Supplementary Material for

Assessment of kinship detection using RNA-seq data

Authors

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Supplementary Table 1

Supplementary Figure 1

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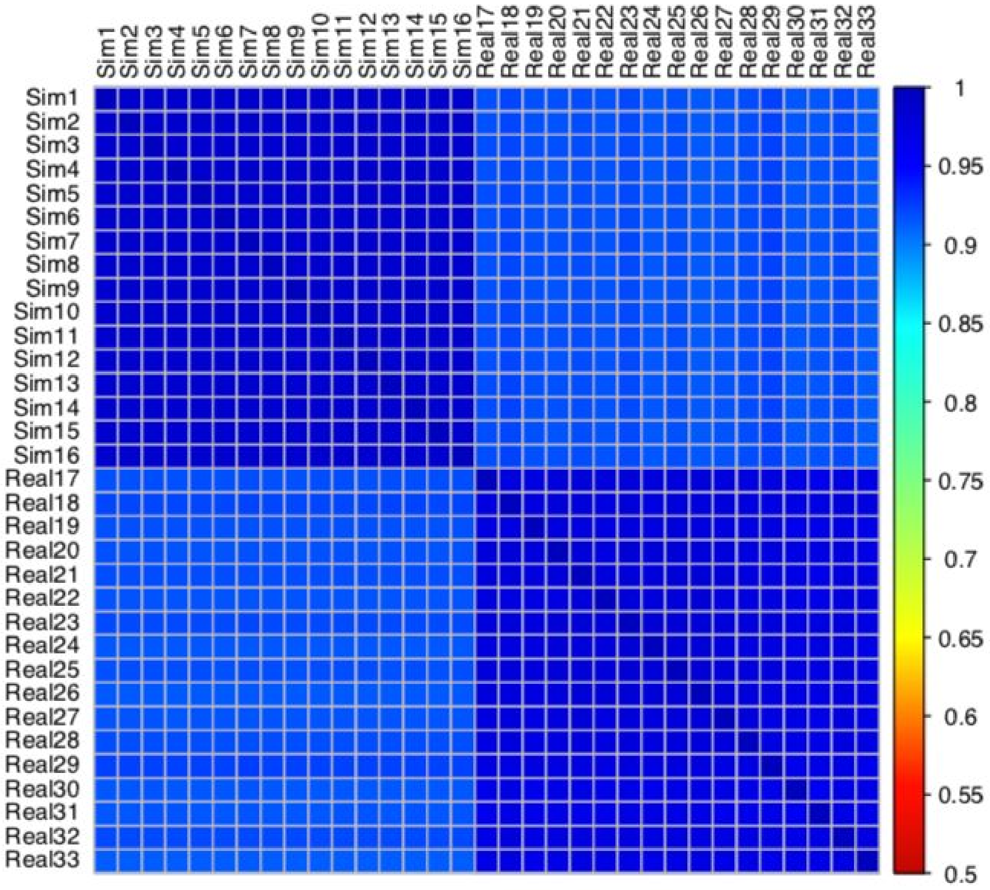
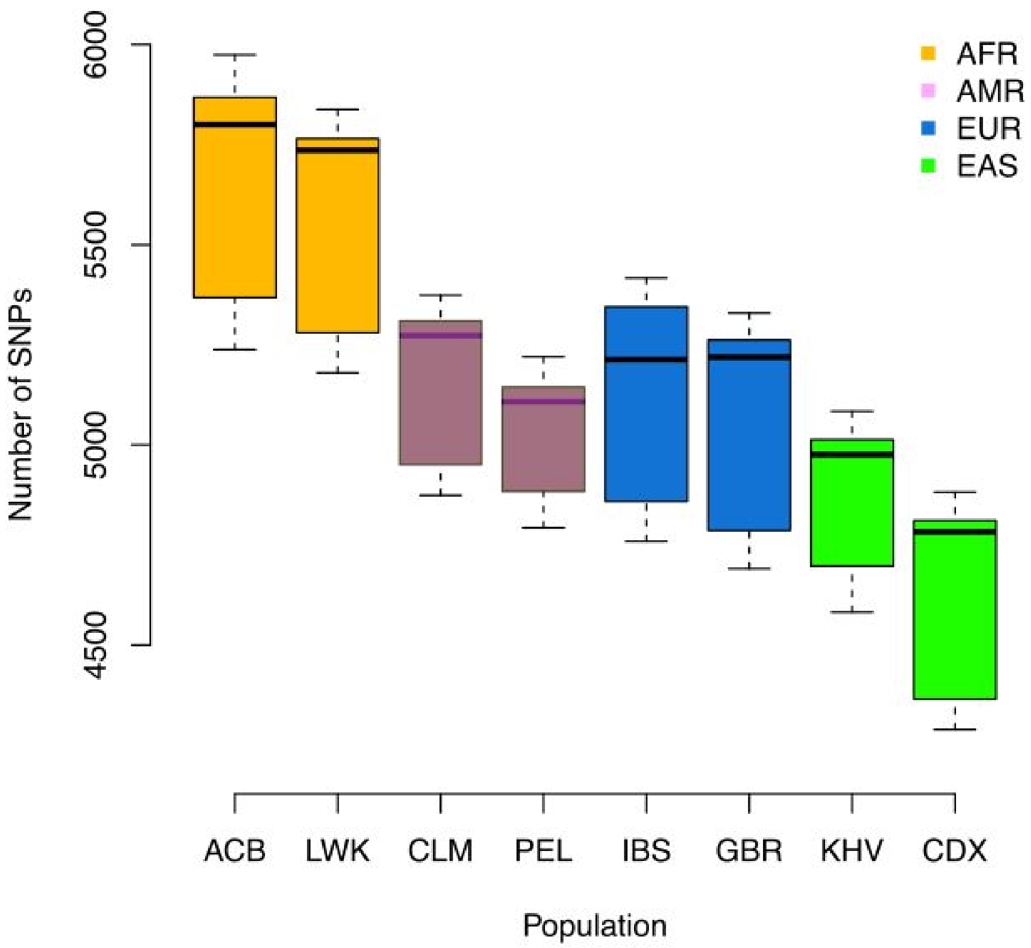
Supplementary Table 1. Expected IBD probabilities of different relationships and degrees of relatedness. Z0, Z1 and Z2 represent the probabilities that a pair of individuals share 0, 1 or 2 identical by descent alleles respectively.

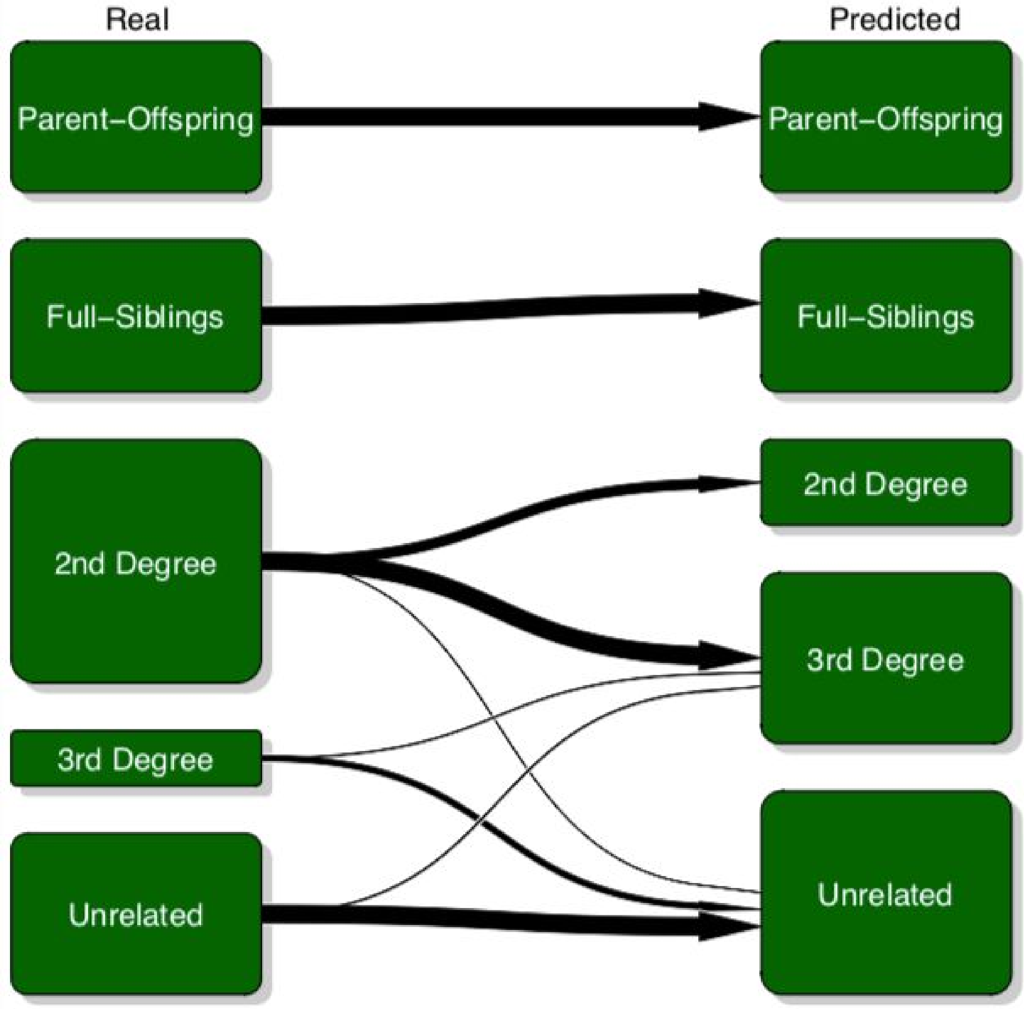
Degree	**Relationship**	**Z0**	**Z1**	**Z2**
1	parent-offspring	0	1	0
	full-siblings	0.25	0.5	0.25
2	grandparental, avuncular, half-siblings	0.5	0.5	0
3	First-cousins, great-grandparental, great-avuncular, half-avuncular	0.75	0.25	0
∞	unrelated	1	0	0



Supplementary Figure 1. Correlation matrix of the number of reads per gene in logarithmic scale between Simulated data (Sim1 - Sim16: individuals 1 - 16 of a type 1 simulated family) and Real data (Real1 - Real17: SRR1258217 - SRR1258233). Mean correlation between Real data: 0.975, between Simulated data: 0.988, between Real data and Simulated data: 0.918.



Supplementary Figure 2: Number of SNPs used for pairwise comparison of the simulated families per population. Each color represents a super population (AFR: African, AMR: Ad Mixed American, EUR: European, EAS: East Asian).



Supplementary Figure 3: Kinship classification by PRIMUS for simulated families (pairs with higher than third degree relationship are represented here as unrelated).