S1 Appendix: Pseudocode for adjustment of kinship coefficients

The following pseudo-code illustrates the adjustment of kinship coefficients using detected full-sibling pairs iteratively. The objective of the iterations is to capture a sufficient amount of full-sibling pairs (1000 by default) which are then used to estimate the adjustment factor. $\Phi^{\alpha i}(j, k)$ *r*epresents the kinship coefficient between the individuals *j* and *k* at the *i*-iteration using the adjustment factor α_i. $\pi_2^{\alpha i}(j, k)$ denotes the IBD2 segment proportion between the individuals *j* and *k* at the *i*-iteration. $F(\alpha_i)$ is the number of full-sibling pairs at the *i*-th iteration.

```
i = 0, min_num_fs = 50, prev_adj_num_fs = 0, max_num_fs = 1000, Φ_min^αi=0.1

For j, k in S:  // S is the set of pairs sharing IBD segments between two pairs j and k
        Compute Φ^αi (j, k), π_2^αi (j, k)
        If (Φ^αi > Φmin^αi AND (|F (α_i)| < min_num_fs OR |F (α_i)| - prev_adj_num_fs < min_adj_intervals) :

                Infer relationship of j, k and store it temporarily

        Else if |F (α_i)| >= min_num_fs AND |F (α_i)| - prev_adj_num_fs > min_adj_intervals:

                prev_adj_num_fs = |F (α_i)|

                compute α_i+1

                i = i +1

                Update the relatedness (boundaries) using α_i

        If |F (α_i)| > max_num_fs:

                Return α_i
```

Pseudo-code for adjustment of kinship coefficients iteratively.