

Table SF1: The modified (and default) PLINK parameters for this study

Description in text	PLINK tag	Default	This study
Sliding window size	--homozyg-window-snp	100	50
Heterozygous calls per window	--homozyg-window-het	1	2
Missing calls per window	--homozyg-window-missing	5	10
Homozygous windows	--homozyg-window-threshold	0.05	0.025
Minimum ROH length	--homozyg-kb	1000	500
Minimum SNPs per ROH	--homozyg-snp	100	50
Minimum SNP density	--homozyg-density	50	500

To ensure that downstream inferences were not driven by parameter choice, the ROH calling results with PLINK's default ROH detection parameters and the WGS-optimized ROH parameters (Table SF1) were compared, and the concordance between the two parameterizations assessed.

Table SF2: Sensitivity of ROH detection with default and WGS-optimized parameter settings

Population	ROH class	PLINK default ROH parameters		PLINK ROH parameters used in this study	
		mean nROH	mean size (kb)	mean nROH	mean size (kb)
Ankole	0.5–1 Mb	-	-	2369	1579955.760
	1–2 Mb	319	408465.139	483	625525.079
	2–4 Mb	43	104169.02	72	185717.953
	>4 Mb	1	5952.349	14	82716.172
Karamojong	0.5–1 Mb	-	-	1029	677930.447
	1–2 Mb	52	66487.012	125	153654.944
	2–4 Mb	4	9898.831	10	23335.292
	>4 Mb	-	-	2	9508.169
Nganda10	0.5–1 Mb	-	-	1488	1018388.803
	1–2 Mb	6	7263.917	425	550458.307
	2–4 Mb	-	-	36	87390.014
	>4 Mb	-	-	1	4235.150
Nganda17	0.5–1 Mb	-	-	1707	1132273.082
	1–2 Mb	342	451234.485	381	512092.884
	2–4 Mb	78	202656.28	100	274722.089
	>4 Mb	6	29030.619	44	259366.702

Nkedi	0.5–1 Mb	-	-	1844	1232009.376
	1–2 Mb	372	494016.985	434	563136.944
	2–4 Mb	77	197142.266	113	307911.759
	>4 Mb	7	30130.922	49	297652.248
Ntuku	0.5–1 Mb	-	-	2203	1467419.437
	1–2 Mb	472	622217.585	549	724417.322
	2–4 Mb	99	259525.567	157	434324.753
	>4 Mb	13	62039.555	55	319369.053

Comparison of the number and total length of runs of homozygosity (ROH) detected using PLINK's default parameters and WGS-optimized parameters. WGS-optimized settings increased sensitivity to shorter ROH segments (<1 Mb) (Table SF2).

Table SF3: The F_{ROH} estimates and mean number (nROH) obtained using default PLINK parameters and WGS-optimized parameters

Population	<i>n</i>	PLINK default ROH parameters			PLINK ROH parameters used in this study		
		mean F_{ROH}	SD F_{ROH}	mean nROH	mean F_{ROH}	SD F_{ROH}	mean nROH
Ankole	19	0.0110	0.0063	19.1053	0.0523	0.0140	154.6316
Karamojong	11	0.0028	0.0016	5.0909	0.0316	0.0043	106.0000
Nganda10	10	0.0003	0.0004	0.6000	0.0667	0.0693	195.0000
Nganda17	17	0.0161	0.0199	25.0588	0.0515	0.0278	131.2941
Nkedi	19	0.0152	0.0400	24.0000	0.0508	0.0581	128.4211
Ntuku	19	0.0200	0.0163	30.7368	0.0623	0.0240	156.0000

The F_{ROH} estimates (Table SF3) obtained using WGS-optimized ROH parameters were highly concordant with those derived using PLINK's default settings. Individual-level F_{ROH} values showed strong rank and linear agreement between parameterizations (Spearman $\rho = 0.75$; Pearson $r = 0.77$; both $p < 10^{-18}$), indicating that relative patterns of autozygosity were preserved despite differences in absolute ROH calling thresholds.

Given higher marker density and uneven coverage associated with whole-genome sequencing data, we therefore adopted results derived with WGS-optimized ROH parameters for downstream analyses.