Genetic Determinants of Serum Testosterone Concentrations in Men

Ohlsson, Claes; Wallaschofski, Henri; Lunetta, Kathryn L.; Stolk, Lisette; Perry, John R. B.; Koster, Annemarie; Petersen, Ann-Kristin; Eriksson, Joel; Lehtimaki, Terho; Huhtaniemi, Ilpo T.; Hammond, Geoffrey L.; Maggio, Marcello; Coviello, Andrea D.; Ferrucci, Luigi; Heier, Margit; Hofman, Albert; Holliday, Kate L.; Jansson, John-Olov; Kahonen, Mika; Karasik, David; Karlsson, Magnus; Kiel, Douglas P.; Liu, Yongmei; Ljunggren, Osten; Lorentzon, Mattias; Lyytikainen, Leo-Pekka; Meitinger, Thomas; Mellstrom, Dan; Melzer, David; Miljkovic, Iva; Nauck, Matthias; Nilsson, Maria; Penninx, Brenda; Pye, Stephen R.; Vasan, Ramachandran S.; Reincke, Martin; Rivadeneira, Fernando; Tajar, Abdelouahid; Teumer, Alexander; Uitterlinden, Andre G.; Ulloor, Jagadish; Viikari, Jorma; Voelker, Uwe; Voelzke, Henry; Wichmann, H. Erich; Wu, Tsung-Sheng; Zhuang, Wei Vivian; Ziv, Elad; Wu, Frederick C. W.; Raitakari, Olli

Published in:
PLoS Genetics

DOI:
10.1371/journal.pgen.1002313

2011

Link to publication

Citation for published version (APA):
Genetic Determinants of Serum Testosterone Concentrations in Men

Claes Ohlsson1,*, Henri Wallaschofski2,3, Kathryn L. Lunetta3,4,5,9, John R. B. Perry7,8,*,
Annemarie Koster9*, Ann-Kristin Petersen10, Joel Eriksson1, Terho Lehtimäki11, Ilpo T. Huhtaniemi12,*,
Geoffrey L. Hammond13,*, Marcello Maggio14, Andrea D. Covillo6,15, EMAS Study Group16, Luigi
Ferrucci17, Margit Heier18, Albert Hofman6,19, Kate L. HolliDay20, John-Olov Jansson21, Mika Kähönen22,*,
David Karasik23, Magnus K. Karlsson24, Douglas P. Kiel3,23, Yongmei Liu25, Östen Ljunggren26, Mattias
Lorentzon27, Leo-Pekka Lytyikäinen11, Thomas Meiting27,28, Dan Mellström3, David Melzer29, Iva
Miljkovic30, Matthias Nauck2, Maria Nilsson31, Brenda Penninx31, Stephen R. Pye20, Ramachandran S.
Vasan3,15, Martin Reincke32, Fernando Rivadeneira5,6,19, Abdelouahid Tajar20, Alexander Teumer33,*,
André G. Uitterlinden5,6,19, Jagadish Ullumo15, Jorma Vilkari34, Uwe Völker33, Henry Völzke35, H. Erich
Wichmann36,37,38, Tsung-Sheng Wu13, Wei Vivian Zhuang3, Elad Ziv39,40, Frederick C. W. Wu41, Olli
Raitakari42,43, Anna Eriksson1,*, Martin Bidlingmaier32,*, Tamara B. Harris9, Anna Murray1,7,8,*, Frank H. de
Jong5*, Joanne M. Murabito3,15, Shalender Bhasin3,15, Liesbeth Vandenput1, Robin Haring25.

1 Center for Bone and Arthritis Research, Department of Internal Medicine, Institute of Medicine, Sahlgrenska Academy, University of Gothenburg, Gothenburg, Sweden, 2 Institute of Clinical Chemistry and Laboratory Medicine, University of Greifswald, Greifswald, Germany, 3 The National Heart, Lung, and Blood Institute's Framingham Heart Study, Framingham, Massachusetts, United States of America, 4 Department of Biostatistics, Boston University School of Public Health, Boston, Massachusetts, United States of America, 5 Department of Internal Medicine, Erasmus MC Rotterdam, Rotterdam, The Netherlands, 6 Netherlands Consortium of Healthy Ageing, Rotterdam, The Netherlands, 7 Genetics of Complex Traits, Peninsula Medical School, University of Exeter, Exeter, United Kingdom, 8 Wellcome Trust Centre for Human Genetics, University of Oxford, Oxford, United Kingdom, 9 Laboratory for Epidemiology, Demography, and Biometry, National Institute on Aging, Bethesda, Maryland, United States of America, 10 Institute of Genetic Epidemiology, Helmholtz Zentrum München, Neuherberg, Germany, 11 Department of Clinical Chemistry, University of Tampere and Tampere University Hospital, Tampere, Finland, 12 Department of Surgery and Cancer, Hammersmith Campus, Imperial College London, London, United Kingdom, 13 Institute of Human Genetics, University of British Columbia, Vancouver, Canada, 14 Departments of Internal Medicine and Biomedical Sciences, Section of Genetics, University of Parma, Parma, Italy, 15 Sections of General Internal Medicine, Preventive Medicine, Cardiology, and Endocrinology, Diabetes, and Nutrition, Department of Medicine, Boston University School of Medicine, Boston, Massachusetts, United States of America, 16 The European Male Ageing Study, University of Manchester, Manchester, United Kingdom, 17 Longitudinal Studies Section, Department of Clinical Chemistry and Laboratory Medicine, University of Turku, Finland, 18 Institute of Epidemiology II, Helmholtz Zentrum München, Neuherberg, Germany, 19 Department of Epidemiology, Erasmus MC Rotterdam, Rotterdam, The Netherlands, 20 Arthritis Research UK Epidemiology Unit, University of Manchester, Manchester Academic Health Science Centre, Manchester, United Kingdom, 21 Department of Physiology, Institute of Neuroscience and Physiology, Sahlgrenska Academy, University of Gothenburg, Gothenburg, Sweden, 22 Department of Clinical Physiology, University of Tampere and Tampere University Hospital, Tampere, Finland, 23 Hebrew SeniorLife Institute for Aging Research and Harvard Medical School, Boston, Massachusetts, United States of America, 24 Clinical and Molecular Osteoporosis Research Unit, Department of Clinical Sciences and Department of Orthopaedics, Lund University, Skane University Hospital, Malmo, Sweden, 25 Department of Epidemiology and Prevention, Wake Forest University Health Sciences, Winston-Salem, North Carolina, United States of America, 26 Department of Medical Sciences, University of Upsala, Upsala, Sweden, 27 Institute of Human Genetics, Technische Universität München, München, Germany, 28 Institute of Human Genetics, Helmholtz Zentrum München, Neuherberg, Germany, 29 Peninsula Medical School, University of Exeter, Exeter, United Kingdom, 30 University of Pittsburgh, Department of Epidemiology, Pittsburgh, Pennsylvania, United States of America, 31 Department of Psychiatry and EMGO Institute for Health and Care Research, VU University Medical Center, Amsterdam, The Netherlands, 32 Medizinische Klinik Innenstadt; Ludwig-Maximilians-Universität, München, Germany, 33 Interfaculty Institute for Genetics and Functional Genomics, University of Greifswald, Greifswald, Germany, 34 Department of Medicine, University of Turku and Turku University Hospital, Turku, Finland, 35 Institute for Community Medicine, University of Greifswald, Greifswald, Germany, 36 Institute of Medical Informatics, Biometry and Epidemiology, Ludwig-Maximilians-Universität, München, Germany, 37 Klinikum Großhadern, München, Germany, 38 Institute of Epidemiology I, Helmholtz Zentrum München, Neuherberg, Germany, 39 Division of General Internal Medicine, Department of Medicine, University of California San Francisco, San Francisco, California, United States of America, 40 Department of Epidemiology and Biostatistics, Institute for Human Genetics, University of California San Francisco, San Francisco, California, United States of America, 41 Andrology Research Unit, Developmental and Regenerative Biomedicine Research Group, The University of Manchester, Manchester Academic Health Science Centre, Manchester Royal Infirmary, Manchester, United Kingdom, 42 Research Centre of Applied and Preventive Cardiovascular Medicine, University of Turku, Finland, 43 Department of Clinical Physiology, Turku University Hospital, Turku, Finland

Abstract

Testosterone concentrations in men are associated with cardiovascular morbidity, osteoporosis, and mortality and are affected by age, smoking, and obesity. Because of serum testosterone's high heritability, we performed a meta-analysis of genome-wide association data in 8,938 men from seven cohorts and followed up the genome-wide significant findings in one in silico (n = 871) and two de novo replication cohorts (n = 4,620) to identify genetic loci significantly associated with serum testosterone concentration in men. All these loci were also associated with low serum testosterone concentration defined as <300 ng/dl. Two single-nucleotide polymorphisms at the sex hormone-binding globulin (SHBG) locus (17p13-p12) were identified as independently associated with serum testosterone concentration (rs12150660, p = 1.2 × 10^{-41}; and rs6258, p = 2.3 × 10^{-22}). Subjects with ≥3 risk alleles of these variants had 6.5-fold higher risk of having low serum testosterone than subjects with no risk allele. The rs5934505 polymorphism near VAMP8 on the X chromosome was also associated with testosterone concentrations (p = 5.6 × 10^{-15}). The rs6258 polymorphism in exon 4 of SHBG affected SHBG's affinity for binding testosterone and the measured free testosterone fraction (p<0.01). Genetic variants in the SHBG locus and on the X chromosome are associated with a substantial variation in testosterone concentrations and increased risk of low testosterone. rs6258 is the first reported SHBG polymorphism, which affects testosterone binding to SHBG and the free testosterone fraction and could therefore influence the calculation of free testosterone using law-of-mass-action equation.
GWAS of Testosterone


Editor: Gonçalo R. Abecasis, University of Michigan, United States of America

Received April 4, 2011; Accepted August 11, 2011; Published October 6, 2011

This is an open-access article distributed under the terms of the Creative Commons Public Domain declaration which stipulates that, once placed in the public domain, this work may be freely reproduced, distributed, transmitted, modified, built upon, or otherwise used by anyone for any lawful purpose.

Funding: Framingham Heart Study (FHS): The FHS phenotype-genotype analyses for this work were supported by the National Institute of Aging (Genetics of Reproductive Life Period and Health Outcomes, R21AG092598; JM Murabito, KL Lunetta, D Kurasik, DP Kiel, WZ Zhuang). The Framingham Heart Study is supported by the National Heart, Lung, and Blood Institute’s Framingham Heart Study Contract No. N01-HC-25195 and its contract with Affymetrix for genotyping services (Contract No. N02-HL-6-4278). Sex hormone measurements were funded primarily by National Institute on Aging grant 1R01AG12106 (Pla S Bhasin and RS Vasani); additional support was provided by the Boston Claude D. Pepper Older Americans Independence Center (SP30AG031679) and a grant from the National Institute on Aging and the National Institute of Arthritis Musculoskeletal and Skin Diseases to DP Kiel (RO1 AG/AR 41398). Analyses reflect intellectual input and resource development from the Framingham Heart Study investigators participating in the SNP Health Association Resource (SHARe) project. A portion of this research was conducted using the Linux Cluster for Genetic Analysis (LinGa-II), funded by the Robert Dawson Evans Endowment of the Department of Medicine at Boston University School of Medicine and Boston Medical Medical Center, Study of Heart in Pomerania (SHIP): Computing resources have been made available by the Leibniz Supercomputing Centre of the Bavarian Academy of Sciences and Humanities (HLRB project h1231). SHIP is part of the Community Medicine Research net of the University of Greifswald, Germany, which is funded by the Federal Ministry of Education and Research (grants no. 01Z20003, 01Z20103, and 01Z20003); the Ministry of Cultural Affairs as well as the Social Ministry of the Federal State of Mecklenburg – West Pomerania. Genome-wide data have been supported by the Federal Ministry of Education and Research (grant no. 03Z20012); and a joint grant from Siemens Healthcare, Erlangen, Germany, and the Federal State of Mecklenburg West Pomerania. The University of Greifswald is a member of the “Center of Knowledge Interchange” program of the Siemens AG. This work is also part of the research project Greifswald Approach to Individualized Medicine (GAIN_MED). The GAIN_MED consortium is funded by the Federal Ministry of Education and Research and the Ministry of Cultural Affairs of the Federal State of Mecklenburg – West Pomerania (03IS2001A). The testosterone reagents used were sponsored by Siemens Healthcare Diagnostics, Eschborn, formerly DPC Biermann GmbH, Bad Nauheim, Germany. Novo Nordisk provided partial grant support for the determination of serum samples and data analysis. Gothenburg Osteoporosis and Obesity Disparities (GOOD) Study: Financial support was received from the Swedish Research Council (K2010-54X-09894:19-3, 2006-3832, and K2010-52X-20229-05-3), the Swedish Foundation for Strategic Research, the ALF/LOU grant in Gothenburg, the Lundberg Foundation, the Torsten and Ragnar Söderberg’s Foundation, Petrus and Augusta Hedlunds Foundation, the Västra Götalandsfonden, the Göteborgs stadsfond, the Göteborg Medical Society, the Nordisk Nordisk Foundation, the Canadian Institutes of Health Research (MOP-15261), and the European Commission grant HEALTH-F2-2008-201865-GEFOS. We would like to acknowledge Maria Netherland at the genomics core facility at University of Gothenburg for statistical analyses. We would also like to thank Dr. Tobias A. Knoch, Luc V. de Zeeuw, Anis Abuseiris, and Rob de Graaf as well as their institutions the Erasmus Computing Grid, Rotterdam, The Netherlands, and especially the national German MedGRID and Services#MedGRID part of the German D-Grid, both funded by the German Bundesministerium fuer Forschung und Technologie under grants #01AK 803 A-H and #01 IG 07015 G for access to their grid resources. Cooperative Research in the Region of Augsburg (KORA): The KORA research platform was initiated and financed by the Helmholtz Center Munich, German Research Center for Environmental Health, which is funded by the Federal Ministry of Education and Research (BMBF) and by the State of Bavaria. Part of this work was financed by the German National Genome Research Network (NGFN-2 and NGFNPlus; 01GI05023). Our research was supported within the Munich Center of Health Research (MCHealth) as part of LMU Munich. This study was in part supported by a grant from the German Federal Ministry of Education and Research (BMBF) to the German Center for Diabetes Research (DZD e.V.). Health, Aging, and Body Composition (Health ABC) Study: This study was supported by National Institute on Aging contracts N01-AG-6-2101, N01-AG-6-2103, and N01-AG-6-2106. The genome-wide association study was funded by NIA grant 1R01AG032098-01A1 to Wake Forest University Health Sciences and genotyping services were provided by the Center for Inherited Disease Research (CIDR). CIDR is funded fully through a federal contract from the National Institutes of Health to The Johns Hopkins University, contract number HHSN268200726209GC. This research was supported (in part) by the Intramural Research Program of the NIH, National Institute on Aging, Rotterdam study (RSI): The generation and management of GWAS genotype data for the Rotterdam study is supported by the Netherlands Organisation of Scientific Research NWO Investments (nr. 175.010.2005.011, 911-03-012). This study is funded by the Research Institute for Diseases in the Elderly (014-93-015; RIDE2), the Netherlands Genomics Initiative (NGI) – Netherlands Consortium of Healthy Aging (NCHA) project nr. DSO-060-810, and funding from the European Commission (HEALTH-F2-2008-201865, GEFOs; HEALTH-F2-2008-35627, TREAT-DI). The Rotterdam Study is funded by the Erasmus Medical Center and Erasmus University Rotterdam; Netherlands Organisation for Health Research and Development (ZonMW); the Research Institute for Diseases in the Elderly (RIDE); the Ministry of Education, Culture, and Science; the Ministry for Health, Welfare, and Sports; the European Commission (DG XII); and the Municipality of Rotterdam. We thank Pascal Arp, Mila Jamai, Dr. Michael Moorhouse, Marien Verkerk, and Sander Bervoets for their help in creating the GWAS database. The authors are grateful to the study participants, the staff from the Rotterdam Study, and the participating general practitioners and pharmacists. We would like to thank Dr. Tobias A. Knoch, Luc V. de Zeeuw, Anis Abuseiris, and Rob de Graaf as well as their institutions the Erasmus Computing Grid, Rotterdam, The Netherlands, and especially the national German MedGRID and Services#MedGRID part of the German D-Grid, both funded by the German Bundesministerium fuer Forschung und Technologie under grants #01AK 803 A-H and #01 IG 07015 G for access to their grid resources. Invecchiare in Chianti (InCHIANTI): The InCHIANTI study (1998–2001) was supported by the Italian Ministry of Health and in part by the U.S. National Institute on Aging (Contracts: 263 MD 9164 and 263 MD 821336); the InCHIANTI Follow-up 1 (2001–2003) was funded by the U.S. National Institute on Aging (Contracts: N1-AG-1-1 and N1-AG-1-2); the InCHIANTI Follow-ups 2 and 3 studies (2004–2010) were financed by the U.S. National Institute on Aging (Contract: N01-AG-5-0022); supported in part by the Intramural research program of the National Institute on Aging, National Institutes of Health, Baltimore, Maryland. European Male Ageing Study (EMAS): The EMAS is funded by the Commission of the European Communities Fifth Framework Programme “Quality of Life and Management of Living Resources” Grant QLK5-CT-2001-00258 and supported by funding from the UK Arthritis Research Campaign. The EMAS Principal Investigator is Professor Frederick Wu, MD; Dept of Endocrinology, Manchester Royal Infirmary, UK. The “EMAS Study Group” consists of the following people: Georgy Bartfai, Steven Boonen, Felipe Casanueva, Joseph D Finni, Gianni Forti, Aleksander Gwercman, Thang S Han, Kate L Holliday, Ipo T Huhtaniemi, Krysztof Kula, Michael EJ Lean, David M Lee, Terence W O'Neill, Neil Pendleton, Margus Punab, Stephen R Pye, Alan J Silman, Abdelouahed Tajar, Wendy Thompson, Dirk Vanderschueren, and Frederick CW Wuj. The authors wish to thank the men who participated in the eight countries and the research/nursing staff in the eight centres: C Pott, Manchester, E Wouters, Leuven, M Nilsson, Malmö, M del Mar Fernandez, Santiago de Compostela, M Jedrzejowska, Lodz, H M Tabo, Tartu, A Heredi, Szeged for their data collection and C Moseley, Manchester for data entry and project coordination. Dr. Vanderschueren is a senior clinical investigator supported by the Clinical Research Fund of the University Hospitals Leuven, Belgium. Dr. Boonen is a senior clinical investigator of the Fund for Scientific Research-Flanders, Belgium (F.W.O.–Vlaanderen). Dr. Boonen is holder of the Leuven University Chair in Metabolic Bone Diseases. The Osteoporotic Fractures in Men Study – Sweden (MoOS Sweden): Financial support was received from the Swedish Research Council (K2010-54X-09894-19-3, 2006-3832), the Swedish Foundation for Strategic Research, the ALF/LOU grant in Gothenburg, the Lundberg Foundation, the Torsten and Ragnar Söderberg’s Foundation, Petrus and Augusta Hedlunds Foundation, the Västra Götalandsfonden, the Göteborg Medical Society, the Nordisk Nordisk Foundation, and the European Commission grant HEALTH-F2-2008-201865-GEFOS. The Cardiovascular Risk in Young Finns Study (YFS): YFS has been financially supported by the Academy of Finland (grant no. 117797, 121584, and 126925), the Social Insurance Institution of Finland, Turku University Foundation, Tampere and Turku University Hospital Medical Funds, Emil Aaltonen Foundation (Tl), Juho Vainio Foundation, Paavo Nurmi Foundation, the Tampere Tuberculosis Foundation, the Orion Oyj Foundation, Finnish Foundation of Cardiovascular Research, and Finnish Cultural Foundation. The funders had no role in study design, data collection and analysis, decision to publish, or preparation of the manuscript.

Competing Interests: The authors have declared that no competing interests exist.

* E-mail: claes.ohlsson@medic.gu.se

# These authors contributed equally to this work.

† These authors were joint senior authors on this work.
**Introduction**

Testosterone, the most important testicular androgen in men, is largely bound to two plasma proteins. Most of the circulating testosterone (~50–60%) is bound with high affinity to sex hormone-binding globulin (SHBG), while a smaller fraction (40–50%) is bound loosely to albumin, and 1–3% is unbound and termed free testosterone [1]. In prospective cohort studies, low serum testosterone concentrations are associated with cardiovascular morbidity, metabolic syndrome [2,3], dyslipidemia [4], hypertension [5], type 2 diabetes mellitus [6], stroke [7], atherosclerosis [8–10], osteoporosis, sarcopenia, and increased mortality risk [11–13]. Thus, there is growing evidence that serum testosterone is a valuable biomarker of men's overall health status. Studies in male twins indicate that there is a strong heritability of serum testosterone. Here we perform a large-scale genome-wide association study to examine the effects of common genetic variants on serum testosterone concentrations. By examining 14,429 men, we show that genetic variants in the sex hormone-binding globulin (SHBG) locus and on the X chromosome are associated with a substantial variation in serum testosterone concentrations and increased risk of low testosterone. The reported associations may now be used in order to better understand the functional background of recently identified disease associations related to low testosterone. Importantly, we identified the first known genetic variant, which affects SHBG's affinity for binding testosterone and the free testosterone fraction and could therefore influence the calculation of free testosterone. This finding suggests that individual-based SHBG-testosterone affinity constants are required depending on the genotype of this single-nucleotide polymorphism.

**Author Summary**

Testosterone is the most important testicular androgen in men. Low serum testosterone concentrations are associated with cardiovascular morbidity, metabolic syndrome, type 2 diabetes mellitus, atherosclerosis, osteoporosis, sarcopenia, and increased mortality risk. Thus, there is growing evidence that serum testosterone is a valuable biomarker of men's overall health status. Studies in male twins indicate that there is a strong heritability of serum testosterone. Here we perform a large-scale genome-wide association study to examine the effects of common genetic variants on serum testosterone concentrations. By examining 14,429 men, we show that genetic variants in the sex hormone-binding globulin (SHBG) locus and on the X chromosome are associated with a substantial variation in serum testosterone concentrations and increased risk of low testosterone. The reported associations may now be used in order to better understand the functional background of recently identified disease associations related to low testosterone. Importantly, we identified the first known genetic variant, which affects SHBG's affinity for binding testosterone and the free testosterone fraction and could therefore influence the calculation of free testosterone. This finding suggests that individual-based SHBG-testosterone affinity constants are required depending on the genotype of this single-nucleotide polymorphism.

**Results**

Meta-analyses of genome-wide association studies for autosomal SNPs

We performed a GWAS of serum testosterone concentrations, investigating ~2.5 million SNPs in 8,936 men of Caucasian ancestry, 18 to 98 years, from seven cohorts. Genome-wide significant SNPs were found in the discovery analysis at one locus on chromosome 17 (17p13-p12) using the criteria described in the methods. The strongest association was found for rs12150660 (p = 1.9 × 10^{-17}), located 11.5 kb upstream of the major transcription start site of sex hormone-binding globulin (SHBG), with a minor allele frequency (MAF) of 23% (Table 1 [SNPs rs12150660 and rs6258], Figure 1A and Figures S1A, S2 and S3). Tests for independently associated SNPs with serum testosterone in this region revealed a second SNP, rs6258 (p = 4.1 × 10^{-15}), which represents a missense (P→L) polymorphism located in exon 4 of SHBG (Table 1 [SNPs rs12150660 and rs6258], Figure 1B) and which had a MAF of 2%. Based on HapMap release 22 (CEU), the r^2 between rs12150660 and rs6258 was 0.904. To validate the independence of these two SNPs, conditional meta-analysis of the discovery cohorts including both rs12150660 and rs6258 in an additive genetic linear model adjusted for covariates was calculated. Because the associations remained significant and mostly unchanged (rs12150660, p = 7.0 × 10^{-15}; rs6258, p = 1.6 × 10^{-15}), both SNPs were independently associated with serum testosterone concentrations. No additional autosomal locus fulfilled the criteria for genome-wide significance.

Replication of autosomal hits

The associations of rs12150660 and rs6258 were confirmed in the three replication cohorts (in silico replication in YFS and de novo replication in MrOS Sweden and EMAS), demonstrating a combined p-value in the discovery and the replication cohorts of 1.2 × 10^{-41} and 2.3 × 10^{-22}, respectively (Table 1 [SNPs rs12150660 and rs6258]). Both SNPs showed considerable heterogeneity of results across the studies as measured by the F statistic [18]. The F values for the discovery meta-analysis using the untransformed total testosterone values were 76.7% and 81.6% for rs12150660 and rs6258, respectively. The heterogeneity was reduced to 39.3% and 75.5% for rs12150660 and rs6258, respectively, by meta-analysing the z-score based untransformed total testosterone values and to 30.9% and 78.0%, respectively, by meta-analysing the inverse-normal transformed testosterone values. For rs12150660, a substantial amount of heterogeneity could be explained by phenotypic variation among the cohorts, whereas for rs6258 one cohort (InCHIANTI) showed consistent opposite effect directions in all models used. To take into account this heterogeneity, we additionally calculated a random effects model for untransformed total testosterone values. The association for rs12150660 remained genome-wide significant in the combined discovery and replication stage meta-analysis, the association for
Table 1. Meta-analyses of discovery and replication cohorts.

<table>
<thead>
<tr>
<th>SNPs rs12150660 and rs6258 (on chromosome 17 in SHBG) identified in GWAS for total testosterone</th>
<th>Discovery</th>
<th>Replication</th>
<th>Combined</th>
</tr>
</thead>
<tbody>
<tr>
<td>SNPs</td>
<td>A1/A2</td>
<td>FREQ*</td>
<td>beta</td>
</tr>
<tr>
<td>Testosterone (ng/dl)</td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>rs12150660</td>
<td>T/G</td>
<td>0.23</td>
<td>2.81</td>
</tr>
<tr>
<td>rs6258</td>
<td>T/C</td>
<td>0.02</td>
<td>-74.7</td>
</tr>
<tr>
<td>SHBG (nmol/l)</td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>rs12150660</td>
<td>T/G</td>
<td>0.23</td>
<td>3.6</td>
</tr>
<tr>
<td>rs6258</td>
<td>T/C</td>
<td>0.02</td>
<td>-6.6</td>
</tr>
<tr>
<td>Testosterone (SHBG-adjusted)</td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>rs12150660</td>
<td>T/G</td>
<td>0.23</td>
<td>11.5</td>
</tr>
<tr>
<td>rs6258</td>
<td>T/C</td>
<td>0.02</td>
<td>-41.8</td>
</tr>
<tr>
<td>Calculated Free Testosterone (ng/dl)</td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>rs12150660</td>
<td>T/G</td>
<td>0.23</td>
<td>-0.1</td>
</tr>
<tr>
<td>rs6258</td>
<td>T/C</td>
<td>0.02</td>
<td>-0.2</td>
</tr>
</tbody>
</table>

<table>
<thead>
<tr>
<th>SNP rs5934505 (on chromosome X near FMAB9) identified in GWAS for SHBG-adjusted total testosterone</th>
<th>Discovery</th>
<th>Replication</th>
<th>Combined</th>
</tr>
</thead>
<tbody>
<tr>
<td>SNPs</td>
<td>A1/A2</td>
<td>FREQ*</td>
<td>beta</td>
</tr>
<tr>
<td>Testosterone (ng/dl)</td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>C/T</td>
<td>0.26</td>
<td>14.1</td>
<td>3.2</td>
</tr>
<tr>
<td>SHBG (nmol/l)</td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>C/T</td>
<td>0.26</td>
<td>-0.2</td>
<td>0.3</td>
</tr>
<tr>
<td>Testosterone (SHBG-adjusted)</td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>C/T</td>
<td>0.26</td>
<td>18.1</td>
<td>3.1</td>
</tr>
<tr>
<td>Calculated Free Testosterone (ng/dl)</td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>C/T</td>
<td>0.26</td>
<td>0.4</td>
<td>0.1</td>
</tr>
</tbody>
</table>

Effects size is given per minor allele. All seven discovery cohorts (n = 8,938) were included in the GWAS of chromosomes 1–22 while only the two largest cohorts (FHS and YFS) had GWAS data available for the X chromosome. A1 = allele 1. A2 = allele 2. FREQ* = Frequency of allele 1. In the KORA cohort, testosterone was measured using plasma but the analyses after excluding KORA yielded similar results. Calculated free testosterone was calculated for all subjects with both testosterone and SHBG available by using a modified law of mass action equation. The concentrations of testosterone and SHBG and a fixed value for SHBG’s dissociation constant were used in these calculations.

doi:10.1371/journal.pgen.1002313.t001

rs6258 reached genome-wide significance after excluding the InCHIANTI cohort (Table S3).

The genetic influence on low serum testosterone concentrations

In Table 2, the serum testosterone concentrations according to genotype are given for the three replication cohorts. As expected, mean serum testosterone concentrations were found to be lower in men with GG than in those with TT genotype for rs12150660. Similarly, men with the CT genotype for rs6258 had lower serum testosterone concentrations than those with CC genotype. The TT genotype of rs6258 was extremely rare and only found in two subjects in the replication cohorts. The two autosomal SNPs identified by GWAS had a significant influence on the risk of having low serum testosterone (serum testosterone $<300$ ng/dl) in both the discovery and the replication cohorts with a combined odds ratio (OR) per minor allele of 0.72 (95% CI, 0.65 – 0.79) and 2.7 (95% CI, 2.1 – 3.5) for rs12150660 and rs6258, respectively (Figure 2A). We analyzed the combined effect of the two SNPs on the risk of having low serum testosterone concentrations according to the number of combined risk alleles for rs12150660 (G) and rs6258 (T) in the three replication cohorts (MrOS Sweden, EMAS, and YFS). The risk of having low serum testosterone concentrations increased by the number of risk alleles with an OR of 1.62 (95% CI, 1.41 – 1.86) for each risk allele (Figure S4). Low serum testosterone concentrations were 6.5-times more prevalent in men with ≥3 risk alleles (30.1% prevalence of low serum testosterone) compared to men without any risk allele (4.6% prevalence of low serum testosterone; Figure 2B).

The role of SHBG in the observed associations

As SNP rs12150660 is located 11.5 kb upstream of SHBG and SNP rs6258 is non-synonymous and located in exon 4 of SHBG, we evaluated the influence of these polymorphisms on SHBG concentrations. Both of these polymorphisms demonstrated a significant association with SHBG concentrations in both the discovery and replication cohorts (Table 1 [SNPs rs12150660 and rs6258]). However, even after adjusting for SHBG concentrations, the associations between these two SNPs and serum testosterone concentrations were still significant (p = 9.0×10^{-8} for rs12150660 and p = 4.5×10^{-7} for rs6258). Free testosterone calculated using law-of-mass-action equation was not associated with either of the two polymorphisms (Table 1 [SNPs rs12150660 and rs6258]). As serum testosterone and SHBG are highly correlated (e.g., in MrOS Sweden $r_s = 0.53$), variations in SHBG concentration might have influenced the observed associations of serum testosterone with other non-SHBG-related loci. Therefore, we performed an additional SHBG-adjusted genome-wide meta-analysis among the discovery cohorts, wherein none of the non-SHBG-related autosomal SNPs reached genome-wide significance (Figure S1B).
The rs6258 polymorphism affects SHBG binding affinity for testosterone and the measured free testosterone fraction

As rs6258 is non-synonymous (P156L) and located in exon 4 of SHBG, we evaluated the serum SHBG steroid-binding capacity of the different rs6258 genotypes. As shown in Figure S5, serum SHBG from CT but not CC subjects had a lower steroid-binding capacity than expected from values obtained by an SHBG immunoassay (p = 0.003). Therefore, we analyzed the SHBG affinity for testosterone using Scatchard plots of SHBG in serum of men with the rs6258 genotype (Figure 3A), and revealed (Figure 3B) a higher mean dissociation constant (Kd) indicative of a lower affinity in CT (Kd = 4.5 nM) and TT (Kd = 4.9 nM) individuals than in CC individuals (Kd = 2.8 nM). Recombinant SHBG corresponding to the T genotype demonstrated a higher dissociation constant (lower affinity) compared with recombinant SHBG corresponding to the C genotype (T genotype Kd = 2.5 nM; C genotype Kd = 1.2 nM, Figure 3C). In addition, the free testosterone fraction measured by an equilibrium dialysis method was 22% higher (p = 1.4 × 10^{-2}) in serum from CT subjects than in serum from CC subjects (Figure 3D).

X chromosome analyses

Imputed values for X chromosome-located SNPs were available for the two larger discovery cohorts (SHIP and FHS; n = 5,067). We performed meta-analyses of imputed X chromosome SNPs for serum testosterone concentrations both with and without SHBG adjustment, revealing one genome-wide significant association for SNP rs5934505 (p = 8.5 × 10^{-9}) in the SHBG-adjusted model (Table 1 [SNP rs5934505] and Figures 1B and S3). This SNP was confirmed in the two replication cohorts with de novo genotyping (MrOS Sweden p = 3.6 × 10^{-3}; EMAS p = 1.5 × 10^{-7}). Meta-analysis of discovery and replication cohorts resulted in a combined p-value of 5.6 × 10^{-16}. The rs5934505 SNP is located in a CNV-insertion area (Xp22), 145 kb upstream of the family with sequence similarity 9, member A (FAM9A) and 79 kb downstream of the family with sequence similarity 9, member B (FAM9B) (Figure 1C). In addition, rs5934505 was located 214 kb upstream of Kallmann syndrome 1 sequence (KAL1). SNP rs5934505 was associated with serum testosterone without SHBG-adjustment (combined p-value of 1.7 × 10^{-7}) and with free testosterone (combined p-value of 6.7 × 10^{-11}), but not with SHBG (Table 1 [SNP rs5934505]). The mean serum testosterone and calculated free testosterone but not SHBG concentrations were lower in men with T genotype than in those with C genotype for rs5934505 (Table 2).

Discussion

This GWAS revealed novel genetic variants that significantly affect circulating testosterone concentrations in men. The presence of three or more risk alleles for the two polymorphisms in the
SHBG loci resulted in markedly decreased testosterone concentrations compared to men with two or less risk alleles. Importantly, one of the identified genetic variations was associated with an alteration in SHBG’s binding affinity for testosterone and the measured free testosterone fraction. In addition, we identified a locus on the X chromosome influencing serum testosterone concentrations. The genetic contribution of the polymorphisms to testosterone concentrations reported here is substantial; as a reference for comparison, the effect of these polymorphisms on testosterone concentrations in men is similar or greater than that for known risk factors such as age, smoking, and BMI [19,20].

These findings improve our understanding of the genetic factors that affect serum testosterone concentrations and contribute to the variation in testosterone concentrations in men. These polymorphisms may assist in the identification of men at risk of low serum testosterone, although the clinical usefulness of these findings remains to be established. As rs12150660 and rs6258 were strongly associated with SHBG concentrations, both SNPs may at least partly affect total testosterone concentrations by modulating SHBG concentrations. Our findings that rs6258 substantially affects SHBG binding affinity and the measured free testosterone fraction raise questions about the use of a single consensus value for SHBG’s dissociation constant in the law of mass action equations used to calculate free testosterone concentrations. As emphasized by the Endocrine Society’s expert panel on androgen deficiency syndromes, low testosterone concentrations alone should not necessarily be viewed as evidence of androgen deficiency [16]. Whether rs935405 near the FAM9B and KAL1 genes on Xp22 renders men susceptible to the increased risk of androgen deficiency remains to be determined. Further studies are required to determine the impact of these genetic variations on sex steroid-related disorders, including osteoporosis, cardiovascular diseases, prostate cancer, and male infertility [21].

Our studies add to the evidence that genetic variations within the SHBG gene may explain some of the inter-individual differences in SHBG concentrations. Our finding that SNP rs6258 results in the production of an SHBG variant with reduced affinity for testosterone provides an explanation for the association between rs6258 and low serum testosterone concentrations. This is the first described genetic variant associated with altered SHBG binding for testosterone. As rs6258 is non-synonymous (P156Leu), located in exon 4 of SHBG and associated with altered SHBG binding for testosterone and free testosterone fraction, rs6258 is likely a functional polymorphism with impact on testosterone binding to SHBG as well as testosterone bioavailability and action at target tissue level.

The SNP rs12150660 that is strongly associated with testosterone concentrations is located 11.5 kb upstream of the coding sequence for SHBG mRNA production in the liver. However, it still resides within the human SHBG locus because several other alternative exon 1 sequences are located up to ~13 kb upstream of the exon 1 sequence that encodes the secretion signal polypeptide of the SHBG precursor in the liver [22]. There are no obvious nuclear protein binding sites within the sequences spanning SNP rs12150660, and it remains to be determined whether this SNP disrupts a cis-element that directly influences SHBG transcription. We have found that rs12150660 is in strong LD ($r^2 = 0.89$) with another common SNP (rs1799941) in the SHBG proximal promoter that was shown to be associated with serum SHBG concentrations [23–25]. Thus, it is highly likely that only one of these polymorphisms is actually functional and therefore both SNPs represent the same signal. It should also be noted that rs1799941 is linked to the number of TAAAA repeats within an Alu sequence upstream of SHBG promoter [26] and that the rs1799941 (A allele) is linked with the presence of six TAAAA repeats in this location which has been reported to be associated with higher SHBG concentrations [27]. In addition, while there does not appear to be any putative transcriptional factor binding sites with the sequence comprising rs12150660, it remains to be determined whether rs12150660 or these other associated SNPs in

| Table 2. Serum sex steroids in the three replication cohorts according to rs12150660, rs6258, and rs5934505 genotype. |
|--------------------------------------------------|--------------------------------------------------|--------------------------------------------------|
| SNPs identified in GWAS for total testosterone | SNP identified in GWAS for SHBG-adjusted testosterone |
| rs12150660 | rs6258 | rs5934505 |
| GG | GT | TT | p-value | CC | CT | TT | p-value | C | T | p-value |
| EMAS | (n = 1310) | (n = 833) | (n = 152) | (n = 2261) | (n = 34) | (n = 410) | (n = 1120) |
| Testosterone (ng/dl) | 454±161 | 490±172 | 544±181 | <0.001 | 474±169 | 358±104 | <0.001 | 495±178 | 473±168 | 0.02 |
| Calculated Free Testosterone (ng/dl) | 8.47±2.53 | 8.53±2.53 | 8.84±2.85 | 0.15 | 8.52±2.56 | 8.14±2.14 | 0.39 | 9.00±2.65 | 8.45±2.49 | <0.001 |
| SHBG (nM) | 39.6±17.1 | 45.2±20.4 | 51.6±20.8 | <0.001 | 42.6±19.0 | 26.8±10.6 | <0.001 | 42.4±20.5 | 42.8±18.9 | 0.69 |
| MrOS Sweden | (n = 1317) | (n = 844) | (n = 123) | (n = 2245) | (n = 31) | (n = 530) | (n = 1765) |
| Testosterone (ng/dl) | 435±170 | 475±177 | 526±171 | <0.001 | 456±174 | 331±125 | <0.001 | 473±177 | 448±173 | 0.005 |
| Calculated Free Testosterone (ng/dl) | 7.98±3.07 | 8.30±3.16 | 8.75±2.99 | 0.005 | 8.16±3.08 | 7.59±2.72 | 0.31 | 8.54±3.27 | 8.03±3.03 | 0.001 |
| SHBG (nM) | 41.0±21.6 | 45.8±22.4 | 49.8±23.0 | <0.001 | 43.5±22.0 | 24.3±12.3 | <0.001 | 43.7±24.1 | 43.1±21.5 | 0.51 |
| YFS | (n = 522) | (n = 329) | (n = 51) | (n = 852) | (n = 48) | (n = 2) |
| Testosterone (ng/dl) | 525±182 | 549±246 | 561±158 | 0.063 | 540±209 | 471±157 | 441±75 | 0.065 | NA |
| Calculated Free Testosterone (ng/dl) | 11.89±5.30 | 12.30±8.92 | 11.57±2.46 | 0.71 | 12.04±6.90 | 11.80±3.42 | 11.55±1.23 | 0.80 | NA |
| SHBG (nM) | 30.0±11.7 | 31.3±11.9 | 35.2±13.1 | 0.007 | 31.2±12.0 | 23.0±8.1 | 20.5±4.0 | <0.001 | NA |

NA = not available. Free testosterone was calculated for all subjects with both testosterone and SHBG available by using a modified law of mass action equation. The concentrations of testosterone and SHBG and a fixed value for SHBG’s dissociation constant were used in these calculations.

doi:10.1371/journal.pgen.1002313.t002
the SHBG gene are functionally important or simply represent proxies of SHBG and testosterone concentrations in men.

Our meta-analyses of imputed X chromosome SNPs revealed one genome-wide significant association for SNP rs5934505, located in a CNV-insertion area (Xp22), 145 kb upstream of family with sequence similarity 9, member A (FAM9A) and 79 kb downstream of family with sequence similarity 9, member B (FAM9B). Both genes, FAM9A and FAM9B, are expressed exclusively in the testis [28] and described here for the first time to be associated with total as well as free testosterone concentrations. rs5934505 is located 214 kb upstream of Kallmann syndrome 1 sequence (KAL1). Although the Kallmann syndrome, a type of hypogonadotropic hypogonadism associated with anosmia and other congenital anomalies, has been linked to mutations in the KAL1 gene on the X chromosome, only 11–14% of Caucasian patients with hypogonadotropic hypogonadism have detectable KAL1 mutations [29], reflecting the considerable genetic heterogeneity of this syndrome.
The strengths of our study include a discovery sample size of 8,938 men, which allowed us at the threshold \( \alpha = 5 \times 10^{-8} \), a 90% power to detect SNPs accounting for 0.5% of the total variance in serum testosterone concentrations, and 99% power to detect SNPs accounting for 1% of the total variance. The SNPs rs12150660, rs6258, and rs5934505 explained 2.3%, 0.9%, and 0.6%, respectively, of the variance in serum testosterone concentrations when evaluated in the MrOS Sweden replication cohort. Future meta-analyses including larger samples will probably reveal additional loci associated with serum testosterone. Further research into the functional significance of these variants will be needed to enable the translation of these findings into the mechanisms of sex steroid-related diseases and strategies for risk assessment. As the causal or etiological role of these polymorphisms in the genesis of low testosterone has not been established, the reported polymorphisms associated with low serum testosterone concentration may be viewed currently as risk markers rather than causal risk factors.

In conclusion, genetic variants in the SHBG locus and on the X chromosome are associated with a substantial variation in testosterone concentrations and increased risk of low testosterone in men. Further studies are needed to determine the impact of these genetic variations on sex hormone-related disorders. rs6258 is the first reported SHBG polymorphism, which affects testosterone binding to SHBG and the free testosterone fraction and could therefore influence the calculation of free testosterone using law-of-mass-action equation.

Methods

Study samples and genotyping

The discovery stage of the GWAS included 8,938 Caucasian men of European descent drawn from seven epidemiological cohorts: the Framingham Heart Study (FHS), the Study of Health in Pomerania (SHIP), the Gothenburg Osteoporosis and Obesity Determinants (GOOD) study, the Cooperative Health Research in
the Region of Augsburg (KORA) study, the Health, Aging and Body Composition (HEALTH ABC) study, the Rotterdam Study (RS1), and the Invecchiare in Chianti (InCHIANTI) (Table S1). The replication stage consisted of 4,620 men from two epidemiological cohorts (the European Male Ageing Study [EMAS] and the Osteoporotic Fractures in Men [MrOS] Sweden study) for de novo genotyping of the top SNPs and one additional cohort (the Young Finns Study, [YFS, n = 871]) with genome-wide association data available and joining the study after stage one was finished for in silico replication (Table S2).

Exclusion criteria included chemical or surgical castration and/or medications affecting sex hormones such as steroid 5-alpha reductase inhibitors, and sex hormone antagonists. All studies were approved by local ethics committees and all participants provided written informed consent. Characteristics of the study samples and detailed descriptions of the participating cohorts, genotyping methods, quality control, and imputation procedures are provided in Text S1.

Genotyping and statistical analyses
Altogether, ~2.5 million SNPs, imputed using the HapMap II CEU population, were tested for association with serum testosterone in the discovery stage. Genome-wide association analyses using an additive genetic linear regression model adjusted for age, BMI, and current smoking were conducted twice within each of the discovery cohorts using serum testosterone expressed as ng/dl, as well as inverse-normal transformed serum testosterone as outcomes.

To examine the robustness of the discovery results and to reduce the risk of spurious associations due to possible testosterone measurement heterogeneity between the individual cohorts, three different types of meta-analyses were performed in the discovery stage: 1) an inverse-variance weighted fixed effect model; 2) a z-score based analysis of the untransformed serum testosterone concentrations; and 3) a z-score based meta-analysis of the inverse-normal transformed values. Model 1) was used as main analysis since it allowed the computation of effect estimates, whereas the other two analysis models were used for verification and quality control checks of the main findings. All meta-analyses were performed using METAL (www.sph.umich.edu/csg/abecasis/metal/). The random effects model of the two SHBG locus SNPs was calculated using the R-package metafor (www.r-project.org). Imputed genotypes were analyzed in all cohorts taking the genotype uncertainties into account. Genomic control was applied to each individual cohort’s results and to the discovery stage meta-analysis to correct p-values for potential effects of mild population stratification. The estimated genomic control lambda was low for both the individual cohorts (range of \( \lambda_{GC} \): 1.00–1.07) and the meta-analyses (range of \( \lambda_{GC} \): 1.01–1.02), suggesting little residual confounding due to population stratification (Figure S2).

To reduce the variance on serum testosterone induced by SHBG concentration, the GWAS included a genome-wide test for association of untransformed serum testosterone concentrations adjusted for age, BMI, current smoking, SHBG and SHBG\(^2\) concentrations, again using both an inverse-variance weighted fixed effect as main analysis and a z-score based meta-analysis for quality control purposes.

A threshold of \( p < 5 \times 10^{-8} \) was established a priori as the level for genome-wide significance in the discovery analyses [30]. SNPs that reached genome-wide significance in the inverse-variance weighted meta-analysis of untransformed serum testosterone concentrations with or without adjustment for SHBG and which had association results in at least five of the seven cohorts (for chr X: two cohorts with data available) were selected for further analyses. Notably, all autosomal SNPs that fulfilled these criteria also reached genome-wide significance in the other two types of meta-analyses. From these SNPs, all independent SNPs were taken to the replication stage.

We also assessed whether the lead SNPs from the continuous trait analyses were associated with low serum testosterone concentration (defined as <300 ng/dl [16]; this level is slightly lower than that suggested recently by Wu et al [11 mmol/l = 317 ng/dl] [17]) by binary logistic regression including the same covariates in the model used for the main analysis and meta-analyzing the within-cohort results using inverse-variance weighted fixed-effect model. The KORA cohort was not included in the meta-analyses of low serum testosterone as testosterone was measured using plasma in this cohort.

We determined the number of low serum testosterone concentration risk alleles (0 to 4) for the two lead SNPs of the SHBG locus in each individual and assessed the risk of low serum testosterone concentrations in the three replication cohorts (MrOS Sweden, EMAS, and YFS) using a trend test. Since only two subjects in the replication cohorts had four risk alleles, individuals having three and four risk alleles were grouped into one category to obtain more reliable effect estimates during the subsequent analyses. Details of test for independence, SHBG related analysis to the replication stage meta-analyses were associated with low serum testosterone concentration (defined as <300 ng/dl [16]; this level is slightly lower than that suggested recently by Wu et al [11 mmol/l = 317 ng/dl] [17]) by binary logistic regression including the same covariates in the model used for the main analysis and meta-analyzing the within-cohort results using inverse-variance weighted fixed-effect model. The KORA cohort was not included in the meta-analyses of low serum testosterone as testosterone was measured using plasma in this cohort.

To reduce the risk of spurious associations due to possible testosterone measurement heterogeneity between the individual cohorts, three different types of meta-analyses were performed in the discovery stage: 1) an inverse-variance weighted fixed effect model; 2) a z-score based analysis of the untransformed serum testosterone concentrations; and 3) a z-score based meta-analysis of the inverse-normal transformed values. Model 1) was used as main analysis since it allowed the computation of effect estimates, whereas the other two analysis models were used for verification and quality control checks of the main findings. All meta-analyses were performed using METAL (www.sph.umich.edu/csg/abecasis/metal/). The random effects model of the two SHBG locus SNPs was calculated using the R-package metafor (www.r-project.org). Imputed genotypes were analyzed in all cohorts taking the genotype uncertainties into account. Genomic control was applied to each individual cohort’s results and to the discovery stage meta-analysis to correct p-values for potential effects of mild population stratification. The estimated genomic control lambda was low for both the individual cohorts (range of \( \lambda_{GC} \): 1.00–1.07) and the meta-analyses (range of \( \lambda_{GC} \): 1.01–1.02), suggesting little residual confounding due to population stratification (Figure S2).

To reduce the variance on serum testosterone induced by SHBG concentration, the GWAS included a genome-wide test for association of untransformed serum testosterone concentrations adjusted for age, BMI, current smoking, SHBG and SHBG\(^2\) concentrations, again using both an inverse-variance weighted fixed effect as main analysis and a z-score based meta-analysis for quality control purposes.

A threshold of \( p < 5 \times 10^{-8} \) was established a priori as the level for genome-wide significance in the discovery analyses [30]. SNPs that reached genome-wide significance in the inverse-variance weighted meta-analysis of untransformed serum testosterone concentrations with or without adjustment for SHBG and which had association results in at least five of the seven cohorts (for chr X: two cohorts with data available) were selected for further analyses. Notably, all autosomal SNPs that fulfilled these criteria also reached genome-wide significance in the other two types of meta-analyses. From these SNPs, all independent SNPs were taken to the replication stage.

We also assessed whether the lead SNPs from the continuous trait analyses were associated with low serum testosterone concentration (defined as <300 ng/dl [16]; this level is slightly lower than that suggested recently by Wu et al [11 mmol/l = 317 ng/dl] [17]) by binary logistic regression including the same covariates in the model used for the main analysis and meta-analyzing the within-cohort results using inverse-variance weighted fixed-effect model. The KORA cohort was not included in the meta-analyses of low serum testosterone as testosterone was measured using plasma in this cohort.

We determined the number of low serum testosterone concentration risk alleles (0 to 4) for the two lead SNPs of the SHBG locus in each individual and assessed the risk of low serum testosterone concentrations in the three replication cohorts (MrOS Sweden, EMAS, and YFS) using a trend test. Since only two subjects in the replication cohorts had four risk alleles, individuals having three and four risk alleles were grouped into one category to obtain more reliable effect estimates during the subsequent analyses. Details of test for independence, SHBG related analysis to the replication stage meta-analyses were associated with low serum testosterone concentration (defined as <300 ng/dl [16]; this level is slightly lower than that suggested recently by Wu et al [11 mmol/l = 317 ng/dl] [17]) by binary logistic regression including the same covariates in the model used for the main analysis and meta-analyzing the within-cohort results using inverse-variance weighted fixed-effect model. The KORA cohort was not included in the meta-analyses of low serum testosterone as testosterone was measured using plasma in this cohort.

Sex hormone measurements
Methods for the measurement of serum testosterone and SHBG are given in Text S1. Calculated free testosterone was for all subjects with both testosterone and SHBG available (n = 13833; Table 1 and Table 2) calculated by using a modified law of mass action equation, as described by Mazer [31]. The concentrations of testosterone and SHBG and a fixed value for SHBG’s dissociation constant were used in these calculations.

Free testosterone fraction
Free testosterone fraction was measured by an equilibrium dialysis method in 87 subjects with the CC genotype and 32 subjects with the CT genotype of rs6258 (Figure 3D) [32]. Detailed description of the free testosterone fraction measurements is provided in Text S1.

Sex hormone-binding globulin assays
In experiments evaluating SHBG binding capacity, serum SHBG concentrations were determined by two-site immuno-fluorometric assay (PerkinElmer Life Sciences, Turku, Finland) [33], or by a steroid-binding capacity assay [34]. For steroid-binding assays, serum samples were pre-incubated with dextran-coated charcoal (DCC) to remove endogenous steroids, prior to incubation with either \([3H]5\alpha\)-dihydrotestosterone (\([3H]\)DHT; specific activity 50 Ci/mmol) or \([3H]\)testosterone (specific activity 40 Ci/mmol), bound from free \([3H]\)steroid were separated using DCC as the separation reagent [34]. The steroid-binding properties of SHBG in diluted serum samples or tissue culture medium were determined by Scatchard analysis [34]. For the expression of SHBG protein, wild type (corresponding to the C-genotype of rs6258) and rs6258 (corresponding to the T-genotype of rs6258) SHBG cDNAs in the pRc/CMV expression vector were transfected into CHO cells, and G418 was used for selection of stably transfected cells. At near confluence, cells were washed with PBS and cultured in serum-free SFM4CHO medium (Thermo Scientific HyClone, Logan, UT) for four days before the SHBG-containing medium was harvested.
Supporting Information

Figure S1 Manhattan plots giving genome-wide –log_{10} p-value according to chromosomal location for inverse-variance weighted meta-analysis of untransformed serum testosterone (A) and SHBG-adjusted serum testosterone (B) using an imputation quality filter (observed/expected variance ratio) >0.4 at the individual cohort level during meta-analysis. All seven discovery cohorts (n = 8,938) were included in the GWAS of chromosomes 1–22 while only the two largest cohorts (FHS and SHIP, n = 5,067) had GWAS data available for the X chromosome.

(PDF)

Figure S2 Quantile-quantile plot of the genome-wide association results of the inverse-variance weighted meta-analysis of untransformed serum testosterone including all SNPs (black) and after removal of the SNPs of the SHBG locus (blue).

(PDF)

Figure S3 Associations for (A) rs12150660 and (B) rs6258 with adjusted serum testosterone (B) using an imputation quality filter according to chromosomal location for inverse-variance weighted allele (CT, solid regression line r^2 = 0.866) or heterozygous for the rs6258 variant (CT, dashed regression line r^2 = 0.872) or heterozygous for the rs6258 variant.

(PDF)

Figure S4 Risk of low serum testosterone concentrations (serum testosterone <300 ng/dl), according to the number of combined risk alleles for rs12150660 (G allele) and rs6258 (T allele) in the three replication cohorts (MrOS Sweden, EMAS, and YFS). Bars indicate 95% confidence intervals. Only two individuals in the three replication cohorts had four risk alleles and therefore individuals with three and four risk alleles were pooled into one group with ≥3 risk alleles. Two risk allele counts were used as reference, since this is the most prevalent amount among the cohorts.

(PDF)

Figure S5 Subjects heterozygous for the SHBG allele containing an rs6258 SNP have lower serum SHBG steroid-binding capacity (Y-axis) when compared to the concentrations of SHBG measured by immunoassay (X-axis). Serum SHBG concentrations from 10 individuals homozygous for the wild type SHBG allele (CC, dashed regression line r^2 = 0.872) or heterozygous for the rs6258 variant SHBG allele (CT, solid regression line r^2 = 0.866) were measured by a time-resolved immunofluorometric assay[33], and a steroid-binding capacity assay using [^3H]DHT as the labelled ligand.[34]

(PDF)

Table S1 Characteristics of 14,429 men from 10 cohorts included in the genome-wide association study meta-analysis.

(PDF)

Table S2 Additional genotyping information for the 10 cohorts included in the genome-wide association study meta-analysis.

(PDF)

Table S3 Meta Analysis of untransformed total testosterone using Random Effect Model.

(PDF)

Text S1 Supplemental methods.

(DOC)

Acknowledgments

We are indebted to the participants and staff of all the studies for their important contributions. Full individual study Acknowledgements are listed in Text S1.

Author Contributions


References


