**upplemental Table 1** Genomic information of the candidate SNPs

|  |  |  |  |  |
| --- | --- | --- | --- | --- |
| Gene (chromosome) | SNP | Major/Minor allele | SNP function | MAF in 1000genomics database |
| *GCKR*(2p23) | rs1260326 | T/C | Nonsynonymous | 50% |
| *TFDP2*(3q23) | rs347685 | A/C | unknown | 25.7% |
| *SHROOM3*(4q21.1) | rs17319721 | G/A | Intronic | 10.5% |
| *DAB2*(5p13) | rs11959928 | T/A | Intronic | 15.2% |
| *SLC34A1*(5q35) | rs6420094 | A/G | Intronic | 18.6% |
| *VEGFA*(6p12) | rs881858 | A/G | Intergenic | 19.5% |
| *PIP5K1B*(9q13) | rs4744712 | C/A | Intronic | 50.0% |
| *DACH1*(13q22) | rs626277 | C/A | Intronic | 11.9% |
| *UBE2Q2*(15q24.2) | rs1394125 | G/A | Intronic | 7.62% |
| *SLC7A9*(19q13.1) | rs12460876 | C/T | Intronic | 32.4% |
| *ANXA9/LASS2*(1q21.3) | rs267734 | T/C | Upstream | 2.86% |
| *RKAG2* (7q36.1) | rs7805747 | G/A | Intronic | 0% |
| *UMOD* (16p12.3) | rs12917707 | G/T | Upstream | 0.95% |
| *ALMS1/NAT8* (2p13) | rs13538 | A/G | Nonsynonymous | 0.48% |
| *ATXN2/SH2B3* (12q24.1) | rs653178 | T/C | Intronic | 0.48% |
| *PRKAG2* (7q36.1) | rs7805747 | G/A | Intronic | 0% |

**Supplemental Table 2** Association analyses between CKD risk factor related loci and GFR levels

|  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- |
|  |  |  |  |  |  | **GFR levels** |  |
| **Gene** | **SNPs** | **Pathway** | **Clinical significance** | **MAF** | **Maj/ Het/ Min**  | **Major hom**  | **Hetero-zygote**  | **Minor hom** | **p** |
| *LPA* | rs6415084 | Lipid metabolism | Intron variant | 11.0 | 79.1/20.0/1.0 | 87.23±10.57 | 87.06±10.42 | 88.26±7.57 | 0.886 |
| *APOA5* | rs662799 | Lipid metabolism | -1131T>C, Statin-response | 28.1 | 51.7/40.3/8.0 | 87.50±10.49 | 87.11±10.36 | 85.93±11.52 | 0.240 |
| *LIPG* | rs34474737 | Lipid metabolism | Intron variant | 29.5 | 49.4/42.1/8.4 | 87.21±10.11 | 87.34±10.72 | 86.48±12.20 | 0.661 |
| *CETP* | rs5882 | Lipid metabolism | Val422Ile | 47.1 | 28.3/49.2/22.5 | 87.05±10.09 | 86.93±10.66 | 87.95±10.67 | 0.274 |
| *APOE* | rs10402271 | Lipid metabolism | Intergenic | 15.7 | 70.9/26.8/2.3 | 87.19±10.89 | 87.49±9.49 | 85.97±9.86 | 0.651 |
| *PCSK9* | rs11206510 | Lipid metabolism | Intergenic | 6.2 | 87.9/11.7/0.4 | 87.42±10.23 | 86.12±12.19 | 91.54±9.26 | 0.143 |
| *PCSK9* | rs2479409 | Lipid metabolism | Upstream variant | 29.4 | 50.3/40.6/9.1 | 87.29±10.57 | 87.09±10.55 | 87.41±10.23 | 0.909 |
| *HMGCR* | rs12916 | Lipid metabolism | 3'-UTR | 47.4 | 28.5/48.2/23.3 | 87.20±10.38 | 86.96±10.79 | 88.04±10.00 | 0.231 |
| *HMGCR* | rs3846663 | Lipid metabolism | Intron variant | 47.4 | 28.5/48.2/23.3 | 87.17±10.36 | 86.97±10.77 | 88.19±9.78 | 0.146 |
| *TIMD4* | rs1501908 | Lipid metabolism | Intergenic | 26.4 | 54.7/37.9/7.5 | 87.22±10.52 | 87.46±10.28 | 86.79±11.61 | 0.778 |
| *CRP* | rs1205 | Inflammation | 3'-UTR | 42.6 | 33.1/48.6/18.3 | 87.50±10.39 | 87.20±10.69 | 86.46±10.59 | 0.366 |
| *CRP* | rs3093059 | Inflammation | Upstream variant | 17.1 | 68.5/28.7/2.7 | 87.35±10.35 | 87.00±10.82 | 86.47±11.65 | 0.725 |
| *IL6* | rs1800796 | Inflammation  | Intron variant | 27.9 | 52.3/39.7/8.0 | 87.47±10.39 | 87.08±10.65 | 86.77±10.43 | 0.645 |
| *IL6* | rs1524107 | Inflammation | Intron variant | 28.8 | 51.2/40.1/8.7 | 87.55±10.41 | 87.05±10.53 | 86.53±11.19 | 0.444 |
| *TNF-α* | rs1799724 | Inflammation  | -857C > T | 14.2 | 73.4/24.9/1.7 | 87.25±10.43 | 87.43±10.58 | 85.48±13.12 | 0.626 |
| *ALDH2* | rs671 | Acetaldehyde metabolism | Glu504LysDrug-response | 23.3 | 58.3/36.7/5.0 | 86.98±10.77 | 87.71±10.25 | 87.30±9.26 | 0.398 |
| *FTO* | rs9939609 | Energy metabolism | Intron variant | 12.6 | 76.2/22.5/1.3 | 87.34±10.70 | 86.72±10.08 | 86.15±10.85 | 0.526 |
| *XYLB* | rs17118 | Energy metabolism | Missense variant | 26.4 | 53.4/40.4/6.2 | 87.08±10.29 | 87.46±10.80 | 87.54±10.33 | 0.745 |
| *GCK* | rs4607517 | Glucose metabolism | Intergenic | 23.2 | 58.4/36.9/4.7 | 86.76±10.98 | 87.84±9.79 | 87.83±10.49 | 0.104 |
| *NPPB* | rs198389 | Regulate blood pressure | ‑381T>C | 13.6 | 74.9/23.1/2.0 | 86.97±10.53 | 87.86±10.80 | 87.35±8.80 | 0.332 |
| *MTHFR* | rs1801131 | Regulate blood pressure | Glu429Alagene deficiency | 16.9 | 69.1/28.1/2.8 | 87.01±10.87 | 87.76±9.63 | 87.90±9.40 | 0.374 |
| *MTHFR* | rs1801133 | Regulate blood pressure | Ala222ValGene deficiency | 44.4 | 30.4/50.4/19.2 | 87.59±10.69 | 87.08±10.55 | 86.83±10.39 | 0.530 |
| *MTR* | rs1805087 | Regulate blood pressure | Asp919Gly | 10.7 | 79.8/19.1/1.1 | 87.31±10.66 | 86.99±10.04 | 87.85±4.94 | 0.857 |
| *MTRR* | rs1801394 | Regulate blood pressure | Ile22MetDrug-response | 24.7 | 56.8/36.9/6.3 | 87.30±10.75 | 86.94±10.46 | 88.91±7.89 | 0.194 |
| *MTRR* | rs2287780 | Regulate blood pressure | Arg415TCys | 17.5 | 68.3/28.5/3.2 | 87.20±10.44 | 87.50±10.64 | 86.29±9.71 | 0.681 |
| *MTRR* | rs162036 | Regulate blood pressure | Lys350Arg | 18.6 | 65.6/31.7/2.7 | 87.56±10.33 | 86.83±10.76 | 85.15±11.48 | 0.153 |
| *BHMT* | rs3733890 | Regulate blood pressure | Arg239Gln | 29.9 | 49.4/41.5/9.1 | 87.68±10.05 | 87.05±10.66 | 86.52±11.25 | 0.311 |
| *CYP19A1* | rs10046 | Estrogen biosynthesis | Intron variant | 45.3 | 30.4/48.7/21.0 | 87.13±10.03 | 87.37±10.81 | 87.25±10.47 | 0.922 |
| *CYP19A1* | rs1008805 | Estrogen biosynthesis | Intron variant | 30.3 | 48.6/42.1/9.3 | 87.64±10.13 | 86.88±10.97 | 87.05±9.88 | 0.340 |
| *ESR1* | rs722208 | Transcription factor | Intron variant | 46.5 | 29.5/47.9/22.6 | 87.59±10.12 | 87.35±10.58 | 86.77±10.51 | 0.493 |
| *ESR1* | rs2175898 | Transcription factor | Intron variant | 43.9 | 31.1/50.1/18.8 | 87.72±9.94 | 87.17±10.35 | 86.91±11.48 | 0.485 |
| *ESR2* | rs1256031 | Transcription factor | Intron variant | 42.7 | 31.8/50.9/17.3 | 87.41±10.91 | 87.19±10.31 | 86.82±10.73 | 0.749 |
| *HNF1A* | rs7953249 | Transcription factor | Intergenic | 47.0 | 28.7/48.4/22.8 | 87.70±10.38 | 87.08±10.42 | 87.02±10.74 | 0.516 |
| *CDKN2A/B* | rs2383207 | Regulate gene expression | Intron variant | 32.7 | 45.1/44.5/10.4 | 87.58±10.22 | 87.00±10.82 | 87.16±9.75 | 0.545 |
| *VDR* | rs2228570 | Calcium homeostasis | Initiator codon, Drug-response | 46.0 | 29.7/48.6/21.7 | 86.85±10.83 | 87.29±10.50 | 87.49±9.98 | 0.637 |
| *VDR* | rs1544410 | Calcium homeostasis | Intron variant | 5.1 | 90.1/9.7/0.2 | 87.27±10.48 | 87.34±10.62 | 89.59±11.79 | 0.905 |
| *MMP12* | rs660599 | Tissue remodeling | Intergenic | 14.1 | 74.4/23.1/2.5 | 87.31±10.69 | 87.33±9.65 | 87.32±10.13 | 1.000 |
| *ACTN3* | rs1815739 | Muscle contraction | Stop gained,Gene deficiency | 39.9 | 36.6/47.0/16.4 | 86.80±10.46 | 87.38±10.62 | 87.39±10.62 | 0.535 |
| *C1orf112* | rs10489177 | Catalyze methyl transfer | Upstream variant | 18.1 | 67.7/28.4/3.9 | 87.29±10.54 | 86.99±10.58 | 88.60±8.64 | 0.489 |
| *ABO* | rs505922 | Catalyze carbohydrate transfer | Intron variant | 47.0 | 27.7/50.8/21.6 | 87.50±10.06 | 86.94±10.83 | 87.61±10.27 | 0.486 |
| *FOXO3A* | rs2802292 | Transcriptional activator | Intron variant | 25.0 | 55.8/38.4/5.8 | 86.91±10.82 | 87.53±10.33 | 88.28±8.72 | 0.297 |
| *SIRT6* | rs352493 | DNA repair | Ser46Thr | 26.9 | 53.3/39.5/7.1 | 87.56±10.25 | 86.92±10.89 | 86.28±10.51 | 0.280 |