**S21 Table: Allele frequencies across populations for the most strongly associated variant in chr6 for T2D in single variant association test.**

|  |  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- | --- |
| SNP ID | Chr | Pos (hg19) | Derived Allele Frequencies | | | | | |
| MEC-NH | EUR | EAS | AFR | Oceania | Southeast Asia |
| rs370140172 | 6 | 66205761 | 0.243 (C) | 0 | 0.009 | 0 | 0.020 | 0.0116 |

Allele frequencies were either calculated from the imputed data of the 178 reference MEC Native Hawaiian individuals with estimated PNS ancestry > 90%, or obtained from 1000 Genomes Project (EUR, EAS, and AFR; <https://www.internationalgenome.org/1000-genomes-browsers/>) or the Genome Asia data (Oceania and Southeast Asia; <https://browser.genomeasia100k.org/>). Frequencies were reported with respect to the derived allele, given in parenthesis next to the Native Hawaiian frequency estimates.