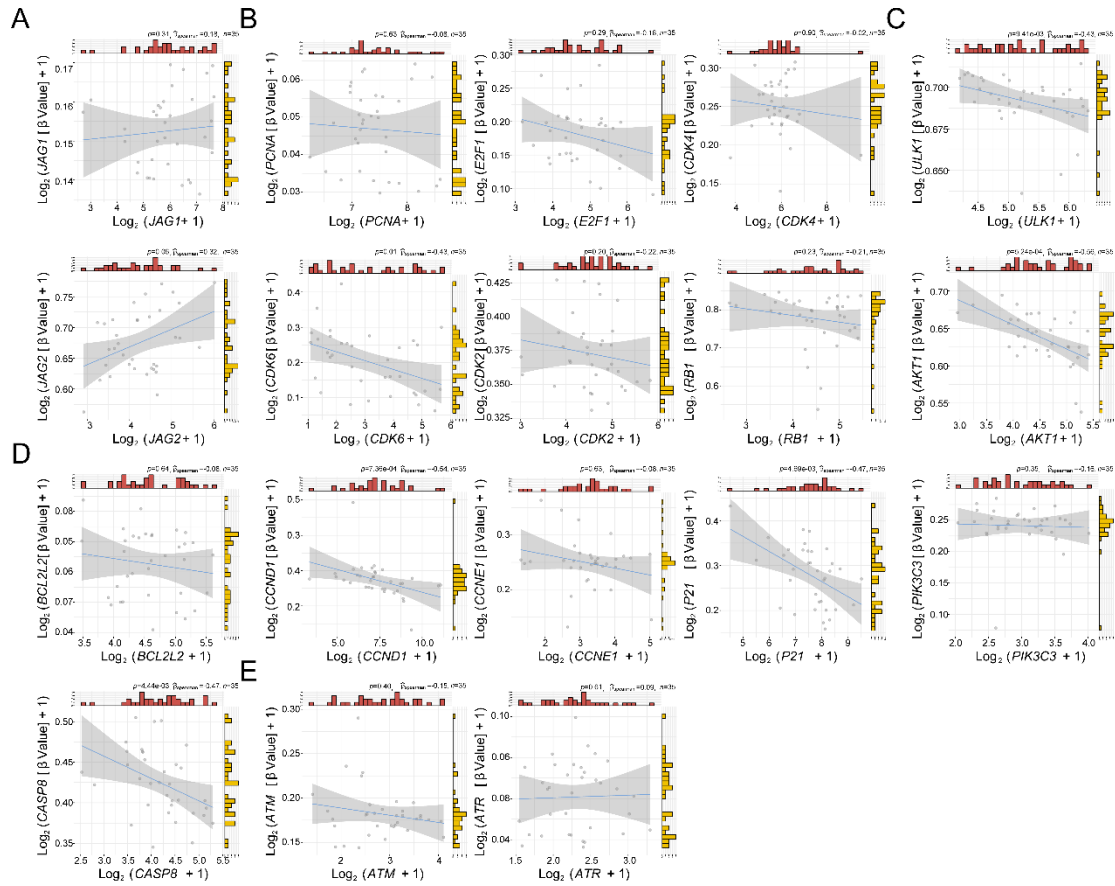


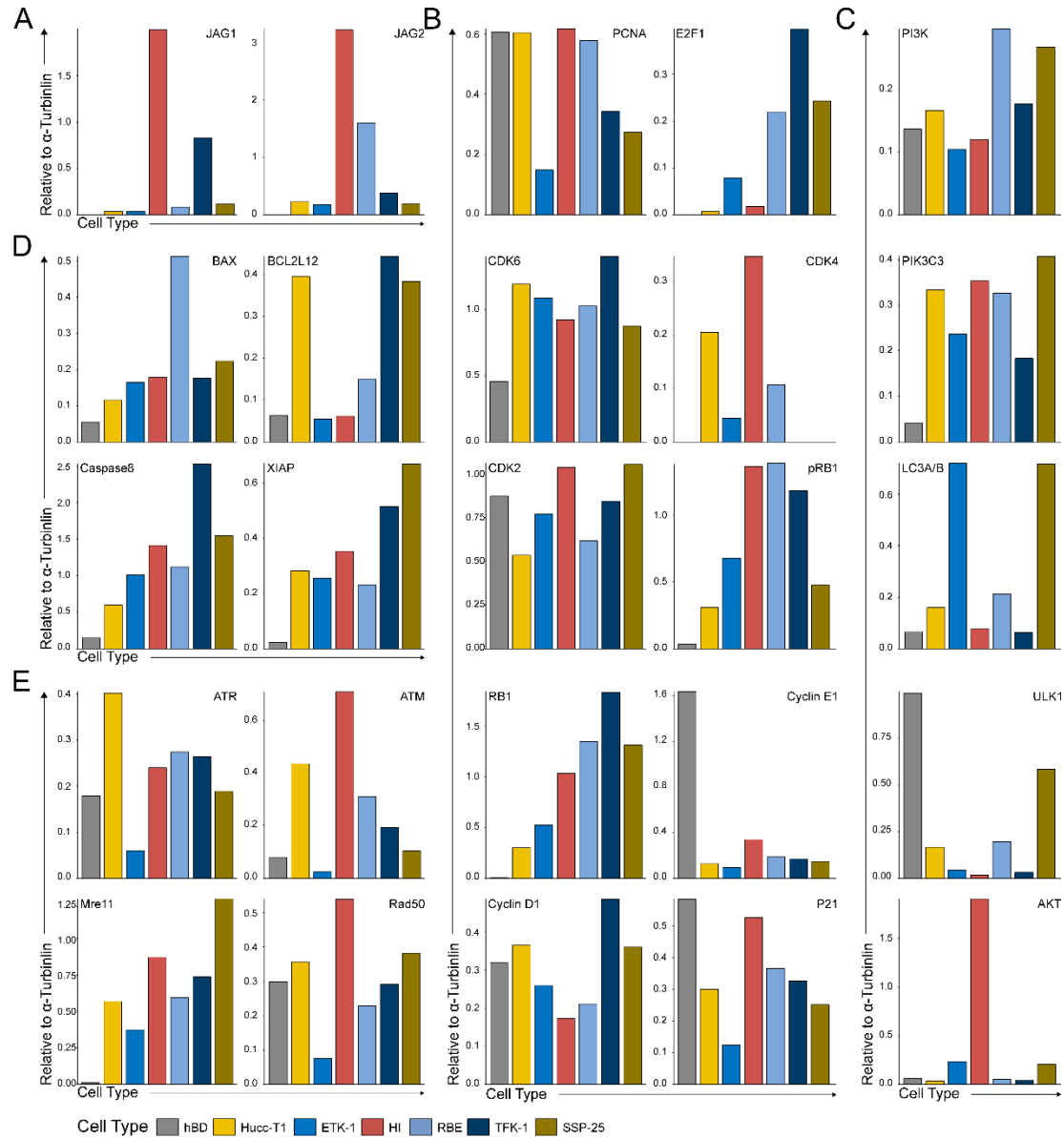
Supplementary Table 1 Sequences of primers used in qRT-PCR

Gene	Forward primer	Reverse primer
<i>JAG1</i>	GCCGAGGTCCTATACGTTGC	CCGAGTGAGAAGCCTTTTCA A
<i>JAG2</i>	GCCCCGCAACGACTTTTTTC	TGGAGCAAATTACACCCTTG TT
<i>PCNA</i>	CCTGCTGGGATATTAGCTCC A	CAGCGGTAGGTGTCGAAGC
<i>E2F1</i>	ACGTGACGTGTCAGGACCT	GATCGGGCCTTGTTTGCTCTT
<i>CDK2</i>	CCAGGAGTTACTTCTATGCC TGA	TTCATCCAGGGGAGGTACAA C
<i>CDK4</i>	ATGGCTACCTCTCGATATGA GC	CATTGGGGACTCTCACACTC T
<i>CDK6</i>	TCTTCATTCACACCGAGTAG TGC	TGAGGTTAGAGCCATCTGGA AA
<i>RB1</i>	TTGGATCACAGCGATACAA ACTT	AGCGCACGCCAATAAAGAC AT
<i>ULK1</i>	GGCAAGTTCGAGTTCTCCCG	CGACCTCCAAATCGTGCTTC T
<i>PIK3C</i> 3	GTCTGGCCTAATGTAGAAG CAG	GGCAAGACGGCTCATCTGAT
<i>BAX</i>	CCCGAGAGGTCTTTTTCCGA G	CCAGCCCATGATGGTTCTGA T
<i>BCL2L</i> 1	GAGCTGGTGGTTGACTTTCT C	TCCATCTCCGATTCAGTCCCT
<i>XIAP</i>	AATAGTGCCACGCAGTCTA CA	CAGATGGCCTGTCTAAGGCA A
<i>CASP</i> 8	AGAGTCTGTGCCCAAATCA AC	GCTGCTTCTCTTTTGCTGAA
<i>ATR</i>	TCCCTTGAATACAGTGGCCT A	TCCTTGAAAGTACGGCAGTT C
<i>ATM</i>	TTGATCTTGTGCCTTGGCTA C	TATGGTGTACGTTCCCCATGT
<i>MRE1</i> 1	GGGGCAGATGCACTTTGTG	GAAGCAAAACCGGACTAAT GTCT
<i>RAD5</i> 0	TTTGGTTGGACCCAATGGGG	CAGGAGGGAAATCTCCAGT ACAA
<i>18S</i>	GAGACTCTGGCATGCTAAC TAG	GGACATCTAAGGGCATCACA G

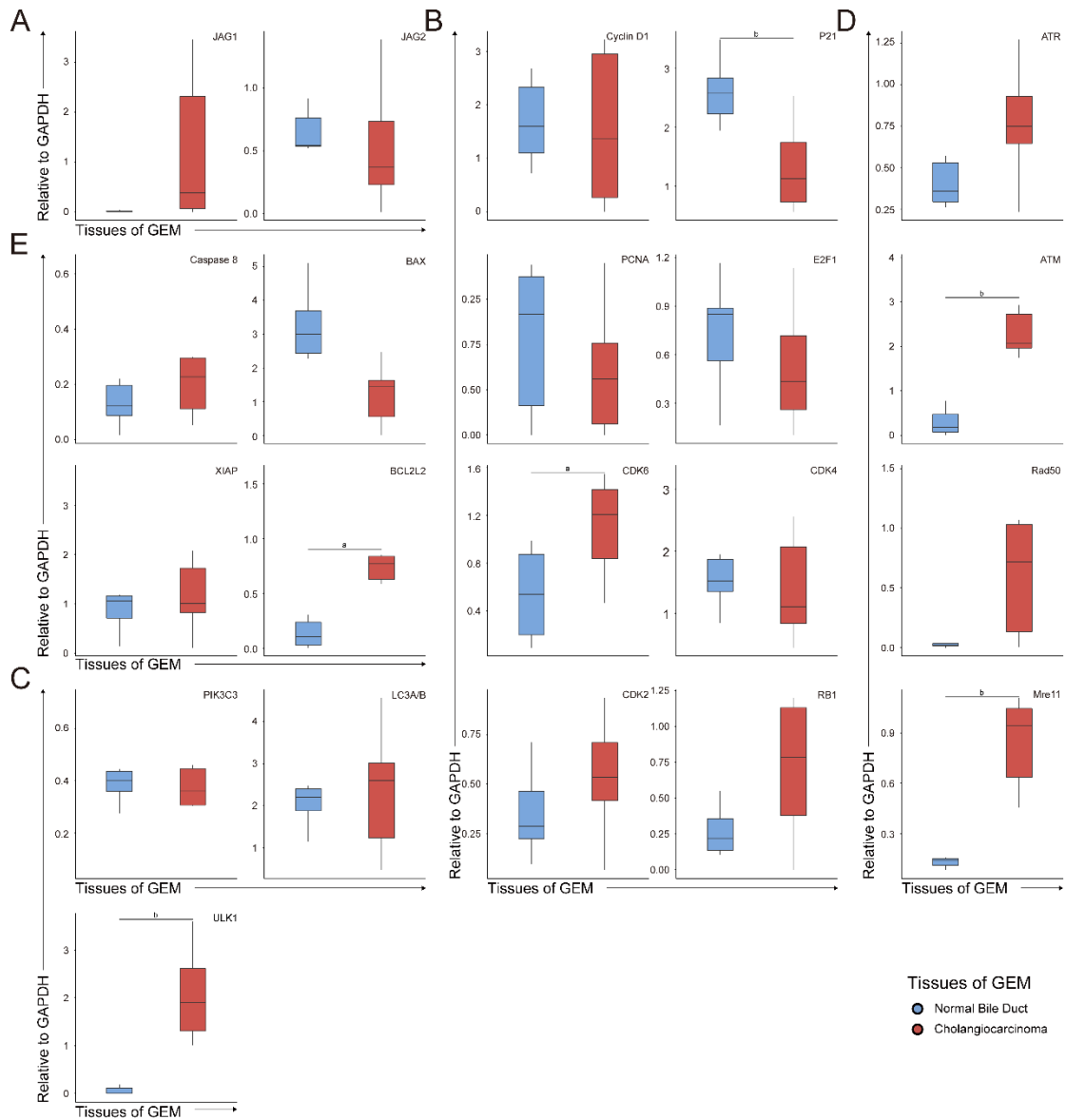
Supplementary Figure 1 The correlations between methylation status and related genes expression. The relationships between the methylation status and its genes expression from (A) cell cycle (B) Notch, (C) autophagy, (D) cell death, and (E) DNA damage associate pathways. The DNA methylation levels of CpG islands were shown as β value. Spearman correlation coefficient (ρ) is used to evaluate the significance of correlations.



Supplementary Figure 2 The quantitative analysis of genes verified in cholangiocarcinoma cell lines. The protein quantification data of leading-edge genes relative to α -Tubulin, including (A) cell cycle, (B) Notch, (C) autophagy, (D) cell death, and (E) DNA damage associate pathways.



Supplementary Figure 3 The quantitative analysis of genes verified in genetically engineered mouse model. The protein quantification data of leading-edge genes relative to GAPDH, including (A) cell cycle, (B) Notch, (C) autophagy, (D) cell death, and (E) DNA damage associate pathways. P values were shown as: ^a $P < 0.05$, ^b $P < 0.01$, and ^c $P < 0.001$.



Supplementary Figure 4. Relationship between levels of tumor infiltrating immune cells and cell cycle and Notch associated genes expression.

Correlations between tumor infiltration of different immune cells, (A) cell cycle, (B) Notch, (C) autophagy, (D) cell death, and (E) DNA damage associate genes. Spearman correlation is used to evaluate the relationships, and the significant levels is shown as ^a $P < 0.05$; ^b $P < 0.01$; and ^c $P < 0.001$. Red: Significant correlations; Black: No significant correlations.

