	4.445795	0.8217567617253585	hg38_knownGene_ENST00000296795.8	26	35	-	atcacttgag

D TMEM139

Matrix ID	Name	Score	Relative score	Sequence ID	Start	End	Strand	Predicted sequence
MA0464.2	MA0464.2.BHLHE40	4.840111	0.8283074267188935	hg38_knownGene_ENST00000409102.5	589	598	+	ttcaagtgat
MA0464.2	MA0464.2.BHLHE40	4.5997477	0.8243143363996307	hg38_knownGene_ENST00000409102.5	589	598	-	atcacttgaa
MA0464.2	MA0464.2.BHLHE40	3.8276465	0.8114876195985217	hg38_knownGene_ENST00000409102.5	1473	1482	+	cacatgtgct

Figure S3 The JASPAR database was used to analyze binding sites of *BHLHE40* in the promoters of *CYP24A1* (A), *GCNT4* (B), *TLR3* (C), and *TMEM139* (D).