Supplementary information

FinnGen samples were genotyped with Illumina and Affymetrix arrays (Thermo Fisher Scientific, Santa Clara, CA, USA). Genotype calls were made with GenCall and zCall algorithms for Illumina and AxiomGT1 algorithm for Affymetrix chip genotyping data. Genotyping data produced with previous chip platforms were lifted over to build version 38 (GRCh38/hg38) following the protocol described here: dx.doi.org/10.17504/protocols.io.nqtddwn. Samples with sex discrepancies, missingness (> 5%), excess heterozygosity (+-4SD) and non-Finnish ancestry were removed. Variants with high missingness (> 2%), deviation from Hardy–Weinberg equilibrium ($P < 1.0 \times 10^{-6}$) and low minor allele count (MAC < 3) were removed. Pre-phasing of genotyped data was performed with Eagle 2.3.5 (https://data.broadinstitute.org/alkesgroup/Eagle/) with the default parameters, except the number of conditioning haplotypes was set to 20,000. Imputation was carried out by using the population-specific Sequencing Initiative Suomi (SISu) v3 imputation reference panel with Beagle 4.1 (version 08Jun17.d8b, https://faculty.washington.edu/browning/beagle/b4_1.html) as described in the following protocol: [dx.doi.org/10.17504/protocols.io.nmndc5e]. SISu v3 imputation reference panel was developed using the high-coverage (25–30x) whole-genome sequencing data generated at the Broad Institute of MIT and Harvard and at the McDonnell Genome Institute at Washington University, USA; and jointly processed at the Broad Institute. Variant callset was produced with Genomic Analysis Toolkit (GATK) HaplotypeCaller algorithm by following GATK best-practices for variant calling. Genotype-, sample- and variant-wise quality control was applied in an iterative manner by using the Hail framework v0.1 (https://Github.com/hail-is/hail/releases/tag/0.2.13, http://Doi.org/10.5281/zenodo.2646680). The resulting high-quality whole genome sequencing data for 3775 individuals were phased with Eagle 2.3.5 as described above. Post-imputation quality control involved excluding variants with INFO score < 0.7.

Supplementary Table 1. The main findings of the previous GWAS studies

1st author	Trait	Sample size	Original GWAS finding		Corresponding finding in FinnGen	Corresponding finding in FinnGen (BMI adjusted)
Tempaku F[13]	Obstructive sleep apnoea trait (AHI, change over time)	706	rs12415421	beta=0.28 P=3.4 x 10^{-8}	beta=0.032 P=0.38	beta=0.048 P=0.26
			rs4731117	beta=0.28 P=4.4 x 10^{-8}	beta=0.014 P=0.37	beta= 0.019 P=0.29
Chen H[14]	Obstructive sleep apnoea trait (AHI) NREM AHI in men	Total: 19,744 Men: 6,737	rs12936587	beta=0.12 P=1.7 × 10^{-8}	beta=0.0023 P=0.86	beta=0.0097 P=0.53
Cade B[15]	Obstructive sleep apnoea trait (apnoea hypopnea index, average respiratory event duration)	12,558	rs116791765	beta=-0.32 P=1. 9 x 10^{-8}	Not defined in the FinnGen data	Not defined in the FinnGen data
			rs35424364	beta=0.03 P=4.9 x 10^{-8}	beta=-0.014 P=0.51	beta=-0.0034 P=0.89

The main results of the previous genome-wide association studies (GWAS) and comparison to the FinnGen data findings. BMI=body mass index, AHI=apnoea-hypopnea index, NREM= non-rapid eye movement sleep.

Supplementary Table 2. The prospective epidemiological and disease-based cohorts, and hospital biobank samples in FinnGen Data Freeze 5

Cohort	N
Auria Biobank	22729
Biobank of Central Finland	1470
Biobank of Eastern Finland	6495
Blood Service Biobank	29047
Borealis Biobank	5441
Biobank Botnia	6691
Biobank Corogene	4753
Biobank FinHealth	5770
Helsinki Biobank	45481
Tampere Biobank	7430
Terveystalo Biobank	102
THL Biobank FinIPF	203
THL Biobank FINRISK 1992	4982
THL Biobank FINRISK 1997	7060
THL Biobank FINRISK 2002	7013
THL Biobank FINRISK 2007	5185
THL Biobank FINRISK 2012	5302
THL Biobank GENERISK	6955
THL Biobank Health 2000	6574
THL Biobank Health 2011	708
THL Biobank HHS	1981
THL Biobank Kuusamo	128
THL Biobank Migraine	7764
THL Biobank SUPER	8543
THL Biobank Diabetes	9405
THL Biobank Twins	11578
Total:	218792

THL= Finnish Institute for Health and Welfare Helsinki, Finland

Supplementary Table 3. ICD-codes for OSA and comorbidities

Phenotype endpoint	ICD-10	ICD-9	ICD-8
OSA	G47.3	3472A	
HYPERTENSION	I10-I13, I15, I67.4	4019X, 4029A, 4029B, 4039A, 4040A, 4059A, 4059B, 4372A, 4059X	400, 401, 402, 403, 404
T2D*	E11	250A	
CHD	I20.0, I21, I22	410, 4110	410, 411,0
STROKE	I61, I63, I64	431, 4330A, 4331A, 4339A, 4340A, 4341A, 4349A, 436	431, 433, 434, 436
DEPRESSION	F32, F33	2961, 2968	790,20, 298,0
HYPOTHYROIDISM	E00, E01, E02, E03.0-E03.5, E03.8, E03.9	243, 2443, 2448, 2449, 2448A, 2448B	243, 244
ASTHMA	J45, J46	493	493
IRD	M05, J99.0, M06.0, M30-M35, M45, M08.0, L40.5	7140A, 7140B, 7141, 7100, 7431, 7101, 7340, 7200, 7143A, 6960A	712,10, 712,4, 712,0, 696,00
SNORING	R06.5		

By combining codes from different registries, we generate phenotype endpoints. Finnish national version for each International Statistical Classification of Diseases (ICD)-codes were used. These ICD-code criteria are all regular expressions for a hierarchical search. T2D* includes also medication purchases for Anatomical Therapeutic Chemical (ATC) code A10B, Blood glucose lowering drugs, excluding insulins. At least three separate purchases were required to ensure the correct diagnosis if diabetic medication was the only evidence. OSA=obstructive sleep apnoea, T2D=type 2 diabetes, CHD=coronary heart disease, IRD= inflammatory rheumatic diseases.

Supplementary Table 4. Characterization of five genome-wide significant OSA loci when snorers were excluded from controls in GRChb38

CHR	Position	RSID	REF	ALT	Nearest gene	Consequence	Fin.enr.	AF	AF cases	AF controls	INFO	OR [95% CI]	P-value	P-value BMIadj
16	53765595	rs9937053	G	A	FTO	intron	0.97	0.43	0.45	0.43	0.999	1.11[1.08-1.13]	1.8×10^{-16}	0.03
12	97359374	rs10507084	C	T	RMST/ NEDD1	intergenic	3.03	0.18	0.19	0.18	0.993	1.12[1.08-1.15]	2.4×10^{-11}	9.5×10^{-10}
10	12656440	rs185932673	C	T	CAMK1D	intron	0.55	0.0033	0.0051	0.0032	0.972	1.85[1.49-2.30]	3.6×10^{-8}	9.4×10^{-6}
9	125379530	rs4837016	G	A	GAPVD1	intergenic	1.12	0.47	0.45	0.47	0.995	0.93[0.91-0.95]	1.5×10^{-8}	2.0×10^{-4}
2	136234237	rs10928560	C	T	CXCR4	downstream	1.04	0.20	0.18	0.20	0.993	0.92[0.89-0.95]	4.7×10^{-8}	1.2×10^{-4}

All effect sizes and allele frequencies are reported in terms of alternate (ALT) allele. The finding of rs185932673 should be interpreted cautiously as the variant is rare in the Finnish population. OSA=obstructive sleep apnoea, GRCh38=Genome Reference Consortium Human genome build 38 co-ordinates, CHR=chromosome, Fin.enr=Finnish enrichment is computed using The Genome Aggregation Database (Gnomad) data comparing Finnish to other European populations in the Gnomad data. AF=allele frequency, OR=odds ratio, CI=confidence interval, P-value BMIadj=P-value after body mass index (BMI) adjustment. FTO=Fat mass and obesity-associated protein, RMST=Rhabdomyosarcoma 2 associated transcript / NEDD1=NEDD1 gamma-tubulin ring complex targeting factor, CAMK1D=Calcium/calmodulin-dependent protein kinase ID, GAPVD1= GTPase activating protein and VPS9 Domains 1, CXCR4=C-X-C motif chemokine receptor 4.

Supplementary Table 5. Bonferroni corrected significant PheWAS findings of the five associated loci

Rs10928560		
Phenotype	**OR**	**P-value**
Lactose intolerance	1.87[1.82-1.93]	2.74×10^{-12}
Lactose intolerance, other/unspecified	1.89[1.84-1.95]	3.20×10^{-11}
Sleep disorders (combined)	0.92[0.89-0.94]	6.53×10^{-9}
Internal derangement of knee	0.93[0.91-0.96]	4.97×10^{-6}
Episodal and paroxysmal disorders	0.95[0.93-0.98]	7.18×10^{-6}
Arthropathies	0.96[0.93-0.99]	1.32×10^{-5}
Neurological diseases	0.96[0.93-0.99]	1.68×10^{-5}
Rs4837016		
Phenotype	**OR**	**P-value**
Sleep disorders (combined)	0.94[0.92-0.97]	8.51×10^{-7}
Rs185932673		
Phenotype	**OR**	**P-value**
Sleep disorders (combined)	1.69[1.64-1.74]	3.81×10^{-7}
Rs10507084		
Phenotype	**OR**	**P-value**
Sleep disorders (combined)	1.11[1.08-1.14]	1.56×10^{-11}
Episodal and paroxysmal disorders	1.05[1.02-1.08]	8.69×10^{-7}
Neurological diseases	1.04[1.01-1.08)	2.98×10^{-6}
Rs9937053		
Phenotype	**OR**	**P-value**
Arthrosis related co-morbidities	1.28[1.24-1.32]	2.47×10^{-44}
Obesity	1.25[1.22-1.29]	4.14×10^{-41}
Obesity and other hyperalimentation	1.25[1.21-1.29]	9.05×10^{-41}
Other nutritional deficiencies	1.23[1.19-1.27]	1.69×10^{-36}
Obesity, other/unspecified	1.30[1.27-1.34]	7.12×10^{-33}
Other (not insulin) diabetes medications	1.14[1.10-1.17]	6.23×10^{-32}
Type 2 diabetes with other specified/multiple/unspecified complications	1.14[1.11-1.17]	1.84×10^{-28}
Type 2 diabetes	1.12[1.09-1.15]	5.67×10^{-28}
Type 2 diabetes, definitions combined, including primary healthcare diagnoses	1.13[1.10-1.16]	9.09×10^{-28}
Type 2 diabetes, strict (exclude DM1)	1.12[1.09-1.16]	6.65×10^{-27}
Obesity due to excess calories	1.24[1.20-1.27]	7.79×10^{-27}

Type 2 diabetes, definitions combined	1.12[1.09-1.16]	7.93×10^{-27}
Diabetes medication	1.11[1.08-1.15]	5.62×10^{-26}
Diabetes mellitus	1.11[1.07-1.14]	1.98×10^{-24}
Diabetes, insuline treatment (Kela reimbursement) (more controls excluded)	1.11[1.08-1.15]	4.48×10^{-24}
Diabetes, insuline treatment (Kela reimbursement)	1.11[1.08-1.15]	5.17×10^{-24}
Type 2 diabetes without complications	1.15[1.12-1.19]	2.36×10^{-23}
Other diabetes, wide definition	1.11[1.08-1.14]	5.29×10^{-23}
Diabetes, varying definitions	1.1[1.07-1.13]	6.46×10^{-23}
Type 2 diabetes, wide definition	1.14[1.10-1.17]	4.59×10^{-22}
Diabetes 1 & 2, IBD comorbidity	1.11[1.08-1.14]	8.54×10^{-18}
Gout-related comorbidities	1.08[1.05-1.12]	2.77×10^{-17}
Sleep disorders (combined)	1.1[1.07-1.13]	3.31×10^{-15}
Rheumatological diseases related comorbidities	1.06[1.03-1.09]	4.55×10^{-15}
Endocrine, nutritional and metabolic diseases	1.06[1.03-1.09]	7.25×10^{-14}
ILD Comorbidities, CVD and metabolic diseases	1.06[1.03-1.09]	3.23×10^{-12}
Comorbidities, CVD and metabolic diseases	1.07[1.04-1.1]	5.13×10^{-12}
Multimorbidity, for COPD	1.05[1.02-1.08]	2.01×10^{-11}
COPD comorbidities, CVD and metabolic diseases	1.06[1.03-1.09]	2.06×10^{-11}
Hypertensive diseases	1.06[1.03-1.09]	1.36×10^{-10}
Hypertensive diseases (excluding secondary)	1.06[1.03-1.09]	1.36×10^{-10}
Hypertension	1.06[1.03-1.09]	1.40×10^{-10}
Hypertension (no controls excluded)	1.06[1.03-1.09]	1.42×10^{-10}
ILD-related co-morbidities	1.05[1.02-1.08]	1.85×10^{-10}
Gonarthrosis	1.08[1.05-1.11]	3.34×10^{-10}
Arthrosis, including primary healthcare diagnoses	1.06[1.03-1.09]	6.59×10^{-10}
Cardiovascular diseases (excluding rheumatic etc)	1.05[1.02-1.08]	6.81×10^{-10}
Arthrosis	1.06[1.03-1.09]	6.90×10^{-10}
Gonarthrosis [arthrosis of knee]	1.07[1.04-1.10]	3.75×10^{-9}
Gonarthrosis, primary	1.07[1.04-1.10]	4.25×10^{-9}
Hypertension, essential	1.06[1.03-1.09]	6.76×10^{-9}
COPD-associated comorbidities	1.04[1.01-1.07]	8.70×10^{-9}
Insulin medication	1.09[1.06-1.12]	3.84×10^{-8}

Asthma associated comorbidities	1.04[1.01-1.07]	7.11×10^{-8}
Primary gonarthrosis, bilateral	1.1[1.07-1.13]	1.29×10^{-7}
Obesity related asthma	1.13[1.10-1.16]	1.56×10^{-7}
Hypertension, essential (no controls excluded)	1.05[1.02-1.08]	1.87×10^{-7}
Gonarthrosis, primary, with knee surgery	1.09[1.06-1.13]	1.88×10^{-7}
Cardiovascular diseases	1.04[1.01-1.07]	3.50×10^{-7}
Antihypertensive medication - note that there are other indications	1.04[1.01-1.07]	4.04×10^{-7}
Neurological diseases	1.05[1.02-1.08]	7.20×10^{-7}
Arthropathies	1.04[1.01-1.07]	8.59×10^{-7}
Heart failure and antihypertensive medication	1.07[1.04-1.1]	1.30×10^{-6}
Carpal tunnel syndrome	1.07[1.04-1.11]	1.77×10^{-6}
Psoriatic arthropathies related comorbidities	1.05[1.02-1.08]	3.64×10^{-6}
Diabetes, several complications	1.1[1.06-1.13]	4.27×10^{-6}
Type 2 diabetes with coma	1.16[1.12-1.19]	5.56×10^{-6}
Extreme obesity with alveolar hypoventilation	1.36[1.32-1.4]	5.58×10^{-6}
Coxarthrosis,	1.07[1.04-1.11]	5.95×10^{-6}
All-cause Heart Failure	1.05[1.02-1.08]	6.56×10^{-6}
Hypertensive Heart Disease	1.12[1.09-1.15]	6.62×10^{-6}
Heart failure, not strict	1.05[1.02-1.08]	7.10×10^{-6}
Heart failure and BMI 25plus	1.05[1.02-1.08]	7.10×10^{-6}
Erysipelas	1.07[1.04-1.10]	8.41×10^{-6}
Type 2 diabetes with ophthalmic complications	1.15[1.12-1.19]	1.63×10^{-5}

Significance Bonferroni corrected threshold was defined at P = 0.05/2925 = 1.71. × 10^{-5}. OR=odds ratio [95% confidence interval]. KELA= Social Insurance Institution of Finland. DM1 = type 1 diabetes, IBD = inflammatory bowel disease, ILD = interstitial lung disease, CVD = cardiovascular disease, COPD = chronic obstructive pulmonary disease, BMI = body mass index.

Supplementary Table 6. Mendelian randomization suggesting a strong causal relationship between BMI and OSA.

Method	number of SNPs	beta	se	P-value
MR Egger	64	0.35	0.24	0.15
Weighted median	64	0.64	0.11	1.53×10^{-8}
Inverse variance weighted	64	0.67	0.08	8.32×10^{-16}
Simple mode	64	1.09	0.30	6.42×10^{-4}
Weighted mode	64	1.08	0.26	1.25×10^{-4}

Mendelian randomization (MR) analysis uses 64 independent body mass index (BMI) associated SNPs[33] as an instrumental variable to predict obstructive sleep apnoea (OSA).

Supplementary Table 7. Replication of the lead variants

RSID	G47.3 OSA UKBB	EAF UKBB	G47.3 OSA ANDIS	EAF ANDIS	G47.3 OSA EGCUT	EAF EGCUT	G47.3 OSA Combined
case/control	4471/403723		947/9829		4930/61056		10348/474608
rs9937053	OR=1.12 [1.07-1.17] $P=5.5 \times 10^{-7}$	0.42	OR=1.13 [1.03-1.24] P=0.01	0.46	OR=1.06 [1.02-1.11] $P=6.55 \times 10^{-3}$	0.48	OR=1.09 [1.06-1.12] $P=2.68 \times 10^{-9}$
rs10507084	OR=1.07 [0.98-1.17] P=0.15	0.06	OR=0.89 [0.73-1.06] P=0.18	0.07	OR=1.01 [0.94-1.09] P=0.80	0.09	OR=1.02 [0.96-1.08] P=0.51
rs185932673	OR=0.96 [0.73-1.26] P=0.74	0.01	Not defined in ANDIS	-	OR=1.09[0.84-1.43] P=0.52	0.01	OR=1.02[0.84-1.23] P=0.82
rs4837016	OR=0.97 [0.93-1.01] P=0.16	0.42	OR=0.87 [0.79-0.95] $P=4.6 \times 10^{-3}$	0.43	OR=0.98 [0.94-1.02] P=0.32	0.51	OR=0.96 [0.94-0.99] P=0.01
rs10928560	OR=1.00 [0.94-1.06] P=0.94	0.17	OR=1.01[0.90-1.15] P=0.38	0.18	OR=1.01 [0.96-1.07] P=0.60	0.21	OR=1.01 [0.97-1.05] P= 0.57

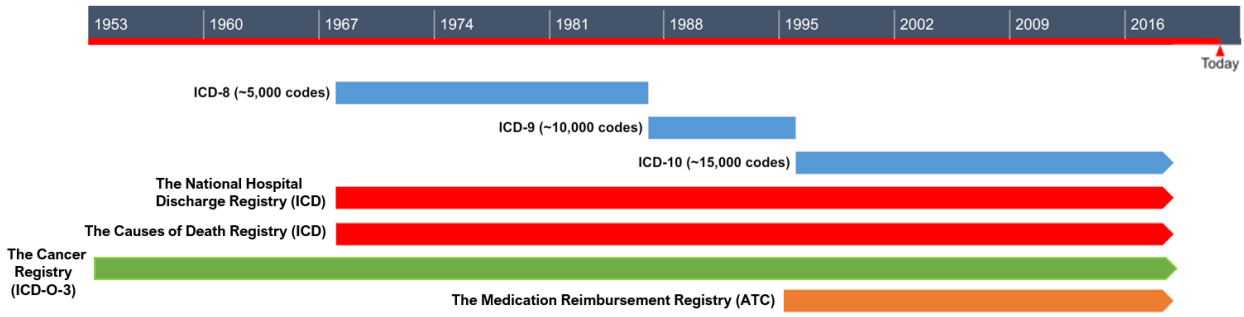
Inverse-variance weighted meta-analysis combining the results of the replication cohorts of the main FinnGen findings considering obstructive sleep apnoea (OSA). All results are presented without BMI-adjustment. EAF=Effect allele frequency, OR=odds ratio, [95% confidence interval], UKBB = UK Biobank, ANDIS = All New Diabetics in Scania, EGCUT = Estonian Genome Center - University of Tartu.

Supplementary Table 8.

	Model 1			Model 2		
	OR	CI	P-value	OR	CI	P-value
OSA_Q1	-	-	-	-	-	-
OSA_Q2	1.07	0.92-1.15	0.080	1.02	0.95-1.10	0.585
OSA_Q3	1.09	1.01-1.18	0.029	1.03	0.95-1.11	0.464
OSA_Q4	1.10	1.02-1.19	0.013	1.00	0.92-1.08	0.966
OSA_Q5	1.24	1.15-1.33	6.89×10^{-9}	1.11	1.03-1.20	4.70×10^{-3}

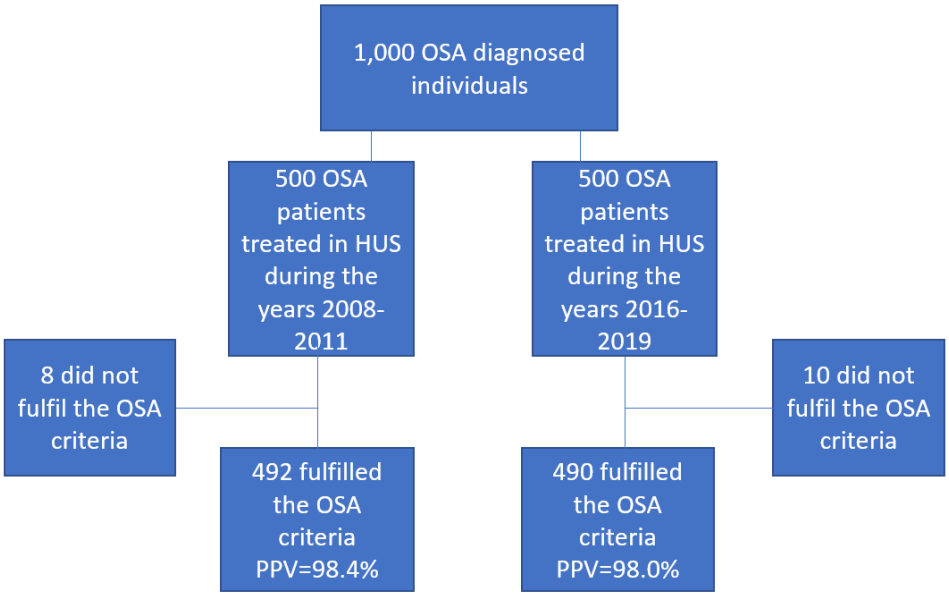
Obstructive sleep apnoea (OSA)'s polygenic risk score (PRS) predicts OSA in the UK Biobank (UKBB) data with P-value thresholded variants ($P < 5.0 \times 10^{-8}$, 5 variants). Model 1 is adjusted for age, sex and 10 first principal components (PC)s. Model 2 is adjusted for body mass index (BMI) in addition to covariates of Model 1. The OSA's PRS was stratified into quintiles and OSA_Q5 is the highest quintile. OR=odds ratio, CI = 95% confidence interval.

Supplementary Figure 1.



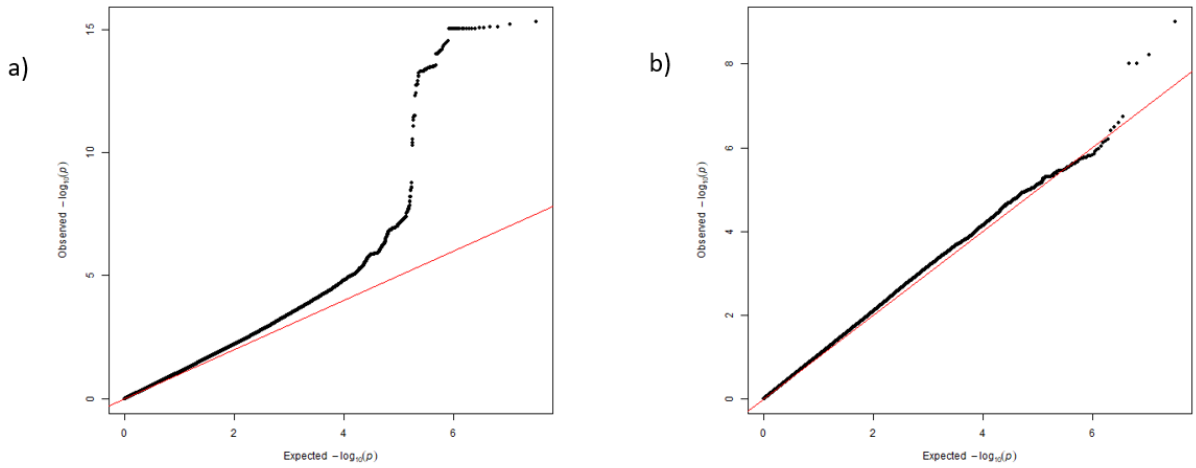
Nationwide registries combined by FinnGen. X-axel represents when a certain registry collection has started. Each arrow on Y-axis shows the origin of the ICD or ATC-code. ICD=International Statistical Classification of Diseases, ICD-O-3=International Classification of Diseases for Oncology, 3rd Edition, ATC=Anatomical Therapeutic Chemical Classification System.

Supplementary Figure 2.



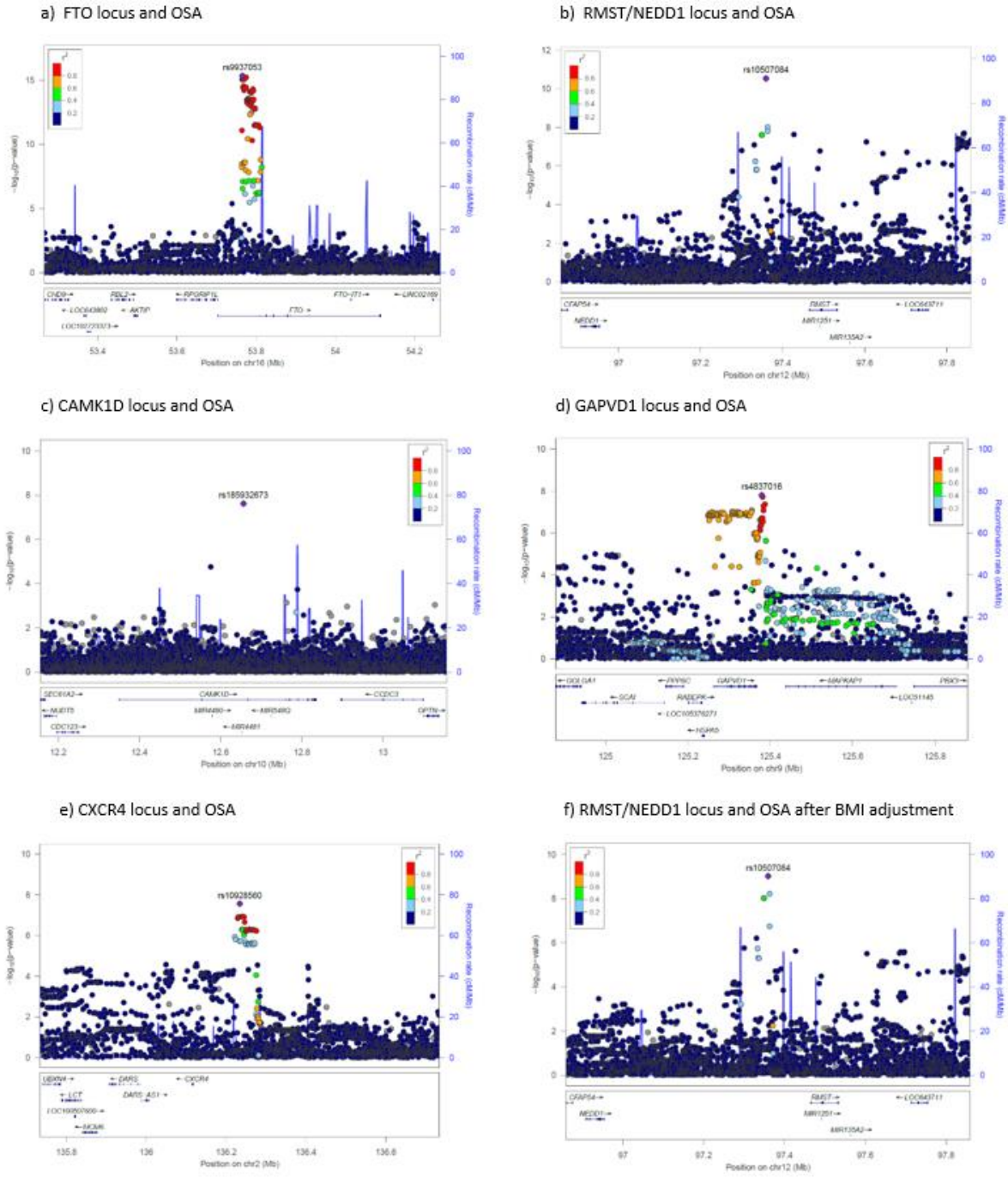
Obstructive sleep apnoea (OSA) diagnosis was validated using HUS's Hospital Discharge Registry collecting information of 1,000 patients and compared the registry data to the patient medical records. OSA diagnosis has a validity showing over 98% positive predictive value (PPV) when using International Classification criteria for Sleep Disorders for OSA [23]. AHI=apnoea-hypopnea-index, PPV=positive predictive value.

Supplementary Figure 3.



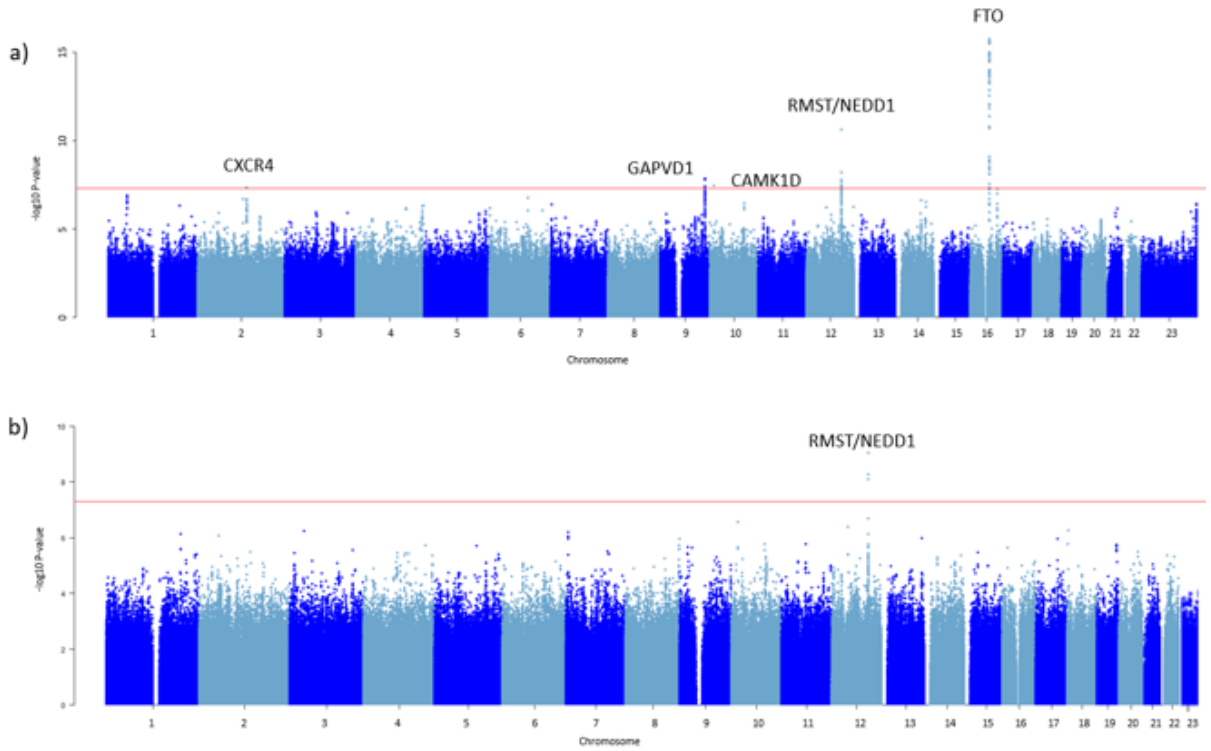
Quantile-Quantile (QQ) plot from the association analysis concerning a) obstructive sleep apnoea (OSA), λ = 1.12, b) body mass index (BMI) adjusted OSA, λ = 1.07. The observed P-values for each single nucleotide polymorphism (SNP) are sorted from largest to smallest and plotted against expected values from a theoretical χ^2-distribution.

Supplementary Figure 4.



Regional plots of 5 associations. Locus Zoom plots a-f show associated P-values on the $-\log_{10}$ scale on the vertical axis, and the chromosomal position along the horizontal axis. Purple diamonds indicate single nucleotide polymorphism (SNP) at each locus with the strongest associated evidence. Linkage disequilibrium (LD, r^2 values) between the lead SNP and the other SNPs are indicated by colour. *FTO*=Fat mass and obesity-associated protein, *RMST*=Rhabdomyosarcoma 2 associated transcript / *NEDD1*=NEDD1 gamma-tubulin ring complex targeting factor, *CAMK1D*=Calcium/calmodulin-dependent protein kinase ID, *GAPVD1*= GTPase activating protein and VPS9 domains 1, *CXCR4*=C-X-C Motif chemokine receptor 4.

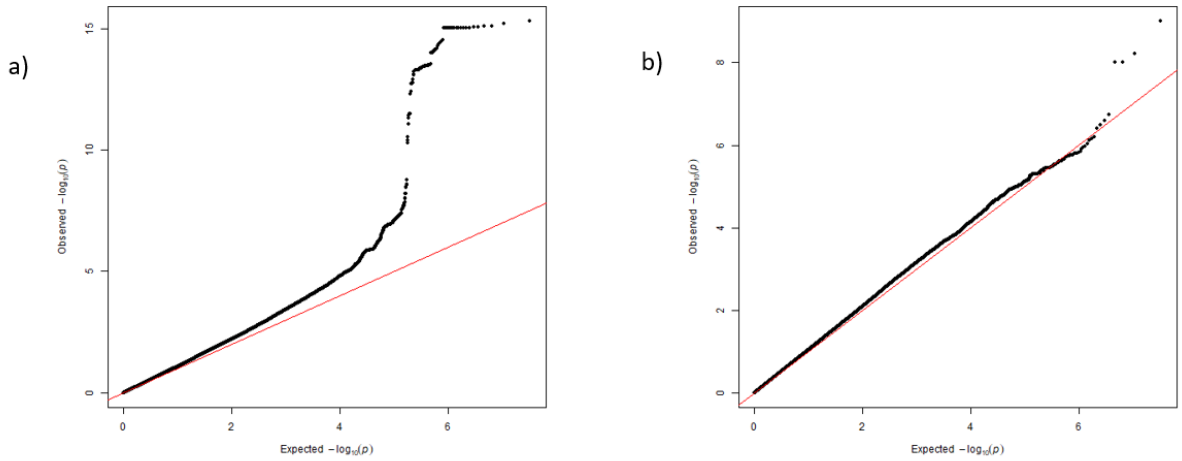
Supplementary Figure 5.



a) Manhattan plot for obstructive sleep apnoea (OSA) after excluding snorers from the control group with 16 761 OSA cases and 197 797 controls. For each genetic variant, the x-axis shows chromosomal position, while y-axis shows the $-\log_{10}$(P) value. The horizontal line indicates the genome-wide significance threshold of $P = 5 \times 10^{-8}$. Five genetic loci were identified at the genome-wide significance level. *CXCR4*=C-X-C motif chemokine receptor 4, *GAPVD1*= GTPase activating protein and VPS9 Domains 1, *CAMK1D*=Calcium/calmodulin-dependent protein kinase ID, *RMST*=Rhabdomyosarcoma 2 associated transcript / *NEDD1*=NEDD1 gamma-tubulin ring complex targeting factor, *FTO*=Fat mass and obesity-associated protein.

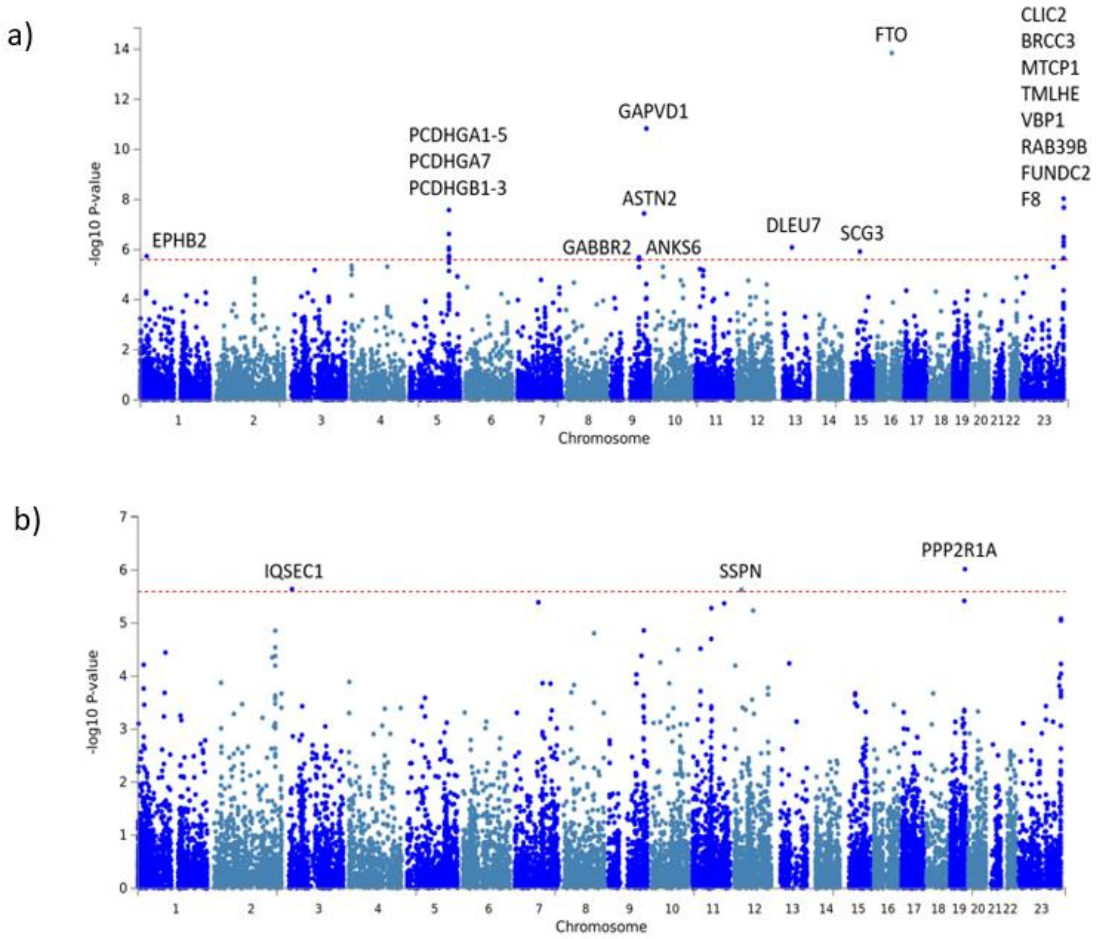
b) Manhattan plot for obstructive OSA after body mass index (BMI) adjustment, snorers excluded with 12 759 OSA cases and 144 583 controls. For each genetic variant, the x-axis shows chromosomal position, while y-axis shows the $-\log_{10}$(P) value. The horizontal line indicates the genome-wide significance threshold of $P = 5 \times 10^{-8}$. One genetic locus was identified at the genome-wide significance level. *RMST*=Rhabdomyosarcoma 2 associated transcript / *NEDD1*=NEDD1 gamma-tubulin ring complex targeting factor.

Supplementary Figure 6.



Quantile-Quantile (QQ) plot from the association analysis concerning a) obstructive sleep apnoea (OSA) after excluding snorers from the control group, $\lambda = 1.12$, b) body mass index (BMI) adjusted OSA after excluding snorers from the control group, $\lambda = 1.07$. The observed P-values for each single nucleotide polymorphism (SNP) are sorted from largest to smallest and plotted against expected values from a theoretical χ^2-distribution.

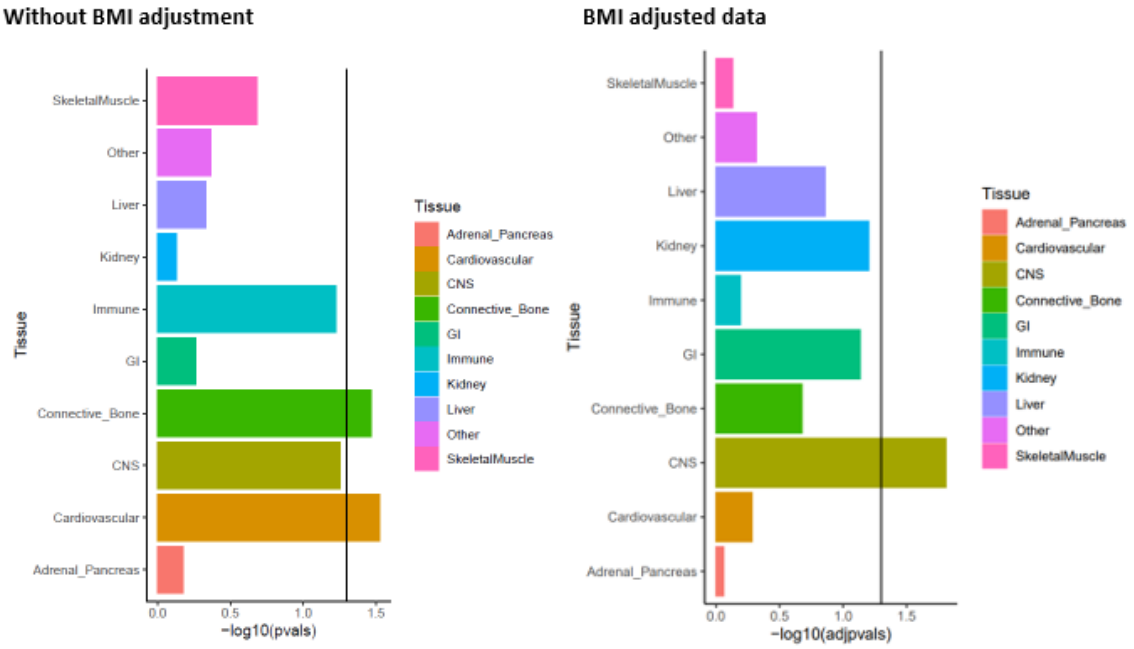
Supplementary Figure 7.



a) Manhattan plot of the gene-based test as computed by Multi-marker Analysis of GenoMic Annotation (MAGMA). Single nucleotide polymorphisms (SNP)s were mapped to 19,651 protein coding genes. Significance Bonferroni corrected threshold was defined at P = 0.05/19,651 = 2.54×10^{-6}. Primarily the same genes were identified as in single variant associations. For each annotated gene x-axis shows the chromosomal position while y-axis shows the −log10(P) value.
EPHB2=Ephrin type-B receptor 2, *PCDHGA*=Protocadherin gamma subfamily A, *PCDHGB*=Protocadherin gamma subfamily B, *GAPVD1*=GTPase activating protein and VPS9 domains 1, *ASTN2*= Astrotactin 2, *GABBR2*=Gamma-aminobutyric acid type A receptor subunit rho2, *ANKS6*=Ankyrin repeat and sterile alpha motif domain containing 6, *DLEU7*=Deleted in lymphocytic leukemia 7, *SCG3*=Secretogranin III, *FTO*=Fat mass and obesity-associated protein, *CLIC2*=Chloride intracellular channel 2, *BRCC3*=BRCA1/BRCA2-containing complex subunit 3, *MTCP1*=Mature T cell proliferation 1, *TMLHE*=Trimethyllysine hydroxylase, epsilon, *VBP1*= VHL binding protein 1, *RAB39B*=RAB39B, member RAS oncogene family, *FUNDC2*=FUN14 domain containing 2 and *F8*= Coagulation factor VIII.

b) Manhattan plot of the gene-based test as computed by MAGMA using body mass index (BMI) adjusted GWAS data. Single nucleotide polymorphisms (SNP)s were mapped to 19,651 protein coding genes. Significance Bonferroni corrected threshold was defined at P = 0.05/19,651 = 2.54×10^{-6}. For each annotated gene x-axis shows the chromosomal position while y-axis shows the −log10(P) value. *IQSEC1*= IQ motif and sec7 domain arfGEF 1, *SSPN*=Sarcospan, *PPP2R1A*= Protein phosphatase 2 scaffold subunit aalpha.

Supplementary Figure 8.



Tissue specific enrichment analysis. Stratified linkage disequilibrium (LD) score regression based on 1000 Genomes Project phase 1. LD was calculated by each tissue types. Each bar represents -log10 P-value for enrichment and computed for obstructive sleep apnoea (OSA) and body mass index (BMI) adjusted OSA. CNS=central nervous system, GI=gastrointestinal.