Supplement 1. The single nucleotide polymorphisms and oligonucleotides

dbSNP ID [1]	Genomic location	Variation	Frequency [2]	PCR primer Sequence 5'-3' [3]	Product size (bp)	MS-primer Sequence 5'-3' [4]
rs715405 $^{\mathrm{VIII}}$	1p31	A/G	57/43	AGGTATTACTCTGCTTACCACA	174	ATGCCAGGTCGTAGTCGAATAAAGACTGCTCACTGACAAAG
				CTGAGATGTTATTTGCTAGTTCA		TAGTCAGGTTGGATGTCTACCAGGCATTATATTTAGGCTGA
rs2991269 $^{\mathrm{IX}}$	1p32.3	A/G	77/23	ACTCTGCAGGAGGATAAAGAC[5]	195	GTCCTCGCTTCGTCTATGAGATCGACAGTGAGTGTGGCCC
				GAGACACACCTTGCCTAGAC[6]		GAGTAGCCTTCCCGAGCATTGGGTCACTGAGCTTGATGAA
rs5707 $^{\mathrm{VI}}$	1q32	T/G	53/47	GCACAATGGAACAGAACTCAC	174	CGATATAATGCTCGATACGGCACCGTAAGTTGGGCCGCCC
				GAGAGGCCTGGGGACAGAA		CAATGATAGGCTAGTCTCGCGTCCGGGGCAGATGACCT
rs383452 $^{\mathrm{V}}$	2p11.2	G/A	63/37	AACCTCTGAGACCCTGAGACAC	217	ATTCGCGCACCTGAGGATTTCTCCTCCTTGATAGAATGTC
				CCTTATGGTGCTGGGCACA		ATTCACCTGACTCGCGTATAGCACAGTATAAAACTCACTAAA
rs952798 $^{\mathrm{X}}$	2 q32.2	C/T	52/48	AAAGCAAAAAGTGGACCCATAC[5]	273	GCCGACGCTTCGACAGAATTAAAAAGGAAACCTTGCAAGTG
				GCCCTATACAGCACAGATTCTAC[6]		CGTGCAAGTTACCGAGCTGACATCATTCACTCATTTCCCTA
rs1914408 $^{\mathrm{X}}$	2 q32.2	G/A	81/19	GCAGCTTTATCTGCATTCAAAC[5]	262	AACAGTCTAACCTACGCGAGTTTTCTGTCCAGGGTAAGCCAC
				CCCCTTGGGAAATGTTTCAC[6]		ATACGTCTTACCGCACATAGACCCTGAGATGACAATGCCT
rs1400657 $^{\mathrm{X}}$	2 q32.2	A/C	88/12	CAGAATTGCTATGGCAGATTAAGAC[5]	171	GGATACTATTCCGTGCGTGTGAGGTCAGAGGAGTAATATTATTGG
				TGGTCGCAAAGAACCAAAATAC[6]		CGTCACGTTACCTACATGATTATGGCACCTATTACAGCTGTT
rs715710 $^{\mathrm{V}}$	3p25	C/G	67/33	CACCTTCTTGTTGTATCCCCA	121	CTGACTAATCGTGTAGGTGTGAGTAGAGAGCAAGATCAAAC
				GGAGTAATCAGGTCATGAGCA		CTAATACATCGTGATACGGGCCTTATAAGAAGAGATGCAAG
rs5186 $^{\mathrm{II}}$	3q21	A/C	74/26	CCCCAAAAGCCAAATCCCAC	305	ATGATGTGCAAAGTGCCGTCCACTTCACTACCAAATGAGC
				AGAAAAGTCGGTTCAGTCCAC		CTGGACCTTAATCGTGTGCGCCTTCAATTCTGAAAAGTAGCTAA
rs714825 $^{\mathrm{IV}}$	4q12	T/C	55/45	GGTGTCTCCATTATGCTATCCA	187	AGCAGCATCGTAGAGCGTCATGTACATGAGGACTGAGAAAC
				CCAGACTGTCACTTCATATTCTCA		AGCTGCATCCTAGCGTCATGCCTGATTAGTTAGTTGAATAAGT
rs5333 $^{\mathrm{I}}$	4q31	T/C	82/18	CGTCGAGAAGTGGCAAAAACA	190	ACAGGCGCTGCAACCGATATCTTTGCTGGTTCCCTCTTCA
				TACACAGGATCATACCTAAGTAA		AGAGCCCTGCAACGCGATATGTTTTCTTCAATATACGGCTTAA
rs5335 $^{\mathrm{II}}$	4q31	G/C	56/44	CAGTGGAAGAACCACGATCA	192	AATCTATCTACAAGCCGGTCAAAATCACAAGGCAACTGTGA
				TCTTGGGTGTGGGAGTGAA		AAATGATCTCACCGCGTACTTCAGAGAAGAGATTCCCGGA

rs714932[VIII]	5p13.3	G/A	62/38	CAAATCCCAAAAACTTCACCAA TTCAAAGTCTTCAGGATAGCAA	170	AGTCATAGTACCTCATGCTCTCTTCTATCTCACCAGAAAAAA ACTGTCGTCAACGTCAGGCAGGATAGCAAATTCTAGTGTTTTT
rs1042717[II]	5q32	G/A	78/22	GTCACCAACTACTTCATCACTTCAC TGGCAAAGTAGCGATCCAC	205	CTCAACAGTGTATCCGGTGGGCTGATCTGGTCATGGGCCT CTGCGTACTGTATAAGGATGGCCCCAAAGGGCACCACTGC
rs1042719[I]	5q32	G/C	68/32	GATTTCAGGATTGCCTTCCA ATGGCCCACAAAGTCTTCC	180	CTCATTAGTATCATCGTCGGGTCTTCTTTGAAGGCCTATGG GCGTTATTCAGATCGAGTGACCGTTGCTGGAGTAGCCATT
rs714470[VII]	6p21	A/C	67/33	CCTTTGAGTCACATCATTTTCA AGTTAGATGTACAAGGCTGAC	172	ACCGTAGCTCTCGGCAAGATCGAATAGCACATGTGTAAAAAT ACGCTAATGACGGCAGTGCACAAAATCTGGGAGGATAGATG
rs1874328[IX]	7q32	G/A	53/48	ATGTTGGTAACCCTCACCTCAC[5] TCGCACCTGTAATCCCAAC[6]	428	AAACGACGTAGGCCGGACATTTGCCATTCAAAATAATACCA GTCCCACATGGTGCTTCGTAAGGCTCGAGACACTGGAGCTG
rs1799983[I]	7q36	G/T	64/36	CATTCAGCACGGCTGGACC TGCTCCAGGGGCACCTCAA	146	CGTGCCGCTCGTGATAGAATCTGCTGCAGGCCCCAGATGA GCTAGATCGTGCGTTATATGAGAAGGAAGAGTTCTGGGGG
rs1799998[VI]	8q21	T/C	61/39	AATGAACTAAATCTGTGGTATAAAA CCAGGGCTGAGAGGAGTAAA	150	GTATGTGCTGTTATCGAAGCCTATTAAAAGAATCCAAGGC CTATGGCTGAGTATGTAACGCTTATCGTGAGATGAGAGGG
rs1053887[IX]	9p22	G/A	55/45	GGCAGAAGTCATAGAAGTGTGGAC[5] CTGGCACAAATGGGAAGAAT[6]	559	GAAGTGCGTTCAACAGGTCTTTTCTGCTCTGACAACCTCCCA TGCCCTATTGTTGCGTCGGAAGAAGAAATACAGCCCTTGTGC
rs2939[IX]	9p22	G/A	73/27	GGCAGAAGTCATAGAAGTGTGGAC[5] CTGGCACAAATGGGAAGAAT[6]	559	CAACGGGTGGACTCTGCAATATAGAAGTGTGGACTGGTGT ATTGACCAAACTGCGGTGCGAAATGATCTGTATTGACTAA
rs713503[IV]	11p15	G/T	60/40	AGCCTGCTACCACTTTGCCA AGAGGGAGAATCAGCCTACA	297	GAATAGTGTCGTAGGCTCTCGGACCATGCCTTGCTTTTGT GGGCACGTTGCTAAACTGTTTGCTTGAAGGAAACACGGGA
rs5092[I]	11q23	A/G	51/49	TGTTACCACCCAGGAGCCA CACCACACACTGTAGTCCC	206	TCGAGCGATTTATACATCCGAGTGCTGACCAGGTGGCCAC CAATGATCGACCTGGAGTCTCTGAAGTAGTCCCACATCAC
rs714760[IV]	12q24.3	G/T	76/24	GAATTGGGGAAGTGAGAGCA TGGGAAAGAGTGCTGTCAAC	152	TCGGTTGCTTGGATGTACCCTGGTGGGAGTGAAATGTAAG GGCGTTCGTGCAGCTTACTTGTCCCTCACCGTTTGCATG
rs715447[VII]	12q24.11	G/C	55/45	ATATCCATTTGCTCCAGCATCA AAGAATAAAGTGGGAGTAATCAC	223	AGCATATAGGGTACGCTAGATGATGATTGTAGCTGTATTGTA ATGAAGACTCGTCCCTCGATTCTACCTGATTGATACTAAAAC
rs715129[IV]	13q12.3	T/A	57/43	GACTTGCCCACAGTCAAACA ATAGTAGGTACCAGCCTCCA	146	CGGTCCTCTGCATCTATAATCCACTGTACTATACCAGGGT CGCACGCCTCTGGAGTAAATTTGCATTTATCACTTAATATTTATA
rs13841[VII]	14q11.2	C/T	50/50	AGGAAAGAGAGCACCTGCCA	182	ACCATATAGCCATCTAAGCGATCACTCAATCATTTTTCTGGA

				GGAGAATCCTTCAAAATGCTAC		CCTCGATATGTACGGATAGGCCATTTCTAGCTGTTAACCCT
rs2799^{X}	14q32	C/G	95/5	GCTGTCATTGCGAGGTTCTAC[5]	197	CTTAACTATTAGCGTCGGTGGGAGAAGGCACCCAGCCATC
				GGAGATGCAGAATTTGGTATATTTCAC[6]		ATCCCATGACTACTCGTGAGGTTGGCTCCTCGCTGGGTCA
rs6083^{VII}	15q21	A/G	57/43	CCCTTACCCCTGCTTTCCC	198	CAGCCGAATGGACTATCGCTTCTTTCTCCAGATGATGCCA
				CTGTTTGATGCCCACGCTCA		TAGTTGACTTGGAGTATGCCTATGAATGGCATCCACAAAA
rs715296^{IV}	16p13.3	G/C	51/49	GTTTTACCATAGACGGATTTACA	143	CCAGCTCGTACTATCGAATAATTTTGGTTAATATCTTAATACCA
				CTTAATGTCTAATGGATGCAAAC		CACCATCGTCGTATCGAATATTAAAGAGTATAATGCCAAAAGA
rs5882^{VI}	16q21	A/G	72/28	TGCTCCAGGGAGGACTCAC	165	ACAGTCGCCTAGCGGTATATTGCAGAGCAGCTCCGAGTCC
				CAGCCCACACTTACGAGACA		AGGTACGCTCCTAGTCCATAGACTGCAGGAAGCTCTGGA
rs744166^{IX}	17q21	G/A	52/48	GAAAGGGAGGAGTAAGTGACAAC[5]	334	GTTTCTTATTAGCGAGGAGCTGTTCTATAAATTACTGTCA
				AGGGGATGGCAGGTTTTAC[6]		ACTCTCGACCTAGCGTAAGGAATGTCTTGAGGGAATCGAGC
rs713197^{VIII}	18q11	G/T	57/43	AATCGATATTTTGATCCATTGAC	219	GATAAGCGTTCACAGCTCGGTGGGGTCATAAGATTTCTTCAA
				CTCTTTGCCTTGAACCTTGAC		CTCAAATCTTAGCACTCGTGAATATTTAAAAAATGTACCAAAATAT
rs715351^{VI}	18q21.3	A/G	50/50	AGGCGACACCAGTTTGTCCA	275	GACCAAGCTCGTTAGATAGTCCACGGGCCTCAAGTTCAA
				GAGATATGTGGTTTCTGCTTCA		AGCCCAGATCCTACGAGATGGTTGGATCTGAGAGCACTG
rs5930^{II}	19p13.3	G/A	82/18	CCTTCTCTCCTCCTGCCTCA	185	AGGTCGGCTGCACGCTAAATTATGACACCGTCATCAGCAG
				TCTTCACGCCCTTGGTATCC		AGGTCGCATGGACGAACATCCCGTCGGGGGCCTGGATGTC
rs280523^{IX}	19 p13.2	C/T	88/12	ACCTCTGGGCTAGAGAGGAAC[5]	361	CGTTCCTAAAGCTGAGTCTGATCACTGTGGGAGCTGTCGAC
				CGGCAATATGCAAAGTCTAC[6]		GCACGTCGTATTAGGTAGTCAAAGTGGTGGATCTCCTCCTC
rs1578401^{III}	20p 11.2	A/G	57/43	TTTCCTGATGCTACAGACCAC	278	GGCTACTATTCGATCATACGAATGCCATCACTTTTCCTCATT
				AACCTGGGATAATAAATACAGAC		CGCCTATCTGGTAATAACTGCCATATTTACTTATATACCTGAAA
rs890613^{III}	20p11.2	T/C	94/6	CCAATTATATACAAAGGCTACAC	237	TGCGTTGGTTGTCGCTCACAACAGTTGAGCCTTTCCCATC
				ACATCCACTTAAAAATGTCTCAC		GTGTCTGGTGTTCGATACCCTTCTGTTCTTTGAGGATCTTC
rs753381^{IV}	20q12	C/T	58/42	CCCAGGTTGGCAGTGGCA	260	CGTGACAATGTACTATGGAGGAGGACGAGCTGACCTTCA
				GCACACAGGAGACAAGCACA		CGCGTCGATCTAGGTGACTACTGGATGATGGCGCTCTTG
rs715147^{VII}	20q13.2	A/G	66/34	GACAGCCATAGAATTCCAGCA	200	GGTGATACTTCGCTATATGGCTTAGAAACTAGCCAGCCCT
				CTTGACCTGTCTTTGAAGCCA		GGCTATACTTGACAGTGATGGTTGCCTTGTCTGCCAGTG
rs715231^{V}	21q21.3	C/T	68/32	ATTTGATTAGTTGGATTGGGAC	192	CGAGTGCTCCGTGCGAAATAACTGAAAACTAACATCTCTCTG
				CCATTAAAGCCTGAAATACACA		CGCGGTCATCGTGCGAATAATCTTTTTTTATACCTAGTCCC

rs3153 [X]	21q22.11	G/A	66/34	ACTGAGTGTTCCTGCAGATATATAAC[5]	149	ACCAATGACCATATACGGCGGGAGACAAATGGGGACCAGAG
				TTATATTTGAACACCTGACCTGAC[6]		AGTAGTGCGAAAGGCTCCTAGACCTGACCTCTGACATGTGG
rs713625 [VII]	22q11.23	C/T	67/33	TCTGCTAGGAAATCTCAGAAC	162	GGTTCCTCTGATGTGCTAGACTTTCTCCAGCATAGCAAAAG
				GCTCAACACTGCGAGGTCA		CAGTTCTACGATGGCAAGTCTCTCCTGCCTCTGGGGAT
rs713753 [VIII]	22q13.1	C/T	56/44	TAGAGGCAACTCCAGGTCAA	183	GCGGTATGTCGTGCTATAATGTCAAAGGTGGGGAACCAA
				TTGGTGCCTCTCTTTCCACA		GGCGTCTGTCGTGCTCATAACTTTGGGCAGGATCTTGGT
rs715328 [V0]	Xp22.1	C/T	57/43	ACCAAGGACATTAGTGGATTCA	297	ATCGCACCTCGTAGGAGTCAGTGTAAAATGTTGGAGGCAGA
				GCTTCCATCAGGGGTTCTCA		GTTGCCACTCGTTGATAGTCAGTCTGTCTTTAAAGATAATAAC

[1] The identification numbers are from the dbSNP database: http://www.ncbi.nlm.nih.gov/SNP/. The roman indexes (I-X) indicates which SNPs has been amplified together in multiplex PCR (Lindroos, K. et al. (2002) *Nucleic Acids Res*, **30,** e70., Liljedahl, U. et al. (2003) *Pharmacogenetics*, **13,** 7-17.).

[2] Allele frequencies as determined in a pool of Swedish men by solid-phase minisequencing (Syvanen, A.C. et al. (1993) *Am J Hum Genet*, **52,** 46-59.).

[3] PCR primer sequences. The forward primers are given above their corresponding reverse primers.

[4] Minisequencing primers. The primers with the same polarity as the forward PCR primers are given above the primer on the complementary strand. The 20 most 5’ bases of the primer are tag-sequences with complementary cTags included in the printed arrays.

[5] These PCR primers contained the universal sequence TTC TAA TAC GAC TCA CTA TAG or TTC TAA TAC GAC TCA CTA TAG GGA GA in the 5’ end.

[6] These PCR primers contained the universal sequence GCG GTC CCA AAA GGG TCA GT in the 5’ end.