Supplementary Materials

Figure S1. A pedigree showing the genetic relationships of the ten family members that provided a reference sample for this study [1].

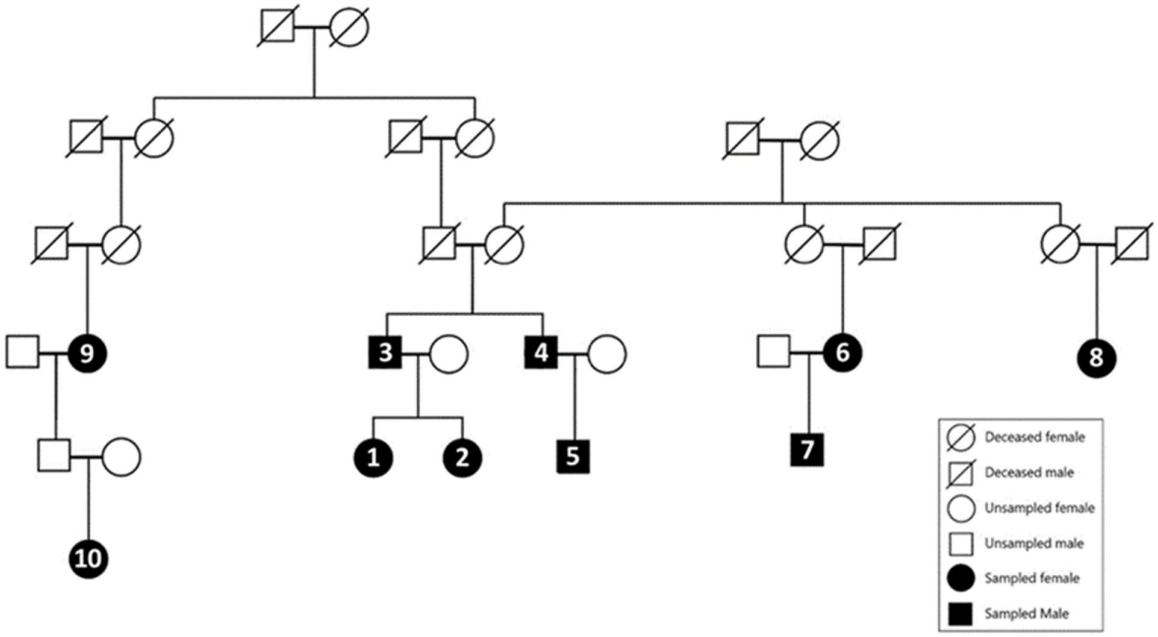


Table S1. The genetic relationships shared by the family sample individuals from Figure S1.

Degree of kinship	Relationship	Pairs	Totals	
1	Parent/child	1, 3	4	6
		2, 3		
		4, 5		
		6, 7		
	Siblings	1, 2	2	
		3, 4		
2	Grandparent/grandchild	9, 10	1	4
	Uncle/nephew	3, 5	1	
	Uncle/niece	1, 4	2	
		2, 4		
3	First cousins	1, 5	7	7
		2, 5		
		3, 6		
		3, 8		
		4, 6		
		4, 8		
		6, 8		
4	First cousins once removed	1, 6	9	9
		1, 8		
		2, 6		

		2, 8 3, 7 4, 7 5, 6 5, 8 7, 8		
5	Second cousins	1, 7 2, 7 3, 9 4, 9 5, 7	5	5
6	Second cousins once removed	1, 9 2, 9 5, 9	3	3
7	Second cousins twice removed	3, 10 4, 10	2	2
8	Third cousins once removed	1, 10 2, 10 5, 10	3	3
0	Unrelated	6, 9 6, 10 7, 9 7, 10 8, 9 8, 10	6	6
	Total		45	

Algorithm S1. Pseudocode describing the workflow of the algorithm for identifying stretches of concordant SNP genotypes shares by a pair of individuals.

Input : A list of dataframes L_p, where each dataframe contains a pair of SNP profiles belonging to individuals i and j.

Output: A list of dataframes L_s, where each dataframe contains the locations of segments where the genotypes of individuals i and j are concordant with IBD.

```
function (L_p);
for dataframe in L_p do
    for each SNP n in dataframe do
        G_{i,n} ← genotype of individual i at SNP n
        G_{j,n} ← genotype of individual j at SNP n
        if G_{i,n} is concordant with G_{j,n} AND G_{i,n+1} is concordant with
         G_{j,n+1} AND G_{i,n-1} is not concordant with G_{j,n-1} then
            Start new segment.
            Store segment start location.
        end
        else if G_{i,n} is concordant with G_{j,n} AND G_{i,n-1} is concordant
         with G_{j,n-1} AND G_{i,n+1} is not concordant with G_{j,n+1} then
            End segment.
            Store segment end location.
        end
        Add segments shared by individuals i and j to L_s
    end
    return L_s
end
```

Algorithm S2. Pseudocode describing the workflow of the algorithm for window-based IBD segment detection.

Input : A list of dataframes L_p, where each dataframe contains a pair of SNP profiles belonging to individuals i and j.

Output: A list of dataframes L_s, where each dataframe contains the locations of windows where the genotypes of individuals i and j are concordant with IBD.

```
function (L_p);
for dataframe in L_p do
    W_{i,j} ← Dataframe for storing windows belonging to individual i and j
    for each chromosome C in dataframe do
        W_c ← Dataframe for storing all windows in chromosome C
        m ← Index of the first SNP in chromosome C
        n ← Index of the last SNP in chromosome C
        for SNP index i in [m, ..., n − 60] do
            Calculate kinship coefficient for window from SNP_i to SNP_{i+60}
            if kinship coefficient > 0.23 then
                Store window start and end locations in dataframe W_c
            end
        end
        while window w in dataframe W_c overlaps with window w + 1 do
            Merge windows w and w + 1
        end
        Store merged windows in dataframe W_{i,j}
    end
    for window w in dataframe W_{i,j} do
        Calculate proportion p of window w wherein at least one allele is shared per genotype
        if p < 0.95 then
            Remove window w from dataframe W_{i,j}
        end
    end
    Add remaining windows from W_{i,j} to L_s
end
return L_s
```

Table S2. Autosomal masked regions used in the identical by descent (IBD) detection and filtering algorithm, which also represent gaps in single nucleotide polymorphism (SNP) coverage in the Verogen® ForenSeq Kintelligence Kit.

Chromosome	Start SNP	End SNP	Start position (Mbp)	End position (Mbp)
1	rs481357	rs6670984	120200843	145561594
2	rs1016839	rs1724120	88770768	96809331

3	rs7649188	rs7630912	88978538	94452002
4	rs4599384	rs1459814	48318390	53239603
5	rs1011814	rs6898102	44335820	49874330
6	rs7760349	rs6934646	57112128	64693014
7	rs10245203	rs4422672	57217249	62203031
8	rs6988483	rs1828494	42351311	50054112
9	rs7037234	rs449851	38771831	70984372
10	rs2505160	rs2744069	37309400	43374226
11	rs11038993	rs1792509	46810916	56670810
12	rs10772019	rs10506125	33085304	39120287
16	rs4889673	rs520151	31580272	48079134
18	rs786002	rs8099549	14914854	19826742
20	rs2076559	rs7271152	25187213	30506673

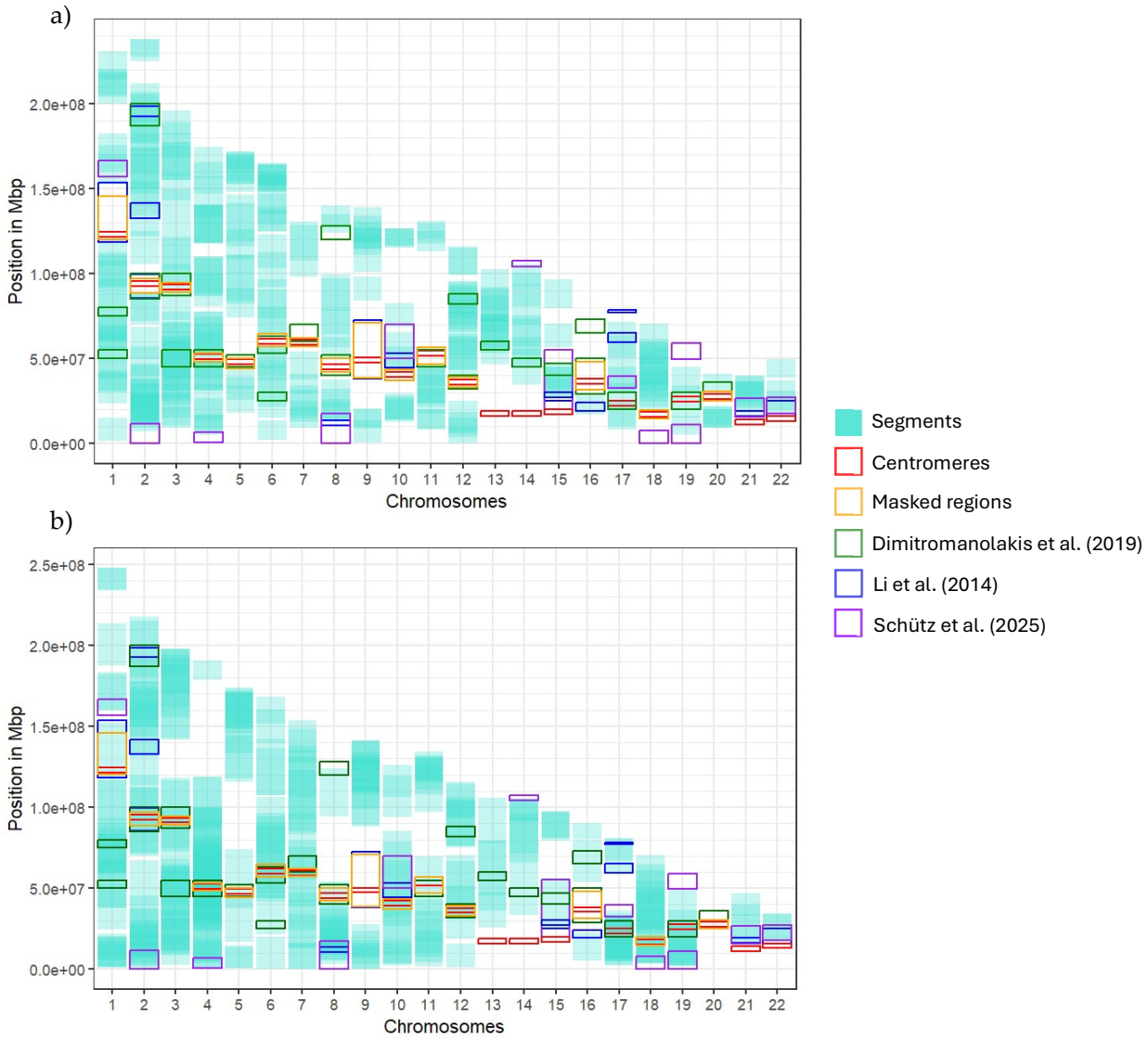


Figure S2. All segments shared by unrelated test individuals for Algorithm S1 (a) and Algorithm S2 (b), mapped alongside the centromeres, increased sharing regions identified in the literature and masked regions used in the IBD segment detection and filtering algorithm [34,46,48].

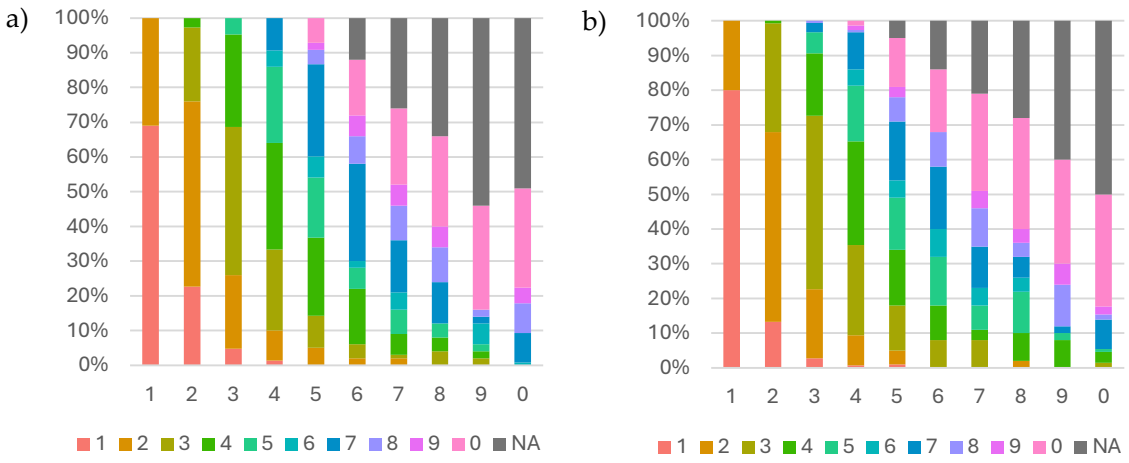


Figure S3. Results for the gamma distribution method of kinship inference for Algorithm S1 (a) and Algorithm S2 (b). 'NA' results indicate pairs whose relationship could not be inferred due to sharing less than two segments.

Table S3. Additional masked regions applied to the unrelated test pairings, which were identified by mapping segments shared by these pairs.

Chromosome	Start SNP	End SNP	Start position (Mbp)	End position (Mbp)
2	rs12471545	rs4665408	12168075	28521057
3	rs6599132	rs12715576	41039907	62044326
4	rs7672883	rs6554464	38006686	58296826
6	rs12210237	rs4708866	151639599	158022745
12	rs771655	rs1405780	77545429	90128655
13	rs9540208	rs9573824	65335655	76833684
18	rs11081813	rs1787531	31075341	47293738
20	rs3761161	rs2076584	10110237	19970705
21	rs6516727	rs2222956	27525506	37101040

References

1. Watson, J.L.; Grisedale, K.; Coakley, L.; McNevin, D.; Ward, J. Extended Kinship Inference Part 1: Evaluation of Short Tandem Repeats and Single Nucleotide Polymorphisms Using Likelihood Ratios and Haplotype Matching. *Forensic Genom.* **2025**, *5*, 13–31. https://doi.org/10.1089/forensic.2025.0001.
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