

Table S1 Primer sequences used in this study.

Primer name	Primer sequence (5'-3')
ISOC1 forward primer (qPCR)	GAGATTCCCGGAGTCAGGAG
ISOC1 reverse primer (qPCR)	TCGTGGTCACTATGATCCCG
miR-4633-5p primer (RT)	GTCGTATCCAGTGCGTGTCTGGAGTCGGCAATTGCACTGGATACGACGAGGAGCT
miR-4633-3p primer (RT)	GTCGTATCCAGTGCGTGTCTGGAGTCGGCAATTGCACTGGATACGACTGCATATG
miR-4633 forward primer (qPCR)	CAGTGCGTGTCTGGAGT
miR-4633-5p reverse primer (qPCR)	ACACTCCAGCTGGGATATGCCTGGCTAG
miR-4633-3p reverse primer (qPCR)	ACACTCCAGCTGGGAGGAGCTAGCCAGGCA
β -actin forward primer (qPCR)	AGAAGGATTCTATGTGGGCG
β -actin reverse primer (qPCR)	GGATAGCACAGCCTGGATAGCA
U6 forward primer (qPCR)	CTCGCTTCGGCAGCACA
U6 reverse primer (qPCR)	AACGCTTCACGAATTTGCGT
CD513B-ISOC1 forward primer	TCTAGAGCCACCATGGCGGCTGCGGAGCCGGCGGT
CD513B-ISOC1 reverse primer	GGATCCCTACTTATCGTCGTCATCCTTGTAATCTACTTTGGAAAGCAGACCCG
CD513B-miR-4633 forward primer	CACAAATGCGTGTGGGAGCGTCACTTACAGCCGAACACAG
CD513B-miR-4633 reverse primer	CCACACGCATTTGTGGCGGAGACTTGCCATGTAACCTGCA
pLL3.7-shISOC1-1 forward primer	TGTACTTCCAAAGACCAAGTTTTTCAAGAGAAAACCTTGGTCTTTGGAAGTATTTTTTC
pLL3.7-shISOC1-1 reverse primer	TCGAGAAAAAATACTTCCAAAGACCAAGTTTTCTCTTGAAAACTTGGTCTTTGGAAGTACA
pLL3.7-shISOC1-2 forward primer	TGCCTCACAAATGTTGTCCACTTATCAAGAGATAAGTGGACAACATTGTGAGGTTTTTC
pLL3.7-shISOC1-2 reverse primer	TCGAGAAAAAACCTCACAAATGTTGTCCACTTATCTCTGAATAAGTGGACAACATTGTGAGGCA
ISOC1 3'-UTR forward primer	GTGTAATTCTAGACATATGGGGCCCGACATTTGAAGAACTGGTATGCTACTCACTG
ISOC1 3'-UTR reverse primer	CCCCGACTCTAGAGAATTCAATTACTTTAATATAAAAGACAGCAGTTTCACATTTAC
ISOC1 sgRNA forward primer	CGACATGCACCGCAAATTCGGTTTTAGAGCTAGAAATAGCAAGTTAA
ISOC1 sgRNA reverse primer	ACCGAATTTGCGGTGCATGTCGCAACAAGGCTTTTCTCCAAGG

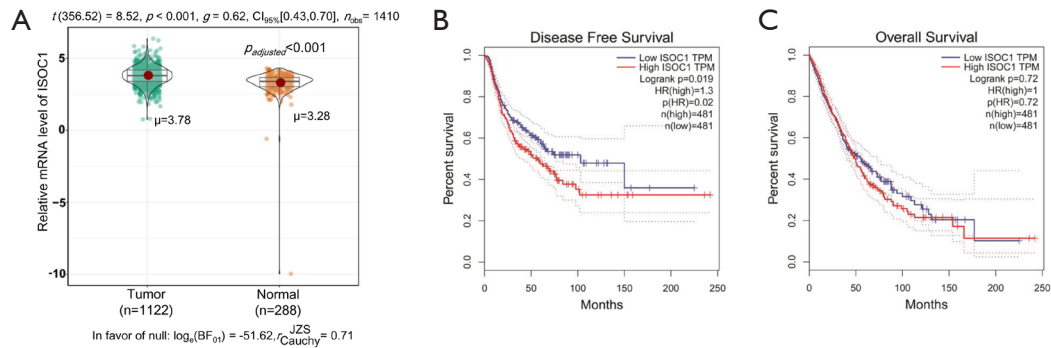


Figure S1 *ISOC1* expression was elevated in NSCLC. (A) The expression level of *ISOC1* mRNA in NSCLC tumor tissues (n=1,122) and normal lung samples (n=288). Analysis of *ISOC1* expression were processed with the data obtained from TCGA and GTEx database using UCSC Xena platform. The horizontal line represents the mRNA expression level [$\log_2(TPM + 0.001)$]. (B) Disease-free survival curve analyses for NSCLC patients based on the expression level of *ISOC1* mRNA. (C) Overall survival curve analyses for NSCLC patients based on the expression level of *ISOC1* mRNA. TCGA, The Cancer Genome Atlas; GTEx, Genotype-Tissue Expression; TPM, transcripts per million; HR, hazard ratio.

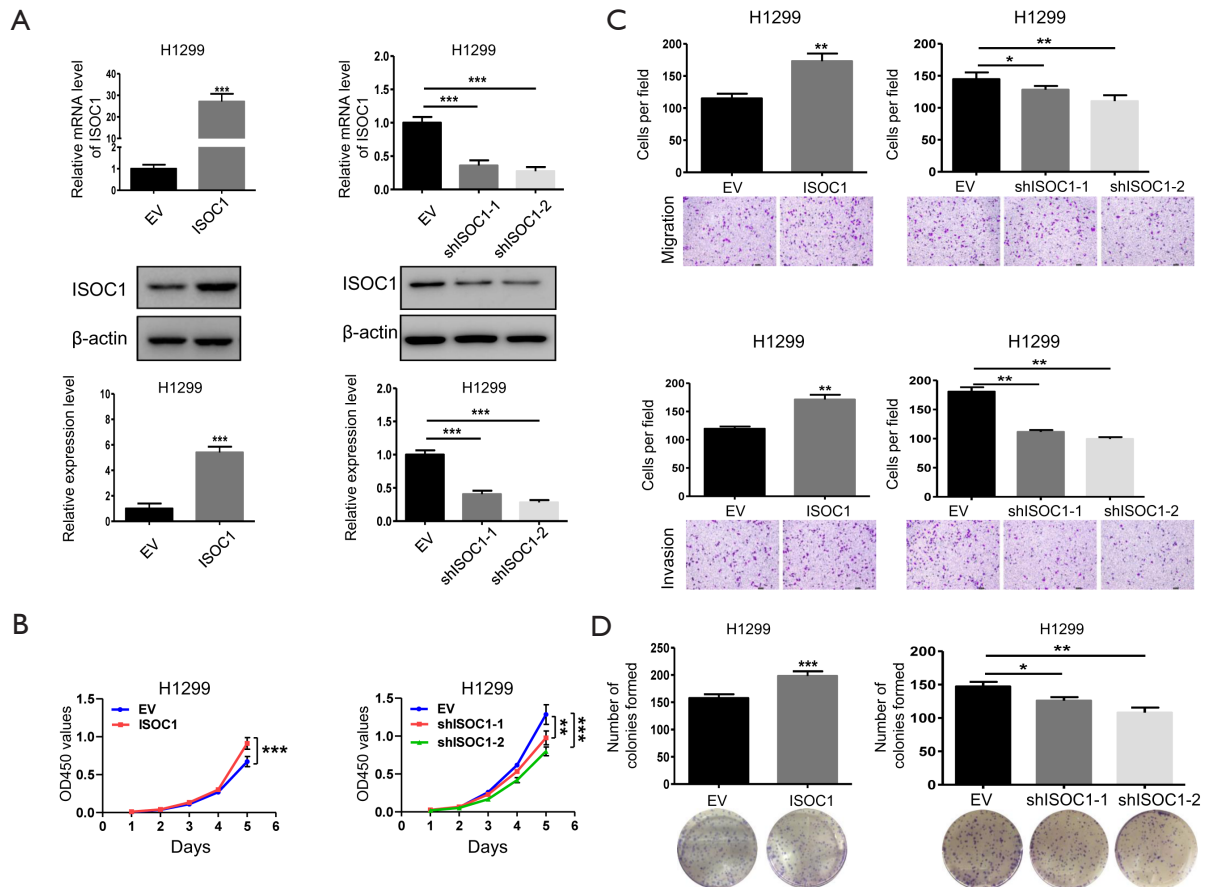


Figure S2 Effects of *ISOC1* on H1299 cell progression, migration, and invasion. (A) OE and KD (shISOC1-1 and shISOC1-2) efficiency of *ISOC1* was determined by Western blot and qRT-PCR. (B) CCK-8 cell proliferation assays in *ISOC1* OE and KD H1299 cells from days 1 to 5. (C) Transwell migration and invasion assays in *ISOC1* OE and KD H1299 cells ($\times 200$). Cells were stained with crystal violet. (D) Effects of *ISOC1* OE and KD on colony formation in the H1299 cell line. *, $P < 0.05$; **, $P < 0.01$; ***, $P < 0.001$. OE, overexpression; KD, knockdown; EV, empty vector.

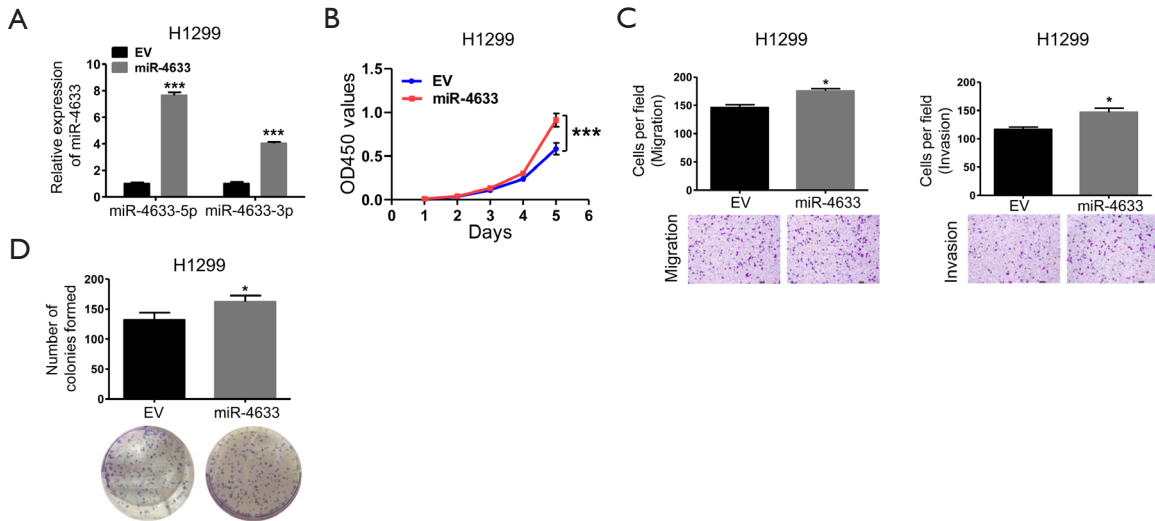


Figure S3 miR-4633 promoted cell viability in the H1299 cell line. (A) Forced expression of miR-4633 in H1299 cells was assessed by qRT-PCR. (B) Effects of miR-4633 on H1299 cell proliferation was examined by CCK-8 assay. (C) Transwell assay was used to assess the effects of miR-4633 on H1299 migration and invasion ($\times 200$). Cells were stained with crystal violet. (D) Colony formation assays in H1299 cells infected with EV or miR-4633 lentivirus. *, $P < 0.05$; ***, $P < 0.001$. EV, empty vector.

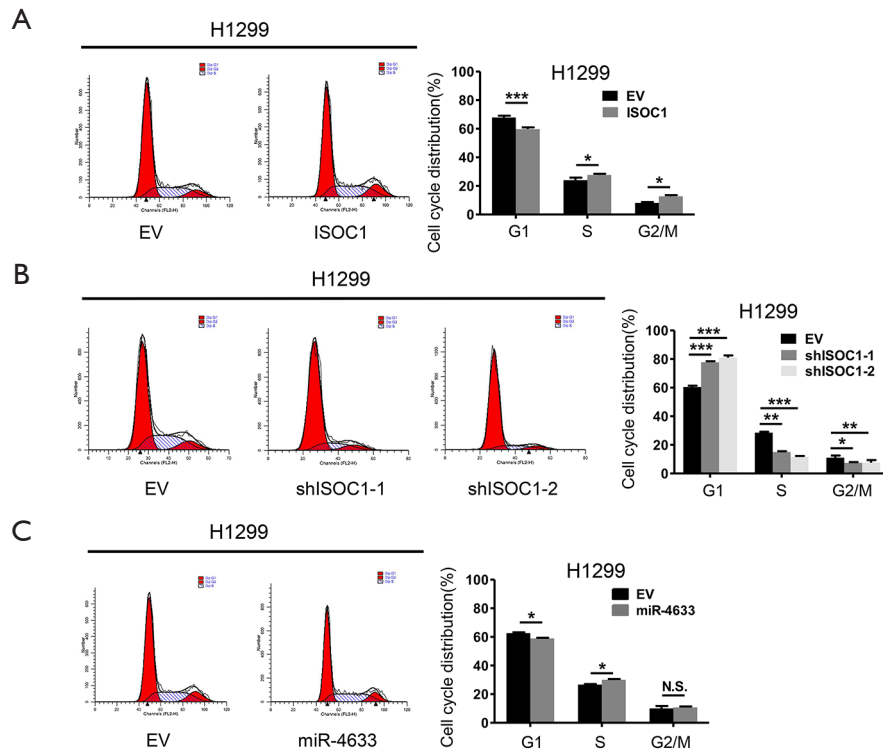


Figure S4 Effects of *ISOC1* and miR-4633 on H1299 cell cycle distribution. (A) *ISOC1* OE H1299 cells caused an increase of cell accumulation in S and G2/M phases. (B) *ISOC1* KD H1299 cell line induced G1 arrest. (C) miR-4633 promoted G1/S progression in the H1299 cell line. *, $P < 0.05$; **, $P < 0.01$; ***, $P < 0.001$. OE, overexpression; KD, knockdown; EV, empty vector; N.S., not significant.