ORIGINAL ARTICLE

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Catalog of 668 SNPs detected among 31 genes encoding potential drug targets on the cell surface

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Abstract We have been publishing a series of detailed maps of single-nucleotide polymorphisms (SNPs) detected within the genomic loci of 145 genes encoding drug-metabolizing enzymes and transporters. As an addition to the maps reported earlier, we provide here high-density SNP maps of 31 genes encoding various receptors and adhesion molecules of medical importance. By examining a total of approximately 382 kb of genomic DNA encompassing these 31 genes, we identified 668 SNPs among 48 healthy Japanese individuals: 86 in 5' flanking regions, 27 in 5' untranslated regions, 45 in coding regions, 399 in introns, 47 in 3' untranslated regions, and 64 in 3' flanking regions. We also discovered 113 variations of other types. Of the 668 SNPs, 371 (55.5%) appeared to be novel, on the basis of comparisons with the dbSNP database of the National Center for Biotechnology Information (US) or with previous publications. The maps constructed in this study will serve as an additional resource for studies of complex genetic diseases and drug-response phenotypes to be mapped by linkage-disequilibrium analyses.

Key words Single-nucleotide polymorphism (SNP) · G-protein-coupled receptor · Adhesion molecule · Cytokine receptor · Tyrosine kinase receptor · Japanese population · High-density SNP map · Drug therapy

Introduction

Single-nucleotide polymorphisms (SNPs) can be useful markers for identifying genes responsible for common diseases and for establishing personalized medicine. In the near future, genome-wide SNP maps should enable investigators to profile DNA variations, in order to predict an individual's response to a particular drug therapy, for example (see a review by Roses 2000). Previously we focused on mapping genomic regions known to contain genes encoding various enzymes and transporters involved in the metabolism of drugs, and constructed integrated gene maps of 145 target regions containing SNPs and other types of variations (Iida et al. 2001a–d; 2002a–e; Saito et al. 2001a, b; 2002a–c; Sekine et al. 2001).

Plasma membrane-bound molecules that initiate a cascade of cellular response to diverse extracellular mediators are considered good potential targets for therapeutic drugs. One of the best-studied groups of drug receptors is the G-protein-coupled receptor (GPCR) family; modulation of GPCR function has already proven to be a successful approach to development of many commercialized therapeutic drugs. Indeed, according to recent estimates, GPCRs are the targets of 50% of all modern drugs (see a review by Howard et al. 2001).

To expand the genetic basis for drug development as well as, eventually, to enable clinicians to predict efficacy and adverse drug reactions, we explored SNPs among 31 genes encoding receptors and adhesion molecules of medical importance. As an addition to the maps reported earlier, the present report provides detailed maps of cell-surface drug targets; the new maps include a total of 688 SNPs and 113 variations of other types that we detected among 96 chromosomes from a Japanese population sample.

Subjects and methods

Samples of peripheral blood were obtained with written informed consent from 48 healthy Japanese volunteers for

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correspond to the left-most column of Table 1). Other types of variations, where present, are indicated below the maps

Cysteinyl leukotriene receptor 1 : genome size 5.1-kb

Cysteinyl leukotriene receptor 2: genome size 6.8-kb

ERBB2: V-erb-b2 erythroblastic leukemia viral oncogene homolog 2: genome size 32.5-kb

Folate receptor 1 : genome size 7.7-kb

Histamine receptor H1: genome size 13.3-kb

Histamine receptor H2: genome size 13.6-kb

Histamine receptor H3: genome size 9.6-kb

5-Hydroxytryptamine (serotonin) receptor 3A: genome size 19.2-kb

Fig. 1. Continued

Interferon alpha receptor 1: genome size 35.6-kb

Interleukin 1 receptor, type I: genome size 42-kb

Interleukin 1 receptor, type II: genome size 41.4-kb

Fig. 1. Continued

Interleukin 2 receptor: genome size 55.5-kb

Integrin, beta 2: genome size 38.5-kb

Melanocortin-2 receptor: 10.7-kb

Progesterone receptor: genome size > 54.1-kb

Platelet-activating factor receptor: genome size > 8.5-kb

Prostaglandin D2 receptor: genome size 10.6-kb

Prostaglandin E receptor 1: genome size 7-kb

Prostaglandin E receptor 2: genome size 18.2-kb

Prostaglandin F receptor: genome size 51.4-kb

Thromboxane A2 receptor: genome size 26.8-kb

Vascular cell adhesion molecule 1: genome size 23.2-kb

Fig. 1. Continued

Table 1. Characterization of 781 variations in 31 gene loci corresponding to drug targets on the cell surface

I.D.	Region	Exon	Position ^a	5' Flanking sequence ^b	Variation ^c	3' Flanking sequence ^b	Substitution	Repetitive sequence	Identity to dbSNP/ previous report
i-ADRB1-1	5' Flanking region	1	-1891	cacttttggggtttttat	A/G	gaaattccccacatatccc			rs2773469
i-ADRB1-2	5' Flanking region	1	-1451	acatttcacgcagcctcaa	C/T	tccctggcctcaagfatcct			
i-ADRB1-3	5' Flanking region	1	-1309	aatctcttacctatgtctcg	T/C	ttatttactacgaataggt			
i-ADRB1-4	5' Flanking region	1	-555	aaagcagcatitggaaata	C/T	tcccttggatgatatagcc			
i-ADRB1-5	5' Untranslated region	1	-2827	agaaaagcaatgcctccac	C/A	cttcgggggcatftaagggt			
i-ADRB1-6	5' Untranslated region	1	-2639	tattttgagactgcccttg	T/C	gggtccagaagaagccagg			rs2429511
i-ADRB1-7	5' Untranslated region	1	-2297	aagcagcaggtctcaggctt	T/G	cagtgacttggataacttgg			rs2050395
i-ADRB1-8	5' Untranslated region	1	-2142	atcactccccagttttaaca	T/C	acttgatctgaggtttgggc			
i-ADRB1-9	Coding region	1	145	tgcctgcctccgcagcgaa	A/G	gccccagccgctgtctcag	Ser49Gly		rs1801252
i-ADRB1-10	Coding region	1	1167	acttccgaagagccttcag	G/C	gactgctctcgtgcgcgc	Arg389Ser		rs1801253
i-ADRB1-11	3' Flanking region	1	1254	taataggtttccatgactca	A/G	taacatagcaaaatgcctcc			
i-ADRB1-12	3' Flanking region	1	1354	eggattcaaggtgtcttaga	C/T	tacttggtagcactttcaag			
i-ADRB1-13	3' Flanking region	1	1488	aactcagcgcgaactttica	C/T	ggaaaagcaggaagactaa			
i-ADRB1-14	5' Flanking region	1	(-138)~(-128)	gftaggctaaaaaaaagtt	(A)11~13	caccaatcataaaatgtagg			
i-ADRB1-15	5' Untranslated region	1	(-1803)~(-1792)	agatatttttaatttttta	(T)10~12	atttcaggccctgagctgagg			
i-ADRB1-16	5' Untranslated region	1	(-1629)~(-1610)	agcaatcaattgccaaetc	(A)19~24	ccacagatacaactttaaat			
i-ADRB1-17	3' Flanking region	1	10	gttcctgtgtgttttttt	(T)del	ctttctttcttcttctt			
i-ADRB1-18	3' Flanking region	1	32~53	ttttctttctttctcttc	(T)15~22	ctgttgtgtgtccggccttc			
i-ADRB1-19	3' Flanking region	1	705~712	atgtgataaaaaaataaac	(A)7~9	ggagtgggttcaaaatgccat			
i-ADRB1-20	3' Flanking region	1	1429~1452	tttggatgtgcgtactcct	(A)20~28	gggacgggtcttaatactc			rs1432622
i-ADRB2-1	5' Flanking region	1	-1046	ctatgtgaataataatagtc	T/C	ttaatcatatttggatt			rs1432623
i-ADRB2-2	5' Flanking region	1	-800	taaaacttcgttaacaacta	C/T	acttgtgtgacactatag			
i-ADRB2-3	5' Flanking region	1	-687	ccttagagacaattggaaat	C/T	aggtaactcgtgatttctct			
i-ADRB2-4	5' Flanking region	1	-199	aaattaatitcactttagca	G/A	taaaagcacaatgccagatgg			
i-ADRB2-5	5' Untranslated region	1	-1531	agtagctgggactacagglia	C/T	gfgccacacactggctaa			rs2400706
i-ADRB2-6	5' Untranslated region	1	-1429	tagcttcaaaatgtcttaa	T/A	gttaagacattcttaact			rs2895795
i-ADRB2-7	5' Untranslated region	1	-1343	tgggtgcgaatttcacatggc	A/G	caaccgaaagatttaacaaa			rs2400707
i-ADRB2-8	5' Untranslated region	1	-1023	ggcaggtgctgaggaatc	A/G	gcagctgttgaagtcacctc			rs2053044
i-ADRB2-9	5' Untranslated region	1	-839	aagccagcgggtgtgttactt	T/G	ctgtgtgtgtcaccatgtct			
i-ADRB2-10	5' Untranslated region	1	-654	ctgtgtgtcggatataagct	G/A	agcagtcttgcacgggtgtga			
i-ADRB2-11	5' Untranslated region	1	-47	agccccgcgtgggtccgcc	C/T	gctgaggcgccccagccag			rs1042711
i-ADRB2-12	5' Untranslated region	1	-20	gcgcccccagccagtgct	C/T	acctgcccagactgcgcgcca			rs1801704
i-ADRB2-13	Coding region	1	46	ccttctgtcgtggcaccat	G/A	gaagccatgcgcggaccac	Gly16Arg		rs1042713
i-ADRB2-14	Coding region	1	79	ctcttcttgaagcctatgg	G/C	aaaggcgaggtgtgtgtgtg	Glu27Gln		rs1042714
i-ADRB2-15	Coding region	1	1053	agtaacaaatgactactgt	G/C	aaaggctactccagcaacgg	Gly351Gly		rs1042719
i-ADRB2-16	Coding region	1	1239	ctacttttaagagcccccc	G/A	taaaagcagtttttacttt	Leu413Leu		rs1042720
i-ADRB2-17	3' Untranslated region	1	1273	tacttttaagagccccccC/G	C/G	C/Gcaacagacactaaacag			
i-ADRB2-18	3' Untranslated region	1	1274	gcaaaagagccccctgaggtg	C/T	ccaacagaacactaaacaga			rs1042721
i-ADRB2-19	3' Flanking region	1	757	ggtaactgtgatttcttctt	(A)11~14	gaattagccctgggttggga			
i-ADRB2-20	5' Flanking region	1	(-665)~(-652)	agttttctacttttaaga	(C)10~13	tgaactagaaggtccaagt			
i-ADRB2-21	5' Untranslated region	1	1266~1276	gcccgtgacaatttttt	T/A	attaaatccccaccaggga			
i-BDKRB1-1	5' Flanking region	1	-1069	acccaactacagtttgaac	G/A	ccttcttttctgcttggat			
i-BDKRB1-2	5' Untranslated region	1	-148	gagggaaggttttagaact	C/G	gttaggaagggttccagtagct			
i-BDKRB1-3	Intron 1	1	240	aaattcatgaacaactt	C/G	acaagtgtttagttcagtaa			
i-BDKRB1-4	Intron 1	1	3069	catittgtaaatittgtcac	G/A	tacgttataaatgtcaatt			
i-BDKRB1-5	Intron 1	1	3129	tcfgaagattgtctggagcc	G/A	cataaatcccgagctgtagg			
i-BDKRB1-6	Intron 1	1	5485	ctctcccgcaagcgtggga	G/A	gccagtcagctgcagctggc			
i-BDKRB1-7	Intron 1	1	5818	cagaccaggttcttggcgt	A/G	gcactgttaaccaccactag			
i-BDKRB1-8	Intron 1	1	5883	ctcaattttctaatggcca	A/G	ctggagatgacaatggcccc			
i-BDKRB1-9	Intron 1	1	6116						

Table 1. Continued

I.D.	Region	Exon	Position ^a	5' Flanking sequence ^b	Variation ^c	3' Flanking sequence ^b	Substitution	Repetitive sequence	Identity to dbSNP/ previous report
i-BDKRB1-10	Intron 1		6279	ttactcatgtcttcttct	C/A	ttttttcttctctctc			rs885842
i-BDKRB1-11	5' Untranslated region	2	-126	tgtgtgtgtgacaggg	C/T	tcaagtcgctgcccagact	+		
i-BDKRB1-12	Intron 2		191	tccaagcctgtaagaggaac	C/T	tcttagactgtcccaccc			
i-BDKRB1-13	Intron 2		302	tccaagccatgacctctgc	C/T	tccatctctgacagcccctg			rs870282
i-BDKRB1-14	Intron 2		621	ctcacatgagtgatgtac	C/T	gggatttggactcaggcacc			rs885845
i-BDKRB1-15	Intron 2		739	agtctctgtacaagctc	G/A	actcccctgtagcatgaa	+		rs2071083
i-BDKRB1-16	Coding region	3	123	ctgctgcacagagtctgcc	A/G	acatttatactctcatctg			rs2071084
i-BDKRB1-17	Coding region	3	462	cagagcgcggagagcaggc	C/T	cgggtcaccctgcgtctcat			
i-BDKRB1-18	Coding region	3	699	ggctccctgcgaacggga	G/A	gggtcagcagagacaagtg			
i-BDKRB1-19	3' Flanking region		1017	ccagcatcttgccttcag	C/A	G/T atgggttccctcaggtt	Pro41Pro		
i-BDKRB1-20	3' Flanking region		1026	tgcgcttcagC/Agagaaagg	G/A	gagaaaggG/AG/T atgggttccc	Ala154Ala		
i-BDKRB1-21	3' Flanking region		1027	ggcgcttcagC/Agagaaagg	G/A	G/T atgggttccctcaggtt	Glu233Glu		
i-BDKRB1-22	3' Flanking region		1250	ggcctccctgcgaacggga	C/T	atgggttccctcaggtt			
i-BDKRB1-23	3' Flanking region		1275	ttctaccctccagggctc	A/G	gggtctctaccctcaggg			
i-BDKRB1-24	3' Flanking region		1432	ggagagacacataaactga	A/G	tcccataaatalgagaactg			
i-BDKRB1-25	3' Flanking region		1668	aaggatggggctccaggc	A/G	gctttgagggccccatfgaa	+		rs945036
i-BDKRB1-26	3' Flanking region		1792	agccagatagagccctac	G/A	tcatgggagttggggatcct			
i-BDKRB1-27	5' Flanking region		(-1069)-(-1068)	ccgtgtgacaatttttt	T/ins	attaaaaatcccacaggga			
i-BDKRB1-28	Intron 1		27	aaatgaccacttttttt	T/del	cttttatgagagtacaatat			
i-BDKRB1-29	Intron 1		2980-2989	ttagatgctgagactcaat	GTCCACTAAA/ delTGATTG	attgatgataatgggaaaa			
i-BDKRB1-30	Intron 1		3014	attgataatgggaaaaataa	A/del	gagaaaaacatlgaaaagt			
i-BDKRB1-31	Intron 1		6307-6326	ttttctctctctctcc	(T)16-18	gttgtgtgtgtgtgtga	+		
i-BDKRB1-32	Intron 1		6327	tttttttttttttttt	G/del	tgttgtgtgtgtgtgtgag	+		
i-BDKRB2-1	5' Flanking region		-817	tattaggctcaagtccctc	G/A	agaccctgtctcctccacag			rs2069575
i-BDKRB2-2	5' Flanking region		-57	ctctccctctctggagaatg	C/A	gtgtattttgcaatcccacag			rs2069577
i-BDKRB2-3	Intron 1		165	gtccagctccctgtgagcct	G/A	tgggagcagaggggaatggt			
i-BDKRB2-4	Intron 1		189	ggagcagaggggaatgtctg	C/T	ggaaactagaggaagagggggc			
i-BDKRB2-5	Intron 1		277	caagtgaacttgggaagtga	A/G	ggaaagagagttaaacattaa			
i-BDKRB2-6	Intron 1		2886	cccggttgataaggagaa	T/C	gtgaatcctccatccagga			
i-BDKRB2-7	Coding region	2	792	aagttcaagagagatccagac	G/A	ggagagggggccacaggtgct			rs2069578
i-BDKRB2-8	3' Untranslated region	2	2002	caataactatgacacaacca	C/T	ctgtccctgccctcagttccc			rs2069587
i-BDKRB2-9	3' Untranslated region	2	2117	ctacgtacatgtggagcatc	A/T	ttacgcagacgaactgggga			rs2069588
i-BDKRB2-10	3' Untranslated region	2	2836	acctggagggctagaaactg	G/A	agggctagaaatctggagagc			
i-BDKRB2-11	3' Flanking region	2	1844	gattgctgctactactaagg	G/T	agcttgcataatccaggggaaa			rs2069598
i-BDKRB2-12	3' Flanking region		1997	ctctggctccagcaagctgg	C/T	gcaatgagagagaggtccacgg			rs2069599
i-BDKRB2-13	3' Flanking region		2249	tcccattctctgacctta	C/T	gtatgctctgctctcttacc			rs2069600
i-BDKRB2-14	3' Flanking region		2275	ttccatcttccccaagat	G/T	aggggtggggagcaggggatga			rs2069601
i-BDKRB2-15	3' Flanking region		1920	ggcaaaaaaagaaaaaaa	A/del	tgtctgggagagcctcccacag			
i-BLTR2-1	5' Flanking region		-1759	ctcccatgaaaagctcact	C/A	gggtgggaaaatgaacaaatg			rs1053649
i-BLTR2-2	5' Flanking region		-1167	ctgctctatccccctaaag	G/A	tggaggggtagagcgggggt			
i-BLTR2-3	5' Flanking region		-749	tttttattctatggaggga	A/C	ttttctggggagcgtttctgg			
i-BLTR2-4	5' Flanking region		-569	tggaaaaatgagaggtgaga	C/G	tgtgtccagggaggggtgtaa			rs2144492
i-BLTR2-5	5' Untranslated region	1	-184	atagtgacagcctgggggtga	T/G	gactttatgccgttttacc			rs2180197
i-BLTR2-6	3' Untranslated region	1	1361	attatgaggggtggatggt	C/T	ccgttaaggactatgtgt			rs1950505
i-CD20-1	5' Flanking region		-462	cttaagtgtagccaatgag	G/A	acaatatgtgggagccctta			
i-CD20-2	5' Flanking region		-327	aggtaaaagtcagtgctaac	G/A	gcccatctttggaccacttc			
i-CD20-3	Intron 1		626	tgaatctctgctcaaatct	A/G	tcacatggggaacacaaagct			rs1443249
i-CD20-4	Intron 1		750	tccagtataaagtgtattcc	C/T	tttccctgtttcccatataaa			

Table 1. Continued

I.D.	Region	Exon	Position ^a	5' Flanking sequence ^b	Variation ^c	3' Flanking sequence ^b	Substitution	Repetitive sequence	Identity to dbSNP/ previous report
i-CD20-5	Intron 1		793	gcttaatctcaclgagaatc	C/T	gg'tggaaaagaaatgtttaat			
i-CD20-6	Intron 1		937	ctcaggggatccaccgtcct	C/T	ggcttcccaagtgctggga	+		
i-CD20-7	Intron 1		1 064	tgtaaactgagctcatagtac	A/C	tagaaaacaggttccctatg			rs1941030
i-CD20-8	Intron 1		2 340	caaaactattttgagtgga	G/A	agaatgaagatagagtaaca			rs2155714
i-CD20-9	Intron 1		2 885	tatatataatcagatata	T/C	atatgaagatagtttccat			
i-CD20-10	Intron 1		3 234	aacaattgatgaccttgca	T/C	tttaagttatcttcaataa			
i-CD20-11	Intron 1		3 831	agtttctctctcttcttc	T/C	agccC/Gatgcccagacagat			
i-CD20-12	Intron 1		3 836	ctctctcttcttcT/Cagcc	C/G	atgcccagacagataatac			
i-CD20-13	Intron 2		215	cttaigtcaaccttttggtt	T/G	ggggcttgataltgcagggg			
i-CD20-14	Coding region	3	216	ctgggggggtctctgtgat	C/T	ccagcagggatctatgccc			
i-CD20-15	Intron 3		128	ggaaatatttgggttaa	G/T	taattaaagacagaggttga			
i-CD20-16	Intron 3		472	gcactctttggcgtttta	C/T	gtacatgttttccaatctg	Ile72Ile		rs2070770
i-CD20-17	Intron 4		169	atgaaaaacttagaagcgag	G/A	tctatcigaagtatgttcat			
i-CD20-18	Intron 4		508	tgggtcttcacaggtataa	A/G	gtactacactgtggtcttgc			
i-CD20-19	Intron 4		-556	gcgtactgggctgattgca	A/G	ccatgtcagcaggaataga			
i-CD20-20	Intron 4		-383	cttcactctcttccctctac	C/G	tattttgaaggcagataat			
i-CD20-21	Intron 6		1 150	ttgttgacaaagggtgcagt	G/T	gtaaaagtaagaatlggtt			rs1941031
i-CD20-22	3' Untranslated region	7	1 077	tagagaatgtagccattgta	G/A	cagctgtgtgtgcacgctt			
i-CD20-23	3' Untranslated region	7	1 225	tttgtctattttcccatca	A/G	caaccagggagac'tgcacct			rs1051756
i-CD20-24	3' Flanking region		258	taictattttacaagtaa	T/C	tcaaaaggccaataaactt			rs1051461
i-CD20-25	3' Flanking region		681	atctgagtcacacagcgccc	T/C	acttttcaattcagatatatac			
i-CD20-26	3' Flanking region		857	tgatatttctacatttttag	C/T	gaccactagtggaaagacatt			
i-CD20-27	3' Flanking region		1 438	tgacctcacataactctta	T/C	aataggagacatctttaatg			rs1051593
i-CD20-28	3' Flanking region		1 501	aattctctacactctccc	C/T	gattatccctttggcaatat			rs1051594
i-CD20-29	3' Flanking region		1 585	aagaagttagaatatatttc	T/C	ctagccttagtttttctccc			
i-CD20-30	5' Flanking region		(-1 161)-(-1 151)	ctaatgaacggctcccaaca	(T)10-12	agatggcactttttaaat			
i-CD20-31	Intron 1		250	ttccacaaaagtagagatt	G/del	cagcatatattataaatcat			
i-CD20-32	Intron 1		2 919	ttccataagaataaaaaa	A/del	caggagaaagcactcatggt			
i-CD20-33	Intron 1		3 032-3 049	ccattttacagagaataat	(CA)8-10	gcccctatggtcattattgc			
i-CD20-34	Intron 6		625-626	atggttgaagggttgaaggct	GACT/ins	aagtctactgttcttgggtt			rs2459141
i-CD20-35	3' Untranslated region	7	1 354-1 363	atcattgttttaaggatgat	(A)8-9	taaacactaggggacaataca			
i-CD33-1	5' Flanking region		-1 750	atgcagctaccctctctatta	G/A	taaaggatgaatgaagagtta			
i-CD33-2	5' Flanking region		-401	tctctggcactaaacaccc	C/A	atgggatctaggtgaggctgc			
i-CD33-3	5' Flanking region		-170	tctctggcactctctggcca	T/C	gagggtcaatctgtgtggag			
i-CD33-4	Coding region	2	41	ccctcgttcccacaggggg	C/T	ccctggctatggatccaatt	Ala14Val		
i-CD33-5	Intron 4		6 773	caggccctaattgtgggaga	G/C	tggccttgggagggccaga			
i-CD33-6	Intron 4		7 511	ccctgcctcttgggtttcca	A/G	ttaccacagtgaaacttcca			rs1354106
i-CD33-7	Intron 4		8 381	ccctgtcttcacaggcccttt	T/G	aaggccaaagggaccacctt			
i-CD33-8	3' Untranslated region	7	1 104	aggaccacagtgagggaacca	C/T	aaggagcatcagggttcagcta			
i-CD33-9	3' Untranslated region	7	1 297	tgtgtctttcatttgttaa	G/C	tgtatgatgtcacacaagct			rs1803254
i-CD33-10	5' Flanking region		773	tagatgtctaaattgagatg	G/T	cagaagaagactcaacaatca			
i-CSF3R-1	5' Flanking region		-936	agttcactgggaactcactgag	C/T	gagcagagcctgtgggatat			
i-CSF3R-2	5' Flanking region		-865	atttgacttgggaactagaac	T/G	acagcccttggctctgcagcat			
i-CSF3R-3	Intron 5		71	ggcatggtagagatgctgggc	A/G	tggcctctggggagggagagg			rs2275471
i-CSF3R-4	Intron 7		58	ggggcaggggggaggggtaag	T/A	cgggctctgagcttggccctag			
i-CSF3R-5	Intron 9		253	gttttctctgccctcttc	C/A	tagaacctagcacaaaggga			
i-CSF3R-6	Intron 9		275	agaacctagcacaaagggaac	A/G	gagggaaaaaggggagggggg			
i-CSF3R-7	Coding region	10	1 260	gccgggacctctctgtccac	T/C	ccgggtgctctctcagaaag	Thr420Thr		
i-CSF3R-8	Intron 11		125	tccagcctttcttgatcctt	C/T	gttgtctctattcataacc			
i-CSF3R-9	Intron 12		90	caatcagaagataggggaac	A/G	tggccttctaccactcttc			rs2275472

Table 1. Continued

I.D.	Region	Exon	Position ^a	5' Flanking sequence ^b	Variation ^c	3' Flanking sequence ^b	Substitution	Repetitive sequence	Identity to dbSNP/ previous report
i-CSF3R-10	Intron 14		106	tgaatttgaatcccttggtc	G/A	gaggaggagaccagcctt			
i-CSF3R-11	Intron 1		496~505	gggtccaggcctccgagtg	(C)8~10	gccactctgggicggcg			
i-CSF3R-12	Intron 2		1771	tcaaggcactggaagacc	C/del	tgaactgcatctttgtg		+	
i-CSF3R-13	Intron 3		3412	gcgtgctgctgctgcaaaa	A/del	ctaattgigacatctcttc		+	
i-CSF3R-14	Intron 3		3494~3495	agctacagtgagagactta	A/ins	caaccgggaaggcacac		+	
i-CYSLT1-1	Coding region	1	927	aggaaaaaggctctacatt	C/T	agaaaggcatctttgtccag	Phe309Phe		rs320995
i-CYSLT1-2	3' Flanking region		667	ttctctccatcatgacata	T/C	aattctcttaagaagcca			rs320996
i-CYSLT1-3	3' Flanking region		835	agaaaattgtaaatgttcac	A/G	ttacaaattctttaagaag			rs320997
i-CYSLT1-4	3' Flanking region		1313	gtaaaactcaaatagactgt	G/A	cccatatttttaataac		+	rs2035190
i-CYSLT1-5	3' Flanking region		1662	aatgttaagtttttaaaaa	G/A	gaatgttaagtttttaaaa			
i-CYSLT1-6	3' Flanking region		1684	cttcaattacttcaagccc	C/T	atatacaagataaatgtt			
i-CYSLT1-7	3' Flanking region		1940	ttacctcagaagaataaat	GAT/ins	atcataaattgtctttttt			
i-CYSLT1-8	3' Flanking region		1158~1159	atacttactctgcatTTTT	T/ins	aactataaagaaaaaagaaa		+	
i-CYSLT1-9	3' Flanking region		1630~1631	ttttgtttttgtttgtt	G/T	ataggcattttgaaaactc		+	
i-CYSLT2-1	5' Flanking region		-556	actctgacctcaggtgac	T/C	ttttttttttttgagatg		+	
i-CYSLT2-2	5' Flanking region		-317	aggagggtctcttctgcca	C/T	gccagcctcagcttcccaa		+	rs 2805152
i-CYSLT2-3	3' Untranslated region	1	2077	aggagggtctcttctgcca	A/G	tgaaacaaggcttaaggatc			
i-CYSLT2-4	3' Untranslated region	1	2533	tttgtttgtttgtttgtG/T	(T)12~15	tcataaacaacaaatccc		+	rs912278
i-CYSLT2-5	5' Flanking region		(-555)~(-542)	gagtcgttggggaggagag	C/T	gagatggagtttgccttfg			rs2952155
i-ERBB2-1	Intron 1		5154	cctggaatctgcatgtagcct	G/A	gtgggggaagaggagggggtg			
i-ERBB2-2	Intron 1		5529	gtttgtccctctctgtt	T/C	tgggaggggagcagtgacc			rs1810132
i-ERBB2-3	Intron 4		300	ttgatgggtaagagtgggca	C/T	taaccgctctctgctgctt			
i-ERBB2-4	Intron 9		14	gacagcctgctgacctcag	C/T	gatgacctgagacagtgtca	Ser423Ser		rs1801201
i-ERBB2-5	Coding region	11	1269	cagagcctgctgacctcag	C/T	gtcttcagaaacctgcaggt	Ile655Val		rs903506
i-ERBB2-6	Coding region	17	1963	cagagcctctgacctcag	A/G	tctctgggtgggtggcatt			rs1058808
i-ERBB2-7	Intron 17		52	tggggtctgacacccggcccc	G/A	gcatcgaccacacccacct			
i-ERBB2-8	Coding region	27	3508	ctggtgacctctgggaagg	C/G	ccaagacctctccccagg	Pro1170Ala		
i-ERBB2-9	Coding region	27	3757	cagaggtacctgggtctggac	G/A	tggcagtggaaccagaagg	Val1253Met		
i-FOLR1-1	5' Flanking region		-1227	ttctctgcccacaaactgc	C/T	ccctccctctcttctcca			
i-FOLR1-2	Intron 1		18	aaaggtagtgagtgagcagg	T/A	ccacaggggcagatfggat			
i-FOLR1-3	Intron 1		160	gaattcaattccaggcttat	A/C	tgaagccctgctgigcagctg		+	rs346074
i-FOLR1-4	Intron 1		560	ggctgcccctggcagcacc	A/G	tgtccctgtagccccccca			rs1809049
i-FOLR1-5	Intron 2		2863	aggactaagaggaggagacac	T/C	gcatgiggaatatctggct			
i-FOLR1-6	Coding region	4	396	aaagaggggtactgaactgt	G/A	ccccigtgcaagaggagactg			
i-FOLR1-7	5' Untranslated region	1	-229	tatcatgttgtattcccc	C/del	ttctacatttaactctgic	Val132Val		
i-HRH1-1	5' Flanking region		-90	cagaaggcatctttaaatc	T/C	attactgtactatctgatt		+	rs346074
i-HRH1-2	3' Untranslated region	3	2161	atgcagctgacacaccac	G/A	tctttaaccccaatttct			rs1809049
i-HRH1-3	3' Flanking region		83	tacagagggtcactctatgc	A/G	tttttaaaagctctgagca		+	
i-HRH1-4	3' Flanking region		1092	ggatggacctgaatcactgt	A/T	gcttgaataagtgicacag			rs346071
i-HRH1-5	Intron 2		(5025)~(5044)	ccacaacagtgatgaagcc	(A)18~21	gcaaaagccaagcaaaacaa		+	
i-HRH1-6	3' Untranslated region	3	2800~2810	acagaagaagactgtcttc	(A)10~12	tacaatattttaacaatgtg		+	
i-HRH1-7	3' Flanking region		880~884	acagaggagactctgtt	AAAAAT/del	gaaatgaaatgaaatgaaat		+	
i-HRH1-8	3' Flanking region		904~905	gaaatgaaatgaaatgaaat	GAAAT/ms	ataaaataaataaataata		+	
i-HRH2-1	5' Flanking region		-6616	ttctgctatgggttga	C/T	caaatgtcttccaggagg			
i-HRH2-2	5' Flanking region		-5244	actgtgggtcagtagctg	A/C	gfgattttaacattaacggg			
i-HRH2-3	5' Flanking region		-5128	acatcacgcccgcacgtgc	A/G	cacacacagactgtgctt			
i-HRH2-4	5' Flanking region		-3954	actgtctgggtctgagccac	G/A	cacacacagactgtgctt			
i-HRH2-5	5' Flanking region		-2185	agggccttgaacctcaaaa	C/T	tctgcccagctctgctatcg			rs2890892
i-HRH2-6	5' Flanking region		-2168	aaC/Tctgcccattgggattt	A/T	aaaaaacacccccttctgt			
i-HRH2-7	5' Flanking region		-1001	gggctcagggtgtgtggc	T/C	ctgatttttggcccttctg			rs645574

Table 1. Continued

I.D.	Region	Exon	Position ^a	5' Flanking sequence ^b	Variation ^c	3' Flanking sequence ^b	Substitution	Repetitive sequence	Identity to dbSNP/ previous report
i-HRH2-8	5' Untranslated region	1	-1018	ctttctgaaaaagtgtgtc	G/A	gccaccgacctagagtatga			rs2067474
i-HRH2-9	5' Untranslated region	1	-592	gagatctagtagaaggacac	A/G	tcttgaattgggtcatgctt			rs686874
i-HRH2-10	Coding region	1	543	aaagtccaggtcaatgaagt	G/A	tacgggctgggtgatgggct	Val181Val		rs1800689
i-HRH2-11	5' Untranslated region	1	(-142)-(-122)	gctctccaccaccttgccc	(A)18-24	ctggacacatttttggatctg			
i-HRH3-1	5' Flanking region	1	-1212	gctataagtagggagtgac	G/A	gfgcatgtcagcgcccgagg			
i-HRH3-2	5' Flanking region	1	-1161	agccctcccccagacagc	G/A	cactctggcctctttagggc			
i-HRH3-3	Intron 1		945	gagggggtgtaagatgaggc	T/C	ggctagttccagaagaagcag			
i-HRH3-4	Coding region	3	978	ctcaaggagggtcccaagcc	G/A	tggcgctctggcctcG/Act	Pro326Pro		
i-HRH3-5	Coding region	3	996	ccG/Atcgggtctctggcctc	G/A	ctggagaagcgcatgaagat	Ser332Ser		
i-HRH3-6	5' Flanking region	1	-1238	gcaggtcccccacagtatggg	G/del	aagcctgctataagtagggga			
i-HRH3-A-1	5' Untranslated region	1	-42	ctggcctctgggtggcctcg	T/C	ccctggcactcgaggcact			rs1062613
i-HTR3A-2	Coding region	1	30	tgggtccagcaggcgctgt	C/T	gccttgcctccccacact	Leu10Leu		
i-HTR3A-3	Intron 1		173	catfttaggcatactggtta	A/G	gctagagagagtttaggaatg			
i-HTR3A-4	Intron 1		574	ctaaactccagtaacgccca	G/A	ttctctcacattccctac			rs1150225
i-HTR3A-5	Intron 1		758	gaggaaagccatccagggtt	T/G	gacagacgtgaaagagctctg			rs1150222
i-HTR3A-6	Intron 1		790	agagctctgggtaagatgic	C/T	ttctcccgaggagcggtgt			
i-HTR3A-7	Intron 1		1079	ctcaccctctgggtgctggg	G/A	gactctgtgtgcaaatagc			
i-HTR3A-8	Intron 1		1198	tttgtgtgtgtgtgtgtgtg	C/T	gtgtgtgtgtgtgtgtgttc		+	rs1176726
i-HTR3A-9	Intron 1		1431	ccatctcccttctgtctgcc	G/A	tatgtgtgcccctctaggttg			
i-HTR3A-10	Intron 1		2155	agatctgtcttctctgca	A/T	tgaatgcataggtctcttct			rs1985242
i-HTR3A-11	Intron 1		2356	ggggggctgtgtgtctacttt	A/G	aactgtctctctccacgcc			rs1176722
i-HTR3A-12	Intron 2		1241	acaaaggaaagccctcttta	G/T	gggctggcatgtgtcagggtg			
i-HTR3A-13	Intron 3		141	gccttgagatccaggagtggt	G/A	aatctctcatctcaggtct			rs2276302
i-HTR3A-14	Intron 4		153	tgtgagctccaaattcccttt	A/G	ttctcccccG/Aacctttt			rs1176719
i-HTR3A-15	Intron 4		165	ttcccttA/Gtcttcccccc	G/A	accttttctgtcttcttct			rs2276303
i-HTR3A-16	Intron 4		1625	tggaaactagacctgacaa	C/T	ggcaggtcaggaaagcctaag			
i-HTR3A-17	Intron 4		1666	ataggaaaggttggaanaacc	G/A	aggccaggcaaaacacacag			
i-HTR3A-18	Intron 5		85	ggagtgctcccaggggcgc	T/C	tctcagtatccagcctact			
i-HTR3A-19	Intron 5		271	attcacattcatgtgtgc	A/G	tatatatacacatacaca			rs909411
i-HTR3A-20	Intron 5		2666	ctgtgtccatcatcacagg	G/T	tccagcagctcttgggtact			rs1150220
i-HTR3A-21	Intron 8		218	tactgacatggatcccat	A/G	ccctgcttacttgggggtgg			
i-HTR3A-22	Coding region	9	1182	atgggagagcccccaggactt	C/T	ggagagagcccgaggggacag	Phe394Phe		
i-HTR3A-23	Coding region	9	1377	ctattccacatttaccgtct	G/A	gcgggtgctggcctacagcat	Leu459Leu		rs1176713
i-HTR3A-24	3' Flanking region		718	gfggagtaggagactaaagg	A/G	gggtatcacagggttctcag			rs1182457
i-HTR3A-25	3' Flanking region		1899	tttccctcccactgttata	C/A	ctctcggaagctgtctctc			
i-HTR3A-26	5' Flanking region		(-758)-(-741)	acagagcagactctgtctc	(A)15-17	gaaagaaagaaagaaagaa		+	
i-HTR3A-27	Intron 1		1181-1216	agacacttaaaaaatgttt	(GT)15-21	tctctctgctctctctgtc		+	
i-HTR3A-28	Intron 3		1699	tgaactgactctctctctggg	G/del	caaggctacatcagcggag			
i-HTR3A-29	3' Flanking region		18	aaactctctcttttttt	T/del	cttttttgtattatcat			
i-ICAM1-1	Intron 2		39	agggcctgtagtagcagacc	C/G	gggtgggagagacgtgcaegg			Okuda et al. (2002)
i-ICAM1-2	Coding region	5	1095	aaaggcccccacagaggacaa	C/T	ggggcgagctctctctgctc	Asn365Asn		rs3198540
i-ICAM1-3	Coding region	6	1405	ctcaaggggagggtcacccgc	A/G	agggtgacggtaagtgtctc	Lys469Glu		rs3093032
i-ICAM1-4	3' Untranslated region	7	1972	ggctatggtagtctgaggg	C/T	cccacagacttacaagaagaa			
i-ICAM1-5	3' Untranslated region	7	2707	tgtgtagacaacgtctcgt	C/T	tgtcacccaggtctggaggtgc		+	
i-ICAM1-6	3' Untranslated region	7	2767	actcagctctgacacttttg	G/A	gctcaagtgatctctccacc		+	rs1135717
i-ICAM1-7	3' Untranslated region	7	2859	atttgatttttttttttt	C/T	cagagacggggtctC/Tgcaac		+	
i-ICAM1-8	3' Untranslated region	7	2874	ttttttC/Tcagagacggggtct	C/T	gcaacattggcccagacttcc		+	rs281437
i-ICAM1-9	3' Flanking region		112	aaaacattgtgggtgtatgg	C/T	cataccctgaggttcttggtc			rs3093030
i-ICAM1-10	3' Flanking region		376	ctggctctctggcggggggc	C/T	ccttagtccgggctttttg			

Table 1. Continued

I.D.	Region	Exon	Position ^a	5' Flanking sequence ^b	Variation ^c	3' Flanking sequence ^b	Substitution	Repetitive sequence	Identity to dbSNP/ previous report
i-ICAM1-11	3' Flanking region		541	tccggagctcagtgccctt	C/A	tgggtgcatgagccccga			
i-ICAM1-12	3' Untranslated region	7	2845-2858	accacacctggcaaatitga	(T)12-14	C/TcagaggggtctC/Tgcaa		+	
i-JFNAR1-1	5' Flanking region		-786	gcatatttcacaaatgact	G/T	gatC/G/TGattactgaggaattt			
i-JFNAR1-2	5' Flanking region		-782	atttcacaaatgactG/Tgat	C/G	T/Gattactgaggaatttaatt			rs2834191
i-JFNAR1-3	5' Flanking region		-781	ttttcacaatgactG/TgatC/G	T/G	attactgaggaatttaatta			rs2843710
i-JFNAR1-4	5' Flanking region		-576	cgcctctgccccgcctctcg	C/G	tctgcacacaggaacggctct			Muldoon et al. (2001)
i-JFNAR1-5	5' Flanking region		-416	gaagagggccggcgccgac	C/T	aggagccaccgcgcctc			rs2850015
i-JFNAR1-6	5' Flanking region		-19	gctaagaggggcagcgctg	T/C	gcagaggggcgctgctgactt			rs2850021
i-JFNAR1-7	Intron 1		6065	actctaccacctgcccctt	G/T	ggctagagctgaagcagfat			
i-JFNAR1-8	Intron 1		6161	gcctaaagctgaagtggiata	C/T	ggcatccagggaaacagggg			
i-JFNAR1-9	Intron 1		6267	aatcagctgcccctggccaac	C/T	gagcagctatgctatccacgg			
i-JFNAR1-10	Intron 1		6765	ggtagaatcaaaagctacaac	C/G	catctctggcgctaaagctg			rs2252930
i-JFNAR1-11	Intron 1		6765	tgtgagcaactactacgtccaa	C/T	ccctgcacagagagaaacc			rs2243590
i-JFNAR1-12	Intron 1		6840	ctcagcaaccaagtgctca	G/A	taggtttgtgagatccctgag			rs2252931
i-JFNAR1-13	Intron 1		6884	acagttgtatataatgttc	T/G	tattctctgtgctttata			rs2243592
i-JFNAR1-14	Intron 2		10372	gtttgtttctatattttt	A/G	gaaatgttacgcctattta			rs2243594
i-JFNAR1-15	Intron 2		187	aaatacatcttgggtgtg	A/C	agcaaaaaattggggatgag			rs2253413
i-JFNAR1-16	Coding region	4	502	taagctttacataatagctta	G/C	ttatcggaaaaactctca			rs2257167
i-JFNAR1-17	Intron 6		648	gcagaggattacttgaggc	C/T	aggaaatggcgtgcagctgt			
i-JFNAR1-18	Intron 9		177	ttttgaaaaatattttaac	G/A	cttaactctcaagtcgggt			
i-JFNAR1-19	Intron 10		141	tatctctcaagcttag	T/G	caattaactttaaaaacagt			
i-JFNAR1-20	Intron 10		1163	aaataattctcaatgtgct	T/G	ctcttgatataatgtgtt			rs2254180
i-JFNAR1-21	Intron 10		1241	catgatccacagagtcgccc	G/A	ctctctctctccctggtt			rs1041867
i-JFNAR1-22	Intron 10		1398	gcaatttagtattgtcttagg	C/T	gacttttataatgcatgccc			rs1041868
i-JFNAR1-23	5' Flanking region		(-85)-(-76)	ggcgctgctgcggaggccg	(GT)5-14	cagaaagcgcgcgctgcg			rs2254315
i-JFNAR1-24	Intron 10		1208-1218	acaaacattttattttc	(A)9-11	gtcatgctccagagctcgc			
i-IL1R1-1	Intron 1a		-581	tctgtataaagggaatttg	A/G	ggacggggtattgtaaggaa			
i-IL1R1-2	Intron 1a		-491	ggaaaagggaaccataaaagc	T/A	ctctggaaacagattgttaa			
i-IL1R1-3	Intron 1a		-327	accctaatctctgagttct	G/A	aagagggcatactacaggggg			rs956730
i-IL1R1-4	Intron 1a		-116	agggggaaagcccaggagg	C/T	tgcagactcgaccactgccc			rs2234650
i-IL1R1-5	5' Untranslated region	1b	-571	atgtattagctcatttttt	T/A	A/Taaaaactgitttcaaccac			
i-IL1R1-6	5' Untranslated region	1b	-570	tgtattagctcattttT/A	A/T	aaaaactgitttcaaccact			
i-IL1R1-7	Intron 1c		1238	tgggggtttctggggcaggg	G/A	tgtggaaactctgatttattt			
i-IL1R1-8	Intron 1c		1760	aggagacaccactcagcagc	C/T	ccaatggagaggagagaggag			
i-IL1R1-9	Intron 1c		2058	gacaaatgggggaaactac	C/T	atagcatatgtgggtggagaa			
i-IL1R1-10	Intron 1c		2287	gcacaagacaaaggatctga	C/A	tgtcagcagccctttctcc			
i-IL1R1-11	Intron 1c		3714	ggggggctaggtctcaaca	T/C	tgtaaatatgttccG/Atcag			
i-IL1R1-12	Intron 1c		3730	aacaT/Cgtaaatatttcc	G/A	tgctatgaacgtctgtgag			
i-IL1R1-13	Intron 1c		4357	gagaacaagctgtcttgc	T/C	gactgggaggcagtgctcca			rs2110727
i-IL1R1-14	Intron 1c		4814	aaataattgagattcatagc	G/A	acacttgaacctcttggga			
i-IL1R1-15	Intron 1c		5298	atcattagggttaggtcact	C/G	cctctaatgtccccacagg			
i-IL1R1-16	Intron 1c		5537	tagatcgtggagattttct	T/C	tctgctcataatagccg			
i-IL1R1-17	Intron 1c		5961	caaaacaacaacaacaaa	C/G	gggttaacaggaaagacatcat		+	
i-IL1R1-18	Intron 1c		6020	agtaacttaacacattccc	G/A	tacatgtttccaccgatttt			
i-IL1R1-19	Intron 1c		6385	ggctccctgggaagaaggaga	G/A	tcatttactgccG/Atctgttc			rs1558641
i-IL1R1-20	Intron 1c		6398	aggaggG/Atcatttactgcc	G/A	tctgttctctctcttgggc			rs1558640
i-IL1R1-21	Intron 1c		7152	gaagctgttaataaatgca	G/A	tgtggctacacagcaggaaa			
i-IL1R1-22	Intron 1c		7712	atgaccagctaggtccttgg	G/A	tcaccttagctctggctga			
i-IL1R1-23	Intron 1c		9657	tataattccacagcagctgct	T/G	tcatacttggggcatactca			

Table 1. Continued

I.D.	Region	Exon	Position ^a	5' Flanking sequence ^b	Variation ^c	3' Flanking sequence ^b	Substitution	Repetitive sequence	Identity to dbSNP/ previous report
i-L1R1-24	Intron 1c		9822	tatcgtgtactgctctcaa	A/G	gtgaataatagcttgggatt			
i-L1R1-25	Intron 2		261	cagtagagaccctgggaatg	A/G	tgggtccagctgtggccc			rs2287049
i-L1R1-26	Intron 2		805	tctctcagaacaactctgca	T/A	gttgggaactatgagctt			rs871656
i-L1R1-27	Intron 2		864	accacactctgtgtatgct	C/T	cagaacatgatgtgttggga			rs871657
i-L1R1-28	Intron 2		1388	ttagatagccgttcaactgc	G/C	agcactatggaggccagtca			rs871658
i-L1R1-29	Intron 2		3071	tttctctctctctttttt	C/A	atacaaaagtctgttagat			
i-L1R1-30	Intron 2		3522	ttatccctttttgtcccca	C/T	cccatcttcaaccagaagt			rs2287048
i-L1R1-31	Intron 2		3577	ttcatgatagtaaaaaacca	G/A	ttcatcagtgactgtggg			rs2287047
i-L1R1-32	Coding region	5	351	gcacaaatttgggagaatga	G/A	ccctaatctgttataatgc	Glu117Glu		
i-L1R1-33	Intron 5		315	actattttacaaaacata	C/T	tatgtgtttttatgaaga			
i-L1R1-34	Intron 5		567	ttcaaacatgtttttctgc	A/C	aaataaatggcctcactt			
i-L1R1-35	Intron 5		669	aaaaagccagttataaaact	T/A	actatatgaaggaaactttt			rs997049
i-L1R1-36	Intron 6		614	ttaatagggttaggatgatt	G/T	ttcttgttaattttctgtg			rs2160227
i-L1R1-37	Intron 6		2092	tttcagtagcacccactct	A/G	tgaatteggaaggtctagct			
i-L1R1-38	Intron 7		19	gggtaaagtgggcttcagtga	G/C	ggatagctgggaatcgG/Ttttt			rs3213736
i-L1R1-39	Intron 7		35	gtgaG/Cgggtatgctggaaatg	G/T	tttttttttttaaacata			rs3213735
i-L1R1-40	Intron 7		3002	actaatgggtgtttttctcg	G/T	gtgggtgggttagggtaatt			
i-L1R1-41	Intron 8		396	actgctcatctatgggacaa	G/A	gaictctggcttccatga	Thr344Met		
i-L1R1-42	Coding region	10	1031	catgattggatatatgttca	C/T	gttgacagtcataaattgtgt	Ile377Leu		
i-L1R1-43	Coding region	10	1129	ctgtctatgattttctccca	A/T	taaaagggtataatttgtat			
i-L1R1-44	Intron 11		655	gtgtggcttgggttcaggag	A/G	gaatgatataaatagaatt			
i-L1R1-45	3' Untranslated region	12	2024	gtcaggagttcagaccagc	C/G	cagccaacatggcaaaacc	+		
i-L1R1-46	3' Untranslated region	12	2537	agaagtttagtgcgaagac	C/A	gaattttattttacagagct			
i-L1R1-47	3' Untranslated region	12	2708	ttctccctggcatgacact	C/G	ctgtcctttgttatctct			
i-L1R1-48	3' Untranslated region	12	2769	aaacagctccctagtggtctc	C/T	tccG/Atctgcaatgtcccttg			
i-L1R1-49	3' Untranslated region	12	2773	gtctccctagtggtctcT/tcc	G/A	tctgcaatgtccctgcaca			rs2110726
i-L1R1-50	3' Untranslated region	12	3010	gggtggccatgtcgctctgcc	C/T	cagcactctctgtctctgc			
i-L1R1-51	3' Untranslated region	12	3094	gcattttctctagctgac	A/G	gaattttaccaaaattcaga			
i-L1R1-52	Intron 1c		2966	gcaaaagtgtcaggaaataaa	A/del	gcaatttggcagagagaga			
i-L1R1-53	Intron 1c		4659-4660	agtgtgcaagaggcttgggg	G/ins	taggtccatccccctgtg			
i-L1R1-54	Intron 1c		5926-5961	cagagcaagactctgtctca	(AAAC)6~11	gggttaacaggaaagacatcat			
i-L1R1-55	Intron 1c		9968-9978	cccaagaataatgaticagac	(A)9~12	ttagactccaaaataactaaa	+		
i-L1R1-56	Intron 7		36~47	tgaG/CgggtatgctggaaatcgG/T	(T)11~13	aaaacataaagagtaagataa			
i-L1R1-57	Intron 7		316~328	tacaggatttggattcttctc	(T)10~14	cacagagttaaaatatattaa			
i-L1R1-58	Intron 8		114~138	tgtctctaactttgtctgcc	(T)20~26	gctaagctaaagtgaattta			
i-L1R1-59	Intron 9		1735	tattttctctctttttt	T/del	ctttttgtctatagtcactaa			
i-L1R1-60	Intron 10		365~372	cttcacgtcaccaggaggtt	(CT)4~6	ccittgtttaactttgcga			
i-L1R1-61	Intron 10		392~403	tctttgtttaaactttgcg	(A)10~12	gggaataccacataatctaaa			
i-L1R1-62	3' Flanking region		1912~1920	aaagtgtgtgtgtgtgtgt	(G)7~11	cgggggtgtttaaattttaag			
i-L1R2-1	Intron 1a		1802	aaacttctgtgtaagaatctt	G/C	tcaagacctacatgtccct			
i-L1R2-2	Intron 1a		1883	accttcttggaaacctccag	C/T	ggccgatggctgcagtgggga			
i-L1R2-3	Intron 1a		2169	agggcagctatctctctcc	C/A	gggggtcttcagtttgcttgg			
i-L1R2-4	Intron 1a		2248	tacatcccatctccatccc	G/A	acctccaaagccgtttttgac			
i-L1R2-5	Intron 1a		2355	ggagtggcctctagcagcaa	C/T	aggagctgaagcagagcagac			rs2871444
i-L1R2-6	Intron 1a		4377	gggtctgtggaataaccagcaa	A/G	tctgggctatcttcaagtgt			rs757918
i-L1R2-7	Intron 1a		4826	atatactactacaaaattga	C/T	gccaaaaataacctttaaa			
i-L1R2-8	Intron 1a		5073	acattgtgtccccaggaggt	C/G	gtgggcagctgattccacag			
i-L1R2-9	Intron 1a		5108	cacacgtgtgtacctgggggt	A/C	ggcactggctctgtgtggaga			rs1108338
i-L1R2-10	Intron 1a		5179	cctgtgggaatactactgtgg	C/T	gtctgtgactgggaaaccc			
i-L1R2-11	Intron 1a		5250	tgtctcatcagaggctacccc	C/T	gtgtgtcctctctctggctc			

Table 1. Continued

I.D.	Region	Exon	Position ^a	5' Flanking sequence ^b	Variation ^c	3' Flanking sequence ^b	Substitution	Repetitive sequence	Identity to dbSNP/ previous report
i-L1R2-12	Intron 1a	5 422		tgtgcacctgaagagctcc	G/A	aggagaccaggaaagccaa			
i-L1R2-13	Intron 1a	5 454		gaaagcaaggagcagaag	G/A	tggagaG/Actcaggccttgg			
i-L1R2-14	Intron 1a	5 461		aaggagcagaagG/Atggaga	G/A	ctcaggccttggggaagtg			
i-L1R2-15	Intron 1a	5 564		atactgaagctgtggcta	C/T	aggtcatctgtcttcac			
i-L1R2-16	Intron 1a	6 184		gtgatcaaggaaatcatia	G/A	gagcatcaattgtttgtgc			
i-L1R2-17	Intron 1b	550		agaggtgaagaactgtgac	T/C	cagagatgagcaaatgact	+		rs2310169
i-L1R2-18	Intron 1b	576		atfgacaaatgactatgfg	T/G	tfgcctaagatacacatggt	+		rs2310170
i-L1R2-19	Intron 1b	752		gtgtgttatatgtaagca	C/T	gcaacatttatatgtgtat			
i-L1R2-20	Intron 1b	1 167		ctccgtatgtcacaccagg	G/T	tatgccatttcacagatga			
i-L1R2-21	Intron 1b	1 400		tgaagttaaaggagggaagaa	T/A	ttagggatccaaatG/Acag	+		
i-L1R2-22	Intron 1b	1 417		aaat/Atttggatccaaatg	G/A	cagacatttctaatttggga			
i-L1R2-23	Intron 1b	1 626		aaccaaggattgtgtaggct	T/C	gggtttacatcctattgtc			
i-L1R2-24	Intron 1b	2 792		tgactcagtgatagggttaa	A/G	ggctgatactatgtgactt			
i-L1R2-25	Intron 1b	9 208		taggtgtctacaaagattcga	C/T	tttagatatgttcagtgaa			
i-L1R2-26	Intron 2	776		agtacccagggtgtgaggtc	T/A	ttttttaggggacaaatgac			rs2302589
i-L1R2-27	Intron 3	5 364		ggatattgtttcttgatca	T/C	gaagttggagatgtcggggg			rs2236930
i-L1R2-28	Intron 3	5 385		gaagttggagatgtcggggg	C/T	tgggtctcaaggaggtccagga			rs3218896
i-L1R2-29	Intron 3	5 585		aaagatcagggacagaagta	T/C	tgcataatagatgtctcgc			rs2073492
i-L1R2-30	Intron 3	5 735		ttcctaaatgggtgagaa	T/C	gcttacaatgacctacagct	+		rs3218900
i-L1R2-31	Intron 3	5 776		gggcaagtcactaacaca	A/T	aagctattttgtataaagc	+		rs3218901
i-L1R2-32	Intron 3	5 895		aaG/Attgaaccatctatgic	G/A	tgaaccatctgtactaatc			rs2282744
i-L1R2-33	Intron 3	5 913		cttttttactgcccataaa	A/G	ggaagacT/Ataaatctgat			rs2282743
i-L1R2-34	Intron 4	61		actagccataaaA/Ggaagac	T/A	taaaataatcgtttttcgaa			
i-L1R2-35	Intron 4	69		tgcacatgtctgcatgacaa	A/T	gtttcagtcacagtaggct	+		rs3218903
i-L1R2-36	Intron 4	284		aatttctatgctcctagac	A/G	tcatactgtctcacaatca	+		rs3218905
i-L1R2-37	Intron 4	368		atgtttagatatgtttat	G/A	tacaaaaactgaccactgtg	+		rs3218906
i-L1R2-38	Intron 4	432		ttctattctgcagagacccc	A/G	ggagacctgtgtccatata			rs2236923
i-L1R2-39	Intron 4	3 060		gtagttaaccaaaactagca	A/C	ttttattgttttatagtta			rs2072482
i-L1R2-40	Intron 4	3 386		tatagttaacaaattcctt	C/T	ccctataataacagtcacaa			rs2072481
i-L1R2-41	Intron 4	3 418		tcccacattgttgataag	A/T	tgatglaattcatagccttt			rs2072480
i-L1R2-42	Intron 4	3 517		gcatgcagagaacaatgac	G/A	gtgcaC/Ttgaatctcttgc			
i-L1R2-43	Intron 5	68		agagacaataatgacG/Agtgca	C/T	gtagaattccttgcaggctc			rs2072479
i-L1R2-44	Intron 5	74		gttgcaagatgaaggctaaa	A/T	caccactcaagagagtcga			rs2072478
i-L1R2-45	Intron 5	252		gtctagctgcccttaatagc	A/T	atatccaataatgacagac			rs2072477
i-L1R2-46	Intron 5	485		catgtgtcaacatttatic	A/G	gtaccaactgtgtgcgggac			rs2072476
i-L1R2-47	Intron 5	590		ataatctgaaacaggatata	C/T	ttgtcttcacaaagccta			rs2072475
i-L1R2-48	Intron 6	228		tggfgccatgaaaatgacaa	C/T	tgggggtttctgtctttcac			rs2072474
i-L1R2-49	Intron 6	498		ggagtggcataggaaggagaa	A/G	gggtggcatctcaaccctgt			rs2236922
i-L1R2-50	Intron 6	1 288		ttagaataactaaattttct	C/G	ccaaggaagaatgtgggtgg			rs3218974
i-L1R2-51	Intron 6	2 160		ttttggagacagtatact	A/G	tgacccacataccacattaa			rs2236921
i-L1R2-52	Intron 7	71		actgttggatgttagaatt	A/G	aaaaaatgtattttgctaa			rs3218977
i-L1R2-53	Intron 7	134		tgcaggtttccagagttagaa	T/A	T/Cagcagtagagatgagaag			rs2318979
i-L1R2-54	Intron 7	997		gcagggtttccagagttagaaG/A	G/A	cagcagtagagatgagaaga			rs2241082
i-L1R2-55	Intron 7	998		agagacggcaccactgaggg	T/C	tggagctctggaaactcctt			rs3218980
i-L1R2-56	Intron 7	1 036		atgggtacttctaaggaga	G/A	tgttagatgtctacattgt			rs2072473
i-L1R2-57	Intron 7	1 365		tgggtctgtccttgggtcact	A/G	atcagctgtctctgcatggc			rs2072472
i-L1R2-58	Intron 8	304		gggaatggcaccacttttc	C/T	tccaactgtgcctgtgcac	+		rs733498
i-L1R2-59	Intron 8	810		cttggccacttacctacga	C/T	gtttctaacaagattttgcc			rs3218984
i-L1R2-60	Intron 8	1 746		ggcccatgtggccctctgac	T/T	agccattgttctgggtatg			
i-L1R2-61	5' Flanking region	(-1 044)-(-1 043)							

Table 1. Continued

I.D.	Region	Exon	Position ^a	5' Flanking sequence ^b	Variation ^c	3' Flanking sequence ^b	Substitution	Repetitive sequence	Identity to dbSNP/ previous report
i-IL1R2-62	Intron 1a		78~97	ggaggagagagagagaaa	(G>A)10~11	gggggagagagagagga	+		
i-IL1R2-63	Intron 1a		1569~1570	gtttctctgtctgtcgt	TT/del	ctctctctctgtctct	+		
i-IL1R2-64	Intron 1a		4475~4494	atccctggggtgttttcagt	(T)19~22	gggggggagatgggctgact			
i-IL1R2-65	Intron 1a		4899	agcccttccactagggc	T/del	ggggaataaagcctgtcgt			
i-IL1R2-66	Intron 1b		5377~5394	gtgaaacatgtgtatttgac	(A)15~18	gataaatcttaactaaat			
i-IL1R2-67	Intron 7		1429~1435	caatcataatgaatgaatg	(A)7~8	aactcagggaatctcagaa			
i-IL2R-1	5' Flanking region		~606	ccacttttgcattgatctctt	T/C	aagagaaaagaatctggag			rs2104286
i-IL2R-2	Intron 1		5006	tagtcatggtaacacaagtc	A/G	tatgtgtaagtactactga			rs706778
i-IL2R-3	Intron 1		5102	ggactgtgaaatttccatca	A/G	tgcattccaggaggagagg			rs706779
i-IL2R-4	Intron 1		5227	tgtaggaaatttccctcaa	A/G	caatgtcctgtctccatg			
i-IL2R-5	Intron 1		5874	tttaacacggagatgaac	T/C	gcgtctgaatggctccatt			
i-IL2R-6	Intron 1		7451	ctggagtcgtgtacatggac	C/T	ggttccatgagtagtaggc			
i-IL2R-7	Intron 1		7852	cagtgctttgtcctgacag	A/C	ccattctccactccacac			
i-IL2R-8	Intron 1		7893	ccaaccagtcccccggggg	T/G	ttttgaccagcagctccgcc			
i-IL2R-9	Intron 1		7929	ccgcctgcagcccctgaccc	G/A	gattcaggcaicctcttaa			rs1924138
i-IL2R-10	Intron 1		8215	gcaagaacaagctgtgtgcaa	T/C	tggactagcagaattgagt			
i-IL2R-11	Intron 1		11958	caagttaatctccctgaaa	G/A	cacctgtgtgagcccttt			
i-IL2R-12	Intron 1		11996	tttcggcgtcaagagctcca	G/A	tcatttccattgctctcagg			
i-IL2R-13	Intron 1		12408	gtatacgtatgggtgagtgcc	G/A	tgtaaagaagaaggagaaa			
i-IL2R-14	Intron 1		14709	ggctgcgtggtcttgaggc	C/A	cccaaggtagaacaacagctt			rs791588
i-IL2R-15	Intron 1		15083	taactactgttcccacccc	G/A	agtaaaaagcaggatctct			rs1107345
i-IL2R-16	Intron 1		16756	ataactagatccctccacc	C/A	accaccccatcttctgtg			rs706780
i-IL2R-17	Intron 1		17025	ccacacgcctcttctctct	G/T	tcccagggaatcagcgaac			
i-IL2R-18	Intron 1		21655	ttaacacgtgtgatttgggt	G/T	ggcagcaatcagaagaattga			
i-IL2R-19	Intron 1		24205	ttattaaacagtaaacctca	C/T	ctcactatacaagatagcct			
i-IL2R-20	Intron 1		24572	ttcctgtctccgtgctgfta	T/C	tctaattctacgtgggtaca			
i-IL2R-21	Intron 1		24707	ctggatttcacccaaggggca	A/G	agaatcttatctcagactcg			
i-IL2R-22	Intron 1		25512	attccacgtcagggagagagc	C/T	ggctgctgcccaagctgct			
i-IL2R-23	Intron 1		25661	agtgacgcggagagcaaga	C/T	caacttatttcccaagttc			
i-IL2R-24	Intron 1		26206	gtagctgtatttccgccaca	A/C	tgatggagggtaggggtggaaa			
i-IL2R-25	Intron 1		26255	gaaacaagtgggattctgcc	A/G	tgtctgtctaalgagcatcc			
i-IL2R-26	Intron 1		26290	gcatcacacagcaaaactcaa	C/T	gggaagatgtgaacaacgctc			
i-IL2R-27	Intron 1		26723	ggagccacactagaacttg	G/A	ccctggcgcagctcacccact			
i-IL2R-28	Intron 1		26860	gaaacctggctctctcagg	G/C	tcccattcaagtgttctgggc			
i-IL2R-29	Intron 3		7	agcagagcttccaggtgaga	G/C	atgaA/Ttctgtctccagctia			
i-IL2R-30	Intron 3		12	gcttccaggtgagagG/Catga	A/T	tctgtctctcagctaactcc			
i-IL2R-31	Intron 3		409	taagcacagacaacagcacc	G/A	caaaaaaattactcttcc			
i-IL2R-32	Coding region	4	516	agcgctctgcaaatgaacca	C/T	gggaagacaggtgggacca	His172His		rs2228149
i-IL2R-33	Intron 4		122	acaagaccttgatctccct	G/A	ggcttccatttttctcatt			
i-IL2R-34	Intron 4		188	agaccagatcagatggactc	T/C	aagggctctcttcaatgaagg			rs2076846
i-IL2R-35	Intron 4		1333	tcagagttagaattcagcct	C/T	gtctgtctctgtgagaccac			rs2274037
i-IL2R-36	Intron 5		52	ggcttagtccaaaaggcag	G/A	gggtgaccaggagccagctc			
i-IL2R-37	Intron 6		761	atctgggaagggtgtacccc	G/A	ggcctctgccaggggctcaag			
i-IL2R-38	Intron 6		958	gaaacccgaccttttcag	G/A	agatgttaaT/Ggtgtcttca			
i-IL2R-39	Intron 6		968	cctctttcagG/Aagatgttaa	T/G	ggtcttctcatcttctcat			
i-IL2R-40	Intron 7		3049	cagggcttccctgacccctg	C/T	cagatccactctggccaac			
i-IL2R-41	Intron 7		3267	agtgtcaaatgtatagcccc	T/C	aggggttatttagtcagggaat			
i-IL2R-42	3' Untranslated region	8	1788	ggaaaggaaagaaagaggaa	G/A	tgaaggaggagaaaggatgg			
i-IL2R-43	3' Untranslated region	8	1827	ggagggtcacactggttagaac	G/A	taaccacgggaaagagcgca			
i-IL2R-44	3' Untranslated region	8	2086	ggctgcagtcagtcagtatg	G/A	caccactgcatctccctctg	+		rs1570538

Table 1. Continued

I.D.	Region	Exon	Position ^a	5' Flanking sequence ^b	Variation ^c	3' Flanking sequence ^b	Substitution	Repetitive sequence	Identity to dbSNP/ previous report
i-IL2R-45	Intron 1		9198	acccccagacgacttgggg	G/del	catctttagagaagcggca			
i-IL2R-46	Intron 1		9446	cctctgagcgtgagggggg	G/del	cgcgttttccctgggaa			
i-IL2R-47	Intron 1		11018~11031	aagcaaaacaacaattacc	(A)12~14	gttggagggtgtttcagaa			
i-IL2R-48	Intron 1		27539~27540	catataagtggaaatcctct	T/ins	gtttattactgtcgaagactt			
i-IL2R-49	Intron 3		1590~1591	caaaacacagattcagctgt	T/ins	gattgtcaaggtgccacatg			
i-IL2R-50	Intron 4		160	attctgagaaaaaataaaa	A/del	tttaaatagaccatcaga			
i-IL2R-51	Intron 5		102	ggcggaggtgacctgtaggg	G/del	agaagcccacagcagcctcc			
i-IL2R-52	Intron 6		1219	cctcgccttgccttttggg	G/del	atgtctcagcctggccctgt			rs2070946
i-ITGB2-1	5' Flanking region		~393	tccgctccattctctggctc	A/G	ggaaattgtctcccccgggtt			rs2070947
i-ITGB2-2	5' Flanking region		~39	aaacagaaagtgtcaggaactt	T/C	acgaccccgccctccagctg			rs760452
i-ITGB2-3	Intron 1		95	accttgggtggccctgttat	A/G	gccccggcccagggtgtct			rs760453
i-ITGB2-4	Intron 1		224	tgggtgtgtcgtggagccttg	C/T	ggcttgaaggatggggccggca			rs760454
i-ITGB2-5	Intron 1		656	atgtatgtgtgcacatgtga	A/G	tgtagtgtgtgtgtgtgtgg			
i-ITGB2-6	Intron 1		792	gtgctgattctgtcaggttg	G/A	ttcagctgtgtgacctggcc			
i-ITGB2-7	Intron 1		874	tgggagggggattgaagcca	C/T	gccccctgtgtccaggccca			rs741961
i-ITGB2-8	Intron 1		1123	ctgcaatggggaaaggggggg	G/T	atggccggagagctcagcct			rs873555
i-ITGB2-9	Intron 1		1150	ggagagctcagcc'ggggagc	G/A	agctgtgggggcataggggga			rs873556
i-ITGB2-10	Intron 1		1500	ccctcagattcttggggat	G/T	agtgggggagctcctctgcC/T			rs1811079
i-ITGB2-11	Intron 1		1520	G/T agtgggggagctcctctg	C/T	ggggaagggttccc'gggctac			
i-ITGB2-12	Intron 1		2539	ggggcccttgcctgcac	G/A	tgtcctgtgtcagagaaaccg			rs2838737
i-ITGB2-13	Intron 1		3171	cagctctcagcccttgcgcc	G/A	tgcctagaggagaggctgggc			
i-ITGB2-14	Intron 1		4975	ccctgaccttgggaaata	C/T	gcttttcaggggtcgcaggt			
i-ITGB2-15	Intron 1		5156	tctctcagttctttatcac	G/A	ttctacaagaagcaaatga			
i-ITGB2-16	Intron 1		5327	catgtccatcacttccgc	G/A	cacctccG/A agtcaatttgat			
i-ITGB2-17	Intron 1		5335	atcacttccgcG/A acctcc	G/A	agtcaatttgatggagtgcc			rs2838736
i-ITGB2-18	Intron 1		5366	atgcgagtgctctctcta	G/A	gacagcgcacagggtgttctc			rs2838735
i-ITGB2-19	Intron 1		5454	gggctcttgggttctcaagc	A/G	gtctcgtctiagggtttttac			
i-ITGB2-20	Intron 1		6418	gggggaaggatgacctctcc	C/G	ccctgtctctcccccctcagc			
i-ITGB2-21	Intron 1		6660	ggccgccttagatggggga	T/A	gtccaagctggaggatgag			
i-ITGB2-22	Intron 1		7292	ccagggctgtctcatggaggga	G/C	caacagtgagggaaggggtgg			
i-ITGB2-23	Intron 1		7667	accctgggggagctctgaagc	C/T	gggtctgggaacctgcaacctgg			
i-ITGB2-24	Intron 1		7982	accctggggtagctccagca	C/T	ggctgggaacctgcaacctgg			
i-ITGB2-25	Intron 1		8051	cgctcatttgcctctggggc	T/C	gcacaggcccttcgaltcagc			rs2280965
i-ITGB2-26	Intron 1		9072	cgctcatttgcctctggggc	C/T	ttccacggaggggagctccac			
i-ITGB2-27	Intron 2		12	tgggtgtcgtgtgagttctgt	G/A	ggggcctctgtgagtgaccac		Ser39Ser	
i-ITGB2-28	Coding region	3	117	tggcgggaatgcatcgagtc	G/A	ggggcctgtgtgagtgaccac			rs2072702
i-ITGB2-29	Intron 3		16	agctgtgaagtgctctcttgg	A/G	ccccctccacctgtccacagc			
i-ITGB2-30	Intron 3		2912	ctctctcttgggtcagcct	C/T	gggtctggagagtgagtgctctg			
i-ITGB2-31	Intron 3		3173	gtggccccctcttgacctct	G/T	actccccctcccgaaactt			
i-ITGB2-32	Intron 5		7	gtccggccgcatgtgggtgagg	C/T	ccagtgcatctgcagggacaaa			
i-ITGB2-33	Intron 6		181	agggaaaggggcagggaagg	G/A	agggtgtaccacaggggctCTg			
i-ITGB2-34	Intron 6		200	gG/A aggggtgaccagagggt	C/T	gaaatattgtacccttggggc			rs2235133
i-ITGB2-35	Intron 6		235	gatttcattgtttgtgtgga	G/A	ttaaattgtacccttggggc			rs2329940
i-ITGB2-36	Intron 6		558	cactgtcacagagtgagg	T/C	cacagccttaggacacagcag			
i-ITGB2-37	Intron 6		919	gggggacccacacacagcttc	C/T	ggggccaccccccacagctctg			
i-ITGB2-38	Coding region	7	819	ttccatttgcggggcagcgg	G/A	aaagtgtggcggccatcttgac			rs2230528
i-ITGB2-39	Coding region	7	849	ggcattcttgaccccaacga	C/T	ggccgctgtctacacctggaggga			
i-ITGB2-40	Intron 7		39	cacccagccacccctggcca	G/A	ggacacactgtacggaggagga			
i-ITGB2-41	Intron 7		270	gggtctccagcccccactggcc	G/C	cctacctgggctgacagctg			
i-ITGB2-42	Intron 7		312	tgtggagggtatagtaaccgc	C/T	cccaaggctacgggctgacccc		Gly273Gly Asp283Asp	

Table 1. Continued

I.D.	Region	Exon	Position ^a	5' Flanking sequence ^b	Variation ^c	3' Flanking sequence ^b	Substitution	Repetitive sequence	Identity to dbSNP/ previous report
i-ITGB2-43	Intron 7		743	gataaagactcagggtcttc	C/T	gccgggagccacagacaggga			rs2838730
i-ITGB2-44	Intron 7		818	agagccgaccctgacactca	C/T	ggccttaccgaaactggagt			rs2838729
i-ITGB2-45	Coding region	8	906	tctcttccaggacttacc	A/G	tcgtgggcccagctggcgca	Pro302Pro		
i-ITGB2-46	Intron 8		42	gcacatctgggtgggggca	T/C	gtttcagccacagccagac			rs2838728
i-ITGB2-47	Intron 8		379	agataaattacacaaaac	G/T	ttcacagcttggagtgcg			
i-ITGB2-48	Intron 8		1856	ccagctacaagctcaacctc	G/A	ttgtgtgtggggccgacag			rs235333
i-ITGB2-49	Intron 8		1974	gaggtgtcttgggggacct	C/G	cgagtggggaccacagagctg			
i-ITGB2-50	Intron 8		2342	catcagtgccacgccccctc	C/T	gagtggtttctgcaccaag			rs2838725
i-ITGB2-51	Intron 8		3960	ggccagtgctgggagatgcc	G/A	tgccacaggtcttagccgtg			rs1970054
i-ITGB2-52	Intron 9		302	tggagaaaggagggtggacag	C/G	tcgtgtgggcaaacagtgacag			rs235329
i-ITGB2-53	Intron 9		446	aagctccaggagaagccctta	A/C	ccccgaatttctccctggt			rs2230529
i-ITGB2-54	Coding region	10	1101	cagaactctctccagggt	C/A	ttcttgatcacaaagccct	Val367Val		
i-ITGB2-55	Intron 10		178	ggcacacaggcatcagaggc	T/A	G/Atctgggagcaggcagcattc			
i-ITGB2-56	Intron 10		179	gcacacaggcatcagaggct/A	G/A	cttgggagcaggcagcattcc			
i-ITGB2-57	Intron 10		333	gtgagagggtctggggagg	T/C	ttctcacacgcttggcc			
i-ITGB2-58	Intron 10		1253	gcccggctgactttggctctc	G/A	gattctgagcatcagctcttc			
i-ITGB2-59	Coding region	11	1323	ggacataagacccgtgcaggt	C/T	cttcccaggtgtgagtgccg	Val441Val		rs235326
i-ITGB2-60	Intron 11		460	tggcagcccttggggcatggg	T/C	cttgtagagagccctctgggga			rs235325
i-ITGB2-61	Intron 11		954	ggactgtagggggtgactcagt	C/T	ggaaacacttggcagggtgtcg			
i-ITGB2-62	Intron 11		1055	aggagagcccgtggcagtgcc	C/A	gtctctgagagtgctcaggg			
i-ITGB2-63	Intron 11		1194	acgaaacagaggaggaggggc	G/A	ggggctgtggcaggaggagct			rs2075884
i-ITGB2-64	Intron 11		1279	accagccactcacagagcac	C/T	gggtatcgacagcagggccat			rs2075883
i-ITGB2-65	Intron 13		193	ccctccctgtgcacctggcc	G/A	cggggcccttgggattcaggctt			
i-ITGB2-66	Intron 14		860	ctctggagccctgtagggtgaca	T/C	ggcttggagctcacacccac			
i-ITGB2-67	Intron 14		1057	caggatggcagagggggggca	C/T	ggggagtgagagtgagcaggtc			rs173098
i-ITGB2-68	Intron 14		1113	ggcacaggaggtgaggggtgc	G/A	gattcagagatggcaggaggcaa			rs1108139
i-ITGB2-69	Intron 15		57	cacgtgcgtccacactatg	C/T	gaacctctgtgcggggagggc			
i-ITGB2-70	3' Untranslated region		2433	cagaataccaagttatttcc	G/A	ccctcaaaatgacagcccatg			rs684
i-ITGB2-71	3' Untranslated region		2456	ctcaaatgacagccatggc	C/A	ggcccggggtgcttcttggggggc			rs1160263
i-ITGB2-72	Intron 7		272	ttctcagcccaacttgcctccc	C/del	tacctggggctgacagctgct			
i-ITGB2-73	Intron 7		759~760	ctccggccgggagccacagac	AG/del	ggggaggggagccctctggggt			
i-ITGB2-74	Intron 10		384~385	tactatcaacctggagccc	C/ms	aaatccctgggtcaggggccac			
i-ITGB2-75	Coding region	11	1325~1328	catagtgcacgtgcagggttc	TTC/del	ccagtggtgagtgccgggtgcc			
i-ITGB2-76	Intron 13		340	ggcccccgttgcggagcccc	C/del	gcacacctggcaccgatggc			
i-MC2R-1	5' Flanking region		-3123	gaaccaagctcagaggaca	C/T	agtcctacactggctctctc			
i-MC2R-2	5' Flanking region		-2842	gtagcattaaactcccttct	A/G	aacC/delacaagtgggtctata			
i-MC2R-3	5' Flanking region		-1089	gggtgagtgagtgatgtcat	C/G	tggaggaattagggtgggtgcc			
i-MC2R-4	5' Untranslated region	1	-1329	acaagtccctagagtgagggc	C/T	gfgatgggctccccgtggagc			rs948322
i-MC2R-5	5' Untranslated region	1	-1211	actgtgcactggccgagtc	C/T	ggcttccccccagagacaca			
i-MC2R-6	5' Untranslated region	1	-807	ggcaaaagaataatcttctgt	A/G	tcactctcggctcaaat			
i-MC2R-7	5' Untranslated region	1	-601	ctgtcatcattcaacttca	G/A	tgttaccatagggttaatt			
i-MC2R-8	5' Untranslated region	1	-524	aatgtccattcacttca	T/C	atccacgtgtatgcatatt			
i-MC2R-9	5' Untranslated region	1	-194	gggaataagttttcttaag	C/T	gagtggtggctgggtttttatt			
i-MC2R-10	3' Untranslated region	1	952	cggtggcaagtgccagaata	G/A	tgttaacattccaacaaatgc			
i-MC2R-11	3' Untranslated region	1	1005	ctggccttcttccctaatg	G/A	atggcaaG/Cgatgtcccacca			
i-MC2R-12	3' Untranslated region	1	1012	ttcttccctaatgG/Aatgcaa	G/C	gatgatccaccagctagtg			
i-MC2R-13	3' Untranslated region	1	1509	gttagtctgattgattgatg	C/T	cacctcagtttccagaaagta			
i-MC2R-14	3' Untranslated region	1	1579	acgagcttcgagtttccaat	G/A	ataaatggacctctctggt			
i-MC2R-15	3' Untranslated region	1	1774	actattgaaagaagctgtaa	C/T	caactatgtgtt/insgttaca			
i-MC2R-16	3' Untranslated region	1	1991	aacaaacaccaaagcagac	A/T	tcaagcaatgggtgctgtatt			

Table 1. Continued

I.D.	Region	Exon	Position ^a	5' Flanking sequence ^b	Variation ^c	3' Flanking sequence ^b	Substitution	Repetitive sequence	Identity to dbSNP/ previous report
i-MC2R-17	3' Untranslated region	1	2777	aatgtaacatatatttatg	T/C	gattaaagTC/Tgtattctca			
i-MC2R-18	3' Untranslated region	1	2788	tattttatgT/Cgattaaagtg	C/T	gtatticaataagaggtaa			
i-MC2R-19	3' Untranslated region	1	3030	actgctcttgatttggta	G/T	ttaatctaagaacaaaatg			rs1940907
i-MC2R-20	3' Untranslated region	1	3286	gfgtgaggaaatcaacaag	C/G	ttcagactttcccatgagg			
i-MC2R-21	5' Flanking region		-2838	catttaactccctctA/Caac	C/del	acaagtgfgtctacaggtc			
i-MC2R-22	3' Untranslated region	1	1787~1788	gctgtaaC/Tcaactatgtgt	TT/ins	gttacaatgtagaagtacaa			
i-MC2R-23	3' Untranslated region	1	1863~1943	gagagagacagagacagaca	(G/A)11~15(GT)12~25	attttcccatgcttttggga			
i-PGR-1	Intron 2		432	tatacatattgtacataca	C/T	gaacatatatacaacatgt			rs529359
i-PGR-2	Intron 2		2892	atgtaagctgcttaatac	G/A	ctiaggaaatgtaaaagtica	+		rs1302678
i-PGR-3	Intron 2		3666	ccagtcatacataactataa	C/T	gccacacttttatttttgg			rs495189
i-PGR-4	Intron 2		4961	ttaagcaccactttacattia	G/T	gggtcattigaacatctact			rs572483
i-PGR-5	Intron 2		-4965	tgttttacactgtgttaga	A/G	tcacaatgttatgttgact			rs778938
i-PGR-6	Intron 2		-4448	tttgatggctcaactctaa	T/C	gtttaaagatgatgaaaagt			rs508533
i-PGR-7	Intron 2		-2632	aagtggtgacagtgggcac	C/A	acataataagaaataagcaaa			rs516693
i-PGR-8	Intron 2		-1136	tggcatitttggcccttggcc	G/A	tttaggctaactcttcccc			
i-PGR-9	Intron 2		-266	atactgacacattaaagaag	A/T	taaacagaatctcttgcaa			rs508653
i-PGR-10	Intron 3		291	tgtcattaaagtaacatgtgt	G/T	ggagctcagggcttctggcc			rs503362
i-PGR-11	Intron 3		664	cacagttatgcaagacaccc	C/G	tactcccttgaattttttca			rs553272
i-PGR-12	Intron 4		575	tatgcccacgaacacagagag	A/G	acttggatataatcacaca			rs545835
i-PGR-13	Intron 4		1373	atttggaaatatgatttct	T/C	tggttttgttgatatagtt			rs518382
i-PGR-14	Intron 4		2061	aaggctgggctcatgggtg	G/A	atgcattttggtagacacaca			rs1144133
i-PGR-15	Intron 4		3991	catitttctgcttttgaagc	G/A	tgcctaaacaaacttttagt			
i-PGR-16	Intron 4		9145	aagtgatgaaagagaagagc	C/T	ttctttttgtctactacct			rs657516
i-PGR-17	Intron 5		43	tttgtattttaaagtgta	T/C	gtaggataattttgaaagt			rs645213
i-PGR-18	Intron 5		490	ttcatgtgaatatattatatt	G/T	ttctagtggtaaatgctgac			
i-PGR-19	Intron 5		535	ttcatataactcacactta	T/C	ataagctcttacaagtttta			rs511484
i-PGR-20	Intron 6		-5599	attcattgtgattttctatga	C/G	aaccacagggagctaaagacc			rs504402
i-PGR-21	Intron 6		-4790	cagggaatagaagaagctgct	G/A	ttaattaatacagC/Gatggga			rs504372
i-PGR-22	Intron 6		-4776	gctgctG/A/taataataacag	C/G	atgggagaagagataatactg			rs542491
i-PGR-23	Intron 6		-4535	agctagaagaataagaaat	A/C	atttcaatctcaataacct			
i-PGR-24	Intron 2		730~731	tcagatttacttgcatagtg	TG/ins	tttcagattttaaactttcaa			
i-PGR-25	Intron 2		-5123	tgaactccctctatttcat	T/del	atgccatgtaacctgtttgt			rs905908
i-PGR-26	Intron 4		2239~2254	acttgccttatttacaagtgag	(AC)7~8	gcacacacacacataataa			rs905909
i-PTAFR-1	Intron 1		72	gctgcctctgcagaatcccca	A/G	ggctgctcagatctcggag			rs5938
i-PTAFR-2	Intron 1		381	aacggacaataatgctctac	G/A	tgatgcagatcctaaaccca			rs313152
i-PTAFR-3	Coding region	2	671	gggtgcagcagcagcacaacg	C/A	tgaagtcgaagcgcggcgcc			
i-PTAFR-4	Intron 2		183	catacaaaaattagccgggc	G/A	tgggtggcacagcctcttagt			
i-PTAFR-5	Intron 2		321~346	acagagcgagattcttttc	(A)22~26	gctttgggcaactactctca		Ala224Asp	
i-PTGDR-1	5' Flanking region		-1933	agttaaagataaaatacac	G/A	ctttacaaataaactccct			rs803010
i-PTGDR-2	5' Flanking region		-1766	aactgcagttaaacatcac	T/C	accataaacacctctatca			
i-PTGDR-3	5' Flanking region		-1525	ctgctaacctagcccttccc	C/T	ccagctctctacagtcactg			
i-PTGDR-4	5' Flanking region		-1257	accgtgaatgccccaaatg	C/T	gctgctatctagagagaagag			
i-PTGDR-5	5' Flanking region		-1193	agaagtgagtattcttacc	T/C	ttctctgactagtaattca			
i-PTGDR-6	5' Flanking region		-1085	cagttcaaacaccagcacca	C/T	tgcctctctctcagggtggct			
i-PTGDR-7	5' Flanking region		-69	cagatgtgcccacagaggagg	C/T	tgcctgtcgggtgctgggta			
i-PTGDR-8	Intron 1		5041	tgggaaaaatgcattcttc	C/T	aggagatgctctctctatggc			
i-PTGDR-9	Intron 1		5553	atattccaatctcttca	T/C	tgattaaaagctctccattct			
i-PTGDR-10	Intron 1		5592	ctattgggtctctccatcat	G/A	tgcacattcaacagggtgac			rs708486
i-PTGDR-11	Intron 1		5910	ctttcccaagctcccacttg	C/G	acctcatcagctctgtggcc			
i-PTGDR-12	3' Flanking region		410	atgattttatcatattggcc	G/A	atggttagttcatcttttgg			

Table 1. Continued

I.D.	Region	Exon	Position ^a	5' Flanking sequence ^b	Variation ^c	3' Flanking sequence ^b	Substitution	Repetitive sequence	Identity to dbSNP/ previous report
i-PTGDR-13	3' Flanking region	439		ttcatttttggccaattga	T/C	ctaagcagcc'tgaattat			
i-PTGDR-14	3' Flanking region	628		accacaaagaagcaaaatttc	A/G	ttttatcttttgaatacca			rs802987
i-PTGDR-15	3' Flanking region	903		caggacttagctcctagtga	C/T	gatagtaacaatggccttaa			
i-PTGDR-16	Intron 1	777~779		gcgatggaatgaattatc	TCC/del	tcaatttgaaggcatttgtt			
i-PTGDR-17	Intron 1	5416~5426		tgcctctagattgaaacaag	(A)10~11	ggatgtcaaccatgaaaaag			
i-PTGDR-18	Intron 1	5515~5519		gtaatttttccaagtcatc	TCAGG/del	tcttttcatttcattatc			
i-PTGDR-19	3' Flanking region	252~263		atttggcttgggtggcccta	(T)11~12	agagaggcct'gagacatac			
i-PTGER1-1	5' Flanking region	-1852		gcaaggggcgc'gggcccaga	A/G	ggcccccacaggaat'gctfegg			
i-PTGER1-2	5' Flanking region	-1626		cgggcacctgtgggctcttc	A/G	gg'gigtG/C'gctgggagccg			
i-PTGER1-3	5' Flanking region	-1618		tggggctcttcA/C'gg'gigt	G/C	tgc'tgggagccgct'feggt			
i-PTGER1-4	5' Flanking region	-1272		gggggtgtgttttctctgg	G/A	tgggggtgt'gctagctct			
i-PTGER1-5	5' Flanking region	-1159		ctaggctct'ggt'gtccagc	G/A	gggggggg'gtcactcttg			
i-PTGER1-6	5' Flanking region	-1072		tgaagggtcattgaaagca	A/T	acagaagt'ggt'caggggcca			
i-PTGER1-7	5' Flanking region	-1017		gagt'gt'gt'gct'gt'gt'gt	A/G	tctctgggg'gccaagt'ga			
i-PTGER1-8	5' Flanking region	-849		cct'gagt'cagggat'gt'ggc	G/A	gcagcaacc'ggc'tg'gt'gctg			
i-PTGER1-9	5' Flanking region	-762		tcttaggg'gt'gag'gct'g'g	C/A	cag'gt'gac'ctact'ctca			
i-PTGER1-10	5' Flanking region	-730		tacttctcagggcagggagcc	G/A	agt'ctt'gt'gt'cttaggagc			
i-PTGER1-11	5' Flanking region	-115		ctggccactccaggcccccag	C/T	ggggcgt'g'cgc'gggg'g'gagc			rs2241359
i-PTGER1-12	Intron 1	59		aggaggccat'gaaagggg'ggg	G/A	ggcaltggccact'gct'gtcc			rs2241360
i-PTGER1-13	Intron 1	328		ggagagccgcag'gt'gagcag	A/G	ggcag'gt'c'calt'ggggcaggg			
i-PTGER1-14	Intron 1	634		tggcagagat'gct'gagggc	G/A	ggg'c'g'gggggg'gaattctgca			
i-PTGER1-15	Intron 2	292		tgcgccgc'ctt'cattcccta	G/T	tcttttcaccacaacccctt			
i-PTGER1-16	Intron 2	419		tttccgcac'ccgttttctcat	C/G	tggatccccatt'acccctcc			
i-PTGER1-17	3' Flanking region	15		tctcgagcccccagcaggac	C/G	gt'gt'gt'cc'cgc'gggg'cttc			rs2241361
i-PTGER1-18	3' Flanking region	215		aagcgacac'gct'ggggcggc	C/G	ggggc'gt'gggg'ctc'cgc'ctggg			rs2241362
i-PTGER1-19	3' Flanking region	242		ggggcctcc'gct'gggagcaga	G/C	acagaagg'gt'gt'gt'ggggc'gt			rs2241364
i-PTGER1-20	3' Flanking region	811		ctctcgtcg'aaagt'gt'gta	C/T	gt'c'gt'g'c'gg'c'c'g'gacagc'g			
i-PTGER1-21	5' Flanking region	(-1654)~(-1653)		cgcagctct'ct'g'g'actcag	GG/del	catcccc'ggg'c'ac'c'gt'gggg			rs2230541
i-PTGER1-22	5' Flanking region	(-1016)~(-1015)		g'gt'gt'gt'g'c'gt'gt'gt'A/Gt	TG/ins	ct'c'gt'gg'gt'g'c'c'a'gt'gag			
i-PTGER1-23	Intron 2	394~401		tgttt'gtttt'gtt'ggccccc	(T)7~8	ccgcact'cc'gtt'ctcatC/G'g			
i-PTGER2-1	5' Flanking region	-1780		taaaaagggtataaaaattat	C/T	ggaaaaataagcac'gt'g'c'caa			rs1254602
i-PTGER2-2	5' Flanking region	-1568		gcaaaagt'ggt'ataaagt	G/A	tta'ct'acct'g'cag'ag'gt'tta			rs1254601
i-PTGER2-3	5' Flanking region	-1391		tgtct'gt'ct'agt'gggaacc	A/C	ccccC/A'cccaact'ccg'cattc			
i-PTGER2-4	5' Flanking region	-1386		gttctagt'gggaaccA/C'cccc	C/A	cccaact'ccg'cattc'caatc			
i-PTGER2-5	5' Flanking region	-854		tccacaaacacaaattctgta	T/C	aagaC/A'acact'ctcttttt			rs1658086
i-PTGER2-6	5' Flanking region	-849		aaacacaaattctgtaI/Caaga	C/A	acact'ctctttttt'aaatg			rs1658087
i-PTGER2-7	5' Flanking region	-660		tcatcccaattt'gt'ccca	A/G	ctctt'agt'gt'at'ct'ctg			rs1254600
i-PTGER2-8	5' Flanking region	-462		ctggcagacc'ccc'caagtg	C/G	tcc'gt'cact'ccct'ccagcc			rs2075797
i-PTGER2-9	5' Flanking region	-361		accccagggaagc'gagaaac	G/A	ccgc'tccc'cc'cc'gt'c'c'gggg			rs1254599
i-PTGER2-10	5' Flanking region	-251		ctct'ccct'cc'cc'cc'ggcgc	G/A	ccccagg'gact'cggaac'cc			rs1353411
i-PTGER2-11	5' Flanking region	-12		ccact'g'c'g'c'g'c'g'ggga	G/A	acccagg'gcaac'cc'cc'g'c			rs1254598
i-PTGER2-12	5' Untranslated region	-72		tct'gagt'ct'ggaac'gt'cc	G/A	gct'ct'cag'ac'ct'ct'ctc			
i-PTGER2-13	Intron 1	1032		ggaagt'g'c'g'gg'c'ct'ctta	C/T	gggggg'ctag'g'aa't'g'gg'agt			
i-PTGER2-14	Intron 1	2260		ccgt'ttat'g'c'ct'ag'gggg	A/G	ggcagat'gg'ag'act'g'aag			rs1254597
i-PTGER2-15	Intron 1	2492		gggaacat'gt'c'ac'ct'ctta	G/A	taagaaaa'tt'at'att'gacc			rs1254596
i-PTGER2-16	Intron 1	3529		aact'tt'g'c'at'aac'ccatt	A/G	tctt'cacaG/A'acac'gt'aggaa			
i-PTGER2-17	Intron 1	3538		attaacccattA/G'ctt'caca	G/A	cacc'gt'agg'aaat'agt'at'ga			
i-PTGER2-18	Intron 1	4107		attt'g'c'at'ggaac'caacaa	C/T	atatt'cacaact'gt'ttattc			rs1254595
i-PTGER2-19	Intron 1	5825		ctgt'g'at'c'agg'caaaaggga	C/T	tctt'tt'aaag'cat'catat'ac			rs1254594
i-PTGER2-20	Intron 1	5929		caggacac'ctt'agt'gt'cttt	C/G	agaag'g'cag'g'g'aaacat'ata			

Table 1. Continued

I.D.	Region	Exon	Position ^a	5' Flanking sequence ^b	Variation ^c	3' Flanking sequence ^b	Substitution	Repetitive sequence	Identity to dbSNP/ previous report
i-PTGER2-21	Intron 1		6363	gtttatgtaataataaaca	A/C	aatatgacctataaatgtct		+	rs1254593
i-PTGER2-22	Intron 1		10391	ctatgccagattctccgc	A/G	taaaacacctatggctgccaa			rs708498
i-PTGER2-23	Intron 1		11658	aaaatacatcattattgtta	C/T	agtttataataaggaagaag			rs1495785
i-PTGER2-24	3' Untranslated region	2	1139	gatcatttgaatgtgtcc	T/C	tggagaaatgaacacagtgt			rs708502
i-PTGER2-25	3' Untranslated region	2	1286	agctacaacacactccctca	G/A	tggagcatgtactctggcctt			rs17197
i-PTGER2-26	3' Untranslated region	2	2005	ataagatgactgtgtgtac	C/T	aaaattcatctgtctatatt			rs1042618
i-PTGER2-27	3' Flanking region		256	tgatcttataaataagtagaa	T/C	caatctattttttcatagt			rs1254582
i-PTGER2-28	3' Flanking region		741	aattttcacccaccttac	T/C	gccccC/Taaatacccagaa			rs1254581
i-PTGER2-29	3' Flanking region		748	caccacaccttacT/Cgcccc	C/T	taaaatcccagaataatgcc			
i-PTGER2-30	3' Flanking region		935	gtccatgtactgtctgaa	C/T	gactaaatcttgggtatttca			rs1254580
i-PTGER2-31	3' Flanking region		1517	caaaagtgggtggaccatg	A/G	caaccaggagcaagacC/Tgaa			
i-PTGER2-32	3' Flanking region		1534	atgA/Gcaaccaggagcaagac	C/T	gaaactctagaacacctcc			
i-PTGER2-33	3' Flanking region		1628	aactgattcacatcacata	C/T	gctcatgtaactcagttaca			rs1254579
i-PTGER2-34	5' Flanking region		(-1390)(-1383)	gctgttctagtgggaacca	(C)6-9	ggggagcagatggagact			
i-PTGER2-35	Intron 1		2254	caatttctgtttatggctt	A/del	aaagaatgaattaggcaag			
i-PTGER2-36	Intron 1		5872-5880	ataatctcccccaaatg	(T)9-10	ccaatttcactctcatta			
i-PTGER2-37	Intron 1		9877	gaattgctcactcttaca	A/del	tgcccaaacatttatgtgc			
i-PTGER2-38	Intron 1		10732	attattcactctctcaac	C/del	tccctattctggggaggat			
i-PTGER2-39	3' Untranslated region	2	1842-1845	attctcataataactcttta	TTTA/del	gagatgctgtttttccaa			
i-PTGER2-40	3' Flanking region		301-312	ttattggatagccactcctt	(A)12-14	ctaacacaccatcttagct			
i-PTGFR-1	5' Flanking region		-325	tgaagctaccactccgacag	T/C	gggctggcgccaggaaggc			
i-PTGFR-2	Intron 1		520	gtagcctaggcagttccact	C/A	agcctccgggaaagttagct			
i-PTGFR-3	Intron 1		556	aaggctggctcccggaattcc	C/T	tatccagtgctgtgtccctca			
i-PTGFR-4	Intron 1		629	aagagtggccgtgacctgt	G/A	gtccctctccaaagtttggga			
i-PTGFR-5	Intron 1		938	ttaacatcaatgaactgtct	G/T	gggtgctggggcagctcagct			
i-PTGFR-6	Intron 1		1356	gataaaacccatccaccac	T/C	gtggatatttgaatgtatg			rs1555541
i-PTGFR-7	Intron 2		2218	gcaaaatttactactcttgg	T/C	gggtgccacttctctttaa			
i-PTGFR-8	Intron 2		2359	cactttacagagaacatttc	T/C	caccacaggA/Gttactttat			
i-PTGFR-9	Intron 2		2464	gtgttagatgggtagtagat	C/A	ttactttaiggcctgtatatt			
i-PTGFR-10	Intron 2		2475	gttagtagatC/Accacaggt	A/G	actctgaacacaaatggtaa			rs1322934
i-PTGFR-11	Intron 2		4211	tgtaggttaacagccaagca	G/A	cttgggtattttatttata			rs2057423
i-PTGFR-12	Intron 2		6235	gaatttcatggacatactag	G/A	gggggacaagaggagaaactt			
i-PTGFR-13	Intron 2		6558	tatctctgagagaatcatgt	T/C	tggtaaatatggaaatttgt			
i-PTGFR-14	Intron 2		6635	tgtcataaaatgaaagctct	G/A	ccagaaataactactgttag			
i-PTGFR-15	Intron 2		10721	aaatcttccaaatccacta	C/T	ttttaccctagctaattggga			
i-PTGFR-16	Intron 2		10761	gtattctgggtgcatctatc	T/C	ggagaaattacaattctggac			
i-PTGFR-17	Intron 2		22053	caaatctggagttttttatt	G/A	gattgatttttaataacag			
i-PTGFR-18	Intron 2		25198	aattaaaaaaattttttica	T/C	gtagtaacctcagtgaaat			
i-PTGFR-19	Intron 2		25362	aagtaaaagagacagagcac	C/T	gacctgataaggacatgta			rs520171
i-PTGFR-20	Intron 2		27893	tgttctaataatttttgacta	T/C	agggtgtgaacctgtccctg			
i-PTGFR-21	Intron 2		30624	catgatgagggcacttgttc	A/C	agaatttatctacttagct			
i-PTGFR-22	Intron 2		31049	cacttgcaatacaaccigtat	C/G	tggcctttttgtgtatgttt			
i-PTGFR-23	Intron 2		32835	gctaaacatgtttctagtct	C/G	ggcatcctaacaatttgcctc			rs473027
i-PTGFR-24	Intron 2		32953	caccatagccacagacatcc	A/G	atctctgaacctggacggg			rs668005
i-PTGFR-25	Intron 2		32976	cactctaacattttgtccta	A/G	ctgtgtctgactcgtagaatta			rs530871
i-PTGFR-26	Intron 2		33311	attaaaaaggatagaaacaa	A/T	tgttggtcagaaatctggag			rs538275
i-PTGFR-27	Intron 2		33591	atgaaatgtcttcttaaaaga	C/T	accataggtctgttacctgg			
i-PTGFR-28	Intron 2		34615	gaaataatgatcagagattt	G/A	taatggatagatgccaggc			rs589598
i-PTGFR-29	Intron 2		35438	gaaccaatgcacacatttca	G/A	cctaactgggtatggcttgtt			
i-PTGFR-30	Intron 2		35657	ggagatgggttactgaaac	G/A				

Table 1. Continued

I.D.	Region	Exon	Position ^a	5' Flanking sequence ^b	Variation ^c	3' Flanking sequence ^b	Substitution	Repetitive sequence	Identity to dbSNP/ previous report
i-PTGFR-31	Intron 2		35 696	tttttctattataaacgacg	T/C	tgcagT/Cggtaataaagt			
i-PTGFR-32	Intron 2		35 703	tattataaacgagT/Ctgcag	T/C	ggtaataaagttagccttt			rs590309
i-PTGFR-33	Intron 2		38 235	tctgtctcccactcaa	G/C	tgttaggtctctctctaat			rs622346
i-PTGFR-34	Intron 2		39 361	tataaatataagaagagg	T/A	tattcttgaatgtactat			
i-PTGFR-35	Intron 2		39 533	ttctgtccagtgtatttc	T/C	taaagaagaattgagaaac			
i-PTGFR-36	Intron 2		39 862	gtaggaagcttgactaga	C/T	aacattttcgtaccctgt			rs501078
i-PTGFR-37	Intron 2		40 043	gggtgagtgccatctagac	G/A	atgctcatatagagagaca			rs686262
i-PTGFR-38	Intron 2		40 141	gcataatatacaaatftacc	A/G	tgtcttgaatagtaaacag			
i-PTGFR-39	Intron 2		40 570	atacaactgtaatgtgcaa	T/C	gttcacagaaagagatttta			
i-PTGFR-40	Intron 2		42 768	acaatgcatcatctctgtgg	A/T	aagtgaatgtaatgtcatct			
i-PTGFR-41	Coding region	3	1 031	cattataaatcttaagg	T/G	tgtctattctgagtcac	Val344Gly		
i-PTGFR-42	3' Untranslated region	3	2 007	cagagaacaagaagaacaga	A/G	tcaatataaaatcaaaag			
i-PTGFR-43	3' Untranslated region	3	2 062	tgtgttctctttacac	A/G	tatacacagacatcagaa			rs899
i-PTGFR-44	Intron 2		347~348	acatttgaacagattgcagt	T/ins	aagttctgtatagaaagtcac			
i-PTGFR-45	Intron 2		6 530	ttcataatgtattttttt	T/del	ggttatttctctgagaga			
i-PTGFR-46	Intron 2		7 472	aaaacatgaccttttttt	T/del	aagaagaagacttatataaa			
i-PTGFR-47	Intron 2		23 217	tttgtacataattttttt	T/del	ctttgagaagtcgttttc			
i-PTGFR-48	Intron 2		31 366~31 399	cactttggacaaatgcaaga	(T)21~37	acigttaatgtatttgacc			
i-PTGFR-49	Intron 2		34 754~34 781	agtaagtccagaagttagc	(A)21~28	gcacaacatcaaatgtct			
i-PTGFR-50	Intron 2		41 157~41 165	gacaataattcatatttgg	(T)8~10	caaaaatggaaatcacacaat			
i-PTGFR-51	3' Untranslated region	3	2 927~2 939	agaaatgacatcaaaaatt	(A)9~13	ggaaatggttttcatgttt			
i-PTGFR-52	3' Flanking region		610~620	gtgaagaagaatggccctta	(T)9~11	ccctagaagcagaaagttaac			
i-TBXA2R-1	5' Flanking region		-2 646	tgcaccacaaaggagatggc	T/C	gtctccaactggcagagaca			
i-TBXA2R-2	5' Flanking region		-2 565	ggggccctgggaccctgaa	G/C	ggctcacggcactgagcctg			
i-TBXA2R-3	5' Flanking region		-2 521	agaggggtctgtggccgaga	A/C	gggtgacggctgccttgcag			
i-TBXA2R-4	5' Flanking region		-2 275	ccaagtcttccaccatggc	C/T	cgaagtccacctgggtctct			
i-TBXA2R-5	5' Flanking region		-1 054	ggaataccctcactcacgc	C/T	tggactagagccctcccg			
i-TBXA2R-6	5' Flanking region		-951	ccctaactcagaagttctgc	C/T	ggctgggggtgtaacaacaag			
i-TBXA2R-7	5' Flanking region		-863	ctgtgctcaggcactcttc	A/T	ggcatttctgttgggtcca			
i-TBXA2R-8	5' Flanking region		-226	ccggcgtgctggggggcacc	A/G	ctgactccaagtgcagcagg			rs2238634
i-TBXA2R-9	Intron 1		1 627	caggcaigtggagggtctggc	C/T	G/Agctccgaagtctcagtc			rs2238633
i-TBXA2R-10	Intron 1		1 628	aggcattggggagggtctggc	G/A	gtccctgaagtctcagtc			rs2238632
i-TBXA2R-11	Intron 1		1 799	gggcagaggaggcctgagct	T/G	agcacccgcaggcatggaga			rs2238631
i-TBXA2R-12	Intron 1		1 979	aggcggggcggcagggtggg	G/T	gtgctgaggagaggggactt			rs2238630
i-TBXA2R-13	Intron 1		2 030	ggatggatgtagtgggtgacg	T/C	gtctccaggaggtggggaggg			
i-TBXA2R-14	Intron 1		2 229	tcacagaccttgcgaagccgg	A/G	tacctgtcagggggtgggcat			
i-TBXA2R-15	Intron 1		2 263	gtggcatcggatgaggagaga	A/G	ctcactgtccgcttccaga			
i-TBXA2R-16	Intron 1		2 524	agttattcaatcagaaaag	C/G	gaatctgggtccacacctct			
i-TBXA2R-17	Intron 1		2 600	agccgcagtgctgcttact	G/C	ccccacggcgtggggggcccc			
i-TBXA2R-18	Intron 1		3 028	accagctctcagaggaggaa	C/T	ggcctgtcccagggggaaatc			
i-TBXA2R-19	Intron 1		3 301	gccagaagccagagccaagc	G/A	tcaacaagtggatggggaggt			
i-TBXA2R-20	Coding region	2	179	gcagggggggttcgcacacgc	G/T	ctctctctctcacttcc	Arg60Leu		Unoki et al. (2000)
i-TBXA2R-21	Coding region	2	243	ttcttggggctgctgtgac	C/T	gggtaccatctgtgtgccca	Thr81Thr		rs5745
i-TBXA2R-22	Coding region	2	435	tgcggccggcgggtcgccctc	G/A	cagcgccgcgcctgggccac	Ser145Ser		rs5748
i-TBXA2R-23	Coding region	3	924	atctgtgaccctgggtgta	T/C	atctgttccgcgcgcgcgt	Tyr308Tyr		rs4523
i-TBXA2R-24	3' Untranslated region	3	1 196	tcaaacccggggaccacca	C/T	tctctcctgatctttttacc			
i-TBXA2R-25	3' Flanking region		4 779	gggatgtcagtgaggagact	C/T	cccG/Agcccaacttcccgct			
i-TBXA2R-26	3' Flanking region		4 783	tgtcagtgaggagactC/Tccc	G/A	cggccaacttcccgctggga			
i-TBXA2R-27	3' Flanking region		5 009	ggagcccttcaggccagccc	C/T	ctcccagccccccccttaa			

Table 1. Continued

I.D.	Region	Exon	Position ^a	5' Flanking sequence ^b	Variation ^c	3' Flanking sequence ^b	Substitution	Repetitive sequence	Identity to dbSNP/ previous report
i-TBXA2R-28	3' Flanking region		5342	tctggccaatcatatctgga	G/A	ggaaacagagtgaggatggc			
i-TBXA2R-29	3' Flanking region		5364	gaacagagtgaggatggcc	A/G	tgggttctgggtggagccac			
i-TBXA2R-30	3' Flanking region		5438	ctttctagaatcttctcc	C/T	cttcaagtgctcttaccat			
i-TBXA2R-31	3' Flanking region		5703	cagaaccggcttagtgca	G/C	gactgagggtctagaacac			
i-TBXA2R-32	3' Flanking region		8234	tcaaggcctatctgacccc	C/T	aggagcttctgcatgtccac			
i-TBXA2R-33	3' Flanking region		8306	ttccgggggagagagacc	T/C	agagttagccagggcatgca			
i-TBXA2R-34	3' Flanking region		8738	aatactagggtgcgctag	T/C	cctaagacctgcccatttt			
i-TBXA2R-35	3' Flanking region		9258	cttctgcagctccctcc	C/T	ccggcccagggcgagacgc			
i-TBXA2R-36	Intron 1		2 099~2 100	agaggcctctgttgggaa	A/ins	ccaaggatcacattccactg			
i-VCAM1-1	5' Flanking region		- 1468	agtatctctgaatcaatt	T/C	tctatcccctagatatttgg			rs10411163
i-VCAM1-2	Intron 2		912	ctaattgattctgcaaca	A/G	ccgcattgtgtctcaagct			rs3176860
i-VCAM1-3	Intron 2		1014	tgtctgtagcctcccgag	C/T	ttctgaaagcttcccttat			rs3176861
i-VCAM1-4	Intron 3		1277	tgctaataattttttgcc	C/T	tttcagtatcaccacaagaat			rs2392221
i-VCAM1-5	Intron 4		2 547	ctcaagtgaccaggaagat	A/G	ttatactaataaagtgtgt			
i-VCAM1-6	Intron 5		721	agttatttttttggggg	G/T	tcactcgcctgttttatt			
i-VCAM1-7	Intron 5		1 495	tfgaaataataactacta	A/T	A/Gtaagatgtgggaaactgat			rs3176869
i-VCAM1-8	Intron 5		1 496	gfgaaataataactacta	A/G	taagatgggtggaactgatg			
i-VCAM1-9	Intron 7		468	attatgagtagccatgact	C/T	gtccttgggtcatcagcct			rs3181088
i-VCAM1-10	Intron 8		284	aatgttaaccatttttca	A/G	accttttccggggagggtat			rs3176876
i-VCAM1-11	Intron 8		823	ttggctattggagtgagcaa	T/A	cacttgtcaatgcagagaaa			
i-VCAM1-12	Intron 8		1 898	aataatgtagcctatccata	A/G	tcattgtgtagtgacatccca			
i-VCAM1-13	Intron 8		1 932	catccattcaaatattacc	T/C	ttatactttagtagctcag			
i-VCAM1-14	Intron 8		2 030	tttttctcaataatttgaa	A/G	aagtgtactcacattatctg			
i-VCAM1-15	Intron 8		2 277	cttcagctgctcttataaag	T/G	taagatgtaagcagatag			
i-VCAM1-16	Intron 8		3 071	tgttctgttataaaactgt	A/T	ccctccctccatttttcaaa			rs3176877
i-VCAM1-17	Coding region	9	2 208	agtctgtagaagcacagaa	G/A	tcaaaagtgtagctaatgct	Lys736Lys		rs3176879
i-VCAM1-18	3' Flanking region		46	aaactgctcctcttagtcac	A/G	tgttagctcttcttgaaagt			rs3181092
i-VCAM1-19	3' Flanking region		130	gatactcaaaaatgacacct	T/C	agactactattataaatt		+	rs3181093
i-VCAM1-20	Intron 1		393~396	tgattccataaactttttg	GCA/G/del	tgacttcgggtgcttttggc			
i-VCAM1-21	Intron 2		102~103	ttaaaatggatattcatga	CA/del	gattcttggcctaaagaacat			
i-VCAM1-22	Intron 2		561	acacatttaggattttttt	T/del	ggtttttttgggtgcttgaa			
i-VCAM1-23	Intron 2		570	ggatttttttttggttttt	T/del	gggtgccaatgaagccttgggtg			
i-VCAM1-24	Intron 3		81~94	aataaactagcagaaaagt	(A)12~15	cttgtatagttttgtattc			
i-VCAM1-25	Intron 5		28~38	gttttcagatgttttactg	(T)10~12	cagttctattggagaagaaa			
i-VCAM1-26	Intron 5		714	accataaagtattttttt	T/del	gaggggG/Ttactctgcttg			
i-VCAM1-27	Intron 8		2 864	catggcaagatttttttt	T/del	ctcttaacgacttattgtg			

dbSNP, database of single-nucleotide polymorphisms; ins, insertion polymorphism; del, deletion polymorphism

^aNucleotide numbering is according to the mutation nomenclature (den Dunnen and Antonarakis 2000)

^bBoth 5' and 3' flanking sequences to each variation are denoted by small letters

^cVariation is shown by capital letters

this study, which was approved by the ethical committee of the RIKEN SNP Research Center. The SNP screening methods described in an earlier report by Haga et al. (2002) were the principal techniques used in this study. In brief, on the basis of genomic sequences from the GenBank database in the US National Center for Biotechnology Information (NCBI), we designed primers to amplify all selected genes in their entirety, excluding only regions that corresponded to repetitive sequences predicted by the RepeatMasker program (<http://repeatmasker.genome.washington.edu/cgi-bin/RepeatMasker>). Each polymerase chain reaction (PCR) was performed with 20 ng of mixed genomic DNA derived from three individuals. All 16 mixed samples were amplified in the GeneAmp PCR system 9700 (PE Applied Biosystems, Foster City, CA, USA) under the following conditions: initial denaturation at 94°C for 2 min, followed by 35 cycles of denaturation at 94°C for 30 s, annealing at 60°C for 30 s, extension at 72°C for 2 min, and post-extension at 72°C for 7 min. Products obtained from the PCR experiments served as templates for direct sequencing and detection of SNPs, using the fluorescent dye-terminator cycle-sequencing method. All SNPs detected by the Polyphred computer program (Nickerson et al. 1997) were confirmed by sequencing both strands of each PCR product.

Accession numbers of the genomic sequences we obtained for this study are as follows: beta-1 adrenergic

receptor (*ADRB1*; AC005886.2), beta-2 adrenergic receptor (*ADRB2*; AC011334.4), bradykinin receptor B1 (*BDKRB1*; AL355102.5), bradykinin receptor B2 (*BDKRB2*; AF378542.2), leukotriene B4 receptor 2 (*BLTR2*; AL096870.5), CD20 antigen (*CD20*; AP001034.4), CD33 antigen (*CD33*; AC063977.5), colony stimulating factor 3 receptor (granulocyte) (*CSF3R*; AL445245.3), cysteinyl leukotriene receptor 1 (*CYSLT1*; AL445202.21), cysteinyl leukotriene receptor 2 (*CYSLT2*; AL137118.20), V-erb-b2 erythroblastic leukemia viral oncogene homolog 2 (*ERBB2*; AC079199.3), folate receptor 1 (*FOLR1*; U20391.1), histamine receptor H1 (*HRH1*; AC020750.3), histamine receptor H2 (*HRH2*; AB023486.1), histamine receptor H3 (*HRH3*; AL078633.32), 5-hydroxytryptamine (serotonin) receptor 3A (*HTR3A*; AP001874.3), intercellular adhesion molecule 1 (*ICAM1*; AC011511.9), interferon alpha receptor 1 (*IFNAR1*; AP001716.1), interleukin 1 receptor, type I (*IL1R1*; AC007271.3), interleukin 1 receptor type II (*IL1R2*; AC005035.1 and AC007165.3), interleukin-2 receptor (*IL2R*; AL137186.18 and AL157395.16), integrin beta 2 (*ITGB2*; AL163300.2), melanocortin 2 receptor (*MC2R*; AP001086.4 and Y10259.1), progesterone receptor (*PGR*; AC020735.5), platelet-activating factor receptor (*PTAFR*; AC027421.3), prostaglandin D2 receptor (*PTGDR*; AL355833.4), prostaglandin E receptor 1 (*PTGER1*;

Table 2. Summary of genetic variations identified in 31 genes encoding drug targets

Gene	5' Flanking region	5' UTR	Coding region	Intron	3' UTR	3' Flanking region	SNP	Other types of variation	Total	Identity to dbSNP/previous report	New SNP
<i>ADRB1</i>	4	4	2	0	0	3	13	7	20	5	8
<i>ADRB2</i>	4	8	4	0	2	1	19	2	21	13	6
<i>BDKRB1</i>	1	2	3	12	0	8	26	6	32	6	20
<i>BDKRB2</i>	2	0	1	4	3	4	14	1	15	11	3
<i>BLTR2</i>	4	1	0	0	1	0	6	0	6	4	2
<i>CD20</i>	2	0	1	18	2	6	29	6	35	9	20
<i>CD33</i>	3	0	1	3	2	1	10	0	10	3	7
<i>CSF3R</i>	2	0	1	7	0	0	10	4	14	2	8
<i>CYSLT1</i>	0	0	1	0	0	6	7	2	9	4	3
<i>CYSLT2</i>	2	0	0	0	2	0	4	1	5	2	2
<i>ERBB2</i>	0	0	4	5	0	0	9	0	9	5	4
<i>FOLR1</i>	1	0	1	4	0	0	6	1	7	0	6
<i>HRH1</i>	1	0	0	0	1	2	4	4	8	3	1
<i>HRH2</i>	7	2	1	0	0	0	10	1	11	5	5
<i>HRH3</i>	2	0	2	1	0	0	5	1	6	0	5
<i>HTR3A</i>	0	1	3	19	0	2	25	4	29	13	12
<i>ICAM1</i>	0	0	2	1	5	3	11	1	12	6	5
<i>IFNAR1</i>	6	0	1	15	0	0	22	2	24	16	6
<i>IL1R1</i>	0	2	3	39	7	0	51	11	62	16	35
<i>IL1R2</i>	0	0	0	60	0	0	60	7	67	38	22
<i>IL2R</i>	1	0	1	39	3	0	44	8	52	11	33
<i>ITGB2</i>	2	0	6	61	2	0	71	5	76	33	38
<i>MC2R</i>	3	6	0	0	11	0	20	3	23	2	18
<i>PGR</i>	0	0	0	23	0	0	23	3	26	19	4
<i>PTAFR</i>	0	0	1	3	0	0	4	1	5	4	0
<i>PTGDR</i>	7	0	0	4	0	4	15	4	19	3	12
<i>PTGER1</i>	11	0	0	5	0	4	20	3	23	7	13
<i>PTGER2</i>	11	1	0	11	3	7	33	7	40	23	10
<i>PTGFR</i>	1	0	1	39	2	0	43	9	52	14	29
<i>TBXA2R</i>	8	0	4	11	1	11	35	1	36	9	26
<i>VCAM1</i>	1	0	1	15	0	2	19	8	27	11	8
Total	86	27	45	399	47	64	668	113	781	297	371

SNP, single-nucleotide polymorphism; UTR, untranslated region

Table 3. Distribution of SNPs by the types of nucleotide substitutions

Gene	A/G	C/T	A/C	C/G	G/T	T/A	Total
<i>ADRB1</i>	3	7	1	1	1	0	13
<i>ADRB2</i>	6	7	0	4	1	1	19
<i>BDKRB1</i>	14	6	2	2	1	1	26
<i>BDKRB2</i>	5	5	1	0	2	1	14
<i>BLTR2</i>	1	1	2	1	1	0	6
<i>CD20</i>	9	14	1	2	3	0	29
<i>CD33</i>	2	3	1	2	2	0	10
<i>CSF3R</i>	4	3	1	0	1	1	10
<i>CYSLT1</i>	3	4	0	0	0	0	7
<i>CYSLT2</i>	1	2	0	0	1	0	4
<i>ERBB2</i>	4	4	0	1	0	0	9
<i>FOLR1</i>	2	2	1	0	0	1	6
<i>HRH1</i>	2	1	0	0	0	1	4
<i>HRH2</i>	5	3	1	0	0	1	10
<i>HRH3</i>	4	1	0	0	0	0	5
<i>HTR3A</i>	13	7	1	0	3	1	25
<i>ICAM1</i>	2	7	1	1	0	0	11
<i>IFNAR1</i>	4	8	1	4	5	0	22
<i>IL1R1</i>	18	12	5	6	4	6	51
<i>IL1R2</i>	22	22	3	3	2	8	60
<i>IL2R</i>	19	14	4	2	4	1	44
<i>ITGB2</i>	28	28	4	5	4	2	71
<i>MC2R</i>	6	9	0	3	1	1	20
<i>PGR</i>	7	7	2	3	3	1	23
<i>PTAFR</i>	3	0	1	0	0	0	4
<i>PTGDR</i>	4	10	0	1	0	0	15
<i>PTGER1</i>	10	2	1	5	1	1	20
<i>PTGER2</i>	13	14	4	2	0	0	33
<i>PTGFR</i>	15	17	3	3	2	3	43
<i>TBXA2R</i>	9	17	1	4	3	1	35
<i>VCAM1</i>	8	6	0	0	2	3	19
Total	246	243	42	55	47	35	668

AC008569.6), prostaglandin E receptor 2 (*PTGER2*; AL365475.1), prostaglandin F receptor (*PTGFR*; AL136324.6), thromboxane A2 receptor (*TBXA2R*; AC005175.1), and vascular cell adhesion molecule 1 (*VCAM1*; AL157715.5).

Results and discussion

By direct sequencing of DNA from 48 healthy individuals, we screened SNPs in a total of approximately 382kb of genomic DNA that accounted for 60% of the 638 kilobases encompassing the loci of 31 selected genes, minus repetitive sequences. We identified a total of 781 variations, including 668 SNPs and 113 variations of other types, and constructed a fine-scale SNP map of each locus (Fig. 1). Detailed information for each variation identified in this study is summarized in Table 1. Regional distributions of the SNPs identified among the 31 loci were as follows: 86 in 5' flanking regions, 27 in 5' untranslated regions, 45 in coding regions, 399 in introns, 47 in 3' un-translated regions, and 64 in 3' flanking regions (Table 2). The 86 SNPs present in 5' flanking regions (putative promoter regions) could affect the quantity of the respective gene products. Moreover, among the 45 SNPs found in coding regions, 15 were nonsynonymous changes; although the minor-allele frequencies of these 15 SNPs were as low as 2.2%, it should be

emphasized that such alterations are likely to influence functions and/or structures of proteins. The overall frequencies of nucleotide substitutions in our test population (96 chromosomes) were counted as 36.8% for A/G, 36.4% for C/T, 8.2% for C/G, 7% for T/G, 6.3% for A/C, and 5.2% for A/T; transitions occurred 2.7 times more frequently than transversions (Table 3). The overall genomic distribution was 1/572bp in the 382 kb of DNA that we sequenced. By comparing our data with earlier reports from elsewhere (Unoki et al. 2000; Muldoon et al. 2001; Okuda et al. 2002) and with the dbSNP database at NCBI, we were able to consider 371 of the 668 SNPs (55.5%) to be novel as of the middle of August 2002.

The 668 SNPs identified here provide genetic data that should be helpful for designing personalized medical care and also for identifying genes associated with drug efficacy and/or adverse drug reactions.

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