

Table 3: Genes with hypermethylated CpG sites that also show genomic loss according to previous analysis (15).

Gene	Name	Chr.	Median difference	95% CI		FDR-q-value	Spearman's correlation	95% CI		p-value
FAM46B	family with sequence similarity 46, member B	1p35.3	0.22	0.10	0.33	0.002	-0.08	-0.39	0.23	0.626
CD164L2	CD164 sialomucin-like 2	1p36.11	0.27	0.13	0.39	0.003	0.23	0.08	0.49	0.138
PER3	period homolog 3 (Drosophila)	1p36.23	0.15	0.07	0.23	0.004	-0.56	-0.74	-0.32	< 0.001
CDKN2A	cyclin-dependent kinase inhibitor 2A (melanoma, p16, inhibits CDK4)	9p21	0.49	0.32	0.70	< 0.001	0.68	0.48	0.82	< 0.001
CDKN2B	cyclin-dependent kinase inhibitor 2B (p15, inhibits CDK4)	9p21	0.38	0.24	0.51	< 0.001	0.22	-0.09	0.49	0.155
NKX6-2	NK6 homeobox 2	10q26.3	0.47	0.33	0.62	< 0.001	0.05	-0.25	0.35	0.733
KCTD4	potassium channel tetramerisation domain containing 4	13q14.12-13	0.20	0.12	0.27	< 0.001	-0.16	-0.44	0.15	0.296
PROZ	protein Z, vitamin K-dependent plasma glycoprotein	13q34	0.23	0.13	0.35	< 0.001	-0.42	-0.64	-0.14	0.004
SOX1	SRY (sex determining region Y)-box 1	13q34	0.20	0.13	0.27	< 0.001	-0.10	-0.39	0.20	0.512
ABCA3	ATP-binding cassette, sub-family A (ABC1), member 3	16p13.3	0.39	0.22	0.48	< 0.001	0.34	0.04	0.58	0.025
DNASE1L2	deoxyribonuclease I-like 2	16p13.3	0.23	0.09	0.36	0.004	0.01	-0.29	0.31	0.933
HBQ1	hemoglobin, theta 1	16p13.3	0.34	0.22	0.48	< 0.001	-0.21	-0.48	0.10	0.183
IGFALS	insulin-like growth factor binding protein, acid labile subunit	16p13.3	0.22	0.12	0.30	0.002	-0.70	-0.83	-0.51	<0.001
SOX8	SRY (sex determining region Y)-box 8	16p13.3	0.19	0.05	0.17	0.005	0.47	0.20	0.68	0.001
NLGN2	neuroligin 2	17p13.2	0.23	0.13	0.30	0.001	0.01	-0.29	0.31	0.935
TCF20	transcription factor 20 (AR1)	22q13.2-31	0.16	0.10	0.20	< 0.001	0.27	-0.03	0.53	0.071
BIK	BCL2-interacting killer (apoptosis-inducing)	22q13.3	0.20	0.09	0.30	0.002	0.08	-0.22	0.38	0.587

Candidates on this list show a significant hypermethylation (FDR-q <0.005) in HCC compared to normal liver controls and loss of genomic information in at least 10% of cases based on aCGH data. Candidates that fit all three selection criteria are highlighted.