

# Prognostic implications of aberrantly expressed methylation-driven genes in hepatocellular carcinoma: A study based on The Cancer Genome Atlas

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**Abstract.** RNA-Sequencing and methylation data for hepatocellular carcinoma (HCC) were downloaded from The Cancer Genome Atlas (TCGA). The aberrantly expressed methylation-driven genes in HCC and normal tissues were identified using the Limma package and the MethylMix algorithm. The Database for Annotation, Visualization and Integrated Discovery and ConsensusPathDB were used for Gene Ontology (GO) enrichment and pathway analysis. Univariate and multivariate Cox regression analyses were used to construct a prognostic risk model of HCC. Survival curve and receiver operating characteristic (ROC) curves were applied to evaluate the clinical utility of the risk model. A total of 238 methylation-driven genes were successfully identified from cancer and normal tissues. GO enrichment analysis indicated that these genes functioned in the extracellular space, interfering with lipid metabolism in hepatocytes and regulating adaptive immune responses. In total, 14 relevant pathways were identified. The following prognostic risk model was generated: Risk score=CALML3 (degree of methylation) x (-4.860) + CCNI2 x (2.071) + TNFRSF12A x (-3.369) + IFITM1 x (1.203) + ENPP7P13 x (-1.366) + DDT x (2.139) + RASAL2-AS1 x (-1.384) + ANKRD22 x (-3.215). The median risk score (0.970) derived from this model was set as cutoff

value for assigning patients to high- or low-risk group. The 5-year survival rate was 35.8% [95% confidence interval (CI)=27.1-47.4%] in the high-risk group and 61.7% (95% CI=51.4-74.2%) in the low-risk group (P<0.0001). The ROC curve showed an area under the curve of 0.742, indicating that this model is appropriate for predicting the survival rate of patients. Furthermore, the methylation and expression levels of two key genes, tumor necrosis factor superfamily member 12A and D-dopachrome decarboxylase, were significantly associated with prognosis and were correlated with cg00510447, cg26808293, cg11060661 and cg16132339 methylation. In conclusion, a prognostic risk model for HCC is proposed based on the bioinformatic analysis of methylation-driven genes. The findings of the present study may improve understanding of the pathogenesis and prognosis of HCC.

## Introduction

Primary liver cancer is the second leading cause of cancer-related mortality in men globally and the sixth leading cause of cancer-related mortality in women (1). According to the statistics from the International Agency for Research on Cancer of the World Health Organization, there were >782,000 cases of primary liver cancer in 2012, making liver cancer the fifth and ninth most common cancer among men and women, respectively (2). Most risk factors for liver cancer, such as alcohol, are commoner in men than in women, so the prevalence of hepatocellular carcinoma (HCC) in men is 2-3 times higher than in women (1).

Cell characteristics are under control of and maintained by both genetic and epigenetic mechanisms (3). Epigenetics is defined as inheritable changes in gene expression with no alterations in DNA sequence (4). Methylation, the most important and common epigenetic modification, is an important means of regulating genome function (5). Decreases in the genome-wide methylation level is an important indicator of early cancer and may be significantly correlated with the severity and metastasis of cancer (6). The main reason underlying this phenomenon is the demethylation of repeat sequences, which leads to genome instability (7,8). Aberrant hypermethylation of CpG islands in specific promoter regions is another important phenomenon in the late stage of cancer,

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**Abbreviations:** BP, biology process; CC, cellular component; DAVID, The Database for Annotation, Visualization and Integrated Discovery; GO, Gene Ontology; HCC, hepatocellular carcinoma; IGF, insulin-like growth factor; IGFs, insulin-like growth factor binding proteins; MF, molecular function

**Key words:** The Cancer Genome Atlas, hepatocellular carcinoma, methylation, biomarkers, Cox proportional hazards regression, survival analysis, prognosis

leading to changes in chromosomal structure, silencing of tumor suppressor genes and other cancer-related genes, thereby promoting cancer cells to adapt to the microenvironment and metastasis (9,10). Previous studies have been conducted to examine the implication of methylation in the diagnosis, treatment response and prognosis of various malignancies, such as lung (11), breast (12), and ovarian cancer (13). It has also been reported that coactivator-associated arginine methyltransferase 1-mediated GAPDH methylation is a key regulatory mechanism of glucose metabolism in liver cancer (14). In addition, it has also been found that the mRNA expression of tumor suppressor P14ARF is regulated by DNA methylation in primary liver cancer; DNA methylation of the P14ARF gene may be related to the occurrence and tumor-node-metastasis stage of primary liver cancer (15).

The Cancer Genome Atlas (TCGA) (16), a public database used in bioinformatics analysis, has complete patient data and is conducive to the analysis of cancer progression and prognosis. In the present study, HCC-related methylation-driven genes were identified from TCGA database, and the correlation between the identified genes and HCC progression and prognosis was analyzed. A series of bioinformatic and survival analyses were conducted to identify the biomarkers associated with methylation and constructed a prognostic risk model for predicting the prognosis of patients with HCC.

## Materials and methods

**Study population and data processing.** The HCC-related level 3 RNA-sequencing (Seq) data and methylation data were downloaded from TCGA (<https://gdc.cancer.gov/>). Specifically, the Perl programming language (<http://www.perl.org/>) was used to extract matrix files from the RNA-seq and methylation data files. There were 122 women and 255 men; 204 patients were aged  $\geq 60$  and 172 patients aged  $< 60$ . The clinical data of the patients with HCC are summarized in Table I. The RNA-Seq and methylation matrix files were merged using the Limma package (17) and the MethylMix algorithm. Following the merge, the genes meeting all of the following three conditions were defined as methylation-driven genes: i) Gene expression levels differ between normal and cancer tissues; ii) methylation levels differ between normal and cancer tissues; and iii) the degree of DNA methylation is correlated with gene expression. The Pheatmap package (1.0.12, <https://CRAN.R-project.org/package=pheatmap>) was used to cluster the methylation-driven genes.

**Gene Ontology (GO) and pathway enrichment analysis of aberrantly expressed methylation-driven genes.** The Database for Annotation, Visualization and Integrated Discovery (DAVID 6.7; <https://david.ncifcrf.gov/>) was used to perform GO enrichment analysis of the aberrant methylation-driven genes. A list of differentially expressed methylation-driven genes was submitted to the functional annotations tool in DAVID (screening criteria,  $P < 0.01$ ).

Differentially expressed methylation-driven genes were analyzed using the overexpression analysis function of ConsensusPathDB 3.4.1 (<http://cpdb.molgen.mpg.de/>). The Kyoto Encyclopedia of Genes and Genomes database

Table I. Summary of the clinical data for hepatocellular carcinoma from The Cancer Genome Atlas.

Characteristics	No. of samples, n (%)
Age, years	
≤50	32 (8.5)
>50	342 (91.5)
Sex	
Female	122 (32.4)
Male	255 (67.6)
Stage	
I	175 (49.6)
II	87 (24.6)
III	86 (24.4)
IV	5 (1.4)
Survival state	
Alive	245 (65.0)
Deceased	132 (35.0)
Race	
American	19 (5.2)
Asian	161 (43.9)
Caucasian	187 (50.9)

(conducted in ConsensusPathDB 3.4.1) was used to perform pathway enrichment analysis for the differentially expressed methylation-driven genes taking  $P < 0.01$  as a cutoff value.

**Screening for prognosis-related signatures and risk score calculations.** The univariate Cox regression model was used to calculate the association between the methylation level of each aberrant methylation-driven gene and the overall survival (OS) of the patient. Genes were considered statistically significant in univariate Cox analysis when  $P < 0.05$ . The amount of Z-value represents the distance between the original score and the parent mean, measured in standard deviation. When the original score is lower than the average, Z is negative and vice versa. Multivariate Cox regression was used in the R language (3.5.1, <https://www.r-project.org/>) Survival Package (2.44-1.1, <https://CRAN.R-project.org/package=survival>) to screen the independent prognostic ability of the aberrant methylation-driven genes (18). A prognostic risk assessment model was constructed by integrating the information of the aberrant methylation-driven genes.

The log-rank test was used to calculate P-values and the prognostic correlation coefficient  $\beta$ . The risk score was defined as follows: Risk score =  $\beta_{\text{gene1}} \times \text{methyl}_{\text{gene1}} + \beta_{\text{gene2}} \times \text{methyl}_{\text{gene2}} + \dots + \beta_{\text{gene(n)}} \times \text{methyl}_{\text{gene(n)}}$ , where  $\beta$  is the prognostic correlation coefficient and methyl is the methylation level of the corresponding gene. The risk score of each sample was calculated and the median risk score was set as the cutoff value for assigning the samples into the low- and high-risk groups (11,19). The Kaplan-Meier method was used to plot the survival curves for the low- and high-risk groups. Differences between groups were evaluated using the log-rank test. Receiver operating characteristic (ROC) curves were drawn to

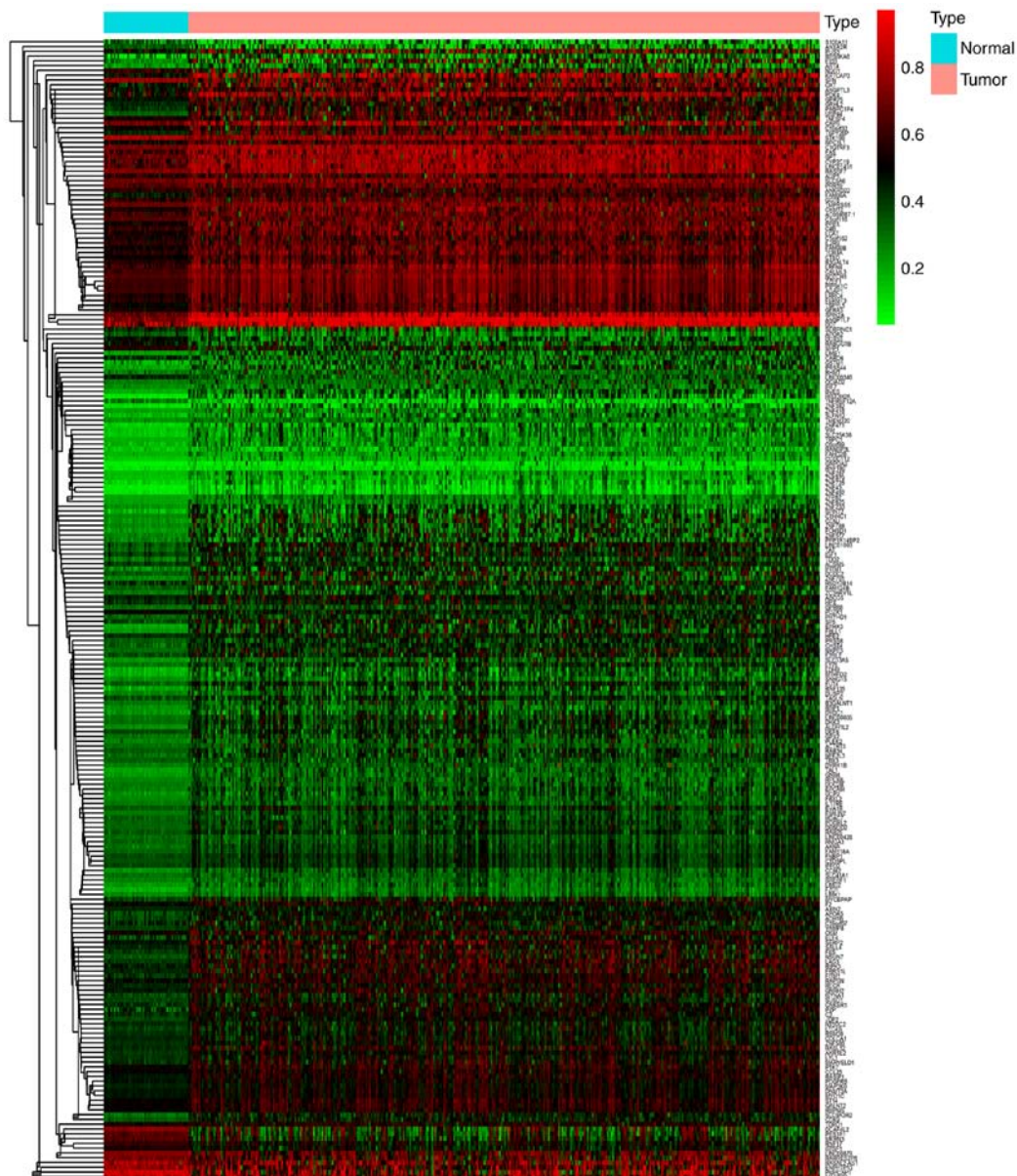


Figure 1. Heat map of the 238 methylation-driven genes. The Pheatmap R package was used for bidirectional hierarchical clustering of differentially expressed methylation-driven genes in hepatocellular carcinoma and adjacent tissues. Red indicates hypermethylation of the gene in the sample and green indicates hypomethylation of the gene.

predict the survival time of patients in terms of the degree of gene methylation.

**Survival and correlation analysis.** Survival analysis was performed by combining the identified prognostic aberrantly expressed methylation-driven genes with the corresponding gene expression data. The survival curves were rendered using the Survival Package in R. The resulting prognostic genes were considered as key genes in HCC because their methylation degree and gene expression level were significantly correlated with prognosis. The abnormal methylation was thought to be associated with gene expression. In order to examine correlation, methylation related loci of the key genes were extracted from the downloaded HCC methylation data to assess the correlation between the key gene methylation loci and gene expression (the screening criteria were  $|Cor| > 0.3$ ;  $P > 0.05$ ;  $Cor$  is correlation).

## Results

**TCGA data processing and screening of differentially expressed methylation-driven genes.** HCC-related level 3 RNA-Seq data (374 HCC samples and 50 control samples) and methylation data (380 HCC samples and 50 control samples) were downloaded from TCGA. A total of 238 methylation-driven genes were identified according to the predefined conditions using Perl script and the R package. The Pheatmap package was used to cluster the methylation-driven genes (Fig. 1). The distribution map of the degree of methylation of some of the differentially methylated genes is shown in Fig. 2.

**GO enrichment and pathway analysis of aberrantly expressed methylation-driven genes.** Functional enrichment analysis was conducted on the identified genes to understand the functional role of the aberrant methylation-driven genes in

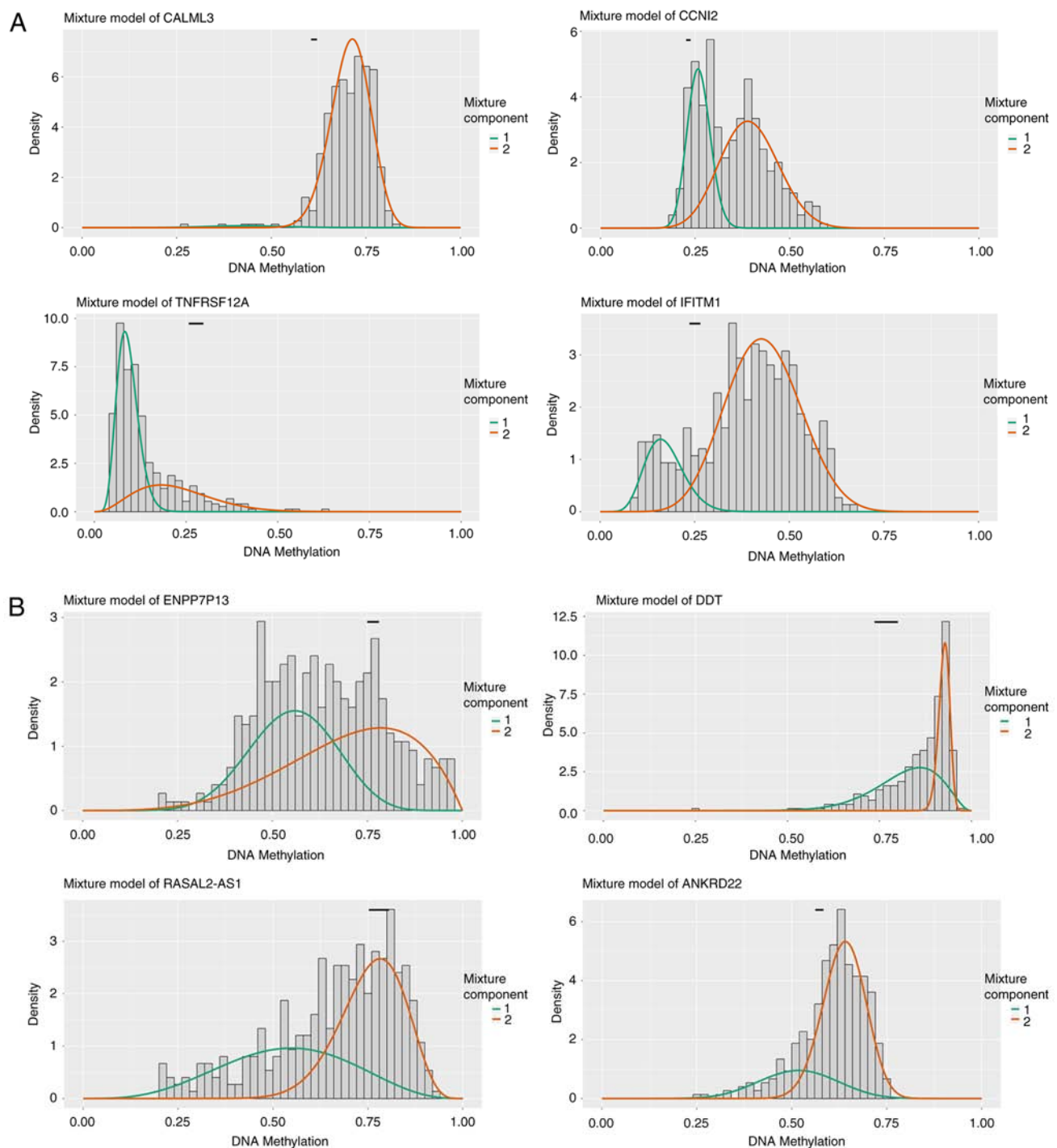


Figure 2. Histogram showing the distribution of the degree of methylation of eight differentially expressed methylation-driven genes. (A and B) The abscissa indicates the degree of methylation and the ordinate represents the number of methylated samples. The histograms display the distribution of methylation levels and the red and green curves are both the simulated trend curve of the methylation distribution of cancer group. The mixture component represents the methylation subgroup distribution. The black horizontal line above the graphs indicate the methylation level distribution of the normal sample. The distribution of methylation is different between the cancer and normal samples. In parts The greater the distance between the cancer and the normal samples, the greater the difference in methylation levels. CALM3, calmodulin-like protein 3; CCNI2, cyclin I family member 2; TNFRSF12A, tumor necrosis factor receptor superfamily member 12A; IFITM1, interferon induced transmembrane protein 1; ENPP7P13, ectonucleotide pyrophosphatase/phosphodiesterase 7 pseudogene 13; DDT, D-dopachrome decarboxylase; RASAL2-AS1, RASAL2-antisense RNA1; ANKRD22, ankyrin repeat domain 22.

HCC. The results showed that the aberrantly expressed methylation-driven genes were associated with molecular functions (MFs), biological processes (BPs) and cellular components (CCs). In the BP cluster, the genes were mainly associated with 'epithelial cell morphogenesis in placental branching', 'positive regulation of lipid catabolism', 'cholesterol homeostasis',

'cholesterol metabolic process' and 'lipoprotein metabolic process'. The MF included 'endopeptidase inhibitor activity', 'cholesterol transporter activity' and 'transcription factor activity', 'sequence-specific DNA binding'. The CC cluster included 'extracellular space', 'blood microparticles' and the 'apical plasma membrane' (Table II).



Table II. GO functional enrichment of aberrantly expressed methylation-driven genes.

Function	Term	Enrichment	Count	P-value	FDR
BP	GO:0060672	Epithelial cell morphogenesis in placental branching	3	0.00036	0.581
	GO:0050996	Positive regulation of lipid catabolic process	3	0.00118	1.897
	GO:0002819	Regulation of adaptive immune response	3	0.00176	2.813
	GO:0042632	Cholesterol homeostasis	5	0.00542	8.427
	GO:0008203	Cholesterol metabolic process	5	0.00671	10.339
	GO:0042157	Lipoprotein metabolic process	4	0.00836	12.724
CC	GO:0072562	Blood microparticle	8	0.00146	1.822
	GO:0005615	Extracellular space	26	0.00682	8.244
	GO:0016324	Apical plasma membrane	9	0.0152	17.546
	GO:0005576	Extracellular region	28	0.0176	19.967
MF	GO:0004866	Endopeptidase inhibitor activity	5	0.00106	1.438
	GO:0017127	Cholesterol transporter activity	3	0.0121	15.423
	GO:0003700	Transcription factor activity, Sequence-specific DNA binding	20	0.0128	16.189

GO, gene ontology; FDR, false discovery rate; BP, biological processes; CC, cell components; MF, molecular function.

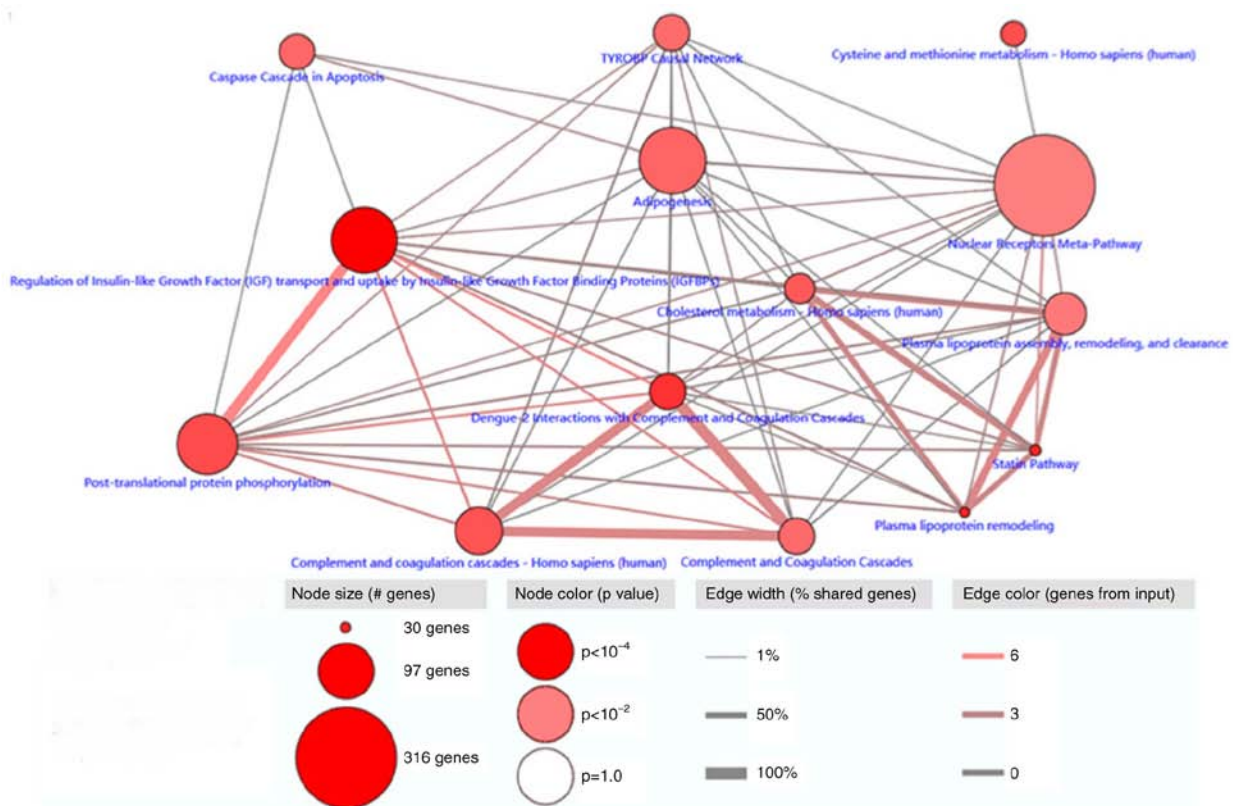


Figure 3. Pathway analysis of the differentially expressed methylation-driven genes. The nodes represent pathways and the lines denote the relationship between the pathways. The node size indicates the number of genes involved in the pathway, with a larger number indicating more genes are involved in the pathway. The node color represents the significance of enrichment, with darker red representing a higher degree of enrichment. The edge width represents the percentage of shared genes and the edge color indicates the number of input of genes.

Pathway enrichment analysis was performed on the 238 differentially expressed methylation-driven genes using ConsensusPathDB. A total of 14 pathways with significance ( $P < 0.01$ ) were identified, the most relevant of which was the pathway responsible for the regulation of insulin-like growth factor (IGF) transport and uptake by insulin-like growth factor

binding proteins (IGFBPs), plasma lipoprotein remodeling and statins (Fig. 3).

*Prognostic implications of aberrantly expressed methylation-driven genes.* Univariate Cox regression analysis of the aberrantly expressed methylation-driven genes in patients

Table III. Methylation-driven genes significantly associated with overall survival in hepatocellular carcinoma using univariate Cox regression analysis.

Gene	HR	Z	P-value
ANKRD22	0.033	-3.352	0.001
LIME1	7.012	3.181	0.001
RASAL2-AS1	0.187	-3.086	0.002
LINC00346	0.064	-3.054	0.002
ENPP7P13	0.164	-2.971	0.003
TNFRSF12A	0.050	-2.944	0.003
GPR75	6.951	2.830	0.005
DDT	24.444	2.442	0.015
PABPC1P4	6.664	2.441	0.015
EPHX3	5.015	2.379	0.017
SFN	0.248	-2.352	0.019
TMPRSS5	0.059	-2.343	0.019
RABGGTB	0.235	-2.249	0.024
IFITM1	10.908	2.242	0.025
CAPS	0.260	-2.199	0.028
IFITM1	4.161	2.179	0.029
CCNI2	7.200	2.152	0.031
RPL39L	6.896	2.148	0.032
USP44	4.258	2.138	0.033
LCAT	9.746	2.130	0.033
RARRES2P8	0.311	-2.069	0.039
HPX	6.227	2.057	0.040
NQO1	0.398	-2.055	0.040
GSTM1	3.443	2.047	0.041
RNF135	3.878	2.030	0.042
PPIEL	6.030	2.030	0.042
LDHB	3.933	1.998	0.046
CALML3	0.067	-1.971	0.049

HR, hazard ratio.

with HCC showed that 28 genes were significantly associated with OS ( $P < 0.05$ ; Table III). Multivariate Cox regression analysis was used to construct a prognostic risk model. As shown in Table IV, eight genes were found with prognostic significance: Calmodulin-like protein 3 (CALML3), cyclin I family member 2 (CCNI2), tumor necrosis factor receptor superfamily member 12A (TNFRSF12A), interferon induced transmembrane protein 1 (IFITM1), ectonucleotide pyrophosphatase/phosphodiesterase 7 pseudogene 13 (ENPP7P13), D-dopachrome decarboxylase (DDT), RASAL2-antisense RNA1 (RASAL2-AS1) and ankyrin repeat domain 22 (ANKRD22). The following risk model was constructed: Risk score = CALML3 (degree of methylation)  $\times$  (-4.860) + CCNI2  $\times$  (2.071) + TNFRSF12A  $\times$  (-3.369) + IFITM1  $\times$  (1.203) + ENPP7P13  $\times$  (-1.366) + DDT  $\times$  (2.139) + RASAL2-AS1  $\times$  (-1.384) + ANKRD22  $\times$  (-3.215). The median risk score derived from this model was set as the cutoff value for stratifying the 376 patients into the high-risk ( $n=188$ ) or low-risk groups ( $n=188$ ). The relationship between HCC risk and the degree

Table IV. Methylation-driven genes significantly associated with overall survival in hepatocellular carcinoma using multivariate Cox regression analysis.

Gene	coef	exp(coef)	se(coef)	Z-value	P-value
CALML3	-4.860	0.008	1.344	-3.617	0.0003
CCNI2	2.071	7.931	1.095	1.891	0.059
TNFRSF12A	-3.369	0.034	1.008	-3.342	0.0008
IFITM1	1.203	3.329	0.716	1.680	0.093
ENPP7P13	-1.366	0.255	0.711	-1.920	0.055
DDT	2.139	8.493	1.351	1.584	0.113
RASAL2-AS1	-1.384	0.251	0.570	-2.426	0.015
ANKRD22	-3.215	0.040	1.060	-3.033	0.002

coef, coefficient; exp (coef), HR-hazard ratio; se, standard error; Z-value, Wald statistic,  $z = \text{coef}/\text{se}(\text{coef})$ ; CALML3, calmodulin-like protein 3; CCNI2, cyclin I family member 2; TNFRSF12A, tumor necrosis factor receptor superfamily member 12A; IFITM1, interferon induced transmembrane protein 1; ENPP7P13, ectonucleotide pyrophosphatase/phosphodiesterase 7 pseudogene 13; DDT, D-dopachrome decarboxylase; RASAL2-AS1, RASAL2-antisense RNA1; ANKRD22, ankyrin repeat domain 22.

of methylation was illustrated in Fig. 4. The Kaplan-Meier method was used to plot the survival curves for the low- and high-risk HCC groups (Fig. 5). The 5-year survival rate of patients was 35.8% [95% confidence interval (CI)=27.1-47.4%] in the high-risk group and 61.7% (95% CI=51.4-74.2%) in the low-risk group. The difference between the groups was significant ( $P < 0.0001$ ). The ROC curve had an area under the curve of 0.742, indicating that this model is able to predict the survival rate of patients with HCC.

*Association between different methylation loci and gene expression.*  $P < 0.05$  was used as a screening standard for combinatorial survival. The methylation degree and gene expression level of TNFRSF12A and DDT were significantly associated with the prognosis of HCC (Fig. 6). In addition, the methylation loci of the prognostic genes were identified using TCGA. The correlation between the different methylation loci and gene expression was analyzed using |Corl|.  $P > |0.3|$  was used as the screening cutoff value. It was found that the expression of TNFRSF12A and DDT was related to the methylation level of multiple loci (Fig. 7). TNFRSF12A was generally in a hypomethylated high expression state in patients with HCC, while DDT was in a hypermethylated low expression state, suggesting that TNFRSF12A may be a proto-oncogene and DDT may be a tumor suppressor gene.

## Discussion

The incidence of hepatitis B (HBV) related HCC is expected to decrease with the increasing rate of vaccinations against HBV and the cumulative impact of new generation antiviral drugs (20). However, alcoholism, diabetes, obesity and metabolic syndrome play an important role in hepatocellular carcinoma in regions with a low prevalence of HBV,

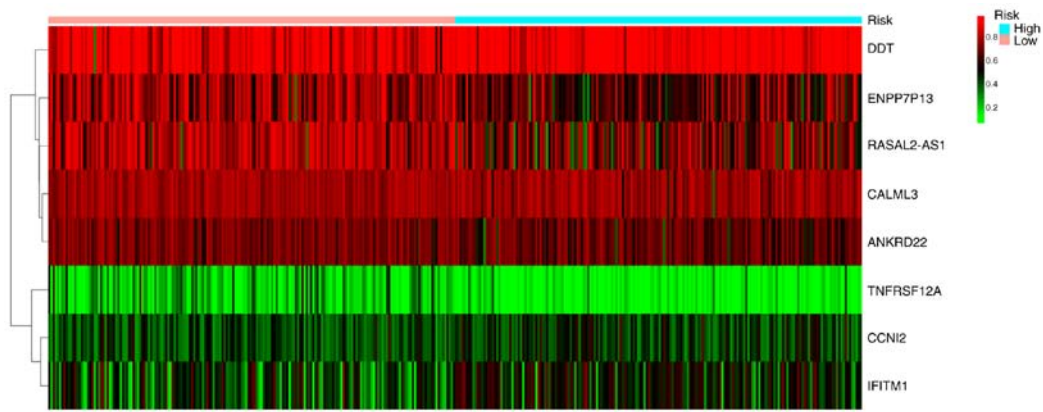


Figure 4. Analysis of the methylation heat map in high- and low-risk groups of liver cancer. The Pheatmap R package was used for the bidirectional hierarchical clustering of prognostic genes in high- and low-risk groups. Pink represents the low-risk group and blue represents the high-risk. Red indicates hypermethylation of the gene in the sample, while green represents hypomethylation. CALML3, calmodulin-like protein 3; CCNI2, cyclin I family member 2; TNFRSF12A, tumor necrosis factor receptor superfamily member 12A; IFITM1, interferon induced transmembrane protein 1; ENPP7P13, ectonucleotide pyrophosphatase/phosphodiesterase 7 pseudogene 13; DDT, D-dopachrome decarboxylase; RASAL2-AS1, RASAL2-antisense RNA1; ANKRD22, ankyrin repeat domain 22.

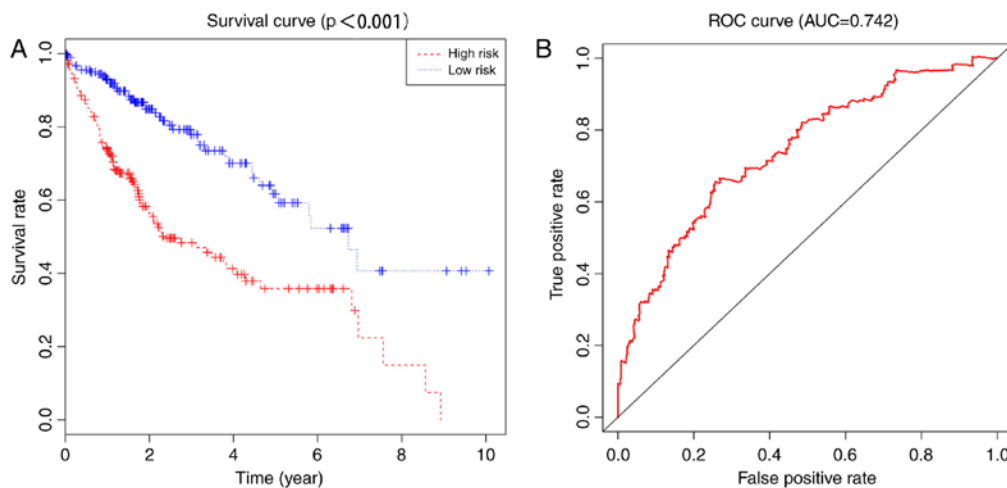


Figure 5. Survival and ROC curve analysis of the prognostic model. (A) Kaplan-Meier survival curves showing the overall survival based on the risk cutoff value. (B) Time-dependent ROC curve analysis of the 5-year survival prediction using the eight genes identified. ROC, Receiver operating characteristic; AUC, area under the curve.

especially in western populations. As a result, the prevalence of HCC will continue to increase (21). Diet is also a primary factors affecting DNA methylation (22). DNA methylation is dependent on the availability of S-adenosylmethionine (SAM), while methyl donors in food (including folate, betaine and choline) are linked to the synthesis of SAM (23,24). A methyl-deficient diet has been reported to reduce the concentration of SAM in the liver, leading to the methylation of CpG islands in 164 genes in the livers of mice; these genes are involved in DNA damage and repair, lipid and glucose metabolism, and the progression of fibrosis, which can ultimately lead to HCC (25,26).

At present, the pathogenesis of HCC has not been clearly elucidated. HCC is related with multiple gene mutations and epigenetic aberrations (27). Mechanistically, DNA methylation leads to transcriptional silencing in one of two ways: i) Methylation at the CpG site hinders the spatial accessibility of transcription factors to homologous binding sites in various gene promoters (28); and ii) the direct binding of methyl-CpG-binding

domain proteins to methylated DNA, causing transcriptional inhibition (29). It was hypothesized that the methylation-driven genes aberrantly expressed between patient with HCC and normal samples may be useful for predicting the prognosis of HCC. To test this, R script was used to combine methylation and transcriptome data, identifying 238 methylation driven-genes. The subsequent functional enrichment of these genes revealed the potential functional targets, such as 'blood microparticles', 'extracellular space' and 'apical plasma membranes', interfering with lipid metabolism in hepatocytes and the 'regulation of adaptive immune responses' by affecting 'endopeptidase inhibitor activity', 'cholesterol transporter activity', 'transcription factor activity', 'sequence-specific DNA binding'. The resulting pathways predominantly regulated IGF transport and IGFBP uptake, plasma lipoprotein remodeling and statins. These results suggested that high-fat, hypomethylated diets can affect DNA methylation, further affecting lipid metabolism in the body. This cycle can lead to liver steatosis, inflammation, fibrosis and cancer.

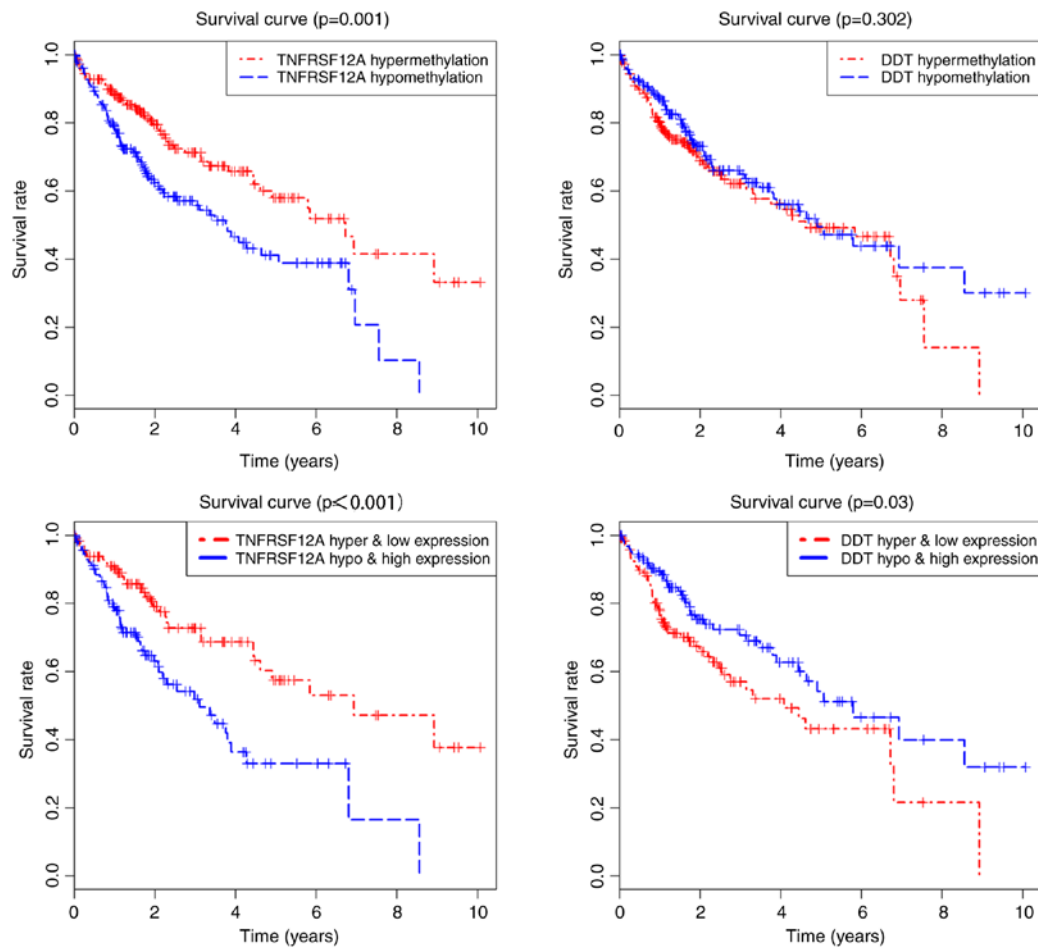


Figure 6. Survival analysis in terms of TNFRSF12A and DDT. Kaplan-Meier survival curves using the methylation status of TNFRSF12A and DDT, and survival curves plotted by combining the methylation and expression data of TNFRSF12A and DDT genes. TNFRSF12A, tumor necrosis factor receptor superfamily member 12A; DDT, D-dopachrome decarboxylase.

Multivariate Cox regression was used to generate a prognostic risk model, which was used to evaluate prognosis. The 5-year survival rate was 35.8% (95% CI=27.1-47.4%) in the high-risk group and 61.7% (95% CI=51.4-74.2%) in the low-risk group ( $P<0.0001$ ). The prognostic model constructed showed a level of accuracy and sensitivity in evaluating the prognosis of patients with HCC.

The expression of TNFRSF12A is increased in various tumors, especially in HCC and breast cancer (30). As the sole signal receptor of the proinflammatory cytokine TNF superfamily member 12, TNFRSF12A is involved in stimulating many signal transduction pathways, including the nuclear factor- $\kappa$ B pathway. It has been reported that the knockout of the differentially expressed TNFRSF12A gene inhibited the proliferation and migration of HCC cells *in vitro* (31). High levels of TNFRSF12A expression are associated with the upregulation of matrix metalloproteinase-9 and may be important for the progression of breast cancer; furthermore, TNFRSF12A-targeted therapy can improve survival (32). In the present study, TNFRSF12A was found to be hypomethylated in patients with HCC and that this was significantly correlated with prognosis. The methylation status of TNFRSF12A was negatively correlated with gene expression. The hypomethylated status of TNFRSF12A and its high expression corresponded to a significantly lower survival rate. Therefore, TNFRSF12A can

be used as an independent prognostic predictor of HCC. Further analysis of the methylation loci showed that cg00510447 and cg26808293 were also negatively correlated with gene expression. It is, therefore, speculated that the hypomethylation of cg00510447 and cg26808293 resulted in the high expression of the TNFRSF12A gene, which may affect metabolism in HCC, and the proliferation and migration of tumor cells.

DDT (MIF2), the second member of the multi-functional proinflammatory protein macrophage mobility inhibitor superfamily, is an important mediator of the inflammation-cancer axis and plays a role in angiogenesis by inducing angiogenic factors, such as vascular endothelial growth factor and interleukin-8 (33). In lung adenocarcinoma cells, MIF and DDT have a cumulative effect on the induction of these carcinogenic factors, indicating that MIF and DDT may play a synergistic role in malignant diseases (34), however, little is known about the methylation of DDT in HCC. In the present study, it was found that DDT was hypermethylated in HCC, and that the prognosis of HCC was poorer in the hypermethylated low expression group. Further analysis indicated that cg11060661 and cg16132339 were also negatively correlated with gene expression. The results suggested that DDT plays a protective role in HCC and may act as a tumor suppressor gene. Further studies are required to elucidate the specific mechanisms underlying the preliminary findings of the present study.



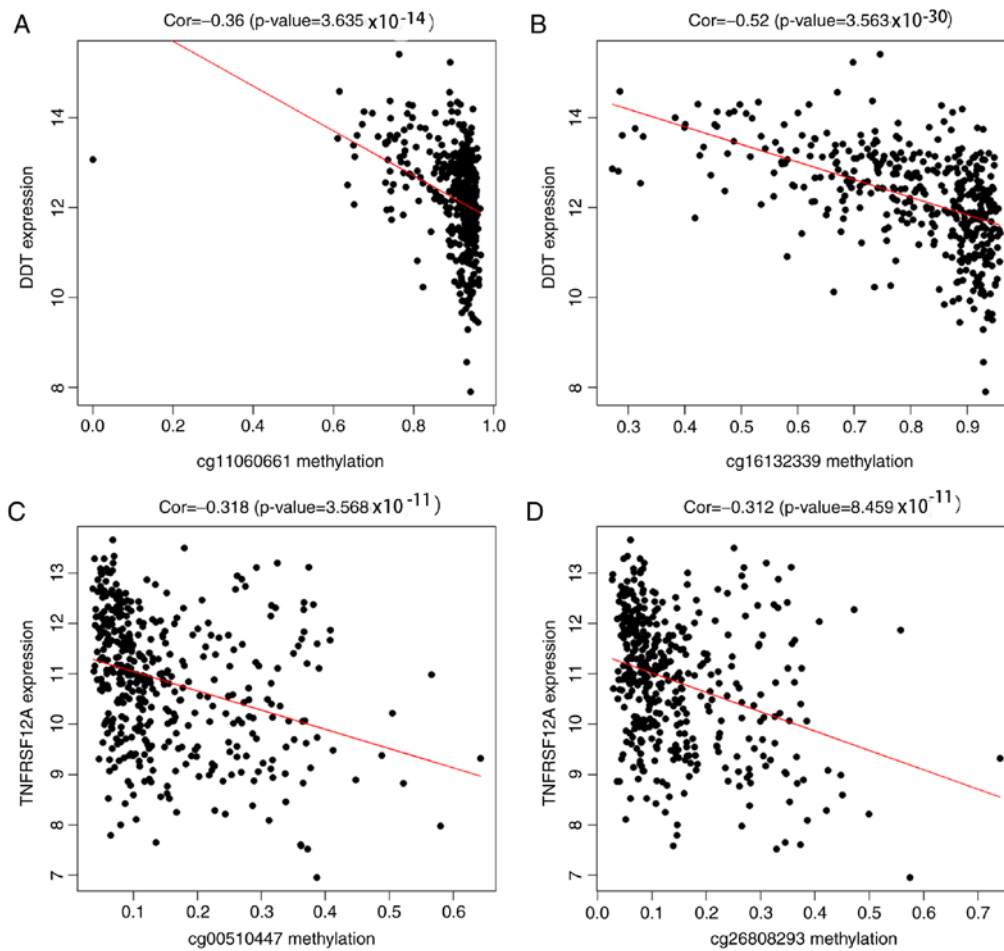


Figure 7. Correlation analysis between the methylation status of the locus and the expression level of TNFRSF12A and DDT. (A and B) Gene expression and methylation locus of DDT; (C and D) gene expression and methylation locus of TNFRSF12A. TNFRSF12A, tumor necrosis factor receptor superfamily member 12A; DDT, D-dopachrome decarboxylase; Cor, correlation.

Unlike mutations, epigenetic changes are reversible, especially DNA methylation and histone modifications (35). The expression of genes silenced by DNA methylation can be promoted in cancer cell lines using demethylating agents, such as 5-azacytidine and 5-azacytidine-2'-deoxycytidine (36), which are used in myelodysplastic syndromes and acute myeloid leukemia (37). As a novel DNA methyltransferase inhibitor, Zebularine can inhibit DNA methylation by forming a covalent complex with DNA methyltransferase 1. The stability and half-life of Zebularine in neutral aqueous solutions is significantly better than azatadine and histamine (38). In animal experiments, Andersen *et al* (39) demonstrated that Zebularine response genes and demethylation signatures predictive of clinical outcome in patients with HCC, could be used as a new diagnostic and prognostic tool for selecting patients with HCC who may benefit from epigenetic therapy. In the target group with the highest degree of DNA CpG methylation, epigenetic therapy with Zebularine successfully inhibited tumor cell proliferation and increased apoptosis.

There have been a number of previous studies on DNA methylation in HCC. For example, the methylation of P14ARF, growth arrest and DNA damage inducible GADD45  $\beta$  and protocadherin 8 is associated with HCC (15,40,41). In addition, Tao *et al* (42) found that seven genes (WNK2, EMILIN2, TLX3, TM6SF1, TRIM58, HIST1H4F and GRASP) were

hypermethylated in HBV-related HCC and hypomethylated in paired adjacent liver tissues. Fan *et al* (43), using  $|\log FC| \geq 2$  and  $P \leq 0.05$ , identified six hub genes that were altered in HCC from The Gene Expression Omnibus; patients with high expression of mitotic arrest deficient 2-like 1, cell division cycle 20 and cyclin B1 and low expression cyclin D1, androgen receptor and estrogen receptor 1 had a shorter OS. However, these previous studies, including (15,40-43), only assessed the value of DNA methylation of single or multiple genes in HCC. Although DNA methylation determines when, where and how genes are expressed, DNA methylation at a single site does not necessarily affect the prognosis of a patient as there are multiple methylation sites on each gene (44). Only when DNA methylation affects gene expression can it affect the prognosis of a patient. Therefore, the present study combined gene expression and DNA methylation ( $Cor \leq -0.3$ ) from TCGA to conduct a comprehensive analysis, using this a prognostic risk model was constructed for HCC using univariate and multivariate COX regression. This model can also be used to quantify the survival time of patients with HCC, and has strong clinical applicability. However, the present study is comprised only of bioinformatics analysis with no experimental verification. Therefore, future studies should collect cancer samples and the clinical data of patients with HCC in order to verify the accuracy of the model by detecting the DNA methylation

status of the eight prognostic genes identified in the present study.

It can be concluded from the analysis conducted in the present study that the occurrence and development of HCC are closely related to the eight methylation-driven genes identified, including CALML3, CCNI2, TNFRSF12A, IFITM1, ENPP7P13, DDT, RASAL2-AS1 and ANKRD22. The degree of methylation and gene expression level of TNFRSF12A and DDT are significantly correlated with the prognosis of HCC and were negatively correlated with the methylation status of the following loci: cg00510447, cg26808293, cg11060661 and cg16132339. Experimental and clinical trials are required to further investigate the findings of the present study, which may be important for the diagnosis, treatment and prognosis of patients with HCC.

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### Availability of data and materials

The datasets used and/or analyzed during the present study are available from the corresponding author on reasonable request.

### Authors' contributions

JL conceived and designed the study. Data analysis was conducted by XG, JL and XG, and NC contributed to study methodology, software use, study administration and data validation. JL and XG wrote, reviewed and edited the manuscript. All authors read and approved the final manuscript.

### Ethics approval and consent to participate

Not applicable.

### Patient consent for publication

Not applicable.

### Competing interests

The authors declare that they have no competing interests.

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