Supplemental Online Content

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This supplemental material has been provided by the authors to give readers additional information about their work.
eMethods 1. Description of Study Cohorts

Genetics of Diabetes Audit and Research in Tayside Scotland (GoDARTS)

GoDARTS is a population-based cohort which aims to identify genetic factors influencing the risk of developing type 2 diabetes (T2D), response to treatment and diabetes related complications. This study comprises 18,306 participants of European-heritage from Tayside, Scotland, of whom 10,149 participants have T2D, and 8,157 participants were diabetes-free at the time of recruitment. Genome-wide chip data are available for 7,857 T2D and 1,108 non-diabetes participants after quality control (QC) at the time of the present study. Median age of the cohort at baseline was 64 years. Participants provided consent for anonymous linkage of baseline and genetic data to routine electronic health records (EHR) including prescribing, laboratory data, mortality, hospital admissions and demography. This allows researchers to use this cohort as a longitudinal cohort for follow-up studies. Also, the participants provided consent to be re-contacted to participate in relevant studies in the future. This study was approved by the Tayside Committee for Medical Research (053/04).

Generation Scotland: Scottish Family Health Study (GS:SFHS)

GS:SFHS is a family-based study with socio-demographic, clinical and biological samples from 24,000 participants of European descent aged 18-98 years. Participants were recruited between 2006 and 2011 through general medical practices across Scotland and if they had at least one first-degree relative aged 18 or more willing to participate. This study received ethical approval from the NHS Tayside committee on research ethics (05/S1401/89). This cohort was set up in order to identify and understand the contribution of genetic factors to major common complex diseases such as cardiovascular disease, diabetes, stroke, mental illness, and cognitive dysfunction. The median age of this cohort was 47.9 years at the time of recruitment. Whole-genome genotyping data are available for 20,032 participants after the QC. All participants provided broad consent to use their genetic data for a wide range of medical research, and for linkage of routine health care records and re-contact for future research purposes.
United Kingdom Biobank (UKBB)

The UKBB is a population-based biomedical resource that aims to investigate the contribution of genetic and non-genetic determinants of diseases and outcomes to improve prevention, diagnosis, and treatment. This prospective cohort comprises 460,000 individuals of European ancestry from across the UK who were recruited 2006-2010 at age between 40 and 69 years. At the time of the recruitment, participants provided electronically signed consent to use their self-completed answers on socio-demographic, lifestyle, health-related information, and a range of physical measures. Also, participants reported if they were currently taking certain important classes of medication information through a touch-screen questionnaire followed by interview with a trained member of staff at the time of assessment centre. They provided the consent for their blood, urine, and saliva samples and longitudinal data through linkage of medical records including hospital inpatient data, death, and cancer register. This cohort received ethical approval from the North West Multi-centre REC (11/NW/0382).
eMethods 2. Self-completed Questionnaire Data

DOLORisk is an international collaboration involving members of established academic institutions and companies in Europe. They designed a questionnaire based on an agreed approach to NP phenotyping by International consensus (NeuroPPIC) led by the Neuropathic Pain Special Interest Group (NeuPSIG) of the International Association for the Study of Pain (IASP) to identify and characterise participants with NP. This self-completed questionnaire included information on pain history, pain medication, the severity of pain, quality of pain, pain location, pain interference, pain catastrophizing, health status, and quality of life, personality and lifestyle factors using validated questionnaire tools. DOLORisk Dundee is a part of the DOLORisk consortium and is based on the two pre-existing population-based cohorts: Genetics of Diabetes Audit and Research in Tayside Scotland and Generation Scotland: Scottish Family Health Study. Living participants of both the GoDARTS (N=5,236) and the GS:SFHS (N=20,221) who had given consent were contacted by mail with a letter of invitation, a Participant Information Leaflet (PIL) and DOLORisk paper questionnaire in optical character recognition (OCR) format labelled with a unique study code, along with a pre-paid return envelope through the Health Informatics Centre (HIC), a research support unit of the University of Dundee. The self-completed questionnaires from the participants were collected and managed by HIC through their secure mailing system and database. Questionnaire data were scanned, processed, and linked with anonymised participant IDs by HIC services for the DOLORisk study. The confidential personal data in the questionnaire were stored securely and processed and entered into the data entry system. Data handling and delivery were conducted by HIC in a secure safe-haven environment to confirm data security and protection. Data were provided in flat file format and released on secure HIC servers for research purposes. Phenotype information was extracted from the questionnaire data and linked to pre-existing genetic and demographic data.
Participants with chronic pain were identified using the following questions in the DOLORisk questionnaire: 1) “Are you currently troubled by pain or discomfort, either all the time or on and off?”; 2) “Are you currently taking medications specifically to treat pain or discomfort?”; and 3) “How long have you been suffering with this pain or discomfort?”.

Participants were also asked to specify characteristics of the pain that bothered them the most, using a validated screening tool, the self-complete version of DN4 questionnaire which comprises seven items: burning, painful cold, electric shocks, tingling, pins and needles, numbness and itching. A positive response (“Yes”) to each item scored as 1, and negative response (“No”) scored as 0. Participants gave positive answers to either the first or second question or both and who reported a pain duration at least three months and scored at least 3 out of 7 on the DN4 questionnaire were classified as possible NP cases. Participants who gave a negative response to the question about current pain at the time of completing the questionnaire, and who were currently not taking pain medications were selected as controls for a case-control GWAS on NP.

UKBB

At the time of this study, direct neuropathic pain phenotyping information is not available in the UKBB. We therefore used the self-reported medical history information records as a proxy for NP phenotype. Dispensed medications information was captured from the answers given by the participants at an assessment centre through an interview with a trained nurse. Hospital admissions data, including the diagnosis associated with the reason for any admission, were extracted by linking to the available nation-wide participants’ electronic records. On the basis of NeuPSIG guidelines for NP treatment, the most relevant medications to include for case identification were gabapentin, pregabalin and duloxetine to identify individuals with likely NP. Duloxetine is used to treat depression, but it is not the first choice of drug for depression disorders treatment (National Institute for Health and Care Excellence. First-choice antidepressant use in adults with depression or generalised anxiety disorder. 2013;1–4). We did not have records of other commonly used medicines, capsaicin, and lidocaine plasters, for
peripheral NP in the UKBB. Individuals who had no recorded history of having been prescribed any of these drugs were selected as controls for the GWAS. Apart from these drugs, subjects with a recorded history of amitriptyline, other tricyclic anti-depressants or tramadol were excluded from controls or cases, as these drugs are used to treat non-neuropathic pain and is not specific to NP. As gabapentin and pregabalin are used for epilepsy treatment, subjects were excluded from cases or controls if they had been admitted to hospital and formally diagnosed with epilepsy or if they had been recorded as receiving any of the following anti-epileptic medications: clobazam, clonazepam, eslicarbazepine, ethosuximide, lamotrigine, levetiracetam, lacosamide, perampanel, phenytoin, phenobarbital, sodium valproate, topiramate, and zonisamide. The International Classification of Diseases 10 (ICD-10) diagnosis codes, G40.0, G40.1, G40.2, G40.3, G40.4, G40.5, G40.6, G40.7, G40.8, G40.9, G41, and R56, were used to classify epilepsy and recurrent seizures in the hospital admissions records. These diagnosis codes were used to identify subjects with epilepsy in addition to their prescription history of gabapentin and pregabalin. Therefore, we have applied exclusion criteria to avoid possible misclassification bias. Moreover, cases and controls were matched for ancestry, and principal components to address any differences.
Genotype data for the GoDARTS\textsuperscript{1}, GS:SFHS\textsuperscript{9} and UKBB\textsuperscript{10} study populations were pre-existing and linked to the phenotype data. Blood samples were collected from the GoDARTS participants and used for genotyping by either Affymetrix 6.0 or Illumina Omni Express chips or Illumina Infinium Broad chips. Samples were excluded based on the following criteria: samples with a call rate less than 95%, the mismatch between clinical data and genotypic gender, batch effects, ancestry outliers using principal components, sample duplicates (IBD score > 0.8). The poor-quality markers were identified and excluded on the basis of monomorphism, Hardy-Weinberg Equilibrium (HWE) p-value less than $1 \times 10^{-6}$ and call rate less than 95%. PLINK 1.07\textsuperscript{11} was used to perform the quality assessment for genotyping data from all platforms. Blood or saliva were collected from the GS:SFHS participants to extract DNA. The samples were genotyped on the Illumina Human Omni Express Exome-8 v1.0 Bead chip, and Illumina Omni Express Exome-8 v1.2 Bead Chip. Quality control assessment was performed for genotyping data using GenABEL 1.7-6\textsuperscript{12} and PLINK 1.07\textsuperscript{11}. Samples were removed if they met the following criteria: samples with a call rate less than 98%, sample duplicates, and samples with gender discrepancies between reported and genotype data. SNVs with a call rate less than 98% HWE p-value less than $1 \times 10^{-6}$ and MAF < 1%. Ancestry outliers were identified by applying a six standard deviation cut-off in a principal component analysis using genotyping data from the GS:SFHS participants merged with 1,092 individuals from the 1,000 Genomes project\textsuperscript{13}. For the UKBB cohort, blood samples were collected to extract DNA from the participants on their visit to the UKBB assessment centre. Genome-wide genotyping was performed using two similar custom-designed genotyping arrays including UK Biobank Axiom (438,427 participants) and UK BiLEVE Axiom Affymetrix array (49,950 participants)\textsuperscript{10}. UKBB’s genotyping, QC, PCA and imputation methodology are described in detail elsewhere\textsuperscript{3}. We selected individuals of European ancestry in the UKBB based on principal component analysis (PCA) and self-reporting ancestry information.
The genotype data from all three cohorts were imputed against a haplotype reference consortium (HRC r1.1) reference panel in NCBI build 37\textsuperscript{14}. Post-imputation QC checks were conducted in all individual studies; monomorphic markers or those with imputation quality score < 0.4 were excluded. The genomic position of the markers is based on the NCBI human genome build 37.
eMethods 5. Genome-Wide Association Analyses and Meta-analyses

We conducted genome-wide association analyses in each of the three cohorts (GoDARTS, GS:SFHS and UKBB) separately. Both genotypic and imputed markers were tested for their association with NP using a linear mixed non-infinitesimal model in BOLT-LMM software to account for relatedness and population structure\textsuperscript{15}. This model assumes an additive genetic model that was corrected for age and gender. The beta estimates and SEs were converted and approximated to traditional odds ratios using the formula below (https://data.broadinstitute.org/alkesgroup/BOLT-LMM/).

\[
\log \text{OR} = \frac{\beta}{(\mu * (1 - \mu))}
\]

\(\mu\) denotes case proportion.

\[
SE_{\beta} = \frac{SE}{(\mu * (1 - \mu))}
\]

We conducted the meta-analysis of GWAS (GoDARTS and GS:SFHS) in stage1 using a fixed effect inverse variance weighted meta-analysis in GWAMA\textsuperscript{16}. The genomic control inflation factor lambda was 1.023. To increase study power, we combined the summary results from all three cohorts in stage2. We calculated genomic inflation factors (\(\lambda\)) in individual data sets for population stratification and applied genomic control. Prior to the meta-analysis, SNVs with low minor allele frequency (< 0.001), low imputation quality score (<0.4) and deviation from Hardy-Weinberg equilibrium (\(P<1\times10^{-6}\)) were removed from the summary GWAS results. The presence of heterogeneity between these studies was examined with the \(I^2\) statistic. Manhattan, Quantile-quantile (QQ) and forest plots were generated to visualize the GWAS results using R 3.4 and metafor R package\textsuperscript{17}. Regional association plots were created using LocusZoom\textsuperscript{18}. ScatterShot is a web application which was used to generate cluster plot images for directly typed variants in the from the UKBB dataset\textsuperscript{19}.
eMethods 6. In-silico Functional Annotation, Expression Quantitative Loci, and Colocalization Analysis

Variants were annotated using the University of California Santa Cruz (UCSC) Genome resource\(^{20}\) based on the Genome Reference Consortium Human genome build 37. Functional annotations of the significant SNVs and genetic risk loci were identified using functional mapping and annotation of genome-wide association studies\(^{21}\) (FUMA) which includes the annotation databases such as RegulomeDB\(^{22}\), HaploReg v1\(^{23}\) and Chromatin states\(^{24}\). ChromHMM state for 127 tissues/cell types indicates the functional effects of gene expression using expression quantitative trait loci (eQTLs) of various tissue types and chromatin interactions using Hi-C. The FINEMAP package was used to identify specific genetic variants that are likely to be causal from the summary statistics of the SNVs at the most significant locus by applying shotgun stochastic search algorithm\(^{25}\).

The Genotype-Tissue Expression (GTEx) v7\(^{26}\) database allow users to view gene expression data and eQTL results, and provides a controlled access system for de-identified individual-level genotype and clinical data. The GTEx project provides a resource that contains information about the relationship between human gene expression and genetic variation by analysing genotype and expression data obtained from multiple human tissues from donors. A recent study by Parisien et al. reported a database of eQTLs in a collection of human dorsal root ganglia and the association of dorsal root ganglion (DRG) eQTLs with pain-related genetic association results\(^{27}\). They also reported eGenes in DRGs, overlapping of DRG eQTLs with cis-eQTLs in brain and blood, and the association of HLA gene loci for DRG eQTLs and pain phenotypes. This can be used for interpreting human GWAS results with sensory components. The eQTL data of DRGs (https://humanpaingenetics.org/DRG-eQTLs/) are freely available online for downstream analysis GWAS focussed on pain and other sensory phenotypes. Brain xQTL serve database provides information about the association between genetic variants and molecular traits derived from the brain cortex\(^{28}\) (mostafavilab.stat.ubc.ca/xqtl).
Co-localisation analyses were conducted to test co-localisation between the expression of eQTL for brain tissues from GTEx v6 and the most significant SNV from this study using the R package “coloc” which is based on Bayesian statistical methods and generates five posterior probabilities (PP0, PP1, PP2, PP3, PP4) for each locus\textsuperscript{29}. We report the gene with the highest probability score (PP4) of being correlated with the most significant signal.

In Silico lookups for the most significant SNVs using GeneATLAS\textsuperscript{30} database to examine the association of pain related traits in the UKBB. It is a large database containing genetic association results for 118 quantitative and 660 case-control traits of 452,264 UKBB participants of European heritage.
eMethods 7. SNV-Based Heritability

SNV-based heritability of NP was estimated from GWAS summary statistics using Linkage Disequilibrium Score Regression (LDSC) (https://github.com/bulik/ldsc) software which accounts for linked markers and expects that each marker contributes equally to the phenotypic variance. The LDSC utilises SNVs across the whole genome that passed the imputation quality score, and strand ambiguity and slope from $\chi^2$ statistics regressed on GWAS SNVs’ LD scores. It does not require an individual study genotype data. We used full summary statistics data from the meta-analysis of GWAS to estimate the SNV-based heritability in a liability scale.\textsuperscript{31}
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### eTable 1. Sensitivity and Specificity of Neuropathic Pain Phenotyping Methods in GoDARTS

| Neuropathic pain phenotype | Cases | Controls | Total |
|---------------------------|-------|----------|-------|
| Cases                     | 257   | 44       | 301   |
| Controls                  | 63    | 358      | 421   |
| Total                     | 320   | 402      |       |

Sensitivity = 80.3%
Specificity = 89.0%
| RSID      | CHR | POS   | EA  | NEA | EAF  | OR  | OR_95L | P          | OR_95U  | P          | I²  | GENE     |
|-----------|-----|-------|-----|-----|------|-----|--------|------------|---------|------------|-----|---------|
| rs3699920026 | 12  | 98585582 | A   | G   | 0.005 | 1.683 | 1.404 | 2.023 | 1.30×10⁻⁶ | 0.00 | SLC25A3 |
| rs185663675 | 12  | 98602402 | A   | G   | 0.006 | 1.612 | 1.350 | 1.924 | 5.46×10⁻⁶ | 0.02 | SLC25A3 |
| rs17027891 | 12  | 98581935 | C   | T   | 0.007 | 1.602 | 1.351 | 1.901 | 7.50×10⁻⁶ | 0.10 | SLC25A3 |
| rs17027910 | 12  | 98586595 | A   | G   | 0.007 | 1.564 | 1.324 | 1.852 | 1.90×10⁻⁷ | 0.00 | SLC25A3 |
| rs7992766 | 13  | 49905672 | A   | C   | 0.747 | 1.091 | 1.054 | 1.141 | 1.22×10⁻⁷ | 0.31 | CAB39L |
| rs150900885 | 3   | 135174848 | C   | T   | 0.007 | 1.580 | 1.321 | 1.883 | 3.04×10⁻⁷ | 0.04 | EPHB1 |
| rs148034142 | 2   | 52976279 | C   | T   | 0.993 | 0.546 | 0.429 | 0.695 | 1.50×10⁻⁶ | -   | CHAC2   |
| rs77526294 | 8   | 49946568 | G   | A   | 0.944 | 1.176 | 1.103 | 1.255 | 1.54×10⁻⁶ | 0.00 | SNAI2   |
| rs4331318 | 15  | 91582257 | C   | T   | 0.948 | 0.853 | 0.799 | 0.909 | 2.01×10⁻⁶ | 0.05 | VPS33B  |
| rs7336018 | 13  | 49906514 | C   | T   | 0.759 | 1.090 | 1.053 | 1.129 | 2.11×10⁻⁶ | 0.48 | CAB39L  |
| rs78726778 | 6   | 65985758 | T   | C   | 0.933 | 0.863 | 0.813 | 0.916 | 2.24×10⁻⁶ | 0.71 | EYS     |
| rs79154996 | 6   | 25736698 | G   | A   | 0.975 | 0.781 | 0.707 | 0.864 | 2.26×10⁻⁶ | 0.35 | HIST1H2AA |
| rs79154996 | 6   | 25736698 | G   | A   | 0.975 | 0.781 | 0.707 | 0.864 | 2.26×10⁻⁶ | 0.35 | HIST1H2BA |
| rs7335286 | 13  | 49897739 | C   | A   | 0.248 | 0.918 | 0.887 | 0.951 | 2.53×10⁻⁶ | 0.51 | CAB39L  |
| rs7322201 | 13  | 49903046 | A   | G   | 0.747 | 1.088 | 1.051 | 1.126 | 2.64×10⁻⁶ | 0.51 | CAB39L  |
| rs145804345 | 12  | 98690315 | C   | T   | 0.994 | 0.631 | 0.523 | 0.761 | 2.66×10⁻⁶ | 0.00 | SLC9A7P1 |
| rs7985932 | 13  | 49911527 | A   | T   | 0.759 | 1.089 | 1.052 | 1.128 | 2.70×10⁻⁶ | 0.47 | CAB39L  |
| rs61692854 | 15  | 91582496 | C   | T   | 0.947 | 0.856 | 0.803 | 0.912 | 3.11×10⁻⁶ | 0.00 | VPS33B  |
| rs13210851 | 6   | 65906043 | C   | T   | 0.951 | 0.847 | 0.792 | 0.907 | 3.18×10⁻⁶ | 0.41 | EYS     |
| rs9535201 | 13  | 49897577 | A   | G   | 0.763 | 1.089 | 1.051 | 1.127 | 3.59×10⁻⁶ | 0.47 | CAB39L  |
| rs115353340 | 1   | 2882483 | C   | T   | 0.988 | 0.704 | 0.608 | 0.815 | 4.47×10⁻⁶ | 0.52 | 56kb 5' of ACTRT2 |
| rs34932751 | 6   | 25762241 | T   | C   | 0.974 | 0.793 | 0.720 | 0.874 | 4.55×10⁻⁶ | 0.29 | SLC17A4 |
| rs4688956 | 4   | 4343240 | C   | T   | 0.421 | 0.931 | 0.904 | 0.959 | 4.87×10⁻⁶ | 0.00 | -       |
| rs72980761 | 6   | 138175666 | G   | A   | 0.847 | 0.906 | 0.869 | 0.944 | 5.04×10⁻⁶ | 0.00 | -       |
| rs9535202 | 13  | 49901738 | A   | C   | 0.759 | 1.086 | 1.049 | 1.125 | 5.17×10⁻⁶ | 0.50 | CAB39L  |
| rs138847726 | 4   | 13020910 | C   | T   | 0.964 | 1.207 | 1.115 | 1.307 | 5.24×10⁻⁶ | 0.00 | -       |
| rs7992582 | 13  | 49905581 | A   | G   | 0.758 | 1.086 | 1.049 | 1.125 | 5.28×10⁻⁶ | 0.45 | CAB39L  |
| rs75616385 | 12  | 70527056 | G   | C   | 0.910 | 0.887 | 0.843 | 0.933 | 5.28×10⁻⁶ | 0.00 | CNOT2/KCNMB4 |
| rs4689309 | 4   | 4343725 | A   | T   | 0.421 | 0.931 | 0.904 | 0.960 | 5.34×10⁻⁶ | 0.00 | -       |
| rs150309683 | 16  | 70284053 | T   | C   | 0.972 | 0.800 | 0.729 | 0.879 | 5.36×10⁻⁶ | 0.10 | EXOSC6   |
| rs150309683 | 16  | 70284053 | T   | C   | 0.972 | 0.800 | 0.729 | 0.879 | 5.36×10⁻⁶ | 0.10 | AARS    |
| RSID        | CHR | POS     | EA | NEA | EAF  | OR   | OR_95L | OR_95U | P          | I²  | GENE                   |
|-------------|-----|---------|----|-----|------|------|--------|--------|------------|-----|------------------------|
| rs12578473 | 12  | 70530616| G  | T   | 0.910| 0.887| 0.843  | 0.933  | 5.92×10⁻⁶  | 0.00| CNOT2/KCNMB4          |
| rs78979790 | 12  | 70533571| A  | G   | 0.910| 0.887| 0.844  | 0.933  | 6.14×10⁻⁶  | 0.00| CNOT2/KCNMB4          |
| rs112906219| 6   | 138212862| C  | T   | 0.843| 0.908| 0.871  | 0.946  | 6.36×10⁻⁶  | 0.00| TNFAIP3               |
| rs77684790 | 12  | 70499715| C  | T   | 0.910| 0.888| 0.844  | 0.934  | 6.36×10⁻⁶  | 0.00| CNOT2/KCNMB4          |
| rs76712326 | 12  | 70501362| T  | C   | 0.910| 0.888| 0.844  | 0.934  | 6.42×10⁻⁶  | 0.00| CNOT2/KCNMB4          |
| rs960591   | 12  | 70512598| A  | G   | 0.910| 0.888| 0.844  | 0.934  | 6.59×10⁻⁶  | 0.00| CNOT2/KCNMB4          |
| rs4761295  | 12  | 70505474| T  | C   | 0.910| 0.888| 0.844  | 0.934  | 6.60×10⁻⁶  | 0.00| CNOT2/KCNMB4          |
| rs74438250 | 12  | 70507017| T  | G   | 0.910| 0.888| 0.844  | 0.934  | 6.65×10⁻⁶  | 0.00| CNOT2/KCNMB4          |
| rs77275828 | 12  | 70501844| C  | T   | 0.910| 0.888| 0.844  | 0.934  | 6.67×10⁻⁶  | 0.00| CNOT2/KCNMB4          |
| rs79376147 | 12  | 70512178| T  | A   | 0.910| 0.888| 0.844  | 0.934  | 6.68×10⁻⁶  | 0.00| CNOT2/KCNMB4          |
| rs4547147  | 12  | 70506188| G  | A   | 0.910| 0.888| 0.844  | 0.934  | 6.75×10⁻⁶  | 0.00| CNOT2/KCNMB4          |
| rs78244236 | 12  | 70503212| A  | G   | 0.911| 0.888| 0.844  | 0.934  | 6.82×10⁻⁶  | 0.00| CNOT2/KCNMB4          |
| rs7335804  | 13  | 49897815| G  | A   | 0.237| 0.921| 0.889  | 0.954  | 7.03×10⁻⁶  | 0.45| CAB39L                |
| rs79512135 | 12  | 70501072| T  | C   | 0.910| 0.888| 0.845  | 0.934  | 7.25×10⁻⁶  | 0.00| CNOT2/KCNMB4          |
| rs78313276 | 12  | 70510115| C  | T   | 0.910| 0.888| 0.845  | 0.935  | 7.38×10⁻⁶  | 0.00| CNOT2                |
| rs12775058 | 10  | 12240680| C  | T   | 0.973| 0.794| 0.720  | 0.876  | 7.42×10⁻⁶  | 0.00| NUDT5                |
| rs12775058 | 10  | 12240680| C  | T   | 0.973| 0.794| 0.720  | 0.876  | 7.42×10⁻⁶  | 0.00| CDC123               |
| rs56364844 | 15  | 91586112| T  | C   | 0.948| 0.859| 0.805  | 0.917  | 7.43×10⁻⁶  | 0.00| -                     |
| rs141456350| 12  | 70510197| C  | A   | 0.910| 0.889| 0.845  | 0.935  | 7.45×10⁻⁶  | 0.00| CNOT2                |
| rs2118427  | 12  | 70508552| C  | T   | 0.910| 0.889| 0.845  | 0.935  | 7.56×10⁻⁶  | 0.00| CNOT2                |
| rs75267777 | 12  | 70501154| A  | G   | 0.910| 0.889| 0.845  | 0.935  | 7.61×10⁻⁶  | 0.00| CNOT2                |
| rs71507307 | 9   | 12233221| G  | A   | 0.964| 1.206| 1.113  | 1.307  | 7.96×10⁻⁶  | 0.00| -                     |
| rs72761306 | 15  | 91584219| G  | A   | 0.948| 0.860| 0.807  | 0.918  | 8.06×10⁻⁶  | 0.00| -                     |
| rs1025692  | 12  | 70513806| A  | G   | 0.910| 0.889| 0.845  | 0.935  | 8.19×10⁻⁶  | 0.00| CNOT2/KCNMB4          |
| rs112990863| 3   | 88714964| T  | A   | 0.007| 1.461| 1.243  | 1.721  | 8.99×10⁻⁶  | 0.85| EPHA3                 |

CHR, chromosome; EA, effect allele; EAF, Effect allele frequency; I², heterogeneity measure; N, number of samples; NEA, noneffect allele; OR, odds ratio; OR_95L, 95% lower confidence interval; OR_95U, 95% upper confidence interval; POS, base position based on NCBI build 37; GoDARTS, Genetics of Diabetes Audit and Research in Tayside Scotland; GS:SFHS, Generation Scotland: Scottish Family Health Study; Stage 1 meta-analysis; UKBB, United Kingdom Biobank.
eTable 3. Sensitivity Analysis of the Most Significant SNVs Associated With NP in the Stage 2 Meta-analysis

| SNVs            | GS:SFHS + UKBB | GoDARTS + UKBB |
|-----------------|----------------|---------------|
|                 | OR (95% CI)    | P             | OR (95% CI)    | P             |
| rs369920026     | 1.27 (1.15-1.41) | 2.48x10^-8   | 1.28 (1.11-1.48) | 1.63x10^-4   |
| rs185663675     | 1.25 (1.13-1.39) | 1.86x10^-7   | 1.28 (1.11-1.47) | 7.56x10^-4   |
| rs17027891      | 1.24 (1.12-1.37) | 1.34x10^-7   | 1.31 (1.13-1.51) | 1.56x10^-4   |
| rs17027910      | 1.23 (1.11-1.37) | 1.71x10^-7   | 1.27 (1.08-1.49) | 1.58x10^-4   |
| rs7992766       | 1.01 (1.06-1.14) | 2.27x10^-7   | 1.08 (1.02-1.14) | 6.2x10^-3    |
| rs112990863     | 1.19 (1.07-1.13) | 4.88x10^-6   | 1.01 (0.77-1.27) | 0.897         |

GoDARTS, Genetics of Diabetes Audit and Research in Tayside Scotland; GS:SFHS, Generation Scotland; Scottish Family Health Study.
eTable 4. The Most Significant SNVs Associated With NP From The Overall Meta-analysis and Related Traits

| SNP-Associated SNV/Gene | Relevant traits association | Effect allele | OR / Beta | P-value | Source |
|-------------------------|-----------------------------|--------------|-----------|---------|--------|
| rs369920026 / rs185663675 SLC25A3 | Viral hepatitis | A | 3.34 / 0.002 | 0.001 | GeneATLAS database using UKBB30 |
|                          | Disc problem | A | 1.23 / 0.003 | 0.04 |        |
|                          | Fibromyalgia | A | 0.48 / -0.001 | 0.04 |        |
| rs17027891 / rs17027910 SLC25A3 | Disc problem Fibromyalgia | C | 1.28 / 0.004 | 0.01 | GeneATLAS database using UK Biobank30 |
|                          |                | C | 0.47 / -0.001 | 0.02 |        |
| rs7992766 / CAB39L | Lymphocyte count | C | NA / -0.004 | 0.0002 | GeneATLAS database using UK Biobank30 |
|                          | Alcohol intake frequency | C | NA / -0.011 | 0.0004 |        |
|                          | Ulcer of lower limb | C | 0.858 / -0.0003 | 0.0014 |        |
|                          | Disorders of brain | C | 0.907 / -0.0003 | 0.01 |        |
|                          | Neck/shoulder pain for 3+ months | C | 0.961 / -0.039 | 0.0012 | UK Biobank Neale v2 (2018) (http://www.nealelab.is/uk-biobank) |
| rs1509000085 / EPHB1 | Back pain | C | 1.49 / -0.001 | 0.066 | GeneATLAS database using UK Biobank30 |
|                          | Pain and other conditions associated with female genital organs and menstrual cycle | C | 1.52 / 0.006 | 0.007 |        |
|                          | Disorders of lipoprotein metabolism | C | 0.886/0.009 | 0.0089 |        |
|                          | Sciatica | C | 0.767/0.002 | 0.064 |        |
|                          | Headaches for 3+ months | C | 1.22/0.195 | 0.005 |        |
### eTable 5. Expression Quantitative Trait Loci Information for the Most Significant Genetic Loci Associated With NP in Human Dorsal Root Ganglia (eQTL DRG) and Brain Cortex (brain xQTL serve)

| SNV                  | TagSNV       | Beta | P-value       | Gene          | Tissue       | Association with NP SNV / Tag SNV |
|----------------------|--------------|------|---------------|---------------|--------------|-----------------------------------|
| rs7334929:T:G        | rs7992766:A:G| -0.23| 8.9×10^{-7}   | CDADC1/ CAB39L | DRG          | 0.002 / 1.22×10^{-7}               |
| rs7992766:A:G        |              |      |               | CAB39L        | Brain Cortex | 8.51×10^{-21}                     |
| rs10049228:T:C       | rs11712544:G:A| 0.12 | 4.9×10^{-5}   | EPHB1         | DRG          | 0.009/0.006                       |

DRG, dorsal root ganglia.
**eTable 6. Most Significant SNVs ($P < 5 \times 10^{-5}$) Associated With NP in Stage 1 (GoDARTS and GS:SFHS) and UKBB Study**

| RSID       | CHR | POS   | EA / NEA | EAF | Study    | OR   | OR_95L | OR_95U | P value   | $I^2$ | N        | GENE                  |
|------------|-----|-------|----------|-----|----------|------|--------|--------|-----------|-------|----------|-----------------------|
| rs112990863| 3   | 88714964 | T/A      | 0.009 | Stage 1  | 1.743 | 1.434  | 2.112  | 3.73×10^{-08} | 0.960 | 2.112 | EPHA3                 |
| rs150675307| 2   | 100319170 | T/G      | 0.991 | Stage 1  | 0.546 | 0.436  | 0.685  | 1.59×10^{-07} | 0.094 | 0.94   | AFF3                  |
| rs182827559| 3   | 140357428 | T/C      | 0.968 | Stage 1  | 0.736 | 0.656  | 0.826  | 3.09×10^{-07} | 0.111 | 0.91   | TRIM42                |
| rs145943613| 3   | 88731531 | T/G      | 0.992 | Stage 1  | 0.549 | 0.438  | 0.689  | 3.61×10^{-07} | 0.00  | 3.273 | EPHA3                 |
| rs72977016  | 3   | 140370012 | C/T      | 0.967 | Stage 1  | 0.752 | 0.672  | 0.841  | 9.91×10^{-07} | 0.00  | 3.978 | TRIM42                |
| rs141384665 | 12  | 91136799 | T/G      | 0.979 | Stage 1  | 0.706 | 0.615  | 0.809  | 1.05×10^{-06} | 0.16  | 3.978 | 66kb 5' of RP11-20L19.1 |
| rs150900085 | 3   | 135174847 | C/T      | 0.007 | Stage 1  | 1.671 | 1.342  | 2.071  | 1.31×10^{-06} | 0.00  | 4.076 | EPHB1                 |
| rs4648390   | 1   | 2700372  | C/T      | 0.825 | Stage 1  | 0.880 | 0.836  | 0.926  | 1.44×10^{-06} | 0.00  | 4.076 | TTC34                 |
| rs182181935 | 9   | 13277439 | G/T      | 0.996 | Stage 1  | 0.444 | 0.321  | 0.614  | 1.46×10^{-06} | 0.121 | 0.15  | MPDZ                  |
| rs74546839  | 3   | 140259531 | T/C      | 0.952 | Stage 1  | 0.801 | 0.732  | 0.875  | 1.62×10^{-06} | 0.00  | 4.076 | CLSTN2                |

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| RSID     | CHR | POS     | EA / NEA | EAF | Study        | OR  | OR_95L | OR_95U | P value       | I²  | N      | GENE |
|----------|-----|---------|----------|-----|--------------|-----|---------|---------|---------------|-----|--------|------|
| rs28647750 | 1   | 2632016 | C/G      | 0.826 | Stage 1 UKBB | 0.880 | 0.836 | 0.926 | 1.68×10⁻⁶   | 0.00 | 4,076  | TTC34 |
| rs7992766  | 13  | 49905672| A/C      | 0.750 | Stage 1 UKBB | 1.097 | 1.051 | 1.145 | 2.41×10⁻⁵   | 0.23 | 3,978  | CAB39L |

CHR, chromosome; EA, effect allele; EAF, Effect allele frequency; I², heterogeneity measure; N, number of samples; NEA, noneffect allele; OR, odds ratio; OR_95L, 95% lower confidence interval; OR_95U, 95% upper confidence interval; POS, base position based on NCBI build 37; GoDARTS, Genetics of Diabetes Audit and Research in Tayside Scotland; GS:SFHS, Generation Scotland: Scottish Family Health Study; Stage 1, meta-analysis of GoDARTS and GS:SFHS GWAS; UKBB, United Kingdom BioBank.
| RSID     | CHR | POS    | EA | NEA | EAF  | Study         | OR  | OR_95L | OR_95U | P_unadj | I²   | GENE     |
|----------|-----|--------|----|-----|------|---------------|-----|--------|--------|---------|------|----------|
| rs1901531| 15  | 45005381| T  | C   | 0.817| Stage 1       | 0.804| 0.899  | 0.991  | 0.023   | 0.0  | B2M      |
|          |     |        |    |     |      | UKBB         | 1.002| 0.939  | 1.069  | 0.951   |      |          |
|          |     |        |    |     |      | Stage 2      | 0.964| 0.928  | 1.003  | 0.041   | 0.1  |          |
| rs6986153| 8   | 108072044| G  | A   | 0.207| Stage 1      | 0.981| 0.936  | 1.028  | 0.427   | 0.2  | HMGB1P46 |
|          |     |        |    |     |      | UKBB         | 0.938| 0.884  | 0.995  | 0.034   |      |          |
|          |     |        |    |     |      | Stage 2      | 0.964| 0.929  | 1.000  | 0.057   | 0.2  |          |
| rs267206 | 6   | 7860815 | C  | T   | 0.185| Stage 1      | 0.975| 0.928  | 1.025  | 0.330   | 0.0  | BMP6     |
|          |     |        |    |     |      | UKBB         | 0.947| 0.890  | 1.008  | 0.086   |      |          |
|          |     |        |    |     |      | Stage 2      | 0.964| 0.927  | 1.002  | 0.071   | 0.0  |          |
| rs1800629| 6   | 31543031| G  | A   | 0.803| Stage 1      | NA  | NA     | NA     | NA      | 0.0  | TNF-A    |
|          |     |        |    |     |      | UKBB         | 1.056| 0.994  | 1.122  | 0.076   |      |          |
|          |     |        |    |     |      | Stage 2      | 1.056| 0.994  | 1.122  | 0.076   |      |          |
| rs7033149| 9   | 32398234| G  | T   | 0.142| Stage 1      | 1.071| 1.014  | 1.129  | 0.015   | 0.0  | ACO1     |
|          |     |        |    |     |      | UKBB         | 0.982| 0.917  | 1.053  | 0.622   |      |          |
|          |     |        |    |     |      | Stage 2      | 1.036| 0.993  | 1.081  | 0.106   | 0.1  |          |
| rs887797 | 17  | 64579445| G  | A   | 0.679| Stage 1      | 1.005| 0.965  | 1.047  | 0.796   | 0.6  | PRKCA    |
|          |     |        |    |     |      | UKBB         | 1.053| 0.999  | 1.108  | 0.051   |      |          |
|          |     |        |    |     |      | Stage 2      | 1.023| 0.991  | 1.056  | 0.165   | 0.6  |          |
| rs71647933| 1   | 33945601| A  | G   | 0.825| Stage 1      | 0.967| 0.919  | 1.017  | 0.201   | 0.0  | ZSCAN20  |
|          |     |        |    |     |      | UKBB         | 0.979| 0.919  | 1.044  | 0.520   |      |          |
|          |     |        |    |     |      | Stage 2      | 0.972| 0.934  | 1.011  | 0.166   | 0.0  |          |
| rs4680   | 22  | 19951271| G  | A   | 0.484| Stage 1      | 0.952| 0.917  | 0.989  | 0.013   | 0.5  | COMT     |
|          |     |        |    |     |      | UKBB         | 1.021| 0.976  | 1.074  | 0.321   |      |          |
|          |     |        |    |     |      | Stage 2      | 0.979| 0.951  | 1.009  | 0.176   | 0.7  |          |
| rs12478318| 2   | 167133540| T  | G   | 0.996| Stage 1     | 0.806| 0.591  | 1.103  | 0.186   | 0.0  | SCN9A    |
|          |     |        |    |     |      | UKBB         | 1.027| 0.617  | 1.712  | 0.920   |      |          |
|          |     |        |    |     |      | Stage 2      | 0.807| 0.590  | 1.102  | 0.187   | 0.0  |          |
| rs4369876 | 2   | 167129256| C  | A   | 0.996| Stage 1     | 0.995| 0.956  | 1.034  | 0.787   | 0.0  | SCN9A    |
|          |     |        |    |     |      | UKBB         | 1.062| 1.012  | 1.115  | 0.014   |      |          |
|          |     |        |    |     |      | Stage 2      | 1.021| 0.990  | 1.052  | 0.196   | 0.4  |          |
| rs1800795| 7   | 22766645| C  | G   | 0.430| Stage 1     | 0.927| 0.822  | 1.044  | 0.221   | 0.0  | IL6      |
|          |     |        |    |     |      | UKBB         | 0.960| 0.821  | 1.123  | 0.611   |      |          |
|          |     |        |    |     |      | Stage 2      | 0.939| 0.854  | 1.033  | 0.203   | 0.0  |          |
| rs16966334| 15  | 45003114| C  | G   | 0.976| Stage 1     | NA  | NA     | NA     | NA      | 0.0  | B2M      |
|          |     |        |    |     |      | UKBB         | NA  | NA     | NA     | NA      |      |          |
|          |     |        |    |     |      | Stage 2      | NA  | NA     | NA     | NA      |      |          |

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| RSID     | CHR | POS     | EA | NEA | EAF | Study       | OR   | OR_95L | OR_95U | P_unadj | I²   | GENE |
|----------|-----|---------|----|-----|-----|-------------|------|--------|--------|---------|------|------|
| rs8007267 | 14  | 55378991| C  | T   | 0.822| Stage 1 UKBB | 1.045| 0.994  | 1.099  | 0.901   | 0.6  | GCH1 |
| rs3024505 | 1   | 206939904| G  | A   | 0.846| Stage 1 UKBB | 1.014| 0.988  | 1.097  | 0.137   | 0.0  | IL10 |
| rs13072552| 3   | 148913126| G  | T   | 0.922| Stage 1 UKBB | 0.960| 0.893  | 1.032  | 0.283   | 0.0  | CP   |
| rs3750904 | 2   | 167055393| T  | C   | 0.996| Stage 1 UKBB | 0.859| 0.641  | 1.154  | 0.323   | 0.0  | FXN  |
| rs2026739 | 9   | 32418237| G  | T   | 0.288| Stage 1 UKBB | 1.026| 0.985  | 1.069  | 0.227   | 0.6  | ACO1 |
| rs270388  | 6   | 7772340 | T  | G   | 0.159| Stage 1 UKBB | 0.991| 0.939  | 1.044  | 0.730   | 0.5  | BMP6 |
| rs2284017 | 22  | 37096927| T  | C   | 0.436| Stage 1 UKBB | 1.066| 0.968  | 1.046  | 0.749   | 0.3  | CACNG2 |
| rs8007201 | 14  | 55324848| A  | G   | 0.669| Stage 1 UKBB | 1.002| 0.963  | 1.043  | 0.909   | 0.4  | GCH1 |
| rs480760  | 3   | 195798258| T  | C   | 0.036| Stage 1 UKBB | 1.001| 0.906  | 1.106  | 0.983   | 0.0  | TFRC |
| rs13075921| 3   | 148915628| T  | C   | 0.896| Stage 1 UKBB | 0.981| 0.925  | 1.039  | 0.502   | 0.0  | CP   |
| rs927312  | 6   | 8559593 | G  | C   | 0.868| Stage 1 UKBB | 1.001| 0.953  | 1.052  | 0.898   | 0.0  | HLA-DQB1*03:02 |
| rs224446  | 12  | 51381718| C  | T   | 0.849| Stage 1 UKBB | 1.001| 0.953  | 1.052  | 0.898   | 0.04 | SLC11A2 |
| rs3816893 | 3   | 148927711| A  | T   | 0.900| Stage 1 UKBB | 0.990| 0.928  | 1.057  | 0.771   | 0.0  | CP   |

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| RSID | CHR | POS   | EA | NEA | EAF | Study     | OR  | OR_95L | OR_95U | P_unadj | I²  | GENE |
|------|-----|-------|----|-----|-----|-----------|-----|--------|--------|----------|-----|------|
| rs11674595 | 2   | 102610992 | T | C   | 0.736 | Stage 2  | 0.984 | 0.935  | 1.034  | 0.530    | 0.0 |       |
|       |     |        |    |     |     | Stage 1 UKBB | 0.993 | 0.950  | 1.038  | 0.764    | 0.0 | IL1R2 |
|       | 8   | 21708824 | G | A   | 0.719 | Stage 1 UKBB | 1.010 | 0.976  | 1.045  | 0.572    | 0.0 |       |
|       |     |        |    |     |     | Stage 2  | 1.010 | 0.977  | 1.044  | 0.579    | 0.0 | GFRA2 |
|       | 7   | 22771039 | T | A   | 0.989 | Stage 1 UKBB | 1.004 | 0.962  | 1.048  | 0.838    | 0.0 | IL6   |
|       | 8   | 21711431 | T | C   | 0.719 | Stage 1 UKBB | 1.012 | 0.960  | 1.045  | 0.933    | 0.0 | GFRA2 |
|       | 6   | 7854236  | G | A   | 0.615 | Stage 1 UKBB | 1.014 | 0.976  | 1.055  | 0.479    | 0.0 | BMP6  |
|       | 2   | 167160735 | A | G   | 0.996 | Stage 1 UKBB | 1.054 | 0.671  | 1.300  | 0.842    | 0.0 |       |
|       | 5   | 20245554 | C | T   | 0.939 | Stage 1 UKBB | 0.992 | 0.918  | 1.074  | 0.693    | 0.0 |       |
|       |     |        |    |     |     | Stage 2  | 1.011 | 0.951  | 1.076  | 0.729    | 0.0 | CDH18 |
|       | 9   | 71659280 | C | T   | 0.958 | Stage 1 UKBB | 1.005 | 0.914  | 1.105  | 0.745    | 0.1 | FXN   |
|       | 8   | 21717841 | G | T   | 0.751 | Stage 1 UKBB | 0.995 | 0.952  | 1.040  | 0.841    | 0.0 | GFRA2 |
|       | 14  | 55360139 | T | A   | 0.797 | Stage 1 UKBB | 1.025 | 0.977  | 1.075  | 0.321    | 0.0 | GCH1  |
|       | 6   | 154360797 | A | G   | 0.874 | Stage 1 UKBB | 1.024 | 0.961  | 1.084  | 0.502    | 0.1 | oprm1 |
|       | 1   | 206944645 | T | C   | 0.199 | Stage 1 UKBB | 1.002 | 0.954  | 1.051  | 0.943    | 0.2 | IL10  |
|       | 22  | 37105180 | G | A   | 0.740 | Stage 1 UKBB | 0.971 | 0.927  | 1.013  | 0.179    | 0.0 | CACNG2 |
| RSID     | CHR | POS   | EA  | NEA | EAF  | Study       | OR   | OR_95L | OR_95U | P_unadj | I² | GENE |
|----------|-----|-------|-----|-----|------|-------------|------|--------|--------|---------|----|------|
| rs1518110 | 1   | 206944861 | A   | C   | 0.199 | Stage 1 UKBB | 1.056 | 0.999  | 1.115  | 0.054   | 0.5 |       |
|          |     |       |     |     |      | Stage 2 UKBB | 1.003 | 0.969  | 1.038  | 0.872   |     |       |
| rs1800896 | 1   | 206946897 | T   | C   | 0.489 | Stage 1 UKBB | 1.004 | 0.967  | 1.042  | 0.832   | 0.0 |       |
|          |     |       |     |     |      | Stage 2 UKBB | 0.988 | 0.942  | 1.037  | 0.641   |     |       |
| rs12596162 | 16  | 87151495 | C   | T   | 0.691 | Stage 1 UKBB | 1.002 | 0.970  | 1.035  | 0.909   | 0.0 | PRKCA |
| rs3917332 | 2   | 102796524 | A   | T   | 0.197 | Stage 1 UKBB | 1.004 | 0.945  | 1.036  | 0.660   | 0.0 | IL1R1 |
| rs1878672 | 1   | 206943713 | G   | C   | 0.489 | Stage 1 UKBB | 1.004 | 0.967  | 1.042  | 0.826   | 0.1 |       |
| rs752688  | 14  | 55311569 | C   | T   | 0.789 | Stage 1 UKBB | 1.002 | 0.957  | 1.050  | 0.917   | 0.0 | IL10  |
| rs4411417 | 14  | 55320563 | T   | C   | 0.789 | Stage 1 UKBB | 1.002 | 0.956  | 1.050  | 0.917   | 0.1 | GCH1  |
| rs2718796 | 3   | 133479200 | G   | C   | 0.025 | Stage 1 UKBB | 0.942 | 0.835  | 1.063  | 0.346   | 0.0 | TF    |
| rs3024496 | 1   | 206941864 | A   | G   | 0.490 | Stage 1 UKBB | 1.005 | 0.967  | 1.043  | 0.803   | 0.0 | IL10  |
| rs10483639 | 14  | 55306457 | G   | C   | 0.788 | Stage 1 UKBB | 0.999 | 0.953  | 1.046  | 0.956   | 0.1 | GCH1  |
| rs2284015 | 22  | 37096573 | C   | G   | 0.741 | Stage 1 UKBB | 0.972 | 0.929  | 1.015  | 0.211   | 0.5 | CACNG2|
| rs4820242 | 22  | 36982675 | G   | A   | 0.385 | Stage 1 UKBB | 1.012 | 0.972  | 1.053  | 0.558   | 0.1 | CACNG2|

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eTable 8. Combined Analysis of the Present Study Summary Statistics (Stage 1 and Stage 2) and the Original Study Summary Statistics

| SNV     | Candidate gene | Effect allele (EAF) | Stage 1 (GoDARTS + GS:SFHS) OR (95% CI) / P<sub>unadj</sub> | Previously reported statistics (Kallianpur et al. 2014) OR (95% CI) / P<sub>unadj</sub> | Stage 1 meta-analysis + previous study OR (95% CI) / P<sub>unadj</sub> | UKBB OR (95% CI) / P<sub>unadj</sub> | Stage 2 meta-analysis OR (95% CI) / P<sub>unadj</sub> | Stage 2 meta-analysis + previous study OR (95% CI) / P<sub>unadj</sub> |
|---------|----------------|--------------------|-------------------------------------------------|-------------------------------------------------|-------------------------------------------------|---------------------------------|------------------------|---------------------------------|---------------------------------|
| rs1901531 | B2M            | C                  | 1.02(0.98-1.07) /0.023                           | 1.60(1.06-2.41) /0.028                           | 1.07(1.02-1.13) /0.004                           | 1.00(0.94-1.07)/0.95       | 1.01(1.00-1.08) /0.040       | 1.04(1.00-1.09) /0.028       |
| rs7033149 | ACO1           | G                  | 1.069(1.014-1.128) /0.015                         | 1.60(1.11-2.40) /0.012                           | 1.08(1.03-1.14) /0.004                           | 0.98(0.92-1.05)/0.62       | 1.03(0.99-1.08)/0.111       | 1.04(1.00-1.08) /0.071       |

EAF, effect allele frequency; OR, odds ratio; OR <sub>95L</sub>, 95% lower confidence interval; OR <sub>95U</sub>, 95% upper confidence interval; GoDARTS, Genetics of Diabetes Audit and Research in Tayside Scotland; GS:SFHS, Generation Scotland: Scottish Family Health Study; UKBB, United Kingdom Biobank.
eFigure 1. Quantile-Quantile Plot for the Results of Stage 2 Meta-analysis (GoDARTS, GS:SFHS, and UKBB) GWAS

X-axis represents $-\log_{10}$ expected P-values and Y-axis represents $-\log_{10}$ observed P-values.
eFigure 2. Scattershot of Directly Typed Variant at Chromosome 12q23.1 From the UKBB Data
eFigure 3. Multitissue eQTL Comparison for a Promising Candidate SNV for NP and Correlation With Expression of CAB39L
eFigure 4. Plots Showing the P Value of Association Tests for SNVs With Possible NP in Stage 1 Meta-analysis (GoDARTS and GS:SFHS)

A) Manhattan plot and B) Quantile-Quantile plot.
eFigure 5. Regional Association Plot of an Index SNV in Stage 1 Meta-analysis (GoDARTS and GS:SFHS)