

Novel Loci Associated with Usual Sleep Duration: The CHARGE Consortium Genome-Wide Association Study

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Supplementary Table 1. Sleep duration questions

Cohort name	Question to ascertain sleep duration	Self- or interviewer administered?	Response options
ARIC and CHS	“How many hours of sleep do you get at night on weekdays (or workdays)?”	Self	Whole numbers
FHS	How many hours were spent... sleeping? (part of an activity questionnaire, where sleep was one of the categories)	Interviewer	Whole numbers
HABC	“How many hours of sleep do you usually get at night?”	Interviewer	Whole numbers
HBCS	“How many hours do you usually sleep per night?”	Self	Whole numbers
HPFS and NHS	Indicate total hours of actual sleep in a 24-hour period	Self	Whole numbers from 5 to 11; values <5 hours coded as 5, values >11 hours coded as 11
InCHIANTI	“During the past month, how many hours of actual sleep did you get at night?”	Self	Whole numbers
MrOS	“During the past month, how many hours of actual sleep did you get each night? (This may be different than the number of hours you spent in bed.)”	Self	Whole numbers
QFS	“How many hours per day, on average, do you actually sleep?”	Self	Whole numbers
QIMR	“On WEEKDAYS, how much sleep do you usually get at night? (hours and minutes)”	Self	Nearest half hour
RS I & II	“In the past month how long did you usually sleep per night?”	Interviewer	Any value from 0 to 20
SHIP	Hours of sleep per 24 hours on weekdays	Interviewer	Whole numbers
SOF	“On most nights, how many hours do you sleep each night?”	Self	Nearest half hour
TwinsUK	On average, how many hours per night do you sleep during a working week (Sun-Thur night)?	Self	Less than 6, 6-7, 7-8, 8-9, >9
WiSC	"How many hours of sleep do you usually get during a workday night?"	Self	Whole numbers
YFS	How many hours the participant usually sleeps, in 24 hours	Interviewer	5 or less, 6, 6.5, 7, 7.5, 8, 8.5, 9, 9.5, 10 or more

Supplementary Table 2a. Genotyping and quality control of discovery cohorts

Cohort name	Individual sample quality control parameters
ARIC	Call rate <95%, sex mismatch, 1 st degree relatives, genotype mismatch with reference panel, outliers based on IBS clustering or Eigenstrat
CHS	Call rate, <95%, sex mismatch, sample failure
FHS	Call rate <97%, subject heterozygosity >5 SD from the sample mean, large Mendelian error rate
HABC	Call rate <97%, sample failure; genotypic sex mismatch, first-degree relative of an included individual based on genotype data
HBCS	Call rate <95%, sex mismatch, relatedness based on IBS >20% with another individual
HPFS	Call rate <95%, sex mismatch, unexpected duplicates, 1st and 2nd degree relatives, outliers based on Eigenstrat
InCHIANTI	Call rate <97%, heterozygosity rate <30%, sex mismatch
MrOS	Call rate <97%, genotypic sex mismatch, relatedness by estimated IBD, gross chromosomal abnormalities by BAF in >5 chromosomes, non-European ethnic outliers from PCA.
NHS	Call rate <95%, sex mismatch, unexpected duplicates, 1st and 2nd degree relatives, outliers based on Eigenstrat
QFS	Call rate <95%
QIMR	Call rate <95%
RS I & II	Call rate <97.5% sex mismatch, excess autosomal heterozygosity 0.336, outliers identified by the IBS clustering analysis
SHIP	Call rate <92%, sex mismatch, duplicate samples by estimated IBD
SOF	Call rate <97%, genotypic sex mismatch, relatedness by estimated IBD, gross chromosomal abnormalities by BAF in >5 chromosomes, non-European ethnic outliers from PCA
TwinsUK	Call rate <98%, heterozygosity across all SNPs ≥ 2 SD from the sample mean, non-European ancestry as assessed by PCA comparison with HapMap3 populations, observed pairwise IBD probabilities suggestive of sample identity errors. Misclassified monozygotic and dizygotic twins corrected based on IBD probabilities.
WiSC	Call rate <95%, sex mismatch, IBS >25% with another individual, non-Caucasian by self-report or PCA
YFS	Call rate <95%, pHWE < 10^{-6} , sex mismatch, relatedness

Supplementary Table 2b. Genotyping and quality control of discovery cohorts

Cohort name	Genotyping platform	Pre-imputation quality control			Imputation software	Reference panel
		SNP call rate	HWE p-value	MAF cutoff		
ARIC	Affymetrix 6.0	0.90	10 ⁻⁶	0.01	MACH	HapMap2, v22, CEU
CHS	Illumina 370 CNV	0.97	10 ⁻⁵	---	BIMBAM	HapMap2, v22, CEU
FHS	Affymetrix 500K and MIPS 50K combined	0.97	10 ⁻⁶	---	MACH	HapMap2, v22, CEU
HABC	Illumina Human1M-Duo	0.97	10 ⁻⁶	0.01	MACH	HapMap2, v22, CEU
HBCS	Modified Illumina 610Quad	0.95	10 ⁻⁶	0.01	MACH	HapMap2, v22, CEU
HPFS - CHD, T2D	Affymetrix SNP 6.0	0.98	10 ⁻⁴	0.02	MACH	HapMap2, v22, CEU
HPFS – KS	Illumina 610Q	0.95	10 ⁻⁵	0.01	MACH	HapMap2, v22, CEU
InCHIANTI	Illumina HumanHap 550K	0.98	10 ⁻⁴	0.01	IMPUTE	HapMap2, v22, CEU
MrOS	Illumina HumanOmni 1 Quad	0.97	10 ⁻⁴	0.01	MACH	HapMap2, v22, consensus haplotypes
NHS - CHD, T2D	Affymetrix SNP 6.0	0.98	10 ⁻⁴	0.02	MACH	HapMap2, v22, CEU
NHS - KS sample	Illumina 610Q	0.95	10 ⁻⁵	0.01	MACH	HapMap2, v22, CEU
NHS - BrCa sample	Illumina 550K	0.90	---	0.01	MACH	HapMap2, v22, CEU
QFS	Illumina 610Q	0.95	10 ⁻⁴	0.01	MACH	HapMap2, v22, CEU
QIMR	Illumina 317k + 3870k + 610k	0.95	10 ⁻⁶	0.01	MACH	HapMap2, v22, CEU
RS I & II	Illumina Infinium II HumanHap 550, v3	0.90	---	0.01	MACH	HapMap2, v22, CEU
SHIP	Affymetrix SNP 6.0	---	---	---	IMPUTE	HapMap2, v22, CEU
SOF	Illumina HumanOmni 1 Quad	0.97	10 ⁻⁴	0.01	MACH	HapMap2, v22, consensus haplotypes
TwinsUK	Illumina 610Q	0.90	10 ⁻⁴	0.01	IMPUTE	HapMap2, v22, CEU+YRI+ASN
WiSC	Affymetrix SNP 6.0	0.95	10 ⁻³	0.01	BEAGLE	HapMap2, v22, CEU
YFS	Illumina 670k custom	0.95	10 ⁻⁶	---	MACH	HapMap2, v22, CEU

Supplementary Table 3. Association testing methods

Cohort name	Software for association testing	Covariates to control for population stratification
ARIC	ProbABEL	None
CHS	R	Clinic site
FHS	LMEKIN package in R	First 10 principal components
HABC	ProbABEL (R)	Two clinic sites and first 2 principal components
HBCS	ProbABEL (imputed), Plink (genotyped)	First 3 principal components
HPFS - KS, T2D	ProbABEL (R)	First 4 principal components
HPFS – CHD	ProbABEL (R)	First 3 principal components
InCHIANTI	SNPTEST	None
MrOS	R	First 4 principal components
NHS - CHD, T2D	ProbABEL (R)	First 3 principal components
NHS - KS, BrCa	ProbABEL (R)	First 4 principal components
QFS	GWAF (LME) package in R	None
QIMR	MERLIN - fastassoc	No correction for population stratification was made. Individuals who were outliers when projecting principal components against other Europeans were removed from the analysis.
RS I & II	ProbABEL	None
SHIP	QUICKTEST v0.95	None
SOF	R	First 4 principal components
TwinsUK	GenABEL v1.4	None
WiSC	PLINK	None
YFS	ProbABEL, Plink	First 2 principal components

Supplementary Table 4. Expression quantitative trait locus databases queried

eQTL Tissue Description	PMID citation (if published)
B-lymphoblastoid cell lines	17873874
B-lymphoblastoid cell lines	18193047
B-lymphoblastoid cell lines	19644074
B-lymphoblastoid cell lines	22286170
B-lymphoblastoid cell lines	22941192
B-lymphoblastoid cell lines (asthmatics)	17873877
B-lymphoblastoid cell lines (asthmatics)	23345460
Brain cortex	19222302
Brain cortex	19361613
CD11+ dendritic cells (before and after M. tuberculosis stimulation)	22233810
CD19+ B cells	22446964
CD4+ T cells	20833654
Cerebellum	22685416
Cerebellum	unpublished
Cerebellum	20485568
Endometrial carcinomas	21226949
ER+ and ER- breast tumor cells	23374354
Frontal cortex	20485568
Leukocytes	19966804
Leukocytes (Celiac disease)	19128478
Liver	18462017
Liver	21602305
Liver	21637794
Lung	23209423
Lymphocytes	17873875
micro-RNAs in B-lymphoblastoid cell lines	21691150
micro-RNAs in gluteal and abdominal adipose	22102887
Omental and/or subcutaneous adipose	18344981
Omental and/or subcutaneous adipose	21602305
Omental and/or subcutaneous adipose	22941192
Osteoblasts	19654370
Peripheral blood monocytes	19222302
Peripheral blood monocytes	20502693
Peripheral blood monocytes	22446964
Pons	20485568
Prefrontal cortex	unpublished
Prefrontal cortex	22031444
Prefrontal cortex	20351726
Primary fibroblasts	19644074
Primary PHA-stimulated T cells	19644074

Skin	21129726
Skin	22941192
Stomach	21602305
Temporal cortex	22685416
Temporal cortex	20485568
Visual cortex	unpublished
Whole blood	18344981
Whole blood	21829388
Whole blood	22692066

FIGURE LEGENDS

Supplementary Figure 1. Quantile-quantile plot for meta-analysis of usual sleep duration in cohorts of European ancestry.

Supplementary Figure 2. Cohort-specific association of rs1823125 with usual sleep duration (mean and standard error). TwinsUK is absent from the graph because this SNP did not impute well.

Supplementary Figure 3. Linkage disequilibrium (LD) pattern around rs1191685, rs1807282 and *PAX8* on chromosome 2 (113650kb to 113890kb from Hapmap2r22). LD pattern shown for blacks (YRI, top) and whites (CEU, bottom). rs1191685 is indicated with green arrows and green lines. rs1807282 is indicated with red arrows and red lines. r^2 color scheme used, where darkest black indicates the highest r^2 correlation between SNPs. Location of the *PAX8* gene is shown in the center in blue. The *PSD4* gene is 5' (13kb) and *CBW2D* gene is 3' (159kb, not shown) of *PAX8*. Figure was constructed using Haploview 4.2; Barrett, et al. Bioinformatics 2005.