Supplementary Tables

Table S1. Linkage disequilibrium between pairs of variation sites observed along the coding region of the *HFE* gene in patients and healthy control individuals.

POPULATION	SNP 1	SNP 2	*P* value
HH	rs1799945 (H63DC>G)	rs2071303 (IVS2(+4)T>C)	0.010
	rs1799945 (H63DC>G)	rs1800562 (C282YG>A)	0.041
	rs2071303 (IVS2(+4)T>C)	rs1800562 (C282YG>A)	0.034
HCV-IO^{+}	rs1799945 (H63DC>G)	rs2071303 (IVS2(+4)T>C)	< 0.001
	rs2071303 (IVS2(+4)T>C)	rs1800708 (IVS4(–44)T>C)	< 0.001
HCV-IO^{-}	rs1799945 (H63DC>G)	rs2071303 (IVS2(+4)T>C)	< 0.001
	rs2071303 (IVS2(+4)T>C)	rs1800708 (IVS4(–44)T>C)	< 0.001
HCC HCV-IO^{+}	rs1799945 (H63DC>G)	rs2071303 (IVS2(+4)T>C)	0.001
	rs2071303 (IVS2(+4)T>C)	rs1800708 (IVS4(–44)T>C)	0.001
HCC-IO$^{?}$	rs2071303 (IVS2(+4)T>C)	rs1800708 (IVS4(–44)T>C)	0.015
CTL	rs1799945 (H63DC>G)	rs2071303 (IVS2(+4)T>C)	< 0.001
	rs2071303 (IVS2(+4)T>C)	rs1800708 (IVS4(–44)T>C)	< 0.001
GLOBAL TEST	rs1799945 (H63DC>G)	rs2071303 (IVS2(+4)T>C)	< 0.001
	rs807209 (G>C)	rs1800562 (C282YG>A)	< 0.001

Patients with hereditary hemochromatosis (HH), hepatitis C presenting (HCV-IO+) or not (HCV-IO-) iron overload (IO), hepatocellular carcinoma (HCC) associated with HCV-IO^{+} (HCC HCV-IO^{+}) and associated with other causes and presenting no information regarding iron overload (HCC-IO$^{?}$), and healthy control individuals (CTL).

Table S2. Linkage disequilibrium among the H63DC>G (rs1799945), IVS2(+4)T>C (rs2071303) and C282YG>A (rs1800562) variations sites observed along the *HFE* gene in hereditary hemochromatosis (HH) and healthy control (CTL) individuals.

		OBSERVED FREQUENCY		EXPECTED FREQUENCY		STANDARDIZED VALUE OF DISEQUILIBRIUM (*D'*)		STANDARDIZED VALUE OF CORRELATION (r^2)	QUI^2 VALUE	*P* VALUE OF QUI^2
				IVS2(+4)T>C						
	H63DC>G	T	C	T	C	T	C			
	C	24	1	21.43	3.57	1.0000	-1.0000	0.7200	20.1600	**0.0000**
	G	**0**	3	**2.57**	0.43	-1.0000	1.0000	0.7200	20.1600	**0.0000**
				C282YG>A						
HH	**H63DC>G**	G	A	G	A	G	A			
	C	5	20	7.14	17.86	-1.0000	1.0000	0.3000	8.4000	**0.0038**
	G	3	**0**	0.86	2.14	1.0000	-1.0000	0.3000	8.4000	**0.0038**
				C282YG>A						
	IVS2(+4)T>C	G	A	G	A	G	A			
	T	4	20	6.86	17.14	-1.0000	1.0000	0.4267	11.6667	**0.0006**
	C	4	**0**	1.14	2.86	1.0000	-1.0000	0.4267	11.6667	**0.0006**
				IVS2(+4)T>C						
	H63DC>G	T	C	T	C	T	C			
	C	122	43	100.65	64.35	1.0000	-1.0000	0.3318	66.3559	**0.0000**
	G	**0**	35	**21.35**	13.65	-1.0000	1.0000	0.3318	66.3559	**0.0000**
				C282YG>A						
CTL	**H63DC>G**	G	A	G	A	G	A			
	C	156	9	157.57	7.42	-1.000	1.000	0.0100	1.9990	0.1574
	G	35	**0**	33.42	1.57	1.000	-1.000	0.0100	1.9990	0.1574
				C282YG>A						
	IVS2(+4)T>C	G	A	G	A	G	A			
	T	114	8	116.51	5.49	-0.7151	0.7151	0.0154	3.0811	0.0792

	C	77	1	74.49	3.51	0.7151	-0.7151	0.0154	3.0811	0.0792

Polymorphic sites were defined according to NCBI (http://www.ncbi.nlm.nih.gov) and Ensembl (http://www.ensembl.org) databases. Significant *P* values are shown in bold. Shaded cells are showing the pairs with higher LD.

Table S3. Linkage disequilibrium analyses encompassing the *HFE* gene (*HFE* allele, H63DC>G and C282YG>A) and classical and non-classical HLA loci.

LOCUS 1	***LOCUS 2***	***P* VALUE**	**STANDARD DEVIATION**
HLA-A	*HFE*	0.22	0.03
HLA-B	*HFE*	0.59	0.04
HLA-C	*HFE*	0.33	0.04
HLA-DRB1	*HFE*	0.11	0.02
HLA-DQB1	*HFE*	0.51	0.03
TNFa	*HFE*	0.22	0.03
TNFb	*HFE*	0.49	0.03
TNFc	*HFE*	0.65	0.01
TNFd	*HFE*	0.35	0.03
HLA-G 14pb	*HFE*	0.54	0.01
HLA-A	H63D	0.09	0.01
HLA-B	**H63D**	**0.03**	**0.00**
HLA-C	H63D	0.15	0.01
DRB1	H63D	0.51	0.02
DQB1	H63D	0.31	0.01
TNFa	H63D	0.26	0.01
TNFb	H63D	0.90	0.00
TNFc	H63D	0.27	0.00
TNFd	H63D	0.67	0.01
HLA-A	C282Y	0.31	0.01
HLA-B	C282Y	0.57	0.01
HLA-C	C282Y	0.91	0.00
DRB1	C282Y	0.96	0.00
DQB1	C282Y	0.82	0.00
TNFa	C282Y	0.80	0.01
TNFb	C282Y	0.66	0.00
TNFc	C282Y	0.26	0.00
TNFd	C282Y	0.89	0.00
H63D	C282Y	0.79	0.00

Alleles (ensemble of coding region single nucleotide polymorphisms); SNPs (H63DC>G and C282YG>A); Classical HLA (*HLA-A, -B, -C*) loci; Non-classical HLA class I (*HLA-G* 14*bp* INDEL), class III (*TNFa-e* microsatellites), and class II (*HLA-DRB1* and -*DQB1*) loci. Significant results are shown in bold.