

Supplementary Table S8 The 80 probes (70 genes) that were included among the non-alcoholic steatohepatitis (NASH) specifically affected probes whose DNA methylation alterations were inherited by or strengthened in NASH-related hepatocellular carcinoma (NASH-T) samples (Jonckheere-Terpstra trend test) and that showed significant differences in DNA methylation levels even between NASH-T samples and hepatitis virus-related hepatocellular carcinoma (viral-T) samples.

| Target ID ^a | Chromosome | Gene symbol ^b | DNA methylation levels (mean±SD) | | |
|------------------------|------------|--------------------------|----------------------------------|----------------|---------------------------|
| | | | NASH-T (n=22) | Viral-T (n=37) | P (Welch's <i>t</i> test) |
| cg08679807 | 1 | <i>ACOT7</i> | 0.673±0.039 | 0.769±0.054 | 8.450x10 ⁻⁵ |
| cg10555853 | 1 | N/A | 0.525±0.050 | 0.439±0.041 | 2.281x10 ⁻² |
| cg23108607 | 1 | <i>KIAA0754</i> | 0.675±0.051 | 0.767±0.054 | 2.487x10 ⁻² |
| cg19777710 | 1 | <i>AKR7A2P1</i> | 0.681±0.037 | 0.753±0.050 | 2.868x10 ⁻² |
| cg01815906 | 1 | <i>SMYD3</i> | 0.677±0.035 | 0.759±0.052 | 8.411x10 ⁻⁴ |
| cg26534993 | 2 | <i>TSSC1</i> | 0.499±0.040 | 0.594±0.058 | 4.734x10 ⁻⁴ |
| cg10328259 | 2 | <i>TSSC1</i> | 0.678±0.043 | 0.794±0.068 | 3.380x10 ⁻⁵ |
| cg01400712 | 2 | <i>EFR3B</i> | 0.485±0.037 | 0.394±0.065 | 2.793x10 ⁻³ |
| cg25116269 | 2 | <i>PRORSDIP</i> | 0.160±0.023 | 0.089±0.058 | 2.241x10 ⁻² |
| cg01287788 | 2 | <i>SNORD94</i> | 0.684±0.024 | 0.776±0.077 | 1.278x10 ⁻² |
| cg13896783 | 2 | <i>PKP4</i> | 0.443±0.043 | 0.331±0.086 | 6.176x10 ⁻³ |
| cg01779076 | 2 | <i>CFLAR</i> | 0.376±0.038 | 0.292±0.044 | 3.465x10 ⁻⁴ |
| cg12198254 | 3 | <i>ATG7</i> | 0.668±0.026 | 0.737±0.052 | 6.425x10 ⁻³ |
| cg09352908 | 3 | N/A | 0.783±0.041 | 0.895±0.054 | 1.830x10 ⁻⁶ |
| cg13003239 | 3 | <i>WDR6</i> | 0.453±0.034 | 0.271±0.136 | 5.926x10 ⁻⁴ |
| cg08081407 | 3 | <i>ARF4</i> | 0.268±0.027 | 0.169±0.051 | 9.340x10 ⁻⁸ |
| cg07804735 | 3 | <i>WDR52</i> | 0.695±0.048 | 0.806±0.043 | 2.750x10 ⁻⁵ |
| cg10757852 | 3 | <i>RASA2</i> | 0.535±0.032 | 0.633±0.072 | 1.209x10 ⁻³ |
| cg18185028 | 3 | <i>DHX36</i> | 0.390±0.044 | 0.282±0.059 | 5.610x10 ⁻⁵ |
| cg05788437 | 3 | <i>FYTTD1</i> | 0.142±0.014 | 0.081±0.051 | 1.142x10 ⁻² |
| cg03150409 | 4 | <i>WHSC1</i> | 0.637±0.045 | 0.773±0.093 | 2.625x10 ⁻⁴ |
| cg21843114 | 4 | <i>RBPJ</i> | 0.440±0.035 | 0.519±0.054 | 3.863x10 ⁻³ |
| cg17404403 | 4 | <i>GARI</i> | 0.199±0.054 | 0.090±0.038 | 7.511x10 ⁻⁴ |
| cg14497545 | 4 | <i>MAML3</i> | 0.538±0.045 | 0.704±0.096 | 1.210x10 ⁻⁶ |
| cg15285494 | 4 | N/A | 0.671±0.029 | 0.787±0.096 | 8.839x10 ⁻³ |
| cg07893230 | 5 | <i>CTNNA1</i> | 0.290±0.035 | 0.216±0.041 | 1.051x10 ⁻³ |
| cg12152193 | 5 | <i>RNF44</i> | 0.578±0.053 | 0.703±0.077 | 4.464x10 ⁻⁴ |
| cg09741240 | 6 | <i>NQO2</i> | 0.235±0.034 | 0.118±0.048 | 1.720x10 ⁻⁹ |
| cg14047339 | 6 | <i>SUPT3H</i> | 0.325±0.023 | 0.215±0.083 | 6.199x10 ⁻⁴ |
| cg10616859 | 7 | <i>BRATI</i> | 0.670±0.033 | 0.743±0.041 | 5.981x10 ⁻⁴ |
| cg11213199 | 7 | <i>MRPS24</i> | 0.485±0.026 | 0.408±0.044 | 1.290x10 ⁻⁵ |
| cg04205664 | 7 | <i>CLEC2L</i> | 0.259±0.108 | 0.496±0.189 | 4.114x10 ⁻² |
| cg25009327 | 7 | <i>ZNF425</i> | 0.287±0.060 | 0.432±0.110 | 8.531x10 ⁻³ |
| cg08499057 | 7 | <i>ABCF2</i> | 0.631±0.044 | 0.715±0.052 | 1.132x10 ⁻² |
| cg13810766 | 7 | <i>PRKAG2</i> | 0.458±0.053 | 0.630±0.101 | 4.080x10 ⁻⁶ |
| cg01994308 | 8 | <i>PLAG1</i> | 0.301±0.068 | 0.150±0.089 | 8.452x10 ⁻⁴ |
| cg13560760 | 9 | <i>PMPCA</i> | 0.563±0.032 | 0.658±0.051 | 3.080x10 ⁻⁶ |
| cg14495033 | 9 | <i>EHMT1</i> | 0.654±0.029 | 0.730±0.062 | 2.190x10 ⁻² |
| cg27435660 | 10 | <i>FBXO18</i> | 0.577±0.034 | 0.731±0.051 | 7.501x10 ⁻³ |
| cg02732134 | 10 | <i>DNMBP</i> | 0.677±0.068 | 0.768±0.112 | 2.830x10 ⁻⁵ |
| cg08206623 | 11 | <i>CDKN1C</i> | 0.306±0.046 | 0.156±0.109 | 6.244x10 ⁻⁴ |
| cg18089569 | 11 | N/A | 0.229±0.020 | 0.143±0.067 | 1.859x10 ⁻³ |
| cg12375876 | 11 | N/A | 0.657±0.037 | 0.732±0.042 | 1.954x10 ⁻³ |
| cg24240077 | 11 | <i>AAMDC</i> | 0.682±0.023 | 0.753±0.052 | 1.459x10 ⁻³ |
| cg20090957 | 12 | <i>MAPKAPK5</i> | 0.231±0.030 | 0.172±0.028 | 3.669x10 ⁻³ |

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| | | | NASH-T (n=22) | Viral-T (n=37) | P (Welch's <i>t</i> test) |
| cg07449447 | 14 | <i>SAMD4A</i> | 0.740±0.026 | 0.804±0.052 | 4.934x10 ⁻² |
| cg03468541 | 14 | <i>ZC3H14</i> | 0.213±0.038 | 0.116±0.052 | 2.450x10 ⁻⁵ |
| cg11021810 | 14 | <i>FOXP3</i> | 0.688±0.029 | 0.745±0.040 | 4.998x10 ⁻² |
| cg08707819 | 14 | <i>RCOR1</i> | 0.443±0.037 | 0.358±0.062 | 9.061x10 ⁻³ |
| cg21937244 | 14 | <i>CDC42BPB</i> | 0.781±0.018 | 0.845±0.051 | 6.516x10 ⁻³ |
| cg00470768 | 15 | <i>INO80</i> | 0.507±0.050 | 0.634±0.066 | 1.360x10 ⁻⁵ |
| cg13417485 | 15 | <i>UNC45A</i> | 0.613±0.038 | 0.697±0.055 | 3.259x10 ⁻³ |
| cg02205746 | 16 | <i>KCTD5</i> | 0.185±0.042 | 0.097±0.030 | 2.868x10 ⁻⁴ |
| cg04548722 | 16 | <i>SMIM22</i> | 0.556±0.030 | 0.621±0.048 | 2.372x10 ⁻² |
| cg09141413 | 16 | <i>GPRC5B</i> | 0.273±0.030 | 0.197±0.051 | 1.044x10 ⁻³ |
| cg08213792 | 16 | N/A | 0.576±0.032 | 0.676±0.049 | 2.850x10 ⁻⁷ |
| cg01684248 | 16 | <i>FENDRR</i> | 0.420±0.049 | 0.310±0.089 | 4.311x10 ⁻² |
| cg12774921 | 16 | <i>SPG7</i> | 0.523±0.030 | 0.605±0.047 | 2.760x10 ⁻⁵ |
| cg03321231 | 17 | <i>RPH3AL</i> | 0.603±0.047 | 0.726±0.065 | 1.280x10 ⁻⁵ |
| cg19105961 | 17 | <i>ZZEF1</i> | 0.431±0.043 | 0.336±0.071 | 1.651x10 ⁻² |
| cg11855759 | 17 | <i>USP43</i> | 0.308±0.051 | 0.192±0.064 | 1.858x10 ⁻⁴ |
| cg07138452 | 17 | <i>FLCN</i> | 0.280±0.043 | 0.187±0.053 | 8.615x10 ⁻⁴ |
| cg06361278 | 17 | N/A | 0.252±0.044 | 0.168±0.055 | 1.956x10 ⁻² |
| cg25629442 | 17 | <i>ENGASE</i> | 0.267±0.043 | 0.172±0.059 | 1.933x10 ⁻³ |
| cg08109808 | 17 | <i>CCDC40</i> | 0.648±0.036 | 0.734±0.053 | 4.053x10 ⁻⁴ |
| cg25270498 | 17 | <i>METRNL</i> | 0.258±0.043 | 0.152±0.065 | 2.033x10 ⁻⁴ |
| cg06808467 | 18 | <i>LINC00526</i> | 0.240±0.034 | 0.141±0.070 | 7.596x10 ⁻⁴ |
| cg25538450 | 19 | <i>REXO1</i> | 0.219±0.045 | 0.139±0.040 | 1.733x10 ⁻² |
| cg23084309 | 19 | <i>MLLT1</i> | 0.276±0.036 | 0.183±0.055 | 6.920x10 ⁻⁵ |
| cg09112613 | 19 | <i>PRAMI</i> | 0.685±0.045 | 0.773±0.062 | 3.560x10 ⁻² |
| cg07783291 | 19 | N/A | 0.581±0.045 | 0.667±0.056 | 2.089x10 ⁻² |
| cg05910615 | 19 | <i>PROSER3</i> | 0.173±0.044 | 0.077±0.041 | 1.097x10 ⁻⁴ |
| cg06684987 | 19 | <i>CLASRP</i> | 0.642±0.021 | 0.704±0.055 | 4.281x10 ⁻² |
| cg01198024 | 21 | <i>MRAP</i> | 0.549±0.035 | 0.631±0.044 | 1.019x10 ⁻⁴ |
| cg17499729 | 21 | <i>CBR3-AS1</i> | 0.497±0.059 | 0.636±0.075 | 9.030x10 ⁻⁵ |
| cg11381792 | 21 | <i>TRAPPC10</i> | 0.240±0.034 | 0.151±0.045 | 9.370x10 ⁻⁶ |
| cg05998816 | 21 | <i>PCNT</i> | 0.772±0.045 | 0.876±0.045 | 3.410x10 ⁻⁵ |
| cg05367846 | 22 | <i>MICAL3</i> | 0.191±0.032 | 0.106±0.069 | 2.059x10 ⁻² |
| cg09020181 | 22 | N/A | 0.184±0.034 | 0.115±0.043 | 5.466x10 ⁻³ |
| cg25152348 | 22 | <i>NCAPH2</i> | 0.311±0.048 | 0.180±0.097 | 2.558x10 ⁻³ |

^aProbe ID of the Infinium HumanMethylation450 BeadChip. ^bNational Center for Biotechnology Information (NCBI) database (Genome Build 37). N/A, not annotated (designed in the intergenic regions).