**Supplemental Table 1. List of SNP selected from various GWAS and confirmatory studies (**[**1**](#_ENREF_1)**;** [**2**](#_ENREF_2)**;** [**3**](#_ENREF_3)**;** [**4**](#_ENREF_4)**;** [**5**](#_ENREF_5)**) shown to be associated with high serum uric acid (SNPhsua)**

|  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- |
| **Variant** | **Location** | **Risk allele****(Higher SUA)** | **Other allele****(Lower SUA)** | **Population, references** | **Minor Allele Frequency** | **Status** |
| ***SLC2A9 (chromosome 4)*** |  |  |  |  |  |  |
| **rs1014290** | **Intron 3** | **T**  | **C** | **European ancestry(**[**6**](#_ENREF_6)**)** | **G=0.33** | **A** |
| **rs6449213** | **Intron 4** | **T** | **C** | **White (**[**6**](#_ENREF_6)**;** [**7**](#_ENREF_7)**;** [**8**](#_ENREF_8)**;** [**9**](#_ENREF_9)**;** [**10**](#_ENREF_10)**), AA(**[**11**](#_ENREF_11)**;** [**12**](#_ENREF_12)**), Hispanic(**[**2**](#_ENREF_2)**)** | **C=0.14** | **A** |
| rs734553 | Intron 6 | T | G | White,([13](#_ENREF_13); [14](#_ENREF_14); [15](#_ENREF_15)) Icelandic,([16](#_ENREF_16)) AA([12](#_ENREF_12)) | G=0.30 | D |
| **rs7442295** | **Intron 6** | **A** | **G** | **White(**[**7**](#_ENREF_7)**;** [**14**](#_ENREF_14)**;** [**15**](#_ENREF_15)**;** [**17**](#_ENREF_17)**)** | **G=0.26** | **A** |
| rs737269 | Intron 7 | T | C | European ancestry([6](#_ENREF_6); [15](#_ENREF_15)) | T=0.41 | C |
| rs6855911 | Intron 7 | A | G | White, ([7](#_ENREF_7); [14](#_ENREF_14); [15](#_ENREF_15); [17](#_ENREF_17)) AA([12](#_ENREF_12)) | G=0.30 | D |
| **rs13129697** | **Intron 7** | **T** | **G** | **White,(**[**15**](#_ENREF_15)**;** [**18**](#_ENREF_18)**) AA(**[**12**](#_ENREF_12)**), Hispanic(**[**2**](#_ENREF_2)**)** | **G=0.48** | **A** |
| **rs2241480** | **Intron 8** | **T** | **A/C** | **European ancestry(**[**12**](#_ENREF_12)**)** | **T=0.33** | **B** |
| rs7663032 | Intron 9 | T | G/C | AA,([12](#_ENREF_12)) Croatian([15](#_ENREF_15)) | C=0.37 | D |
| rs3775948 | Intron 9 | C | G | Croatian,([15](#_ENREF_15)) AA([11](#_ENREF_11)) | G=0.34 | D |
| rs16890979 | Intergenic | C | T | White,([15](#_ENREF_15); [19](#_ENREF_19); [20](#_ENREF_20)) AA([12](#_ENREF_12)), Amish,([21](#_ENREF_21)) Croatian, ([15](#_ENREF_15)) Pacific Islander,([20](#_ENREF_20)) New Zealander([20](#_ENREF_20)) | T=0.26 | D |
| rs717615 | Intergenic | A | G | Croatian([15](#_ENREF_15)) | G=0.43 | C |
| rs6856396 | Intergenic | T | A | AA([11](#_ENREF_11)) | A=0.14 | C |
| rs11942223 | Intergenic | T | C | European([22](#_ENREF_22)) | C=0.27 | D |
| rs11723388 | Intergenic | G | A | Hispanic([2](#_ENREF_2)) | A=0.12 | C |
| rs11721501 | Intergenic | G | A | Hispanic([2](#_ENREF_2)) | A=0.13 | D |
| rs6843466 | Intergenic | G | A | Hispanic([2](#_ENREF_2)) | T=0.49 | E |
| rs17251963 | Intergenic | A | G | Hispanic([2](#_ENREF_2)) | C=0.13 | D |
| rs13113918 | Exon 3 | G | A | Hispanic([2](#_ENREF_2)) | A=0.18 | D |
| rs7683856 | Intron | G | A | Hispanic([2](#_ENREF_2)) | A=0.18 | D |
| **rs9991278** | **Intron** | **G** | **A** | **Hispanic(**[**2**](#_ENREF_2)**)** | **T=0.17** | **A** |
| rs11723439 | Intron | G | A | Hispanic([2](#_ENREF_2)) | T=0.12 | C |
| rs4697745 | Intergenic | G | A | Hispanic([2](#_ENREF_2)) | A=0.19 | C |
| rs7675964 | Intron | G | A | Hispanic([2](#_ENREF_2)) | T=0.47 | D |
| rs938552 | Intron | G | A | Hispanic([2](#_ENREF_2)) | T=0.26 | D |
| rs12510549 | Intergenic | A | G | Hispanic([2](#_ENREF_2)) | C=0.17 | C |
| rs11722228 | Intron | T | C | Chinese([3](#_ENREF_3)) | T=0.31 | C |
| **rs12498742** | **Intron** | **A** | **G** | **European(**[**5**](#_ENREF_5)**)** | **G=0.30** | **A** |
| ***ABCG2 (chromosome 4)*** |  |  |  |  |  |  |
| rs2231137 | Exon 2 | A | G | Japanese([23](#_ENREF_23)) | A= 0.16 | D |
| rs72552713 (Q126X) | Exon 4 | T | C | Japanese([23](#_ENREF_23)) | A=0.001 | F |
| **rs2231142(Q141K)** | **Exon 5** | **T** | **G** | **White,(**[**13**](#_ENREF_13)**;** [**14**](#_ENREF_14)**;** [**15**](#_ENREF_15)**;** [**19**](#_ENREF_19)**;** [**24**](#_ENREF_24)**), European,(**[**5**](#_ENREF_5)**) African, (**[**12**](#_ENREF_12)**;** [**19**](#_ENREF_19)**)Chinese,(**[**3**](#_ENREF_3)**;** [**25**](#_ENREF_25)**)****Icelandic,(**[**16**](#_ENREF_16)**) Japanese, (**[**23**](#_ENREF_23)**;** [**26**](#_ENREF_26)**) Pacific Islander,(**[**27**](#_ENREF_27)**) New Zealander(**[**27**](#_ENREF_27)**;** [**28**](#_ENREF_28)**)** | **T=0.12** | **A** |
| rs2199936 | Intergenic | A | G | White([13](#_ENREF_13); [15](#_ENREF_15); [18](#_ENREF_18)) | N/A | E |
| rs4148152 | Intron | T | C | Chinese([3](#_ENREF_3)) | C=0.16 | C |
| rs3114018 | Intron | G | T | Chinese([3](#_ENREF_3)) | C=0.50 | C |
| ***SLC22A12 (chromosome 11)*** |  |  |  |  |  |  |
| rs11231825 | Exon 1 | C | T | Chinese,([29](#_ENREF_29)) White,([13](#_ENREF_13); [30](#_ENREF_30)) AA([12](#_ENREF_12)) | C=0.39 | D |
| rs12800450 | Exon 2 | G | T | AA([12](#_ENREF_12)) | **T=0.01**([12](#_ENREF_12)) | E |
| rs559946 | Intron 3 | C | T | Chinese([31](#_ENREF_31)) | T=0.43 | C |
| rs893006 | Intron 4 | G | T | Japanese,([32](#_ENREF_32)) Chinese([33](#_ENREF_33)) | G/T=0.50 | C |
| rs1529909 | Intron 4 | T | C | Korean([34](#_ENREF_34)) | C=0.39 | E |
| rs17300741 | Intron 4 | A | G | European([13](#_ENREF_13); [35](#_ENREF_35)) | G=0.33 | C |
| **rs7932775** | **Exon 8** | **C** | **T** | **German,(**[**30**](#_ENREF_30)**) Chinese,(**[**29**](#_ENREF_29)**;** [**31**](#_ENREF_31)**)****Solomon Islander(**[**29**](#_ENREF_29)**)** | **C=0.40** | **A** |
| rs505802 | Intergenic | C | T | European,([13](#_ENREF_13); [15](#_ENREF_15)) AA([12](#_ENREF_12)) | T=0.43 | D |
| rs11602903 | Intergenic | A | T | German,([30](#_ENREF_30)) Chinese([31](#_ENREF_31)) | T=0.39 | D |
| rs3825018 | Intergenic | G | A | European([22](#_ENREF_22)) | A=0.39 | D |
| ***SLC16A9 (chromosome 10)*** |  |  |  |  |  |  |
| rs12356193 | Intron 1 | A | G | European,([13](#_ENREF_13)) Icelandic([16](#_ENREF_16)) | G=0.09 | C |
| ***SLC17A1 (chromosome 6)*** |  |  |  |  |  |  |
| rs1165196 | Exon 7 | A | G | White,([18](#_ENREF_18)) Icelandic,([16](#_ENREF_16)) Japanese([19](#_ENREF_19); [36](#_ENREF_36)) | G=0.28 | D |
| rs1183201 | Intron 10 | T | A | European([13](#_ENREF_13)) | A=0.29 | D |
| rs11751616 | Intergenic | A | G | AA([12](#_ENREF_12)) | G=0.02 | C |
| rs2051541 | Intergenic | G | A | European ancestry([12](#_ENREF_12)) | A=0.50 | C |
| **rs3799344** | **Intergenic** | **C** | **T** | **European(**[**37**](#_ENREF_37)**)** | **T=0.37** | **A** |
| ***SLC17A3 (chromosome 6)*** |  |  |  |  |  |  |
| rs1165205 | Intron 1 | C | T | White([19](#_ENREF_19)) | T=0.31 | C |
| ***SLC22A11 (chromosome 11)*** |  |  |  |  |  |  |
| rs10792443 | Intron 4 | G | C | European ancestry([12](#_ENREF_12)) | C=0.39 | C |
| rs2078267 | Intron 6 | C | T | European([5](#_ENREF_5)), White,([18](#_ENREF_18)) Icelandic([16](#_ENREF_16)) | T=0.23 | C |
| ***GCKR (chromosome 2)*** |  |  |  |  |  |  |
| rs780094 | Intron 16 | T | C | European([13](#_ENREF_13); [35](#_ENREF_35)) | T=0.30 | C |
| rs780093 | Intron 17 | T | C | White,([18](#_ENREF_18)) Icelandic([16](#_ENREF_16)) | T=0.29 | D |
| rs814295 | Intron 17 | G | A | AA([12](#_ENREF_12)) | G=0.23 | C |
| **rs1260326** | **Exon 15** | **T** | **C** | **European(**[**5**](#_ENREF_5)**)** | **T=0.29** | **A** |
|  |  |  |  |  |  |  |
| ***LRRC16A (chromosome 6)*** |  |  |  |  |  |  |
| rs9321453 | Intron 12 | T | C | AA([12](#_ENREF_12)) | T=0.24 | C |
| **rs742132** | **Intron 30** | **A****(G increases SUA in our sample)** | **G** | **European(**[**13**](#_ENREF_13)**;** [**35**](#_ENREF_35)**)** | **G=0.29** | **A** |
| ***PDZK1 (chromosome 1)*** |  |  |  |  |  |  |
| rs882211 | Intron 1 | C | G | AA([12](#_ENREF_12)) | G=0.06 | C |
| rs1967017 | Intergenic | T | C | White([18](#_ENREF_18)), European([22](#_ENREF_22)) | C=0.30 | C |
| ***R3HDM2-INHBC region (chromosome 12)*** |  |  |  |  |  |  |
| rs1106766 | Intergenic | C | T | White, ([18](#_ENREF_18)) Icelandic([16](#_ENREF_16)) | T=0.14 | C |
| ***RREB1 (chromosome 6)*** |  |  |  |  |  |  |
| rs675209 | Intergenic | T | C | White, ([18](#_ENREF_18)) Icelandic,([16](#_ENREF_16)) Croatian([15](#_ENREF_15)), European([5](#_ENREF_5); [22](#_ENREF_22)) | C=0.45 | C |
| ***NRXN2 (chromosome 11)*** |  |  |  |  |  |  |
| **rs478607** | **Intron** | **G** | **A** | **European(**[**5**](#_ENREF_5)**)** | **G=0.28** | **B** |
| ***UBE2Q2******(chromosome 15)*** |  |  |  |  |  |  |
| rs1394125 | Intron | A | G | European([5](#_ENREF_5)) | G=0.26 | C |
| ***IGF1R******(chromosome15)*** |  |  |  |  |  |  |
| rs6598541 | Intron | A | G | European([5](#_ENREF_5)) | A=0.45 | C |
| ***NFAT5******(chromosome16)*** |  |  |  |  |  |  |
| **rs71931165778** | **Intergenic** | **C** | **T** | **European(**[**5**](#_ENREF_5)**)** | **C=0.08** | **B** |
| ***HLF******(chromosome 17)*** |  |  |  |  |  |  |
| **rs7224610** | **Intron** | **C** | **A** | **European(**[**5**](#_ENREF_5)**)** | **C=0.22** | **A** |
|  |  |  |  |  |  |  |
| ***Excluded SNPs of n=68***  |  |  |  |  |  |  |
| Reason #1: Missing from database |  |  |  |  |  |  |
| 4 SNPs were not available in the HANDLS genotype imputed database: Status E.  |  |
| AA | rs12800450 |  |  |  |  |  |
| Korean | rs1529909 |  |  |  |  |  |
| Whites | rs2199936 |  |  |  |  |  |
| Hispanic | rs6843466 |  |  |  |  |  |
| Reason #2: Poor imputation quality |  |  |  |  |  |  |
| SNP rs72552713 has poor imputation quality (imputation quality measure of R2 = 0.0073: Status F |  |
| Reason #3: High linkage disequilibrium with another SNP |  |  |  |  |  |  |
| At LD R2 of 0.8, in 500 kb window, LD pruning was done, regardless of MAF; 20/63 were excluded, resulting in 43 tag SNPs.12 found to be associated with baseline SUA (Status A)3 found to be associated with SUA rate of change (Status B)28 non-significant (Status C)20 remaining SNPs (Status D) |  |
| ***Initially selected SNPs: n=43*** |  |  |  |  |  |  |
| ***Finally selected SNPs:*** ***N=15 (12 for baseline and 3 for rate of change in SUA)*** |  |  |  |  |  |  |
|  |  |  |  |  |  |  |

Note: Minor allele frequency is obtained from: <http://www.ncbi.nlm.nih.gov/snp>, except when bolded (the MAF is obtained from a study). The risk allele is determined from the largest study. Both risk allele and other allele indicate the direction of reported association with serum uric acid (SUA) in previous studies regardless of their allele frequency in the population. Minor Allele Frequency indicates which allele (risk or other) is the less frequent one.

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