

## Supporting Information

### **Characterizing key nucleotide polymorphisms of hepatitis C virus-disease associations via mass-spectrometric genotyping**

Yuta Horiuchi<sup>1\*</sup>, Jason Lin<sup>2\*</sup>, Yui Shinojima<sup>3</sup>, Kyoko Fujiwara<sup>34</sup>, Mitsuhiko Moriyama<sup>1</sup> and  
Hiroki Nagase<sup>2</sup>

<sup>1</sup>Institute of Gastroenterology, Nihon University School of Medicine. Itabashi-ku, Tokyo 173-8610 Japan; <sup>2</sup>Laboratory of Cancer Genetics, Chiba Cancer Center Research Institute. Chuo-ku, Chiba 260-8717 Japan; <sup>3</sup>Department of Cancer Genetics, Nihon University School of Medicine. Itabashi-ku, Tokyo 173-8610 Japan; <sup>4</sup>Division of General Medicine, Department of Medicine, Nihon University School of Medicine, Tokyo 173-8610 Japan.

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Supporting information available at: [www.github.com/cccri-jlin/marray\\_si](http://www.github.com/cccri-jlin/marray_si)

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Table S1, list of selected SNPs and corresponding primers.

RsID/Symbol	Forward	Reverse	Extend
rs5491/ICAM1	ACGTTGGATGTGACATGCAGC ACCTCCTGT	ACGTTGGATGGGAGCAACTC CTTTTAGGC	CTTCTCTATGCCCAACAAC
rs5497/ICAM1	ACGTTGGATGACCCACCTCCA TGTCATCTC	ACGTTGGATGAGTTTCCCGGA CAATCCCTC	AGTCCCTCTCGTCCAGT GGAGGATCAGCAGCTCGTAG AA
rs34677/AMACR	ACGTTGGATGGGAATTCATGG CTGTTGGAG	ACGTTGGATGGACGCGTGAA GTTCACTTAC	CCAGTTCTCCATAATCA
rs213950/CFTR	ACGTTGGATGGATGGGTTTTA TTTCCAGAC	ACGTTGGATGCTCTGAAGGCT CCAGTTCTC	AACCTGGTGTCCAAAAG CAAATACCACATTGGAAAGT CAATGCCA
rs235768/BMP2	ACGTTGGATGACAGCCAACCTC GAAATTCCC	ACGTTGGATGTTTCCACCTG CTTGCACTC	GAAGCTTCTTTAAATGTTCC ATTTTA
rs766173/BRCA2	ACGTTGGATGTCTTCAGAGGT ATCTACAAC	ACGTTGGATGGCAAAGACCA CATTGGAAAAG	CCTGCAAAGCGCCAGTCATTT GCTC
rs766874/CFTR	ACGTTGGATGCTGTGTCTGTA AACTGATGG	ACGTTGGATGCAGCTTTCTTT AAATGTTCC	AAGATGGAAAGGCCATGTCC CCTCCCCCTCCTCACTTTGCC GTAAC
rs799917/BRCA1	ACGTTGGATGCAGAGAATGTT GCACATTCC	ACGTTGGATGTCAAGGTTTCA AAGCGCCAG	GGCAACTTCGGCTGAAAGGC GTGGTGCGGATCAAGACGAC ATAC
rs812936/FUT3	ACGTTGGATGTCCCAGACAGG ACACCACTC	ACGTTGGATGAGCCACAGGG ATGTGAAAAG	TGCGTGATGATGAAATCG
rs867228/FPRI	ACGTTGGATGAGTGACACAG CTACCAATTG	ACGTTGGATGAGCTCCCTCCT CACTTTGC	AAGATCTTCAGCACCC
rs1019747/ADAMT S16	ACGTTGGATGCACTAGGCTGC TGGAAGTC	ACGTTGGATGTTGAGTCTCTT CACCTTCGG	CGACGATGTAGTCTCCTTCT
rs1051624/CDH17	ACGTTGGATGACTCATGCCCG ACTGTCTAC	ACGTTGGATGCATTGATGCGG ATCAAGACG	TGACGGCTATTCCCA GGGTGCTGTCAACCTCAACTA AACTA
rs1801133/MTHFR	ACGTTGGATGACCTGAAGCA CTTGAAGGAG	ACGTTGGATGGAAAAGCTGC GTGATGTG	CCCTGTTCTTGTTCATCAAGC TGAG
rs2071762/ARHGA P8	ACGTTGGATGTGCTCCCTGT TCCCATGGT	ACGTTGGATGGAGTACTATGA AAAGATCTTC	CTCCCCGCACGACGTCTTCCA GTACC
rs2227567/PLAU	ACGTTGGATGGGGACTAAGC TGTTTGATGG	ACGTTGGATGCCAGGTAGAC GATGTAGTCC	CCAAATACATCTCCCTTCACA GCAGAA
rs2230922/SCD1	ACGTTGGATGTGGAGGTGGA GGCAGCTGTA	ACGTTGGATGAAGGACACGC AGTCCCTGA	GTGAGCACCTTAACATAGAT GGT
rs2235000/ATM	ACGTTGGATGTGGCTTACTTG GAGCCATAA	ACGTTGGATGAGGCTGACCC AGTAAATAAC	GTGTGTTCAAACATTTCCC ACATCCAAAAAGGATGTTTTCT
rs2243191/IL19	ACGTTGGATGAGCTCGACGTC TTTCTAGCC	ACGTTGGATGCATAACAGG TTCCTTGTC	TCCGTATCTGCCCC CCTACTTCATTAATATTGCTT GACT
rs17577/MMP9	ACGTTGGATGTAGTGTGGTGT CTCACGAAG	ACGTTGGATGTTGGACACGCA CGACGCTCT	GATCCAGACAGTTTACGAATA TATTTAA
rs2276331/CDH1	ACGTTGGATGTGGGTCGTGT ACTGAATGG	ACGTTGGATGTTCTCCCAAT ACATCTCCC	CCCAACTCATCATCTGCACAG GTATGCACAGAGGGCAGAAT A
rs2305948/KDR	ACGTTGGATGTGTACAATCCT TGGTCACTC	ACGTTGGATGAGTCTGGGAGT GAGATGAAG	TTGAATCAATGACCTGACCCT TG
rs3730017/NOS2	ACGTTGGATGGCTGTTGCAGG TCTTCGATG	ACGTTGGATGACGTGTCTGCA GATGTGTTT	CCCCGTTTTCTTCTCCCCAG AG
rs4148356/ABCC1	ACGTTGGATGGCAGGCCTGG ATTCAGAATG	ACGTTGGATGCGGACCTGTAA TATGGTTCC	GAGTGGAGGGCTTCT
rs4149637/TNFRSF 1A	ACGTTGGATGCCCATTACAG GAACCTACT	ACGTTGGATGACACTCCCTGC AGTCCGTAT	ACCTTCTTCTAATAATTACTA CAAGCTA
rs4986852/BRCA1	ACGTTGGATGAGCCGTAATA ACATTAGAG	ACGTTGGATGTCAATTAGTACT GGAACCTAC	TGCTGATGTCGGATTTTAC CTTCATGTACCAATACATCCT GC
rs5745549/MSH4	ACGTTGGATGGTCTGGGAA AATCTTCTTTG	ACGTTGGATGACTCTCAATTG GATCCAGAC	
rs6135876/OTOR	ACGTTGGATGGTATGTGCTGT GCATGGAAT	ACGTTGGATGTCCTTACAGAC ACACTCATC	
rs10306140/PTGS1	ACGTTGGATGCACATGACTAC ATCAGCTGG	ACGTTGGATGCAATCTTTAGG CACAGAGGG	
rs10941112/AMAC R	ACGTTGGATGGGCTCTTTTGG ACCGCACAC	ACGTTGGATGGGCATCTACCC CAATTAATAC	
rs12037099/LAMC2	ACGTTGGATGAGCTGGGTCAC AGTCACAC	ACGTTGGATGGTTGTGAAGCA TTTGGAAGC	
rs17101180/GIPC2	ACGTTGGATGATTTCAAACGC GCCCGCGAT	ACGTTGGATGGTAGTGCCACG GGCCGAGT	
rs17208397/PCDHG B7	ACGTTGGATGTCCCGATCCAG GGCCTCAT	ACGTTGGATGGTAGAGGTGTT CCATTTAAG	
rs17313892/MCC	ACGTTGGATGAGTGCCTTGGA GAGACTCAC	ACGTTGGATGCCCCTTTAGA TCATTACAG	
rs5361/SELE	ACGTTGGATGTGGTCTCTACA CATTCACCG	ACGTTGGATGGTATTTTCCGT AGTCGCCTG	

rs12917/MGMT	ACGTTGGATGCGAGGCTATCG AAGAGTTCC	ACGTTGGATGAGATGGCTTAG TTACCGACC	AAAACGGGATGGTGAA
rs16942/BRCA1	ACGTTGGATGTGAAAGGGCT AGGACTCCTG	ACGTTGGATGGACATTAAGG AAAGTTCTGC	ATCCTGCTAAGCTCTCCT
rs25496/XRCC1	ACGTTGGATGGAATGATGGCT CAGCTTTCG	ACGTTGGATGTACCTCATAGT CTTGCTCCC	CTCCCCAGCTGAACTGCCC
rs357564/PTCH1	ACGTTGGATGCCCCCAGAGA AGGCTTGTG	ACGTTGGATGCCAGAATGCCC TTCAGTAGA	CATAGAAGGCTTGTGGCCACC CC
rs459552/APC	ACGTTGGATGTCTCAGACAAC AAAGATTCC	ACGTTGGATGCATTATTTGGG AGCTTATC	GGTCTTTGGGAGCTTATCATT GAAG
rs799917/BRCA1	ACGTTGGATGCAGAGAATGTT GCACATTCC	ACGTTGGATGTCAAGGTTTCA AAGCGCCAG	CGCCAGTCATTTGCTC
rs1042522/TP53	ACGTTGGATGGGTGTAGGAG CTGCTGGTG	ACGTTGGATGAGACCCAGGT CCAGATGAAG	CCAGGCCAGAGGCTGCTCCCC
rs1061695/SBDS	ACGTTGGATGAATGTTTCTAA AGGTCAGG	ACGTTGGATGTGGTCATCTGT TCCAAACGC	CACTGATGAGATCTTCCTT
rs1073123/TSC1	ACGTTGGATGAACTCAGAGTC TGAGGTAGC	ACGTTGGATGGCTACTTCTAC CCCTTACTC	CCGGCTGATGTTGTAAATA
rs1145232/PMS1	ACGTTGGATGCGGAAATTTCT GCAGATGAG	ACGTTGGATGGGTTCATATT CTCTCCAC	CTCCCACTGAATTTTAAAGTA TATTTC
rs1346044/WRN	ACGTTGGATGCTAATCAAAG AAGTTTGCAG	ACGTTGGATGCTCTAAGTTGA TAAATCCCCC	CCCCTCCCCACCTTCTGATAA C
rs1799801/ERCC4	ACGTTGGATGGGACCAGGAT TATACTTCTC	ACGTTGGATGCGACAGCACT GGCCATTACA	TGGCCATTACAGCAGATTTC
rs1799931/NAT2	ACGTTGGATGGGGTGATACAT ACACAAGGG	ACGTTGGATGAAAATCTCGTGC CCAAACCTG	CTCTTGCCCAACCTGGTGAT G
rs1799969/ICAM1	ACGTTGGATGACCTGGGCCTC CGAGACTG	ACGTTGGATGGGTCTAGAG GTGGACAC	GGGGTGTCTGTTCCCTGGAC
rs1801018/BCL2	ACGTTGGATGTACTTCATCAC TATCTCCCG	ACGTTGGATGTTTCCTCTGG GAAGGATGG	GCACGCTGGGAGAAC
rs1801052/NF1	ACGTTGGATGAGCCATATCAG TCTGTGGGA	ACGTTGGATGATAGGCATTTT GGAACCTGG	GCTCCAGATGAATTTACAAAA CT
rs1801376/BUB1B	ACGTTGGATGTATCCAAAAAC CACACTCAC	ACGTTGGATGTGTGCTTCCCA GTTTCACTC	GTGGAAGAGACTGCAC
rs1815811/PDZD3	ACGTTGGATGCTCTGTCTCAA CCAGTGAGG	ACGTTGGATGCTCCTCTTCTT GGAGAACAC	CCGTCTCCCGCTCGCCCC
rs2070065/CENPF	ACGTTGGATGTTGAGTTCTGC CTCCAGGTG	ACGTTGGATGTGAAGAAGGA AAACAACCTC	CTCCAACAACCTCCTTAAGAG TCA
rs2228001/XPC	ACGTTGGATGAACTGGTGGGT GCCCCCTA	ACGTTGGATGAGCAGCTTCCC ACCTGTTT	CAGATTCCCACCTGTTCCCAT TTGAG
rs2234909/FGFR3	ACGTTGGATGAGCACGGTAA CGTAGGGTGT	ACGTTGGATGATCCAGTGGCT CAAGCACG	GCTAAAGCACGTGGAGGTGA A
rs2362974/SKP2	ACGTTGGATGCTCCCCAACTC TTTCCATAC	ACGTTGGATGATGAAAGCTCT GTGGCCAAC	GATCTGATTGGCCCTTG
rs2464196/HNF1A	ACGTTGGATGTCTGCAGCTGA GCCATGGT	ACGTTGGATGCACCTGTGCAG AGCCATGT	GGGGCCATGTGACCCAGA
rs3733542/KIT	ACGTTGGATGAAGTGACGTCT GGTCTATG	ACGTTGGATGTGAAGTTGTCT TTGGCAAGG	AAGGATCATTTTACCTAAAGA GAA
rs3826007/BCL2A1	ACGTTGGATGCTGCCAGAAC ACTATTCAAC	ACGTTGGATGTGGTTACAATT CTTCCACAG	TACCATTCTTCCCAGTTAAT GATG
rs3917408/SELE	ACGTTGGATGGTGTGTGTACC TTTGCTGAC	ACGTTGGATGTGGTCTTACAA CACCTCCAC	AAAGACAACACCTCCACGGA AGCTAT
rs4148725/CFTR	ACGTTGGATGCTTAGACTTGC ACTTGCTTG	ACGTTGGATGTCTTCCGGCAA GCCATCAGC	AAGCTCTTTCCCCAC
rs4755228/EXT2	ACGTTGGATGAGTAGATTCGG TGCTTGGTC	ACGTTGGATGTTATGTGTGCG TCGGTCAAG	GGGTTCGTCGGTCAAGTATAA TATC
rs7167216/BLM	ACGTTGGATGAAGAAGTGCC GCTGAGGAG	ACGTTGGATGTTTACTTGCAA AGTAGTGGG	GCAAAGTAGTGGAAGATA
rs9282655/CDH1	ACGTTGGATGTCAGCGTGTGT GACTGTGAA	ACGTTGGATGGAATTTGCAAT CCTGCTTCG	TCTGCTGTGCCTTCCTAC
rs11568591/ABCC3	ACGTTGGATGGAGGTGGAGT TCCGGAATTA	ACGTTGGATGTGCAGACTCAG GTCTCTCAG	AGCCCCAGGTCTAGGCCCGG CCGGTAG
rs34749508/BIRC2	ACGTTGGATGGGAGAAGGAA AAACAAGCTG	ACGTTGGATGGCTCCACTGAG AAACAATGC	CCCCAAATACCTGATGC
rs5273/PTGS2	ACGTTGGATGCCAGATGCCAT CTTTGGTGA	ACGTTGGATGCCATAAGTCCT TTCAAGGAG	GGGCGGAGAATGGTGCTCCA
rs5789/PTGS1	ACGTTGGATGTCTGTCCACAG GTAGACCTC	ACGTTGGATGTCTTAAAGAG CCGCAGTTG	AGGTGATACTGACGCTCCA
rs12628/HRAS	ACGTTGGATGATAGTGGGGTC GTATTCGTC	ACGTTGGATGAAGAGTGCGC TGACCATCCA	CTCCAGCTGATCCAGAACCA
rs16941/BRCA1	ACGTTGGATGTCATTAGTACT GGAACCTAC	ACGTTGGATGAGCCGTAATA ACATTAGAG	TAACATTAGAGAAAATGTTTT TAAAG

rs17655/ERCC5	ACGTTGGATGTCTCAGAATCA TCTGATGG	ACGTTGGATGGCTGTTCTCCT TTGTACATTC	TTAAAGATGAACTTTCAGCAT
rs72942/ RABGGTA	ACGTTGGATGAACTTGCTGCG CAGGTCATC	ACGTTGGATGACATGCATACC CTGCCAC	GGGCAAGGCCGTGGACCCCA TGCGGGCA
rs1044115/DUSP26	ACGTTGGATGTGACACACAC GTCGAAGCAG	ACGTTGGATGACCGAATGTG AGACCGAGTC	CGAGTCCCTTTATGTAC
rs1799977/MLH1	ACGTTGGATGGTTAGGACACT ACCCAATGC	ACGTTGGATGTCGACATACCG ACTAACAGC	GGGCCTAACAGCATTTCCTAAA GA
rs1805107/CDX2	ACGTTGGATGTTTAGCACCCCC CCCAGTTG	ACGTTGGATGTTGAGTCCGGT GTCTTCCCT	GGCTGCAAGCCTCAGTG
rs1805321/PMS2	ACGTTGGATGTCCGTGACTGG AACTCACTG	ACGTTGGATGGTCTTCTAGCA CTTCAGGTG	AGGGCAAAGGCGTCTGAGA
rs1805794/NBN	ACGTTGGATGTCAATTTGTGG AGGCTGCTT	ACGTTGGATGGGACGTCCAAT TGTAAGGCC	ATTGTACTGAATTCCTGAAAG CAGTT
rs1863968/ADAMT S16	ACGTTGGATGTTGAGTCTCTT CACCTTCGG	ACGTTGGATGCACTAGGCTGC TGGAAGTC	GTGCGGGAAGTCTCAGATCC A
rs1870134/XPC	ACGTTGGATGTCTTGCCCTTG GATTCTGG	ACGTTGGATGAAGCAACATG GCTCGGAAAC	GAGGGGAGCCGCGGGGACGC GAA
rs1991517/TSHR	ACGTTGGATGTCTTCCATGTT GTGGAGACC	ACGTTGGATGGTCTCTCCAAA GAACAGCAC	ATAGTCAGGTTCAAAAGGTTA CCCACGA
rs2020955/ERCC4	ACGTTGGATGACAAAGTGCA GGACTCACCG	ACGTTGGATGACTTAGACCTA GTAAGAGGC	TAGTAAGAGGCACAGCA
rs2023748/MET	ACGTTGGATGTTTTCTGAACT GGTGTCCCG	ACGTTGGATGCGTTCACATGG ACATAGTGC	ATCCCCAATGAAAGTAGAGA AGAT
rs2032582/ABCB1	ACGTTGGATGGAAAATGTTGT CTGGACAAGC	ACGTTGGATGCATATTTAGTT TGACTCAC	CATAGTTAGTTTGACTCACCT TCCCAG
rs2069398/CDK2	ACGTTGGATGACGTGTCCAGG CGGATTTTC	ACGTTGGATGCAAAGCCAGA AACAAGTTGAC	GAACAAGTTGACGGGAGA
rs2229362/BCL6	ACGTTGGATGACAGCATGCA GAGATGTGCC	ACGTTGGATGTACTCAGACTG GGTCTCTCC	CAGGGAACGTGGGGCCAG
rs2235036/ABCB1	ACGTTGGATGACCATTGTGAT AGCTCATCG	ACGTTGGATGCCACAATGACT CCATCATCG	CCTAATCCATCATCGAAACCA G
rs2285892/NF1	ACGTTGGATGCCTTGACTCTC AGGATAGTG	ACGTTGGATGACTTCTAGTTT GGTCTGGGC	GGCTTGTCGGCAAAT
rs3219489/MUTYH	ACGTTGGATGTTGGCTTGAGT AGGGTTCGG	ACGTTGGATGTCCGAGGGAG GCAGGCACA	GCCTAGGGAGGCAGGCACAG GTGGCA
rs3744124/FLCN	ACGTTGGATGAGAAGCTCGCT GGTGAGGCA	ACGTTGGATGAGAGCAGACA GCTGGTACCG	CCGCCCCACGGCCATC
rs3751489/MMP14	ACGTTGGATGATGCTGCTCTC TTCTGGATG	ACGTTGGATGAGGGGTTGAG GTCTTACTTG	TTAGGTCTTACTTGTCTTCCA
rs1130821/CDH11	ACGTTGGATGCTTTCACTCTT CCTACTTCC	ACGTTGGATGATGTCTTCTTC TTCTAGGCG	ACGCGTCTAGGCGTATACCAG AT
rs7837891/EXT1	ACGTTGGATGATTTGCGCTTC ACAGTGTTG	ACGTTGGATGAGAGTTATCCC AGAAGTGGC	GGTACCCCAACAATCCT
rs9462088/FANCE	ACGTTGGATGCCAAGGCCCTA TCAATACTC	ACGTTGGATGTATGCCAAGCT CATGCTGAC	CCCTCCAGTGATGACCAAGTA TCAG
rs9648696/BRAF	ACGTTGGATGCAGCTTTCAGT CAGATGTAT	ACGTTGGATGAAGGTAAGTGT CCAGTCATC	CAGTCATCAATTCATACAGAA CAAT
rs2227983/EGFR	ACGTTGGATGCTGTGCCATGCC TTGTGCTC	ACGTTGGATGCTGACATTCCG GCAAGAGAC	CAAGAGACGCAGTCC
rs11586699/LAMC2	ACGTTGGATGATGTCTGCCAG GCTTCCACA	ACGTTGGATGGGGATGCAAA TACTCACAGC	CTAGGTGCACCCCGCATCC
rs16875054/ADAM TS16	ACGTTGGATGTACGGGCAGTT ACTAGTAGC	ACGTTGGATGGGCTTTGGCTG ATCAGCAAG	GGGAAAGGCAGATAGCTTGA G
rs1137282/KRAS	ACGTTGGATGCACACTTTGTC TTTGACTTC	ACGTTGGATGGTTCGAGAAAT TCGAAAAC	CCCGAAAGAAAAGATGAGCA AAGA
rs13021/PNN	ACGTTGGATGGAGAAGGGAT ACTTCAGGAC	ACGTTGGATGCCTTTGATCCT TTGTATCTC	CCCGTTGATCCTTTTGTATCTC TACTAC
rs13181/ERCC2	ACGTTGGATGCTCAGAGCTGC TGAGCAATC	ACGTTGGATGAGCCTGGAGC AGCTAGAATC	GAGATAATCAGAGGAGACGC TG
rs17655/ERCC5	ACGTTGGATGCCCCAGCTAAG GATCATAAAC	ACGTTGGATGCCAAGAAGGTT GCCAGTAGC	CGGTACTTTATCATACTAAAT CTTTAA
rs85440/TGIF2	ACGTTGGATGTTCTCCACC CCCATTG	ACGTTGGATGCCATAAAACA GGGCTCTATC	CTTATGCTGAGGAACAAGG
rs429433/MFHAS1	ACGTTGGATGTTGATCTGGAC ACTGTAGCG	ACGTTGGATGGCTGAGCAGTT GCAGATTG	GCTTTCCTTTTACTTTTCCAC
rs466443/REEP5	ACGTTGGATGGGACTAGTGG AACTACACAG	ACGTTGGATGGAGATTATGGC AGTGAATCC	AAACTGGCAGTGAATCCCATT GG
rs9344/CCND1	ACGTTGGATGTACTACCGCTT CACACGCTT	ACGTTGGATGAAGGCTGCCTG GGACATCAC	TGTACATCACCTCACTTAC
rs659403/S100A6	ACGTTGGATGTTTGAACCAC CCAGTCTCA	ACGTTGGATGTCTCTCTCTCC CCTTCAAGC	TGCTGTCTCTCTGATGC

rs913588/KDM4C	ACGTTGGATGGAGCTCCAGGT TTAAGAAATG	ACGTTGGATGGGCACTTCTTC TGGAAAAGAG	TATTCAAAAAAGTGCGGTATA
rs1071695/CD44	ACGTTGGATGGTTGTTTGCTG CACAGATGG	ACGTTGGATGTCTCTTACAGG TATGGGTTC	GGGTTCATAGAAGGGCA
rs1531111/HECW2	ACGTTGGATGCTATCGAACAC AATGGCCAC	ACGTTGGATGAGTTTCGGAGA GGCACCCAT	GCAGGTGCGTGTCCC
rs2066852/CYLD	ACGTTGGATGGCTTGATTTTT CCAGCTGAG	ACGTTGGATGTATGTGGAGG GCTTGCAATG	GTGTAGAGAATGCTACGA
rs2071313/MEN1	ACGTTGGATGACTGCCCTCCT CCCATTG	ACGTTGGATGTCCAGGACCCT GAGTGCTTC	CCGGCTGCGATTCTACGA
rs2229080/DCC	ACGTTGGATGTCTTGCCCTCT GGAGCATTG	ACGTTGGATGATTTTCGAGCTG AGCATCGGT	CCAGCCCCCGGTTGGAGTC
rs2229333/TGIF1	ACGTTGGATGCAAACCCAAC CCTAGGGAG	ACGTTGGATGAGATCACTGAT GGACGAGCC	CACTTATGGACGAGCCAAAA CTGATCCC
rs2239359/FANCA	ACGTTGGATGGAGATGTAGTC TGTGAGGAG	ACGTTGGATGCTATCCTCAGG TGCACATTC	TGTGCTCCACCCACCCCTGGT TCCC
rs2275145/BAZ1A	ACGTTGGATGGTTCATCAATT TCCATCTC	ACGTTGGATGGTTAAGTGAG GAAAACAAGG	GATAATTA AAACTGTGAATG AAGA
rs2304329/HECW1	ACGTTGGATGCCCAATGCATT CTGTTGCTT	ACGTTGGATGTGTGAGTTCAC TGGAGAAAAG	CTGGAGAAAAGTGACCC
rs2589951/IQGA1	ACGTTGGATGCTCAATCTTAC TACTAACC	ACGTTGGATGCTTTGCTAGTC TGATAGCTG	GGTGATATTGTTACTTTACTT TG
rs1801195/WRN	ACGTTGGATGGCTAATGAAG AATTGTGTCC	ACGTTGGATGAAAATGCAGA AGTTACAAG	TCACAATGAACCTAGGCAGA AG
rs3791153/S100A10	ACGTTGGATGAATGGAATGT GACCAGGATG	ACGTTGGATGGTCAACCAGA AAATGGCTAC	CCTCGCTACCTTCAGGTCCAA AAACC
rs4151539/RB1	ACGTTGGATGGCCTTCTGCTT TGATAAAAC	ACGTTGGATGCCATGGATTG TGAATGTGC	GATTCTGAATGTGCTTAATTT AAAAG
rs4244612/RECQL4	ACGTTGGATGTGCTCTCCTGC TGGACCTGT	ACGTTGGATGAGCAGCAGTG GAGGCGAGAA	GAAGAGGAGATGGAACGAGG A
rs6786409/ZNF639	ACGTTGGATGGAGAATTTAAT TGGATAGTGG	ACGTTGGATGGAGGTCACATT CAACGTTCC	GCTTTCCACTGAGAACACAAC AC
rs7071768/MKI67	ACGTTGGATGCTTCCTCTACG TCTGCTTTC	ACGTTGGATGACAACCAGAC CCAGTGGAC	CCCGAAACGGCCCAAGAGAA TTTTTAGCAATTTCCAAAAA GAAA
rs8076741/PPM1D	ACGTTGGATGAGGGTGTGCGT TAGATTCTG	ACGTTGGATGCCGGTTGGGA ACTATCTGAA	CTGGAAAAGAATAATGGTGAA GATGA
rs9289556/TXNDC6	ACGTTGGATGTGCTCATTGGT TCTGCACTC	ACGTTGGATGATGTGTTTCCC ATGGAAAAG	CGTAAAAATTGTTATCACTAAT GCAG
rs10772947/LMO3	ACGTTGGATGGCTTGGGTTTA ATGTGGACG	ACGTTGGATGCAGAAGAGCA CACCAAAGCA	GTTTAGTGAAGTTGATATTGT TATAAG
rs10955788/EIF3H	ACGTTGGATGAGCTGCTGATA ACCAGTGGG	ACGTTGGATGTTTCATATTTTA GTGAAGTTG	ACGAGCACAAGCTGAAGAAA TCCGAAC
rs1051169/S100B	ACGTTGGATGGACTCACCTCT AAGAAATGG	ACGTTGGATGGAGACAAGCA CAAGCTGAAG	CCAACGCCAGCACC
rs12891473/SRP54	ACGTTGGATGTGGCACTCCGT TGGTCTTC	ACGTTGGATGGATAAAGTAG GGTCCCAACG	CCCCTAAATCTACAACAAA ATGGT
rs17439799/LRRN3	ACGTTGGATGCAAGTCTTTTT CTTTTGTC	ACGTTGGATGCGAACGATTGT CTCAAGTAA	
rs34661910/IL1RAP	ACGTTGGATGTTTTCTAGGCC AGCCTTGAG	ACGTTGGATGGCCTCCTGGTT GTTCTAAGC	GTTCTAAGCCCCAACTAC

Table S2, genotypes and alleles for all candidate SNPs. HCC, hepatocellular carcinoma; LC, liver cirrhosis; CH, chronic hepatitis. N/A, data not available.

RsID Symbol	Allele A/B	Ancestral Allele	Phenotype	Genotype			Sum	Call rate (%)	Allele	
				AA	AB	BB			A	B
rs5491	A/T	A	HCC	160	3	23	186	93	343	29
ICAM1			LC	67	0	10	77	96.3	144	10
			CH	163	2	31	196	98	357	35
rs5497	A/G	G	HCC	0	0	188	188	94	0	376
ICAM1			LC	0	0	78	78	97.5	0	156
			CH	0	0	197	197	98.5	0	394
rs34677	T/G	G	HCC	4	22	149	175	87.5	30	320
AMACR			LC	3	6	56	65	81.3	12	118
			CH	1	17	158	176	88	19	333
rs213950	A/G	A	HCC	28	81	69	178	89	137	219
CFTR			LC	10	34	30	74	92.5	54	94
			CH	26	86	79	191	95.5	138	244
rs2357768	A/T	A	HCC	7	64	123	194	97	78	310
BMP2			LC	1	22	53	76	95	24	128
			CH	7	60	130	197	98.5	74	320
rs766173	T/G	T	HCC	140	47	1	188	94	327	49
BRCA2			LC	47	24	0	71	88.8	118	24
			CH	144	47	1	192	96	335	49
rs766874	A/G	G	HCC	0	0	187	187	93.5	0	374
CFTR			LC	0	0	77	77	96.3	0	154
			CH	0	0	187	187	93.5	0	374
rs799917	T/C	T	HCC	27	80	86	193	96.5	134	252
BRCA1			LC	7	42	30	79	98.8	56	102
			CH	15	99	82	196	98	129	263
rs812936	A/G	A	HCC	108	6	0	114	57	222	6
FUT3			LC	62	1	0	63	78.8	125	1
			CH	141	2	0	143	71.5	284	2
rs867228	A/C	A	HCC	13	24	85	122	61	50	194
FPR1			LC	4	5	42	51	63.8	13	89
			CH	5	5	90	100	50	15	185
rs1019747	T/C	T	HCC	38	74	53	165	82.5	150	180
ADAMTS16			LC	20	18	23	61	76.3	58	64
			CH	37	71	55	163	81.5	145	181
rs1051624	A/C	A	HCC	26	58	48	132	66	110	154
CDH17			LC	2	5	17	24	30	9	39
			CH	18	36	45	99	49.5	72	126

rs1801133			HCC	44	74	61	179	89.5	162	196
MTHFR	T/C	C	LC	11	30	33	74	92.5	52	96
			CH	32	75	73	180	90	139	221
rs2071762			HCC	38	73	78	189	94.5	149	229
ARHGAP8	T/C	C	LC	13	29	36	78	97.5	55	101
			CH	20	94	81	195	97.5	134	256
rs2227567			HCC	109	0	0	109	54.5	218	0
PLAU	A/C	A	LC	79	0	0	79	98.8	158	0
			CH	105	0	0	105	52.5	210	0
rs2230922			HCC	0	0	188	188	94	0	376
SCD1	T/C	N/A	LC	0	0	79	79	98.8	0	158
			CH	0	0	198	198	99	0	396
rs2235000			HCC	0	0	193	193	96.5	0	386
ATM	A/G	G	LC	0	0	79	79	98.8	0	158
			CH	0	0	188	188	94	0	376
rs2243191			HCC	41	65	15	121	60.5	147	95
IL19	T/C	C	LC	0	33	6	39	48.8	33	45
			CH	27	81	9	117	58.5	135	99
rs17577			HCC	5	50	126	181	90.5	60	302
MMP9	A/G	N/A	LC	2	22	46	70	87.5	26	114
			CH	4	55	125	184	92	63	305
rs2276331			HCC	176	2	0	178	89	354	2
CDH1	G/C	G	LC	39	2	0	41	51.3	80	2
			CH	171	1	0	172	86	343	1
rs2305948			HCC	0	25	158	183	91.5	25	341
KDR	T/C	C	LC	0	9	57	66	82.5	9	123
			CH	2	27	148	177	88.5	31	323
rs3730017			HCC	0	1	139	140	70	1	279
NOS2	T/C	C	LC	0	0	79	79	98.8	0	158
			CH	0	2	127	129	64.5	2	256
rs4148356			HCC	1	26	166	193	96.5	28	358
ABCC1	A/G	G	LC	1	10	67	78	97.5	12	144
			CH	4	25	169	198	99	33	363
rs4149637			HCC	0	0	189	189	94.5	0	378
TNFRSF1A	T/C	C	LC	0	0	79	79	98.8	0	158
			CH	0	0	198	198	99	0	396
rs4986852			HCC	0	0	172	172	86	0	344
BRCA1	A/G	G	LC	0	0	77	77	96.3	0	154
			CH	0	0	178	178	89	0	356
rs5745549			HCC	0	7	114	121	60.5	7	235
MSH4	A/G	G	LC	0	4	41	45	56.3	4	86



			CH	0	43	50	93	46.5	43	143
rs6135876			HCC	102	70	11	183	91.5	274	92
OTOR	T/C	T	LC	40	30	7	77	96.3	110	44
			CH	77	85	12	174	87	239	109
rs10306140			HCC	0	0	193	193	96.5	0	386
PTGS1	T/G	G	LC	0	0	70	70	87.5	0	140
			CH	0	0	196	196	98	0	392
rs10941112			HCC	25	70	77	172	86	120	224
AMACR	A/G	G	LC	9	27	33	69	86.3	45	93
			CH	26	69	89	184	92	121	247
rs12037099			HCC	172	22	0	194	97	366	22
LAMC2	A/T	A	LC	74	2	0	76	95	150	2
			CH	185	13	0	198	99	383	13
rs17101180			HCC	1	0	82	83	41.5	2	164
GIPC2	T/C	N/A	LC	0	12	60	72	90	12	132
			CH	0	5	84	89	44.5	5	173
rs17208397			HCC	152	6	0	158	79	310	6
PCDHGB7	G/C	G	LC	70	2	0	72	90	142	2
			CH	107	1	0	108	54	215	1
rs17313892			HCC	0	0	189	189	94.5	0	378
MCC	A/T	T	LC	0	0	79	79	98.8	0	158
			CH	0	0	198	198	99	0	396
rs5361			HCC	180	2	0	182	91	362	2
SELE	A/C	A	LC	74	2	0	76	95	150	2
			CH	180	2	0	182	91	362	2
rs12917			HCC	5	48	142	195	97.5	58	332
MGMT	T/C	C	LC	0	25	55	80	100	25	135
			CH	4	42	152	198	99	50	346
rs16942			HCC	85	76	26	187	93.5	246	128
BRCA1	A/G	A	LC	29	45	6	80	100	103	57
			CH	82	101	15	198	99	265	131
rs25496			HCC	195	0	0	195	97.5	390	0
XRCC1	T/C	N/A	LC	80	0	0	80	100	160	0
			CH	198	0	0	198	99	396	0
rs357564			HCC	0	0	0	0	0	0	0
PTCH1	A/G	G	LC	0	0	0	0	0	0	0
			CH	0	0	0	0	0	0	0
rs459552			HCC	0	18	86	104	52	18	190
APC	A/T	T	LC	0	0	3	3	3.8	0	6
			CH	0	1	36	37	18.5	1	73
rs799917	T/C	T	HCC	27	78	82	187	93.5	132	242

BRCA1			LC	6	44	30	80	100	56	104
			CH	15	101	82	198	99	131	265
rs1042522	TP53	G/C	HCC	73	88	24	185	92.5	234	136
			LC	38	32	9	79	98.8	108	50
			CH	76	100	22	198	99	252	144
rs1061695	SBDS	A/G	HCC	185	0	0	185	92.5	370	0
			LC	79	1	0	80	100	159	1
			CH	192	1	0	193	96.5	385	1
rs1073123	TSC1	A/G	HCC	168	25	2	195	97.5	361	29
			LC	74	5	1	80	100	153	7
			CH	182	12	0	194	194	376	12
rs1145232	PMS1	A/G	HCC	0	0	160	160	80	0	320
			LC	0	0	78	78	97.5	0	156
			CH	0	0	195	195	97.5	0	390
rs1346044	WRN	T/C	HCC	14(AA)	50(AG)	111(GG)	175	87.5	78(A)	272(G)
			LC	4(AA)	33(AG)	38(GG)	75	93.8	41(A)	109(G)
			CH	29(AA)	76(AG)	87(GG)	192	96	134(A)	250(G)
rs1799801	ERCC4	T/C	HCC	120	61	11	192	96	301	83
			LC	44	32	3	79	98.8	120	38
			CH	116	72	9	197	98.5	304	90
rs1799931	NAT2	A/G	HCC	4	37	154	195	97.5	45	345
			LC	0	19	61	80	100	19	141
			CH	2	28	166	196	98	32	360
rs1799969	ICAM1	A/G	HCC	0	0	191	191	95.5	0	382
			LC	0	0	79	79	98.8	0	158
			CH	0	1	197	198	99	1	395
rs1801018	BCL2	A/G	HCC	158	34	3	195	97.5	350	40
			LC	74	6	0	80	100	154	6
			CH	165	29	4	198	99	359	37
rs1801052	NF1	A/G	HCC	0	0	0	0	0	0	0
			LC	0	0	0	0	0	0	0
			CH	0	0	0	0	0	0	0
rs1801376	BUB1B	A/G	HCC	0	0	0	0	0	0	0
			LC	0	0	0	0	0	0	0
			CH	1	0	0	1	0.5	2	0
rs1815811	PDZD3	A/G	HCC	0	0	0	0	0	0	0
			LC	0	0	0	0	0	0	0
			CH	0	0	0	0	0	0	0
rs2070065	CENPF	G/C	HCC	3	44	144	191	95.5	50	332
			LC	0	16	63	79	98.8	16	142
			CH	6	37	154	197	98.5	49	345

rs2228001			HCC	90	80	15	185	92.5	260	110
XPC	A/C	A	LC	25	35	28	78	97.5	85	91
			CH	63	89	21	173	86.5	215	131
rs2234909			HCC	137	32	3	172	86	306	38
FGFR3	T/C	C	LC	60	20	0	80	100	140	20
			CH	141	42	2	185	92.5	324	46
rs2362974			HCC	26	104	61	191	95.5	156	226
SKP2	T/C	C	LC	17	36	24	77	96.3	70	84
			CH	33	100	64	197	98.5	166	228
rs2464196			HCC	53	99	43	195	97.5	205	185
HNF1A	T/C	C	LC	25	33	22	80	100	83	77
			CH	67	101	30	198	99	235	161
rs3733542			HCC	180	13	1	194	97	373	15
KIT	G/C	G	LC	72	8	0	80	100	152	8
			CH	179	15	1	195	97.5	373	17
rs3826007			HCC	7	22	86	115	57.5	36	194
BCL2A1	A/G	G	LC	4	6	36	46	57.5	14	78
			CH	5	13	51	69	34.5	23	115
rs3917408			HCC	0	0	193	193	96.5	0	386
SELE	T/G	G	LC	0	1	79	80	100	1	159
			CH	0	0	196	196	98	0	392
rs4148725			HCC	2	12	181	195	97.5	16	374
CFTR	T/C	C	LC	0	3	77	80	100	3	157
			CH	0	10	188	198	99	10	386
rs4755228			HCC	0	0	0	0	0	0	0
EXT2	A/C	C	LC	0	0	0	0	0	0	0
			CH	0	0	0	0	0	0	0
rs7167216			HCC	0	17	175	192	96	17	367
BLM	A/G	G	LC	0	3	77	80	100	3	157
			CH	0	17	181	198	99	17	379
rs9282655			HCC	191	0	0	191	95.5	382	0
CDH1	T/C	T	LC	80	0	0	80	100	160	0
			CH	198	0	0	198	99	396	0
rs11568591			HCC	0	0	190	190	95	0	380
ABCC3	A/G	N/A	LC	0	0	80	80	100	0	160
			CH	0	0	181	181	90.5	0	362
rs34749508			HCC	0	0	195	195	97.5	0	390
BIRC2	A/G	N/A	LC	0	0	80	80	100	0	160
			CH	0	0	198	198	99	0	396
rs5273	T/C	T	HCC	169	0	0	169	84.5	338	0
PTGS2			LC	79	0	0	79	98.8	158	0

			CH	195	0	0	195	97.5	390	0
rs5789			HCC	0	0	185	185	92.5	0	370
PTGS1	A/C	C	LC	0	0	79	79	98.8	0	158
			CH	0	0	193	193	96.5	0	386
rs12628			HCC	122	55	6	183	91.5	299	67
HRAS	T/C	N/A	LC	55	22	2	79	98.8	132	26
			CH	132	55	5	192	96	319	65
rs16941			HCC	57	63	24	144	72	177	111
BRCA1	A/G	A	LC	26	41	6	73	91.3	93	53
			CH	72	99	15	186	93	243	129
rs17655			HCC	71	75	35	181	90.5	217	145
ERCC5	G/C	C	LC	21	39	19	79	98.8	81	77
			CH	63	84	45	192	96	210	174
rs729421			HCC	0	0	0	0	0	0	0
RABGGTA	A/G	G	LC	0	1	0	1	1.3	1	1
			CH	0	1	2	3	1.5	1	5
rs1044115			HCC	50	50	26	126	63	150	102
DUSP26	T/C	C	LC	27	35	17	79	98.8	89	69
			CH	64	88	22	174	87	216	132
rs1799977			HCC	138	5	0	143	71.5	281	5
MLH1	A/G	A	LC	77	2	0	79	98.8	156	2
			CH	180	11	0	191	95.5	371	11
rs1805107			HCC	139	37	8	184	92	315	53
CDX2	T/C	T	LC	59	18	2	79	98.8	136	22
			CH	141	51	4	196	98	333	59
rs1805321			HCC	13	50	74	137	68.5	76	198
PMS2	T/C	N/A	LC	3	42	28	73	91.3	48	98
			CH	8	82	81	171	85.5	98	244
rs1805794			HCC	31	65	51	147	73.5	127	167
NBN	G/C	G	LC	22	42	15	79	98.8	86	72
			CH	41	96	49	186	93	178	194
rs1863968			HCC	60	44	16	120	60	164	76
ADAMTS16	T/C	T	LC	33	32	14	79	98.8	98	60
			CH	78	91	24	193	96.5	247	139
rs1870134			HCC	87	31	4	122	61	205	39
XPC	G/C	G	LC	53	22	4	79	98.8	128	30
			CH	129	52	8	189	94.5	310	68
rs1991517			HCC	5	51	120	176	88	61	291
TSHR	G/C	C	LC	0	32	46	78	97.5	32	124
			CH	2	39	151	192	96	43	341
rs2020955	T/C	T	HCC	186	0	0	186	93	372	0

ERCC4			LC	79	0	0	79	98.8	158	0
			CH	196	0	0	196	98	392	0
rs2023748	MET	A/G	HCC	26	28	36	90	45	80	100
			LC	17	18	23	58	72.5	52	64
			CH	55	41	38	134	67	151	117
rs2069398	CDK2	A/G	HCC	0	2	183	185	92.5	2	368
			LC	0	0	79	79	98.8	0	158
			CH	0	3	193	196	98	3	389
rs2229362	BCL6	A/G	HCC	5	20	62	87	43.5	30	144
			LC	0	7	66	73	91.3	7	139
			CH	6	10	106	122	61	22	222
rs2235036	ABCB1	A/G	HCC	0	0	187	187	93.5	0	374
			LC	0	0	79	79	98.8	0	158
			CH	0	0	196	196	98	0	392
rs2285892	NF1	A/G	HCC	50	75	41	166	83	175	157
			LC	22	38	19	79	98.8	82	76
			CH	51	102	41	194	97	204	184
rs3219489	MUTYH	G/C	HCC	46	62	30	138	69	154	122
			LC	21	44	14	79	98.8	86	72
			CH	60	92	33	185	92.5	212	158
rs3744124	FLCN	A/G	HCC	7	51	126	184	92	65	303
			LC	4	20	55	79	98.8	28	130
			CH	4	67	125	196	98	75	317
rs3751489	MMP14	A/G	HCC	0	1	168	169	84.5	1	337
			LC	0	1	78	79	98.8	1	157
			CH	0	2	194	196	98	2	390
rs1130821	CDH11	A/G	HCC	27(TT)	92(TC)	63(CC)	182	91	146(T)	218(C)
			LC	9(TT)	49(TC)	19(CC)	77	96.3	67(T)	87(C)
			CH	26(TT)	91(TC)	75(CC)	192	96	143(T)	241(C)
rs7837891	EXT1	T/C	HCC	13	69	100	182	91	95	269
			LC	3	32	44	79	98.8	38	120
			CH	17	78	98	193	96.5	112	274
rs9462088	FANCE	A/G	HCC	0	23	155	178	89	23	333
			LC	0	6	73	79	98.8	6	152
			CH	0	14	182	196	98	14	378
rs9648696	BRAF	T/C	HCC	95	25	1	121	60.5	215	27
			LC	58	16	1	75	93.8	132	18
			CH	94	53	5	152	76	241	63
rs2227983	EGFR	A/G	HCC	58	18	36	112	56	134	90
			LC	26	1	20	47	58.8	53	41
			CH	70	40	39	149	74.5	180	118

rs11586699			HCC	0	0	182	182	91	0	364
LAMC2	T/C	C	LC	0	0	79	79	98.8	0	158
			CH	0	0	196	196	98	0	392
rs16875054			HCC	9	11	105	125	62.5	29	221
ADAMTS16	A/G	G	LC	2	10	60	72	90	14	130
			CH	2	22	141	165	82.5	26	304
rs1137282			HCC	128	35	4	167	83.5	291	43
	A/G	N/A	LC	60	14	2	76	95	134	18
KRAS			CH	142	37	8	187	93.5	321	53
rs13021			HCC	45	34	4	83	41.5	124	42
PNN	A/G	A	LC	35	7	7	49	61.3	77	21
			CH	83	49	17	149	74.5	215	83
rs13181			HCC	188	10	0	198	99	386	10
ERCC2	T/G	G	LC	67	2	0	69	86.3	136	2
			CH	188	9	1	198	99	385	11
rs17655			HCC	91(AA)	42(AG)	5(GG)	138	69	224	52
ERCC5	G/C	C	LC	31(AA)	6(AG)	4(GG)	41	51.3	68	14
			CH	99(AA)	26(AG)	8(GG)	133	66.5	224	42
rs85440			HCC	0	72	38	110	55	72	148
TGIF2	A/G	G	LC	0	18	39	57	71.3	18	96
			CH	0	70	64	134	67	70	198
rs429433			HCC	0	0	192	192	96	0	384
MFHAS1	T/C	C	LC	0	0	69	69	86.3	0	138
			CH	0	0	197	197	98.5	0	394
rs466443			HCC	84	64	6	154	77	232	76
REEP5	A/G	G	LC	48	18	1	67	83.8	114	20
			CH	132	51	5	188	94	315	61
rs9344			HCC	53	85	57	195	97.5	191	199
CCND1	A/G	N/A	LC	14	31	18	63	78.8	59	67
			CH	47	90	58	195	97.5	184	206
rs659403			HCC	4	33	160	197	98.5	41	353
S100A6	G/C	C	LC	3	9	57	69	86.3	15	123
			CH	0	40	159	199	99.5	40	358
rs913588			HCC	4	35	160	199	99.5	43	355
KDM4C	A/G	G	LC	2	18	49	69	86.3	22	116
			CH	4	52	142	198	99	60	336
rs1071695			HCC	1	24	173	198	99	26	370
CD44	T/C	N/A	LC	0	5	64	69	86.3	5	133
			CH	0	18	180	198	99	18	378
rs1531111			HCC	190	7	0	197	98.5	387	7
HECW2	A/G	G	LC	70	0	0	70	87.5	140	0

			CH	192	7	0	199	99.5	391	7
rs2066852			HCC	2	29	168	199	99.5	33	365
CYLD	T/C	C	LC	2	11	56	69	86.3	15	123
			CH	2	26	170	198	99	30	366
rs2071313			HCC	26	68	71	165	82.5	120	210
MEN1	T/C	N/A	LC	14	11	29	54	67.5	39	69
			CH	16	82	76	174	87	114	234
rs2229080			HCC	93	79	25	197	98.5	265	129
DCC	G/C	C	LC	33	30	6	69	86.3	96	42
			CH	94	83	22	199	99.5	271	127
rs2229333			HCC	0	18	133	151	75.5	18	284
TGIF1	T/C	C	LC	0	0	55	55	68.8	0	110
			CH	0	11	152	163	81.5	11	315
rs2239359			HCC	105	49	8	162	81	259	65
FANCA	T/C	T	LC	51	51	0	69	86.3	153	51
			CH	138	40	4	182	91	316	48
rs2275145			HCC	45	93	46	184	92	183	185
BAZ1A	A/G	G	LC	22	23	11	56	70	67	45
			CH	50	88	55	193	96.5	188	198
rs2304329			HCC	146	6	44	196	98	298	94
HECW1	T/C	T	LC	48	4	17	69	86.3	100	38
			CH	138	6	50	194	97	282	106
rs2589951			HCC	34	77	60	171	85.5	145	197
IQGAP1	T/C	C	LC	8	27	30	65	81.3	43	87
			CH	32	84	69	185	92.5	148	222
rs1801195			HCC	73	98	25	196	98	244	148
WRN	T/G	T	LC	28	27	12	67	83.8	83	51
			CH	70	90	37	197	98.5	230	164
rs3791153			HCC	107	63	11	181	90.5	277	85
S100A10	T/C	T	LC	33	30	6	69	86.3	96	42
			CH	99	79	19	197	98.5	277	117
rs4151539			HCC	0	0	103	103	51.5	0	206
RB1	G/C	C	LC	0	0	18	18	22.5	0	36
			CH	0	0	173	173	86.5	0	346
rs4244612			HCC	78	76	32	186	93	232	140
RECQL4	G/C	G	LC	32	29	8	69	86.3	93	45
			CH	90	86	21	197	98.5	266	128
rs6786409			HCC	15	91	81	187	93.5	121	253
ZNF639	T/C	C	LC	5	17	29	51	63.8	27	75
			CH	15	64	91	170	85	94	246
rs7071768	T/C	C	HCC	4	98	40	142	71	106	178

MKI67			LC	25	32	12	69	86.3	82	56
			CH	22	101	42	165	82.5	145	185
rs8076741	T/C	C	HCC	139	38	0	177	88.5	316	38
PPM1D			LC	52	16	0	68	85	120	16
			CH	151	33	3	187	93.5	335	39
rs9289556	T/C	C	HCC	122	41	5	168	84	285	51
TXNDC6			LC	48	19	1	68	85	115	21
			CH	128	52	4	184	92	308	60
rs10772947	A/G	A	HCC	24	42	71	137	68.5	90	184
LMO3			LC	9	24	28	61	76.3	42	80
			CH	24	85	80	189	94.5	133	245
rs10955788	T/C	T	HCC	23	25	28	76	38	71	81
EIF3H			LC	12	21	22	55	68.8	45	65
			CH	44	57	46	147	73.5	145	149
rs1051169	G/C	N/A	HCC	46	91	56	193	96.5	183	203
S100B			LC	13	31	25	69	86.3	57	81
			CH	38	98	60	196	98	174	218
rs12891473	T/C	C	HCC	5	67	127	199	99.5	77	321
SRP54			LC	4	24	41	69	86.3	32	106
			CH	17	66	116	199	99.5	100	298
rs17439799	T/C	T	HCC	120	55	10	185	92.5	295	75
LRRN3			LC	27	1	12	40	50	55	25
			CH	114	43	13	170	85	271	69
rs34661910	T/C	N/A	HCC	0	0	198	198	99	0	396
IL1RAP			LC	0	0	69	69	86.3	0	138
			CH	0	0	198	198	99	0	396



Table S3, putative paired variants of HCV-associating SNPs by linkage disequilibria. Proxy, candidate proxy variants in linkage disequilibria with those in Table 1 (“SNP”);  $R^2$ , pairwise correlation coefficient; RS, RegulomeDB scores for regulation; Dist, distance in proximity between A and B (bp); Function, predicted function of the proxy variant; Syn, synonymous.

SNP	Proxy	$R^2$	RS	Dist	Function
rs16875054	rs12652633	0.894	5	18081	None
rs17439799	rs2301733	0.881	2a	-4428	None
rs1799801	rs2276464	0.979	5	972	None
rs1799801	rs2276466	0.979	5	1217	None
rs1799801	rs3136211	0.979	5	-2310	None
rs1799801	rs56012340	0.936	5	2823	None
rs1799801	rs4781562	0.895	5	3278	None
rs1799801	rs4781563	0.895	5	3441	None
rs1799801	rs3136199	0.979	5	-4306	None
rs1799801	rs9646271	0.895	5	5460	None
rs1799801	rs3136168	0.979	4	-9504	None
rs1799801	rs3136160	0.979	5	-10895	None
rs1799801	rs3136155	0.957	4	-11598	None
rs1799801	rs3136085	0.979	5	-22377	None
rs1799801	rs3136213	0.957	5	-1805	None
rs1799801	rs3136189	0.957	3a	-7257	None
rs1799801	rs3136187	0.957	4	-7459	None
rs1799801	rs3136172	0.957	5	-9082	None
rs1799801	rs957078	0.957	5	-22254	None
rs1799801	rs3136079	0.957	5	-22721	None
rs1799801	rs2238463	0.957	3a	-24056	None
rs1799801	rs3136070	0.957	2b	-24239	None
rs1799801	rs74684179	0.957	5	-24674	None
rs1799801	rs9646272	0.936	5	6886	None
rs1799801	rs2238462	0.936	5	-26648	None
rs1799801	rs762521	0.936	3a	-27718	None
rs1799801	rs1799797	0.936	4	-27965	None
rs1799801	rs6498486	0.936	2b	-28292	None
rs1799801	rs3136038	0.936	4	-28579	None
rs1799801	rs6498485	0.936	5	-30964	None
rs1799801	rs11649492	0.936	5	-32540	None
rs1799801	rs11648436	0.936	5	-33284	None
rs1799801	rs4781560	0.936	5	-36207	None
rs1799801	rs12924220	0.936	5	-36825	None
rs1799801	rs7200442	0.936	2b	-38302	None
rs1799801	rs2081273	0.936	5	-39706	None
rs1799801	rs9928336	0.916	5	-40091	None
rs1799801	rs4078751	0.916	4	-41240	None
rs1799801	rs753192	0.916	4	-41564	None
rs1799801	rs12933628	0.916	3a	-43078	None
rs1799801	rs7191182	0.916	3a	-43262	None

rs1799801	rs7195395	0.916	5	-43934	None
rs1799801	rs3136080	0.936	5	-22549	None
rs1799801	rs6498483	0.859	3a	-42987	None
rs1799801	rs7190692	0.859	5	-43875	None
rs1799801	rs1646332	0.874	5	7769	None
rs1799801	rs1646331	0.833	5	8048	None
rs1799801	rs11644737	0.874	3a	-46708	None
rs1799801	rs7204841	0.855	4	-46866	None
rs1799801	rs11648736	0.813	5	8934	None
rs1805321	rs62456177	1.000	5	-1143	None
rs1805321	rs62456178	0.942	5	3299	None
rs1805321	rs2286681	0.922	1a	8440	None
rs1805321	rs3779106	0.922	1f	28894	None
rs1805321	rs10951974	0.885	5	24380	None
rs2071762	rs2071764	1.000	5	290	None
rs2071762	rs2071761	1.000	5	-382	None
rs2071762	rs11704168	0.960	5	-2555	None
rs2071762	rs3830108	0.939	5	-2145	None
rs2071762	rs5766136	0.862	2b	4125	None
rs2071762	rs35200938	0.861	5	5749	None
rs2071762	rs2213531	0.807	4	948	None
rs2228001	rs2733532	0.938	5	250	None
rs2228001	rs2257984	1.000	5	1698	None
rs2228001	rs2607770	0.938	2b	-1822	None
rs2228001	rs2607769	0.938	2b	-1856	None
rs2228001	rs2279017	0.979	2b	2788	None
rs2228001	rs1043943	0.938	5	-4039	None
rs2228001	rs2607734	0.979	5	5055	None
rs2228001	rs2607736	0.979	5	5484	None
rs2228001	rs2607767	0.859	3a	-6897	None
rs2228001	rs34574722	0.882	5	8565	None
rs2228001	rs2607772	0.979	5	31553	None
rs2228001	rs2607739	0.979	5	35122	None
rs2228001	rs11925757	0.865	2b	54532	None
rs2228001	rs2305843	0.920	5	54699	None
rs2228001	rs2305842	0.865	5	54949	None
rs2228001	rs1127122	0.979	5	54993	None
rs2228001	rs17039107	0.865	4	55244	None
rs34677	rs34284851	0.953	5	-2497	None
rs34677	rs34681	1.000	5	2557	None
rs34677	rs42440	1.000	4	2936	None
rs34677	rs40601	1.000	5	3087	None
rs34677	rs39663	1.000	5	3186	None
rs34677	rs840409	1.000	5	-3825	None
rs34677	rs34683	1.000	2b	4415	None
rs34677	rs40507	1.000	4	4593	None
rs34677	rs34684	1.000	5	6794	None
rs34677	rs34685	1.000	5	7435	None

rs34677	rs112667834	0.903	5	-7639	None
rs34677	rs34686	1.000	5	7717	None
rs34677	rs34687	1.000	5	7742	None
rs34677	rs34688	0.951	4	8891	None
rs34677	rs34689	0.951	2b	8941	None
rs34677	rs253195	1.000	5	11538	None
rs34677	rs253196	1.000	5	11548	None
rs34677	rs253197	1.000	4	11744	None
rs34677	rs253198	1.000	5	11871	None
rs34677	rs253199	1.000	5	12905	None
rs34677	rs253201	1.000	5	14492	None
rs5361	rs3917410	1.000	1f	48	None
rs5361	rs5362	1.000	3a	-99	None
rs5361	rs3917411	1.000	1f	-304	None
rs5361	rs1800016	1.000	5	841	Syn
rs5361	rs1800015	1.000	5	844	Syn
rs5361	rs3917417	1.000	5	-998	None
rs5361	rs5363	1.000	5	-2271	Syn
rs5361	rs5367	1.000	5	-3984	None
rs5361	rs3917425	1.000	1f	-4306	None
rs5361	rs75337769	1.000	4	5621	None
rs5361	rs76249441	1.000	3a	5764	None
rs5361	rs76036595	1.000	5	6183	None
rs5361	rs76904074	1.000	5	6674	None
rs5361	rs3917441	1.000	3a	-8939	None
rs5361	rs3917448	1.000	5	-9839	None
rs5361	rs76991533	1.000	5	10517	None
rs5361	rs80355141	1.000	5	11538	None
rs5361	rs75007377	1.000	4	13207	None
rs5361	rs10489180	1.000	5	18369	None
rs5361	rs79774551	1.000	3a	20634	None
rs5361	rs17527744	1.000	5	20908	None
rs5361	rs1569457	1.000	5	-20986	None
rs5361	rs12145504	1.000	5	21219	None
rs5361	rs80165835	1.000	5	21714	None
rs5361	rs76660846	1.000	4	21797	None
rs5361	rs77507144	1.000	4	21880	None
rs5361	rs4987299	1.000	1f	-25711	None
rs5361	rs4987308	1.000	5	-26944	None
rs5361	rs114538842	1.000	4	27215	None
rs5361	rs190949251	1.000	3a	27230	None
rs5361	rs12137905	1.000	5	-28193	None
rs5361	rs4987317	1.000	3a	-29272	None
rs5361	rs4987395	1.000	3a	-29674	None
rs5361	rs4987323	1.000	1f	-29783	None
rs5361	rs4987324	1.000	1f	-29823	None
rs5361	rs4987325	1.000	4	-29843	None
rs5361	rs4987326	1.000	4	-30119	None

rs5361	rs4987327	1.000	4	-30120	None
rs5361	rs12130784	1.000	5	30258	None
rs5361	rs12123942	1.000	5	30613	None
rs5361	rs12121313	1.000	5	30807	None
rs5361	rs12120647	1.000	5	31161	None
rs5361	rs75589232	1.000	5	31219	None
rs5361	rs75800947	1.000	5	31457	None
rs5361	rs116005144	1.000	5	31564	None
rs5361	rs79018991	1.000	5	31604	None
rs5361	rs79650530	1.000	5	32514	None
rs5361	rs74830193	1.000	5	32781	None
rs5361	rs78177553	1.000	5	33083	None
rs5361	rs75460658	1.000	5	33791	None
rs5361	rs17593568	1.000	5	33877	None
rs5361	rs144225401	1.000	4	33918	None
rs5361	rs12121606	1.000	4	34137	None
rs5361	rs12129443	1.000	4	34213	None
rs5361	rs12121681	1.000	4	34339	None
rs5361	rs77151202	1.000	3a	34503	None
rs5361	rs116581594	1.000	2b	34505	None
rs5361	rs76670206	1.000	3a	34769	None
rs5361	rs76140670	1.000	4	48051	None
rs5361	rs79593867	1.000	4	48330	None
rs5361	rs12132633	1.000	5	55155	None
rs5361	rs12130372	1.000	1f	56256	None
rs766173	rs1801439	1.000	5	500	Syn
rs766173	rs11571605	1.000	2b	-8242	None
rs766173	rs11571598	1.000	5	-9758	None
rs766173	rs11571591	0.940	4	-11742	None
rs766173	rs11571671	1.000	5	11742	None
rs766173	rs11571699	1.000	5	20174	None
rs766173	rs11571809	1.000	5	59284	None
rs766173	rs11571813	1.000	5	60766	None

Table S4, stratified comparisons of significant SNPs among disease phenotypes. Genotypic significance is evaluated for genotypic frequencies, allele frequencies, dominant (AA+AB/BB) and recessive allele models (AA/AB+BB), respectively. *p*, *p*-values of significance of a particular subgroup compared against all three disease phenotypes (*All*) or individual subgroups. *OR*, odds ratio with 95% confidence interval shown in parentheses; red values indicate genes with call rate >80%. "\*\*\*", *p* < 0.001; "-", not available.

ID (Symbol, rsID)	Allele	Ancestral Allele	Grouping (or JSNP/NCBI set ID)	Genotype				Allele				Genotype dominant model (AA+AB/BB)								Genotype recessive model (AA/AB+BB)							
				All <i>p</i>	HCC <i>p</i>	LC <i>p</i>	CH <i>p</i>	All <i>p</i>	HCC <i>p</i>	LC <i>p</i>	CH <i>p</i>	All <i>p</i>	HCC <i>p</i>	LC <i>p</i>	CH <i>p</i>	All <i>p</i>	HCC <i>p</i>	LC <i>p</i>	CH <i>p</i>								
1 (AMACR, rs34677)	T/G	G	NCBI 12675253 NCBI 68931918 JSNP IMS-JST038996	HCC	-	-	0.511	0.259	-	-	-	0.82	0.92 (0.46-1.86)	0.099	0.61 (0.34-1.10)	-	-	-	0.844	1.09 (0.48-2.46)	0.19	1.53 (0.81-2.91)	-	-	-		
				LC	-	-	-	0.092	-	-	-	-	-	-	-	-	-	-	-	-	-	0.429	1.41 (0.60-3.32)	-	-	-	
				CH	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	
				0.032	0.106	0.147	0.002	**	0.023	0.53 (0.30-0.92)	0.127	0.57 (0.28-1.18)	**	0.32 (0.17-0.60)	0.013	0.036	0.51 (0.27-0.97)	0.077	0.47 (0.20-1.10)	0.001	0.33 (0.17-0.66)	0.123	0.248	0.48 (0.12-1.97)			
				**	**	**	**	**	**	0.29 (0.18-0.48)	0.001	0.31 (0.16-0.62)	**	0.18 (0.10-0.31)	0.022	0.055	0.54 (0.29-1.02)	0.104	0.50 (0.21-1.16)	0.002	0.35 (0.18-0.70)	**	**	0.07 (0.02-0.22)			
2 (ARHGAP8, rs2071762)	T/C	C	NCBI 12527661 NCBI 69271108 NCBI 71647951 JSNP IMS-JST007439	HCC	-	-	0.712	0.017	-	-	-	0.368	1.20 (0.81-1.76)	0.146	1.24 (0.93-1.67)	-	-	-	0.463	1.22 (0.72-2.07)	0.957	1.01 (0.67-1.52)	-	-	-		
				LC	-	-	-	0.159	-	-	-	-	-	-	0.842	1.04 (0.71-1.54)	-	-	-	-	-	0.486	0.83 (0.49-1.41)	-	-	-	
				CH	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	
				0.111	0.988	0.818	0.053	0.458	0.905	1.02 (0.71-1.47)	0.492	0.86 (0.55-1.34)	0.294	0.82 (0.57-1.19)	0.896	0.88	1.04 (0.63-1.73)	0.609	0.85 (0.46-1.57)	0.913	1.03 (0.62-1.71)	0.042	0.984	1.01 (0.54-1.88)			
				0.065	0.862	0.659	0.014	0.392	0.895	0.98 (0.68-1.40)	0.371	0.82 (0.52-1.27)	0.193	0.79 (0.55-1.13)	0.896	0.88	1.04 (0.63-1.73)	0.609	0.85 (0.46-1.57)	0.913	1.03 (0.62-1.71)	0.024	0.684	0.88 (0.48-1.62)			
3 (KDR, rs2305948)	T/C	C	NCBI 48430022 NCBI 68899172 JSNP IMS-JST063410	0.111	0.988	0.818	0.053	0.458	0.905	1.02 (0.71-1.47)	0.492	0.86 (0.55-1.34)	0.294	0.82 (0.57-1.19)	0.896	0.88	1.04 (0.63-1.73)	0.609	0.85 (0.46-1.57)	0.913	1.03 (0.62-1.71)	0.042	0.984	1.01 (0.54-1.88)			
				0.012	0.056	0.102	0.029	0.046	0.491	0.92 (0.74-1.16)	0.138	0.77 (0.55-1.09)	0.011	0.74 (0.59-0.93)	0.04	0.08	0.75 (0.55-1.04)	0.04	0.62 (0.39-0.98)	0.065	0.74 (0.54-1.02)	0.055	0.346	1.21 (0.81-1.79)			
				HCC	-	-	0.59	0.316	-	-	-	0.996	1.00 (0.46-2.21)	0.335	0.76 (0.44-1.32)	-	-	-	0.996	1.00 (0.44-2.28)	0.469	0.81 (0.45-1.44)	-	-	-		
				LC	-	-	-	0.646	-	-	-	-	-	0.489	0.76 (0.35-1.65)	-	-	-	-	-	0.6	0.81 (0.36-1.81)	-	-	-		
				CH	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	
4 (SELE, rs5361)	A/C	A	NCBI 48428825 NCBI 68784305 JSNP	0.647	0.374	0.438	0.603	0.775	0.635	0.85 (0.43-1.68)	0.707	0.85 (0.36-2.02)	0.755	1.11 (0.58-2.15)	0.879	0.622	0.84 (0.41-1.70)	0.695	0.83 (0.34-2.06)	0.921	1.04 (0.52-2.08)	0.281	-	-			
				0.651	0.401	0.461	0.599	0.778	0.686	0.87 (0.44-1.72)	0.749	0.87 (0.36-2.07)	0.7	1.14 (0.59-2.20)	0.887	0.674	0.86 (0.42-1.75)	0.738	0.86 (0.35-2.12)	0.862	1.06 (0.53-2.13)	0.279	-	-			
				0.158	0.044	0.302	0.389	0.035	0.015	0.59 (0.38-0.91)	0.127	0.59 (0.29-1.17)	0.195	0.77 (0.52-1.14)	0.056	0.025	0.60 (0.38-0.94)	0.158	0.60 (0.29-1.23)	0.172	0.74 (0.48-1.14)	0.361	-	-			
				HCC	-	-	0.338	0.689	-	-	-	0.339	0.41 (0.06-2.97)	0.688	1.00 (0.14-7.14)	-	-	-	0.338	0.41 (0.06-2.97)	0.689	1.00 (0.14-7.18)	-	-	-		
				LC	-	-	-	0.338	-	-	-	-	-	0.339	2.41 (0.34-17.29)	-	-	-	-	-	0.338	2.43 (0.34-17.59)	-	-	-		
5 (XPC, rs2228001)	A/C	A	NCBI 44411054 NCBI 66856826 NCBI 68853585 JSNP IMS-JST086794	0.188	0.091	0.413	0.091	0.191	0.092	0.24 (0.04-1.31)	0.414	0.57 (0.10-3.18)	0.092	0.24 (0.04-1.31)	0.188	0.091	0.23 (0.04-1.30)	0.413	0.57 (0.10-3.19)	0.091	0.23 (0.04-1.30)	-	-	-			
				0.201	0.095	0.424	0.095	0.205	0.097	0.24 (0.04-1.34)	0.425	0.59 (0.11-3.25)	0.097	0.24 (0.04-1.34)	0.201	0.095	0.24 (0.04-1.33)	0.424	0.58 (0.10-3.26)	0.095	0.24 (0.04-1.33)	-	-	-			
				0.001	0.001	0.145	0.001	0.001	0.005	0.17 (0.04-0.70)	0.149	0.41 (0.10-1.69)	0.001	0.17 (0.04-0.70)	0.001	0.005	0.16 (0.04-0.68)	0.145	0.40 (0.10-1.67)	0.005	0.16 (0.04-0.68)	-	-	-			
				HCC	-	-	0.001	0.054	-	-	-	**	0.40 (0.27-0.57)	0.021	0.69 (0.51-0.95)	-	-	-	0.002	0.42 (0.24-0.72)	0.019	0.60 (0.40-0.92)	-	-	-		
				LC	-	-	-	0.086	-	-	-	-	-	0.002	1.76 (1.22-2.54)	-	-	-	-	-	0.196	1.44 (0.83-2.52)	-	-	-		
6 (FANCA, rs2239359)	T/C	T	NCBI 16702260 NCBI 43872290 NCBI 66860952 NCBI 69355410 JSNP IMS-JST010482	0.011	0.523	0.092	0.656	**	0.263	0.81 (0.55-1.18)	0.001	2.04 (1.33-3.12)	0.44	1.16 (0.80-1.69)	0.008	0.316	0.77 (0.46-1.28)	0.054	1.84 (0.99-3.44)	0.358	1.28 (0.76-2.15)	**	0.416	0.71 (0.30-1.64)			
				0.01	0.365	0.108	0.847	**	0.168	0.77 (0.53-1.12)	0.002	1.94 (1.27-2.97)	0.603	1.10 (0.76-1.61)	0.009	0.177	0.70 (0.42-1.17)	0.103	1.68 (0.90-3.14)	0.569	1.16 (0.69-1.96)	**	0.416	0.71 (0.30-1.64)			
				0.012	0.326	0.185	0.555	**	0.168	0.77 (0.53-1.12)	0.002	1.94 (1.27-2.97)	0.603	1.10 (0.76-1.61)	0.008	0.316	0.77 (0.46-1.28)	0.054	1.84 (0.99-3.44)	0.358	1.28 (0.76-2.15)	**	0.172	0.57 (0.26-1.28)			
				0.003	0.001	0.371	0.165	**	0.64 (0.50-0.81)	0.002	1.62 (1.19-2.21)	0.492	0.92 (0.73-1.17)	0.006	0.005	0.64 (0.46-0.87)	0.088	1.52 (0.94-2.46)	0.771	1.05 (0.75-1.47)	**	0.002	0.42 (0.24-0.74)				
				HCC	-	-	0.117	0.061	-	-	-	0.072	1.67 (0.95-2.94)	0.015	1.65 (1.10-2.48)	-	-	-	0.177	1.54 (0.82-2.88)	0.025	1.70 (1.07-2.72)	-	-	-		
7 (LRRN3, rs17439799)	T/C	C	NCBI 24455640 JSNP	0.169	0.366	0.191	0.581	0.069	0.211	1.36 (0.84-2.22)	0.528	0.81 (0.43-1.54)	0.453	0.83 (0.50-1.37)	0.134	0.165	1.49 (0.85-2.63)	0.935	0.97 (0.48-1.98)	0.655	0.88 (0.49-1.56)	0.177	0.563	1.12 (0.33-3.82)			
				0.169	0.366	0.191	0.581	0.069	0.211	1.36 (0.84-2.22)	0.528	0.81 (0.43-1.54)	0.453	0.83 (0.50-1.37)	0.134	0.165	1.49 (0.85-2.63)	0.935	0.97 (0.48-1.98)	0.655	0.88 (0.49-1.56)	0.177	0.563	1.12 (0.33-3.82)			
				0.169	0.366	0.191	0.581	0.069	0.211	1.36 (0.84-2.22)	0.528	0.81 (0.43-1.54)	0.453	0.83 (0.50-1.37)	0.134	0.165	1.49 (0.85-2.63)	0.935	0.97 (0.48-1.98)	0.655	0.88 (0.49-1.56)	0.177	0.563	1.12 (0.33-3.82)			
				0.087	0.029	0.504	0.488	0.055	0.022	1.42 (1.05-1.92)	0.529	0.85 (0.51-1.42)	0.366	0.86 (0.62-1.19)	0.139	0.067	1.39 (0.98-1.98)	0.718	0.90 (0.52-1.57)	0.277	0.820 (0.56-1.18)	0.06	0.028	2.64 (1.13-6.17)			
				HCC	-	-	**	0.5	-	-	-	0.032	0.56 (0.33-0.96)	0.994	1.00 (0.69-1.44)	-	-	-	0.751	1.13 (0.54-2.33)	0.663	1.10 (0.71-1.71)	-	-	-		
8 (BRCA2, rs766173)	T/G	T	NCBI 5586314 NCBI 66862596 NCBI 69130493	0.019	0.008	**	0.01	0.006	0.003	3.07 (1.42-6.64)	**	4.17 (1.81-9.60)	0.004	3.00 (1.39-6.48)	0.002	0.002	3.34 (1.50-7.43)	**	4.98 (2.07-11.98)	0.003	3.25 (1.46-7.22)	0.842	0.686	-			
				0.013	0.005	**	0.006	0.004	0.002	3.22 (1.49-6.96)	**	4.37 (1.90-10.07)	0.002	3.15 (1.46-6.79)	0.001	0.001	3.51 (1.58-7.79)	**	5.23 (2.18-12.58)	0.002	3.42 (1.54-7.57)	0.837	0.676	-			
				0.013	0.005	<0.001	0.003	0.004	0.002	3.22 (1.49-6.96)	**	4.37 (1.90-10.07)	0.002	3.15 (1.46-6.79)	0.001	0.001	3.51 (1.58-7.79)	**	5.23 (2.18-12.58)	0.002	3.42 (1.54-7.57)	0.837	0.676	-			
				HCC	-	-	0.518	0.147	-	-	-	0.518	1.37 (0.27-6.89)	0.149	4.16 (0.50-34.81)	-	-	-	0.518	1.38 (0.27-7.02)	0.147	4.22 (0.50-35.59)	-	-	-		
				LC	-	-	-	0.351	-	-	-	-	-	0.352	3.03 (0.27-33.71)	-	-	-	-	-	0.351	3.06 (0.27-34.36)	-	-	-		
9 (PCDHGB7, rs17208397)	G/C	G	NCBI 24621861 NCBI 68951534	0.004	0.026	0.04	0.002	0.005	0.027	0.33 (0.12-0.92)	0.484	0.24 (0.05-1.11)	0.002	0.08 (0.01-0.62)	0.004	0.024	0.32 (0.11-0.90)	0.044	0.23 (0.05-1.08)	0.002	0.07 (0.01-0.60)	-	-	-			
				0.004	0.026	0.04	0.002	0.005	0.027	0.33 (0.12-0.92)	0.484	0.24 (0.05-1.11)	0.002	0.08 (0.01-0.62)	0.004	0.024	0.32 (0.11-0.90)	0.044	0.23 (0.05-1.08)	0.002	0.07 (0.01-0.60)	-	-	-			
				HCC	-	-	0.573	-	-	-	0.536	1.15 (0.74-1.78)	0.68	1.07 (0.77-1.51)	-	-	-	0.377	0.65 (0.18-2.39)	0.604	0.79 (0.32-1.95)	-	-	-			
				LC	-	-	-	0.815	-	-	-	-	-	0.761	0.94 (0.61-1.44)	-	-	-	-	-	0.534	1.21 (0.32-4.60)	-	-	-		
				CH	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-		
10 (ERCC4, rs1799801)	T/C	C	NCBI 52072800 NCBI 66861998	0.156	0.027	0.237	0.07	0.061	0.009	1.69 (1.14-2.52)	0.115	1.47 (0.91-2.39)	0.023	1.58 (1.06-2.34)	0.403	0.299	1.65 (0.64-4.25)	0.169	2.53 (0.65-9.91)	0.136	2.09 (0.78-5.61)	0.059	0.007	2.00 (1.20-3.33)			
				0.156	0.027																						

Table S5, statistically overrepresented Reactome pathways for genes with candidate SNPs considered to be significant and their common interacting partners. Statistical criterion:  $p < .05$  ( $\log_{10} p < -1.30$ ) after Bonferroni correction; *RID*, Reactome pathway accession number; *BG*, number of *Homo sapiens* genes in specified pathway; *Found*, number of enriched genes in specified pathway; *Expected*, the number of expected genes. *FE*, fold enrichment.

<b>RID</b>	<b>Reactome pathways</b>	<b>BG</b>	<b>Found</b>	<b>Expected</b>	<b>FE</b>	<b>log <i>p</i></b>
73894	DNA Repair	292	10	0.52	19.41	-6.921
69481	G2/M Checkpoints	151	7	0.27	26.28	-4.818
69239	Synthesis of DNA	100	6	0.18	34.01	-4.370
69620	Cell Cycle Checkpoints	183	7	0.32	21.68	-4.252
69306	DNA Replication	108	6	0.19	31.49	-4.173
1640170	Cell Cycle	575	10	1.01	9.86	-4.124
69206	G1/S Transition	115	6	0.2	29.57	-4.013
201681	TCF dependent signaling in response to WNT	201	7	0.35	19.74	-3.979
162909	Host Interactions of HIV factors	124	6	0.22	27.43	-3.821
69242	S Phase	128	6	0.23	26.57	-3.742
68867	Assembly of the pre-replicative complex	68	5	0.12	41.68	-3.595
453279	Mitotic G1-G1/S phases	139	6	0.25	24.47	-3.533
68949	Orc1 removal from chromatin	71	5	0.13	39.92	-3.503
69052	Switching of origins to a post-replicative state	71	5	0.13	39.92	-3.503
69300	Removal of licensing factors from origins	73	5	0.13	38.82	-3.444
69304	Regulation of DNA replication	76	5	0.13	37.29	-3.358
195253	Degradation of beta-catenin by the destruction complex	82	5	0.14	34.56	-3.196
69002	DNA Replication Pre-Initiation	85	5	0.15	33.34	-3.119
68874	M/G1 Transition	85	5	0.15	33.34	-3.119
405531	Regulation of mRNA stability by proteins that bind AU-rich elements	86	5	0.15	32.95	-3.095
2467813	Separation of Sister Chromatids	178	6	0.31	19.11	-2.910
195721	Signaling by Wnt	296	7	0.52	13.40	-2.851
69275	G2/M Transition	185	6	0.33	18.38	-2.812
68882	Mitotic Anaphase	186	6	0.33	18.28	-2.799
2555396	Mitotic Metaphase and Anaphase	187	6	0.33	18.19	-2.785
453274	Mitotic G2-G2/M phases	187	6	0.33	18.19	-2.785
597592	Post-translational protein modification	826	10	1.46	6.86	-2.682
69278	Cell Cycle, Mitotic	471	8	0.83	9.63	-2.606
1236978	Cross-presentation of soluble exogenous antigens (endosomes)	50	4	0.09	45.34	-2.449
211733	Regulation of activated PAK-2p34 by proteasome mediated degradation	50	4	0.09	45.34	-2.449
69017	CDK-mediated phosphorylation and removal of Cdc6	51	4	0.09	44.46	-2.416
169911	Regulation of Apoptosis	51	4	0.09	44.46	-2.416
69229	Ubiquitin-dependent degradation of Cyclin D1	51	4	0.09	44.46	-2.416
350562	Regulation of ornithine decarboxylase (ODC)	51	4	0.09	44.46	-2.416
75815	Ubiquitin-dependent degradation of Cyclin D	51	4	0.09	44.46	-2.416
180534	Vpu mediated degradation of CD4	52	4	0.09	43.60	-2.382
349425	Autodegradation of the E3 ubiquitin ligase COP1	52	4	0.09	43.60	-2.382
162906	HIV Infection	221	6	0.39	15.39	-2.370
69613	p53-Independent G1/S DNA damage checkpoint	53	4	0.09	42.78	-2.350
69610	p53-Independent DNA Damage Response	53	4	0.09	42.78	-2.350
69601	Ubiquitin Mediated Degradation of Phosphorylated Cdc25A	53	4	0.09	42.78	-2.350
180585	Vif-mediated degradation of APOBEC3G	53	4	0.09	42.78	-2.350
450408	AUF1 (hnRNP D0) binds and destabilizes mRNA	54	4	0.1	41.99	-2.318

174113	SCF-beta-TrCP mediated degradation of Emi1	55	4	0.1	41.22	-2.287
69541	Stabilization of p53	55	4	0.1	41.22	-2.287
4641257	Degradation of AXIN	55	4	0.1	41.22	-2.287
5362768	Hh mutants that don't undergo autocatalytic processing are degraded by ERAD	56	4	0.1	40.49	-2.256
4641258	Degradation of DVL	57	4	0.1	39.78	-2.225
5218921	VEGFR2 mediated cell proliferation	236	6	0.42	14.41	-2.207
68827	CDT1 association with the CDC6:ORC:origin complex	59	4	0.1	38.43	-2.166
5676590	NIK-->noncanonical NF-kB signaling	59	4	0.1	38.43	-2.166
5387390	Hh mutants abrogate ligand secretion	59	4	0.1	38.43	-2.166
5607761	Dectin-1 mediated noncanonical NF-kB signaling	60	4	0.11	37.79	-2.138
187577	SCF(Skp2)-mediated degradation of p27/p21	60	4	0.11	37.79	-2.138
5610785	GLI3 is processed to GLI3R by the proteasome	60	4	0.11	37.79	-2.138
5610783	Degradation of GLI2 by the proteasome	60	4	0.11	37.79	-2.138
5610780	Degradation of GLI1 by the proteasome	60	4	0.11	37.79	-2.138
5678895	Defective CFTR causes cystic fibrosis	61	4	0.11	37.17	-2.110
174084	Autodegradation of Cdh1 by Cdh1:APC/C	63	4	0.11	35.99	-2.055
69580	p53-Dependent G1/S DNA damage checkpoint	64	4	0.11	35.43	-2.028
69563	p53-Dependent G1 DNA Damage Response	64	4	0.11	35.43	-2.028
4608870	Asymmetric localization of PCP proteins	64	4	0.11	35.43	-2.028
5358346	Hedgehog ligand biogenesis	65	4	0.11	34.88	-2.001
69615	G1/S DNA Damage Checkpoints	66	4	0.12	34.35	-1.975
1169091	Activation of NF-kappaB in B cells	67	4	0.12	33.84	-1.951
174154	APC/C:Cdc20 mediated degradation of Securin	67	4	0.12	33.84	-1.951
5658442	Regulation of RAS by GAPs	68	4	0.12	33.34	-1.924
69202	Cyclin E associated events during G1/S transition	69	4	0.12	32.86	-1.900
69656	Cyclin A:Cdk2-associated events at S phase entry	70	4	0.12	32.39	-1.876
174184	Cdc20:Phospho-APC/C mediated degradation of Cyclin A	72	4	0.13	31.49	-1.827
174178	APC/C:Cdh1 mediated degradation of Cdc20 and other APC/C:Cdh1 targeted proteins in late mitosis/early G1	72	4	0.13	31.49	-1.827
179419	APC:Cdc20 mediated degradation of cell cycle proteins prior to satisfaction of the cell cycle checkpoint	73	4	0.13	31.06	-1.804
109581	Apoptosis	159	5	0.28	17.82	-1.801
68886	M Phase	281	6	0.5	12.10	-1.777
5357801	Programmed Cell Death	162	5	0.29	17.49	-1.762
176409	APC/C:Cdc20 mediated degradation of mitotic proteins	75	4	0.13	30.23	-1.759
176814	Activation of APC/C and APC/C:Cdc20 mediated degradation of mitotic proteins	76	4	0.13	29.83	-1.735
8852276	The role of GTSE1 in G2/M progression after G2 checkpoint	77	4	0.14	29.44	-1.714
176408	Regulation of APC/C activators between G1/S and early anaphase	80	4	0.14	28.34	-1.650
5619084	ABC transporter disorders	81	4	0.14	27.99	-1.627
5632684	Hedgehog 'on' state	83	4	0.15	27.32	-1.587
1168372	Downstream signaling events of B Cell Receptor (BCR)	177	5	0.31	16.01	-1.577
1236974	ER-Phagosome pathway	84	4	0.15	26.99	-1.567
351202	Metabolism of polyamines	84	4	0.15	26.99	-1.567
4420097	VEGFA-VEGFR2 Pathway	307	6	0.54	11.08	-1.561
174143	APC/C-mediated degradation of cell cycle proteins	86	4	0.15	26.36	-1.527
453276	Regulation of mitotic cell cycle	86	4	0.15	26.36	-1.527
194138	Signaling by VEGF	316	6	0.56	10.76	-1.491
5687128	MAPK6/MAPK4 signaling	88	4	0.16	25.76	-1.488
4086400	PCP/CE pathway	92	4	0.16	24.64	-1.412
5689603	UCH proteinases	96	4	0.17	23.62	-1.341
5668541	TNFR2 non-canonical NF-kB pathway	96	4	0.17	23.62	-1.341
5607764	CLEC7A (Dectin-1) signaling	97	4	0.17	23.37	-1.323