**Table S2.** Power estimation for each SNP locus to replicate the results of original study

|  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- |
| SNP | Nearby Gene | Risk alleles a | RAF b | Reported OR c  | Power |
| rs6813195 | *TMEM154* | C | 0.47 | 1.08 (1.06-1.10) | 58% |
| rs9505118 | *SSR1* | A | 0.56 | 1.06 (1.04-1.08) | 37% |
| rs17106184 | *FAF1* | G | 0.90 | 1.10 (1.07-1.14) | 32% |
| rs3130501 | *POU5F1* | G | 0.57 | 1.07 (1.04-1.09) | 47% |
| rs702634 | *ARL15* | A | 0.82 | 1.06 (1.04-1.09) | 23% |
| rs4275659 | *MPHOSPH9* | C | 0.67 | 1.06 (1.04-1.08) | 33% |

Power estimation was performed using CaTS power calculator, CaTS: http://www.sph.umich.edu/csg/abecasis/CaTS/)

The prevalence of type 2 diabetes is assumed to be 10%, α = 0.05

a Risk allele for type 2 diabetes reported in the original trans-ethnic GWAS

b Risk allele frequency in the Japanese population (controls) in the present study

c Information in the original trans-ethnic GWAS is shown