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Citation

Published Version
doi:10.1371/journal.pgen.1002791

Accessed
April 19, 2017 2:10:02 PM EDT

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(Article begins on next page)
GWAS Identifies Novel Susceptibility Loci on 6p21.32 and 21q21.3 for Hepatocellular Carcinoma in Chronic Hepatitis B Virus Carriers

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Abstract

Genome-wide association studies (GWAS) have recently identified KIF1B as susceptibility locus for hepatitis B virus (HBV)-related hepatocellular carcinoma (HCC). To further identify novel susceptibility loci associated with HBV-related HCC and replicate the previously reported association, we performed a large three-stage GWAS in the Han Chinese population. 523,663 autosomal SNPs in 1,538 HBV-positive HCC patients and 1,465 chronic HBV carriers were genotyped for the discovery stage. Top candidate SNPs were genotyped in the initial validation samples of 2,112 HBV-positive HCC cases and 2,208 HBV carriers and then in the second validation sample of 1,021 cases and 1,491 HBV carriers. We discovered two novel associations at rs9272105 (HLA-DQA1/DRB1) on 6p21.32 (OR = 1.30, P = 1.71 × 10−5) and rs455804 (GRIK1) on 21q21.3 (OR = 0.84, P = 1.86 × 10−6), which were further replicated in the fourth independent sample of 1,298 cases and 1,026 controls (rs9272105: OR = 1.25, P = 1.71 × 10−5; rs455804: OR = 0.84, P = 6.92 × 10−6). We also revealed the associations of HLA-DRB1*0405 and 0901*0405, which could partially account for the association at rs9272105. The association at rs455804 implicates GRIK1 as a novel susceptibility gene for HBV-related HCC, suggesting the involvement of glutamate signaling in the development of HBV-related HCC.


Editor: Mark R. Thurz, Imperial College London, United Kingdom

Received December 16, 2011; Accepted May 13, 2012; Published July 12, 2012

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Funding: This work is partly funded by the China National High-Tech Research and Development Program Grant (2009AA022701, 2009AA022705, and 2009AA022706), the National Key Basic Research Program Grant (2010CB529600, 2011CB503802), National Major S&T Projects (2008ZX10002-010, 2008ZX10002-015, 2008ZX10002-017, 2008ZX10002-018, and 2009ZX1004_904), the National Natural Science Foundation of China (81072344, 81130022, 30800946, 31000553, 30872372), NSFC Science Fund for Creative Research Groups (30921006), State Key Laboratory funding of Oncology in South China (303041077008), Foundation for the Author of National Excellent Doctoral Dissertation (grants 201081, 201026), the Program for New Century Excellent Talents in University (NCET-09-0550, NCET-10-0178), a project funded by the Priority Academic Program Development of Jiangsu Higher Education Institutions (public health and preventive medicine), and funds from the Agency for Science, Technology, and Research (A*STAR) of Singapore. The funders had no role in study design, data collection and analysis, decision to publish, or preparation of the manuscript.

Competing Interests: The authors have declared that no competing interests exist.

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† These authors contributed equally to this work.
**Results**

We performed a genome-wide discovery analysis by analyzing 523,663 common autosomal SNPs in two independent cohorts of the Han Chinese: 480 cases and 484 controls from central China and 1,058 cases and 981 controls from southern China (Table S1 and Figure S1). The principal component analysis (PCA) confirmed all the samples to be Chinese, but indicated moderate genetic mismatch between the cases and controls in the cohort of southern China (Figure S2). To minimize the effect of population stratification, we performed the genome-wide association analysis using PCA-based correction for population stratification. After the adjustment by the first principal component, the age of the genome-wide association results is 1.013 for the cohort of central China, 1.003 for the cohort of southern China and 1.012 for the combined samples. Furthermore, for all the three genome-wide analyses of central, southern and combined samples, the quantile-quantile (QQ) plot of the observed P values revealed a good overall fit with the null distribution (Figure S3). Taken together, these results clearly indicate that the final association results from our genome-wide discovery analysis are free of inflation effect due to population stratification.

The genome-wide discovery analysis revealed multiple suggestive associations (P<10\(^{-5}\)) on 2q22.1, 6p21.32, 11p15.1 and 20q12 (Figure S4 and Table S2). To validate these findings, 39 SNPs were selected according to their overall association evidence in three GWAS analyses as well as their consistencies of association between the two independent GWAS samples (Central and Southern China) (see the Methods for the selection criteria). The 39 SNPs were genotyped in additional 2,112 HBV–positive HCC cases and 2,208 HBV carriers (Phase I validation) (Table S1). Of the 39 SNPs, only 3 (rs9272105 on 6p21.32, rs11148740 on 13q21.32 and rs455804 on 21q21.3) were validated, showing consistent association between the GWAS discovery and Phase I validation samples (Table S3). These 3 SNPs were then genotyped in additional 1,021 HBV–positive HCC cases and 1,491 HBV carriers (Phase II validation). The Phase II validation analysis (Table 1) confirmed the associations at rs9272105 on 6p21.32 (OR = 1.41, \(P = 7.63\times10^{-3}\)) and rs455804 on 21q21.3 (OR = 0.83, \(P = 3.63\times10^{-3}\)), but not the association at rs11148740 on 13q21.32 (Table S3).

For both rs9272105 and rs455804, no heterogeneity of associations were observed among the GWAS and validation samples (I\(^2\)>0.05), and the associations in the combined GWAS and validation samples achieved genome-wide significance (P<5.0×10\(^{-8}\)) (rs9272105: OR = 1.30, \(P = 1.13\times10^{-19}\) and rs455804: OR = 0.84, \(P = 1.86\times10^{-10}\)) (Table 1). As a replication, these two SNPs were genotyped in the fourth independent samples of 1,298 cases and 1,026 controls from central China, which further confirmed the associations at rs9272105 (OR = 1.25, \(P = 1.71\times10^{-4}\)) and rs11148740 (OR = 0.84, \(P = 6.92\times10^{-3}\)) (Table 1). When combining all the five groups of samples, the two SNPs resulted in a 28% increased, and a 16% decreased risk (Table 1) confirmed the associations at rs9272105 on 6p21.32 and rs455804 on 21q21.3 among subgroups, except that the association at rs9272105 showed a stronger effect in the non-smoking group than the smoking one (OR = 1.36 vs. 1.19, \(P = 0.0044\)) (Table S4B). Pair-wise interaction analysis among these two SNPs, smoking and drinking status did not reveal any significant interaction (data not shown). The samples used in the GWAS, validation and replication analyses are summarized in Table S1, and the multi-stage design of the whole study is shown in Figure S5.

We further investigated the association of HLA alleles in our GWAS samples through imputation. After QC filtering (see the Methods), 37 HLA alleles were successfully imputed, and 5 alleles showed nominal association (P<0.05) (Table S5 and Table 2). Further stepwise conditional analysis revealed that only two DRB1 alleles, HLA-DQA1*0101/DRB1*0102 and HLA-DQA1*0103/DRB1*0201, independent of the SNPs, accounted for 28% increased risk and 16% decreased risk, respectively.
alleles showed independent associations (\textit{DRB1}^*0405: \textit{OR} = 0.69, \textit{P} = 6.18\times 10^{-5}; \textit{DRB1}^*0901: \textit{OR} = 0.82, \textit{P} = 3.62\times 10^{-5}) (Table 2). Conditioning on rs9272105 could abolish the associations of the \textit{DRB1} alleles, and conditioning on the \textit{DRB1} alleles could weaken, but not eliminate, the association at rs9272105 (Table 2). The haplotype analysis of rs9272105 and the two \textit{DRB1} alleles revealed consistent result, showing that both the \textit{DRB1} alleles sit on the haplotypes carrying the protective \textit{G} allele of rs9272105 (Table S6). Taking together, there seems to be additional risk effect beyond the ones carried by the \textit{DRB1} alleles.

We further explored whether the SNPs rs9272105 and rs455804 play any role in HBV infection. First, we compared the frequencies of these 2 SNPs between 408 non-symptomatic HBV carriers and 521 symptomatic chronic HBV patients from southern China (GWA scanned). The analysis revealed a protective effect of rs9272105 (\textit{OR} = 0.80, \textit{P} = 8.39\times 10^{-5}) on the development of symptomatic chronic hepatitis B, but no association at rs455804 (Table S7A). Furthermore, we genotyped these 2 SNPs in 1,344 individuals with HBV nature clearance and compared their frequencies with those in 4,183 asymptomatic HBV carriers (all from the Central China). The analysis also revealed a protective association at rs9272105 for HBV chronic infection (\textit{OR} = 0.88, \textit{P} = 3.78\times 10^{-5}) (Table S7B).

**Discussion**

SNP rs9272105 is located between \textit{HLA-DQA1} and \textit{HLA-DRB1} on 6p21.32 (Figure 1A). SNP imputation in the GWA discovery samples revealed additional SNPs showing association, but rs9272105 remained to be the top SNP within the region (Figure 1A). The residual association at rs9272105 after conditioning the association effects of the \textit{HLA} alleles \textit{DRB1}^*0403 and \textit{*0901} suggests that there may be additional risk effect beyond the \textit{DRB1} alleles in Chinese population. The associations of the \textit{DRB1} alleles revealed by this study are consistent with the previous reports that \textit{HLA-DQ}/ \textit{DR} alleles associated with HCC risk [9,10]. In addition, we investigated the previously reported HBV infection-associated SNPs rs3077, rs9277535, rs7453920, and rs2856718 within the \textit{HLA-DP}/ \textit{DQ} locus has also been shown to be associated with HCV-related HCC in Japanese GWAS (rs9275572, \textit{OR} = 1.30, \textit{P} = 9.38\times 10^{-5}) [13]. SNPs rs9275572 and rs9272105 are 79 kb away from each other and in weak LD ($D'$ = 0.43, $r^2 = 0.08$ in the HepMap CHB/JPT samples), suggesting that the associations at rs9275572 and rs9272105 may be independent.

The \textit{HLA-DQ} locus has also been shown to be associated with HCV-related HCC in a Japanese GWAS (rs9275572, \textit{OR} = 1.30, \textit{P} = 9.38\times 10^{-5}) [13]. SNPs rs9275572 and rs9272105 are 79 kb away from each other and in weak LD ($D'$ = 0.43, $r^2 = 0.08$ in the HepMap CHB/JPT samples). The SNP rs9275572 did not show any association with HBV-related HCC in our GWAS discovery (\textit{OR} = 0.93, \textit{P} = 0.24) (Table S8 and Figure S6B). In addition to \textit{HLA-DQ}/ \textit{DP}/ \textit{DQ} association, we found the evidence of the association at rs9277535 with HCC (\textit{rs9277535: OR} = 1.30, \textit{P} = 7.93\times 10^{-5}). However, there is no linkage disequilibrium (LD) between rs9277535 and our SNP rs9272105 ($r^2 = 0.016$ according the HapMap CHB-JPT samples), suggesting that the associations at rs9277535 and rs9272105 may be independent.

<table>
<thead>
<tr>
<th>SNP</th>
<th>Study</th>
<th>Cases ($n=5,969$)</th>
<th>Controls ($n=6,190$)</th>
<th>MAF</th>
<th>OR (95% CI)</th>
<th>Pd</th>
<th>P_Q</th>
</tr>
</thead>
<tbody>
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<td>6p21.32:rs9272105</td>
<td>GWAS Southern</td>
<td>346/456/251</td>
<td>239/450/286</td>
<td>0.55</td>
<td>0.48</td>
<td>1.28(1.13–1.46)</td>
<td>1.80E-04</td>
</tr>
<tr>
<td>A/G</td>
<td>GWAS Central</td>
<td>129/229/122</td>
<td>81/249/154</td>
<td>0.51</td>
<td>0.42</td>
<td>1.41(1.16–1.72)</td>
<td>6.45E-04</td>
</tr>
<tr>
<td>Joint GWAS</td>
<td>477/885/373</td>
<td>320/699/440</td>
<td>0.53</td>
<td>0.46</td>
<td>1.32(1.19–1.46)</td>
<td>2.26E-07</td>
<td>6.20E-01</td>
</tr>
<tr>
<td>Validation 1</td>
<td>580/976/556</td>
<td>436/1118/653</td>
<td>0.51</td>
<td>0.45</td>
<td>1.24(1.14–1.35)</td>
<td>5.15E-07</td>
<td></td>
</tr>
<tr>
<td>Validation 2</td>
<td>278/420/242</td>
<td>260/770/459</td>
<td>0.52</td>
<td>0.43</td>
<td>1.41(1.25–1.58)</td>
<td>7.63E-09</td>
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<tr>
<td>Joint Validation</td>
<td>858/1396/798</td>
<td>696/1888/1112</td>
<td>0.51</td>
<td>0.44</td>
<td>1.30(1.21–1.39)</td>
<td>8.73E-14</td>
<td>8.10E-02</td>
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<td>GWAS+Validation 1&amp;2</td>
<td>1335/2081/1171</td>
<td>1016/2587/1552</td>
<td>0.52</td>
<td>0.45</td>
<td>1.30(1.23–1.38)</td>
<td>1.13E-19</td>
<td>3.36E-01</td>
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<tr>
<td>Replication</td>
<td>335/621/342</td>
<td>195/516/315</td>
<td>0.50</td>
<td>0.44</td>
<td>1.25(1.11–1.40)</td>
<td>1.71E-04</td>
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</tr>
<tr>
<td>All combined</td>
<td>1670/2702/1513</td>
<td>1211/3103/1867</td>
<td>0.51</td>
<td>0.48</td>
<td>1.28(1.21–1.33)</td>
<td>5.24E-22</td>
<td>3.88E-01</td>
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<tr>
<td>21q21.3:rs455804</td>
<td>GWAS Southern</td>
<td>110/397/551</td>
<td>126/440/415</td>
<td>0.29</td>
<td>0.35</td>
<td>0.74(0.64–0.85)</td>
<td>3.37E-05</td>
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<tr>
<td>A/C</td>
<td>GWAS Central</td>
<td>47/215/218</td>
<td>56/215/213</td>
<td>0.32</td>
<td>0.34</td>
<td>0.94(0.76–1.16)</td>
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<tr>
<td>Joint GWAS</td>
<td>157/612/769</td>
<td>182/655/628</td>
<td>0.30</td>
<td>0.35</td>
<td>0.81(0.72–0.90)</td>
<td>1.65E-04</td>
<td>1.09E-01</td>
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<tr>
<td>Validation 1</td>
<td>201/888/1021</td>
<td>262/962/976</td>
<td>0.31</td>
<td>0.34</td>
<td>0.87(0.79–0.95)</td>
<td>1.62E-03</td>
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<tr>
<td>Validation 2</td>
<td>89/426/506</td>
<td>154/689/648</td>
<td>0.30</td>
<td>0.33</td>
<td>0.83(0.74–0.94)</td>
<td>3.63E-03</td>
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<tr>
<td>Joint Validation</td>
<td>290/1314/1527</td>
<td>416/1651/1624</td>
<td>0.30</td>
<td>0.34</td>
<td>0.85(0.79–0.92)</td>
<td>2.05E-05</td>
<td>5.41E-01</td>
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<tr>
<td>GWAS+Validation 1&amp;2</td>
<td>447/1926/2296</td>
<td>598/2306/2252</td>
<td>0.30</td>
<td>0.34</td>
<td>0.84(0.79–0.89)</td>
<td>1.86E-08</td>
<td>3.15E-01</td>
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<tr>
<td>Replication</td>
<td>123/530/645</td>
<td>106/476/444</td>
<td>0.30</td>
<td>0.34</td>
<td>0.84(0.74–0.95)</td>
<td>6.92E-03</td>
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<tr>
<td>All combined</td>
<td>570/2456/2941</td>
<td>704/2782/2696</td>
<td>0.30</td>
<td>0.34</td>
<td>0.84(0.80–0.89)</td>
<td>5.24E-10</td>
<td>3.14E-01</td>
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*Minor allele/major allele;\n\textsuperscript{a}Variant homozygote/Heterozygote/Wild type homozygote;\n\textsuperscript{b}Minor allele frequency (MAF);\n\textsuperscript{c}Adjusted by the first principal component;\n\textsuperscript{d}P value of heterogeneity based on Cochrane's Q test.

doi:10.1371/journal.pgen.1002791.t001
supportive evidence for these two loci (rs2596542: OR = 1.06, [13,14]. But, our GWAS discovery analysis did not reveal any SNPs that showed stronger association than rs455804. GRIK1 encodes GLUR5, which is involved in the glutamate signaling, as one of the ionotropic glutamate receptor, kainite 1 protein (GLUR5), a subunit of ligand-activated channels and involved in glutamate signaling. Our discovery of the association of GRIK1 with HCC has enhanced the emerging evidences for the important role of glutamate signaling pathway in cancer development. Glutamate has been shown to play a central role in the malignant phenotype of gliomas through multiple cellular mechanisms [20]. Inhibition of glutamate release and/or glutamate receptor activity can inhibit the proliferation and/or invasion of tumor cells in breast cancer [21], laryngeal cancer [22], and pancreatic cancer [23], and ionotropic glutamate receptor (GLUR6) was also suggested to play a tumor-suppressor role in gastric cancer [24]. Recently, the exome sequencing analysis revealed that GRIN2A (encoding the ionotropic glutamate receptor N-methyl D-aspartate subunit 2A) was mutated in 33% of melanoma tumors, clearly indicating the involvement of glutamate signaling in melanoma development. Finally, SNPs within GRIK1 have also been found significantly associated with paclitaxel response in NCI60 cancer cell lines, and may play a role in the cellular response to paclitaxel treatment in cancer [25]. Consistent with the previous observations, our discovery of GRIK1 as a HBV-related HCC susceptibility gene has suggested the importance of glutamate signaling in HBV-related HCC development, and, although still speculative, has highlighted the glutamate signaling pathway as a potentially novel target for the treatment of HCC.

We also assessed the previously reported susceptibility locus KIF1B on 1p36.22 (rs17401966) for HBV-related HCC [6]. Our GWAS discovery analysis did reveal the consistent result for the association at rs17401966, but the strength of association in our GWAS discovery sample (OR = 0.90) is much weaker than the previously reported one (OR = 0.61) (Table S8). SNP imputation in our GWAS discovery samples did not reveal any stronger association than the association at rs17401966 within the LD region surrounding the 1p36.22 locus (Figure S6A).

Previous studies have clearly shown the existence of subpopulation structure of Chinese Han population along the north-south axis, and further demonstrated that geographic matching can be used as a good surrogate for genetic matching, and PCA-based correction is very effective in controlling the inflation effect of population stratification [26]. In the current study, all the cases and controls were matched by their geographic origin of residence. Moreover, the GWAS discovery samples were from central and southern China, while all the validation and replication samples were from central China. Our PCA analysis indicates that while there was mild population stratification in the sample of southern China, the cases and controls from central China were well matched without any indication of population stratification. In our study, the PCA-based correction was used in the GWAS analysis, and all the validation and replication analyses were from central China. Therefore, our findings should be free of adverse effect of population stratification in Chinese population.

In conclusion, the current GWAS identified two biologically plausible, novel loci on 6p21.3 and 21q21 for HBV-related HCC. These findings highlight the importance of HLA-DQ/DR molecules and glutamate signaling in the development of HBV-related HCC.

Table 2. Summary of the association results of five imputed HLA alleles in the GWAS discovery samples.

<table>
<thead>
<tr>
<th>CHR</th>
<th>HLA-allele</th>
<th>position</th>
<th>OR*</th>
<th>P*</th>
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<tr>
<td>6</td>
<td>HLA_DQA1_0301</td>
<td>32716284</td>
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Conditional on HLA_DRB1_0405

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Conditional on HLA_DRB1_0405 and HLA_DRB1_0901

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Conditional on the five HLA alleles

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Conditional on rs9272105

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*Adjusted by the first principal component.

doi:10.1371/journal.pgen.1002791.t002

Methods

Patient samples

The genome-wide discovery analysis was performed by genotyping 731,442 SNPs in 1,575 HBV positive HCC patients.
GWAS and Hepatocellular Carcinoma

(A)

Plotted SNPs

Combined $P = 1.13 \times 10^{-19}$

(B)

Plotted SNPs

Combined $P = 1.86 \times 10^{-08}$
and 1,490 HBV positive controls derived from two independent case-control cohorts of 500 cases and 500 controls from Central China (Shanghai) and 1,075 cases and 990 controls from Southern China (Guangdong). The first stage validation samples included 2,112 HBV-positive cases and 2,208 HBV-positive controls recruited from Jiangsu. The second stage validation samples consisted of 1,021 HBV-positive cases and 1,491 HBV carriers recruited from Shanghai. The replication samples of 1,298 HBV-positive cases and 1,026 HBV carriers were recruited from Central China (Shanghai and Jiangsu). (Table S1 and Figure 1) All the samples are Han Chinese and partially participated in the previously published studies [27,28]. The diagnosis of HCC was confirmed by a pathological examination and/or α-fetoprotein elevation (>400 ng/ml) combined with imaging examination (Magnetic resonance imaging, MRI and/or computerized tomography, CT). Because HCV infection is rare in Chinese, we excluded HCC with HCV infection. Cancer-free HBV+ control subjects from central China were recruited from those receiving routine physical examinations in local hospitals or those participating in the community-based screening for the HBV/HCV markers and frequency-matched for age, gender, and geographic regions to each set of the HCC patients. Almost all these community-based controls are asymptomatic HBV carriers. Similarly, cancer-free control subjects from southern China are all HBV+ and 408 of them were asymptomatic HBV carriers and 521 were symptomatic chronic hepatitis B patients. All the HBV+ controls were positive for both HBsAg and antibody to hepatitis B core antigen (anti-HBc), and negative for anti-HCV.

We also recruited a HBV natural clearance cohort from Jiangsu Province (Zhangjiagang and Changzhou cities) through a population based screening for the HBV/HCV markers in 2004 and 2009, respectively (38,142 persons). Subjects with HBV natural clearance were negative for HBsAg and anti-HCV, positive for both antibody to hepatitis B surface antigen (anti-HBs) and anti-HBc. About 9,610 subjects with HBV natural clearance were identified. No history of hepatitis B vaccination was reported for these people. Then, we randomly selected 1,344 HBV natural clearance people without self-reported history of cancer in the current study. The age for the 1,344 people were 52.6 ± 10.2 years, and 217 (16.2%) were females.

We collected smoking and drinking information through interviews. Those who had smoked an average of less than 1 cigarette per day and less than 1 year in their lifetime were defined as nonsmokers; otherwise, they were considered as smokers. Individuals were classified as alcohol drinkers if they drank at least twice a week and continuously for one year during their lifetime; otherwise, they were defined as nondrinkers. At recruitment, the marker SNPs of the associations are shown in purple, and the $r^2$ values of the rest SNPs with the marker one are indicated in different colors based on the strengths. The annotated genes within the critical region of the association are shown in bottom.

**SNPs selection and genotyping in validation phases**

SNPs for the first stage validation were selected based on the following criteria: (i) not mapped on autosomal chromosomes; (ii) had a call rate <95% in all GWA samples or in either of Central cohort study or Southern study samples; (iii) had minor allele frequency (MAF) <0.05 in either of Central cohort study or Southern study samples; and (iv) genotype distributions deviated from those expected by Hardy-Weinberg equilibrium ($P<1\times10^{-5}$ in either of Central cohort study or Southern study samples). We detected population outliers and stratification using a principal component analysis (PCA) based method. After removing MHC SNPs on chromosome 6 from 25–37 Mb, PCA was performed by using common autosomal SNPs with low LD ($r^2<0.2$) in the reference samples of the HapMap project (YRI (n = 90), CEU (n = 90), CHB (n = 45) and JPT (n = 44)) as the internal controls and our 3,010 participants of the GWAS discovery samples (after removal of samples with low call rates, ambiguous gender, and familial relationships). Projection onto the multidimensional scaling axes is shown in Figure S2. 7 outliers (more than 6 standard deviations) were identified and excluded. Finally, 523,663 autosomal SNPs in 1,538 cases and 1,465 controls, consisting of 480 cases and 484 controls from Central China and 1,058 cases and 981 controls from Southern China, were retained for association testing (Table S1).

**Quality control in GWA Scan**

We performed standard quality control on the raw genotyping data to filter both unqualified samples and SNPs. The samples with overall genotype completion rates <95% were excluded from further analysis (26 subjects). Eight subjects were excluded as they showed discrepancy between the recorded and genetically inferred genders. An additional 21 duplicates or probable familial relatives were excluded based on the IBD analysis implemented in PLINK (all PIHAT>0.25). SNPs were excluded when they fit the following criteria: (i) not mapped on autosomal chromosomes; (ii) had a call rate <95% in all GWA samples or in either of Central cohort study or Southern study samples; (iii) had minor allele frequency (MAF) <0.05 in either of Central cohort study or Southern study samples; and (iv) genotype distributions deviated from those expected by Hardy-Weinberg equilibrium ($P<1\times10^{-5}$ in either of Central cohort study or Southern study samples). We detected population outliers and stratification using a principal component analysis (PCA) based method. After removing MHC SNPs on chromosome 6 from 25–37 Mb, PCA was performed by using common autosomal SNPs with low LD ($r^2<0.2$) in the reference samples of the HapMap project (YRI (n = 90), CEU (n = 90), CHB (n = 45) and JPT (n = 44)) as the internal controls and our 3,010 participants of the GWAS discovery samples (after removal of samples with low call rates, ambiguous gender, and familial relationships). Projection onto the multidimensional scaling axes is shown in Figure S2. 7 outliers (more than 6 standard deviations) were identified and excluded. Finally, 523,663 autosomal SNPs in 1,538 cases and 1,465 controls, consisting of 480 cases and 484 controls from Central China and 1,058 cases and 981 controls from Southern China, were retained for association testing (Table S1).

**SNPs selection and genotyping in validation phases**

SNPs for the first stage validation were selected based on the following criteria: (i) SNP had $P_{\text{joint}}\leq1.0\times10^{-4}$ in the analysis of the combined GWA samples or either the Central China sample or the Southern China sample, and had a consistent association in the two participant studies, meaning that the ORs from the two samples are both either above or below 1; (ii) only SNP with the lowest $P$ value was selected when multiple SNPs showed a strong LD ($r^2\geq0.8$). As a result, a total of 39 SNPs were included in the first stage validation. 3 SNPs that were significantly associated with HCC risk in the first validation stage were further genotyped in the second stage validation samples. Genotyping in the two validation samples were done by using the iPLEX platform (Sequenom) or the TaqMan assays (Applied Biosystems). The primers and probes were available upon request (Table S9). Laboratory technicians who performed genotyping experiments were blinded to case/control status. For TaqMan assay, ten percent of random samples were done by using the iPLEX platform (Sequenom) or the TaqMan assays (Applied Biosystems). The primers and probes were available upon request (Table S9).

**Statistical analysis**

Population structure was evaluated by the PCA in the software package EIGENSTRAT 3.0 [26]. PCA revealed one significant ($P<0.05$) eigenvector which was included in the logistic regression with other covariates of age, gender, smoking and drinking status for both the genome-wide discovery analysis and the joint analysis of the combined discovery and replication samples. Ancestral origin checking by PCA confirmed all the samples to be Han Chinese and further demonstrated moderate genetic stratification.

**Figure 1. Regional plots of the susceptibility loci at rs9272105 on 6p and rs455804 on 21q.** The association result ($-\log_{10}P$) is shown against the map position for each SNP within the region of 400 kb surrounding the validated association. The marker SNPs of the associations are shown in purple, and the $r^2$ values of the rest SNPs with the marker one are indicated in different colors based on the strengths.
between the cases and the controls of the Southern cohort (Figure S2). The genome-wide association analysis was therefore performed in logistic regression using PCA-based correction for population stratification and by treating the samples of two cohorts as independent studies. The genome-control inflation factor ($\hat{\lambda}_{GC}$) after adjustment by the first PC was calculated for the Central cohort samples ($\hat{\lambda}_{GC} = 1.013$), the Southern cohort samples ($\hat{\lambda}_{GC} = 1.003$) and the combined GWAS discovery samples ($\hat{\lambda}_{GC} = 1.012$). Consistently, the QQ plot of the observed $P$ values also showed a minimal inflation of genome-wide association results due to population stratification (Figure S3).

Statistical analyses were performed by using PLINK 1.07 [29] and R 2.11.1. The Manhattan plot of $-\log_{10}P$ was generated using Haploview (v4.1) [30]. Untyped genotypes were imputed in the GWAS discovery samples by using IMPUTE2 [31] and the haplotype information from the 1000 Genomes Project (ASN samples as the reference set) and HapMap3 (CHB and JPT samples as the reference samples). The regional plot of association was created by using an online tool, LocusZoom 1.1. $P$ value was two-sided, and OR presented in the manuscript was estimated by using additive model and logistic regression analyses if not specified.

To impute classical HLA alleles, we used 180 phased haplotypes from the HapMap CHB and JPT samples as our reference panel. This panel comprised dense SNP data and HLA allele types at 4-digit resolution for the HLA class I (HLA-A, B, C) and II (DQA1, DQB1 and DRB1) genes as previously described [32]. Genotypes, probability and allelic dosages were then imputed separately in the two discovery samples of Central and Southern Chinese using the BEAGLE program. Association testing was performed by using a logistic regression model on the best-guessed genotypes and allelic dosages. The results were checked for consistency between the two methods, and the results from best-guessed genotypes were presented.

Supporting Information

**Figure S1** The map of China. The regions of the sample collection were highlighted in red. (DOCX)

**Figure S2** Plots of principal components from the PCA for genetic matching. (A) a-b-c plot of the first two PCs from the PCA of GWAS (central and southern) samples and the HapMap individuals. (B) plots between the 1st–8th PCs, which derived from PCA of 964 Central samples. (C) plots between the 1st–8th PCs, which derived from PCA of 2039 Southern samples. (D) plots between the 1st–8th PCs, which derived from PCA of 3033 Central and Southern samples. (DOCX)

**Figure S3** Quantile-Quantile plot. (A) QQ plot of Central Samples. (B) QQ plot of Southern Samples. (C) QQ plot of combined GWAS Samples. (DOCX)

**Figure S4** Manhattan plot of the genome-wide $P$ values of association. Association was assessed using logistic regression analysis with adjustment for the first principal components of population stratification. (A) Manhattan plot for Central Samples. (B) Manhattan plot for Southern Samples. (C) Manhattan plot for combined GWAS Samples. (DOCX)

**Figure S5** Workflow of the study. (DOCX)

**Figure S6** Regional plots of 4 interested regions. (DOCX)

**Table S1** Summary description of the samples used in this study. (DOCX)

**Table S2** Summary of all the SNPs with $P$ values less than $10^{-4}$. (DOCX)

**Table S3** A: Associations of the 39 fast-track replicated SNPs from the GWAS scan. B: Associations of 39 SNPs in GWAS scan and validations. (DOCX)

**Table S4** Adjusted and stratified analyses of the 2 validated SNPs. (DOCX)

**Table S5** Results of all the HLA alleles that have been successfully imputed after quality controls. (DOCX)

**Table S6** The haplotype analysis of the two DRB1 alleles and rs9272105. (DOCX)

**Table S7** A: Association of two SNPs in the subjects with asymptomatic and symptomatic HBV infection from the southern Chinese cohort. B: Association of rs9272105 and rs455804 in asymptomatic HBV carriers and HBV natural clearance samples from central China. (DOCX)

**Table S8** Association results of rs17401966, rs2596542, rs1012068, and rs9275572 in the GWAS samples. (DOCX)

**Table S9** Information of primers and probes for the 39 fast-track replicated SNPs of the GWAS scan. (DOCX)

**Author Contributions**

Study concept and design: Weiping Zhou, Shengping Li, Jianjun Liu, Zhibin Hu, Yongyong Shi, Ji Qian. Subject recruitment and sample preparation: Weiping Zhou, Yuan Yang, Ji Qian, Jingmin Yang, Feng Shen, Jiamei Yang, Yi Wang, Lehua Shi, Yequn Yan, Shuqun Cheng, Jiaye Yang, Aijun Li, Li Jin (Shanghai samples); Shengli Li, Shuhong Li, Jun Wang, Boping Zhou, Weihua Jia, Ying Zhang, Xinchun Chen, Guofang Zhang, Xianrong Luo, Hongbo Qin, Minshan Chen (Guangzhou samples); Zhibin Hu, Li Liu, Shandong Pan, Minjie Chu, Xiangjun Zhai, Jibin Liu, Hua Wang (Jiangsu samples). GWAS data processing: Zhiqiang Li, Jiawei Shen, Weiping Zhou, Xiaohua Jia, Yong Zhang, Xinchun Chen, Guofang Zhang, Zhibin Hu, Li Liu, Shandong Pan, Minjie Chu (Validation stages). Analysis and interpretation of data: Weiping Zhou, Shengping Li, Jianjun Liu, Zhibin Hu, Yongyong Shi, Ji Qian, Yuan Yang, Juncheng Dai, Wanting Zhao. Drafting of the manuscript: Jianjun Liu, Zhibin Hu. Critical revision of the manuscript for important intellectual content: Weiping Zhou, Shengping Li, Jianjun Liu, Zhibin Hu, Yongyong Shi, Ji Qian. Administrative, technical, or material support: Hongbing Shen, Lin He, Hongyang Wang, Yi-Xin Zeng, Mengchao Wu. Statistical analysis: Zhibin Hu, Yongyong Shi, Jin-Xin Bei, Dongxin Lin, Hongbing Shen, Lin He, Hongyang Wang, Yi-Xin Zeng, Mengchao Wu. Study supervision: Weiping Zhou, Shengping Li, Jianjun Liu, Zhibin Hu, Yongyong Shi, Ji Qian.

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**GWS and Hepatocellular Carcinoma**

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**Table S10** Summary description of the samples used in this study. (DOCX)

**Table S11** Summary of all the SNPs with $P$ values less than $10^{-4}$. (DOCX)

**Table S12** Adjusted and stratified analyses of the 2 validated SNPs. (DOCX)

**Table S13** Results of all the HLA alleles that have been successfully imputed after quality controls. (DOCX)

**Table S14** The haplotype analysis of the two DRB1 alleles and rs9272105. (DOCX)

**Table S15** A: Association of two SNPs in the subjects with asymptomatic and symptomatic HBV infection from the southern Chinese cohort. B: Association of rs9272105 and rs455804 in asymptomatic HBV carriers and HBV natural clearance samples from central China. (DOCX)

**Table S16** Association results of rs17401966, rs2596542, rs1012068, and rs9275572 in the GWAS samples. (DOCX)

**Table S17** Information of primers and probes for the 39 fast-track replicated SNPs of the GWAS scan. (DOCX)

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**Author Contributions**

Study concept and design: Weiping Zhou, Shengping Li, Jianjun Liu, Zhibin Hu, Yongyong Shi, Ji Qian, Yuan Yang. Subject recruitment and sample preparation: Weiping Zhou, Yuan Yang, Ji Qian, Jingmin Yang, Feng Shen, Jiamei Yang, Yi Wang, Lehua Shi, Yequn Yan, Shuqun Cheng, Jiaye Yang, Aijun Li, Li Jin (Shanghai samples); Shengli Li, Shuhong Li, Jun Wang, Boping Zhou, Weihua Jia, Ying Zhang, Xinchun Chen, Guofang Zhang, Xianrong Luo, Hongbo Qin, Minshan Chen (Guangzhou samples); Zhibin Hu, Li Liu, Shandong Pan, Minjie Chu, Xiangjun Zhai, Jibin Liu, Hua Wang (Jiangsu samples). GWAS data processing: Zhiqiang Li, Jiawei Shen, Weiping Zhou, Xiaohua Jia, Yong Zhang, Xinchun Chen, Guofang Zhang, Zhibin Hu, Li Liu, Shandong Pan, Minjie Chu (Validation stages). Analysis and interpretation of data: Weiping Zhou, Shengping Li, Jianjun Liu, Zhibin Hu, Yongyong Shi, Ji Qian. Administrative, technical, or material support: Hongbing Shen, Lin He, Hongyang Wang, Yi-Xin Zeng, Mengchao Wu. Statistical analysis: Zhibin Hu, Yongyong Shi, Jin-Xin Bei, Dongxin Lin, Hongbing Shen, Lin He, Hongyang Wang, Yi-Xin Zeng, Mengchao Wu. Study supervision: Weiping Zhou, Shengping Li, Jianjun Liu, Zhibin Hu, Yongyong Shi, Ji Qian.
References