

Gene symbol	Gene name	SNP	Mutation type	Variant frequency	Flanking sequence
<b>A2M</b>	$\alpha$ -2-macroglobulin	A2M_1	mis (V/I)	0.32	CTCCAGAG[G/A]TCAAGTCC
<b>ABCA1</b>	ATP-binding cassette, subfamily A, member 1	ABCA1_1	mis (R/K)	0.26	TTTGTGGCCTACCAA[G/A]GGAGAAACTGGCTGC
<b>ACADM</b>	acyl coenzyme A dehydrogenase, C4-C12 straight chain; MCAD	ACADM_1	silent	0.26	TACAGAATATCCTGT[A/G]GAAAACTAATGAGG
<b>ACAT2</b>	acetyl coenzyme A acetyltransferase 2	ACAT2_1	mis (K/R)	0.41	TGGTGTCAACTAGAA[A/G]AGGTGAGTATATCAT
<b>ACAT2</b>	acetyl coenzyme A acetyltransferase 2	ACAT2_2	silent	0.18	TGGTGCTGCAGCTGT[T/C]GTTCTTATGAAGAAG
<b>ACE</b>	angiotensin I converting enzyme (peptidyl-dipeptidase A) 1	DCP1_1	silent	0.42	GAATGTGATGGCCAC[A/G]TCCC GGAAATATGAA
<b>ACE</b>	angiotensin I converting enzyme (peptidyl-dipeptidase A) 1	DCP1_2	mis (P/L)	0.43	CGATGCTGGAGAAGC[C/T]GGCCGACGGGCGGGA
<b>ACE</b>	angiotensin I converting enzyme (peptidyl-dipeptidase A) 1	DCP1_3	silent	0.38	GTACAAGGATCTGCC[C/T]GTCTCCCTGCGTCGG
<b>ACE</b>	angiotensin I converting enzyme (peptidyl-dipeptidase A) 1	DCP1_4	silent	0.43	CTGCTCCAGGTACTT[T/C]GTCAGCTTCATCATC
<b>ADRA2B</b>	adrenergic, $\alpha$ -2B-, receptor	ADRA2B_1	I/D	0.41	GCATCTCCAGAGGATGAAGCT[-/GAAGAGGAG]
<b>ADRB2</b>	adrenergic receptor, $\beta$ 2	ADRB2_1	mis (E/Q)	0.44	CACGACGTCACGCAG[G/C]AAAGGGACGAGGTGT
<b>AGT</b>	angiotensinogen	AGT_1	mis (M/T)	0.42	CTGGCTGCTCCCTGA[T/C]GGGAGCCAGTGTGGA
<b>AGTR1</b>	angiotensin receptor 1	AGTR1_1	3' UTR	0.30	ACTACCAAATGAGC[A/C]TTAGCTACTTTTCAGA
<b>ANXA4</b>	annexin IV; lipocortin IV	ANXA4_1	mis (T/M)	0.16	TTGTGGGGATGATGA[C/T]GCCACGGTGCTGTA
<b>APOA1</b>	apolipoprotein AI	APOA1_1	promoter	0.17	AGCAGCAACAGGGCC[G/A]GGGCTGGGCTTATCA
<b>APOB</b>	apolipoprotein B	APOB_1	mis (R/Q)	0.09	GGAAAAATGAAGTCC[G/A]GATTCATTCTGGGTC
<b>APOB</b>	apolipoprotein B	APOB_2	silent	0.50	CAAATTCCGAGAGAC[C/T]CTAGAAGATACACGA
<b>APOC3</b>	apolipoprotein CIII	APOC3_1	3' UTR	0.08	GCCTATCCATCCTGC[C/G]AGCTCCTTGGGTCTT
<b>APOE</b>	apolipoprotein E	APOE_1	mis (C/R)	0.13	GACATGGAGGACGTG[T/C]GCGGCCGCT GGTGC
<b>BDKRB1</b>	bradykinin receptor B1	BDKRB1_1	silent	0.16	GCACAGAGTGCTGCC[G/A]ACATTTATCATCTCC
<b>BDKRB2</b>	bradykinin receptor B2	BDKRB2_1	silent	0.16	CAAGGAGATCCAGAC[G/A]GAGAGGAGGGCCACG
<b>CCKBR</b>	cholecystokinin B receptor	CCKBR_1	mis (V/I)	0.05	TTCATCTTTGGCACCC[G/A]TCATCTGCAAGGCGG
<b>CCL2</b>	chemokine (C-C motif) ligand 2	SCYA2_1	silent	0.39	CCCAGTCACCTGCTG[T/C]TATAACTTCACCAAT
<b>CD14</b>	CD14 antigen	CD14_1	promoter	0.49	TCCTTCCTGTTACGG[C/T]CCCCCTCCCTGAAAC
<b>CD36</b>	CD36 antigen; thrombospondin receptor	CD36_2	promoter	0.42	GTGACTCATCAGTTC[A/C]TTCCTGTAAAATTC
<b>CD36</b>	CD36 antigen; thrombospondin receptor	CD36_3	intronic	0.42	ATAATTTTTTGGT[A/G]TCATAATCGCCTCAT
<b>CD36</b>	CD36 antigen; thrombospondin receptor	CD36_4	silent	0.01	TTTGAGTTTGGTTCC[G/T]TACCCTGTTACTACC
<b>CETP</b>	cholesterol ester transfer protein	CETP_1	mis (A/P)	0.07	GTGACTACCGTCCAG[G/C]CCTCCTATTCTAAGA

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<i>CETP</i>	cholesterol ester transfer protein	CETP_2	mis (I/V)	0.33	AGCAGCTCCGAGTCC[A/G]TCCAGAGCTTCCTGC
<i>CETP</i>	cholesterol ester transfer protein	CETP_3	silent	0.06	CTCTGAGCGAGTCTT[C/T]CACTCGCTGGCCAAG
<i>CETP</i>	cholesterol ester transfer protein	CETP_4	intronic	0.43	GAATCACTGGGGTTC[G/A]AGTTAGGGTTCAGAT
<i>COL5A2</i>	collagen, type V, alpha 2	COL5A2_1	silent	0.18	CCCAACGGGCTCTCC[G/A]GGTACCTCTGGTCCT
<i>COMP</i>	cartilage oligomeric matrix protein (TSP-5)	COMP_1	mis (N/D)	0.05	CGCAACCAGGCCGAC[A/G]ACTGCCCTAGGGTAC
<i>COMP</i>	cartilage oligomeric matrix protein (TSP-5)	COMP_2	3' UTR	0.16	GCACACAGGCCCTGC[C/T]GGCCTTCTCAGCCCT
<i>CYBA</i>	p22 phox	CYBA_1	mis (H/Y)	0.36	CCCAGGGGACAGAAG[T/C]ACATGACCCCGCTGG
<i>ECE1</i>	endothelin converting enzyme 1	ECE1_1	silent	0.28	TCTCATCAACACCAC[C/T]GACAGATGCCTGCTC
<i>ECE1</i>	endothelin converting enzyme 1	ECE1_2	silent	0.06	GAGGGTCACTGCCG[A/T]CAGCTCAGGAAAGCC
<i>EDN1</i>	endothelin 1	EDN1_1	intronic	0.23	TTAAAGACTATTAAT[T/C]ACACTAATATAGTTT
<i>EDN1</i>	endothelin 1	EDN1_2	mis (K/N)	0.20	CAAGCTGAAAGGCAA[G/T]CCCTCCAGAGAGCGT
<i>EDN1</i>	endothelin 1	EDN1_3	silent	0.14	GGCAACAGACCGTGA[G/A]AATAGATGCCAATGT
<i>EDNRA</i>	endothelin A receptor	EDNRA_1	intronic	0.39	ACAAGGCAACTGTGA[C/G]TCCGGGAATCTCTTC
<i>EDNRB</i>	endothelin B receptor	EDNRB_1	silent	0.40	AAAAGATTGGTGGCT[G/A]TTCAGTTTCTATTTT
<i>ESR1</i>	estrogen receptor 1	ESR1_1	silent	0.18	GGGTTTCCCTGCCAC[A/G]GTCTGAGAGCTCCCT
<i>F10</i>	coagulation factor X	F10_1	silent	0.13	TTTCTGTGGTGAAC[C/T]ATTTGAGCGAGT TC
<i>F11</i>	coagulation factor XI	F11_1	silent	0.12	TGCGTCTGTTTCGTGG[C/T]GAGTGGCCGTGGCAG
<i>F11</i>	coagulation factor XI	F11_2	silent	0.03	AAGATGCACGGATGA[C/T]GTCCACTGCCACTTT
<i>F11</i>	coagulation factor XI	F11_3	silent	0.13	TGGATTGCCAGTAC[G/A]CGCATTAAAAAGAGC
<i>F13A1</i>	coagulation factor XIII A-1	F13A1_1	mis (Q/E)	0.21	ATGACTGTGACAGTT[C/G]AGTTTACCAATCCTT
<i>F13A1</i>	coagulation factor XIII A-1	F13A1_2	mis (L/P)	0.21	TCTACACCGGGTCC[T/C]GAAGGCAGAATTCAA
<i>F13A1</i>	coagulation factor XIII A-1	F13A1_3	intronic	0.20	GGGCAGGCAGTGCAG[A/G]GCTGTGGGAAGCTTT
<i>F13A1</i>	coagulation factor XIII A-1	F13A1_4	mis (M/K)	0.24	ATGCCAATTTGCAAA[A/T]GGACATCTT CCTGGA
<i>F2</i>	coagulation factor II; prothrombin	F2_1	mis (T/M)	0.12	CCGACAGCAGCACCA[C/T]GGGACCCTGGTGCTA
<i>F2</i>	coagulation factor II; prothrombin	F2_2	3' UTR	0.01	AAAGTGA CTCTCAGC[G/A]AGCCTCAATGCTCCC
<i>F2</i>	coagulation factor II; prothrombin	F2_3	intronic	0.06	CTGCCTCCTGTACCC[G/A]CCCTGGGAC AAGAAC
<i>F5</i>	coagulation factor V	F5_1	mis (R/Q)	0.02	GATCCCTGGACAGGC[G/A]AGGAATACAGGTATT
<i>F5</i>	coagulation factor V	F5_2	mis (N/T)	0.04	ACCTCATTGGCAAGA[A/C]CTCAGTTCT CAATTC
<i>F5</i>	coagulation factor V	F5_3	intronic	0.26	AGAATGAGGCCCTGG[A/G]AGGACCCTC CTAGTG
<i>F5</i>	coagulation factor V	F5_4	mis (V/M)	0.31	GACAGCAACATGCCT[G/A]TGGACATGAGAGAAT
<i>F7</i>	coagulation factor VII	F7_1	silent	0.14	CTCCTGTCCGGTGCCA[C/T]GAGGGTACTCTCTG
<i>F7</i>	coagulation factor VII	F7_2	mis (R/Q)	0.11	ATGCCACCCACTACC[A/G]GGGCACGTG GTACCT
<i>F7</i>	coagulation factor VII	F7_3	intronic	0.11	GCTGCAGGTGCGTCC[G/A]GGGAGGTTTCTCCA

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<b>F9</b>	coagulation factor IX	F9_1	mis (A/T)	0.30	CTCACCCGTGCTGAG[G/A]CTGTTTTTCTGATG
<b>FABP3</b>	fatty acid binding protein 3	FABP3_1	mis (K/R)	0.04	ACATTCTCACCTAA[A/G]AACACACAGCACCTT
<b>FASN</b>	fatty acid synthase	FASN_1	mis (V/I)	0.03	AGCAGCACCTCCCAC[G/A]TCCCGGAGGTGGACC
<b>FGA</b>	fibrinogen, $\alpha$	FGA_1	mis (T/A)	0.24	TCTGGACCTGGAAGT[A/G]CTGGAAGCTGGAAC
<b>FGB</b>	fibrinogen, $\beta$	FGB_1	silent	0.21	TGAGACTGTGAATAG[C/T]AATATCCCAACTAAC
<b>FGB</b>	fibrinogen, $\beta$	FGB_2	mis (R/K)	0.21	CATGGTACTCAATGA[G/A]GAAGATGAGTATGAA
<b>FGB</b>	fibrinogen, $\beta$	FGB_3	promoter	0.22	TGACAAGTAAATAAG[C/T]TTTGCTGGGAAGATG
<b>FGB</b>	fibrinogen, $\beta$	FGB_4	promoter	0.24	CTATTGATTTTAAATG[A/G]CCCCTTTTGAAATAG
<b>FGG</b>	fibrinogen, $\gamma$	FGG_1	mis (G/R)	0.04	GGAGCTAAACAGAGC[G/A]GGCTTTACTTTATTA
<b>GBE1</b>	glucan (1,4- $\alpha$ )-branching enzyme 1 (glycogen branching enzyme)	GBE1_1	mis (T/A)	0.03	AACATGAGTGTCTCTG[A/G]CTCCTTTTACTCCAG
<b>GP1BA</b>	glycoprotein 1B (platelet), $\alpha$	GP1BA_1	mis (T/M)	0.06	CCCCAGGGCTCCTGA[C/T]GCCACACCCAAGCT
<b>HFE</b>	haemochromatosis	HFE_1	mis (C/Y)	0.06	ATATACGT[G/A]CCAGGTGG
<b>HRG</b>	histidine-rich glycoprotein	HRG_1	mis (H/R)	0.20	ATGGGGCCCAAAGAC[A/G]TTCTCATAATAATAA
<b>HRG</b>	histidine-rich glycoprotein	HRG_2	mis (N/I)	0.39	CTCTAAAGCCAGACA[A/T]TCAGCCCTTCTCTCA
<b>HSD17B4</b>	hydroxysteroid (17 $\beta$ ) dehydrogenase 4	HSD17B4_1	mis (W/R)	0.10	CGCCTCAGTGGAGAC[T/C]GGAATCCCTTACACA
<b>IL1A</b>	interleukin 1, $\alpha$	IL1A_1	mis (A/S)	0.29	ATCAAGCCTAGGTCA[G/T]CACCTTTTAGCTTCC
<b>IL1B</b>	interleukin 1, $\beta$	IL1B_1	silent	0.21	AGAACCTATCTTCTT[C/T]GACACATGG GATAAC
<b>IL1R1</b>	interleukin 1 receptor, type 1	IL1R1_1	mis (A/G)	0.03	ACTTATGTTATAATG[C/G]ACAAGCCATATTTAA
<b>IL1R2</b>	interleukin 1 receptor, type II	IL1R2_1	intronic	0.02	CTCTGTCAGCCCCCG[C/A]ATCAACCTGACATGG
<b>IL1RN</b>	interleukin 1 receptor antagonist	IL1RN_1	mis (S/G)	0.15	AGTGGCCCCACCACC[A/G]GTTTTGAGTCTGCCG
<b>IL1RN</b>	interleukin 1 receptor antagonist	IL1RN_2	silent	0.28	CATCCGCTCAGACAG[T/C]GGCCCCACCACCAGT
<b>IL1RN</b>	interleukin 1 receptor antagonist	IL1RN_3	intronic	0.28	CAACCAACTAGTTGC[T/C]GGATACTTGCAAGGA
<b>IL6</b>	interleukin 6	IL6_1	promoter	0.41	CTAGTTGTGTCTTGC[C/G]ATGCTAAAGGACGTC
<b>INS</b>	insulin	INS_1	intronic	0.29	CTCAGCCCTGCCTGTC[T/A]
<b>IRS2</b>	insulin receptor substrate 2	IRS2_1	intronic	0.13	GTCACATGTGAGAGA[A/G]TATCATTAAGAAG
<b>ITGA2B</b>	integrin, $\alpha$ 2B	ITGA2B_1	silent	0.36	CGTGTACCCCCAGGT[C/T]GGCTTCTTCAAGCGG
<b>ITGA2B</b>	integrin, $\alpha$ 2B	ITGA2B_2	mis (I/S)	0.36	ACTGGGGGCTGCCCA[T/G]CCCCAGCCCCCTCCCC
<b>ITGB1</b>	integrin, $\beta$ 1	ITGB1_1	silent	0.09	TATGGACCTGTCTTA[T/C]TCAATGAAAGACGAT
<b>ITGB1</b>	integrin, $\beta$ 1	ITGB1_2	silent	0.08	AGGAACATTATCTGC[A/C]AATTCTAGCAATGTA
<b>ITGB2</b>	integrin, $\beta$ 2; CD18	ITGB2_1	silent	0.24	TTTCGCGGGCGACGG[A/G]AAGCTGGGCGCCATC
<b>ITGB2</b>	integrin, $\beta$ 2; CD18	ITGB2_2	silent	0.24	ACTCTCCTCCAGGGT[C/A]TTCCTGGATCACAAAC

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<i>ITGB3</i>	integrin, $\beta$ 3	ITGB3_1	mis (L/P)	0.16	TACAGGCCCTGCCTC[T/C]GGGCTCACCTCGCTG
<i>ITGB3</i>	integrin, $\beta$ 3	ITGB3_2	silent	0.29	TTCCAGCAGGACGA[G/A]TGCAGCCCCCGAGAG
<i>ITGB3</i>	integrin, $\beta$ 3	ITGB3_3	silent	0.08	AGGCATTGTCCAGCC[T/C]AATGACGGGCAGTGT
<i>ITGB3</i>	integrin, $\beta$ 3	ITGB3_4	silent	0.30	CGAGTGCAGCCCCCG[A/G]GAGGGTCAGCCCGTC
<i>ITPKB</i>	inositol 1,4,5-trisphosphate 3-kinase B	ITPKB_1	silent	0.28	GGACCCCAACTCAGC[T/C]TTCCTGCATACCCTG
<i>LDLR</i>	low density lipoprotein receptor	LDLR_1	silent	0.45	AAGCATCGATGTCAA[T/C]GGGGGCAACCGGAAG
<i>LDLR</i>	low density lipoprotein receptor	LDLR_2	silent	0.46	CCCAGAGGATATGGT[T/C]CTCTTCCACAACCTC
<i>LDLR</i>	low density lipoprotein receptor	LDLR_3	silent	0.11	AGTGGGCGACAGATG[C/T]GAAAGAAACGAGTTC
<i>LDLR</i>	low density lipoprotein receptor	LDLR_4	silent	0.26	GCACACAACCACCCG[G/A]CCTGTTCCCGACACC
<i>LIPA</i>	lysosomal acid lipase A; acid cholesteryl ester hydrolase	LIPA_1	mis (P/T)	0.32	TGTTTGGTTCTCTGG[C/A]CCCTGCATTCTGAGG
<i>LIPA</i>	lysosomal acid lipase A; acid cholesteryl ester hydrolase	LIPA_2	mis (G/R)	0.11	AGGGGTCT[G/A]GAGGGAAA
<i>LIPC</i>	hepatic lipase	LIPC_1	mis (V/M)	0.04	CCTCAGGTGGACGGC[G/A]TGCTAGAAAACTGGA
<i>LIPC</i>	hepatic lipase	LIPC_2	silent	0.41	CTTCCAGGAATCTGT[T/G]CAACTCTCTCGAAGC
<i>LIPC</i>	hepatic lipase	LIPC_3	mis (N/S)	0.37	CTCCAGATGATGCCA[A/G]TTTTGTGGATGCCAT
<i>LIPC</i>	hepatic lipase	LIPC_4	silent	0.49	CATTCATACCTTTAC[C/G]CGGGAGCACATGGGC
<i>LIPC</i>	hepatic lipase	LIPC_5	promoter	0.22	ACACAGTAGCTTTAA[G/A]TTGATTAATTTGGAA
<i>LPL</i>	lipoprotein lipase	LPL_1	intronic	0.29	TATAGGATTTAAAGC[T/G]TTTATACTAA ATGTG
<i>LRP1</i>	low density lipoprotein-related protein 1 ( $\alpha$ 2 macroglobulin receptor)	LRP1_2	silent	0.27	TGAGTACCCGACCTG[C/T]GGCCCCAGTGAGTTC
<i>LRP1</i>	low density lipoprotein-related protein 1 ( $\alpha$ 2 macroglobulin receptor)	LRP1_3	silent	0.31	CTTCCGGCTGAAGGA[C/T]GACGGCCGGACGTGT
<i>LRP1</i>	low density lipoprotein-related protein 1 ( $\alpha$ 2 macroglobulin receptor)	LRP1_4	silent	0.31	CCCCTTCGGGCTGGC[C/T]GTGTATGGGGAGCAC
<i>LRP1</i>	low density lipoprotein-related protein 1 ( $\alpha$ 2 macroglobulin receptor)	LRP1_5	silent	0.31	TGAGGGCGAGCTCTG[C/T]GGTGAGGCCTGGTCC
<i>LRP2</i>	lipoprotein-related protein 2; glycoprotein 330 megalin low density	LRP2_1	mis (A/T)	0.28	TCCAATGC[G/A]CATCTGGG
<i>LRP2</i>	lipoprotein-related protein 2; glycoprotein 330 megalin low density	LRP2_2	mis (N/S)	0.31	GACAATGCATCCCCA[A/G]CTCCTGGGTGTGTGA
<i>LRPAP1</i>	low density lipoprotein-related protein-associated protein 1; RAP; MRAP	LRPAP1_1	silent	0.10	CTACAGCACTGAGGC[T/C]GGTGAGTGCCCGCCC
<i>LRPAP1</i>	low density lipoprotein-related protein-associated protein 1; RAP; MRAP	LRPAP1_2	3' non- coding	0.27	CGAACTCTGAAGGCA[C/T]TGGGGAGCCCAGCCC

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<i>MMP9</i>	matrix metalloproteinase 9; gelatinase B	MMP9_1	mis (R/Q)	0.33	CAGGACTCTACACCC[G/A]GGACGGCAATGCTGA
<i>MMP9</i>	matrix metalloproteinase 9; gelatinase B	MMP9_2	mis (Q/R)	0.14	ACGTCTTCCAGTACC[A/G]AGGTGAGGGCTGAGG
<i>MMP9</i>	matrix metalloproteinase 9; gelatinase B	MMP9_3	mis (A/V)	0.02	GCTGCTGCTTTGCTG[C/T]CCCCAGACAGCGCCA
<i>MOG</i>	myelin oligodendrocyte glycoprotein	MOG_1	mis (L/V)	0.23	AGATCACT[C/G]TTGGCCTC
<i>MTHFR</i>	methylenetetrahydrofolate reductase	MTHFR_1	mis (A/V)	0.32	AGGTGTCTGCGGGAG[T/C]CGATTTTCATCATCAC
<i>NOS2A</i>	nitric oxide synthase 2 (inducible, hepatocytes)	NOS2A_1	silent	0.26	CCGGGACTTCTGTGA[C/T]GTCCAGCGCTACAAC
<i>NOS2A</i>	nitric oxide synthase 2 (inducible, hepatocytes)	NOS2A_2	silent	0.20	GGCCCTGGTCCAAGG[C/T]ATCCTGGAGCGAGTG
<i>NOS2A</i>	nitric oxide synthase 2 (inducible, hepatocytes)	NOS2A_3	mis (S/L)	0.20	AGAAACTGAAGAAAT[C/T]GCTCTTCATGCTGAA
<i>NOS3</i>	nitric oxide synthase 3 (endothelial); ENOS	NOS3_1	mis (D/E)	0.31	GCAGGCCCCAGATGA[G/T]CCCCAGAAGCTTTC
<i>NOS3</i>	nitric oxide synthase 3 (endothelial); ENOS	NOS3_2	I/D	0.17	GGCTGGAGGAGGGGAAA[GAAGTCTAGACCTGCTGCA GGGG TGAG/-]
<i>P2RY1</i>	purinergic receptor P2Y, G-protein coupled, 1 (ADP receptor)	P2RY1_1	silent	0.03	CGCTGCCTTCTGGC[C/T]GGTCCGGGTTCGTCC
<i>P2RY1</i>	purinergic receptor P2Y, G-protein coupled, 1 (ADP receptor)	P2RY1_2	silent	0.15	ATCGATTTACCTGGT[A/G]ATCATTGTACTGACT
<i>PAI1</i>	serine (or cysteine) proteinase inhibitor, clade E (nexin, plasminogen activator inhibitor type 1), member 1	PAI1_1	I/D	0.47	TCTGGACACGTGGGG[G/del]AGTCAGCCGTGTATC
<i>PAI2</i>	serine (or cysteine) proteinase inhibitor, clade B (ovalbumin), member 2	PAI2_1	mis (S/C)	0.22	TTTTCGGCAGATTTT[C/G]CTCACCTAAAATA
<i>PAI2</i>	serine (or cysteine) proteinase inhibitor, clade B (ovalbumin), member 2	PAI2_2	mis (N/K)	0.22	GCATAAGATAACCAA[C/G]TGCATTTTATTTTTC
<i>PAI2</i>	serine (or cysteine) proteinase inhibitor, clade B (ovalbumin), member 2	PAI2_3	mis (N/D)	0.22	AATGCATCCACAGGG[A/G]ATTATTTACTGGAAA
<i>PAI2</i>	serine (or cysteine) proteinase inhibitor, clade B (ovalbumin), member 2	PAI2_4	intronic	0.21	TGTTTTTTTCTTCCT[C/G]TCTTTGCTTCTAGAT
<i>PCSK1</i>	proprotein convertase subtilisin/kexin type 1	PCSK1_1	intronic	0.19	GAGCCAGGAGTGGTC[T/C]AGAGCCCGAGGGTGG
<i>PDGFA</i>	platelet derived growth factor, A chain	PDGFA_1	silent	0.24	AGCTCACGGGGTCCA[C/T]GCCACTAAGCATGTG
<i>PDGFRA</i>	platelet derived growth factor receptor, $\alpha$	PDGFRA_1	silent	0.13	AGTGAGCTGGCAGTA[C/T]CCCATGTCTGAAGAA
<i>PECAMI</i>	platelet/endothelial cell adhesion molecule (CD31 antigen); ELAM1	PECAM1_1	mis (N/S)	0.35	CCAAGCAGAAGGCTA[A/G]CAAGGAACAGGAGGG
<i>PECAMI</i>	platelet/endothelial cell adhesion molecule (CD31 antigen); ELAM1	PECAM1_2	intronic	0.46	CCGAGAAGAACAGAT[G/A]ATCCCTGTATTTCAA
<i>PECAMI</i>	platelet/endothelial cell adhesion molecule (CD31 antigen); ELAM1	PECAM1_3	silent	0.49	ACTGCAGAGTACCAG[C/G]TGTTGGTGGAAGGAG

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	antigen); ELAM1				
<i>PIK3R1</i>	phosphatidylinositol 3-kinase, regulatory, 1	PIK3R1_1	mis (M/I)	0.17	TATGAATAACAATAT[G/A]TCCTTACAAAATGCT
<i>PLAU</i>	plasminogen activator, urokinase	PLAU_1	mis (P/L)	0.22	AGGTGGGCCTAAAGC[C/T]GCTTGTCCAAGAGTG
<i>PLAU</i>	plasminogen activator, urokinase	PLAU_2	silent	0.10	GCTTGCTCACCACAA[C/T]GACATTGCCTTGCTG
<i>PLCG1</i>	phospholipase C, gamma 1	PLCG1_1	mis (I/T)	0.46	ACGAGCTGACCTTCA[T/C]CAAGAGCGCCATCAT
<i>PLCG1</i>	phospholipase C, gamma 1	PLCG1_2	mis (S/G)	0.17	CAGGAGTTCATGCTC[A/G]GCTTCCTCCGAGACC
<i>PLOD2</i>	lysine hydrolase 2	PLOD2_1	intronic	0.51	TGAAATTTATTTGG[G/A]TGAATGACTGGCATG
<i>PON1</i>	paraoxonase 1, serum, alt transcript 1	PON1_1	mis (M/L)	0.29	CTGGCTCTGAAGAC[A/T]TGGAGATACTGCCTAA
<i>PON2</i>	paraoxonase 2, serum	PON2_1	silent	0.22	TGAAGAAG[C/G]AGAAAATT
<i>PPARG</i>	peroxisome proliferative activated receptor, gamma	PPARG_1	mis (P/A)	0.12	GATTCTCCTATTGAC[G/C]CAGAAAGCGATTCCCT
<i>PPARG</i>	peroxisome proliferative activated receptor, gamma	PPARG_2	silent	0.14	GATTGTACGGAACA[C/T]GTGCAGCTACTGCAG
<i>PRCP</i>	prolylcarboxypeptidase (angiotensinase C)	PRCP_1	mis (T/S)	0.03	AGGATATCACAGACA[C/G]TCTGGTTGCAGTCAC
<i>PRCP</i>	prolylcarboxypeptidase (angiotensinase C)	PRCP_2	mis (E/D)	0.18	GGATGTGGCTGAGGA[A/C]CTGAAAGCTATGTTG
<i>PROC</i>	protein C	PROC_1	silent	0.29	CTTCCTCAATTGCTC[T/G]CTGGACAACGGCGGC
<i>PROC</i>	protein C	PROC_2	silent	0.36	GGCCCACTGCATGGA[T/C]GAGTCCAAGAAGCTC
<i>PROS1</i>	protein S ( $\alpha$ )	PROS1_1	silent	0.39	AGCTCACTCATGTCC[A/G]TCAGTTTGG AAAAAG
<i>PTGS2</i>	cyclooxygenase (COX2)	PTGS2_1	silent	0.17	AATTATGAGTTATGT[C/G]TTGACATCCAGATCA
<i>SAA1</i>	serum amyloid A1, $\beta$	SAA1_1	mis (H/R)	0.12	AGAGATTCTTTGGCC[A/G]TGGTGCGGAGGACTC
<i>SAA1</i>	serum amyloid A1, $\beta$	SAA1_2	mis (K/R)	0.01	GGGGCAGGAGTGGCA[A/G]AGACCCCAATCACTT
<i>SCARB1</i>	scavenger receptor class B, member 1	SRB1_2	silent	0.49	TCACTTCCTCAACGC[C/T]GACCCGGTT CTGGCA
<i>SCARB1</i>	scavenger receptor class B, member 1	SRB1_3	silent	0.01	CCCCACCTATCGCTT[C/T]GTGGCTCCCAAACC
<i>SCARB1</i>	scavenger receptor class B, member 1	SRB1_4	mis (V/I)	0.01	GAGAGCGACTACATC[G/A]TCATGCCCAACATCC
<i>SCARB1</i>	scavenger receptor class B, member 1	SRB1_5	intronic	0.05	AGC[C/G]TGCGGCCCCAGCTC
<i>SCARB1</i>	scavenger receptor class B, member 1	SRB1_6	mis (G/S)	0.10	AGGCGCGCAGACATG[G/A]GCTGCTCCGCCAAAG
<i>SCARB1</i>	scavenger receptor class B, member 1	SRB1_7	intronic	0.10	AGGGGAGGGTGGGCC[C/T]GGCCATGGCTGCTCG
<i>SDC4</i>	syndecan 4 (amphiglycan, ryudocan	SDC4_1	mis (F/L)	0.38	TTCGCGCTGCTGCTG[T/C]TCTTCGTAGGCGGAG
<i>SELE</i>	E-selectin	SELE_1	mis (S/R)	0.09	CCTAAACCTTTGGGT[G/T]AAAAGAACTCTTGAA
<i>SELE</i>	E-selectin	SELE_2	mis (S/R)	0.08	ACCAATACATCCTGC[A/C]GTGGCCACGGTGAAT
<i>SELL</i>	L-selectin	SELL_1	mis (P/S)	0.12	ATGGACTGTACTCAC[C/T]CTTTGGGAAACTTCA
<i>SELL</i>	L-selectin	SELL_2	mis (F/L)	0.27	GGCCCCAGTGTGAG[T/C]TTGGTAAGTCTCTTT
<i>SELL</i>	L-selectin	SELL_3	silent	0.20	AACCAACAAATCTCT[C/T]ACTGAAGAA GCAGAG
<i>SELP</i>	P-selectin	SELP_1	mis (T/P)	0.11	AATGGCCACTGGTCA[A/C]CTACCGTGCCAACCT
<i>SELP</i>	P-selectin	SELP_2	mis (V/L)	0.10	CTTCCTACTCCAGGG[G/T]TGCAATGTCCAGCCC

Gene symbol	Gene name	SNP	Mutation type	Variant frequency	Flanking sequence
<i>SELP</i>	P-selectin	SELP_3	mis (S/N)	0.14	ACCTGGAAGCCCCCA[G/A]TGAAGGAACCATGGA
<i>SELP</i>	P-selectin	SELP_4	mis (N/D)	0.06	TGTCATTTCTCTTGT[A/G]ACAATGGCTTTAAGC
<i>SELPLG</i>	P-selectin ligand	SELPLG_1	mis (M/I)	0.06	CCAGAAAT[G/A]CTGAGGA
<i>SERPINA5</i>	protein C inhibitor; PCI, PLANH3; PAI3	SERPINA5_1	mis (A/V)	0.10	TTGACCTCTACAGGG[C/T]CTTGGCTTCCGCTGC
<i>SERPINA5</i>	protein C inhibitor; PCI, PLANH3; PAI3	SERPINA5_2	mis (K/E)	0.09	CAGAAAAGCTCAGAG[A/G]AGGAGCTGCACAGAG
<i>SERPINC1</i>	serine (or cysteine) proteinase inhibitor, clade C (antithrombin), member 1	AT3_1	silent	0.36	GAGCCTGGCCAAGGT[G/A]GAGAAGGAACCTACC
<i>SERPIND1</i>	serine (or cysteine) proteinase inhibitor, clade D (heparin cofactor), member 1	HCF2_1	silent	0.45	CCTCATCTACGAGCA[C/T]CGCACCAGCTGCCTG
<i>SREBF2</i>	sterol regulatory element binding protein 2	SREBF2_1	mis (R/S)	0.04	CCCCCACTCTCCAG[G/C]AGCTCCGTGCTCAAG
<i>SREBF2</i>	sterol regulatory element binding protein 2	SREBF2_2	intronic	0.07	TGAGAGTGGTGGGA[A/G]GAGCCTTGT CTTCTT
<i>SREBF2</i>	sterol regulatory element binding protein 2	SREBF2_3	mis (A/G)	0.29	TTGCAGCTGCTGCCG[C/G]CAACCTACAAACCTG
<i>TBXA2R</i>	thromboxane A2 receptor	TBXA2R_1	silent	0.36	GGACCCCTGGGTGTA[T/C]ATCCTGTTCCGCCGC
<i>TGFBI</i>	TGFBI	TGFBI_1	silent	0.27	TTCTGTGCAGAGCCT[C/T]TGCATTGAGAACAGC
<i>TGFBI</i>	TGFBI	TGFBI_2	silent	0.48	GAAGTGTGCCCGGCT[C/G]CTGAAAGCCGACCAC
<i>THBD</i>	thrombomodulin	THBD_1	intronic	0.37	TGAGATGTAAAAGGT[A/G]TTAAATTGATGTTGC
<i>THBD</i>	thrombomodulin	THBD_2	mis (A/V)	0.19	CCGACTCGGCCCTTG[C/T]CCGCCACATTGGCAC
<i>THBS1</i>	thrombospondin I	THBS1_1	mis (N/S)	0.10	CTGGCCCA[A/G]TGAGAACC
<i>THBS1</i>	thrombospondin I	THBS1_2	silent	0.10	CAGCCCCCAGATGAA[T/C]GGGAAACCCTGTGAA
<i>THBS1</i>	thrombospondin I	THBS1_3	intronic	0.15	ATGGGCTTGAGAAAA[C/T]CCCCAGGATCACTTC
<i>THBS1</i>	thrombospondin I	THBS1_5	silent	0.15	CATCAGTGAGACCGA[T/C]TTCCGCCGATTCCAG
<i>THBS1</i>	thrombospondin I	THBS1_6	silent	0.11	TCAGGAGTGTGACAA[A/G]AGATGTAAGCATCTT
<i>THBS1</i>	thrombospondin I	THBS1_7	intronic	0.11	CCTCTGCACCCAGCC[C/T]GTTAGCATGAACCTT
<i>THBS1</i>	thrombospondin I	THBS1_8	silent	0.03	TCGTCTCTGCAACAA[C/T]CCNCACCCAGTTT
<i>THBS1</i>	thrombospondin I	THBS1_9	mis (A/T)	0.12	CTCTGCAACAACCC[C/G]CACCAGTTTGGAG
<i>THBS2</i>	thrombospondin II	THBS2_1	3' UTR	0.13	TGCAAATGGGTGTGA[T/C]GCGGTTCCAGATGTG
<i>THBS2</i>	thrombospondin II	THBS2_2	3' UTR	0.29	AAATATCAATGGAAC[T/G]CAGAGATGAACATCT
<i>THBS2</i>	thrombospondin II	THBS2_3	intronic	0.01	CTTCATTAATGTAG[C/T]GACTGTCAACAGCGT
<i>THBS2</i>	thrombospondin II	THBS2_4	intronic	0.13	ATGCCAACAGGAAC[G/A]ATCCATAACTTTAGT
<i>THBS4</i>	thrombospondin IV	THBS4_1	mis (A/P)	0.20	GAGTGTGCAAATGGA[G/C]CGTGCCTTCCCAACT
<i>THBS4</i>	thrombospondin IV	THBS4_3	mis (G/S)	0.02	GCTTACCAGACCGTG[G/A]GCCTGGATCCTGAAG
<i>THBS4</i>	thrombospondin IV	THBS4_4	intronic	0.50	AAGGCTGTCAGTCAG[C/T]GGGTGCTCGGATCTC
<i>THPO</i>	thrombopoietin	THPO_1	intronic	0.51	CATCAGCATTGTCTC[A/G]TGTACAGCTCCCTTC

<b>Gene symbol</b>	<b>Gene name</b>	<b>SNP</b>	<b>Mutation type</b>	<b>Variant frequency</b>	<b>Flanking sequence</b>
<i>TIMP1</i>	tissue inhibitor of metalloproteinase 1	TIMP1_1	silent	0.48	CACTACCTGCAGTTT[T/C]GTGGCTCCCTGGAAC
<i>VWF</i>	von Willebrand factor	VWF_1	silent	0.11	CCCCTTCAGCGAGGC[A/C]CAGTCCAAAGGGGAC
<i>VWF</i>	von Willebrand factor	VWF_2	silent	0.12	GTACTTGGCCTCAAC[C/T]GCCACCAATGACTGT
<i>VWF</i>	von Willebrand factor	VWF_3	mis (A/T)	0.38	GAAGGGCTCGAGTGT[A/G]CCAAAACGTGCCAGA
<i>VWF</i>	von Willebrand factor	VWF_4	mis (V/L)	0.09	GACATCCTGCAGCGG[G/T]TGCGAGAGATCCGCT
<i>VWF</i>	von Willebrand factor	VWF_5	silent	0.37	GCTGTCCCCCGTCTA[C/T]GCCGGGAAGACCTGC
<i>ZNF239</i>	zinc finger protein 239	ZNF239_1	silent	0.21	CGCCTTGCTCGTGC[C/G]GTGGACACACGGCTG