**S6 Table. Supplemental Table 6:** Power of association analyses for the full set of participants presented in Table 2.

|  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- |
|  |  | **rs4238001** | Combined  (MESA + Additional cohorts) | | | |
| **Group** | **MAF**† | N  (events) | Beta=0.05  (OR=1.05) | Beta=0.10  (OR=1.11) | Beta=0.20  (OR=1.22) |
| All | White | 0.104 | 11957  (871) | 9.3% | 26.0% | 72.2% |
| African American | 0.055 | 5962  (355) | 6.0% | 9.7% | 23.4% |
| Hispanic | 0.098 | 1255  (39) | 5.2% | 5.9% | 8.4% |
| Meta-analysis |  | 19174  (1255) | 10.4% | 31.2% | 81.5% |
| Male | White | 0.103 | 5402  (554) | 7.6% | 17.6% | 51.0% |
| African American | 0.053 | 2417  (180) | 5.5% | 7.2% | 13.7% |
| Hispanic | 0.103 | 618  (29) | 5.1% | 5.7% | 7.6% |
| Meta-analysis |  | 8432  (758) | 8.1% | 20.3% | 58.9% |
| Female | White | 0.105 | 6555  (317) | 6.6% | 12.7% | 34.8% |
| African American | 0.056 | 3546  (175) | 5.5% | 7.4% | 14.2% |
| Hispanic | 0.094 | 637  (10) | 5.1% | 5.2% | 5.9% |
| Meta-analysis |  | 10742  (507) | 7.2% | 15.6% | 45.2% |

†MAF denotes Minor Allele Frequency

Power calculations were completed in QUANTO (1) based on logistic regression analysis for the stated effects (Beta) and corresponding odds ratios (ORs), minor alleles frequencies (MAF), sample sizes, numbers of events and assuming a nominal Type I error rate of =0.05. The ORs included in power analysis reflect a realistic range of SNP effects presented in recent genome-wide studies of CHD (2). Power calculation for meta-analysis across race/ethnic groups assumes the weighted mean MAF of 0.088.

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