**Table S1** General characteristics of examined SNPs.

|  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- |
| **No** | **SNP** | **Allelic Change** | **Strand** | **Location (Ch:Loc)1** | **Target Gene** | **Gene ID2** | **Functional change** |
| 1 | rs4994 | C/T | Reverse strand | 8:37823798 | Adrenoceptor beta 3 (ADRB3) | 155 | 155 (W64R) |
| 2 | rs699 | C/T | Reverse strand | 1:230845794 | Angiotensinogen (serpin peptidase inhibitor, clade A, member 8) (AGT) | 183 | 183 (M268T) |
| 3 | rs4783961 | A/G | Forward strand | 16:56994894 | Choslesteryl ester transfer protein, plasma (CETP) | 1071 |  |
| 4 | rs1800775 | A/C | Forward strand | 16:56995236 | Choslesteryl ester transfer protein, plasma (CETP) |  |  |
| 5 | rs1800255 | A/G | Forward strand | 2:18964080 | Collagen, type III, alpha I (COL3A1) | 1281 | (A698T) |
| 6 | rs4673 | C/T | Reverse strand | 16:88713236 | Cytochrome b-245, alpha polypeptide (CYBA) | 1535 | (Y72H) |
| 7 | rs1048943 | A/C/G/T | Reverse strand | 15:75012985 | Cytochrome P450, family 1 A polypeptide 1 (CYP1A1) | 1543 | (I462L) |
| 8 | rs2071307 | A/G | Forward strand | 7:7340714 | Elastin (ELN) | 2006 | (G427S) (G412S) (G422S) |
| 9 | rs16944 | A/G | Forward strand | 2:113594867 | Interleukin 1 beta (IL1B) | 3553 |  |
| 10 | rs1800896 | A/G | Reverse strand | 1:206946897 | Interleukin 10 (IL10) | 3586 |  |
| 11 | rs1800871 | C/T | Reverse strand | 1:206946634 | IL10 | 3586 |  |
| 12 | rs1800872 | A/C | Reverse strand | 1:206946407 | IL10 | 3586 |  |
| 13 | rs11706052 | A/G | Forward strand | 3:49064110 | IMP (inosine 5'-monophosphate) dehyrogenase 2 (IMPDH2) | 3615 |  |
| 14 | rs2333227 | C/T | Forward strand | 17:56358762 | Myeloperoxidase (MPO) | 4353 |  |
| 15 | rs1801133 | C/T | Reverse strand | 1:11856378 | Methylenetetrahydrofolate reductase (NAD(P)H) (MTHFR) | 4524 | (A222V) |
| 16 | rs2070744 | C/T | Forward strand | 7:15069079 | Nitiric oxide synthase 3 (endothelial cell) (NOS3) | 4846 |  |
| 17 | rs1800779 | A/G | Forward strand | 7:15089943 | NOS3 | 4846 |  |
| 18 | rs1799983 | G/T | Forward strand | 7:150696111 | NOS3 | 4846 | (D298E) |
| 19 | rs2229523 | A/G | Forward strand | 6:86199233 | 5'-nucleotidase, ecto (CD73) (NT5E) | 4907 | (T376A) |
| 20 | rs1052133 | C/G | Forward strand | 3:9798773 | 8-oxoguanine DNA glycosylase 1(OGG1) | 4968 | (P332A) (S326C) |
| 21 | rs662 | A/G | Reverse strand | 7:94937446 | Paraoxonase 1 (PON1) | 5444 | (Q192R) |
| 22 | rs1799964 | C / T | Forward strand | 6:31542308 | Tumor necrosis factor (TNF) | 7124 |  |
| 23 | rs1042522 | C/G | Reverse strand | 17:7579472 | Tumor protein p53 (TP53) | 7157 | (P33R) (P72R) |
| 24 | rs2241766 | G/T | Forward strand | 3:186570892 | Adiponectin,C1Q and collagen domain containing (ADIPOQ) | 9370 | (G15) |
| 25 | rs1501299 | A/C | Reverse strand | 3:186571123 | ADIPOQ | 9370 |  |
| 26 | rs3765534 | C/T | Forward strand | 13:95815415 | ATP-binding cassette, sub-family C (CFTR/MRP), member 4 (ABCC4) | 10257 | (E757K) |
| 27 | rs1799864 | A/G | Forward strand | 3:46399208 | Chemokine (C-C motif) receptor 2 (CCR2) | 729230 | (V64I) |
|  |  |  |  |  |  |  |  |
| 1(Ch: Loc) indicates Chromosome: Location  2All information was extracted from dbSNP138 database, GRCh38 version (http://ncbi.nlm.gov/)  Amino acid abbreviations: V: Valine, I: Isoleucine, E: Glutamic acid, K: Lysine, G: Glycine, P: Proline, R: Arginine, Q: Glutamine, C: Cysteine, A: Alanine, T: Threonine, D: Aspartic acid, Y: Tyrosine, M: Methionine, W: Tryptophan | | | | | | | |

**Table S2** General characteristics of the examined genes.

|  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- |
| **No** | **Gene** | **Functions of genes** | **Key features of genes** | **OMIM1** | **MetS.2** | **Can.3** |
| 1 | Adrenoceptor beta 3 (ADRB3) | Receptor | Is involved in lipid metabolism, thermogenesis | 109691 | 52 | 53 |
| 2 | Angiotensinogen (serpin peptidase inhibitor, clade A, member 8) (AGT) | Cytokine/hormone/growth factor | Maintains blood pressure and pathogenesis of essential hypertension and preeclampsia | 106150 | 54 | 55 |
| 3 | Choslesteryl ester transfer protein, plasma (CETP) | Receptor/Enzyme | Transfers of cholesteryl ester from high density lipoprotein (HDL) | 118470 | 56 | 57 |
| 4 | Collagen, type III, alpha I (COL3A1) | Structural protein | Encodes for collagen found in extensible connective tissues such as skin, lung etc. Associated with Ehlers-Danlos Syndrome | 120180 | 58 | 59 |
| 5 | Cytochrome b-245, alpha polypeptide (CYBA) | Receptor/Enzyme | Encodes a primary component of the microbial oxidase system of phagocytes | 608508 | 60 | 61 |
| 6 | Cytochrome P450, family 1 A polypeptide 1 Receptor/Enzyme (CYP1A1) | Receptor/Enzyme | Drug metabolism, cholesterol synthesis and steroids | 108330 | 62 | 63 |
| 7 | Elastin (ELN) | Structural protein | Encodes elastic fibers which are hydrophobic rich | 130160 | 64 | 65 |
| 8 | Interleukin 1 beta (IL1B) hormone / growth factor | Cytokine/hormone/growth factor | Inflammatory and proprotein activating cytokine. Cell proliferation, differentiation, and apoptosis | 147720 | 66 | 67 |
| 9 | Interleukin 10 (IL10) hormone / growth factor | Cytokine/hormone/growth factor | Has pleiotropic effects in immunoregulation and inflammation | 124092 | 68 | 69 |
| 10 | Receptor/Enzyme dehyrogenase 2 |  | Involved in maintaining cellular guanine deoxy-and ribonuclotide pools needed for DNA and RNA synthesis. May cause malignancy | 146691 | 76 | 77 |
| 11 | Myeloperoxidase (MPO) | Receptor/Enzyme | Constitutes the major component of neutrophil azurophilic granules | 606989 | 78 | 79 |
| 12 | reductase (NAD(P)H) Receptor/Enzyme (MTHFR) | Receptor/Enzyme | Converts 5, 10-methylenetetrahydrofolate to 5-methyltetrahydro- folate. May influence vascular diseases, colon cancer, neural tube defects | 607093 | 80 | 81 |
| 13 | Nitiric oxide synthase 3 (endothelial cell) (NOS3) | Receptor/Enzyme | Neurotransmission and antimural activities may cause coronary spasm. | 163729 | 82 | 83 |
| 14 | 5'-nucleotidase, ecto (CD73)Receptor/Enzyme (NT5E) | Receptor/Enzyme |  | 129190 | 84 | 85 |
| 15 | 8-oxoguanine DNA glycosylase Receptor/Enzyme (OGG1) | Receptor/Enzyme |  | 601982 | 86 | 87 |
| 16 | Paraoxonase 1 (PON1) | Receptor/Enzyme |  | 168820 | 88 | 89 |
| 17 | Tumor necrosis factor (TNF) | Cytokine/hormone/growth factor |  | 191160 | 90 | 91 |
| 18 | Tumor protein p53 (TP53) | DNA repair & Tumor suppressor |  | 191170 | 92 | 93 |
| 19 | Adiponectin, C1Q and collagen domain containing (ADIPOQ) ATP-binding cassette, sub-family C | Cytokine/hormone/growth factor |  | 605441 | 94 | 95 |
| 20 | (CFTR/MRP), member 4 (ABCC4) | Receptor/Enzyme |  | 605250 | 96 | 97 |
| 21 | Chemokine (C-C motif) receptor 2 (CCR2) | Receptor/Enzyme |  | 601267 | 98 | 99 |
| 1OMIM:Online Mendelian Inheritance in Man (http://omim.org/)  2MetS.:Metabolic syndrome related publication  3Can.:Cancer related publication  nf:Not found in NBCI database (http://ncbi.nlm.gov/) | | | | | | |

**Table S3** Allelic and genotypic distributions of 27 SNPs.

|  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- |
| **SNP** | **Alleles** | | **Genotypes** | | | **p(HWE)2** | **MAF3** | **SNP** | **Alleles** |  |  | **Genotypes** |  | **p(HWE)** | **MAF** |
|  | **T** | **C** | **TT** | **CT** | **CC** |  |  |  | **C** | **T** | **CC** | **CT** | **TT** |  |  |
| rs4994 (%)1 Missing | 2442 | 556 | 991 | 460 | 48 |  |  | rs4673 (%) Missing | 2701 | 273 | 1224 | 253 | 10 | 0.431 | 0.09 |
| -81 | -19 | -66 | -31 | -3 | 0.543 | 0.19 | -91 | -9 | -82 | -17 | -1 |  |  |
| 3 |  |  |  |  |  |  | 16 |  |  |  |  |  |  |
|  | **T** | **C** | **TT** | **CT** | **CC** |  |  |  | **A** | **G** | **AA** | **AG** | **GG** |  |  |
| rs699 (%) Missing | 558 | 2444 | 63 | 432 | 1006 |  |  | rs1048943 (%) Missing | 2350 | 646 | 925 | 500 | 73 |  |  |
| -19 | -81 | -4 | -29 | -67 | 0.057 | 0.19 | -78 | -22 | -62 | -33 | -5 | 0.608 | 0.22 |
| 2 |  |  |  |  |  |  | 5 |  |  |  |  |  |  |
|  | **G** | **A** | **GG** | **AG** | **AA** |  |  |  | **G** | **A** | **GG** | **AG** | **AA** |  |  |
| rs4783961 (%) Missing | 2170 | 820 | 785 | 600 | 110 |  |  | rs2071307 (%) Missing | 2433 | 549 | 1000 | 433 | 58 |  |  |
| -73 | -27 | -53 | -40 | -7 | 0.751 | 0.27 | -82 | -18 | -67 | -29 | -4 | 0.198 | 0.18 |
| 8 |  |  |  |  |  |  | 12 |  |  |  |  |  |  |
|  | **A** | **C** | **AA** | **AC** | **CC** |  |  |  | **C** | **T** | **CC** | **CT** | **TT** |  |  |
| rs1800775 (%) Missing | 1644 | 1332 | 458 | 728 | 302 |  |  | rs16944 (%) Missing | 1614 | 1382 | 421 | 772 | 305 |  |  |
| -55 | -45 | -31 | -49 | -20 | 0.682 | 0.45 | -54 | -46 | -28 | -52 | -20 | 0.152 | 0.46 |
| 15 |  |  |  |  |  |  | 5 |  |  |  |  |  |  |
|  | **G** | **A** | **GG** | **AG** | **AA** |  |  |  | **A** | **G** | **AA** | **AG** | **GG** |  |  |
| rs1800255 (%) Missing | 2139 | 825 | 768 | 603 | 111 |  |  | rs1800896 (%) Missing | 2854 | 140 | 1361 | 132 | 4 |  |  |
| -72 | -28 | -52 | -41 | -7 | 0.621 | 0.28 | -95 | -5 | -91 | -8 | -1 | 0.673 | 0.05 |
| 21 |  |  |  |  |  |  | 6 |  |  |  |  |  |  |
|  | **C** | **T** | **CC** | **CT** | **TT** |  |  |  | **C** | **T** | **CC** | **CT** | **TT** |  |  |
| rs1800871 (%) Missing | 1973 | 1009 | 657 | 659 | 175 |  |  | rs2070744 (%) Missing | 312 | 2688 | 16 | 280 | 1204 |  |  |
| -66 | -34 | -44 | -44 | -12 | 0.619 | 0.34 | -10 | -90 | -1 | -19 | -80 | 0.95 | 0.1 |
| 12 |  |  |  |  |  |  | 3 |  |  |  |  |  |  |
|  | **A** | **C** | **AA** | **AC** | **CC** |  |  |  | A | **G** | **AA** | **AG** | **GG** |  |  |
| rs1800872 (%) Missing | 1964 | 996 | 655 | 654 | 171 |  |  | rs1800779 (%) Missing | 2679 | 313 | 1200 | 279 | 17 |  |  |
| -66 | -34 | -44 | -44 | -12 | 0.689 | 0.34 | -90 | -10 | -80 | -19 | -1 | 0.862 | 0.1 |
| 23 |  |  |  |  |  |  | 7 |  |  |  |  |  |  |
|  | **A** | **G** | **AA** | **AG** | **GG** |  |  |  | **G** | **T** | **GG** | **GT** | **TT** |  |  |
| rs11706052 (%) Missing | 2857 | 131 | 1367 | 123 | 4 |  |  | rs1799983 (%) Missing | 2725 | 247 | 1249 | 227 | 10 |  |  |
| -96 | -4 | -91 | -8 | -1 | 0.486 | 0.04 | -92 | -8 | -84 | -15 | -1 | 0.928 | 0.08 |
| 9 |  |  |  |  |  |  | 17 |  |  |  |  |  |  |
|  | **C** | **T** | **CC** | **CT** | **TT** |  |  |  | **G** | **A** | **GG** | **AG** | **AA** |  |  |
| rs2333227 (%) Missing | 2673 | 317 | 1196 | 281 | 18 |  |  | rs2229523 (%) Missing | 1811 | 1129 | 561 | 689 | 220 |  |  |
| -89 | -11 | -80 | -19 | -1 | 0.744 | 0.11 | -62 | -38 | -38 | -47 | -15 | 0.722 | 0.38 |
| 8 |  |  |  |  |  |  | 33 |  |  |  |  |  |  |
|  | **C** | **T** | **CC** | **CT** | **TT** |  |  |  | **C** | **G** | **CC** | **CG** | **GG** |  |  |
| rs1801133 (%) Missing | 1750 | 1226 | 519 | 712 | 257 |  |  | rs1052133 (%) Missing | 1560 | 1416 | 414 | 732 | 342 |  |  |
| -59 | -41 | -35 | -48 | -17 | 0.632 | 0.41 | -52 | -48 | -28 | -49 | -23 | 0.593 | 0.48 |
| 15 |  |  |  |  |  |  | 15 |  |  |  |  |  |  |
|  | **A** | **G** | **AA** | **AG** | **GG** |  |  |  | **C** | **A** | **CC** | **AC** | **AA** |  |  |
| rs662 (%) Missing | 1980 | 1002 | 653 | 674 | 164 |  |  | rs1501299 (%) Missing | 2070 | 886 | 718 | 634 | 126 |  |  |
| -66 | -34 | -44 | -45 | -11 | 0.614 | 0.34 | -70 | -30 | -49 | -43 | -8 | 0.401 | 0.3 |
| 12 |  |  |  |  |  |  | 25 |  |  |  |  |  |  |
|  | **T** | **C** | **TT** | **CT** | **CC** |  |  |  | **C** | **T** | **CC** | **CT** | **TT** |  |  |
| rs1799964 (%) Missing | 2376 | 526 | 969 | 438 | 44 |  |  | rs3765534 (%) Missing | 2482 | 442 | 1054 | 374 | 34 |  |  |
| -82 | -18 | -67 | -30 | -3 | 0.516 | 0.18 | -85 | -15 | -72 | -26 | -2 | 0.903 | 0.15 |
| 52 |  |  |  |  |  |  | 41 |  |  |  |  |  |  |
|  | **C** | **G** | **CC** | **CG** | **GG** |  |  |  | **A** | **G** | **AA** | **AG** | **GG** |  |  |
| rs1042522 (%) Missing | 1027 | 1963 | 187 | 653 | 655 |  |  | rs1799864  (%)  Missing | 844 | 2136 | 135 | 574 | 781 |  |  |
| -34 | -66 | -12 | -44 | -44 | 0.223 | 0.34 | -28 | -72 | -9 | -39 | -52 | 0.05 | 0.28 |
| 8 |  |  |  |  |  |  | 13 |  |  |  |  |  |  |
|  | **T** | **G** | **TT** | **TG** | **GG** |  |  |  | | | | | | | |
| rs2241766 (%) Missing | 2102 | 878 | 736 | 630 | 124 |  |  |
| -71 | -29 | -50 | -42 | -8 | 0.505 | 0.29 |
| 13 |  |  |  |  |  |  |
|  |  |  |  |  |  |  |  |  | | | | | | | |
| 1(%) indicates percentage value of either each allele or genotype within their respective category  2p(HWE): probabilistic value of Hardy-Weinberg equilibrium.  3MAF: (Observed) minor allele frequency | | | | | | | | | | | | | | | |