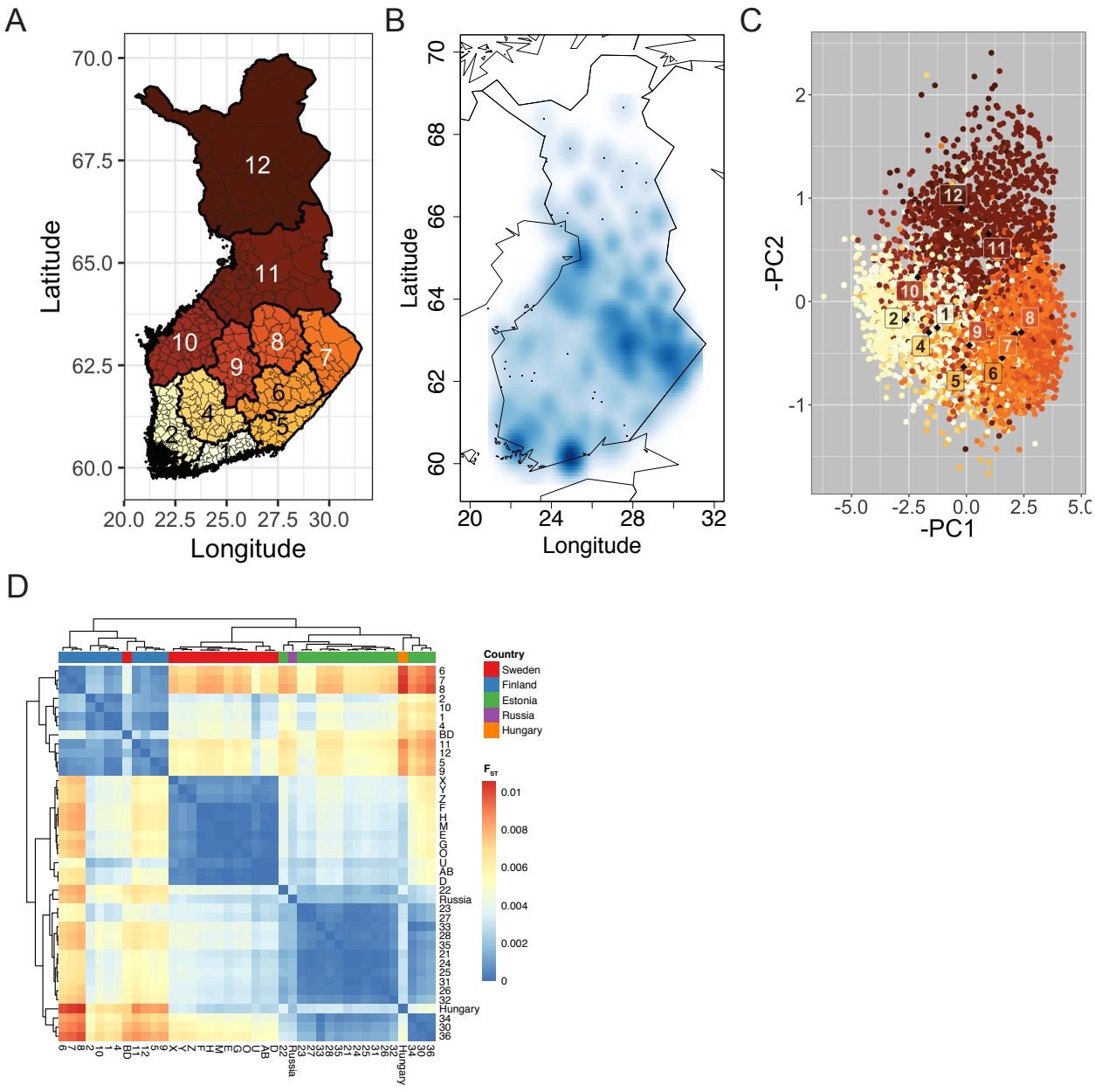

Figure S1 – Principal components analysis recapitulates geographical birth record data by region. A) Labeled map of Finland, as in Figure 1A, with colors highlighting regional differences. Notably, forced relocation uprooted many individuals and communities following WWII for example, when Finland ceded its eastern parts (e.g. Karelia) to the Soviet Union and resettled everyone living in the lost areas into the remaining parts of

the country [1]. B) Smoothed geographical density map of all Finrisk97 samples with birth record data at the centroids of municipalities (N=5,448). Regional-level birth records not shown. C) PCA positions for all Finrisk97 samples with birth record data. Numbers label the average PC coordinates for all individuals born in a region. Colors are as in A). D) Clustered F_{ST} heat map between individuals born in different regions of Finland, Sweden, Estonia, St Petersburg, Russia, and Hungary. Regions with fewer than 10 individuals were not included. Region labels and names are as in **Table S3**.

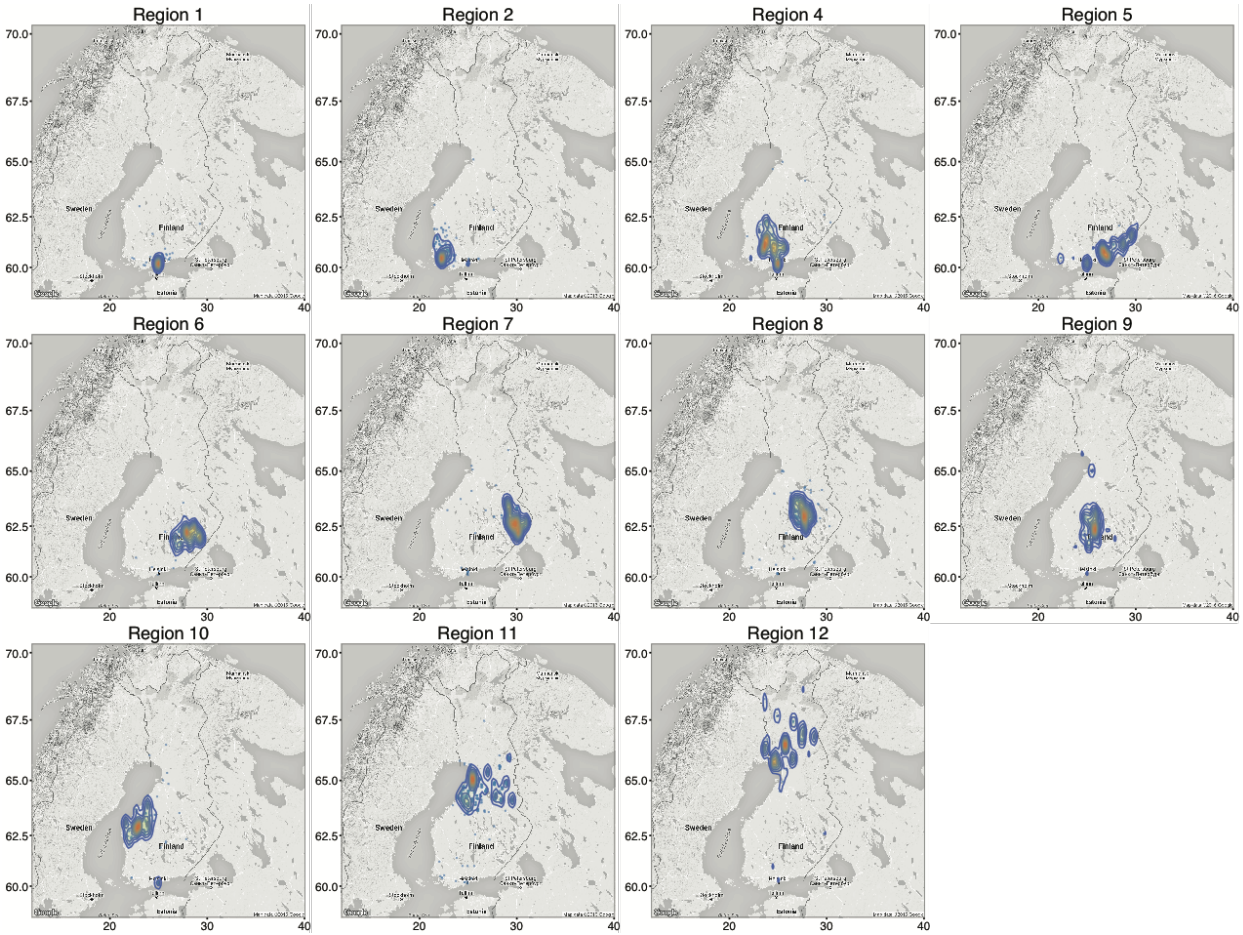

Figure S2 – Birthplace of offspring whose parents are both born in the same region (N=3,132), as indicated by panel titles.

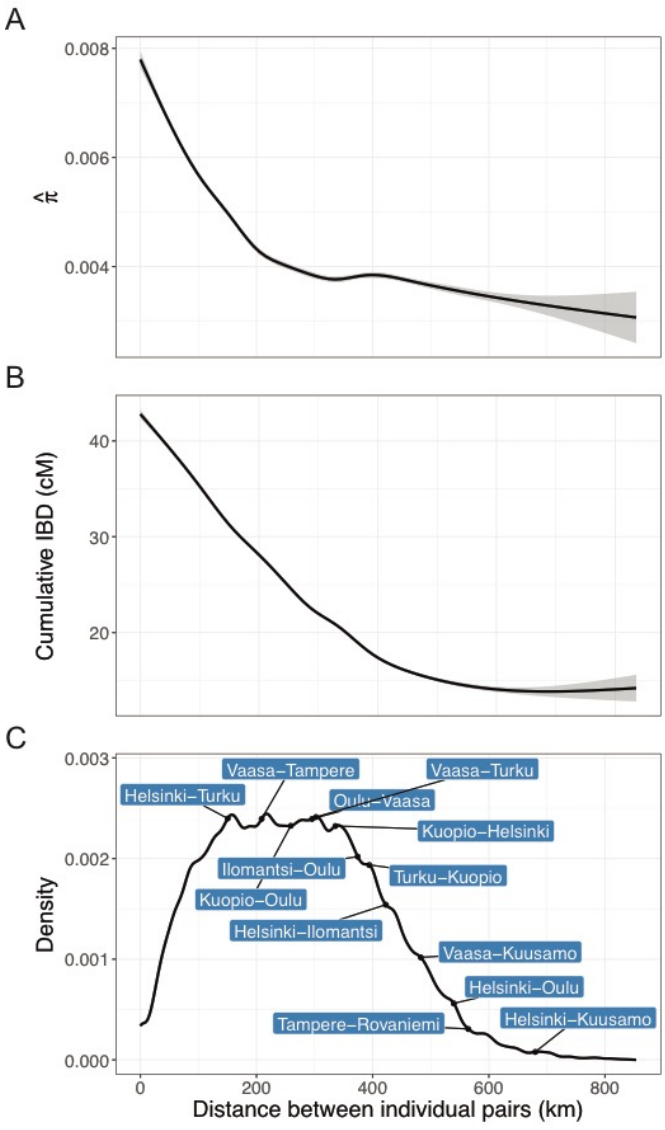

Figure S3 – Geographical distance between pairs of Finnish individuals and genetic sharing. A) Pairwise genetic sharing among unrelated individuals by geographical distance. B) Cumulative IBD sharing (minimum haplotype length ≥ 3 cM) across the genome among unrelated individuals by geographical distance. C) Density of

genetic distance between pairs of individuals by geographical distance. The distance between representative city pairs are shown in blue.

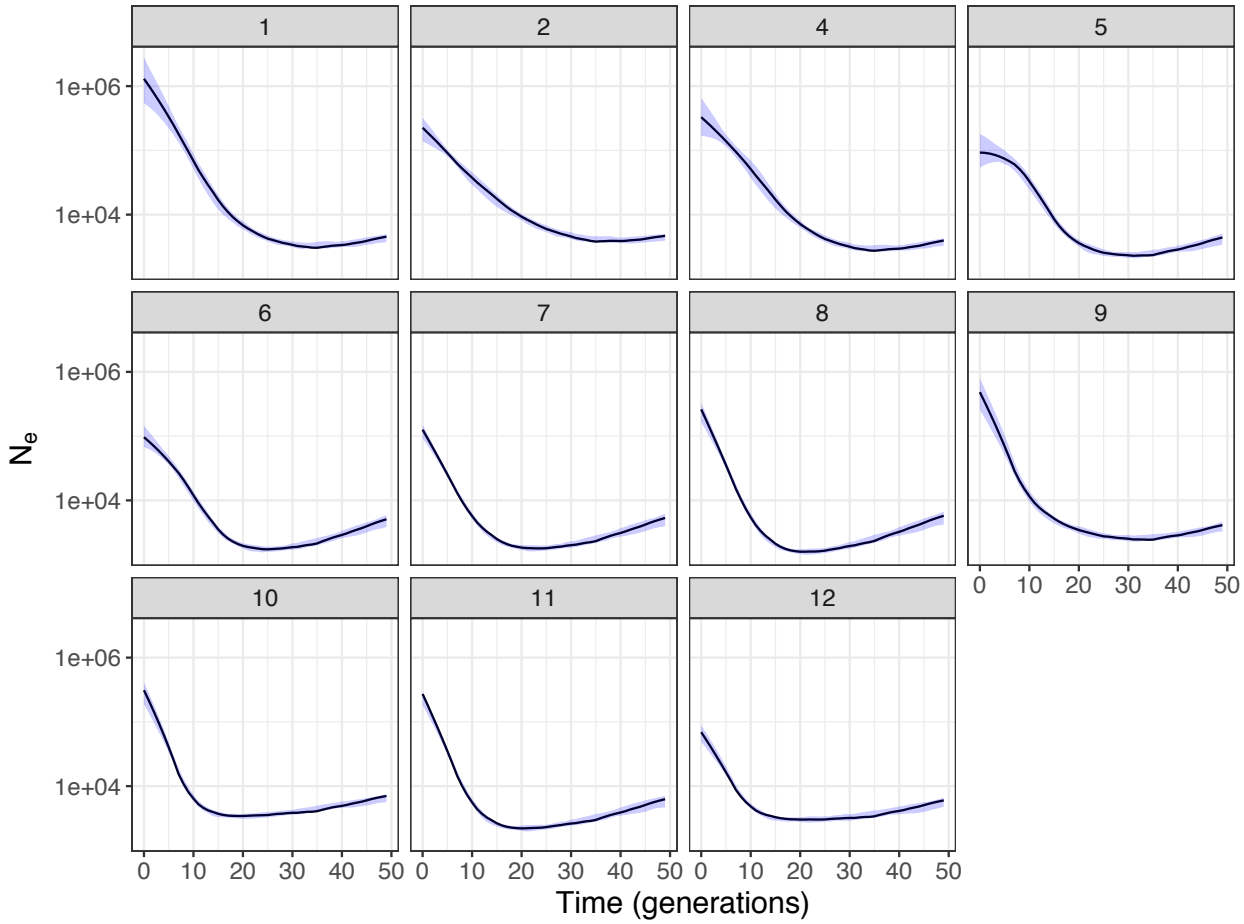

Figure S4 – Effective population size change over time by region of Finland.

Number of individuals in each region are: 1: 1,123, 2: 1,078, 4: 378, 5: 224, 6: 304, 7: 1,581, 8: 1,547, 9: 225, 10: 288, 11: 1,697, 12: 184.

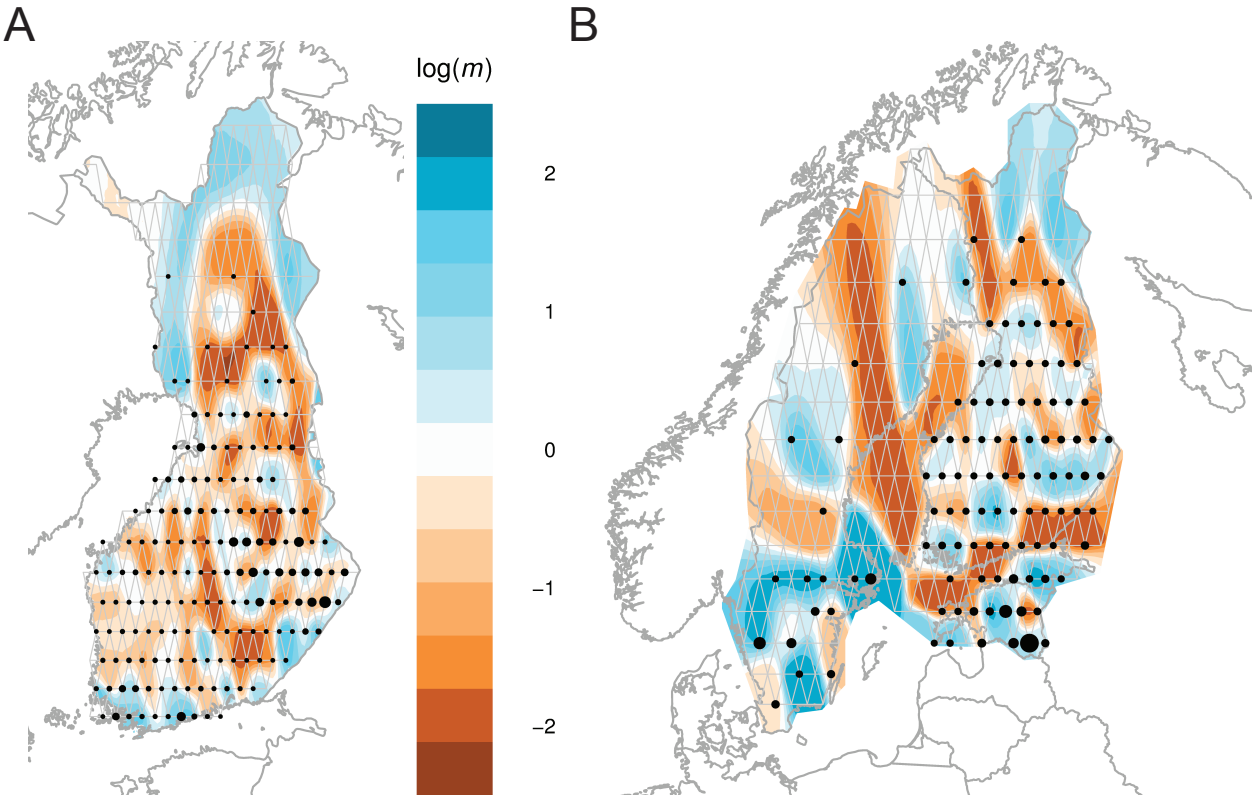

Figure S5 – Deme assignment for EEMS analyses in/near Finland. Black dots at center of demes are proportional to sample size. A) Finland deme assignment from municipality-level birth records. B) Deme assignment in Finland with municipality-level birth records and for region-level birth records in neighboring countries/regions of Sweden, Estonia, and St. Petersburg, Russia.

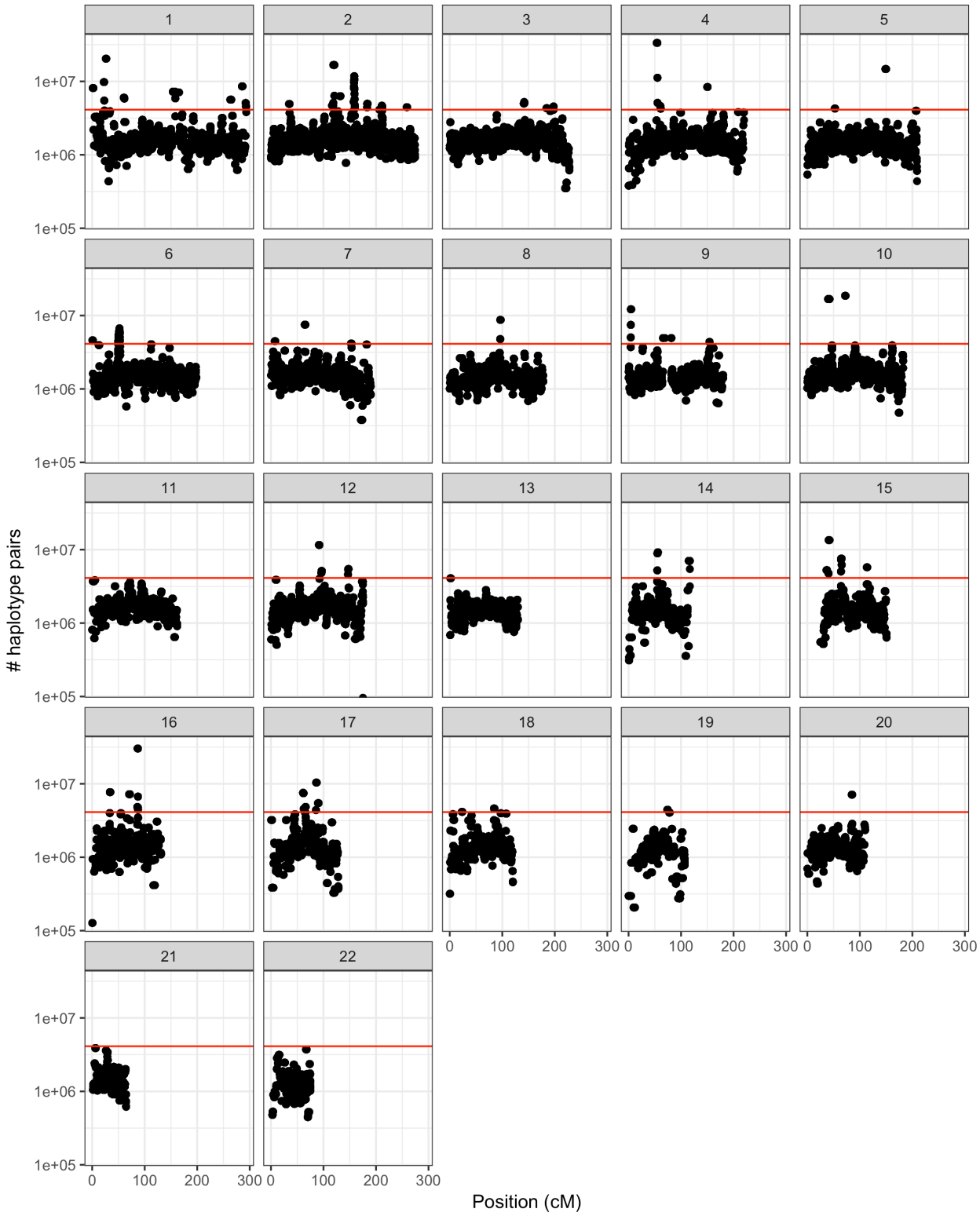
1
2
3
4
5
6
7
8
9
10
11
12
13
14
15
16
17
18
19
20
21
22
1e+07
1e+06
1e+05
0
100
200
300
haplotype pairs
Position (cM)

Figure S6 – Haplotype sharing rate genome-wide by chromosome. At each best-guess genotype used to call haplotypes, we quantified the number of pairs of individuals who shared haplotypes. Included individuals are unrelated and have corresponding exome sequencing data (N=9,363). Red line indicates the mean sharing plus 3 * standard deviation. Total possible number of pairs is $\binom{N}{2}$ = 43,828,203.

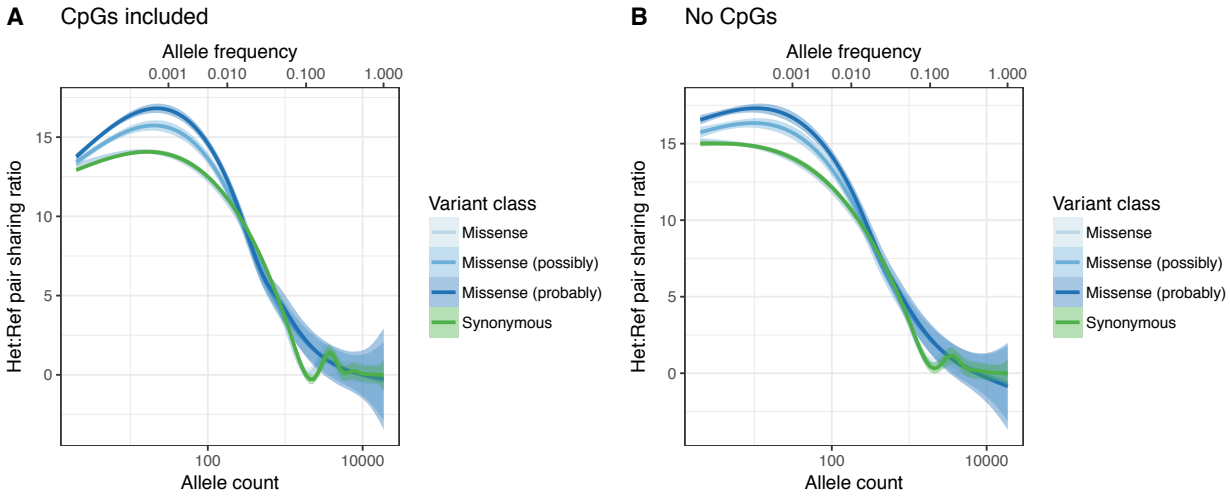

Figure S7 – Depletion of haplotype sharing at CpG sites shows evidence of mutational recurrence. A) Enrichment of haplotype sharing across all variants. B) Enrichment of haplotype sharing across non-CpG variants.

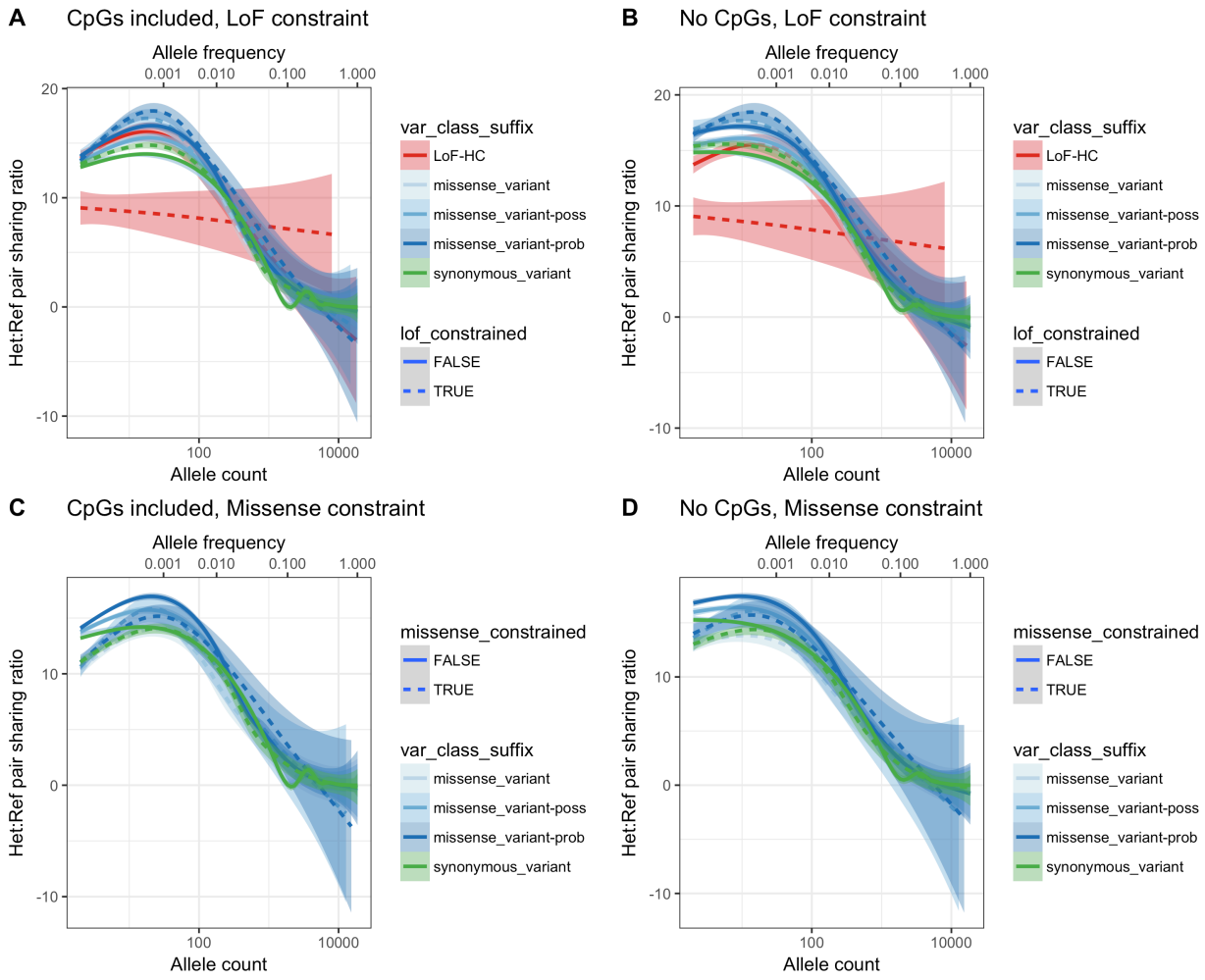

Figure S8 – Depletion of haplotype sharing in missense and loss-of-function (LoF) constrained regions. As calculated in Lek et al, missense constraint indicates regions depleted of missense variation, and LoF constrained regions indicate regions depleted of LoF variation [2].

Table S1 – **Finnish sample genotyping summaries**. Note that some FINRISK samples with birth records have been included as controls for multiple different projects.

Population	Array	Project name	SNPs genotyped	Sample size
Finland	Affymetrix 6.0	MIGen	666,979	339
Finland	Illumina 370k	NFBC	324,674	5,363

Finland	Illumina 610k	Corogene, GenMets	535,787	6,240
Finland	Illumina 670k	HBCS, YFS, FTC	521,500	6,492
Finland	Illumina CoreExome	FINRISK, CoreEX	322,929	10,641
Finland	Illumina CoreExome	ENGAGE	342,869	11,639
Finland	Illumina OmniExpress	PredictCVD, SUMMIT	606,310	2,542
Sweden	Illumina OmniExpress	Sw5	733,202	4,465
Sweden	Illumina OmniExpress	Sw6	733,202	3,873
Hungary	Illumina OmniExpressExome	HTB	943,987	506
Estonia	Illumina OmniExpress	EGCUT	710,831	6,946
Russia	Illumina GlobalScreeningArray	RussiaSiege	633,183	262
TOTAL				59,309

Table S2 – **Birth record data by cohort**. Municipality-level birth records were available for FR97, regional-level birth records were available for FR07 for this study.

Project/Array	**FR07**	**FR97**
ENGAGE	0	3969
FIN610K	634	458
MIGen	0	110
FINRISK, CoreEX	3065	0
PredictCVD, SUMMIT	243	911
TOTAL (N=9,390)	3942	5448

Table S3 – Region names by country in Finland, Sweden, and Estonia.

Country	**Code**	**Name**
Finland	1	Southern Finland
Finland	2	Southwestern Finland
Finland	3	Åland
Finland	4	Tavastia
Finland	5	Southern Karelia
Finland	6	Southern Savonia
Finland	7	North Karelia
Finland	8	Northern Savonia
Finland	9	Central Finland
Finland	10	Ostrobothnia
Finland	11	Northern Ostrobothnia
Finland	12	Lapland
Sweden	AB	Stockholm
Sweden	AC	Västerbotten
Sweden	BD	Norrbotten

Sweden	C	Uppsala
Sweden	D	Södermanland
Sweden	E	Östergötland
Sweden	F	Jönköping
Sweden	G	Kronoberg
Sweden	H	Kalmar
Sweden	I	Gotland
Sweden	K	Blekinge
Sweden	M	Skåne
Sweden	N	Halland
Sweden	O	Västra Götaland
Sweden	S	Värmland
Sweden	T	Orebro
Sweden	U	Västmanland
Sweden	W	Dalarna
Sweden	X	Gävleborg
Sweden	Y	Västernorrland
Sweden	Z	Jämtland
Estonia	21	Harju
Estonia	22	Hiiu
Estonia	23	Ida-Viru
Estonia	24	Järva
Estonia	25	Jõgeva
Estonia	26	Lääne
Estonia	27	Lääne-Viru
Estonia	28	Pärnu
Estonia	29	Peipsi
Estonia	30	Põlva
Estonia	31	Rapla
Estonia	32	Saare
Estonia	33	Tartu
Estonia	34	Valga
Estonia	35	Viljandi
Estonia	36	Võru

Table S4 – Exome sequencing data included in haplotype analyses. Cohorts are ordered by number of individuals contributing to this study. Full descriptions of each cohort are in supplementary note.

Cohort name	Number of individuals included
FINRISK_population_cohort	7014

IBD_FINRISK	845
NFBC	525
Health 2000	271
FINRISK_AD	238
Fusion	214
UK10K	68
Migraine	57
METSIM	45
Eufam	42
NFID	30
Twins_AD	25
ADGEN	9
IBD	4
AUTISM_ASDFI	2
AUTISM_TAMPERE	1
EPILEPSY_EPI25	1
Botnia_T2D	1

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1. Haukka J, Suvisaari J, Sarvimäki M, Martikainen P (2017) The Impact of Forced Migration on Mortality. Epidemiology 28:587-593

2. Lek M, Karczewski KJ, Minikel EV, Samocha KE, Banks E, Fennell T, O'Donnell-Luria AH, Ware JS, Hill AJ, Cummings BB, Tukiainen T, Birnbaum DP, Kosmicki JA, Duncan LE, Estrada K, Zhao F, Zou J, Pierce-Hoffman E, Berghout J, Cooper DN, Deflaux N, DePristo M, Do R, Flannick J, Fromer M, Gauthier L, Goldstein J, Gupta N, Howrigan D, Kiezun A, Kurki MI, Moonshine AL, Natarajan P, Orozco L, Peloso GM, Poplin R, Rivas MA, Ruano-Rubio V, Rose SA, Ruderfer DM, Shakir K, Stenson PD, Stevens C, Thomas BP, Tiao G, Tusie-Luna MT, Weisburd B, Won H, Yu D, Altshuler DM, Ardissino D, Boehnke M, Danesh J, Donnelly S, Elosua R, Florez JC, Gabriel SB, Getz G, Glatt SJ, Hultman CM, Kathiresan S, Laakso M, McCarroll S, McCarthy MI, McGovern D, McPherson R, Neale BM, Palotie A, Purcell SM, Saleheen D, Scharf JM,

1 Sklar P, Sullivan PF, Tuomilehto J, Tsuang MT, Watkins HC, Wilson JG, Daly MJ,
2 MacArthur DG (2016) Analysis of protein-coding genetic variation in 60,706 humans.
3 Nature 536:285-291