

Figure S1 Expression of TP53 in hepatocellular carcinoma tissues by immunohistochemical staining.

Study participants	<ul style="list-style-type: none"> ○ HCC with dual exposure of HBV and AFB1 in Guangxi
Inclusion criteria	<ul style="list-style-type: none"> ○ 1. HCC with positive for hepatitis B surface antigen ○ 2. Epidemiology & clinical pathology data were complete ○ 3. TP53 249Ser mutation detection was successful
Exclusion criteria	<ul style="list-style-type: none"> ○ 1. Combined HCV infection ○ 2. Recurrence of HCC
Genome-wide association study	
Phase one	<ul style="list-style-type: none"> ○ 1. 165 mutation and 320 non-mutation cases were enrolled ○ 2. Genotyped using Illumina HumanExome BeadChip-12-1_A
Phase two	<ul style="list-style-type: none"> ○ 1. 180 mutation and 178 non-mutation cases were enrolled ○ 2. Genotyped using iPLEX Gold SNP typing technology
Quality control (QC)	<ul style="list-style-type: none"> ○ 1. Samples were excluded under the following conditions. <ul style="list-style-type: none"> (i) genotyping rate < 95%, (ii) ambiguous gender (iii) genome-wide identity-by-descent (IBD) > 0.1875 (iv) outliers in principal components analysis ○ 2. SNPs were removed under the following conditions. <ul style="list-style-type: none"> (i) genotype call rate < 95% (ii) P value in HWE < 1×10^{-6} (iii) MAF < 0.05
Expression quantitative trait loci (eQTL)	<ul style="list-style-type: none"> ○ Candidate SNP loci for eQTL analysis

Figure S2 Study flowchart.

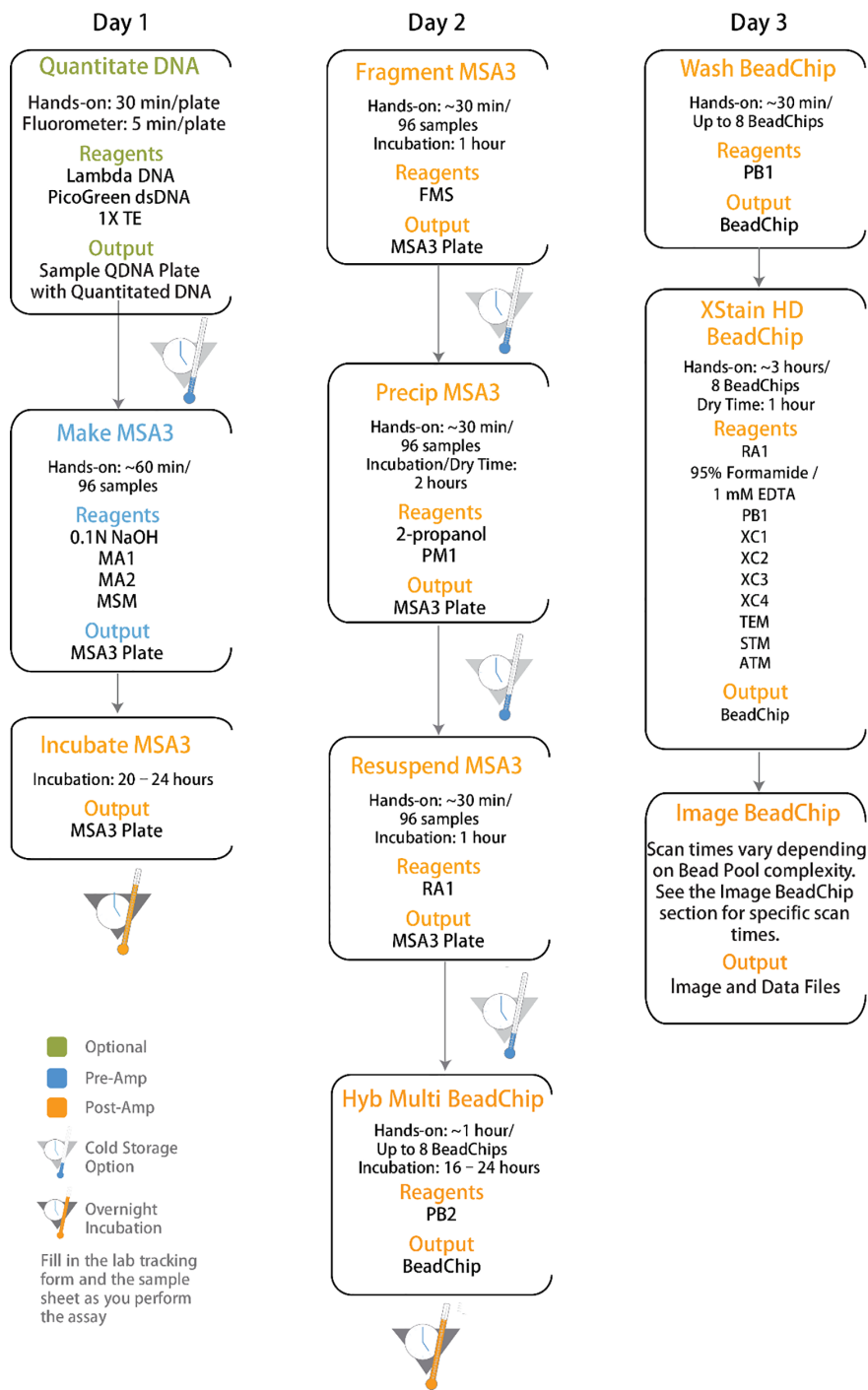


Figure S3 Genotyping procedure of BeadChip-12-1_A in the GWAS. GWAS, genome-wide association study.

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459 founders and 0 non-founders found
2637 heterozygous haploid genotypes; set to missing
Writing list of heterozygous haploid genotypes to [ chd_clean2.hh ]
Total genotyping rate in remaining individuals is 0.983547
0 SNPs failed missingness test < GENO > 1 >
0 SNPs failed frequency test < MAF < 0 >
After frequency and genotyping pruning, there are 21501 SNPs
After filtering, 159 cases, 300 controls and 0 missing
After filtering, 407 males, 52 females, and 0 of unspecified sex
Writing main association results to [ chd_clean2.assoc ]

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QC: Genotype failure rate vs heterozygosity across all individuals.

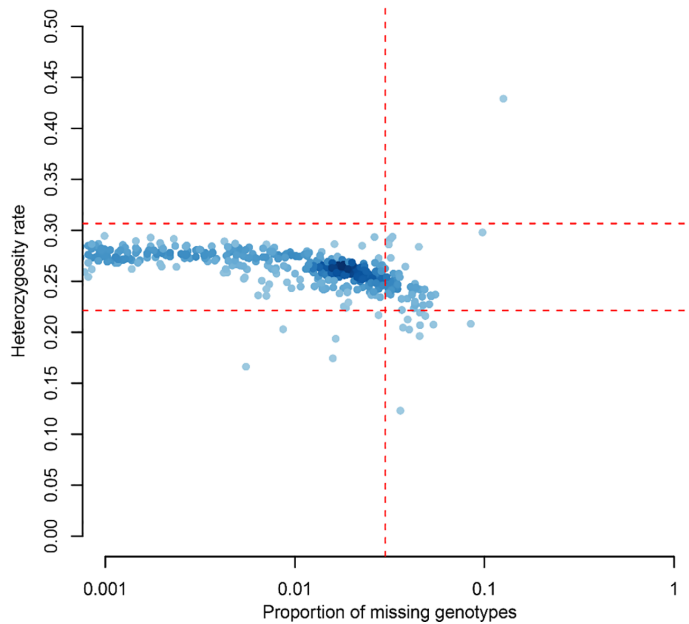


Figure S4 Quality control overview chart. (A) Overall overview of BeadChip-12-1_A after QC. (B) Genotype failure rate and heterozygosity across all individuals.

Table S1 Primers for TP53 R249S mutation detection

Gene	Primers	Sequences
TP53	Forward	5'-CTTGCCACAGGTCTCCCCAA-3'
	Reverse	5'-AGGGGTCAGAGGCAAGCAGA-3'

The following conditions were applied: 35 cycles of denaturation for 30 sec at 94 °C; 30 sec of annealing at 62 °C; and primer extension for 1 min at 72 °C.

Table S2 Associations between TP53 R249S mutation and whole-exon SNPs (TOP-29)

SNP	Chr	Position and gene	Number	HWE	MAF	P*	Mutation group	Non-mutation group	AF of mutation group	AF of non-mutation group
rs3758354	9	9:75764565_A/C_Intergenic	447	0.974	0.109	0.0000543	155	292	0.048	0.140
rs10001249	4	4:1535004_G/A_Intergenic	447	0.974	0.272	0.0000627	154	293	0.351	0.230
rs6104	18	18:61570529_C/G_ Nonsynonymous:SERPINB2	448	0.976	0.462	0.000168	155	293	0.626	0.491
rs4646450	7	7:99266318_G/A_ Intron:CYP3A5	453	0.987	0.328	0.000249	156	297	0.407	0.286
rs9895154	17	17:42267949_G/A_ Nonsynonymous:TMUB2	459	1.000	0.063	0.000261	159	300	0.104	0.042
rs6585827	10	10:124165615_G/A_ Intron:PLEKHA1	444	0.967	0.368	0.000270	151	293	0.715	0.589
rs7414489	1	1:64165243_C/A_Intergenic	444	0.967	0.452	0.000285	152	292	0.536	0.408
rs2288101	2	2:31135184_G/T_ Nonsynonymous:GALNT14	458	0.998	0.216	0.000285	159	299	0.283	0.181
rs9930984	16	16:77353973_G/T_ Nonsynonymous:ADAMTS18	437	0.952	0.126	0.000334	148	289	0.936	0.843
rs5951426	X	X:22291606_C/A_ Nonsynonymous:ZNF645	437	0.952	0.489	0.000460	154	283	0.620	0.452
rs75218075	3	3:167320010_T/C_ Nonsynonymous:WDR49	459	1.000	0.179	0.00047	159	300	0.120	0.210
rs1619714	11	11:115552918_A/G_ Intron:AP000797.3	443	0.965	0.409	0.000609	152	291	0.671	0.550
rs12012519	X	X:87190349_T/C_Intergenic	459	1.000	0.107	0.000648	159	300	0.170	0.073
rs11901030	2	2:40998751_A/G_Intergenic	451	0.983	0.269	0.000728	156	295	0.340	0.232
rs11640912	16	16:77359919_A/T_ Nonsynonymous:ADAMTS18	443	0.965	0.138	0.000749	151	292	0.921	0.832
rs714106	19	19:42083849_C/A_ Nonsynonymous:CEACAM21	453	0.987	0.373	0.000783	156	297	0.551	0.667
rs3745936	19	19:42092815_T/A_Essential_ Splice_Site:CEACAM21	437	0.952	0.365	0.000798	149	288	0.557	0.675
rs893817	15	15:74229065_G/A_ Intron:LOXL1	457	0.996	0.479	0.000832	158	299	0.405	0.518
rs11023787	11	11:15952294_C/T_Intergenic	447	0.974	0.497	0.000999	155	292	0.571	0.457
rs55752830	11	11:124947396_A/G_ Nonsynonymous:SLC37A2	452	0.985	0.108	0.00109	156	296	0.154	0.084
rs2056822	19	19:15739597_A/C_ Exon:CYP4F8	444	0.967	0.274	0.00139	149	295	0.792	0.693
rs3812629	10	10:75407290_G/A_ Nonsynonymous:SYNPO2L	453	0.987	0.205	0.00154	156	297	0.141	0.239
rs34051490	16	16:20966362_T/C_ Nonsynonymous:DNAH3	442	0.963	0.181	0.00154	155	287	0.126	0.211
rs8022091	14	14:70655751_A/C_ Utr5:SLC8A3	437	0.952	0.360	0.00155	148	289	0.561	0.680
rs1442801	15	15:98768182_C/T_Intron:CTD- 2544M6.1	449	0.978	0.296	0.00161	155	294	0.639	0.738
rs922948	3	3:69442637_G/A_ Intron:FRMD4B	451	0.983	0.369	0.00174	155	296	0.700	0.595
rs10842496	12	12:25311489_G/T_ Nonsynonymous:CASC1	453	0.987	0.171	0.00177	155	298	0.226	0.143
rs117866676	12	12:123342706_C/T_ Nonsynonymous:HIP1R	457	0.996	0.053	0.00183	157	300	0.083	0.037
rs12192544	6	6:46620252_C/G_ Nonsynonymous:CYP39A1	459	1.000	0.149	0.00294	159	300	0.195	0.125

*, adjusted for age, sex, race, smoking status, and drinking status. SNP, single nucleotide polymorphism; Chr, chromosome; MAF, minor allele frequency; AF, allele frequency; HWE, Hardy-Weinberg equilibrium.

Table S3 Primers of candidate SNPs in the GWAS (TOP-29)

SNP	5' to 3'		Product (bp)	Tm (°C)
	Forward primer	Reverse primer		
rs10001249	GCCTGCCAGGAACATCAGTT	GTGGCGATTTCGGCGTTA	477	62
rs10842496	ATTACTGGTAGCTATGGGCTGAGA	TCTTGAAGAAAGGAGAACTGACACT	358	60
rs11023787	ATGGAAGCACATTCATTTGGG	AGGGCATTTCGACCGTGAG	332	60
rs11640912	TTTGATACAAGCAGCAATTTCTTCTG	TGAGTGAACAGTGGTAATGAAAAGAA	507	62
rs117866676	GTGGCCCATGGGTCATTCCAG	TCTGTAAACCTCCCCAAAAGGCAAGA	508	62
rs11901030	TTGTAAATGGCAGAGTTGAGTGTTG	CTTGTGCAGGGGAATGACG	556	63
rs12012519	AAGGCGTCAAAGGTCAGGAA	GCATCGGATATGCCATAGAGTG	315	60
rs12192544	TGTTCTAGCCCTGCACTTAAGAGT	CGCGCTGGCTGAGATTCAAAGA	495	62
rs1442801	CGTTATGGCTGTAGGCTGTTTG	GGCTCCAATTTCTTTGTTTTCC	291	60
rs1619714	GCCAGGGTGGTAGGAATGAG	GGGAGGCTGAGGTAGGACAA	398	60
rs2056822	ATCCCCAAAGGTGCCCTCCAT	AAGTCAGGCATCTGACAAGGCA	493	62
rs2288101	TTTCTCTCTTTCTGCTCATCAGA	TTGTTGTTCCAGACTCCTGCCCAA	505	62
rs34051490	ACCGTATCTTACTGGCAACCCTATC	GCTCTAAAACGTTGGGTCCATTGT	394	60
rs3745936	GCAGTGAATAACAGGAGGTGGTGA	GCCATAGGCCCATTCACCTTCC	502	62
rs3758354	ATGAGGAAGCTGTGGGGAGA	TGTTGCTGCTATTACCAGTGCC	793	62
rs3812629	ACCACATACTGTCCGCACG	CTCGCGAGCAGCGCATCT	496	60
rs4646450	ACAGGACCTCTATGCTGAAAATAT	GTGTCAATTCAACTGTCCGTGAT	635	60
rs55752830	GGGACATAGAATCTGGTAGGAGGCA	GGATGGCTGTGGGTGGATTGTA	536	60
rs5951426	TGAACAAGATGCCTGCTGGTGA	GCATATGTTGCACAGACGGTAGTGA	588	60
rs6104	TCTGAGAAGCATGGGCATGGA	GGGTAGCAGAAGTTGTTCCAGAAGAGCA	411	62
rs6585827	TCCTCTTCTCTCTCCCCTCT	ACCTTGCTAAGTTCAACACCGT	592	60
rs714106	GTGAAGAGACCTGCACCCAGGA	TGACAATCCTGCGTATGTGAAGCA	509	60
rs7414489	TGATTCCCTTCGCCTCAAG	ACCACAATAAACACCACTCCAAC	658	60
rs75218075	TCAGAGAAATTCAGATCCCAGAGTT	GGGACTATATGTTTTCTTTCACCTCAT	502	60
rs8022091	CAGCTGTCAGGGAGCTGCG	TCCCAGCTGATAGGGTGACGTT	493	60
rs893817	CCCGCTCAGCACATATTTCA	TCTCACAACCCCTACAGACGAT	377	62
rs922948	TGGAGGTGGGAGGTCAGTCA	CCTATTCAGCGTCTATTCTTTGG	420	62
rs9895154	GCCTGTTTGCCTTCTCATTCC	CTGCCACATTGACACCAAG	274	62
rs9930984	CCTTTGAACTAGAAGGACTGGAGTT	GCCACATACATTTTCTCTAGTGTCT	545	60

SNP, single nucleotide polymorphism; GWAS, genome-wide association study.

Table S4 Association results of SNPs in the replication study

SNP	Chr	Position and gene	Number	HWE	MAF	P	Mutation group	Non-mutation group	AF of mutation group	AF of Non-mutation group
rs8022091	14	14:70655751_A/C_Utr5:SLC8A3	248	0.961	0.347	0.0232	78	170	0.731	0.618
rs9930984	16	16:77353973_G/T_ Nonsynonymous:ADAMTS18	252	0.977	0.091	0.0255	78	174	0.962	0.885
rs75218075	3	3:167320010_T/C_ Nonsynonymous:WDR49	252	0.977	0.147	0.0295	79	173	0.095	0.171
rs11023787	11	11:15952294_C/T_Intergenic	251	0.973	0.478	0.0592	78	173	0.545	0.448
rs117866676	12	12:123342706_C/T_ Nonsynonymous:HIP1R	256	0.992	0.064	0.0858	79	177	0.095	0.051
rs12012519	X	X:87190349_T/C_Intergenic	258	1.000	0.118	0.130	80	178	0.163	0.098
rs6104	18	18:61570529_C/G_ Nonsynonymous:SERPINB2	255	0.988	0.410	0.154	78	177	0.468	0.384
rs3758354	9	9:75764565_A/C_Intergenic	250	0.969	0.142	0.167	78	172	0.109	0.157
rs5951426	X	X:22291606_C/A_ Nonsynonymous:ZNF645	258	1.000	0.426	0.223	80	178	0.519	0.598
rs11640912	16	16:77359919_A/T_ Nonsynonymous:ADAMTS18	249	0.965	0.094	0.259	79	170	0.930	0.894
rs893817	15	15:74229065_G/A_Intron:LOXL1	253	0.981	0.476	0.338	77	176	0.442	0.491
rs9895154	17	17:42267949_G/A_ Nonsynonymous:TMUB2	250	0.969	0.062	0.377	76	174	0.046	0.069
rs55752830	11	11:124947396_A/G_ Nonsynonymous:SLC37A2	252	0.977	0.099	0.414	79	173	0.082	0.107
rs10842496	12	12:25311489_G/T_ Nonsynonymous:CASC1	243	0.942	0.200	0.425	77	166	0.221	0.190
rs2056822	19	19:15739597_A/C_Exon:CYP4F8	247	0.957	0.292	0.487	76	171	0.730	0.699
rs3745936	19	19:42092815_T/A_Essential_ Splice_Site:CEACAM21	247	0.957	0.370	0.501	75	172	0.607	0.640
rs2288101	2	2:31135184_G/T_ Nonsynonymous:GALNT14	254	0.985	0.209	0.639	79	175	0.222	0.203
rs3812629	10	10:75407290_G/A_ Nonsynonymous:SYNPO2L	252	0.977	0.177	0.653	77	175	0.188	0.171
rs34051490	16	16:20966362_T/C_ Nonsynonymous:DNAH3	247	0.957	0.200	0.677	77	170	0.188	0.206
rs7414489	1	1:64165243_C/A_Intergenic	248	0.961	0.413	0.726	80	168	0.425	0.408
rs1442801	15	15:98768182_C/T_Intron:CTD- 2544M6.1	251	0.973	0.299	0.730	78	173	0.712	0.697
rs4646450	7	7:99266318_G/A_Intron:CYP3A5	257	0.996	0.296	0.785	79	178	0.304	0.292
rs714106	19	19:42083849_C/A_ Nonsynonymous:CEACAM21	257	0.996	0.181	0.860	80	177	0.825	0.816
rs922948	3	3:69442637_G/A_Intron:FRMD4B	250	0.969	0.418	0.862	79	171	0.576	0.585
rs11901030	2	2:40998751_A/G_Intergenic	252	0.977	0.266	0.917	78	174	0.263	0.267
rs10001249	4	4:1535004_G/A_Intergenic	255	0.988	0.235	0.938	80	175	0.238	0.234
rs1619714	11	11:115552918_A/G_ Intron:AP000797.3	249	0.965	0.392	0.987	78	171	0.609	0.608
rs12192544	6	6:46620252_C/G_ Nonsynonymous:CYP39A1	254	0.985	0.152	0.992	76	178	0.151	0.152
rs6585827	10	10:124165615_G/A_ Intron:PLEKHA1	245	0.950	0.400	1.000	75	170	0.600	0.600

*, adjusted for age, sex, race, smoking status and drinking status. SNP, single nucleotide polymorphism.

Table S5 Primers for MassARRAY genotyping

SNP	2ND-PCR	1ST-PCR	Product (bp)	UEP_SEQ	EXT1_SEQ	EXT2_SEQ
rs8022091	ACGTTGGATGCATTAAGCTGCCGGAAGAAG	ACGTTGGATGTGTCTCCCAGCTGATAGGGT	102	ATCTCCAAGCCTCCA	ATCTCCAAGCCTCCAC	ATCTCCAAGCCTCCAA
rs75218075	ACGTTGGATGTTGGACGGCTATTACTG	ACGTTGGATGTTGCCTTTGGAATCCCTATG	99	GGACACCCACTGGTT	GGACACCCACTGGTTC	GGACACCCACTGGTTT
rs7414489	ACGTTGGATGTTCCCAGCCTTGATCCATAC	ACGTTGGATGAAGACTCATGCCAGCATAAC	105	CCTTGCCTGCCTGCAC	CCTTGCCTGCCTGCAGG	CCTTGCCTGCCTGCACT
rs55752830	ACGTTGGATGACCTGATGAACATGCCGATG	ACGTTGGATGCCATCTGCTTTCAGACAAGG	115	ACGATGGCATAGGCGA	ACGATGGCATAGGCGAC	ACGATGGCATAGGCGAT
rs4646450	ACGTTGGATGGCCTTGTCCAGAATACACAC	ACGTTGGATGTAACAAAGAGCGAGAGGACG	103	ATCACTTCACGTGGCA	ATCACTTCACGTGGCAC	ATCACTTCACGTGGCAT
rs11023787	ACGTTGGATGATGGCATGTCCTACCTTCTG	ACGTTGGATGAACATTGAGGGAAGGGTCAG	99	TCCTACCTTCTGCTCCTT	TCCTACCTTCTGCTCCTC	TCCTACCTTCTGCTCCTT
rs3812629	ACGTTGGATGTTACAAGACCCTGCCTCAGG	ACGTTGGATGGAGTCTTAGGAGTCATAGGG	103	CGACACCTAAGACCCCCC	CGACACCTAAGACCCCCC	CGACACCTAAGACCCCCCT
rs34051490	ACGTTGGATGCCATTCTGGAGAATGCTGAC	ACGTTGGATGCGTTGGTCCATTGTTCTTC	100	GGAAACTTCTCTGATGGA	GGAAACTTCTCTGATGGAC	GGAAACTTCTCTGATGGAT
rs2288101	ACGTTGGATGTCTCTTCTCCCCAGGTATG	ACGTTGGATGACAAGGTGATGACTGACAGG	102	GGCCTTCACATACACCAG	GGCCTTCACATACACCAGC	GGCCTTCACATACACCAGA
rs12012519	ACGTTGGATGCTGTATTCTTGACAGAGGG	ACGTTGGATGAAGAAGGACCGCTTCTAGAC	90	ACAGGGTGCCTTTAATTTA	ACAGGGTGCCTTTAATTTAC	ACAGGGTGCCTTTAATTTAT
rs117866676	ACGTTGGATGAGCTTGCTCACGGCCTCCTG	ACGTTGGATGAGGCTGCTGGACGAGCAGTT	103	GGAGCGGCAGCAGCGCCCC	GGAGCGGCAGCAGCGCCCCA	GGAGCGGCAGCAGCGCCCCG
rs10001249	ACGTTGGATGATGTGAGATGCGCCCGAGA	ACGTTGGATGAAATCCACCTGGACGCGAAC	120	CACACCCAGGCCAGAAAAC	CACACCCAGGCCAGAAAACC	CACACCCAGGCCAGAAAACCT
rs1619714	ACGTTGGATGAAGGATGACTGTCTCTCTGG	ACGTTGGATGCAGTATCCTGCTTCCCTAAG	99	GGGTCGTTATGAGGATTCAA	GGGTCGTTATGAGGATTCAAC	GGGTCGTTATGAGGATTCAAT
rs922948	ACGTTGGATGTCTCCCTTAAAGAAGGTGGC	ACGTTGGATGAAAAGCATCCAAATGGGAGG	101	ACCATGATCCACTGGACTTCC	ACCATGATCCACTGGACTTCCC	ACCATGATCCACTGGACTTCT
rs3745936	ACGTTGGATGATCTGCTTTGTGGTCGATCC	ACGTTGGATGGGGTCAAGACCTCTTCTCTG	103	TCGTCAGAGTGTAGCAATTCC	TCGTCAGAGTGTAGCAATTCCA	TCGTCAGAGTGTAGCAATTCT
rs3758354	ACGTTGGATGCTCCAGAGAAATGACTCACC	ACGTTGGATGGTTTGTAAAGTAAAGTGGAGC	94	GCTGTTTCTAGAAGATGATGA	GCTGTTTCTAGAAGATGATGAG	GCTGTTTCTAGAAGATGATGAT
rs714106	ACGTTGGATGTGCATTTCCAGAACGTCACC	ACGTTGGATGGGTGAGATGCCTGTTCAATC	110	GGGAGGGACACGGGATACTACA	GGGAGGGACACGGGATACTACAC	GGGAGGGACACGGGATACTACAA
rs6585827	ACGTTGGATGCCATTACATTCTACCAAC	ACGTTGGATGCAGGTGCTAACAACCAGTTC	97	ACCACATACACATTTTATTTTCAT	ACCACATACACATTTTATTTTCATC	ACCACATACACATTTTATTTTCATT
rs1442801	ACGTTGGATGCTGATTTCTGAGCCAAGTCC	ACGTTGGATGCCCTGTAAAATCTAAATGC	111	ATTTATGAGCCAAGTCCACTGTT	ATTTATGAGCCAAGTCCACTGTTA	ATTTATGAGCCAAGTCCACTGTTG
rs11640912	ACGTTGGATGAATACGGCTAGAACCTGGAC	ACGTTGGATGTGAGCCCTTTGATTACTAAC	110	ACGTCTAGAACCTGGACAGAATA	ACGTCTAGAACCTGGACAGAATAA	ACGTCTAGAACCTGGACAGAATAT
rs893817	ACGTTGGATGAAACAGGTGAGGTGTGGACG	ACGTTGGATGAAATCTGTTCCCTCCTGCC	120	AAGTTGTGGACGAGCAATGGGAA	AAGTTGTGGACGAGCAATGGGAAA	AAGTTGTGGACGAGCAATGGGAAG
rs9930984	ACGTTGGATGGGTGGAATTCAGACATGTTT	ACGTTGGATGCTCCTGGATTTTCGATGCTTC	112	GGTTGAGAATATTATCCGGTGGTC	GGTTGAGAATATTATCCGGTGGTCC	GGTTGAGAATATTATCCGGTGGTCA
rs6104	ACGTTGGATGGTGGCAGATCATCTTTTCT	ACGTTGGATGAGCAGCACGCTTAGTTTTAG	120	TGCCTTTTATTTTTCGGCAGATTTT	TGCCTTTTATTTTTCGGCAGATTTT	TGCCTTTTATTTTTCGGCAGATTTG
rs5951426	ACGTTGGATGTAGCTTAGATGGTCCCTGTC	ACGTTGGATGGTTCGTCTCATATTGCTCC	100	CCATGTCTTGCAGTCTTTTAGGGAT	CCATGTCTTGCAGTCTTTTAGGGATG	CCATGTCTTGCAGTCTTTTAGGGATT
rs2056822	ACGTTGGATGATCAGCAGCCTTAACTTGCC	ACGTTGGATGAAGCCATAGGTGACCTTTC	108	CTCGATGACCCCTTCCGCTTCGACCC	CTCGATGACCCCTTCCGCTTCGACCCC	CTCGATGACCCCTTCCGCTTCGACCCA
rs10842496	ACGTTGGATGGCTGTATTTCAAGCCTTTCC	ACGTTGGATGACAGTGATCTATTCACTGAG	119	CCGTTCTTCTTCTCATATTTCAAAC	CCGTTCTTCTTCTCATATTTCAAACG	CCGTTCTTCTTCTCATATTTCAAACCT
rs12192544	ACGTTGGATGCCTTGCTCTGTTCTTACTCC	ACGTTGGATGCTCCAATCCAAGGAATCCAG	100	GACTGGCTCTGTTCTTACTCCTTCAGC	GACTGGCTCTGTTCTTACTCCTTCAGCC	GACTGGCTCTGTTCTTACTCCTTCAGCG
rs11901030	ACGTTGGATGTGGTTTCAGACACTAAAAGC	ACGTTGGATGGGACTGCAGTTTCTCAGAAC	106	AAAATCAACTAATGTTGACACTTAAAT	AAAATCAACTAATGTTGACACTTAAATA	AAAATCAACTAATGTTGACACTTAAATG
rs9895154	ACGTTGGATGTGAAACTGATCTACCAGGGC	ACGTTGGATGGTGAATCACACAGTTGTCGG	106	ATGCGACAAGACCCAGCCCGCACACTGCG	ATGCGACAAGACCCAGCCCGCACACTGCA	ATGCGACAAGACCCAGCCCGCACACTGCG

Table S6 Primers used in quantitative RT-PCR assays

Genes	Primers	Sequences
GAPDH	Forward	GTCAGCCGCATCTTCTTT
	Reverse	CGCCAATACGACCAAAT
ADAMTS18	Forward	GAGGTGCAGCAATGCTTCTAT
	Reverse	CAGCACACGTAGACACAGC
WDR49	Forward	CCATTATGAGTTGCCAGAAAGC
	Reverse	CCCACGCTGAGTTGGTTTT
SLC8A3	Forward	GACGACAAAGGGCTACTGGAA
	Reverse	AGCATTAGGAAGCAAGAGCGT