

SUPPLEMENTARY MATERIAL

Table S1. *OPRM1* primers used for allele-specific multiplex PCR of *OPRM1* 118A>G (dbSNP rs1799971) and IVS2+691G>C (dbSNP rs2075572).

PCR	Primer	Sequence (5' – 3')	Fragment size (bp)	[Primer] (μM)
First PCR Set A	μ EX1 FW	aaa gtc tcg gtg ctc ctg gct	420	0.10
	μ EX1 RV	tgg gag tta ggt gtc tct ttg ta		0.10
	μ INT2 FW	tag att tcc gta ctc ccc gaa	1020	0.20
	μ INT2 RV	cgc aag atc atc agt cca tag		0.20
Second PCR Set 1				
Common primer	μ EX1 RV	tgg gag tta ggt gtc tct ttg ta		0.25
Wild-type primers	μ 118 A FW	caa ctt gtc cca ctt aga tgg ca	267	0.25
Mutant-type primers	μ 118 G FW	caa ctt gtc cca ctt aga tgg cg		0.25
Second PCR Set 2				
Common primer	μ INT2 RV	cgc aag atc atc agt cca tag		0.15
Wild-type primers	μ 691G FW	gct ctg gtc aag gct aaa aat g	240	0.15
Mutant-type primers	μ 691C FW	gct ctg gtc aag gct aaa aat c		0.15

Table S2. Genotype and allele distributions for 118A>G and IVS2+691G>C polymorphisms among opioid-dependent participants.

Polymorphism	Genotype/ allele	N	Frequency (%)	95% CI		HWE P value *
				Lower limit	Upper limit	
118A>G						
Genotype (N = 148)	AA	53	35.8	28.1	43.5	1.000
	AG	71	48.0	40.0	56.0	
	GG	24	16.2	10.3	22.1	
Allele (N = 296)	A	177	59.8	54.2	65.4	
	G	119	40.2	34.6	45.8	
Dominant model	AA	53	35.8	28.1	43.5	
	AG + GG	95	64.2	56.5	71.9	
Recessive model	AA + AG	124	83.8	77.9	89.7	
	GG	24	16.2	10.3	22.1	
IVS2+691G>C						
Genotype (N = 148)	GG	1	0.7	0.0	2.0	0.078
	GC	48	32.4	24.9	39.9	
	CC	99	66.9	59.3	74.5	
Allele (N = 296)	G	50	16.9	12.6	21.2	
	C	246	83.1	78.8	87.4	
Dominant model	GG	1	0.7	0.0	2.0	
	GC + CC	147	99.3	98.0	100.0	
Recessive model	GG + GC	49	33.1	25.5	40.7	
	CC	99	66.9	59.3	74.5	

*Fisher's exact test evaluates the probability of genotype counts that are equally or less likely than the observed counts under HWE for biallelic locus

N, number of subject/allele; CI, confidence interval; HWE, Hardy-Weinberg equilibrium

Table S3. Haplotype and diplotype distributions for 118A>G and IVS2+691G>C polymorphisms among opioid-dependent patients.

Haplotype/diplotype	<i>N</i>	Frequency (%)	95% CI		
			Lower limit	Upper limit	
Haplotype ^a (N = 296)					
1. AC	132	44.6	38.9	50.3	
2. GC	114	38.5	33.0	44.0	
3. AG	45	15.2	11.1	19.3	
4. GG	5	1.7	0.2	3.2	
Diplotype (N = 148)					
1. AC/GC	48	32.4	24.9	39.9	
2. AC/AC	31	20.9	14.3	27.5	
3. AC/AG	22	14.9	9.2	20.6	
4. GC/AG	22	14.9	9.2	20.6	
5. GC/GC	20	13.5	8.0	19.0	
6. GC/GG	4	2.7	0.1	5.3	
7. AG/GG	1	0.7	0.0	2.0	

^aHaplotype patterns were constructed from the two polymorphisms of *OPRM1* (118A>G and IVS2+691G>C)

N, number of haplotype/diplotype; CI, confidence interval