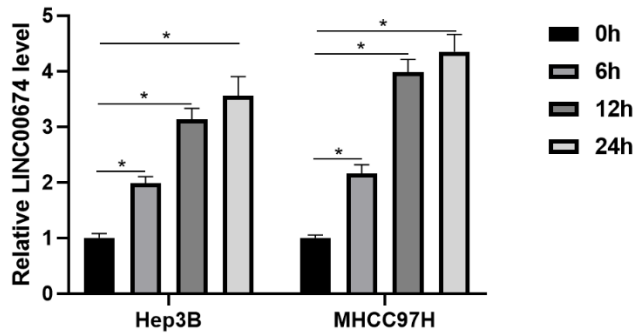
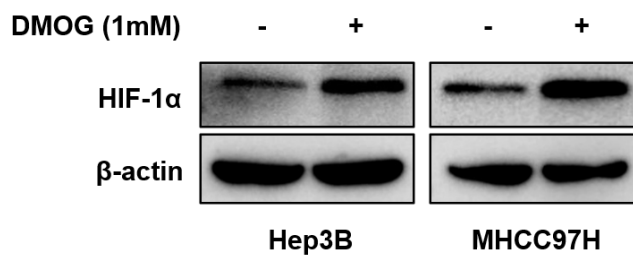


**Supplementary Table 1 The primer sequences used in this study**

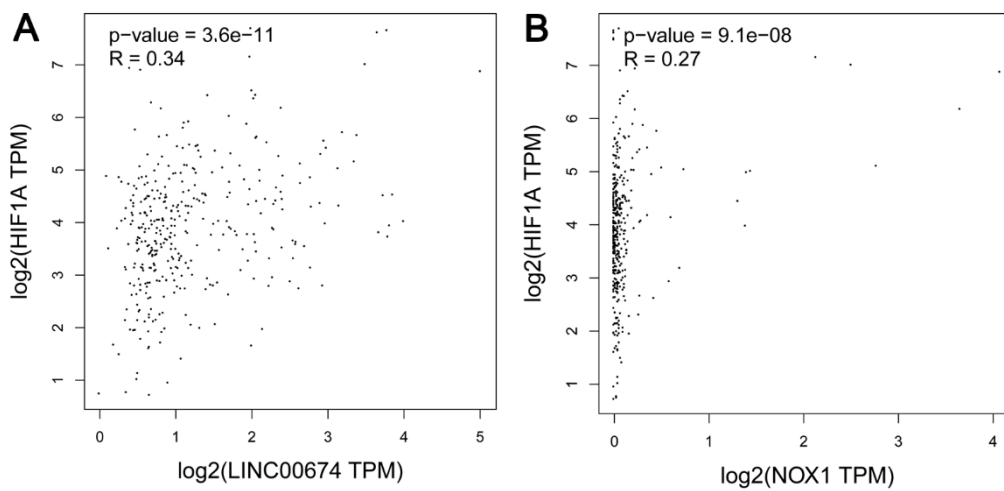
<b>Gene</b>	<b>Primer</b>	<b>Sequence (5'-3')</b>
LINC00674	forward	GAGCACGTCCACATAGCTGA
	reverse	TGGA CT CCTAGCAGGAGCAT
NOX1	forward	GTTTTACCGCTCCCAGCAGAA
	reverse	GGATGCCATTCCAGGAGAGAG
18S	forward	CGGCGACGACCCATTCGAAC
	reverse	GAATCGAACCCCTGATTCCCCGTC
HRE-1	forward	TGTTTTCTGGCTGGACACAG
	reverse	CCACCACACCTGGCTAACTT
HRE-2	forward	CTTAAATTGTGCCACCACCA
	reverse	GGCTGAGGAAAGTGAGCCTA



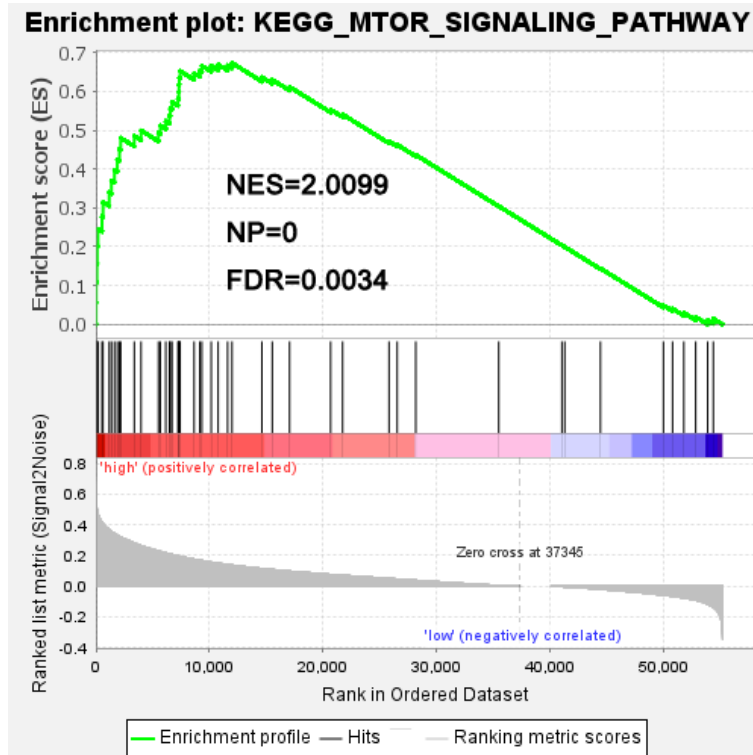
**Supplementary Figure 1** The level of LINC00674 in Hep3B and MHCC97H cells under hypoxic conditions at different time points.



**Supplementary Figure 2** The level of HIF-1 $\alpha$  in Hep3B and MHCC97H cells with or without DMOG (1mM) treatment.



**Supplementary Figure 3** The correlations between HIF-1 $\alpha$  mRNA and LINC00674/NOX1 mRNA in HCC tissues from TCGA database. (A) HIF-1 $\alpha$  mRNA was positively correlated with LINC00674 expression in HCC tissues. (B) HIF-1 $\alpha$  mRNA was positively correlated NOX1 mRNA level in HCC tissues.



**Supplementary Figure 4 KEGG pathway enrichment analysis indicates a close correlation between LINC00674 and the mTOR signaling pathway in HCC.**