## S5 Table. The number of inferred relatedness at exhaustive and parsimony designs.

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| --- | --- | --- | --- |
| **Designa** | **Method** | **Number of inferred relatedness** | **Total** |
| **Identical** | **1st-degree** | **2nd-degree** |
| Exhaustive design | KING | 38 | 7,965 | 6,632 | 14,635 |
| encG-reg | 38 | 7,913 | 7,022 | 14,973 |
| Parsimony design | encG-reg | 38 | 7,903 | 5,435 | 13,376 |

aExhaustive design denotes the use of the intersected SNPs between each pair of cohorts and parsimony design denotes the use of intersected SNPs of all participated cohorts. When performing encG-reg at 19 cohorts in UKB, experiment-wise Bonferroni correction is based on the number of paired samples between each two cohorts ($n\_{i}×n\_{j}$) for exhaustive design and based on total number of paired samples among all cohorts ($N=\sum\_{i<j}^{C}n\_{i}n\_{j}$, where there are $C$ cohorts and $n\_{i}$ is the sample size of cohort $i$ for parsimony design.