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| --- | --- | --- | --- | --- | --- |
| **Table S1.** The top 88 genetic loci identified from the initial GWAS screen of Taiwanese FSS. | | | | | |
| **dbSNP ID** | **Chromosome** | **Position** | **A1/A2** | **Gene Symbol** | ***p*-value** |
| rs75002618 | 1 | 18,146,409 | AG | *IGSF21* | 4.59E-05 |
| rs75856337 | 1 | 35,787,786 | AG | *AGO4* | 4.49E-05 |
| rs12059301 | 1 | 35,855,300 | TG | *AGO4* | 5.54E-05 |
| rs2152388 | 1 | 76,142,666 | TA | *ST6GALNAC3* | 4.44E-06 |
| rs822611 | 1 | 98,244,390 | AG | *LINC01776* | 1.12E-10 |
| rs10158900 | 1 | 201,125,443 | AG | - | 2.88E-05 |
| rs4653894 | 1 | 228,000,403 | TC | *WNT9A / WNT3A* | 5.63E-05 |
| rs6544781 | 2 | 45,051,655 | CG | - | 5.34E-06 |
| rs938659 | 2 | 45,736,761 | GA | *PRKCE* | 9.93E-05 |
| rs4428032 | 2 | 71,474,222 | AG | *DYSF* | 7.59E-05 |
| rs6731651 | 2 | 164,375,125 | AG | - | 6.05E-24 |
| rs10209887 | 2 | 179,240,039 | TC | *SESTD1* | 4.47E-05 |
| rs13417919 | 2 | 179,252,034 | CT | *SESTD1* | 4.31E-05 |
| rs17446700 | 2 | 200,255,505 | CT | - | 6.57E-07 |
| rs10931894 | 2 | 200,260,598 | GT | - | 2.57E-05 |
| rs12621262 | 2 | 200,271,396 | GA | - | 1.43E-05 |
| rs17630248 | 2 | 200,273,059 | CT | - | 3.62E-05 |
| rs78804475 | 2 | 204,209,362 | GA | *PARD3B / ICOS* | 7.61E-06 |
| rs12619767 | 2 | 204,211,467 | AG | *PARD3B / ICOS* | 2.23E-06 |
| rs16840902 | 2 | 204,224,539 | GA | *PARD3B / ICOS* | 2.23E-06 |
| rs7571816 | 2 | 232,212,354 | AG | *DIS3L2* | 8.35E-05 |
| rs1369117 | 3 | 10,699,638 | CT | *ATP2B2* | 5.29E-05 |
| rs12054035 | 3 | 25,227,730 | TC | - | 4.62E-05 |
| rs34436682 | 3 | 107,406,092 | AG | - | 7.40E-05 |
| rs59778278 | 3 | 121,090,749 | AC | *STXBP5L* | 2.27E-05 |
| rs16828530 | 3 | 157,932,964 | TC | - | 6.22E-26 |
| rs9290657 | 3 | 178,599,686 | CT | - | 9.91E-09 |
| rs7683687 | 4 | 10,521,221 | GA | *-* | 6.47E-05 |
| rs2286465 | 4 | 10,531,010 | GA | - | 8.96E-05 |
| rs7672919 | 4 | 17,795,832 | TG | *LOC105374509* | 4.80E-05 |
| rs12500509 | 4 | 39,061,994 | TG | *KLHL5* | 6.05E-06 |
| rs7658917 | 4 | 39,332,767 | TC | *RFC1* | 2.04E-05 |
| rs17584703 | 4 | 39,363,236 | CT | *RFC1* | 1.43E-05 |
| rs6857589 | 4 | 95,292,732 | TC | *UNC5C* | 6.76E-05 |
| rs6831808 | 4 | 95,292,777 | AG | *UNC5C* | 3.58E-05 |
| rs10028040 | 4 | 150,743,640 | TG | *LRBA* | 3.35E-10 |
| rs11743270 | 5 | 5,190,934 | GT | *ADAMTS16* | 2.34E-05 |
| rs1366595 | 5 | 89,045,356 | GA | *MEF2C* | 5.75E-05 |
| rs6899208 | 5 | 113,198,027 | TC | *MCC* | 3.09E-05 |
| rs1432929 | 5 | 166,806,051 | CT | - | 8.59E-05 |
| rs9405156 | 6 | 1,973,345 | CT | *GMDS* | 5.58E-05 |
| rs11965495 | 6 | 89,952,574 | TC | *BACH2* | 2.86E-05 |
| rs1415701 | 6 | 130,024,690 | AG | *L3MBTL3* | 2.26E-07 |
| rs1336369 | 6 | 140,640,515 | GA | - | 6.96E-05 |
| rs4394230 | 6 | 140,667,204 | TC | *LOC105378027* | 7.35E-05 |
| rs3804532 | 6 | 143,121,662 | AT | - | 7.65E-05 |
| rs3127409 | 6 | 166,120,196 | TC | - | 4.75E-05 |
| rs11767364 | 7 | 96,403,573 | GA | *LOC105375410* | 8.78E-06 |
| rs1207716 | 7 | 97,038,835 | CT | - | 5.67E-05 |
| rs10086016 | 8 | 36,990,191 | CT | - | 9.37E-05 |
| rs10955009 | 8 | 36,994,383 | AC | - | 8.43E-05 |
| rs9886374 | 8 | 79,396,368 | AG | *IL7* | 5.82E-05 |
| rs7014528 | 8 | 79,398,623 | GA | *IL7* | 7.39E-05 |
| rs1863593 | 8 | 80,536,906 | CT | - | 9.90E-10 |
| rs16900402 | 8 | 125,160,485 | GA | *NSMCE2* | 2.76E-26 |
| rs28786672 | 9 | 88,760,260 | CA | - | 3.45E-17 |
| rs7852806 | 9 | 93,846,345 | GT | *LOC101928014* | 8.65E-27 |
| rs16916289 | 9 | 111,675,744 | CT | - | 4.42E-05 |
| rs2416835 | 9 | 121,916,935 | CT | *TTLL11* | 6.94E-05 |
| rs12349999 | 9 | 126,017,533 | CT | - | 7.19E-06 |
| rs11254854 | 10 | 6,888,693 | TC | *LOC105376387* | 9.97E-05 |
| rs11023999 | 11 | 2,756,853 | AG | *KCNQ1* | 6.84E-05 |
| rs7945156 | 11 | 3,678,234 | GA | *NUP98* | 7.62E-05 |
| rs11032025 | 11 | 32,853,380 | AG | *PRRG4* | 7.70E-06 |
| rs10767971 | 11 | 32,874,118 | CT | - | 6.02E-05 |
| rs72901219 | 11 | 32,876,297 | CG | - | 6.39E-05 |
| rs4547071 | 11 | 36,030,588 | TC | *LDLRAD3* | 8.20E-05 |
| rs78430417 | 12 | 11,286,180 | AG | *-* | 6.73E-06 |
| rs2172912 | 12 | 26,045,337 | AG | *RASSF8* | 5.42E-18 |
| rs3816804 | 12 | 56,286,961 | TC | *CS* | 6.65E-05 |
| rs12826453 | 12 | 102,567,076 | CT | *IGF1* | 4.16E-11 |
| rs10444453 | 12 | 126,621,615 | TC | - | 3.34E-05 |
| rs9520911 | 13 | 108,501,255 | GA | *MYO16* | 2.34E-13 |
| rs12879229 | 14 | 39,027,867 | AG | - | 3.40E-05 |
| rs4902308 | 14 | 39,029,954 | AC | *SEC23A* | 3.84E-05 |
| rs17097800 | 14 | 98,791,403 | TC | *BCL11B* | 9.57E-05 |
| rs1257636 | 14 | 99,011,850 | AG | *BCL11B* | 3.50E-05 |
| rs4905794 | 14 | 99,013,332 | GA | *BCL11B* | 6.91E-06 |
| rs8055182 | 16 | 86,793,922 | AG | - | 1.58E-05 |
| rs311753 | 17 | 6,940,165 | GA | - | 2.17E-05 |
| rs17732181 | 17 | 6,957,288 | GT | - | 4.90E-24 |
| rs550510 | 17 | 48,849,253 | GA | *CALCOCO2* | 8.95E-05 |
| rs36084614 | 18 | 22,377,013 | TG | - | 9.90E-05 |
| rs7505525 | 18 | 70,369,400 | TC | - | 2.52E-05 |
| rs60104364 | 19 | 8,932,507 | AC | *MUC16* | 8.73E-05 |
| rs4815179 | 20 | 23,162,329 | CT | *LOC100505664* | 4.01E-12 |
| rs6005363 | 22 | 27,293,529 | TC | *MIAT / MN1* | 7.12E-05 |
| rs13054961 | 22 | 27,296,093 | AG | *MIAT / MN1* | 2.26E-05 |
| The top 88 SNPs (*p*–value <1×10-4) are identified by the genome-wide association study (GWAS) between FSS cases and controls under the additive inheritance model. These SNPs are ordered by the chromosome and position.  SNP, single nucleotide polymorphism; A1, allele 1 (minor-allele based the defined control whole samples); A2, allele 2 (major-allele based the defined control whole samples).  The positions are based on the NCBI GRCh38 version. Gene is identified based on the gene containing the SNP or the closest gene (within 100 kb up- or downstream) to the SNP. | | | | | |