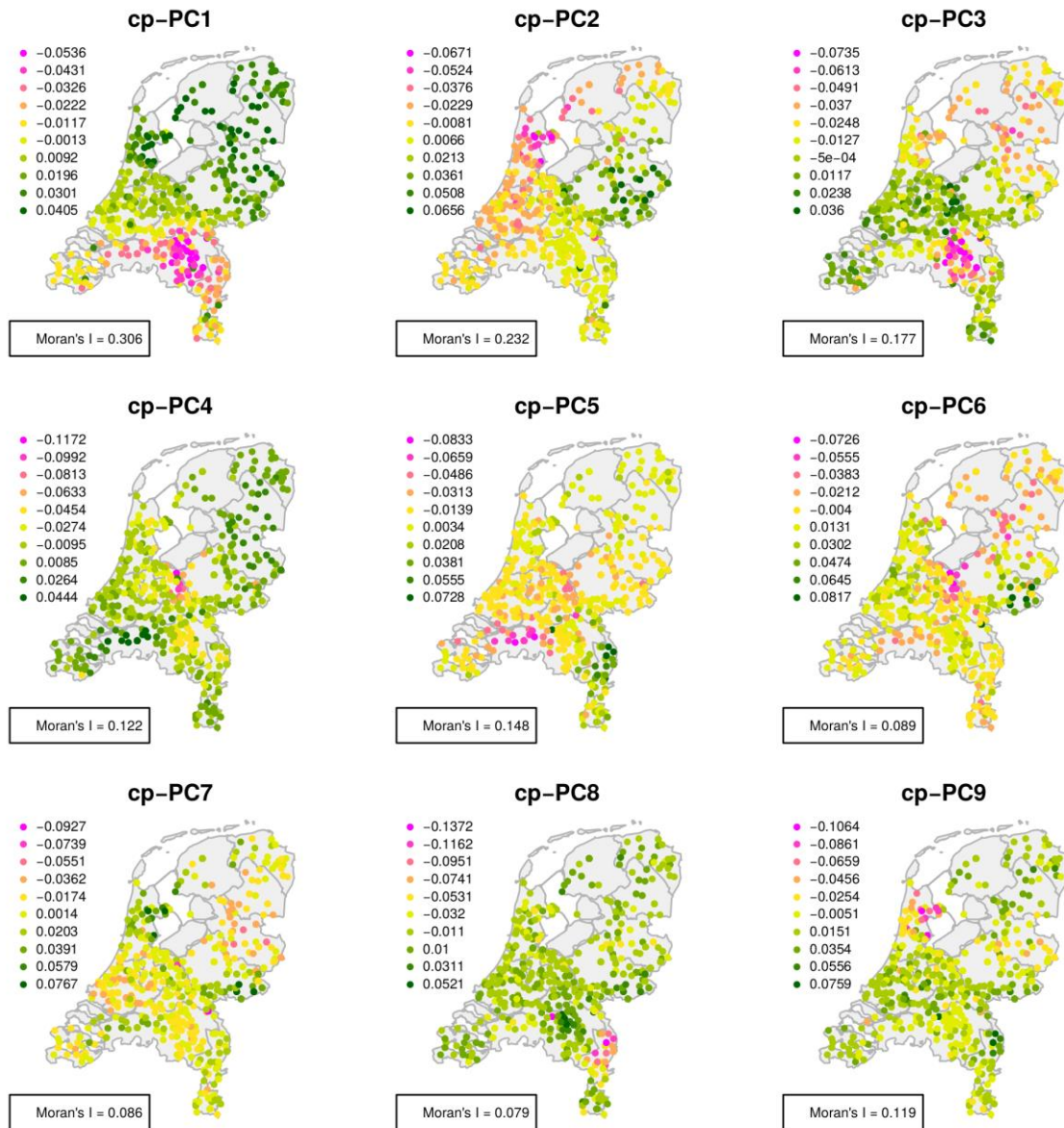


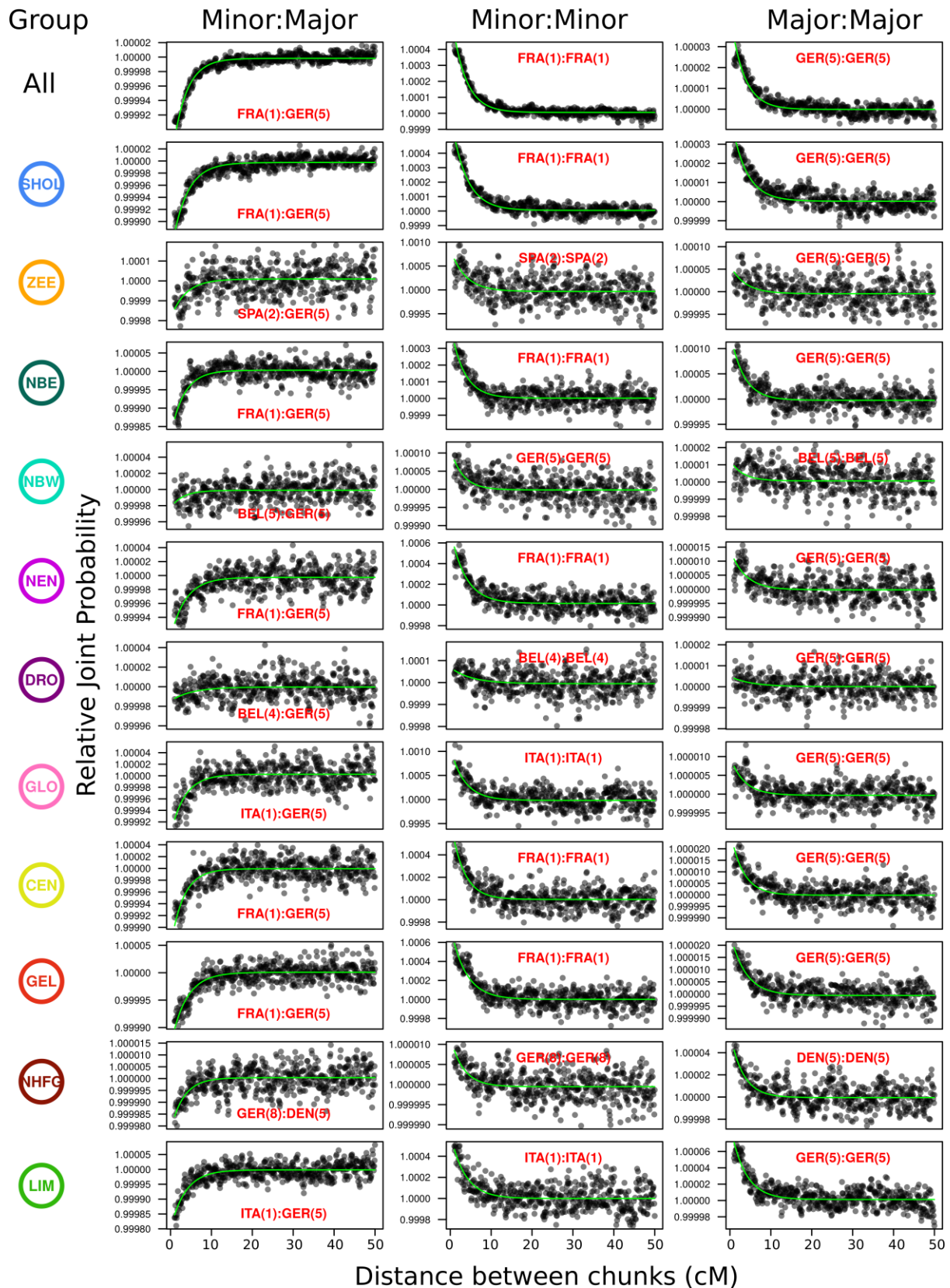
Dutch population structure across space, time and GWAS design

Byrne *et al.*

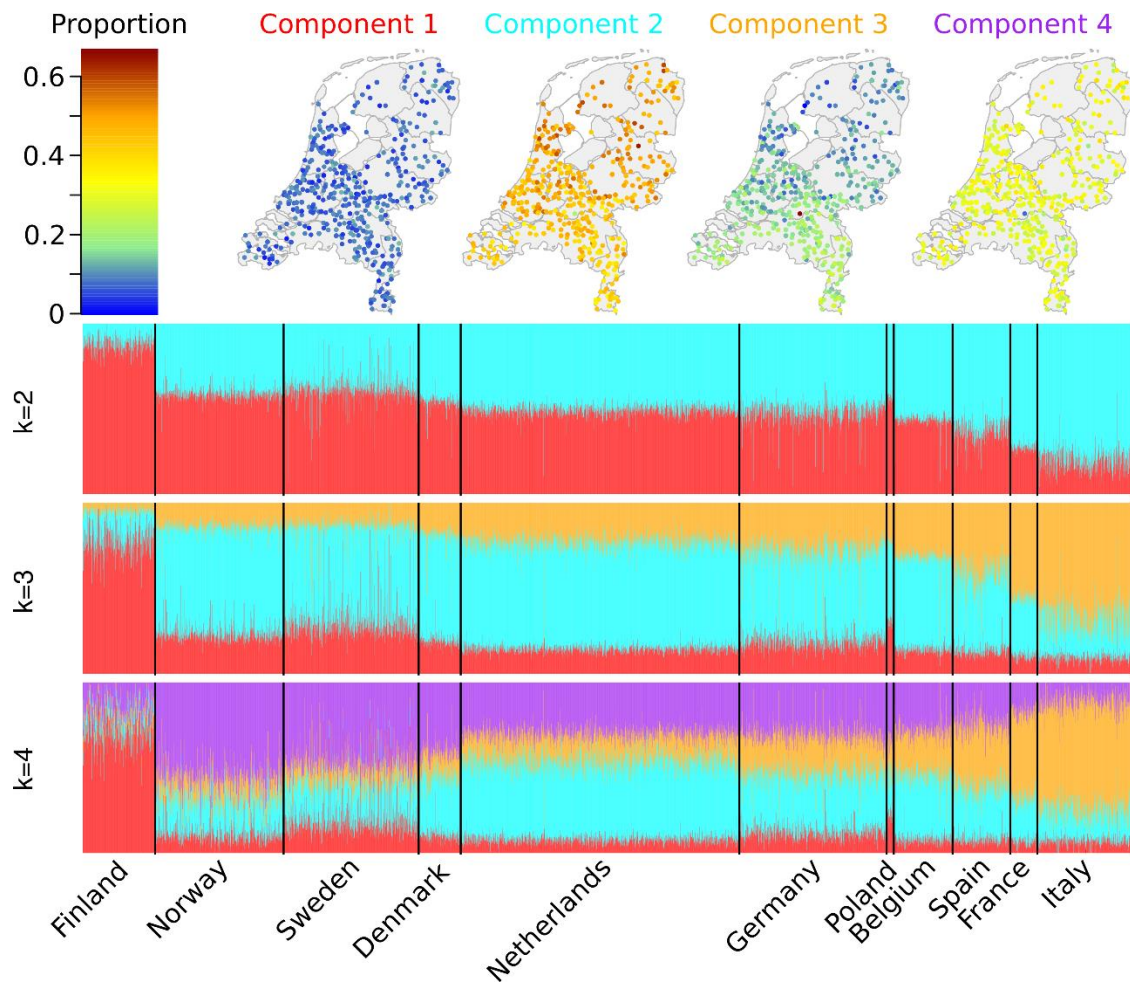
Supplementary material



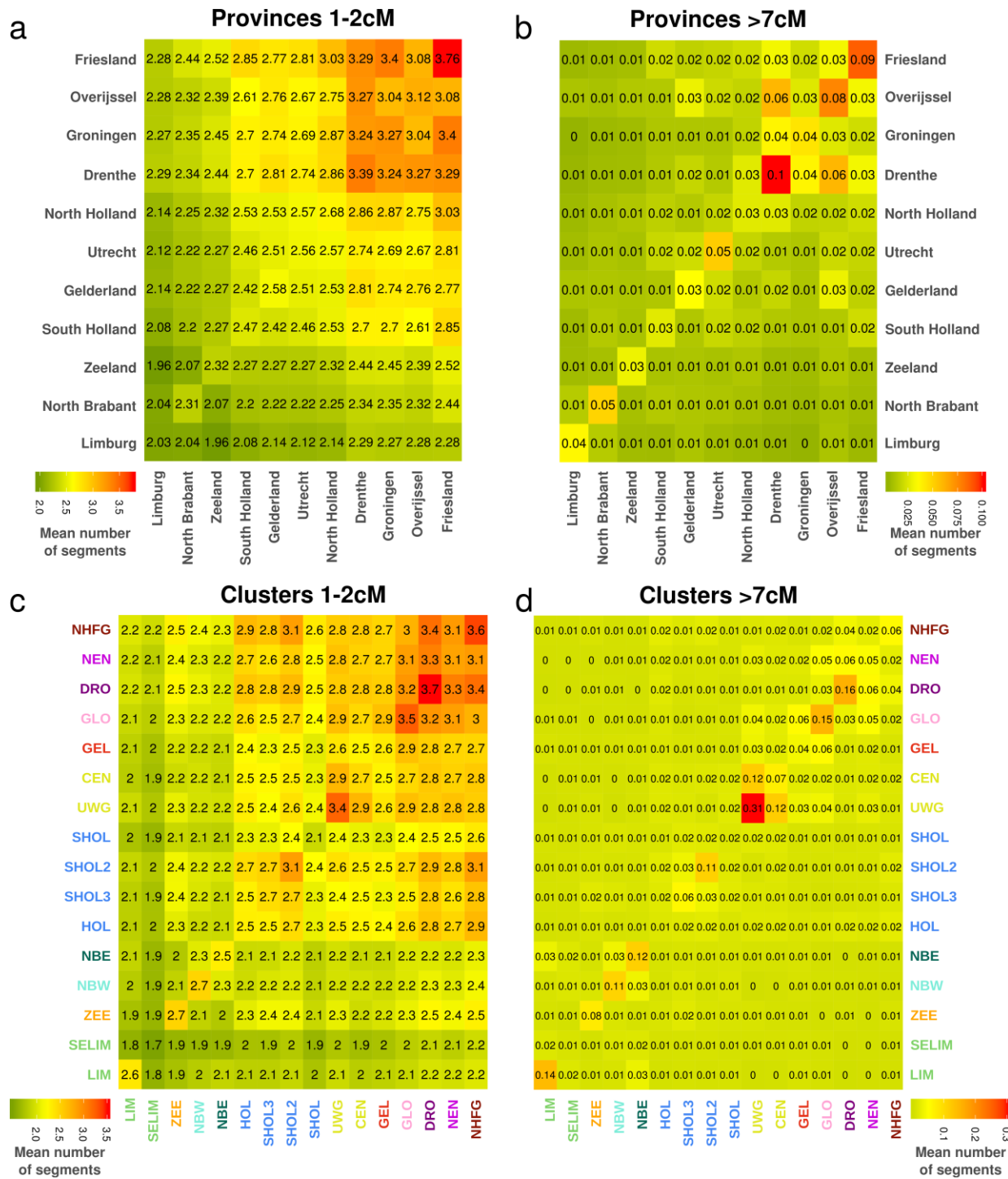
Supplementary Fig. 1 ChromoPainter-PCs relationship to geography. Points on maps are coloured by the average PC value per town of sampling. Each displayed PC shows a significant relationship with geography as tested by Moran's I ($p < 0.0001$ for all PCs). PCs have been split into 10 bins for visualisation purposes as in previous works¹. Map boundary data from the Database of Global Administrative Areas (GADM; <https://gadm.org>).



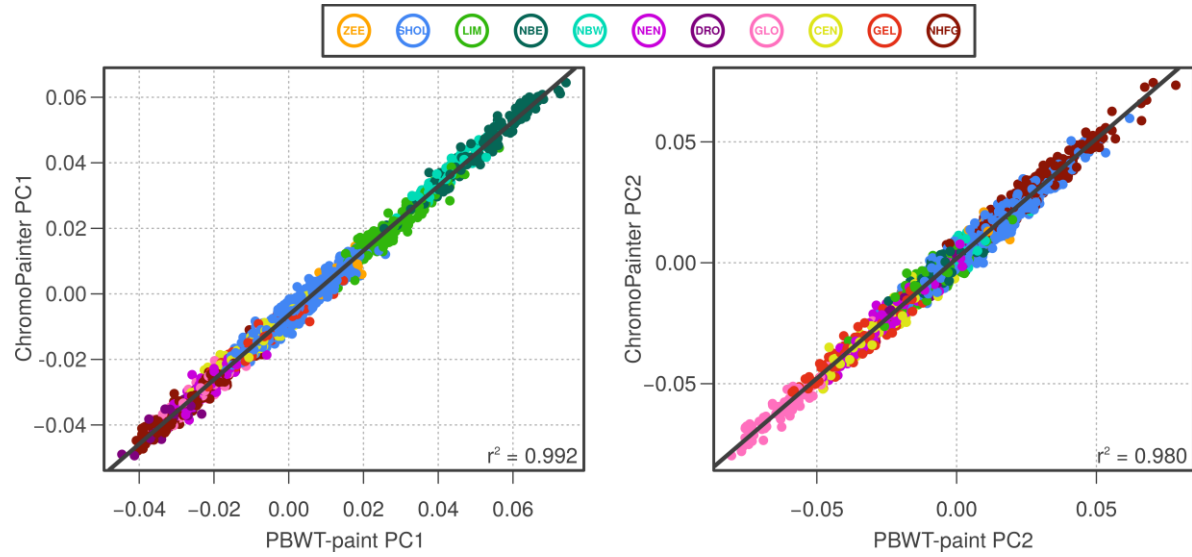
Supplementary Fig. 2 GLOBETROTTER coancestry curves. Example coancestry curves from donors representative of minor and major mixing sources in the GLOBETROTTER analysis of the 12 Dutch groups in Table 1. Each row displays 3 curves for a given Dutch group as labelled on the left (following Fig. 1 and Table 1). The y-axis represents the probability of copying from the two mixing sources (labelled in red eg FRA:GER) at sites separated by a given distance (x-axis; cM). The scaled probabilities are plotted in black, and the GLOBETROTTER fitted curve is in green. Where the fitted slope is positive the mixing sources come from different admixing groups; a negative curve indicates mixing sources come from the same admixing groups.



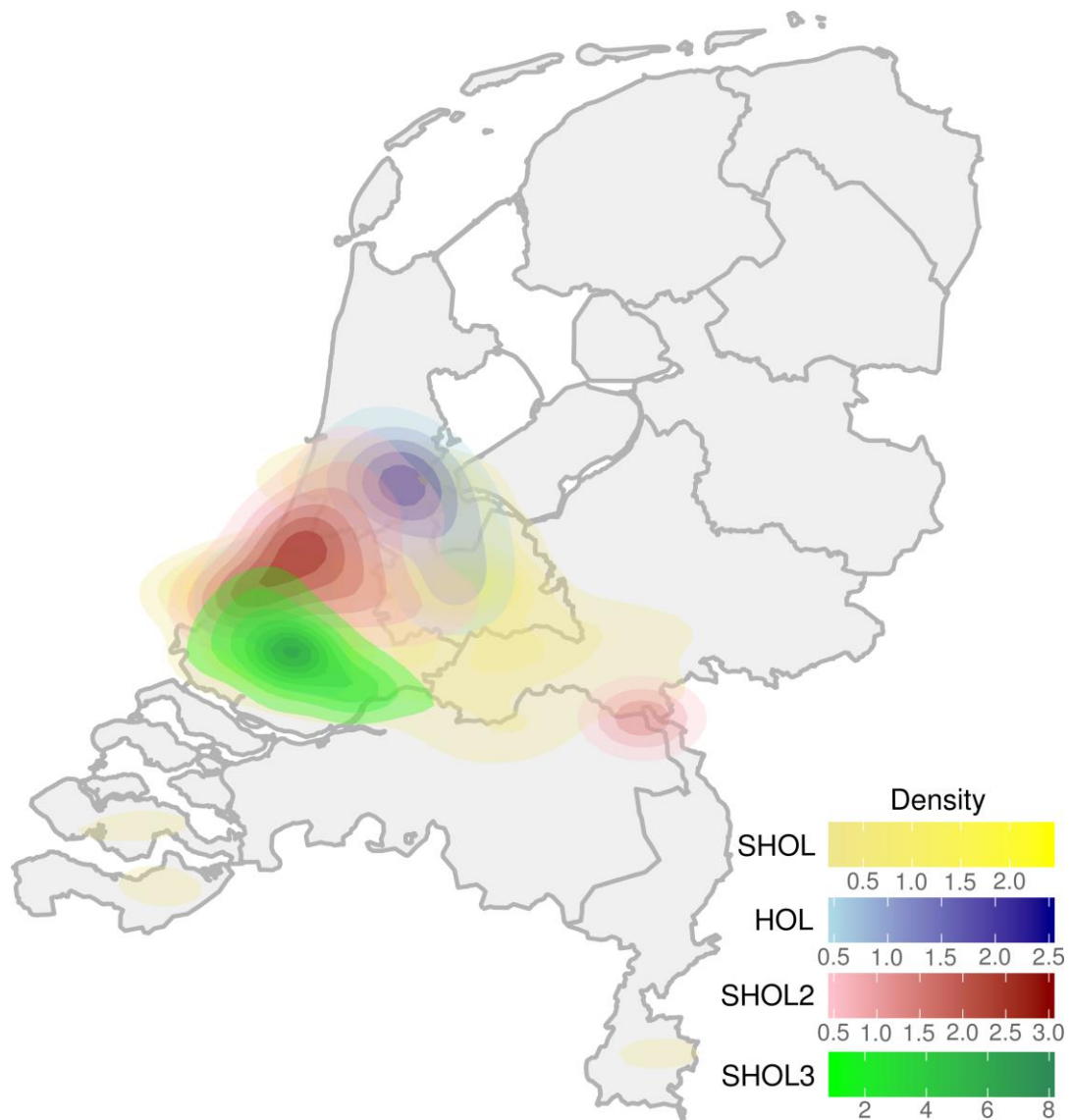
Supplementary Fig. 3 ADMIXTURE modelling for Dutch and European samples. Maps depict the regional breakdown of ADMIXTURE components for $k=4$ split. Dutch samples have a high value for admixture component 2, which is next highest in Germany and Belgium. Components 2 and 3 show opposing north-south gradients in the Netherlands, with component 2 highest in the north and component 3 highest in the south. Component 3 is best represented in southern European countries such as Italy. Map boundary data from the Database of Global Administrative Areas (GADM; <https://gadm.org>).



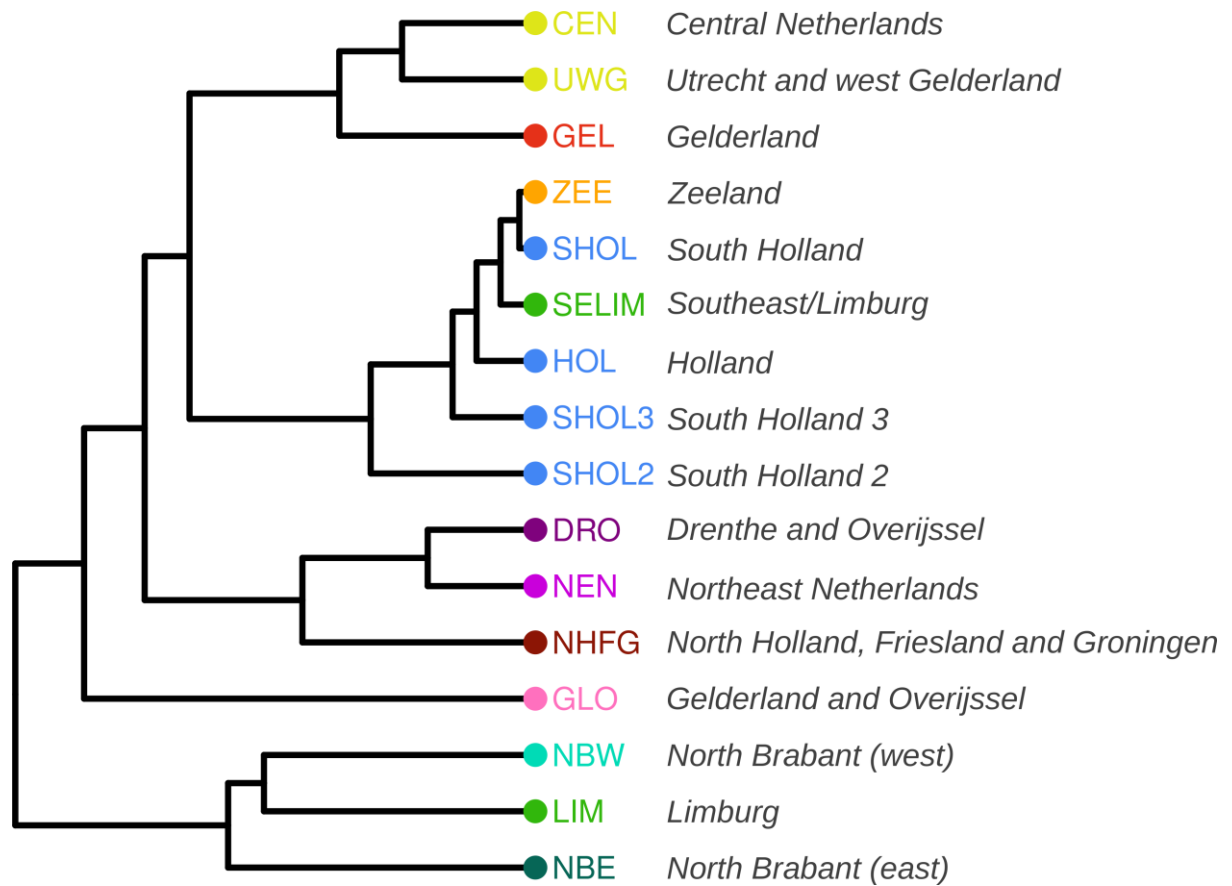
Supplementary Fig. 4 Old and recent IBD sharing per province and per cluster. Average sharing of IBD segments between provinces and clusters respectively is described for old (short) segments (1-2 cM) in (a) provinces and (c) clusters and for recent (long) segments (>7cM) in (b) provinces and (d) clusters. Average sharing of old (short) segments is enriched in northern provinces and clusters (a and c). Average sharing of recent (long) segments is higher on average within clusters than within provinces, indicating haplotypic clustering captures marginally more recent ancestry.



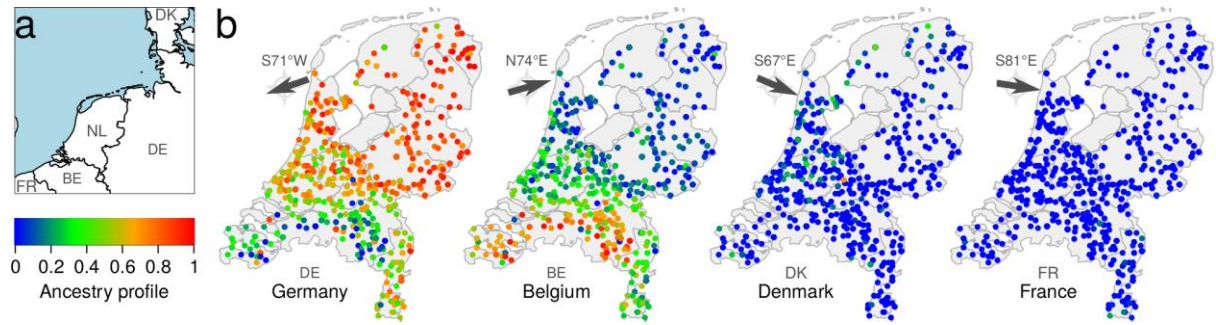
Supplementary Fig. 5 Benchmark of PBWT-paint vs ChromoPainter. Scatterplots comparing the first two principal components (PCs) of the coancestry matrices produced by ChromoPainter and PBWT-paint, showing strong correlation. Points are coloured by cluster groups defined in Fig. 1. For all pairwise comparisons in the two coancestry matrices, Pearson's $\rho = 0.82$ (0.82-0.821; t-statistic = 2332.4 with 2642248 degrees of freedom; $p < 2 \times 10^{-16}$; exact p-value not reported due to numerical precision limit in R).



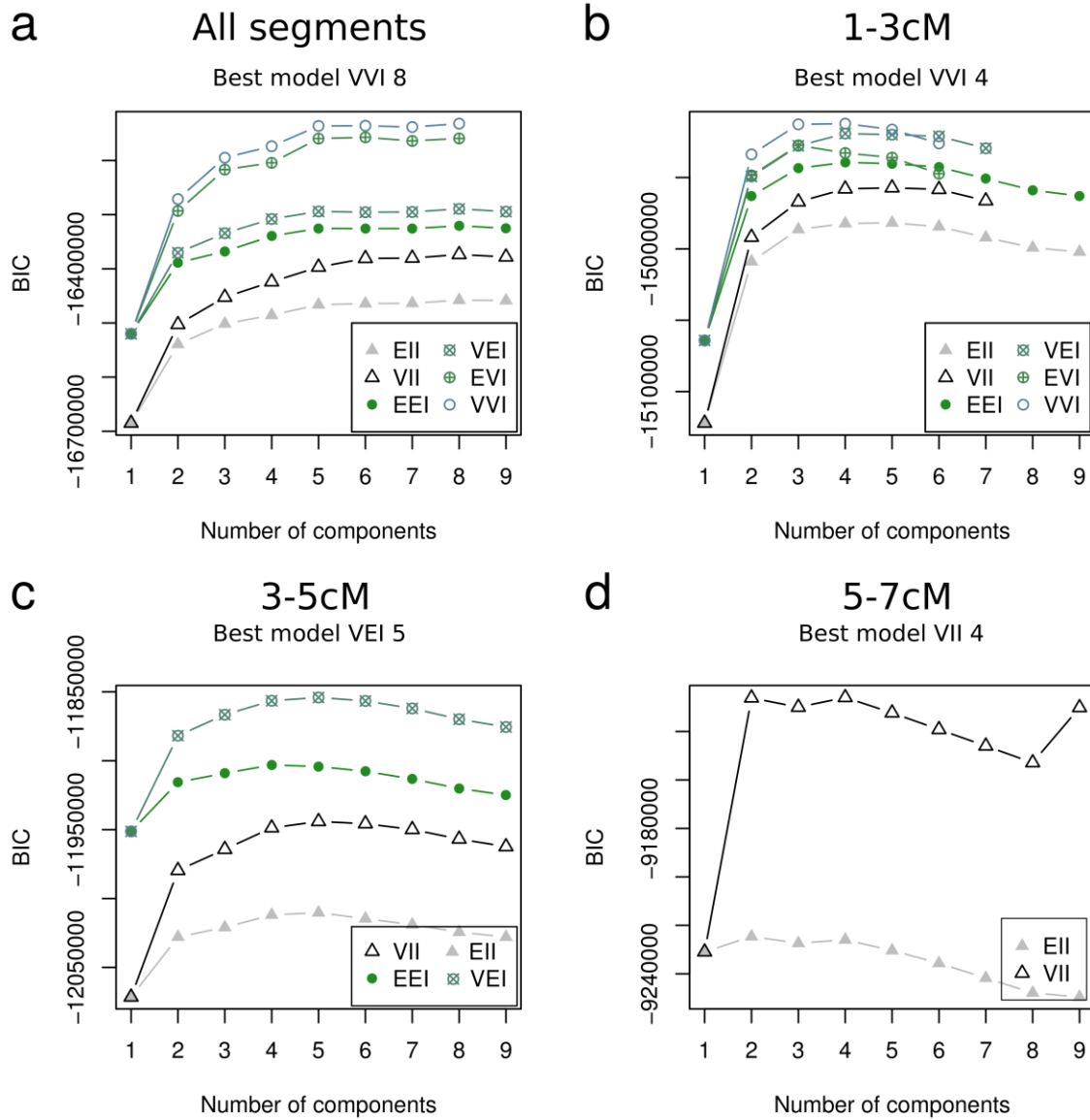
Supplementary Fig. 6 Geographic distribution of South Holland clusters from the SHOL cluster group. 2D kernel density estimates are shown for the geographic spread of samples from clusters SHOL (yellow), HOL (blue), SHOL2 (red), and SHOL3 (green) which form the SHOL cluster group in Fig. 1. Kernel density estimates were calculated using the `stat_density2d` function in `ggplot2` (R version 3.2.3) with default settings. >80% of samples are contained within plotted polygons for each cluster. Notably, although overlapping, three of the four clusters show quite distinct geographic ranges. Map boundary data from the Database of Global Administrative Areas (GADM; <https://gadm.org>).



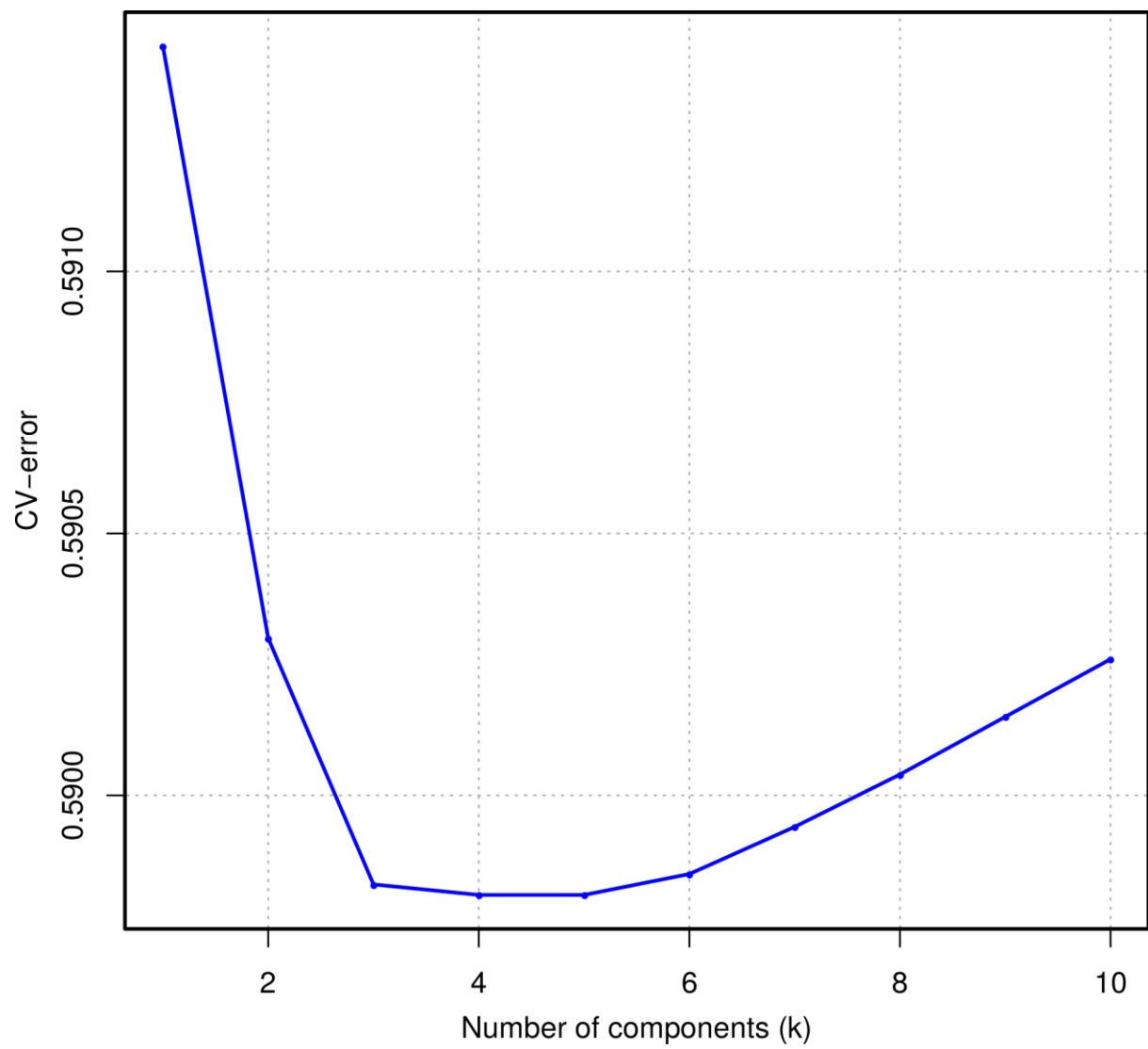
Supplementary Fig. 7 Total variation distance (TVD) tree for k=16 split in the Netherlands. TVD tree analysis provides an alternative view of the relationship between fineSTRUCTURE clusters based on their pairwise TVD scores (Fig. 1a) which should be robust to differences in cluster size. Notably this tree prioritises the split between NBE/NBW/LIM with the rest of the Netherlands, which may reflect the geographic boundary seen in Fig. 5. This tree is based on mean sharing between clusters and may thus miss subtle nuanced relationships where within cluster variation in sharing is non-zero. Clusters are coloured and labelled according to scheme in Fig. 1.



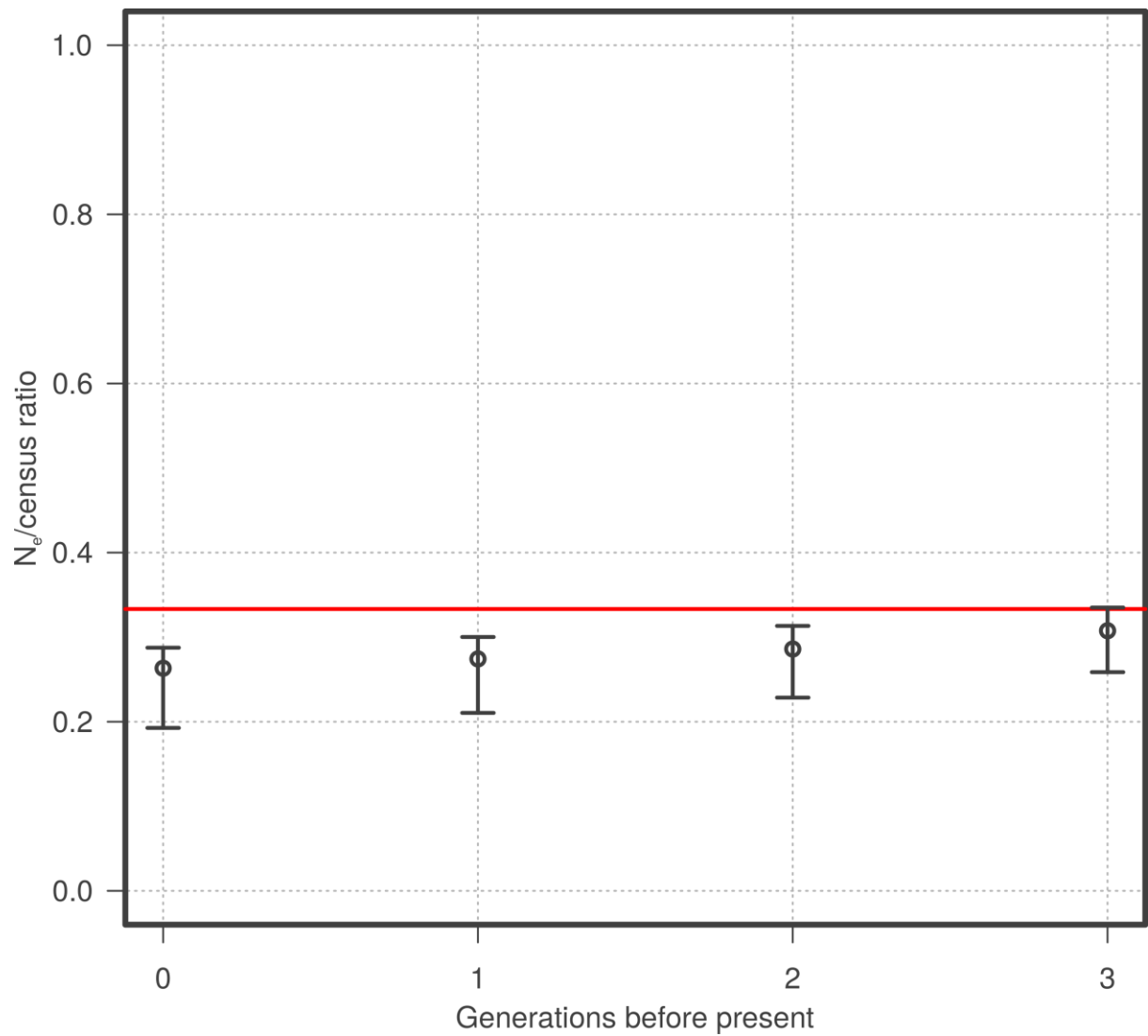
Supplementary Fig. 8 SOURCEFIND ancestry gradients. (a) The Netherlands and its geographical relationship to neighbouring lands. (b) German, Belgian, Danish and French haplotypic ancestry profiles estimated using the alternative method SOURCEFIND for 1,422 Dutch individuals. Arrows indicate the predominant directions along which the ancestry gradients are arranged across the Netherlands. Major ancestry sources from the NNLS method (Fig. 2) are strongly correlated with these estimates ($r^2_{DE} = 0.92$; $r^2_{BE} = 0.97$; $r^2_{DK} = 0.71$). Map boundary data from the Database of Global Administrative Areas (GADM; <https://gadm.org>) and Natural Earth.



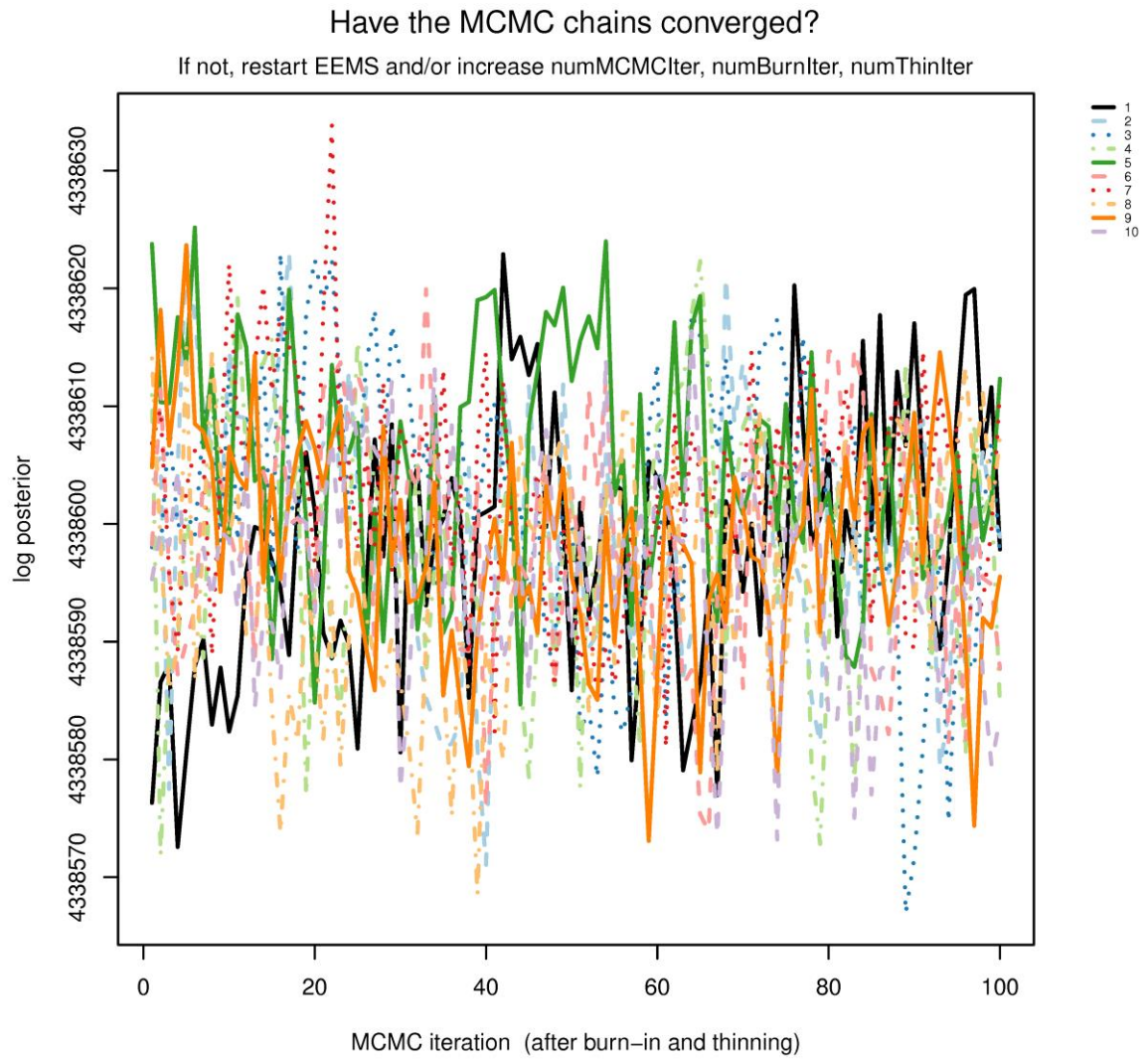
Supplementary Fig. 9 Bayesian information criterion (BIC) versus number of clusters for model choice in mclust. BIC values for mclust models are shown with a range of geometric models (e.g. EII - spherical shape with equal shape and volume²) versus number of components fit for IBD sharing datasets in Fig. 3. Models are fit to IBD sharing matrices between Dutch individuals including (a) segments of all lengths, (b) segments of lengths 1-3cM, (c) segments of lengths 3-5cM and (d) segments of lengths 5-7cM. The model with the maximum BIC was chosen for clustering for each IBD bin. Note that missing values here represent instances where models could not be estimated due to occurrence of a singularity in the covariance matrix often resulting from one or more components being fit to a single point. Under these conditions model likelihood trends to infinity and is uninterpretable. Legend abbreviations represent models with different geometric characteristics described in the mclust paper².



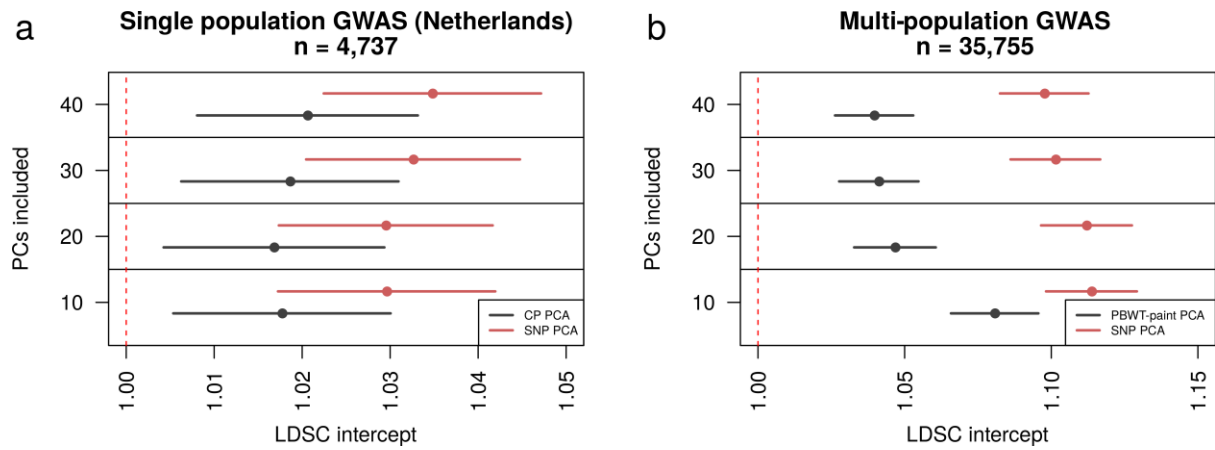
Supplementary Fig. 10 ADMIXTURE CV-error plot. Displays the cross-validation (CV) error for ADMIXTURE run with 1-10 components. Models with 4 and 5 components are tied for lowest CV error, suggesting choice of either is suitable.



Supplementary Fig. 11 Ratio of estimated Ne/Census is stable over the past 3 generations. The red line at 0.33 corresponds to the expected ratio of N_e to census if lifespan is 3 times the generation time. Point estimates represent the ratio of estimated N_e to census value for a given generation in the full Netherlands dataset, while error bars represent 95% confidence interval for this value calculated using 80 bootstrap resamples in IBDNe (note this is not necessarily symmetric on the point estimate).



Supplementary Fig. 12 Convergence of MCMC chains for EEMS run in The Netherlands. 10 independently seeded MCMC chains reach approximate convergence.



Supplementary Fig. 13 LDSC intercepts from ALS GWAS using haplotype PCs vs SNP PCs. Displays LDSC intercepts (points) and 95% confidence intervals (whiskers) for (a) a single population GWAS and (b) a multi-population GWAS of ALS, fitting PCs calculated from haplotype sharing matrices (black) and SNPs (red) as covariates. Using PCs from haplotype sharing matrices reduces the LDSC intercept relative to using SNP PCs, suggesting haplotype sharing matrices correct for confounding not captured by SNP PCA. Error bars represent 95% confidence interval centred on the LDSC intercepts. Abbreviations: CP PCA, ChromoPainter PCA; LDSC, LD score regression; PBWT-paint, positional Burrows-Wheeler transform-paint.

Supplementary Table 1 Mean pairwise F_{ST} ($\times 10^{-3}$) for Dutch clusters and European groups from Sawcer *et al.*³

Finland	0.0	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	
Sweden	3.9	0.0	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	
Norway	5.1	0.4	0.0	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	
Germany	5.9	0.7	0.9	0.0	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	
Italy	11.1	4.9	5.0	2.8	0.0	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	
Denmark	5.6	0.4	0.4	0.4	4.1	0.0	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	
Belgium	6.7	1.1	1.1	0.3	2.3	0.5	0.0	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	
Spain	10.0	3.8	3.7	2.1	1.2	3.0	1.5	0.0	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	
Poland	5.8	1.8	2.6	1.3	5.4	2.1	2.4	4.6	0.0	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	
France	7.6	1.8	1.8	0.7	1.6	1.2	0.4	0.7	2.8	0.0	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	
ZEE	6.8	1.0	1.0	0.5	3.4	0.5	0.3	2.4	2.7	0.9	0.0	-	-	-	-	-	-	-	-	-	-	-	-	-	-	
SHOL	6.4	0.8	0.8	0.3	3.2	0.3	0.2	2.3	2.4	0.8	0.2	0.0	-	-	-	-	-	-	-	-	-	-	-	-	-	
HOL	6.4	0.8	0.8	0.4	3.7	0.3	0.4	2.7	2.5	1.0	0.2	0.0	0.0	-	-	-	-	-	-	-	-	-	-	-	-	
SHOL2	6.7	1.0	1.0	0.7	4.2	0.5	0.7	3.1	2.9	1.4	0.5	0.3	0.2	0.0	-	-	-	-	-	-	-	-	-	-	-	
SHOL3	6.5	0.9	0.9	0.5	3.7	0.4	0.4	2.7	2.6	1.1	0.2	0.1	0.1	0.2	0.0	-	-	-	-	-	-	-	-	-	-	
LIM	7.1	1.4	1.4	0.7	3.0	0.8	0.5	2.2	2.8	0.9	0.6	0.5	0.6	0.8	0.7	0.0	-	-	-	-	-	-	-	-	-	
SELIM	6.5	0.9	0.9	0.2	2.5	0.4	0.1	1.8	2.2	0.5	0.3	0.1	0.2	0.6	0.3	0.3	0.0	-	-	-	-	-	-	-	-	
NBE	6.8	1.2	1.2	0.6	3.3	0.7	0.4	2.4	2.7	1.0	0.6	0.4	0.5	0.8	0.6	0.6	0.3	0.0	-	-	-	-	-	-	-	
NBW	6.9	1.3	1.3	0.7	3.3	0.8	0.4	2.4	2.9	1.1	0.6	0.5	0.5	0.9	0.5	0.8	0.4	0.5	0.0	-	-	-	-	-	-	
NEN	6.5	0.9	0.9	0.6	4.3	0.4	0.6	3.2	2.8	1.4	0.5	0.2	0.1	0.4	0.3	0.8	0.5	0.7	0.8	0.0	-	-	-	-	-	
DRO	6.9	1.1	1.1	0.9	4.7	0.6	0.9	3.6	3.0	1.8	0.6	0.5	0.3	0.6	0.4	1.0	0.7	1.1	1.1	0.1	0.0	-	-	-	-	
GLO	6.8	1.2	1.2	0.9	4.4	0.7	0.9	3.4	3.1	1.6	0.6	0.5	0.5	0.8	0.6	1.1	0.7	1.0	1.0	0.2	0.6	0.0	-	-	-	
UWG	7.0	1.3	1.3	1.0	4.3	0.8	0.9	3.2	3.0	1.6	0.7	0.6	0.6	0.9	0.7	1.0	0.7	1.1	1.0	0.6	0.8	0.8	0.0	-	-	
CEN	6.6	0.9	0.9	0.5	3.7	0.4	0.4	2.7	2.5	1.1	0.3	0.1	0.1	0.3	0.2	0.7	0.3	0.6	0.6	0.2	0.5	0.4	0.0	0.0	-	
GEL	6.4	0.8	0.8	0.4	3.6	0.3	0.3	2.6	2.6	1.0	0.3	0.1	0.1	0.4	0.2	0.6	0.2	0.5	0.5	0.1	0.4	0.1	0.5	0.0	0.0	
NHFG	6.6	1.1	1.0	0.9	4.7	0.6	0.9	3.6	3.1	1.7	0.6	0.4	0.2	0.4	0.3	1.1	0.7	1.0	1.0	0.2	0.3	0.7	0.9	0.4	0.4	
	Finland	Sweden	Norway	Germany	Italy	Denmark	Belgium	Spain	Poland	France	ZEE	SHOL	HOL	SHOL2	SHOL3	LIM	SELIM	NBE	NBW	NEN	DRO	GLO	UWG	CEN	GEL	NHFG

Supplementary note 1

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