Meta-Analysis of Genome-Wide Association Studies Identifies Six New Loci for Serum Calcium Concentrations


1 National Heart, Lung, and Blood Institute’s Framingham Heart Study and Center for Population Studies, Framingham, Massachusetts, United States of America, 2 Renal Division, Massachusetts General Hospital, Boston, Massachusetts, United States of America, 3 Department of Biostatistics, Boston University, Boston, Massachusetts, United States of America, 4 Department of Medicine, University of Washington, Seattle, Washington, United States of America, 5 Department of Epidemiology, Erasmus Medical Center, Rotterdam, The Netherlands, 6 Institute of Social and Preventive Medicine (IUMSP), Lausanne University Hospital, Lausanne, Switzerland, 7 Unit of Population Epidemiology, Division of Primary Care Medicine, Department of Community Medicine and Primary Care and Emergency Medicine, Geneva University Hospitals, Geneva, Switzerland, 8 Geriatric Unit, Azienda Sanitaria Firenze (ASF), Florence, Italy, 9 Department of Pharmacology and Toxicology, University of Lausanne, Lausanne, Switzerland, 10 Renal Division, Freiburg University Hospital, Freiburg, Germany, 11 Department of Epidemiology, Johns Hopkins Bloomberg School of Public Health, Baltimore, Maryland, United States of America, 12 Interfaculty Institute for Genetics and Functional Genomics, Ernst-Moritz-Arndt-University Greifswald, Greifswald, Germany, 13 Swiss Institute of Bioinformatics, Lausanne, Switzerland, 14 King’s College London, St. Thomas’ Hospital Campus, London, United Kingdom, 15 Department of Epidemiology, Erasmus Medical Center, Rotterdam, The Netherlands, 16 Catheter Lab, Cardiology, Ealing Hospital, Southall, Middlesex, United Kingdom, 17 Department of Epidemiology and Biostatistics, School of Public Health, Imperial College London, London, United Kingdom, 18 Icelandic Heart Association Research Institute, Kopavogur, Iceland, 19 Cardiovascular Health Research Unit, University of Washington, Seattle, Washington, United States of America, 20 Clinical Research Branch, National Institute on Aging, Baltimore, Maryland, United States of America, 21 Institute of Population Genetics, CNR-Traversa La Crucca, Reg. Baldinca Li Punti, Sassari, Italy, 22 Centre for Cognitive Ageing and Cognitive Epidemiology, The University of Edinburgh, Edinburgh, United Kingdom, 23 MRC Human Genetics Unit, MRC IGMM, University of Edinburgh, Edinburgh, United Kingdom, 24 Cardiovascular Research Group, ClinPhenomics GmbH&Co KG, Frankfurt-Sachsenhausen, Germany, 25 Laboratory of Molecular Medicine, Human Genome Center, Institute of Medical Science, University of Tokyo, Tokyo, Japan, 26 BHF Glasgow Cardiovascular Research Centre, Division of Cardiovascular and Medical Sciences, University of Glasgow, Glasgow, Scotland, 27 Institute of Genetics and Biophysics ‘Adriano-Buzzi Traverso’, CNR, Napoli, Italy, 28 Institute for Maternal and Child Health - IRCCS “Burlo Garofolo”, Trieste, Italy, 29 Institute of Genetic Epidemiology, Helmholtz Zentrum München - German Research Center for Environmental Health, Neuherberg, Germany, 30 Department of Medicine I, University Hospital Grosshadern, Ludwig-Maximilians University Munich, Munich, Germany, 31 Department of Internal Medicine II – Cardiology, University of Ulm Medical Centre, Ulm, Germany, 32 Mannheim Institute of Public Health, Social and Preventive Medicine, Medical Faculty Mannheim, University of Heidelberg, Mannheim, Germany, 33 Wellcome Trust Centre for Human Genetics, Roosevelt Drive, Oxford, United Kingdom, 34 University of Iceland, Reykjavik, Iceland, 35 Laboratory of Epidemiology, Demography and Biometry, National Institute on Aging, Bethesda, Maryland, United States of America, 36 University of Texas Health Science Center at Houston, Houston, Texas, United States of America, 37 McKusick-Nathans Institute of Genetic Medicine, Johns Hopkins University School of Medicine, Baltimore, Maryland, United States of America, 38 Cambridge Institute of Medical Research, University of Cambridge, Cambridge, United Kingdom, 39 Department of Internal Medicine, Erasmus Medical Center, Rotterdam, The Netherlands, 40 Departments of Medicine and Epidemiology, University of Washington, Seattle, Washington, United States of America, 41 Group Health Research Institute, Group Health Cooperative, Seattle, Washington, United States of America, 42 Departments of Medicine, Epidemiology and Health Services Research, University of Washington, Seattle, Washington, United States of America, 43 Department of Medicine, Internal Medicine, Lausanne University Hospital, Lausanne, Switzerland, 44 Faculty of Medicine, University of Split, Split, Croatia, 45 Department of Pharmacology, Faculty of Medicine, University of Split, Split, Croatia, 46 Division of Laboratory Medicine, Geneva University
Hospitals, Geneva, Switzerland, 47 Department of Internal Medicine, Wake Forest School of Medicine, Winston-Salem, North Carolina, United States of America, 48 Department of Human Genetics, Wellcome Trust Sanger Institute, Hinxton, Cambridge, United Kingdom, 49 Molecular Genetics Section, Laboratory of Neurogenetics, National Institute on Aging, Bethesda, Maryland, United States of America, 50 Institute of Human Genetics, Helmholtz Zentrum München - German Research Center for Environmental Health, Neuherberg, Germany, 51 Department of Computer Science and Networking, Wentworth Institute of Technology, Boston, Massachusetts, United States of America, 52 Institute of Epidemiology II, Helmholtz Zentrum München - German Research Center for Environmental Health, Neuherberg, Germany, 53 Epidemiology and Biostatistics, Imperial College London, Norfolk Place, London, United Kingdom, 54 Ulm University Medical Centre, Department of Internal Medicine I, Ulm University, Ulm, Germany, 55 LKC School of Medicine, Imperial College London and Nanyang Technological University, Singapore, Singapore, 56 Department of Epidemiology, Rollins School of Public Health, Emory University, Atlanta, Georgia, United States of America, 57 Division of Primary Care Medicine, Department of Community Medicine and Primary Care and Emergency Medicine, Geneva University Hospitals, Geneva, Switzerland, 58 Centre for Population Health Sciences, The University of Edinburgh Medical School, Edinburgh, Scotland, United Kingdom, 59 Institute of Clinical Chemistry and Laboratory Medicine, University Medicine Greifswald, Ernst-Moritz-Arndt University Greifswald, Greifswald, Germany, 60 Department of Prosthetic Dentistry, Gerostomatology and Dental Materials, University Medicine Greifswald, Greifswald, Germany, 61 Institute for Community Medicine, University Medicine Greifswald, Greifswald, Germany, 62 Human Genetics, Wellcome Trust Sanger Institute, Hinxton, United Kingdom, 63 Department of Biostatistical Sciences, Division of Public Health Sciences, Wake Forest School of Medicine, Winston-Salem, North Carolina, United States of America, 64 Clinical Chemistry Laboratory, Lausanne University Hospital, Lausanne, Switzerland, 65 William Harvey Research Institute, Bart’s and The London School of Medicine and Dentistry, Queen Mary University of London, London, United Kingdom, 66 Sylab Centre of Laboratory Diagnostics, Heidelberg, Germany, 67 Institute of Medical Sciences, Uppsala University Hospital, Uppsala, Sweden, 68 Department of Epidemiology and Prevention, Division of Public Health Sciences, Wake Forest School of Medicine, Winston-Salem, North Carolina, United States of America, 69 Department of Medicine, Division of Nephrology, University of Washington, Seattle, Washington, United States of America, 70 Faculty of Medicine, National Heart & Lung Institute, Cardiovascular Science, Hammersmith Hospital, Hammersmith Campus, Imperial College London, London, United Kingdom, 71 Imperial College Healthcare NHS Trust, London, United Kingdom, 72 Welch Center for Prevention, Epidemiology and Clinical Research, John Hopkins University, Baltimore, Maryland, United States of America, 73 Service of Nephrology, Lausanne University Hospital, Lausanne, Switzerland, 74 Division of Endocrinology, Brigham and Women’s Hospital and Harvard Medical School, Boston, Massachusetts, United States of America.

Abstract

Calcium is vital to the normal functioning of multiple organ systems and its serum concentration is tightly regulated. Apart from CASR, the genes associated with serum calcium are largely unknown. We conducted a genome-wide association meta-analysis of 39,400 individuals from 17 population-based cohorts and investigated the 14 most strongly associated loci in a replication analysis of 39,400 individuals from 17 population-based cohorts and investigated the 14 most strongly associated loci in a replication analysis of 39,400 individuals from 17 population-based cohorts and investigated the 14 most strongly associated loci in a replication analysis of 39,400 individuals from 17 population-based cohorts and investigated the 14 most strongly associated loci in a replication analysis of 39,400 individuals from 17 population-based cohorts and investigated the 14 most strongly associated loci in a replication analysis of 39,400 individuals from 17 population-based cohorts and investigated the 14 most strongly associated loci in a replication analysis of 39,400 individuals from 17 population-based cohorts and investigated the 14 most strongly associated loci in a replication analysis of 39,400 individuals from 17 population-based cohorts and investigated the 14 most strongly associated loci in a replication analysis of 39,400 individuals from 17 population-based cohorts and investigated the 14 most strongly associated loci in a replication analysis of 39,400 individuals from 17 population-based cohorts and investigated the 14 most strongly associated loci in a replication analysis of 39,400 individuals from 17 population-based cohorts and investigated the 14 most strongly associated loci in a replication analysis of 39,400 individuals from 17 population-based cohorts and investigated the 14 most strongly associated loci in a replication analysis of 39,400 individuals from 17 population-based cohorts and investigated the 14 most strongly associated loci in a replication analysis of 39,400 individuals from 17 population-based cohorts and investigated the 14 most strongly associated loci in a replication analysis of 39,400 individuals from 17 population-based cohorts and investigated the 14 most strongly associated loci in a replication analysis of 39,400 individuals from 17 population-based cohorts and investigated the 14 most strongly associated loci in a replication analysis of 39,400 individuals from 17 population-based cohorts and investigated the 14 most strongly associated loci in a replication analysis of 39,400 individuals from 17 population-based cohorts and investigated the 14 most strongly associated loci in a replication analysis of 39,400 individuals from 17 population-based cohorts and investigated the 14 most strongly associated loci in a replication

Introduction

Normal calcium homeostasis is regulated by three major hormones acting on their corresponding receptors in gut, kidney, and bone: parathyroid hormone (PTH) release governed by the calcium-sensing receptor (CASR), calcitonin, and the active metabolite of vitamin D, 1,25(OH)2-D. Despite heritability estimates of 33–78%, the genetic determinants of serum calcium are poorly understood [1,2,3]. We have previously reported a variant in CASR associated with calcium concentrations in European-ancestry individuals [4,5]. To detect additional loci, we conducted a two-stage genome-wide association meta-analysis.


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E-mail: foxca@nhlbi.nih.gov (CSF); Murielle.Bochud@chuv.ch (MB)

These authors contributed equally to this work.

Writing group.

* E-mail: foxca@nhlbi.nih.gov (CSF); Murielle.Bochud@chuv.ch (MB)

† Writing group.
Author Summary

Calcium is vital to many biological processes and its serum concentration is tightly regulated. Family studies have shown that serum calcium is under strong genetic control. Apart from CASR, the genes associated with serum calcium are largely unknown. We conducted a genome-wide association meta-analysis of 39,400 individuals from 17 population-based cohorts and investigated the 14 most strongly associated loci in ≤21,679 additional individuals. We identified seven loci (six new regions) as being robustly associated with serum calcium. Three loci implicate regions involved in rare monogenic diseases including disturbances of serum calcium levels. Several of the newly identified loci harbor genes linked to the hormonal control of serum calcium. In mice experiments, we characterized the expression of these genes in gut, kidney, and bone, and explored the influence of dietary calcium intake on the expression of these genes in these organs. Our results shed new light on the genetics of calcium homeostasis and suggest a role for dietary calcium intake in bone-specific gene expression.

of serum calcium and studied expression of identified genes in key calcium homeostatic organs in the mouse under various calcium diets.

Results

Genome-wide association meta-analysis in Europeans

The discovery analysis consisted of 39,400 individuals from 17 population-based cohorts of European descent (Table 1 and Table S1). There was little evidence for population stratification at study level (median genomic inflation factor, λ = 1.006) or meta-analysis level (λ = 1.03), and we detected an excess of association signals beyond those expected by chance (Figure S1).

The CASR locus, previously identified in Europeans, was confirmed in our meta-analysis (P = 6.5E-59, Figure S2).[4,5]. In addition, SNPs from five independent regions reached genome-wide significance (P<5E-08) in the overall discovery meta-analysis (Figure 1, Table 1, Table S2: rs1550532 (in DGKD, P = 4.60E-08), rs780094 (in GCKR, P = 3.69E-11), rs17171172 (near VKORC1L1, P = 2.78E-11), rs7481584 (in CARS, P = 9.21E-10) and rs1570669 (near CYP24A1, P = 3.98E-08).

Fourteen SNPs from Stage 1 were sent for Stage 2 validation in at least 21,679 additional Europeans: the twelve independent (≥1 Mb apart) SNPs with lowest P values (6.5E-59 to 8.1E-06) in Europeans and two additional genome-wide significant loci (rs9447004 and rs10491003) from a combined sample including Europeans and two additional genome-wide significant loci (rs9447004 and rs10491003) from a combined sample including 8318 Indian-Asians (Table 1). Of the 14 SNPs, seven were considered successfully replicated (i.e. were in the same direction of effect as the discovery meta-analysis, had a one-side replication P<0.05 and were genome-wide significant (P<5E-8) in combined meta-analysis of discovery and replication sets). These were rs1801725 at CASR, rs1550532 in DGKD, rs780094 in GCKR, rs736933 near KLLA0564 and DGKD, rs10491003 (closest gene GATA3), rs7481584 in CARS and rs1570669 near CYP24A1 (Table 1). Regional association plots are presented in Figure S3. Details on the seven SNPs that did not replicate are presented in Table S2. Association results for serum calcium in Caucasians for all SNPs with P value<5E-5 are listed in Table S3. In a secondary analysis, all SNPs identified in the primary analysis showed consistent and significant association with serum calcium adjusted for serum albumin (Table S4, Figure S4), as well as an excess of association signals beyond those expected by chance (Figure S5); no additional locus was identified using albumin-corrected serum calcium (Table S5).

Copy number variations (CNVs) and eQTL analyses

We found no significant association of the 7 replicated SNPs known to provide reliable tags for copy number variations (CNVs) in a list of 40 SNPs. We then queried each of these SNPs in the eQTL database of the University of Chicago (http://eqtl.uchicago.edu/cgi-bin/gbrowse/eqtl/). Three of the seven SNPs are in strong linkage disequilibrium with an eQTL, as illustrated in Table S6.

Information on genes mapping into the replicated genomic regions

Proposed functions of the genes mapping into the associated intervals (±250 kb) are in Box 1 and in Table S7 for the gene-rich GCKR region. We report in Table S8 the mechanism and/or location of all available biological processes, cellular components and molecular functions related to the genes mapping into the associated intervals from the AmiGo 1.8 gene ontology database. We also queried the OMIM database for each genes located within ±250 kb of the replicated loci (Table S9).

Validation across ethnicities

In Indian-Asians, all 7 replicated SNPs had beta-coefficients that were direction-consistent with the primary analysis and 3 were statistically significant (P<0.05): rs1801725 (CASR, P = 1.4E-31), rs1550532 (DGKD, P = 0.002) and rs10491003 (GATA3, P = 0.009) (Table S10). In Japanese, 3 SNPs had betas that were direction-consistent with the primary analysis, but only rs1801725 (CASR) was associated with serum calcium (P = 0.001) (Table S10).

Associations with related phenotypic traits

We conducted analyses of related bone mineral and endocrine phenotypic traits for the 7 replicated loci (Table 2). Several SNPs were associated (P<0.05) with bone mineral density (BMD) in the GEFOs consortium[6]: rs1801725 at CASR (P = 0.025; previously reported [4,5]) and rs780094 (GCKR) at the lumbar spine (P = 0.006), rs1570669 at CYP24A1 at the femoral neck (P = 0.04), and rs1550532 at DGKD at both the lumbar spine (P = 0.003) and the femoral neck (P = 0.003). For endocrine phenotypes, rs1570669 at CYP24A1 was associated with higher PTH concentrations (P = 0.0005) and rs1801725 at CASR with higher serum PTH concentrations (P = 0.028) and lower serum phosphate concentrations, as previously reported [4,5]. No SNP was associated significantly with circulating 25-OH vitamin D concentrations (all P>0.05) in the SUNLIGHT consortium[7].

Animal studies

We selected biologically plausible gene(s) at each locus for in vivo studies in a mouse model as described in Methods* section. We
Table 1. Genome-wide significant and replicated loci for serum calcium in Europeans.

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**Discussion**

We have identified and replicated one known and six new loci for serum calcium near genes linked to bone metabolism and endocrine control of calcium. Of these, 4 loci (DGKD, GCKR, CASR, and CYP24A1) were nominally associated with BMD in the general population. In supporting mouse studies, we demonstrate expression of several of these genes in tibia, and show regulation of gene expression in response to dietary calcium intake. We also demonstrate expression in nephron segments known to regulate calcium homeostasis. Taken together, these results shed new light on the genetics of calcium balance.

The vast majority of total body calcium is bound in the skeleton as hydroxyapatite and other calcium-phosphate complexes [10]. Apart from providing skeletal strength, bone serves as a calcium reservoir to maintain tightly controlled circulating concentrations vital to cellular signaling, muscle contraction and coagulation [10]. However, the genetic basis of the dynamic cross talk that occurs between these compartments is poorly understood. Our results advance our understanding in this area. Eight genes identified in the GWAS are constitutively expressed in bone and are regulated with serum calcium after adjustment for albumin (Figure 2).

In order to determine regulation of gene expression by calcium intake, we measured gene expression levels in mice fed low and high calcium diets (0.17% vs. 1.69% calcium) for one week, with normal diet as control (0.82%). For rs780094 and rs7481584, I^2 were 0.79 and 0.43 with I^2 = 0.19, respectively. For these latter SNPs, sample size weighted meta-analysis P values were 2.93E-10 and 2.03E-10, respectively.

The A allele of rs1570669 (I^2 = 0.03) was associated with increased expression, as were GATA3, KIAA0564 and CYP24A1 (I^2 = 1.2E-10) in the proximal tubule, CASR in the thick ascending limb, and GATA3 predominantly in the distal nephron and collecting duct (Figure 3).

No significant effect of GCKR (rs780094) was observed in any organ tested, which is of interest considering the strong attenuation of the association of rs780094 with serum calcium after adjustment for albumin (Table S4). In micro-dissection of nephron segments [8,9], DGKD, DGKH, CASR, KIAA0564 and CYP24A1 were primarily transcribed in the proximal tubule, CASR in the thick ascending limb, and GATA3 predominantly in the distal nephron and collecting duct (Figure 3).
documented role in vitamin D metabolism, discussed below, and/or its association with higher PTH concentrations identified in the present analysis.

We observed specific expression patterns of several genes in the mouse nephron: DGKD, DGKH, CASR, KIAA0564, and CYP24A1 were primarily transcribed in the proximal tubule, CASR expression was mostly localized to the thick ascending limb, whereas GATA3 was predominantly found in the distal part of the nephron and the collecting duct. This pattern of expression in segments known to be involved in calcium reabsorption suggests a role in renal calcium handling and is consistent with previous exploratory transcriptome analyses in humans and mice [12,13]. Both DGKD and DGKH were significantly upregulated in the kidney in response to low calcium diet, suggesting specific involvement of these genes in renal calcium handling.

Several of the newly identified loci harbor genes linked to the hormonal control of serum calcium. First, the association of CASR with PTH concentrations is consistent with its known role in PTH signaling. Second, several lines of evidence implicate rs1570669 (CYP24A1) in the vitamin D pathway: its association with serum calcium and PTH concentrations, its selective expression in the proximal tubule where 1,25(OH)2-D metabolism occurs, and that loss-of-function CYP24A1 mutations cause vitamin D-induced hypercalcemia in children (idiopathic infantile hypercalcemia). Third, we identified variants linked to 2 chromosomally distinct isoforms of diacylglycerol kinase, part of the phosphoinositol second messenger system, that may interact with each other at the protein level [14,15].

Strengths of this study are the large sample size and consistent mouse studies to support the statistical associations and advance our knowledge of the biology at these loci. Human and mice largely share physiological processes linked to calcium metabolism, including tissue-specific gene expression. Limitations include the lack of a direct marker of bone remodeling and the potential for bias in gene selection for experimental follow-up. Mice may display subtle differences in the regulation of the genes tested compared to humans.

We have identified and replicated one known and six new loci for serum calcium near genes linked to bone metabolism and endocrine control of serum calcium. Supporting experimental mouse studies suggest a role for dietary calcium in bone-specific gene expression. Further work is needed to identify the causal variants and to understand how they influence calcium homeostasis.

Materials and Methods

Ethics statement

In each human study, the local institutional review board approved the study and participants signed written informed consent, including for DNA analyses. The experimental protocol in mice was approved by the local veterinarian authorities and fulfilled Swiss federal regulations for experiences with animals.

Participating studies (human data)

Discovery and replication cohorts. A list of all discovery and replication studies, their sample size, mean serum calcium levels, age and serum albumin as well as proportion of women can be found in Table S1. We replicated findings using de novo genotyping in the Bus Santé Study and in silico data in all other cohorts. In most studies, serum calcium was measured using a colorimetric assay. The size of discovery tables varied from 488 to 9,049 for a total of 39,400 participants. A detailed description of the characteristics of discovery and replication cohorts, including laboratory method for serum calcium measurement, can be found in Table S12.

Genotyping

Detailed information on the genotyping platforms and data cleaning procedures for each discovery and replication cohort can be found in Table S13. De novo replication genotyping was performed in 4670 participants to the Bus Santé Study using KASPar v4.0 after whole genome amplification by primer extension pre-amplification (PEP) using thermostable DNA polymerases.

Figure 1. Genome-wide association for serum calcium in discovery analysis in Europeans. Manhattan plot showing $-\log_{10}(P$ values) for all SNPs in the discovery GWAS for uncorrected serum calcium in Europeans ($N=39,400$), ordered by chromosomal position. The plot is truncated at $-\log_{10}P$ values of 10 (truncated $-\log_{10}P$ values for GCKR and CASR). The values correspond to the association of uncorrected serum calcium, including age and sex as covariates in the model as well as study-specific covariates if needed. The gene closest to the SNP with the lowest $P$ value is CYP24A1. The seven loci that reached genome-wide significance at the combined analysis following replication are highlighted in red (GCKR, DGKD, CASR, GATA3, CARS, DGKH-KIAA0564 and CYP24A1).

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<td>0.9</td>
<td>4181</td>
<td>0.035</td>
<td>0.010</td>
<td>0.0005</td>
<td></td>
<td></td>
</tr>
</tbody>
</table>

NA, not available. P values <0.05 were considered as statistically significant. A1, effect allele. β, regression coefficient for allele A1, SE, standard error. P, two-sided P value. Zscore, z score. doi:10.1371/journal.pgen.1003796.t002
previously published GWAS meta-analysis, including 16,264 participants of European ancestry [18]. Serum phosphorus concentrations were quantified using an automated platform in which inorganic phosphorus reacts with ammonium molybdate in an acidic solution to form a colored phosphomolybdate complex [18]. The 25-hydroxyvitamin D was looked-up in the SUNLIGHT consortium [7], which includes data from 33,996 individuals of European descent from 15 cohorts. 25-hydroxyvitamin D concentrations were measured by radioimmunoassay, chemiluminescent assay, ELISA, or mass spectrometry.

Figure 2. Relative mRNA expression of replicated genes in three calcium-transporting tissues (kidney, duodenum, tibia). The expression (based on delta CT [cycle threshold] normalized to actin) of the selected genes is compared to the expression of the CASR gene in the duodenum, thereby providing a relative expression. Cut-off was set at delta CT=15. Data are means ± standard error of the mean (SEM) of values obtained from 5 mice fed a normal diet. GCKR was not expressed.

doi:10.1371/journal.pgen.1003796.g002

Figure 3. Relative mRNA expression of identified genes in kidney tubule segments. The renal tubular segments analyzed were the proximal tubule (PROX), the thick ascending limb of the loop of Henle (TAL), the distal convoluted tubule and connecting tubule (DCT-CNT), and the cortical collecting duct (CCD). The expression (based on the delta CT [cycle threshold]) of the selected genes is compared to the expression of the CASR gene in the PROX, thereby providing a relative expression. Data are means of values obtained from 3 mice fed a normal diet. GCKR was not expressed.

doi:10.1371/journal.pgen.1003796.g003
[7]. PTH was looked-up in the SHIP and SHIP-Trend studies. The serum parathyroid hormone concentration was measured on the IDS-iSYS Multi-Discipline Automated Analyser with the IDS-iSYS Intact PTH assay (Immunodiagnostic Systems Limited, Frankfurt am Main, Germany) according to the instructions for use. This chemiluminescence immunosassay detects the full-length parathyroid hormone (amino acids 1–84) and the large parathyroid hormone fragment (amino acids 7–84). The measurement range of the assay was 5–5000 pg/mL. The limits of blank, detection and quantitation were 1.3 pg/mL, 1.4 pg/mL, and 3.6 pg/mL, respectively. As recommended by the manufacturer, three levels of control material were measured in order to verify a decent working mode. During the course of the study, the coefficients of variation were 14.02% at low, 6.64% at medium, and 6.84% at high serum parathyroid hormone concentrations in the control material in SHIP and the corresponding percentages were 16.8% at low, 10.7% at medium, and 9.0% at high serum parathyroid hormone concentrations in the control material in SHIP-Trend.

Copy Number Variation (CNV) analysis

The Hypergene dataset (a 4296 samples case-control study concerning hypertension genotyped using the Illumina 1M chip) has been used to call CNVs and to check their correlation with the SNPs of interest. The CNVs calls have been done using pennCNV software [19]. A SNP by sample matrix with the copy number status was created. Then the square correlation (Pearson correlation) between value of each SNP of interest and the SNPs of interest for which no correspondence has been found in the Hypergene dataset have been replaced by the closest SNPs in high linkage disequilibrium (LD) and present in the Hypergene dataset. LD between the SNPs of interest and a list of SNPs tagging CNVs from the GIANT consortium has also been calculated. The SNPs from the GIANT list are in LD higher than 0.8 with their corresponding CNV.

Gene ontology classification analysis

We queried the AmiGo 1.8 gene ontology database for each gene located within ±50 kb of the seven replicated SNPs, including rs1801725 (CASR; [http://amigo.geneontology.org/cgi-bin/amigo/go.cgi, last accessed November 6, 2012]). We used Homo sapiens as a filter for species.

Expression quantitative trait locus (eQTL) Analyses

For each of the 7 replicated SNPs, we identified all proxy SNPs with r2>0.8 in HapMap CEU (releases 21, 22, and HapMap 3 vers. 2) using the online SNAP database (http://www broadinstitute.org/mpg/snap/). We then queried each of these 40 SNPs in the eQTL database of the University of Chicago (http://eqtl.uchicago.edu/cgi-bin/gbrowse/eqtl/).

Rationale for gene selection for experimental analyses in mouse

The rs1801725 SNP encodes a missense variant in exon 7 of the CASR gene leading to an alanine to serine substitution (A968S). Given the key physiological role of CASR in calcium homeostasis (monogenic disorders of calcium balance), this gene was the logical candidate for analysis in mouse at this previously identified locus.

For the 6 newly identified loci, the precise rationale for gene selection varied from one locus to the other, but the main criteria was to focus on the most biologically relevant gene. Rs1550532 on chromosome 2 is an intronic SNP of GDF5, which was the most likely biological candidate for this locus and was therefore selected for analysis in mouse. None of the other genes located in this region (±250 Kb) has a known link with calcium homeostasis (Table S6). We also took into account the fact that another member of the DGK family, namely DGKH was located near one of the other replicated loci, on chromosome 13.

Rs780094, on chromosome 2, is located in intro 16 of GCKR and is in strong linkage disequilibrium (r2=0.93) in Caucasians [20], with a common non-synonymous SNP (P446L, rs1260326) associated with glucokinase activity in vitro [20,21]. This SNP has been associated with multiple other phenotypes in previous GWAS and it is in strong linkage disequilibrium with an eQTL (Table S6). Previous fine mapping analysis of this locus has attributed the signal from rs780094 to the functional rs1260326 variant [20]. The GCKR locus may indirectly influence calcium concentrations via its association with albumin levels [22]. In line with this, we observed an attenuation of the association of rs780094 with albumin-corrected serum calcium compared to the association with uncorrected serum calcium and we found GCKR not to be expressed in any of the key organs involved in calcium homeostasis that we tested in mice. We selected GCKR for analysis in mouse at this locus.

Rs10491003 on chromosome 10 is located within a long non-coding RNA. For this locus, we selected GATA3, the nearest and only gene located within this region, for analysis in mouse. GATA3 is implicated in monogenic disorders of calcium balance.

Rs7481584 is located within CARS (intronic SNP) in an imprinted region known to play a role in multiple cancers, which makes this locus a plausible candidate for malignancy-related hypercalcaemia. Other plausible biological candidates in this locus are NAP1L4, PHLDA2 and CKDN1C (Box 1). Rs7481584 is in strong LD with 2 eQTLs, one associated with the expression of NAP1L4 (rs2583435) and the other one associated with the expressions of SLC22A18 and SLC22A18AS. We selected CARS, NAP1L4, PHLDA2 and CKDN1C for analyses in mouse.

For rs7336953, we selected the two only genes (DGKH and KLA03564) located under this association peak on chromosome 13 for analyses in mouse.

Finally, rs1570669 is an intronic SNP of CYP24A1, a strong biological candidate implicated in monogenic disorders of calcium balance. The two other genes of this region (BCAS1 and PFDN4) have no known link with calcium homeostasis. Furthermore, rs1570669 and PFDN4 are separated by a recombination hot spot. We selected CYP24A1 for analysis in mouse.

As animal experiments started while the replication process was underway, we had also initially selected the following genes for analysis in mouse: RSG14 and SLC34A1 at locus rs4074995 (discovery P value = 2.4E-07), VKORC1L1 at locus rs17711722 (discovery P value = 2.8E-11), PYGB at locus rs2281558 (discovery...
### Box 1. Genes Located within Replicated Loci for Serum Calcium

We here summarize the information on genes located within ±250 kb from the top SNP at each locus. Because it is a gene dense region, details of genes located in the GCKR genomic region are presented in Table S4.

**Chromosome 2, locus rs1550532**  
**DGKD** rs1550532 is an intronic SNP located near the 5’UTR region of DGKD. DGKD encodes diacylglycerol kinase delta, a member of the diacylglycerol kinase (DGK) enzyme family. Alternative splicing of the DGKD gene results in two isoforms, which differ in their expression profiles and regulatory mechanisms [24]. DGKs play an important role in signal transduction by modulating the balance between the diacylglycerol (DAG) and phosphatidic acid (PA), important second messengers in signaling cascades. Recent findings suggest that DAG is involved in calcium signaling in parathyroid cells [25]. CASR signaling influences intracellular DAG levels in cardiomyocytes [26].

**SAG** encodes S-antigen (also called arrestin), a soluble photoreceptor protein expressed in the retina and pineal gland. Mutations in this gene are associated with Oguchi disease (OMIM #258100), a rare autosomal recessive form of night blindness. Arrestin is a calcium-binding protein that plays an important role in phototransduction.

**ATG16L1** encodes autophagy related 16-like 1 protein, part of a complex involved in autophagia. Mutations in this gene are responsible for inflammatory bowel disease 10 (OMIM #611081). There is no known direct link with calcium signaling.

**SCARNAs and SCARNA6** encode small Cajal body-specific RNAs 5 and 6, which are small nuclear RNAs, belonging to non-coding RNAs involved in the RNA-processing machinery. There is no known direct link with calcium signaling.

**USP40** encodes ubiquitin specific peptidase 40. USP40 functions as a deubiquinating enzyme involved in the degradation of unwanted intracellular proteins in eukaryotic cells. There is no known direct link with calcium signaling.

**INPP5D** encodes inositol polyphosphate-5-phosphatase, expressed in hematopoietic cells. This protein regulates myeloid cell proliferation. The presence of a recombination peak between this gene and rs1550532 makes it an unlikely candidate for this signal.

**Chromosome 10, locus rs10491003**  
rs10491003, located within a long non-coding RNA with GATA3 as its nearest gene may influence the expression of GATA3 [27].

**GATA3** GATA3 encodes a GATA transcription factor involved in T cell lymphopoeisis [28], renal and vestibular morphogenesis [29,30], and parathyroid gland development [31]. GATA3 haploinsufficiency causes hypoparathyroidism and hypocalcemia in the autosomal dominant HDR syndrome (hypoparathyroidism, sensorineural deafness and renal dysplasia) (OMIM #146255) [32,33]. Although GATA3 is the closest gene to rs10491003, this variant lies 1.2 Mb downstream from that gene. However, GATA3 has a very large flanking regulatory region - greater than 450 kbp - [34] and mammalian enhancers may lie more than 1 Mbp away from the gene they regulate [35]. GATA3 may play a role in preserving high degree of differentiation of parathyroid gland and of calcium transporting epithelia [36].

**Chromosome 11, locus rs7481584**  
This region is located in the imprinted gene domain of 11p15.5, an important tumor suppressor gene region [37].

**CARS** rs7481584 is an intronic SNP of **CARS**. CARS encodes a cysteinyl-tRNA synthetase and is located within the imprinted gene domain of 11p15.5. This region is linked to Beckwith-Wiedemann syndrome, which is associated with hypocalcemia and hypercalciuria.  

**NAPIL4** encodes nucleosome assembly protein 1-like 4, a member of the nucleosome assembly protein, potentially involved in histone chaperoning and ubiquitously expressed. NAPIL1 and NAPIL4 have been recently identified as being involved in the regulation of DGKH nucleocytoplasmic shuttling [38]. A link with calcium homeostasis could be possible via the DGKs pathway.

**PHLD2A** encodes pleckstrin homology-like domain, family A, member 2. This gene has been recently highlighted as potentially relevant for osteoporosis on the basis of a bioinformatics pathway analysis approach [39]. Imprinting of this gene appears to play a role in fetal growth, including fetal bone growth, birth weight and bone mass in childhood.[40,41,42,43]. In cancer, PHLD2A is activated by parathyroid hormone-like hormone (PTHHLH) [44]. PTHHLH is associated with malignancy-related hypercalcemia [45], lactation [46], the expression of PHLD2A is upregulated in osteosarcoma progression [47].

**OSBPL5** encodes oxysterol-binding protein-like 5, an intracellular lipid receptor involved in cholesterol balance. There is no known direct link with calcium homeostasis.

**MRGPRE and MRGPRG** encode MAS-related G-protein-coupled receptors, member E and G. This family of receptors is expressed in nociceptive sensory neurons. There is no known direct link with calcium homeostasis.

**C11orf36** encodes MRGPRG antisense RNA 1. Little is known about this gene.

**SNORA54** encodes small nucleolar RNA, H/ACA box. The gene product belongs to non-coding RNAs involved in the RNA-processing machinery. There is no known direct link with calcium homeostasis.

**SLC22A18 and SLC22A18AS** encode solute carrier family 22, member 1 and solute carrier family 22, member 1 antisense. SLC22A18 is an organic cation transporter. Mutations in SLC22A18 have been found in several cancers. There is no known direct link with calcium homeostasis.

**CDKN1C** encodes cyclin-dependent kinase inhibitor 1C (p57, Kip2), a protein involved in cell-cycle progression. This imprinted gene is responsible for the IMAGE syndrome (OMIM #300290) characterized by intrauterine growth restriction, metaphyseal dysplasia, delayed bone aging, adrenal hypoplasia congenital, genetic anomalies, and sometimes hypercalciuria [48].

**KCNQ1** encodes voltage-gated potassium channel, KQT-like subfamily, member 1. **KCNQ1OT1** represents KCNQ1 opposite strand transcript 1 and is an unspliced long non-coding RNA, which regulates the transcription of many target genes. Mutations in KCNQ1 are associated with hereditary long and short QT syndromes (OMIM #192500 & 609621), Jervell and Lange-Nielsen syndrome (OMIM #220400), familial atrial fibrillation (OMIM #607554), type 2 diabetes. **KCNQ1OT1** is also imprinted in a tissue-specific manner. There is no known direct link with calcium homeostasis.

**Chromosome 13, locus rs7336933**  
**DGKH** encodes diacylglycerol kinase eta, a member of the diacylglycerol kinase (DGK) enzyme family. See **DGKD** (above) for discussion.

**KIAA0564** this gene encodes a large uncharacterized protein containing a putative ATP-ase domain. The sequence of this gene is conserved across a large array of organisms,
from humans to mouse, zebrafish and to C. elegans, which suggests an important biological function. Yet, little is known on the nature of the function of this gene so far.

**Chromosome 20, locus rs1570669**

*CYP24A1*: rs1570669 is an intronic SNP of CYP24A1. CYP24A1 encodes a cytochrome P450 enzyme that hydroxylates 1,25-(OH)_{2}D, into metabolites targeted for degradation and appears to be one of the central regulator of 1,25-(OH)_{2}D metabolism. CYP24A1 is highly regulated by its own substrate 1,25(OH)_{2}D, as well as by PTH [49,50], serum phosphate and fibroblast growth factor-23 (FGF-23) [51,52,53]. Sequence variants of CYP24A1 impacting on 1,25(OH)_{2}D metabolism have been described recently and explain the strong heritability of 1,25(OH)_{2}D concentrations.

*Bcas1* encodes breast carcinoma amplified sequence 1, considered as an oncogene. *Bcas1* is highly differentially expressed in some cancers. However, there is no direct link with calcium homeostasis.

**Pfdn4** encodes prefoldin subunit4. Prefoldin is a chaperone complex involved in polypeptide folding. There is no known link of this gene with calcium homeostasis.

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P value = 6.4E-07, *CD109* at locus rs9447004 (discovery P value = 8.1E-06). No gene was selected for the rs2885836 and rs11967485 and rs12150338 loci in the absence of obvious candidate. Results for these unreplicated loci can be found in **Figures S6, S7 and S8**. We present these results for quality control purposes: *SLC34A1* (also known as NAPI-3 or NPT2), which encodes solute carrier family 34 (sodium phosphate), member 1, was expressed in the kidney, but neither in duodenum nor in bone, as expected based on current knowledge on this phosphate transporter. In the kidney *SLC34A1* was mainly expressed proximally and *SLC34A1* expression was upregulated under low calcium diet, which is in line with the known function of this gene.

**Mouse experiments**

Five C57bl/6 mice (Janvier) per group were fed, for one week, three different diets in which the percentage of calcium were 0.17% (low calcium diet), 0.82% (normal calcium diet) and 1.69% (high calcium diet), and had free access to water. 12:12 hours light/dark alternance was imposed. At the end of the week of the specific diet, spot urine were collected and mice were anesthetized. Blood was collected by retro-orbital puncture. Organs were immediately harvested and snap frozen. RNA was extracted using Trizol reagent Kit (Takara Bio Inc). Calcium, sodium, phosphate and creatinine in plasma and urine were analyzed at the central lab of the Lausanne University hospital using a Cobas-Mira analyzer (Roche).

**Microdissection.** A separate set of three mice was kept under normal calcium diet. Proximal Tubule (Prox), thick ascending limb of the loop of Henle (TAL), distal convoluted tubule and connecting tubule (DCT-CNT) and cortical collecting duct (CCD) were isolated by microdissection of the left kidney after the mice were perfused with Liberase TM (Roche). A separate set of three mice was kept under normal calcium diet. Proximal Tubule (Prox), thick ascending limb of the loop of Henle (TAL), distal convoluted tubule and connecting tubule (DCT-CNT) and cortical collecting duct (CCD) were isolated by microdissection of the left kidney after the mice were perfused with Liberase TM (Roche). DNA was extracted from the above mentioned tubules following TR Reagent Solution protocol (Applied Biosystems) and purified with RNasey Micro Kit (Qiagen). Reversed transcription was performed with PrimeScriptTM RT reagent Kit (Takara Bio Inc). Quantitative PCR were performed (7500 Software v 2.0.4.) using TaqMan gene expression assays for the different genes (Applied Biosystems) and comparative CT method was applied. Expression levels were normalised to beta tubulin (endogenous reference gene).

**Statistics.** Comparison of groups was performed using unpaired Student’s t-test.

**Supporting Information**

**Figure S1** QQ-plot of uncorrected serum calcium GWAS meta-analysis. Quantile-quantile plot showing observed p-values of the uncorrected serum calcium meta-analysis vs. expected p values by chance. The second genomic control step was applied to correct for the post meta-analysis of λ = 1.03.

**Figure S2** Regional association plot for the CASR locus. Regional association plot showing −log10 p-values for the association of all SNPs ordered with their chromosomal position with uncorrected serum calcium at the CASR loci. The −log10 P value for each SNP is colored according to the correlation of the corresponding SNP with the SNP showing the lowest p-value (index SNP) within the locus using different colors for selected levels of linkage disequilibrium (r²). Correlation structures correspond to HapMap 2 CEU.

**Figure S3** Regional association plot for the newly identified loci. Regional association plot showing −log10 p-values for the association of all SNPs ordered with their chromosomal position with uncorrected serum calcium within the replicated loci. The −log10 P value for each SNP is colored according to the correlation of the corresponding SNP with the SNP showing the lowest p-value (index SNP) within the locus using different colors for selected levels of linkage disequilibrium (r²). Correlation structures correspond to HapMap 2 CEU.

**Figure S4** Manhattan plot of corrected serum calcium. Manhattan plot showing −log10 P values for all SNPs ordered, ordered by their chromosomal position. The values correspond to the association of albumin-corrected serum calcium, including age and sex as covariates in the model as well as study-specific covariates if needed.

**Figure S5** QQ-plot of corrected serum calcium. Quantile-quantile plot showing observed p-values of the corrected serum calcium meta-analysis vs. expected P values by chance in Europeans at discovery. The second genomic control step was applied to correct for the post meta-analysis of λ = 1.03.

**Figure S6** Relative expression of genes in non-replicated loci in kidney, duodenum and tibia. The expression (based on delta CT normalized to actin) of the selected genes is compared to the expression of the CASR gene in the duodenum, thereby providing a relative expression. Cut-off was set at delta CT≤15. Data are means ± SEM of values obtained from 5 mice fed a normal diet.

**Figure S7** Relative expression in segments of kidney tubules of genes located in non-replication loci. The renal tubular segments analyzed were the proximal tubule (PROX), the thick ascending
limb of the loop of Henle (TAL), the distal convoluted tubule and connecting tubule (DCT-CNT), and the cortical collecting duct (CCD). The expression (based on the delta CT) of the selected genes is compared to the expression of the CASR gene in the PROX. Data are means of values obtained from 3 mice fed a normal diet. GCKR was not expressed.

Figure S8 Relative expression of genes in non-replicated loci under various calcium diets. Data are means± SEM of values obtained from 5 mice fed a low (0.17%) and high (1.69%) calcium diet compared to mice fed a normal calcium diet (0.82%). Expression levels were normalized to actin. Statistical difference was calculated using unpaired t-test. *: P value≤0.05 (low compared to high); #: P value≤0.05 (low compared to normal); ¥: P value≤0.05 (high compared to normal).

Table S1 Characteristics of study participants in discovery and replication cohorts. Data are mean (SD) unless otherwise specified for each discovery and replication studies.


Table S3 SNPs with P value<5*E-05 for uncorrected calcium in Europeans (discovery). Chr, chromosome. Position on build 36. A1, allele 1 (effect allele). A2, allele 2. Freq A1, frequency of allele 1. InRefGen, gene symbol if SNP is located within a specific gene.

Table S4 Comparison of association with uncorrected versus corrected serum calcium. Chr, chromosome. Freq A1, frequency of allele A1. Beta, regression coefficient for the A1 allele. SE, standard error. A1, allele 1 (effect allele). Only replicated loci are included in this table.

Table S5 Genome-wide significant loci for corrected calcium in Europeans (discovery). Chr, chromosome. Position on build 36. A1, allele 1 (effect allele). A2, allele 2. Freq A1, frequency of allele 1. InRefGen, gene symbol if SNP is located within a specific gene.

Table S6 eQTL analysis for the seven genome-wide replicated loci for serum calcium. We used the online eQTL database of the University of Chicago (http://eqtl.uchicago.edu/cgi-bin/gbrowse/eqtl/., last accessed, November 5, 2012). All eQTL were acting in cis.

Table S7 Details on genes located in the GCKR genomic region.

Table S8 Gene Ontology classification (AmiGo). Data are GO numbers, ontology and mechanism/location from the AmiGo 1.8 gene ontology database for each gene located within ±250 kb of the seven replicated SNPs, including rs1801725 (CASR).

Table S9 OMIM disorders associated with the genes located within the replicated loci. This table includes all Mendelian disorders or other types of genetic disorders included in the OMIM database described for each gene located within ±250 kb of any of the six new loci and for CASR.


Table S11 Plasma and Urine electrolytes values by calcium diet in mice. Data are means ± SEM of values obtained from 3 to 5 mice. *: P value≤0.05 compared to normal or high calcium diet.

Table S12 Study information.

Table S13 Genotyping information for each cohort (discovery, replication and look-ups).

Text S1 Study specific acknowledgements.

Acknowledgments
The full list of acknowledgments for each study is provided in the Supporting Information files (Text S1).

Author Contributions
Conceived and designed the experiments: CMOS HWu QY KK WHLK HBa OB CSF MBoc. Performed the experiments: CMOS HWu QY KK IG AMZ AK CSi ZK TH GE LJL VG DEA LF DSS BMP OAh AGo AUG JCMW JID JMS MP EMB PV SBe CH VV SBa IR OP JW HC JSK JCC AHa CSc MN RB UV PBM MBJ JMT JMG TDS WH APm LL WM BOB BRW CG CM WHLK HWa OB Csf MBoc. Analyzed the data: CMOS HWu QY KK IK AMZ AK AT ZK YL TH JD KL AVS GE LJL VG TT GL AD FR LML LP FM JH AMAc SBe CH VV JFW WZ AGo AGU FR KE SP MM FDe AMah WH APm Mek ACB GB Wb HWa OB Csf MBoc. Contributed reagents/materials/analysis tools: IG YL VG EB DH AS DSS BMP AGU FR JID JMS MP PV GD Vv CH JSK JCC PBM MM SYS APm MEK TM WHLK HWa OB CSF MBoc. Performed the experiments: CMOS IG AK HWa OB Csf MBoc. Contributing to and reviewing the manuscript for important intellectual content: CMOS HWu QY KK IG AMZ AK CSi ZK TH MM AD VZ GE GL TT LP LML CH KL KM SP DF RS SU ACB MEK AMAh FDe VG LJL AMAc EB DEA CT VN MBJ JMG JMT DSS BMP SBe PV VV AWF TZ MBoh IK PN EMB KE JID TWH SBa DH ABS GR DR AP TM CM GD JMS JCC BOB BRW JH FM SHW HC APm OAh AGo AF UV AAhes RB WH SYS PL HH CSc PBM PG NP MC CG WM LL TDS AVS IR JFW OP IJD MP LF YL BK JSK JCWM MN WHLK HWa OB Csf MBoc.

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