## 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 () for exhaustive design and based on total number of paired samples among all cohorts (, where there are cohorts and is the sample size of cohort for parsimony design.