

Supplementary Data

Contents

Supplementary Table 1: Demographics of cluster headache cases.....	2
Supplementary Table 2: Quality control.....	3

Supplementary Table 1: Demographics of cluster headache cases

Summary of clinical phenotype and demographics of cluster headache (CH) patients and controls		
Origin:	UK CH (n=852)	Swedish CH (n=591)
Gender:		
Male	546 (64 %)	396 (67%)
Female	306 (46%)	195 (33%)
Smoking:		
Current smoker	204 (23.9%)	155 (26.2%)
Previous smoker	271 (31.8%)	237 (40.1%)
Never smoked	241 (28.2%)	160 (27.1%)
NA	136 (15.9%)	39 (6.6%)
Subtype:		
Episodic	448 (52.6%)	524 (88.6%)
Chronic	261 (30.6%)	64 (10.9%)
Uncharacterised	143 (16.8%)	3 (0.5%)
Concurrent Migraine:		
Migraine	195 (22.9%)	94 (15.9%)
No Migraine	460 (54.0%)	441 (74.7%)
Not available	197 (23.1%)	56 (9.5%)

Supplementary Table 2: Quality control

COHORTS	UK CH n=1,003	UK controls n=463	1958bc n=2,699	NBS n=2,501	Swedish CH n=643	Swedish controls n=1,229
GENOTYPING						
Genotyping Centre	Human Genotyping Facility (HuGe-F)	Human Genotyping Facility (HuGe-F)	Wellcome Trust Sanger Institute	Wellcome Trust Sanger Institute	SNP&SEQ Technology Platform, Uppsala Universitet	deCODE, Iceland
Genotyping Array	Illumina Infinium® GSA-24v1.0	Illumina Infinium® GSA-24v1.0	Illumina 1.2M (custom) chip	Illumina 1.2M (custom) chip	Illumina Infinium® GSA-24v1.0	
SAMPLE QC						
Samples with call rate > 0.98	947 (-56)		5,663 (-18)		643 (-0)	1,218 (-11)
No sex mismatch	945 (-2)		5,660 (-3)		640 (-3)	1,203 (-15)
Not heterozygosity outlier	943 (-2)		5,658 (-2)		631 (-9)	1,185 (-18)
Relatedness IBD < 0.2	912 (-31)		5,648 (-10)		628 (-8)	1,179 (-6)
Population stratification European	852 (-60)		5,614 (-34)		591 (-32)	1,134 (-45)
For analysis	852		5,614		591	1,134
SNP QC						

Shared biallelic SNPs	119,527		549,330	
SNPs with call rate > 0.95	118,159 (-1,368)	119,526 (-1)	549,119 (-211)	549,167 (-163)
SNPs not deviating from HWE ($<10^{-6}$)	116,891 (-1,268)	119,463 (-63)	548,961 (-158)	549,167 (-0)
SNPs with shared call rate > 0.98	115,200 (4,327)		549,070 (-260)	
SNPs with non-sig different call rate cases vs controls (p < 0.00001)	113,445 (-1,755)		548,603 (-467)	
Imputation checker tool pass	109,898 (-3,547)		532,979 (-15,624)	

CH = Cluster headache, GSA = Global screening array, HWE = Hardy-Weinberg equilibrium, IBD = Identity-by-descent, NBS= National blood service, QC = Quality

control, SNP = Single nucleotide polymorphism, UK = United Kingdom, 1958bc = 1958 birth cohort.