

Table 1. Primer sequences for *HSD11B1* sequence variant screening

Primer		Sequence
HSD11B1_1	Forward	TGGACAAGAAAAACCTTGAAA
	Reverse	GGGACTACAGCATGTCAAAAC
HSD11B1_2	Forward	GGCTAGCACTGCCTGAGACT
	Reverse	TGGTCAGCTAAAATGCTGG
HSD11B1_3	Forward	GGCAACACACACACAAACATA
	Reverse	ACTTCTCTGCATGGAAACTGA
HSD11B1_4	Forward	GGCTAGCACTGCCTGAGACT
	Reverse	TGGTCAGCTAAAATGCTGG
HSD11B1_5	Forward	CCCACAGTGATTACGGAGTT
	Reverse	TGCATGGGTATGAGGATATGT
HSD11B1_6	Forward	GGCAACACACACACAAACATA
	Reverse	ACTTCTCTGCATGGAAACTGA
HSD11B1_7	Forward	GCAGTATAACTCCATGGGA
	Reverse	GAGGTCAAGGAGTTCAGCA
HSD11B1_8	Forward	CCTGACAGCTAAGTGGTTGATG
	Reverse	GGTGATTCTTCCACTCAGGAA
HSD11B1_9	Forward	GCAGGCCAGCAGTTGTAAAAT
	Reverse	CCCTGATCAATATAGGGCTTT

Table 2. Frequencies of *HSD11B1* gene polymorphisms in a Korean population

Locus	Position	rsSNP	Genotype			Frequency	Heterozygosity	HWE*
			C/C	C/R	R/R			
-19966C>T	Promoter	rs45441700	23	1	0	0.02	0.04	0.99
-19835G>A	Promoter	rs846908	693	578	111	0.29	0.41	0.53
-19609A>G	Promoter	rs701950	871	458	63	0.21	0.33	0.78
+1932 G insdel	Intron 4	novel	17	6	1	0.17	0.28	0.62
+27447G>C	Intron 5	rs932335	955	390	41	0.17	0.28	0.88
+27810C>T	Intron 6	rs13306422	1128	224	10	0.09	0.16	0.76
+29813G>A	Exon 7	rs6752	17	6	1	0.17	0.28	0.62
+30249T>C	3'downstream	novel	23	1	0	0.02	0.04	0.99

\* p values of deviation from HWE in normal subjects

C/C, C/R and R/R represent homozygotes for common allele, heterozygotes and homozygotes for rare allele, respectively.

Table 3. Sequences of amplifying, TaqMan probes including demand on Assay (AssayID), SnapShot primer and for genotyping of *HSD11B1* SNPs

Loci		Sequence or Assay ID
<i>-19835G&gt;A</i>	Forward	GCAAGCAAAAGTGTCAATTCAAAGAAC
	Reverse	GGAGAACACCATTAGACAGATTTGGA
	VIC	AATGTTCCACGTTGGCT
	FAM	ATGTTCCACATTGGCT
<i>-19609A&gt;G</i>		C____8887140_10
<i>+27447G&gt;C</i>		C____8887192_20
<i>+27810C&gt;T</i>	Forward	ATGCATGTGCCATGTTGGTG
	Reverse	ATGAGGTCAGGGAGTTCAGCA
	Extension	GGTATATCTCCTAATGCTATCCCTCCCCCTTCC