suppl. Table 2. 88 SNPs which were significantly associated with sICAS patients compared with healthy control groups

|  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- |
| Gene | SNP ID | Ref allele | Alt allele | FreqAlt (1000g) | P value | HWE sICAS (P) | HWE Contral (P) |
| *ADIPOQ-AS1* | rs1501298 | G | A | 0.984026 | 0.0001123 | 1 | 1 |
| *AGT* | rs699 | G | A | 0.705072 | 0.01071 | 0.6889 | 0.1902 |
| *BAAT* | rs1572983 | C | T | 0.562899 | 0.02898 | 0.4104 | 0.8919 |
| *CLCN6* | rs3737965 | G | A | 0.0646965 | 0.02455 | 0.7939 | 0.826 |
| *CMIP* | rs17777059 | A | G | 0.148962 | 0.002233 | 0.6598 | 0.8667 |
| *COL18A1* | rs1131100 | C | T | 0.163139 | 0.004629 | 0.6117 | 0.5645 |
|  | rs1131102 | C | A | 0.140375 | 0.01438 | 1 | 0.5398 |
|  | rs73370824 | C | A | 0.135783 | 0.02561 | 0.6116 | 0.5374 |
|  | rs1131101 | C | T | 0.157348 | 0.02861 | 1 | 0.5398 |
| *COL4A1* | rs41275104 | A | G | 0.189896 | 0.03751 | 1 | 0.3264 |
| *CP* | rs561633350 | AA | - | 0.241214 | 0.002765 | 0.3883 | 0.6377 |
| *CUBN* | rs10795440 | G | A | 0.911142 | 0.0017 | 1 | 0.3621 |
|  | rs1801225 | C | T | 0.35603 | 0.03322 | 0.3656 | 0.2725 |
|  | rs41289315 | G | A | 0.0884585 | 0.03444 | 1 | 0.08985 |
|  | rs2273737 | T | G | 0.0820687 | 0.03444 | 1 | 0.08985 |
|  | rs41289313 | G | A | 0.0846645 | 0.03949 | 1 | 0.0835 |
|  | rs41289311 | G | A | 0.0642971 | 0.0495 | 1 | 0.05723 |
| *DDAH1* | rs2076699 | G | A | 0.139776 | 0.0306 | 0.7086 | 0.6606 |
|  | rs2230820 | T | C | 0.124601 | 0.04658 | 0.7086 | 0.4746 |
| *DOCK2* | rs9791113 | C | G | 0.486222 | 0.003118 | 0.4108 | 0.3775 |
| *ERAP1* | rs469783 | C | T | 0.557109 | 0.0009531 | 0.4182 | 0.1657 |
| *FBN1* | rs140598 | G | C | 0.0597045 | 0.003149 | 0.7673 | 0.9373 |
| *FBN1* | rs55699652 | T | C | 0.061901 | 0.003291 | 0.7679 | 0.8129 |
|  | rs57512865 | T | C | 0.0654952 | 0.004044 | 0.3645 | 0.5695 |
| *HNF1A* | rs1169288 | A | C | 0.298522 | 0.008132 | 0.101 | 1 |
|  | rs1169289 | C | G | 0.428514 | 0.01504 | 0.5029 | 0.7461 |
| *HPS3* | rs58796831 | AG | - | 0.164936 | 0.02664 | 0.7359 | 1 |
| *HTRA1* | rs2272599 | G | A | 0.627995 | 0.04219 | 0.2356 | 0.1487 |
| *GFALS* | rs17559 | G | A | 0.25619 | 0.01176 | 0.156 | 0.4404 |
| *INSR* | rs3835070 | - | GA | 0.233626 | 0.005277 | 1 | 0.108 |
|  | rs1799817 | G | A | 0.292532 | 0.01218 | 0.7627 | 0.211 |
|  | rs2229429 | G | A | 0.256589 | 0.02654 | 0.5821 | 0.3551 |
|  | rs78312382 | C | T | 0.0509185 | 5.007×10-7 | 0.07988 | 0.4359 |
| *ITLN1* | rs35779394 | T | C | 0.116813 | 0.02095 | 0.5996 | 0.8988 |
|  | rs2297560 | C | T | 0.117013 | 0.0494 | 0.5996 | 0.6928 |
|  | rs74315633 | T | C | 0.117013 | 0.0494 | 0.5996 | 0.6928 |
| *ITPA* | rs8362 | G | A | 0.470447 | 0.007867 | 0.602 | 0.612 |
| *JMJD1C* | rs3211105 | G | A | 0.58107 | 0.03131 | 0.4016 | 0.07642 |
| *KCNJ11* | rs5218 | G | A | 0.227436 | 0.002441 | 0.07157 | 0.2031 |
|  | rs5210 | G | A | 0.467652 | 0.0176 | 0.4474 | 0.09507 |
| *KCNK16* | rs3734619 | C | T | 0.386182 | 0.006353 | 0.6812 | 0.3012 |
|  | rs11756070 | G | A | 0.583666 | 0.03666 | 0.9203 | 0.2047 |
|  | rs3734618 | A | G | 0.603435 | 0.03698 | 0.8409 | 0.2282 |
| *LPA* | rs1801693 | A | G | 0.648163 | 0.0449 | 0.193 | 0.06592 |
| *MMP9* | rs17576 | A | G | 0.455471 | 0.01381 | 0.7873 | 0.1154 |
| *MTHFR* | rs1476413 | C | T | 0.251198 | 0.005193 | 0.5613 | 0.7375 |
| *MTHFR* | rs1994798 | G | A | 0.579273 | 0.01849 | 0.7725 | 0.7473 |
|  | rs2066462 | G | A | 0.103435 | 0.02207 | 1 | 0.818 |
|  | rs3820192 | G | T | 0.11242 | 0.02958 | 0.5814 | 0.6248 |
|  | rs1537516 | G | A | 0.111422 | 0.04467 | 0.2836 | 1 |
|  | rs1801133 | C | T | 0.245407 | 6.622×10-7 | 0.3787 | 0.2811 |
| *NINJ2* | rs4980959 | C | A | 0.370607 | 0.007127 | 0.1856 | 0.7935 |
| *NOS3* | rs2853796 | G | T | 0.524561 | 0.005207 | 0.05108 | 0.7844 |
|  | rs1800780 | A | G | 0.569489 | 0.005997 | 0.121 | 0.6774 |
|  | rs1549758 | T | C | 0.817692 | 0.03184 | 0.2733 | 0.3113 |
|  | rs1800781 | G | A | 0.108427 | 0.04859 | 0.3403 | 0.2489 |
| *PCSK9* | rs505151 | G | A | 0.898962 | 0.02499 | 0.2422 | 0.1162 |
| *PDE4D* | rs72769729 | C | T | 0.0886581 | 0.00106 | 0.6255 | 0.7998 |
| *PHACTR1* | rs693758 | G | A | 0.220847 | 0.03965 | 0.3688 | 0.5868 |
| *PON1* | rs662 | G | A | 0.220847 | 0.04442 | 0.3103 | 1 |
| *RAPGEF4* | rs2258180 | G | T | 0.526957 | 0.03563 | 0.2779 | 0.3256 |
| *RBP4* | rs56401591 | C | T | 0.167532 | 0.0005549 | 0.4553 | 0.2217 |
| *RCL1* | rs15583 | A | G | 0.580671 | 0.02733 | 0.3575 | 0.6585 |
| *RNF213* | rs8082521 | C | A | 0.558307 | 0.002467 | 0.3027 | 0.5382 |
|  | rs55996424 | A | T | 0.329673 | 0.02748 | 0.1528 | 0.6925 |
| *RPS12* | rs371269086 | TTT | - | 0.0557109 | 0.0003596 | 1 | 1 |
| *SELE* | rs5368 | G | A | 0.150958 | 0.001992 | 0.7657 | 0.4805 |
|  | rs3917432 | T | A | 0.123802 | 0.002827 | 0.7604 | 0.5735 |
|  | rs3917428 | G | A | 0.123602 | 0.003213 | 0.8808 | 0.4749 |
|  | rs5356 | A | G | 0.148363 | 0.004118 | 0.7604 | 0.4695 |
|  | rs5367 | A | G | 0.0549121 | 0.01019 | 1 | 1 |
| *SELE* | rs3917410 | A | G | 0.0555112 | 0.01207 | 1 | 1 |
|  | rs5362 | A | G | 0.0549121 | 0.01217 | 1 | 1 |
|  | rs5361 | T | G | 0.0549121 | 0.01217 | 1 | 1 |
|  | rs5363 | A | G | 0.0549121 | 0.01227 | 1 | 1 |
|  | rs1800016 | T | C | 0.0549121 | 0.01227 | 1 | 1 |
|  | rs1800015 | T | C | 0.0549121 | 0.01227 | 1 | 1 |
|  | rs1805193 | C | A | 0.0549121 | 0.01453 | 1 | 1 |
| *SMARCA4* | rs2075021 | C | G | 0.450879 | 0.02522 | 0.1331 | 0.6527 |
| *SPINK5* | rs6892205 | C | G | 0.450879 | 0.002156 | 0.3141 | 0.2434 |
| *THADA* | rs7605661 | C | G | 0.450879 | 0.03125 | 1 | 0.1145 |
|  | rs33979934 | T | A | 0.213259 | 0.03144 | 1 | 0.09912 |
|  | rs35340152 | T | A | 0.245208 | 0.03296 | 1 | 0.09379 |
| *TMEM59L* | rs709679 | T | C | 0.509385 | 0.03731 | 0.1395 | 0.09043 |
| *ZBTB2* | rs11155787 | C | T | 0.423922 | 0.01638 | 0.7917 | 0.06159 |
| *ZC3HC1* | rs1464890 | T | C | 0.476038 | 0.0392 | 0.3346 | 0.05963 |
| *ZFPM1* | rs59292167 | C | G | 0.202276 | 0.01207 | 0.2947 | 0.5419 |
| *ZFPM2* | rs3735953 | C | T | 0.720248 | 9.348×10-7 | 0.4551 | 0.7513 |

Footnotes: P value﹤0.05 was considered as significant; Allele frequency was ≥ 0.05 in 1000 Genome Project; Weinberg equilibrium (HWE) test P value >0.05. Allele frequency was ≥ 0.05 in 1000 Genome Project.