

## Supplementary data:

# Understanding gene expression in coronary artery disease through global profiling, network analysis and independent validation of key candidate genes

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**Table 1.** List of the 25 key genes for validation by RT-PCR.

Gene name	Gene description
	Gene expression by TaqMan assay
<i>CXCL1</i>	Chemokine (C-X-C motif) ligand 1
<i>EGR3</i>	Early growth response 3
<i>IL8</i>	Interleukin 8
<i>CD69</i>	CD69 molecule
<i>MMP8</i>	Matrix metalloproteinase 8
<i>OLR1</i>	Oxidized low density lipoprotein (lectin-like) receptor 1
<i>PTGS2</i>	Prostaglandin-endoperoxide synthase 2
<i>PTX3</i>	Pentraxin 3
<i>FASLG</i>	Fas ligand (TNF superfamily, member 6)
<i>IFNG</i>	Interferon, gamma
	Gene expression by SYBR Green assay
<i>ADAMTS</i>	A disintegrin and metalloproteinase with thrombospondin motifs
<i>CCL4</i>	Chemokine (C-C motif) ligand 4
<i>CDC42</i>	Cell division cycle 42
<i>DDX58</i>	DEAD (Asp-Glu-Ala-Asp) box polypeptide 58
<i>EGR1</i>	Early growth response 1
<i>EGR2</i>	Early growth response 1
<i>MYOM2</i>	Myomesin 2
<i>NFKBID</i>	Nuclear factor of kappa light polypeptide gene enhancer in B-cells inhibitor, delta
<i>NR4A2</i>	Nuclear receptor subfamily 4, group A, member 2
<i>PPARG</i>	Peroxisome proliferator-activated receptor gamma
<i>RGS1</i>	Regulator of G-protein signalling 1
<i>SERPINE</i>	Serpin peptidase inhibitor, clade A (alpha-1 antitrypsin, antitrypsin), member 5
<i>SFN</i>	Stratifin
<i>SNX31</i>	Sorting nexin 31
<i>TAGAP</i>	T-cell activation RhoGTPase activating protein

**Table 2.** Differentially expressed genes in CAD compared to age and gender matched controls.

Upregulated genes				
Probe ID	Gene name	Gene symbol	FCA	P value
A_24_P282416	V-abl Abelson murine leukaemia viral oncogene homolog 1	<i>ABL1</i>	2.45	0.0001
A_24_P46130	Acid phosphatase, prostate	<i>ACPP</i>	2.27	0.0004
A_33_P3378081	ATP/GTP binding protein-like 1	<i>AGBL1</i>	2.26	0.0003
A_33_P3396010	Advanced glycosylation end product-specific receptor	<i>AGER</i>	2.35	0.0003
A_33_P3415340	Amyotrophic lateral sclerosis 2 (juvenile)	<i>ALS2</i>	2.08	0.0004
A_23_P92642	Ankyrin repeat and KH domain containing 1	<i>ANKHD1</i>	2.08	0.0001
A_33_P3419190	Amphiregulin (schwannoma-derived growth factor)	<i>AREG</i>	10.58	0.0003
A_33_P3343101	Hypothetical protein FLJ10154	<i>ARGLU1</i>	3.67	0.0002
A_23_P18372	UDP-GlcNAc:betaGal beta-1,3-N-acetylglucosaminyltransferase 5	<i>B3GNT5</i>	2.12	0.0005
A_33_P3249595	B-cell CLL/lymphoma 11A (zinc finger protein)	<i>BCL11A</i>	2.29	0.0003
A_24_P268676	Basic Helix-Loop-Helix Family, Member	<i>BHLHE40</i>	2.51	0.0004
A_33_P3385453	BRCA1/BRCA2-containing complex, subunit 3	<i>BRCC3</i>	4.42	0.0000
A_23_P425104	Bromodomain containing 4	<i>BRD4</i>	2.03	0.0004
A_23_P88184	BTB (POZ) domain containing 7	<i>BTBD7</i>	2.02	0.0004
A_24_P152404	Chromosome 10 open reading frame 76	<i>C10orf76</i>	2.25	0.0001
A_32_P85330	Chromosome 15 open reading frame 37	<i>C15orf37</i>	2.62	0.0001
A_33_P3272948	chromosome 17 open reading frame 107	<i>C17orf107</i>	2.73	0.0005
A_23_P211584	Chromosome 22 open reading frame 32	<i>C22orf32</i>	2.17	0.0004
A_24_P927325	C2 calcium-dependent domain containing 3	<i>C2CD3</i>	5.28	0.0000
A_33_P3407339	Chromosome 6 open reading frame 204	<i>C6orf204</i>	2.71	0.0000
A_23_P405873	Chromosome 9 open reading frame 72	<i>C9orf72</i>	2.74	0.0003
A_33_P3316068	Carbonic anhydrase VB, mitochondrial	<i>CA5B</i>	4.50	0.0000
A_33_P3606465	chromobox homolog 3 pseudogene 2	<i>CBX3P2</i>	2.05	0.0002
A_24_P50950	Coiled-coil domain containing 88B	<i>CCDC88B</i>	3.12	0.0004
A_23_P87879	CD69 molecule	<i>CD69</i>	2.58	0.0003
A_23_P70670	CD83 molecule	<i>CD83</i>	5.45	0.0005
A_33_P3419545	Cytidine and dCMP deaminase domain containing 1	<i>CDADC1</i>	2.01	0.0004
A_23_P300056	Cell division cycle 42 (GTP binding protein, 25kDa)	<i>CDC42</i>	2.55	0.0001
A_33_P3265224	Centrosomal protein 68kDa	<i>CEP68</i>	2.06	0.0005
A_23_P139919	Carbohydrate (chondroitin 4) sulfotransferase 11	<i>CHST11</i>	2.17	0.0001
A_23_P151895	Cartilage intermediate layer protein, nucleotide pyrophosphohydrolase	<i>CILP</i>	2.22	0.0004
A_33_P3424462	consortin, connexin sorting protein	<i>CNST</i>	3.97	0.0003
A_23_P121011	cysteine-serine-rich nuclear protein 1	<i>CSRNP1</i>	3.58	0.0003
A_23_P148541	Cancer/testis antigen 1A	<i>CTAG1A</i>	6.36	0.0001
A_23_P7144	Chemokine (C-X-C motif) ligand 1 (melanoma growth stimulating activity, alpha)	<i>CXCL1</i>	4.60	0.0001
A_23_P155755	Chemokine (C-X-C motif) ligand 6 (granulocyte chemotactic protein 2)	<i>CXCL6</i>	2.13	0.0001
A_24_P376129	Deafness, autosomal recessive 31	<i>DFNB31</i>	7.30	0.0001
A_33_P3411357	DiGeorge syndrome critical region gene 11	<i>DGCR11</i>	2.91	0.0000
A_23_P216225	Early growth response 3	<i>EGR3</i>	57.35	0.0000
A_24_P398810	Eukaryotic translation initiation factor 5	<i>EIF5</i>	2.97	0.0000
A_23_P104188	E74-like factor 3 (ets domain transcription factor, epithelial-specific )	<i>ELF3</i>	2.38	0.0001
A_33_P3210848	extracellular leucine-rich repeat and fibronectin type III domain containing 1	<i>ELFN1</i>	5.04	0.0002
A_33_P3351566	Ethanolamine kinase 1	<i>ETNK1</i>	4.98	0.0001
A_33_P3390024	Exocyst complex component 7	<i>EXOC7</i>	3.68	0.0001
A_23_P74737	Eyes absent homolog 3 (Drosophila)	<i>EYA3</i>	2.71	0.0002
A_33_P3248424	Family with sequence similarity 105, member B	<i>FAM105B</i>	3.26	0.0001
A_24_P937325	FYVE, RhoGEF and PH domain containing 4	<i>FGD4</i>	3.32	0.0001
A_33_P3337977	FIG4 homolog (S. cerevisiae)	<i>FIG4</i>	2.89	0.0002
A_33_P3695899	Hypothetical gene supported by AK055666; BC039324	<i>FLJ31104</i>	2.39	0.0004
A_33_P3288219	<i>FLJ45684</i> locus	<i>FLJ45684</i>	2.23	0.0002
A_23_P429998	FBJ murine osteosarcoma viral oncogene homolog B	<i>FOSB</i>	5.67	0.0001
A_23_P74609	G0/G1 switch 2	<i>G0S2</i>	24.94	0.0000
A_23_P256663	Galanin receptor 3	<i>GALR3</i>	3.37	0.0003
A_33_P3265159	GTPase activating protein and VPS9 domains 1	<i>GAPVD1</i>	2.63	0.0002
A_24_P926400	Golgi associated, gamma adaptin ear containing, ARF binding protein 1	<i>GGAI</i>	2.77	0.0004
A_24_P53976	Glutamate-ammonia ligase (glutamine synthetase)	<i>GLUL</i>	2.03	0.0001
A_23_P37623	Golgi autoantigen, golgin subfamily a, 8A	<i>GOLGA8A</i>	2.89	0.0003
A_33_P3221119	Gon-4-like (C. elegans)	<i>GON4L</i>	2.09	0.0001
A_33_P3358943	Glutamate receptor, metabotropic 2	<i>GRM2</i>	2.86	0.0004
A_33_P3410194	H3 histone, family 3B (H3.3B)	<i>H3F3B</i>	2.07	0.0003
A_23_P213153	Heterogeneous nuclear ribonucleoprotein D-like	<i>HNRPDL</i>	2.44	0.0001
A_23_P133739	HUS1 checkpoint homolog b (S. pombe)	<i>HUS1B</i>	4.40	0.0000
A_23_P252306	Inhibitor of DNA binding 1, dominant negative helix-loop-helix protein	<i>ID1</i>	12.37	0.0001
A_32_P87013	Interleukin 8	<i>IL8</i>	16.98	0.0000
A_24_P154037	Insulin receptor substrate 2	<i>IRS2</i>	2.43	0.0003

**Table 2** (contd)

Probe ID	Gene name	Gene symbol	FCA	P value
A_33_P3213169	Integrin, alpha X (complement component 3 receptor 4 subunit)	<i>ITGAX</i>	4.54	0.0000
A_24_P119545	Inositol 1,4,5-trisphosphate 3-kinase B	<i>ITPKB</i>	3.05	0.0000
A_23_P311616	Jumonji domain containing 6	<i>JMJD6</i>	2.49	0.0002
A_33_P3324909	Jun D proto-oncogene	<i>JUND</i>	2.07	0.0003
A_33_P3213797	Potassium channel, subfamily K, member 7	<i>KCNK7</i>	2.39	0.0004
A_33_P3242659	Kinesin family member 13A	<i>KIF13A</i>	2.52	0.0001
A_32_P195647	Kelch-like 15 (Drosophila)	<i>KLHL15</i>	3.01	0.0001
A_33_P3233764	LATS, large tumor suppressor, homolog 1 (Drosophila)	<i>LATS1</i>	2.66	0.0004
A_23_P103110	V-maf musculoaponeurotic fibrosarcoma oncogene homolog F (avian)	<i>MAFF</i>	3.82	0.0001
A_24_P330112	mago-nashi homolog B (Drosophila)	<i>MAGOHB</i>	3.04	0.0000
A_33_P3246505	Mitogen-activated protein kinase kinase kinase 8	<i>MAP3K8</i>	4.05	0.0001
A_33_P3375576	Microtubule-associated protein 7	<i>MAP7</i>	2.46	0.0002
A_33_P3269388	membrane bound O-acyltransferase domain containing 7	<i>MBOAT7</i>	3.54	0.0000
A_33_P3526315	Hypothetical protein MGC12488	<i>MGC12488</i>	2.31	0.0005
A_33_P3346936	MON2 homolog (S. cerevisiae)	<i>MON2</i>	2.44	0.0004
A_33_P3230528	myosin phosphatase Rho interacting protein	<i>MPRI1</i>	2.10	0.0003
A_33_P3223088	Mitochondrial ribosomal protein L19	<i>MRPL19</i>	2.43	0.0000
A_23_P113825	NACC family member 2, BEN and BTB (POZ) domain containing	<i>NACC2</i>	2.53	0.0000
A_33_P3364869	nicotinamide phosphoribosyltransferase	<i>NAMPT</i>	3.87	0.0002
A_33_P3368358	Neural precursor cell expressed, developmentally down-regulated 9	<i>NEDD9</i>	3.26	0.0002
A_23_P383422	nuclear factor of kappa light polypeptide gene enhancer in B-cells inhibitor, delta	<i>NFKBID</i>	4.33	0.0001
A_32_P797019	Aminopeptidase-like 1	<i>NPEPL1</i>	3.84	0.0001
A_24_P250227	Nuclear receptor subfamily 1, group D, member 1	<i>NR1D1</i>	2.22	0.0001
A_23_P131208	Nuclear receptor subfamily 4, group A, member 2	<i>NR4A2</i>	6.17	0.0001
A_33_P3356731	NudC domain containing 3	<i>NUDCD3</i>	2.01	0.0001
A_33_P3273906	Olfactory receptor, family 10, subfamily G, member 4	<i>OR10G4</i>	2.04	0.0001
A_33_P3217119	organic solute carrier partner 1	<i>OSCP1</i>	2.32	0.0003
A_23_P256244	Oxidation resistance 1	<i>OXR1</i>	3.91	0.0000
A_24_P92183	Poly(A) binding protein, cytoplasmic 1-like	<i>PABPC1L</i>	2.18	0.0003
A_33_P3377459	PAP associated domain containing 5	<i>PAPD5</i>	2.78	0.0002
A_33_P3229898	Pyruvate dehydrogenase (lipoamide) alpha 1	<i>PDHA1</i>	2.73	0.0001
A_23_P35977	PDZ domain containing 3	<i>PDZD3</i>	2.66	0.0003
A_23_P89589	Period homolog 1 (Drosophila)	<i>PER1</i>	3.89	0.0003
A_24_P943566	Phosphatase and actin regulator 1	<i>PHACTR1</i>	6.34	0.0001
A_23_P51646	Polo-like kinase 3 (Drosophila)	<i>PLK3</i>	3.82	0.0001
A_33_P3280603	Protein phosphatase 4, regulatory subunit 1-like	<i>PPP4R1L</i>	2.09	0.0003
A_24_P116017	Proteasome (prosome, macropain) 26S subunit, nonATPase, 9	<i>PSMD9</i>	2.81	0.0001
A_33_P3309561	Protein tyrosine phosphatase, receptor type, J	<i>PTPRJ</i>	2.10	0.0001
A_23_P134517	Purine-rich element binding protein B	<i>PURB</i>	2.09	0.0001
A_19_P00317871	Pvt1 oncogene homolog, MYC activator (mouse)	<i>PVT1</i>	3.61	0.0000
A_23_P81760	Quaking homolog, KH domain RNA binding (mouse)	<i>QKI</i>	2.02	0.0005
A_33_P3243524	Rap guanine nucleotide exchange factor (GEF) 6	<i>RAPGEF6</i>	8.03	0.0000
A_33_P3217020	Ras association (RalGDS/AF-6) and pleckstrin homology domains 1	<i>RAPH1</i>	4.82	0.0002
A_33_P3349827	RNA binding motif (RNP1, RRM) protein 3	<i>RBM3</i>	2.27	0.0005
A_23_P97141	Regulator of G-protein signaling 1	<i>RGS1</i>	5.40	0.0002
A_33_P3291349	Regulation of nuclear pre-mRNA domain containing 1A	<i>RPRD1A</i>	2.11	0.0002
A_33_P3367795	Ribosomal protein S6	<i>RPS6</i>	3.66	0.0001
A_24_P590560	RRN3 RNA polymerase I transcription factor homolog (S. cerevisiae)	<i>RRN3</i>	2.12	0.0002
A_24_P34155	Runt-related transcription factor 1 (acute myeloid leukaemia 1; aml1 oncogene)	<i>RUNX1</i>	4.17	0.0002
A_33_P3255229	SET domain containing (lysine methyltransferase) 7	<i>SETD7</i>	4.29	0.0000
A_33_P3389286	Stratifin	<i>SFN</i>	4.04	0.0000
A_23_P19673	serum/glucocorticoid regulated kinase 1	<i>SGK1</i>	2.14	0.0003
A_33_P3333033	Small G protein signaling modulator 2	<i>SGSM2</i>	2.80	0.0004
A_33_P3317009	Solute carrier family 11 (proton-coupled divalent metal ion transporters), member 1	<i>SLC11A1</i>	5.18	0.0001
A_23_P139669	Solute carrier family 2 (facilitated glucose transporter), member 3	<i>SLC2A3</i>	2.52	0.0003
A_24_P927716	proteoglycan 3 pseudogene	<i>SLED1</i>	10.92	0.0001
A_24_P352116	Small nucleolar RNA host gene (nonprotein coding) 7	<i>SNHG7</i>	2.40	0.0003
A_33_P3258467	Spectrin, beta, nonerythrocytic 1	<i>SPTBN1</i>	2.69	0.0001
A_33_P3366146	serine/arginine-rich splicing factor 5	<i>SRSF5</i>	2.28	0.0005
A_24_P332647	Slingshot homolog 1 (Drosophila)	<i>SSH1</i>	2.30	0.0003
A_23_P342600	Serine/threonine kinase 35	<i>STK35</i>	2.75	0.0003
A_23_P339588	T-cell activation GTPase activating protein	<i>TAGAP</i>	4.35	0.0002
A_33_P3266719	tet methylcytosine dioxygenase 2	<i>TET2</i>	2.36	0.0001
A_24_P357465	Tumor protein p53 inducible nuclear protein 2	<i>TP53INP2</i>	3.36	0.0001
A_33_P3297517	transformer 2 beta homolog (Drosophila)	<i>TRA2B</i>	2.28	0.0004
A_33_P3319905	Triggering receptor expressed on myeloid cells 1	<i>TREM1</i>	2.74	0.0003

**Table 2** (contd)

Probe ID	Gene name	Gene symbol	FCA	<i>P</i> value
A_24_P252497	Tribbles homolog 1 ( <i>Drosophila</i> )	<i>TRIB1</i>	2.50	0.0002
A_33_P3274332	Ubiquitin-conjugating enzyme E2, J1 (UBC6 homolog, yeast)	<i>UBE2J1</i>	2.21	0.0001
A_23_P212595	Vpr (HIV-1) binding protein	<i>VPRBP</i>	2.50	0.0002
A_33_P3339376	WAS/WASL interacting protein family, member 1	<i>WIPF1</i>	2.76	0.0000
A_24_P342086	WW domain containing E3 ubiquitin protein ligase 2	<i>WWP2</i>	2.00	0.0004
A_24_P325046	Zinc finger, CCHC domain containing 7	<i>ZCCHC7</i>	2.14	0.0002
A_23_P406071	Zinc finger protein 36, C3H type-like 1	<i>ZFP36L1</i>	3.06	0.0003
A_33_P3384775	Zinc finger protein 295	<i>ZNF295</i>	3.59	0.0002
A_33_P3285235	Zinc finger protein 507	<i>ZNF507</i>	2.03	0.0001
A_33_P3228642	Zinc finger protein 584	<i>ZNF584</i>	3.09	0.0000
A_33_P3304516	Zinc finger, NFX1-type containing 1	<i>ZNFX1</i>	2.13	0.0001
Down regulated genes				
A_32_P123255	Ankyrin repeat domain 58	<i>ANKRD58</i>	2.68	0.0001
A_33_P3330211	Autism susceptibility candidate 2	<i>AUTS2</i>	2.23	0.0003
A_32_P235796	Bardet–Biedl syndrome 12	<i>BBS12</i>	2.56	0.0001
A_33_P3366301	Chromosome 14 open reading frame 23	<i>C14orf23</i>	2.36	0.0003
A_23_P259333	Chromosome 6 open reading frame 203	<i>C6orf203</i>	2.02	0.0003
A_23_P43425	Chromosome 9 open reading frame 40	<i>C9orf40</i>	2.54	0.0003
A_33_P3217584	Cholinergic receptor, nicotinic, alpha 4	<i>CHRNA4</i>	2.01	0.0004
A_33_P3346083	Doublecortin domain containing 1	<i>DCDC1</i>	2.19	0.0003
A_23_P12896	Fanconi anemia, complementation group F	<i>FANCF</i>	2.09	0.0003
A_33_P3411907	Fibroblast growth factor 5	<i>FGF5</i>	3.14	0.0004
A_33_P3297155	gem (nuclear organelle) associated protein 2	<i>GEMIN2</i>	2.23	0.0004
A_23_P429092	HBS1-like ( <i>S. cerevisiae</i> )	<i>HBS1L</i>	2.05	0.0004
A_24_P200854	Homeobox A2	<i>HOXA2</i>	3.34	0.0001
A_33_P3268174	Kelch repeat and BTB (POZ) domain containing 6	<i>KBTD6</i>	2.52	0.0003
A_23_P106505	Leucine carboxyl methyltransferase 2	<i>LCMT2</i>	2.04	0.0003
A_33_P3405168	Methylmalonic aciduria (cobalamin deficiency) cblA type	<i>MMAA</i>	2.02	0.0003
A_23_P146855	Metallophosphoesterase domain containing 1	<i>MPPED1</i>	2.95	0.0003
A_32_P117170	N-acyl phosphatidylethanolamine phospholipase D	<i>NAPEPLD</i>	2.13	0.0002
A_23_P64611	Pyrimidinergic receptor P2Y, G-protein coupled, 6	<i>P2RY6</i>	2.39	0.0001
A_23_P23669	Palmdelphin	<i>PALMD</i>	2.18	0.0004
A_23_P51291	Prolyl-tRNA synthetase 2, mitochondrial (putative)	<i>PARS2</i>	2.05	0.0003
A_24_P416411	Peroxisomal biogenesis factor 12	<i>PEX12</i>	2.15	0.0003
A_33_P3246663	phosphoinositide-interacting regulator of transient receptor potential channels	<i>PIRT</i>	2.78	0.0004
A_24_P315346	POM121 transmembrane nucleoporin-like 8 pseudogene	<i>POM121L8P</i>	2.97	0.0002
A_33_P3420020	diphosphoinositol pentakisphosphate kinase 1	<i>PPIP5K1</i>	2.14	0.0004
A_23_P56146	Retina and anterior neural fold homeobox 2	<i>RAX2</i>	2.71	0.0004
A_23_P154962	RIMS binding protein 3	<i>RIMBP3</i>	2.24	0.0004
A_23_P166797	Receptor (chemosensory) transporter protein 4	<i>RTP4</i>	3.03	0.0002
A_23_P129458	short chain dehydrogenase/reductase family 42E, member 1	<i>SDR42E1</i>	2.14	0.0001
A_23_P334263	SUMO/sentrin specific peptidase family member 8	<i>SENP8</i>	2.31	0.0005
A_23_P382811	sorting nexin 31	<i>SNX31</i>	3.52	0.0001
A_33_P3273457	Spermatogenesis associated 21	<i>SPATA21</i>	2.13	0.0004
A_24_P134302	Serine peptidase inhibitor-like, with Kunitz and WAP domains 1 (eppin)	<i>SPINLW1</i>	2.67	0.0004
A_23_P36187	Synaptotagmin VIII	<i>SYT8</i>	2.45	0.0002
A_32_P184394	Transcription factor EC	<i>TFEC</i>	2.37	0.0002
A_23_P106391	THAP domain containing 10	<i>THAP10</i>	2.13	0.0002
A_24_P350437	THAP domain containing, apoptosis associated protein 2	<i>THAP2</i>	2.19	0.0004
A_23_P24751	Tetratricopeptide repeat domain 9C	<i>TTC9C</i>	2.06	0.0002
A_23_P214408	Unc-93 homolog A ( <i>C. elegans</i> )	<i>UNC93A</i>	2.22	0.0004
A_33_P3342300	Visual system homeobox 1	<i>VSX1</i>	2.84	0.0004
A_33_P3362861	Zinc finger protein 30 homolog (mouse)	<i>ZFP30</i>	2.19	0.0005
A_32_P48244	Zinc finger protein 100	<i>ZNF100</i>	3.20	0.0002
A_24_P393565	Zinc finger protein 396	<i>ZNF396</i>	2.36	0.0003
A_23_P51202	Zinc finger protein 436	<i>ZNF436</i>	2.43	0.0002
A_23_P90542	Zinc finger protein 540	<i>ZNF540</i>	2.96	0.0003
A_33_P3268144	Zinc finger protein 614	<i>ZNF614</i>	2.22	0.0002
A_33_P3399019	ZNF816-ZNF321P readthrough	<i>ZNF816</i>	2.05	0.0005
A_23_P165984	Zinc finger, SWIM-type containing 3	<i>ZSWIM3</i>	2.66	0.0003

FCA, fold change absolute.

**Table 3.** Differentially expressed candidate gene between cases and controls and their functional impact on CAD.

Gene name	Functional effect of candidate genes on CAD
<i>CCL4</i>	An inflammatory chemokine which activates the CCR 5, which is widely expressed in cardiovascular tissues and mediates the persuasive vaso constriction of human arteries (Maguire <i>et al.</i> 2014).
<i>CDC42</i>	Member of GTPase family and regulates the signalling pathways that control the cellular function like cell proliferation, migration and morphology (Van Aelst and D'Souza-Schorey 1997)
<i>CXCL-1</i>	An inflammatory chemokines which promotes the uptake of LDL by macrophages and secretion of matrix mettaloproteinases from vascular smooth muscle cells (Breland <i>et al.</i> 2008)
<i>DDX58</i>	An RNA helicase which encodes RIG-1 double standard RNA helicase enzyme. It acts as a cytoplasmic sensor for viral infection and induces the activation of IFNG and other proinflammatory cytokines (Hou <i>et al.</i> 2014)
<i>EGR1</i>	EGR1 regulates cell mitogenesis and differentiations (Min <i>et al.</i> 2008)
<i>EGR2</i>	Play essential roles in adipogenesis, and immune tolerance (Fang <i>et al.</i> 2011).
<i>EGR3</i>	It is a member of Zinc-finger transcription factor which is up regulated by Vascular endothelial growth factor which leads to angiogenesis (Liu <i>et al.</i> 2008)
<i>FASLF</i>	Transmembrane protein involved in T-cell mediated apoptosis (Cahuzac <i>et al.</i> 2006)
<i>IFNG</i>	Anti/proinflammatory gene has an important role in the control of neointimaproliiferation (Zohinhofer <i>et al.</i> 2001)
<i>IL8</i>	Stimulates the cell proliferation, migrationand the inflammatory responses of human smooth muscle cells (Wang <i>et al.</i> 1996)
<i>NFKBID</i>	Involves in the regulation of inflammatory responces (Touma <i>et al.</i> 2011)
<i>NR4A2</i>	Involve is asociated with both HDL level and blood pressure (Kardys <i>et al.</i> 2009)
<i>PTX3</i>	Gene is considered as an endogenous modulator of vascular inflammation (Suzuki <i>et al.</i> 2008)
<i>PTGS2</i>	Gene has a prominent role in inflammation and mitogenesis and PTX3, which is considered as an endogenous modulator of vascular inflammation (Suzuki <i>et al.</i> 2008)

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