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| **Supplementary Table 5a Results of association analysis for nephrolithiasis in stage3/replication**  |
| **SNP** | **Chra** | **Position** | **gene** | **Case MAFb**  | **Control MAFb**  | ***P*c**  | **ORd**  | **95%CId**  |
| rs13023094 | 2 | 27910706 | *SLC4A1AP* | 0.410  | 0.400  | 2.84x10-1  | 1.04  | 0.97-1.12  |
| rs12654812 | 5 | 176794191 | *RGS14* | 0.386  | 0.350  | 5.27x10-5  | 1.17  | 1.08-1.26 |
| rs11746443 | 5 | 176798306 | *RGS14* | 0.278  | 0.250  | 4.64x10-4  | 1.16  | 1.07-1.26 |
| rs12669187 | 7 | 30915478 | *FAM188B* | 0.205  | 0.182  | 1.59x10-3  | 1.16  | 1.06-1.27 |
| rs1000597 | 7 | 30937178 | No gene | 0.230  | 0.203  | 5.43x10-4  | 1.17  | 1.07-1.28  |
| rs7981733 | 13 | 42690060 | *DGKH* | 0.318  | 0.334  | 7.05x10-2  | 1.08 | 0.99-1.16 |
| rs1170155 | 13 | 42702711 | *DGKH* | 0.339  | 0.353  | 1.32x10-1  | 1.06  | 0.98-1.15 |
| rs1170178 | 13 | 42705808 | *DGKH* | 0.465  | 0.450  | 1.11x10-1  | 1.06  | 0.99-1.14 |
| rs4142110 | 13 | 42754522 | *DGKH* | 0.431  | 0.459  | 2.18x10-3  | 1.12  | 1.04-1.20 |
| rs3765623 | 18 | 3086065 | *MYOM1* | 0.109  | 0.098  | 3.71x10-2  | 1.13  | 1.01-1.28 |
| Note: 2,109 Nephrolithiasis cases and 4,622 controls were analyzed. aChr: Chromosome. bMAF: minor allele frequency. c*P* value obtained from Cochrane-Armitage trend test. dOdds ratios (OR) and confidence interval (CI) are calculated using the non-susceptible allele as reference. |

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| **Supplementary Table 5b Results of meta analysis of 3stages**  |
| Chra  | SNP | stage | allele | gene | Case MAFb  | Control MAFb  | *P*c | ORd  | 95%CId  | Phete |
| 2 | rs13023094 | GWAS | C/A | *SLC4A1AP*(2p23.2) | 0.438  | 0.389  | 7.05x10-5  | 1.22  | (1.11-1.35) |  |
| Screening2 | 0.427  | 0.395  | 5.84x10-5  | 1.14  | (1.07-1.22) |  |
| Screening3 | 0.410  | 0.400  | 2.84x10-1  | 1.04  | (0.97-1.12) |  |
| Combinede  | 　 | 　 | 3.61x10-7  | 1.12  | (1.07-1.17) | 0.027  |
| 5 | rs12654812 | GWAS | T/C | *RGS14*(5q35.3) | 0.397  | 0.346  | 1.98x10-5  | 1.24  | (1.13-1.37) | 　 |
| Screening2 | 0.381  | 0.354  | 1.34x10-7  | 1.14  | (1.09-1.2) |  |
| Screening3 | 0.386  | 0.350  | 5.27x10-5  | 1.17  | (1.11-1.23) |  |
| Combinede  | 　 | 　 | 4.42x10-11  | 1.16  | (1.11-1.22) | 0.267  |
| 5 | rs11746443 | GWAS | T/C | *RGS14*(5q35.3) | 0.290  | 0.244  | 1.62x10-5  | 1.27  | (1.14-1.41) | 　 |
| Screening2 | 0.283  | 0.252  | 3.00x10-8  | 1.17  | (1.1-1.23) |  |
| Screening3 | 0.278  | 0.250  | 4.64x10-4  | 1.16  | (1.07-1.26) |  |
| Combinede  | 　 | 　 | 8.51x10-12  | 1.19  | (1.13-1.24) | 0.378  |
| 7 | rs12669187 | GWAS | T/C | *FAM188B*(7p14.3) | 0.223  | 0.176  | 1.04x10-6  | 1.34  | (1.19-1.51) | 　 |
| Screening2 | 0.214  | 0.184  | 2.70x10-8  | 1.19  | (1.12-1.26) |  |
| Screening3 | 0.205  | 0.182  | 1.59x10-3  | 1.16  | (1.06-1.27) |  |
| Combinede  | 　 | 　 | 1.48x10-12  | 1.25  | (1.17-1.33) | 0.150  |
| 7 | rs1000597 | GWAS | G/A | No gene(7p14.3) | 0.247  | 0.202  | 1.06x10-5  | 1.29  | (1.15-1.45) | 　 |
| Screening2 | 0.241  | 0.204  | 1.42x10-10  | 1.21  | (1.14-1.28) |  |
| Screening3 | 0.230  | 0.203  | 5.43x10-4  | 1.17  | (1.07-1.28) |  |
| Combinede  | 　 | 　 | 2.16x10-14  | 1.22  | (1.15-1.28) | 0.370  |
| 13 | rs7981733 | GWAS | A/G | *DGKH*(13q14.1) | 0.283  | 0.342  | 4.08x10-7  | 1.32  | (1.19-1.47) | 　 |
| Screening2 | 0.314  | 0.341  | 1.54x10-4  | 1.11  | (1.05-1.16) |  |
| Screening3 | 0.318  | 0.334  | 7.05x10-2  | 1.08  | (0.99-1.16) |  |
| Combinede  | 　 | 　 | 1.43x10-8  | 1.14  | (1.09-1.20)  | 0.009  |
| 13 | rs1170155 | GWAS | A/G | *DGKH*(13q14.1) | 0.306  | 0.359  | 1.15x10-5  | 1.27  | (1.14-1.41) | 　 |
| Screening2 | 0.328  | 0.364  | 1.32x10-5  | 1.12  | (1.07-1.18) |  |
| Screening3 | 0.339  | 0.353  | 1.32x10-1  | 1.06  | (0.98-1.15) |  |
| Combinede  | 　 | 　 | 3.89x10-9  | 1.15  | (1.10-1.20)  | 0.021  |
| 13 | rs1170178 | GWAS | A/G | *DGKH*(13q14.1) | 0.494  | 0.440  | 1.60x10-5  | 1.24  | (1.13-1.37) | 　 |
| Screening2 | 0.466  | 0.437  | 2.91x10-4  | 1.09  | (1.04-1.15) |  |
| Screening3 | 0.465  | 0.450  | 1.11x10-1  | 1.06  | (0.99-1.14) |  |
| Combinede  | 　 | 　 | 1.91x10-7  | 1.12  | (1.08-1.17) | 0.043  |
| 13 | rs4142110 | GWAS | A/G | *DGKH*(13q14.1) | 0.410  | 0.460  | 7.15x10-5  | 1.22  | (1.11-1.35) | 　 |
| Screening2 | 0.430  | 0.458  | 4.72x10-6  | 1.12  | (1.07-1.18) |  |
| Screening3 | 0.431  | 0.459  | 2.18x10-3  | 1.12  | (1.04-1.20) |  |
| Combinede  | 　 | 　 | 4.62x10-9  | 1.14  | (1.09-1.19) | 0.301  |
| 18 | rs3765623 | GWAS | A/G | *MYOM1*(18p11.3) | 0.115  | 0.086  | 3.82x10-5  | 1.38  | (1.18-1.61) | 　 |
| Screening2 | 0.108  | 0.091  | 1.13x10-4  | 1.17  | (1.08-1.27) |  |
| Screening3 | 0.109  | 0.098  | 3.71x10-2  | 1.13  | (1.01-1.28) |  |
| Combinede  | 　 | 　 | 1.28x10-7  | 1.21  | (1.13-1.30)  | 0.141  |
| Note: 5,796 (904 in GWAS, 2,783 in stage2 and 2,109 in stage3) Nephrolithiasis cases and 17,344 (7,471 in GWAS, 5251 in stage2 and 4,622 in stage3) controls were analyzed. aChr: chromosome  bMAF: minor allele frequency c*P* value obtained from Cochrane-Armitage trend test. dOdds ratios (OR) and confidence interval (CI) are calculated using the non-susceptible allele as reference. eThe *P* values of heterogeneities (*P*het) across three stages examined by using the Breslow-Day test fMeta-analysis: Odds ratio and *P* value for independence test were calculated by Mantel-haenszel test in the Meta-analysis.  |