Supplementary Materials

Lalu Muhammad Irham [1,2], Wan-Hsuan Chou [1,3], Yu-Shiuan Wang [4,5], Wirawan Adikusuma[1,6], Henry Sung-Ching Wong [1,3], Dyah Aryani Perwitasari [2], Wan-Chen Huang [4], Ben-Kuen Chen [7,8,*], Hwai-I Yang [9,10*], Wei-Chiao Chang [1,3,11,12,*]

[1] Department of Clinical Pharmacy, School of Pharmacy, College of Pharmacy, Taipei Medical University, Taipei 11031, Taiwan
[2] Faculty of Pharmacy, University of Ahmad Dahlan, Yogyakarta 55164, Indonesia
[3] Master Program for Clinical Pharmacogenomics and Pharmacoproteomics, School of Pharmacy, Taipei Medical University, Taipei 11031, Taiwan
[4] Institute of Cellular and Organismic Biology, Academia Sinica, Taipei 115, Taiwan
[5] Ph.D Program in Clinical Drug Development of Chinese Herbal Medicine, College of Pharmacy, Taipei Medical University, Taipei 11031, Taiwan

[6] Departement of Pharmacy, University of Muhammadiyah Mataram, Mataram 83127, Indonesia
[7] Ph.D. Program for translational Medicine, College of Medical Science and Technology, Taipei Medical University, Taipei 11031, Taiwan
[8] Department of Pharmacology, College of Medicine, National Cheng Kung University, Tainan 701, Taiwan
[9] Genomics Research Center, Academia Sinica, Taipei 115, Taiwan
[10] Institute of Clinical Medicine, National Yang-Ming University, Taipei 112, Taiwan
[11] Integrative Therapy Center for Gastroenterologic Cancers, Wan Fang Hospital, Taipei Medical University, Taipei 116, Taiwan
[12] Department of Medical Research, Shuang Ho Hospital, Taipei Medical University, New Taipei City 23561, Taiwan
* Correspondence: bkchen58@mail.ncku.edu.tw (B.-K.C.); hiyang@gate.sinica.edu.tw (H.-I.Y.); wcc@tmu.edu.tw (W.-C.C.)

Contents:

Supporting Information Tables

Supporting Information Figures

Supplementary Table 1. Association between *STIM1* haplotypes and hepatocellular carcinoma (HCC) in hepatitis B virus (HBV) patients

Haplotype	Frequency		*p* value	q value
	Case[a]	Control[b]		
Block 3: rs11030209/ rs10835270/ rs11030210/ rs7929653/ rs6578418/ rs10835272/ rs10742189				
A/G/G/G/C/A/A	0.231	0.226	0.7364	0.8426
A/G/G/A/C/G/A	0.168	0.158	0.5272	0.8426
C/T/G/A/C/G/C	0.159	0.151	0.5677	0.8426
A/G/G/G/C/G/A	0.126	0.131	0.7349	0.8426
A/G/G/G/C/A/C	0.061	0.072	0.2828	0.8426
C/T/G/G/C/G/C	0.057	0.042	0.0836	0.8426
A/G/T/A/G/A/C	0.032	0.027	0.4395	0.8426
A/G/G/A/C/A/A	0.021	0.028	0.3342	0.8426
A/G/G/G/C/G/C	0.021	0.026	0.4307	0.8426
C/T/G/A/C/A/C	0.013	0.019	0.3192	0.8426
A/G/G/A/C/G/C	0.016	0.014	0.7236	0.8426
A/G/G/A/C/A/C	0.006	0.013	Reference	
Block 6: rs7924984/ rs2412338/ rs10835402/rs11030472/ rs11030478/ rs11030486/ rs727152/rs2959081				
G/G/T/A/G/C/A/T	0.039	0.024	**0.0163**	0.3097
A/T/C/G/G/C/A/T	0.224	0.196	0.0711	0.8426
A/T/T/A/A/T/A/T	0.195	0.192	0.8426	0.8426
G/G/T/A/G/C/G/T	0.095	0.103	0.5102	0.8426
A/T/C/A/G/C/A/T	0.077	0.084	0.565	0.8426
G/G/T/A/G/C/A/C	0.364	0.388	Reference	
Block 7: rs11030639/ rs7116520/ rs1442725/ rs11030841/rs4910882				
A/G/C/G/G	0.366	0.413	**0.015**	0.3000
G/A/C/G/G	0.330	0.305	0.1734	0.8426
A/A/C/A/A	0.223	0.208	0.3784	0.8426
A/A/T/A/A	0.059	0.051	0.3147	0.8426
A/A/C/G/G	0.010	0.013	Reference	

[a] HBV with HCC. [b] HBV without HCC. Significant ($p<0.05$) values are in **bold.** The q value is the false discovery rate (FDR) estimation for multi-testing.

Supplementary Table 2. Association between *ORAI1* haplotypes and hepatocellular carcinoma (HCC) in hepatitis B virus (HBV) patients

Haplotype	Frequency		*p* value	q value
	Case[a]	Control[b]		
Block 1: rs6486795/ rs74936888/ rs3741595				
T/T/C	0.670	0.621	**0.013**	0.2990
C/T/T	0.238	0.269	0.073	0.8426
C/C/C	0.058	0.079	0.047	0.8426
C/T/C	0.035	0.030	Reference	

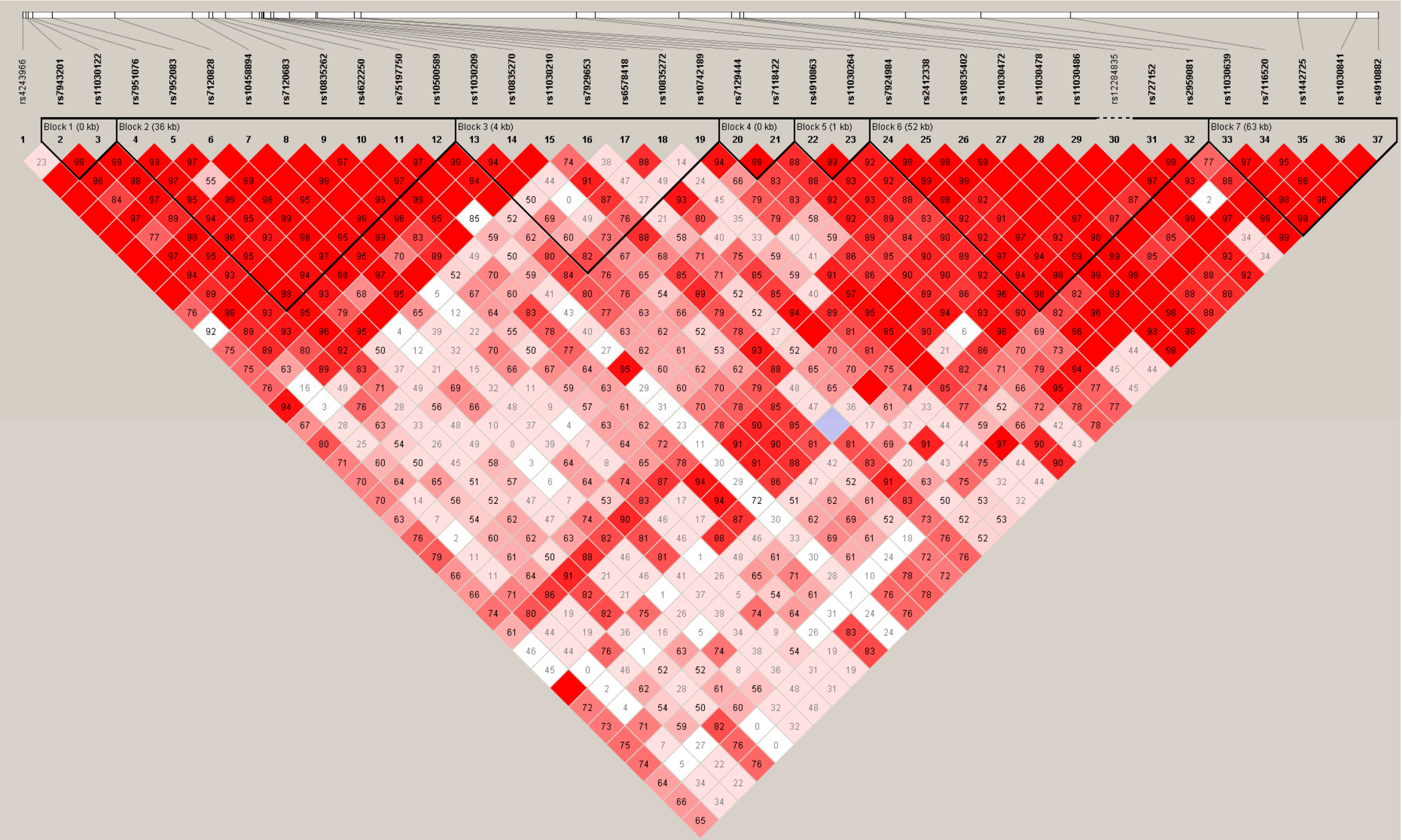
[a] HBV with HCC. [b] HBV without HCC. Significant (p<0.05) values are in **bold.** The q value is the false discovery rate (FDR) estimation for multi-testing.

Supplementary Table S3. Expression Quantitative trail loci (eQTL) results of The SNP from Genotype-tissue expression (GTEx).

SNP ID	Gencode ID (ENSG00000-)	Gene symbol	p value	Effect size	Tissue	Actions
rs7116520	167323.11	*STIM1*	1.1e-9	-0.18	Nerve - Tibial	GG>AG>AA
	167323.11	*STIM1*	2.0e-8	-0.22	Heart-Left Ventricle	GG>AG>AA
rs6578418	NA	NA	NA	NA	NA	NA
rs11030472	NA	NA	NA	NA	NA	NA
rs6486795	276045.2	*ORAI1*	1.30E-17	0.22	Whole Blood	CC>CT>TT
	276045.2	*ORAI1*	9.90E-16	0.29	Esophagus - Mucosa	CC>CT>TT
	276045.2	*ORAI1*	3.30E-13	0.23	Thyroid	CC>CT>TT
	276045.2	*ORAI1*	7.60E-08	0.24	Stomach	CC>CT>TT
	276045.2	*ORAI1*	4.50E-07	0.25	Pancreas	CC>CT>TT
	276045.2	*ORAI1*	4.80E-07	0.11	Muscle - Skeletal	CC>CT>TT
	276045.2	*ORAI1*	1.5E-06	0.21	Colon - Transverse	CC>CT>TT
	276045.2	*ORAI1*	0.000029	0.19	Esophagus - Gastroesophageal Junction	CC>CT>TT
	276045.2	*ORAI1*	0.000058	0.17	Heart - Atrial Appendage	CC>CT>TT
	276045.2	*ORAI1*	0.00016	0.13	Esophagus - Muscularis	CC>CT>TT

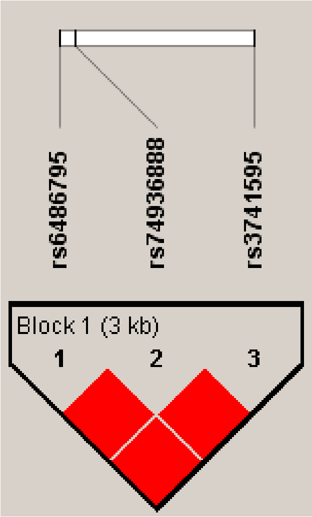
Source: Expression Quantitative trail loci (eQTL) obtained from https://gtexportal.org/home, NA: Not Available

Supplementary Figure



Based on D-prime, D'

Supplementary Figure 1. Linkage disequilibrium plot of the *STIM1* gene.



Based on D-prime, D’

Supplementary Figure 2. Linkage disequilibrium plot of the *ORAI1* gene.

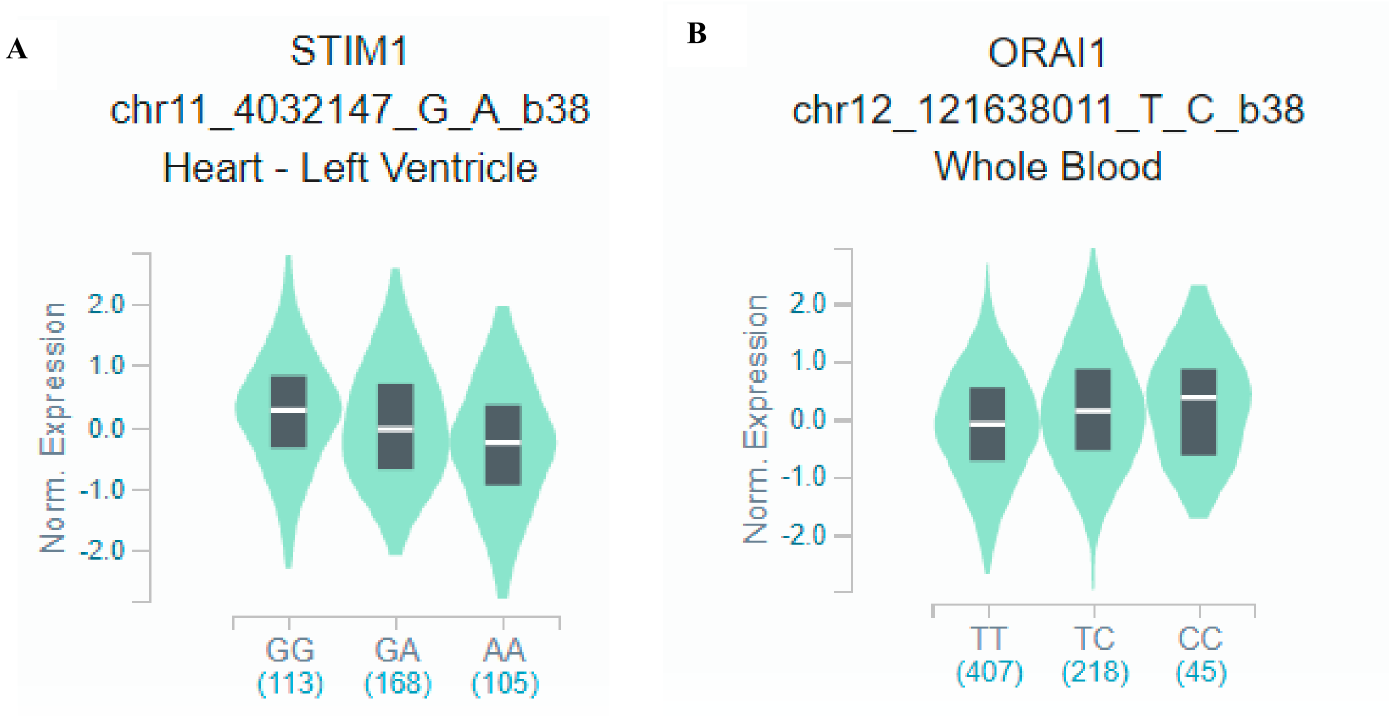


Figure S3. Correlation between genotype and expression in tissue determined by *Cis*-expression quantitative trait loci (*cis*-eQTLs). Figure **A** the expression of *STIM1* between rs7116520 Homozygous (GG), Heterozygous (AG), and Homozygous (AA) in heart-left ventricle tissue. Figure **B** the expression of *ORAI1* between rs6486795 Homozygous(CC), Heterozygous (TC) and Homozygous (TT) in whole blood.

.