Supplementary Table 4. Top 100 differentially modified genes between early HCC and CHB/LC in the training set.

Gene	**Coefficient** [a]	**p-value**	**AUC (Early HCC vs. CHB/LC)** [b]
FIGN	0.275	7.13E-12	75.00%
STAU1	1.276	6.29E-10	60.50%
SYN2	-0.643	4.63E-08	59.50%
TBCE	0.851	6.18E-08	62.70%
ATP10B	-0.434	1.37E-07	57.80%
CD5L	-0.481	1.46E-07	62.30%
HS3ST2	-0.425	1.53E-07	58.90%
GML	-0.530	2.77E-07	62.30%
PIEZO2	0.697	3.04E-07	58.70%
TRAPPC6B	0.685	4.08E-07	59.20%
RPH3A	-0.563	4.51E-07	62.80%
CAMK1D	0.839	6.13E-07	62.00%
GPLD1	0.671	7.78E-07	59.30%
USP14	0.652	9.76E-07	59.80%
RNF175	-0.528	1.14E-06	57.20%
CA8	-0.368	1.29E-06	61.50%
MARCH1	-0.299	1.33E-06	60.30%
PDZK1	0.438	1.50E-06	63.20%
TMC2	-0.521	1.70E-06	62.20%
MUC17	-0.417	1.87E-06	57.20%
HOPX	-0.431	1.95E-06	61.90%
IPPK	0.685	2.08E-06	63.50%
PTPRO	-0.514	2.21E-06	61.90%
RPRD2	0.694	2.32E-06	60.70%
C4orf22	-0.268	2.34E-06	62.40%
CCM2L	-0.528	2.41E-06	58.90%
SYNDIG1	-0.463	2.51E-06	59.60%
KIR3DX1	-0.420	2.64E-06	55.70%
DRG1	0.857	2.82E-06	58.70%
HDLBP	0.913	3.30E-06	59.90%
SIAH3	-0.573	3.44E-06	64.10%
NETO2	-0.467	3.65E-06	59.00%
CPO	-0.540	4.00E-06	60.40%
CACNA1A	-0.539	4.21E-06	59.50%
MCOLN2	-0.505	4.28E-06	60.10%
CREB5	-0.606	4.33E-06	61.70%
SLC24A2	-0.325	4.42E-06	61.10%
JUN	-0.398	4.43E-06	60.80%
STK32B	-0.471	4.53E-06	57.30%
COL15A1	-0.493	5.07E-06	56.80%

PCYOX1	0.603	5.14E-06	60.10%
ZHX2	0.843	5.30E-06	62.90%
ARFGEF2	1.164	5.50E-06	56.60%
BPTF	1.037	5.80E-06	56.10%
BCL6	0.600	5.91E-06	62.80%
DSP	0.492	6.03E-06	59.40%
ADCK3	0.755	6.27E-06	61.30%
THRB	0.395	6.74E-06	57.30%
NNT	0.546	6.97E-06	60.00%
ERICH5	0.431	7.43E-06	61.00%
NLRP1	-0.503	7.55E-06	57.50%
CDK5RAP2	0.883	7.86E-06	60.70%
TADA1	0.594	8.31E-06	58.70%
IKZF3	-0.658	8.48E-06	61.40%
PTPN11	0.969	8.49E-06	55.90%
PEBP4	-0.739	8.52E-06	61.10%
SDHC	0.559	8.66E-06	64.00%
CD300LD	-0.517	9.70E-06	59.40%
MYLK3	-0.622	1.01E-05	58.60%
KLB	0.383	1.03E-05	61.20%
MTFR1	0.594	1.05E-05	60.10%
CPNE4	-0.365	1.08E-05	61.40%
CHCHD6	-0.465	1.09E-05	62.50%
CBFA2T2	0.941	1.16E-05	57.10%
ABL2	0.624	1.16E-05	60.60%
ZNF491	-0.499	1.23E-05	60.40%
METAP2	0.566	1.26E-05	59.90%
RBFOX3	-0.442	1.34E-05	61.10%
ITIH2	0.252	1.35E-05	62.20%
ATRN	0.697	1.36E-05	56.00%
F2	0.385	1.37E-05	62.30%
RAD54L2	0.629	1.45E-05	63.90%
DKK4	0.517	1.45E-05	60.40%
MPHOSPH8	0.945	1.45E-05	58.40%
AIPL1	-0.527	1.46E-05	60.70%
CPAMD8	-0.494	1.50E-05	58.30%
ATP10A	-0.235	1.51E-05	60.30%
WSCD2	-0.362	1.53E-05	58.50%
UNC79	-0.389	1.61E-05	58.40%
AOX1	0.394	1.66E-05	62.50%
CTPS1	0.691	1.69E-05	58.90%
CD53	-0.354	1.69E-05	56.60%
IRF4	-0.536	1.73E-05	57.50%

LILRB4	-0.299	1.73E-05	54.70%
USP6	-0.530	1.74E-05	55.30%
GPR26	-0.354	1.75E-05	58.10%
KLRG1	-0.532	1.77E-05	60.90%
PARD6G	0.436	1.81E-05	63.10%
SYCP1	-0.276	1.87E-05	59.70%
KCNIP1	-0.550	1.87E-05	62.30%
SAP130	0.871	1.98E-05	58.50%
KIAA0226L	-0.439	1.99E-05	57.70%
COG2	0.535	2.22E-05	59.30%
EDN3	-0.416	2.24E-05	61.40%
ZNF445	0.798	2.26E-05	59.80%
URB2	0.660	2.31E-05	58.80%
GAB4	-0.325	2.36E-05	58.50%
POGZ	0.590	2.38E-05	61.20%
SCN10A	-0.372	2.41E-05	61.00%
SYT16	-0.269	2.42E-05	59.80%

Notes: [a] Coefficient was based on the logistic regression adjusted for age and gender for each gene in the training set. [b] AUC was calculated for each gene in the training set. AUC: area under curve; CHB: chronic hepatitis B virus infection; HCC: hepatocellular carcinoma; LC: liver cirrhosis.