LETTER

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Genome-wide association study identifies 74 loci associated with educational attainment

A list of authors and their affiliations appears in the online version of the paper.

Educational attainment is strongly influenced by social and other environmental factors, but genetic factors are estimated to account for at least 20% of the variation across individuals[1]. Here we report the results of a genome-wide association study (GWAS) for educational attainment that extends our earlier discovery sample[1,2] of 101,069 individuals to 293,723 individuals, and a replication study in an independent sample of 111,349 individuals from the UK Biobank. We identify 74 genome-wide significant loci associated with the number of years of schooling completed. Single-nucleotide polymorphisms associated with educational attainment are disproportionately found in genomic regions regulating gene expression in the fetal brain. Candidate genes are preferentially expressed in neural tissue, especially during the prenatal period, and enriched for biological pathways involved in neural development. Our findings demonstrate that, even for a behavioural phenotype that is mostly environmentally determined, a well-powered GWAS identifies replicable associated genetic variants that suggest biologically relevant pathways. Because educational attainment is measured in large numbers of individuals, it will continue to be useful as a proxy phenotype in efforts to characterize the genetic influences of related phenotypes, including cognition and neuropsychiatric diseases.

Educational attainment is measured in all main analyses as the number of years of schooling completed (EduYears, $n = 293{,}723$, mean = 14.3, s.d. = 3.6; Supplementary Information sections 1.1–1.2). All GWAS were performed at the cohort level in samples restricted to individuals of European descent whose educational attainment was assessed at or above age 30. A uniform set of quality-control procedures was applied to the cohort-level summary statistics. In our GWAS meta-analysis of ~9.3 million SNPs from the 1000 Genomes Project, we used sample-size weighting and applied a single round of genomic control at the cohort level.

Our meta-analysis identified 74 approximately independent genome-wide significant loci. For each locus, we define the 'lead SNP' as the SNP in the genomic region that has the smallest P value (Supplementary Information section 1.6.1). Figure 1 shows a Manhattan plot with the lead SNPs highlighted. This includes the three SNPs that reached genome-wide significance in the discovery stage of our previous GWAS meta-analysis of educational attainment[1]. The quantile–quantile (Q–Q) plot of the meta-analysis (Extended Data Fig. 1) exhibits inflation ($\lambda_{GC} = 1.28$), as expected under polygenicity[3].

Extended Data Fig. 2 shows the estimated effect sizes of the lead SNPs. The estimates range from 0.014 to 0.048 standard deviations per allele (2.7 to 9.0 weeks of schooling), with incremental R^2 in the range 0.01% to 0.035%.

To quantify the amount of population stratification in the GWAS estimates that remains even after the stringent controls used by the cohorts (Supplementary Information section 1.4), we used linkage-disequilibrium (LD) score regression[4]. The regression results indicate that ~8% of the observed inflation in the mean χ^2 is due to bias rather than polygenic signal (Extended Data Fig. 3a), suggesting that stratification effects are small in magnitude. We also found evidence for polygenic association signal in several within-family analyses, although these are not powered for individual SNP association testing (Supplementary Information section 2 and Extended Data Fig. 3b).

To further test the robustness of our findings, we examined the within-sample and out-of-sample replicability of SNPs reaching genome-wide significance (Supplementary Information sections 1.7–1.8). We found that SNPs identified in the previous educational attainment meta-analysis replicated in the new cohorts included here, and conversely, that SNPs reaching genome-wide significance in the new cohorts replicated in the old cohorts. For the out-of-sample replication analyses of our 74 lead SNPs, we used the interim release of the UK Biobank[5] (UKB) ($n = 111{,}349$). As shown in Extended Data Fig. 4,

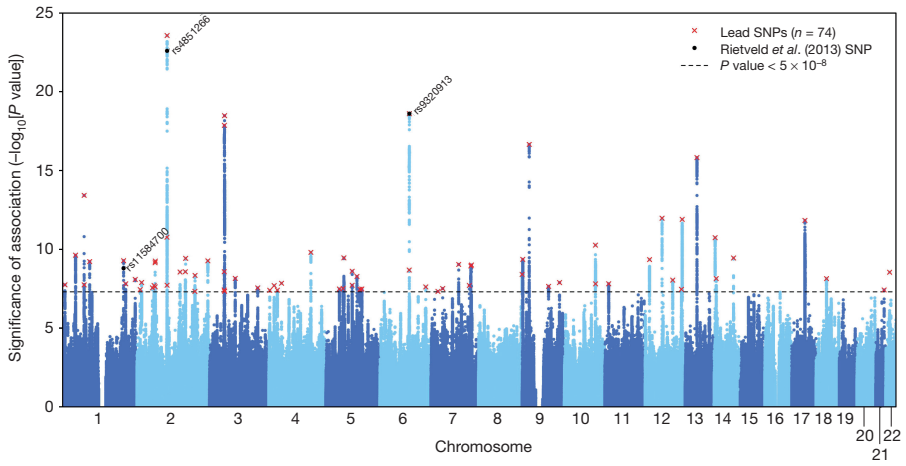

Figure 1 | Manhattan plot for EduYears associations ($n = 293{,}723$). The x axis is chromosomal position, and the y axis is the significance on a $-\log_{10}$ scale (two-tailed test). The black dashed line shows the genome-wide significance level (5×10^{-8}). The red crosses are the 74 approximately independent genome-wide significant associations (lead SNPs). The black dots labelled with rs numbers are the three SNPs identified in ref. 1.

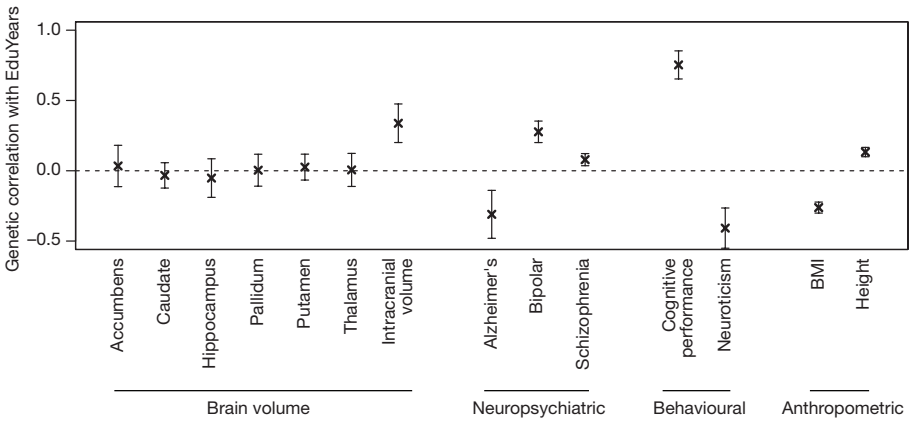

Figure 2 | Genetic correlations between EduYears and other traits. Results from bivariate LD score regressions[9]: estimates of genetic correlation with brain volume, neuropsychiatric, behavioural, and anthropometric phenotypes using published GWAS summary statistics. The error bars show the 95% confidence intervals (CI).

72 out of the 74 lead SNPs have a consistent sign ($P = 1.47 \times 10^{-19}$), 52 are significant at the 5% level ($P = 2.68 \times 10^{-50}$), and 7 reach genome-wide significance in the UK Biobank data set ($P = 1.41 \times 10^{-42}$). For comparison, the corresponding expected numbers, assuming each SNP's true effect size is its estimated effect adjusted for the winner's curse, are 71.4, 40.3, and 0.6. (Supplementary Information section 1.8.2). We also find out-of-sample replicability of our overall GWAS results: the genetic correlation between EduYears in our meta-analysis sample and in the UKB data is 0.95 (s.e. = 0.021; Supplementary Table 1.14).

It is known that educational attainment, cognitive performance, and many neuropsychiatric phenotypes are phenotypically correlated, and several studies of twins find that the phenotypic correlations partly reflect genetic overlap[6–8] (Supplementary Information section 3.3.4). Here we investigate genetic correlation using our GWAS results for EduYears and published GWAS results for 14 other phenotypes, using bivariate LD score regression[9] (Supplementary Information section 3). First, we estimated genetic correlations with EduYears. As shown in Fig. 2, based on overall summary statistics for associated variants, we find genetic covariance between increased educational attainment and increased cognitive performance ($P = 9.9 \times 10^{-50}$), increased intracranial volume ($P = 1.2 \times 10^{-6}$), increased risk of bipolar disorder ($P = 7 \times 10^{-13}$), decreased risk of Alzheimer's ($P = 4 \times 10^{-4}$), and lower neuroticism ($P = 2.8 \times 10^{-8}$). We also found positive, statistically significant, but very small, genetic correlations with height ($P = 5.2 \times 10^{-15}$) and risk of schizophrenia ($P = 3.2 \times 10^{-4}$).

Second, we examined whether our 74 lead SNPs are jointly associated with each phenotype (Extended Data Fig. 5 and Supplementary Information section 3.3.1). We reject the null hypothesis of no enrichment at $P < 0.05$ for 10 of the 14 phenotypes (all the exceptions are subcortical brain structures).

Third, for each phenotype, we tested (in the published GWAS results) each of our 74 lead SNPs (or its proxy) for association at a significance threshold of 0.05/74. We found a total of 25 SNPs meeting this threshold for any of these phenotypes, but only one reaching genome-wide significance. While these results provide suggestive evidence that some of these SNPs may be associated with other phenotypes, further testing of these associations in independent cohorts is required (Supplementary Tables 3.2–3.4, Extended Data Fig. 6).

To consider potential biological pathways, we first tested whether SNPs in particular regions of the genome are implicated by our GWAS results. Unlike what has been found for other phenotypes, SNPs in regions that are DNase I hypersensitive in the fetal brain are more likely to be associated with EduYears by a factor of ~5 (95% confidence interval 2.89–7.07; Extended Data Fig. 7). Moreover, the 15% of SNPs residing in regions associated with histones marked in the central nervous system (CNS) explain 44% of the heritable variation (Extended Data Fig. 8a and Supplementary Table 4.4.2). This enrichment factor of ~3 for CNS ($P = 2.48 \times 10^{-16}$) is greater than that of any of the other nine tissue categories in this analysis.

Given that our findings disproportionately implicate SNPs in regions regulating brain-specific gene expression, we examined whether genes located near EduYears-associated SNPs show elevated expression in neural tissue. We tested this hypothesis using data on mRNA transcript levels in the 37 adult tissues assayed by the Genotype-Tissue Expression Project (GTEx)[10]. Remarkably, the 13 GTEx tissues that are components of the CNS—and only those 13 tissues—show significantly elevated expression levels of genes near EduYears-associated SNPs (false discovery rate <0.05; Extended Data Fig. 8b and Supplementary Table 4.5.2).

To investigate possible functions of the candidate genes from the GWAS-implicated loci, we examined the extent of their overlap with groups of genes ('gene sets') whose products are known or predicted to participate in a common biological process[11]. We found 283 gene sets significantly enriched by the candidate genes identified in our GWAS (false discovery rate <0.05; Supplementary Table 4.5.1). To facilitate interpretation, we used a standard procedure[11] to group the 283 gene sets into 'clusters' defined by degree of gene overlap. The resulting 34 clusters, shown in Fig. 3, paint a coherent picture, with many clusters corresponding to stages of neural development: the proliferation of neural progenitor cells and their specialization (the cluster npBAF complex), the migration of new neurons to the different layers of the cortex (forebrain development, abnormal cerebral cortex morphology), the projection of axons from neurons to their signalling targets (axonogenesis, signalling by Robo receptor), the sprouting of dendrites and their spines (dendrite, dendritic spine organization), and neuronal signalling and synaptic plasticity throughout the lifespan (voltage-gated calcium channel complex, synapse part, synapse organization).

Many of our results implicate candidate genes and biological pathways that are active during distinct stages of prenatal brain development. To directly examine how the expression levels of candidate genes identified in our GWAS vary over the course of development, we used gene expression data from the BrainSpan Developmental Transcriptome[12]. As shown in Extended Data Fig. 9, these candidate genes exhibit above-baseline expression in the brain throughout life but especially higher expression levels in the brain during prenatal development (1.36 times higher prenatally than postnatally, $P = 6.02 \times 10^{-8}$).

A summary overview of some promising candidate genes for follow-up work is provided in Table 1.

We constructed polygenic scores[13] to assess the joint predictive power afforded by the GWAS results (Supplementary Information section 5.2). Across our two holdout samples, the mean predictive

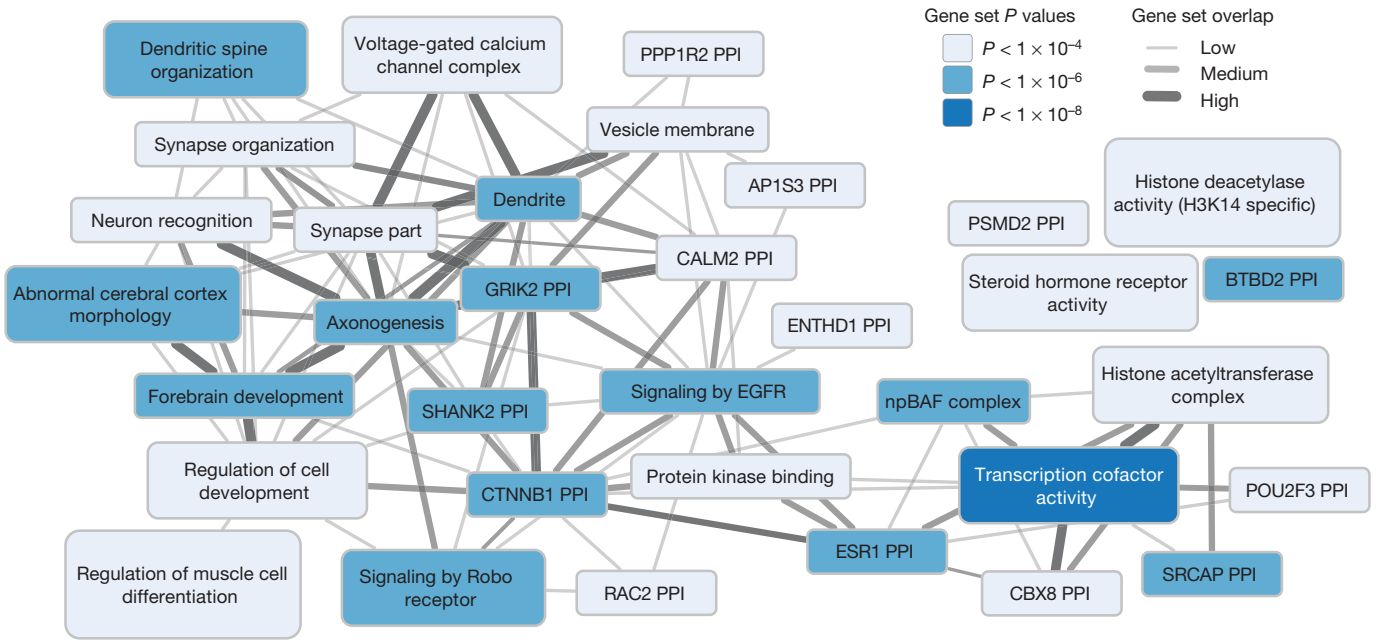

Figure 3 | Overview of biological annotation. Thirty-four clusters of significantly enriched gene sets. Each cluster is named after one of its member gene sets. The colour represents the permutation *P* value of the member set exhibiting the most statistically significant enrichment. Overlap between pairs of clusters is represented by an edge. Edge width represents the Pearson correlation ρ between the two vectors of gene membership scores ($\rho < 0.3$, no edge; $0.3 \leq \rho < 0.5$, thin edge; $0.5 \leq \rho < 0.7$, intermediate edge; $\rho \geq 0.7$, thick edge), where each cluster's vector is the vector for the gene set after which the cluster is named.

power of a polygenic score constructed from all measured SNPs is 3.2% ($P = 1.18 \times 10^{-39}$; Supplementary Table 5.2 and Supplementary Information section 5).

Studies of genetic analyses of behavioural phenotypes have been prone to misinterpretation, such as characterizing identified associated variants as 'genes for education'. Such characterization is not correct for many reasons: educational attainment is primarily determined by environmental factors, the explanatory power of the individual SNPs is small, the candidate genes may not be causal, and the genetic associations with educational attainment are mediated by multiple intermediate phenotypes[14]. To illustrate this last point, we studied mediation of the association between the all-SNPs polygenic score and EduYears in two of our cohorts. We found that cognitive performance can statistically account for 23–42% of the association ($P < 0.001$) and the personality trait 'openness to experience' for approximately 7% ($P < 0.001$; Supplementary Information section 6).

It would also be a mistake to infer from our findings that the genetic effects operate independently of environmental factors. Indeed, a recent meta-analysis of twin studies found that genetic influences on educational attainment are heterogeneous across countries and birth cohorts[15]. We conducted exploratory analyses in the Swedish Twin Registry to illustrate how environmental factors may amplify or dampen the impact of genetic influences (Supplementary Information section 7). We found that the predictive power of the all-SNPs polygenic score is heterogeneous by birth cohort, with smaller explanatory power in younger cohorts (Extended Data Fig. 10; see also Supplementary Information section 7.4 for discussion of the contrast between these

Table 1 | Selected candidate genes implicated by bioinformatics analyses

Gene	SNP	Syndromic	Score	Top-ranking gene sets
TBR1	rs4500960	ID, ASD	6	Developmental biology, decreased brain size, abnormal cerebral cortex morphology
MEF2C	rs7277187	ID, ASD	5	ErbB signalling pathway, abnormal sternum ossification, regulation of muscle cell differentiation
ZSWIM6	rs61160187	–	5	Transcription factor binding, negative regulation of signal transduction, PI3K events in ErbB4 signalling
BCL11A	rs2457660	ASD	5	Dendritic spine organization, abnormal hippocampal mossy fibre morphology, SWI/SNF-type complex
CELSR3	rs11712056	SCZ	5	Dendrite morphogenesis, dendrite development, abnormal hippocampal mossy fibre morphology
MAPT	rs192818565	ID	5	Dendrite morphogenesis, abnormal hippocampal mossy fibre morphology, abnormal axon guidance
SBNO1	rs7306755	SCZ	5	Protein serine/threonine phosphatase complex
NBAS	rs12987662	–	5	–
NBEA	rs9544418	SCZ	4	Developmental biology, signalling by Robo receptor, dendritic shaft
SMARCA2	rs1871109	ID	4	–
MAP4	rs11712056	ASD	4	Developmental biology, signalling by Robo receptor, SWI/SNF-type complex
LINC00461	rs10061788	–	4	Decreased brain size, abnormal cerebral cortex morphology, abnormal hippocampal mossy fibre morphology
POU3F2	rs9320913	–	4	Dendrite morphogenesis, developmental biology, decreased brain size
RAD54L2	rs11712056	SCZ	4	Decreased brain size, SWI/SNF-type complex, nBAF complex
PLK2	rs2964197	–	4	Negative regulation of signal transduction, PI3K events in ErbB4 signalling

Fifteen candidate genes implicated most consistently across various analyses. To assemble this list, each gene in a DEPICT-defined locus (Supplementary Information section 4.5) was assigned a score equal to the number of criteria it satisfies out of ten (see Supplementary Table 4.1 for details). The DEPICT prioritization *P* value was used as the tiebreaker. SNP, the SNP in the gene's locus with the lowest *P* value in the EduYears meta-analysis. Syndromic, which, if any, of three neuropsychiatric disorders have been linked to *de novo* mutations in the gene (Supplementary Information section 4.6). Top-ranking gene sets, DEPICT reconstituted gene sets of which the gene is a top-20 member (Supplementary Table 4.5.1). The three most significant gene sets are shown if more than three are available. ID, intellectual disability; ASD, autism spectrum disorder; SCZ, schizophrenia; ErbB, erythroblastosis oncogene B; PI3K, phosphatidylinositol-4,5-bisphosphate 3-kinase; SWI/SNF, SWitch/sucrose non-fermentable; nBAF, neuronal BRG1- or HRBM-associated factors.

results and findings from a seminal twin study that estimated educational attainment heritability by birth cohort[16]).

Online Content Methods, along with any additional Extended Data display items and Source Data, are available in the online version of the paper; references unique to these sections appear only in the online paper.

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Supplementary Information is available in the online version of the paper.

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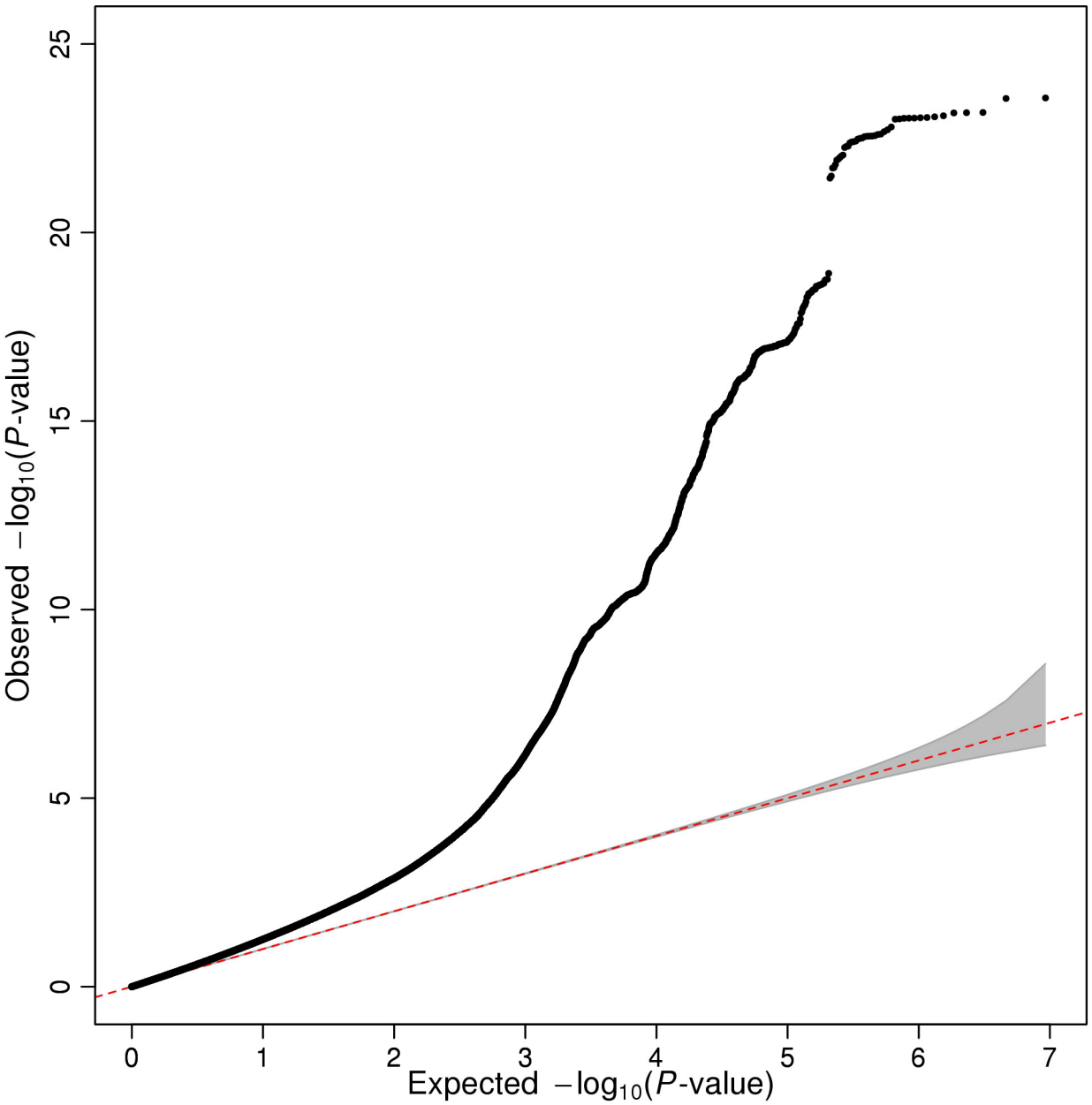
Author Contributions Study design and management: D.J.B., D.Ce., T.E., M.J., P.D.K. and P.M.V. Quality control and meta-analysis: A.O., G.B.C., T.E., M.A.F., C.A.R. and T.H.P. Stratification: P.T., J.P.B., C.A.R. and J.Y. Genetic overlap: J.P.B., M.A.F., P.T. Biological annotation: J.J.L., T.E., T.H.P., J.K.P., J.H.B., J.P.B., L.F., V.E., G.A.M., M.A.F., S.F.W.M., P.Ti., R.A.P., R.d.V. and H.J.W. Prediction and mediation: J.P.B., M.A.F. and J.Y. G×E: D.Co., S.F.L., K.O.L., S.O. and K.T. Replication in UKB: M.A.F. and C.A.R. SSGAC advisory board: D.Co., T.E., A.H., R.F.K., D.I.L., S.E.M., M.N.M., G.D.S. and P.M.V. All authors contributed to and critically reviewed the manuscript. Authors not listed above contributed to the recruitment, genotyping, or data processing for the contributing components of the meta-analysis. For a full list of author contributions, see Supplementary Information section 8.

Author Information Results can be downloaded from the SSGAC website (http://ssgac.org/Data.php). Data for our analyses come from many studies and organizations, some of which are subject to a MTA, and are listed in the Supplementary Information. Reprints and permissions information is available at www.nature.com/reprints. The authors declare no competing financial interests. Readers are welcome to comment on the online version of the paper. Correspondence and requests for materials should be addressed to D.J.B. (daniel.benjamin@gmail.com), D.Ce. (dac12@nyu.edu), P.D.K. (p.d.koellinger@vu.nl) or P.M.V. (peter.visscher@uq.edu.au).

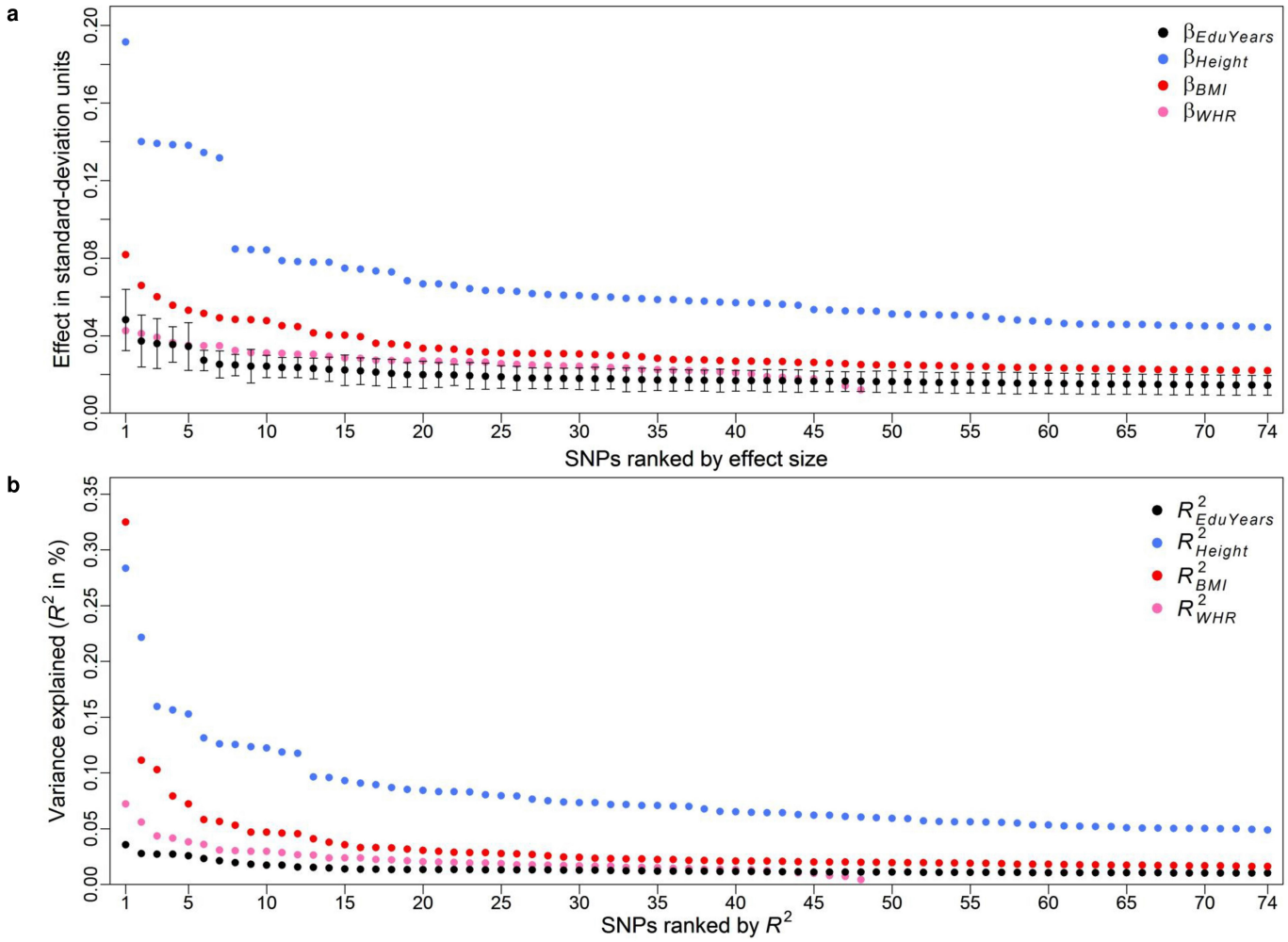
Aysu Okbay[1,2,3]*, Jonathan P. Beauchamp[4]*, Mark Alan Fontana[5]*, James J. Lee[6]*, Tune H. Pers[7,8,9,10]*, Cornelius A. Rietveld[1,2,3]*, Patrick Turley[4]*, Guo-Bo Chen[11], Valur Emilsson[12,13], S. Fleur W. Meddens[3,14,15], Sven Oskarsson[16], Joseph K. Pickrell[17], Kevin Thom[18], Pascal Timshel[8,19], Ronald de Vlaming[1,2,3], Abdel Abdellaoui[20], Tarunveer S. Ahluwalia[9,21,22], Jonas Bacelis[23], Clemens Baumbach[24,25], Gyda Bjornsdottir[26], Johannes H. Brandsma[27], Maria Pina Concas[28], Jaime Derringer[29], Nicholas A. Furlotte[30], Tessel E. Galesloot[31], Giorgia Girotto[32], Richa Gupta[33], Leanne M. Hall[34,35], Sarah E. Harris[36,37], Edith Hofer[38,39], Momoko Horikoshi[40,41], Jennifer E. Huffman[42], Kadri Kaasik[43], Ioanna P. Kalafati[44], Robert Karlsson[45], Augustine Kong[26], Jari Lahti[43,46], Sven J. van der Lee[2], Christiaan de Leeuw[14,47], Penelope A. Lind[48], Karl-Oskar Lindgren[16], Tian Liu[49], Massimo Mangino[50,51], Jonathan Marten[42], Evelin Mihailov[52], Michael B. Miller[6], Peter J. van der Most[53], Christopher Oldmeadow[54,55], Antony Payton[56,57], Natalia Pervjakova[52,58], Wouter J. Peyrot[59], Yong Qian[60], Olli Raitakari[61], Rico Rueedi[62,63], Erika Salvi[64], Börge Schmidt[65], Katharina E. Schraut[66], Jianxin Shi[67], Albert V. Smith[68,69], Raymond A. Poot[27], Beate St Pourcain[70,71], Alexander Teumer[72], Gudmar Thorleifsson[26], Niek Verweij[73], Dragana Vuckovic[32], Juergen Wellmann[74], Harm-Jan Westra[8,75,76], Jingyun Yang[77,78], Wei Zhao[79], Zhihong Zhu[11], Behrooz Z. Alizadeh[53,80], Najaf Amin[2], Andrew Bakshi[11], Sebastian E. Baumeister[72,81], Ginevra Biino[82], Klaus Bønnelykke[21], Patricia A. Boyle[77,83], Harry Campbell[66], Francesco P. Cappuccio[84], Gail Davies[36,85], Jan-Emmanuel De Neve[86], Panos Deloukas[87,88], Ilja Demuth[89,90], Jun Ding[60], Peter Eibich[91,92], Lewin Eisele[65], Niina Eklund[58], David M. Evans[70,93], Jessica D. Faul[94], Mary F. Feitosa[95], Andreas J. Forstner[96,97], Ilaria Gandin[32], Bjarni Gunnarsson[26], Bjarni V. Halldórsson[26,98], Tamara B. Harris[99], Andrew C. Heath[100], Lynne J. Hocking[101], Elizabeth G. Holliday[54,55], Georg Homuth[102], Michael A. Horan[103], Jouke-Jan Hottenga[20], Philip L. de Jager[8,104,105], Peter K. Joshi[66], Astanand Jugessur[106], Marika A. Kaakinen[107], Mika Kähönen[108,109], Stavroula Kanoni[87], Liisa Keltigangas-Järvinen[43], Lambertus A. L. M. Kiemeney[31], Ivana Kolcic[110], Seppo Koskinen[58], Aldi T. Kraja[95], Martin Kroh[91], Zoltan Kutalik[62,63,111], Antti Latvala[33], Lenore J. Launer[112], Maël P. Lebreton[15,113], Douglas F. Levinson[114], Paul Lichtenstein[45], Peter Lichtner[115], David C. M. Liewald[36,85], LifeLines Cohort Study†, Anu Loukola[33], Pamela A. Madden[100], Reedik Mägi[52], Tomi Mäki-Opas[58], Riccardo E. Marioni[11,36,116], Pedro Marques-Vidal[117], Gerardus A. Meddens[118], George McMahon[70], Christa Meisinger[25], Thomas Meitinger[115], Yusplitri Milaneschi[59], Lili Milani[52], Grant W. Montgomery[119], Ronny Myhre[106], Christopher P. Nelson[34,35], Dale R. Nyholt[119,120], William E. R. Ollier[56], Aarno Palotie[8,121,122,123,124,125], Lavinia Paternoster[70], Nancy L. Pedersen[45], Katja E. Petrovic[38], David J. Porteous[37], Katri Räikkönen[43,46], Susan M. Ring[70], Antonietta Robino[126], Olga Rostapshova[4,127], Igor Rudan[66], Aldo Rustichini[128], Veikko Salomaa[58], Alan R. Sanders[129,130], Antti-Pekka Sarin[124,131], Helena Schmidt[38,132], Rodney J. Scott[55,133], Blair H. Smith[134], Jennifer A. Smith[79], Jan A. Staessen[135,136], Elisabeth Steinhagen-Thiessen[89], Konstantin Strauch[137,138], Antonio Terracciano[139], Martin D. Tobin[140], Sheila Ulivi[126], Simona Vaccargiu[28], Lydia Quaye[50], Frank J. A. van Rooij[2,141], Cristina Venturini[50,51], Anna A. E. Vinkhuyzen[11], Uwe Völker[102], Henry Völzke[72], Judith M. Vonk[53], Diego Vozzi[127], Johannes Waage[21,22], Erin B. Ware[79,142], Gonneke Willemsen[20], John R. Attia[54,55], David A. Bennett[77,78], Klaus Berger[73], Lars Bertram[143,144], Hans Bisgaard[21], Dorret I. Boomsma[20], Ingrid B. Borecki[95], Ute Bültmann[145], Christopher F. Chabris[146], Francesco Cucca[147], Daniele Cusi[64,148], Ian J. Deary[36,85], George V. Dedoussis[44], Cornelia M. van Duijn[2], Johan G. Eriksson[46,149], Barbara Franke[150], Lude Franke[151], Paolo Gasparini[32,126,152], Pablo V. Gejman[129,130], Christian Gieger[24], Hans-Jörgen Grabe[153,154], Jacob Gratten[11], Patrick J. F. Groenen[155], Vilmundur Gudnason[12,69], Pim van der Harst[73,151,156], Caroline Hayward[42,157], David A. Hinds[30], Wolfgang Hoffmann[72], Elina Hyppönen[158,159,160], William G. Iacono[6], Bo Jacobsson[23,106], Marjo-Riitta Järvelin[161,162,163,164], Karl-Heinz Jöckel[65], Jaakko Kaprio[33,58,124], Sharon L. R. Kardia[79], Terho Lehtimäki[165,166], Steven F. Lehrer[167,168], Patrik K. E. Magnusson[45], Nicholas G. Martin[169], Matt McGue[6], Andres Metspalu[52,170], Neil Pendleton[171,172], Brenda W. J. H. Penninx[59], Markus Perola[52,58], Nicola Pirastu[32], Mario Pirastu[28], Ozren Polasek[66,173], Danielle Posthuma[14,174], Christine Power[160], Michael A. Province[95], Nilesh J. Samani[34,35], David Schlessinger[60], Reinhold Schmidt[38], Thorkild I. A. Sørensen[9,70,175], Tim D. Spector[50], Kari Stefansson[26,69], Unnur Thorsteinsdottir[26,69], A. Roy Thurik[1,3,176,177], Nicholas J. Timpson[70], Henning Tiemeier[2,178,179], Joyce Y. Tung[30], André G. Uitterlinden[2,180], Veronique Vitart[42], Peter Vollenweider[117], David R. Weir[94], James F. Wilson[42,66], Alan F. Wright[42], Dalton C. Conley[181,182], Robert F. Krueger[6], George Davey Smith[70], Albert Hofman[2], David I. Laibson[4], Sarah E. Medland[48], Michelle N. Meyer[183], Jian Yang[11,93], Magnus Johannesson[184], Peter M. Visscher[11,93]§, Tõnu Esko[7,8,52,185]§, Philipp D. Koellinger[3,14,15]§, David Cesarini[18,186]§ & Daniel J. Benjamin[5]§

[1]Department of Applied Economics, Erasmus School of Economics, Erasmus University Rotterdam, Rotterdam, 3062 PA, The Netherlands. [2]Department of Epidemiology, Erasmus Medical Center, Rotterdam, 3015 GE, The Netherlands. [3]Erasmus University Rotterdam Institute for Behavior and Biology, Rotterdam, 3062 PA, The Netherlands. [4]Department of Economics, Harvard University, Cambridge, Massachusetts 02138, USA. [5]Center for Economic and Social Research, University of Southern California, Los Angeles, California 90089-3332, USA. [6]Department of Psychology, University of Minnesota Twin Cities, Minneapolis, Minnesota 55455, USA. [7]Division of Endocrinology and Center for Basic and Translational Obesity Research, Boston Children's Hospital, Boston, Massachusetts 2116, USA. [8]Program in Medical and Population Genetics, Broad Institute of MIT and Harvard, Cambridge, Massachusetts 02142, USA. [9]The Novo Nordisk Foundation Center for Basic Metabolic Research, Section of Metabolic Genetics, University of Copenhagen, Faculty of Health and Medical Sciences, Copenhagen 2100, Denmark. [10]Statens Serum Institut, Department of Epidemiology Research, Copenhagen 2300, Denmark. [11]Queensland Brain Institute, The University of Queensland, Brisbane, QLD 4072, Australia. [12]Icelandic Heart Association, Kopavogur 201, Iceland. [13]Faculty of Pharmaceutical Sciences, University of Iceland, Reykjavík 107, Iceland. [14]Department of Complex Trait Genetics, VU University, Center for Neurogenomics and Cognitive Research, Amsterdam, 1081 HV, The Netherlands. [15]Amsterdam Business School, University of Amsterdam, Amsterdam, 1018 TV, The Netherlands. [16]Department of Government, Uppsala University, Uppsala 751 20, Sweden. [17]New York Genome Center, New York, New York 10013, USA. [18]Department of Economics, New York University, New York, New York 10012, USA. [19]Center for Biological Sequence Analysis, Department of Systems Biology, Technical University of Denmark Lyngby 2800, Denmark. [20]Department of Biological Psychology, VU University Amsterdam, Amsterdam, 1081 BT, The Netherlands. [21]COPSAC, Copenhagen Prospective Studies on Asthma in Childhood, Herlev and Gentofte Hospital, University of Copenhagen, Copenhagen 2820, Denmark. [22]Steno Diabetes Center, Gentofte 2820, Denmark. [23]Department of Obstetrics and Gynecology, Institute of Clinical Sciences, Sahlgrenska Academy, Gothenburg 416 85, Sweden. [24]Research Unit of Molecular Epidemiology, Helmholtz Zentrum München, German Research Center for Environmental Health, Neuherberg 85764, Germany. [25]Institute of Epidemiology II, Helmholtz Zentrum München, German Research Center for Environmental Health, Neuherberg 85764, Germany. [26]deCODE Genetics/Amgen Inc., Reykjavik 101, Iceland. [27]Department of Cell Biology, Erasmus Medical Center Rotterdam, 3015 CN, The Netherlands. [28]Istituto di Ricerca Genetica e Biomedica U.O.S. di Sassari, National Research Council of Italy, Sassari 07100, Italy. [29]Psychology, University of Illinois, Champaign, Illinois 61820, USA. [30]23andMe, Inc., Mountain View, California 94041, USA. [31]Radboud Institute for Health Sciences, Radboud University Medical Center, Nijmegen, 6500 HB, The Netherlands. [32]Department of Medical, Surgical and Health Sciences, University of Trieste, Trieste 34100, Italy. [33]Department of Public Health, University of Helsinki, 00014 Helsinki, Finland. [34]Department of Cardiovascular Sciences, University of Leicester, Leicester LE3 9QP, UK. [35]NIHR Leicester Cardiovascular Biomedical Research Unit, Glenfield Hospital, Leicester LE3 9QP, UK. [36]Centre for Cognitive Ageing and Cognitive Epidemiology, University of Edinburgh, Edinburgh EH8 9JZ, UK. [37]Centre for Genomic and Experimental Medicine, Institute of Genetics and Molecular Medicine, University of Edinburgh, Edinburgh EH4 2XU, UK. [38]Department of Neurology, General Hospital and Medical University Graz, Graz 8036, Austria. [39]Institute for Medical Informatics, Statistics and Documentation, General Hospital and Medical University Graz, Graz 8036, Austria. [40]Oxford Centre for Diabetes, Endocrinology & Metabolism, University of Oxford, Oxford OX3 7LE, UK. [41]Wellcome Trust Centre for Human Genetics, University of Oxford, Oxford OX3 7BN, UK. [42]MRC Human Genetics Unit, Institute of Genetics and Molecular Medicine, University of Edinburgh, Edinburgh EH4 2XU, UK. [43]Institute of Behavioural Sciences, University of Helsinki, 00014 Helsinki, Finland. [44]Nutrition and Dietetics, Health Science and Education, Harokopio University, Athens 17671, Greece. [45]Department of Medical Epidemiology and Biostatistics, Karolinska Institutet, Stockholm 171 77, Sweden. [46]Folkhälsan Research Centre, 00014 Helsingfors, Finland. [47]Institute for Computing and Information Sciences, Radboud University Nijmegen, Nijmegen, 6525 EC, The Netherlands. [48]Quantitative Genetics, QIMR Berghofer Medical Research Institute, Brisbane, QLD 4029, Australia. [49]Lifespan Psychology, Max Planck Institute for Human Development, Berlin 14195, Germany. [50]Department of Twin Research and Genetic Epidemiology, King's College London, London SE1 7EH, UK. [51]NIHR Biomedical Research Centre, Guy's and St. Thomas' Foundation Trust, London SE1 7EH, UK. [52]Estonian Genome Center, University of Tartu, Tartu 51010, Estonia. [53]Department of Epidemiology, University of Groningen, University Medical Center Groningen, Groningen, 9700 RB, The Netherlands. [54]Public Health Stream, Hunter Medical Research Institute, New Lambton, NSW 2305, Australia. [55]Faculty of Health and Medicine, University of Newcastle, Newcastle, NSW 2300, Australia. [56]Centre for Integrated Genomic Medical Research, Institute of Population Health, The University of Manchester, Manchester M13 9PT, UK. [57]Human Communication and Deafness, School of Psychological Sciences, The University of Manchester, Manchester M13 9PL, UK. [58]Department of Health, THL-National Institute for Health and Welfare, 00271 Helsinki, Finland. [59]Psychiatry, VU University Medical Center & GGZ inGeest, Amsterdam, 1081 HL, The Netherlands. [60]Laboratory of Genetics, National Institute on Aging, Baltimore, Maryland 21224, USA. [61]Research Centre of Applied and Preventive Cardiovascular Medicine, University of Turku, 20521 Turku, Finland. [62]Department of Medical Genetics, University of Lausanne, Lausanne 1005, Switzerland. [63]Swiss Institute of Bioinformatics, Lausanne 1015, Switzerland. [64]Department Of Health Sciences, University of Milan, Milano 20142, Italy. [65]Institute for Medical Informatics, Biometry and Epidemiology, University Hospital of Essen, Essen 45147, Germany. [66]Centre for Global Health Research, The Usher Institute for Population Health Sciences and Informatics, University of Edinburgh, Edinburgh EH8 9AG, UK. [67]Division of Cancer Epidemiology and Genetics, National Cancer Institute, Bethesda, Maryland 20892-9780, USA. [68]Icelandic Heart Association, Kopavogur 201, Iceland. [69]Faculty of Medicine, University of Iceland, Reykjavik 101, Iceland. [70]MRC Integrative Epidemiology Unit, University of Bristol, Bristol BS8 2BN, UK. [71]School of Oral and Dental Sciences, University of Bristol, Bristol BS1 2LY, UK. [72]Institute for Community Medicine, University Medicine Greifswald, Greifswald 17475, Germany. [73]Department of Cardiology, University

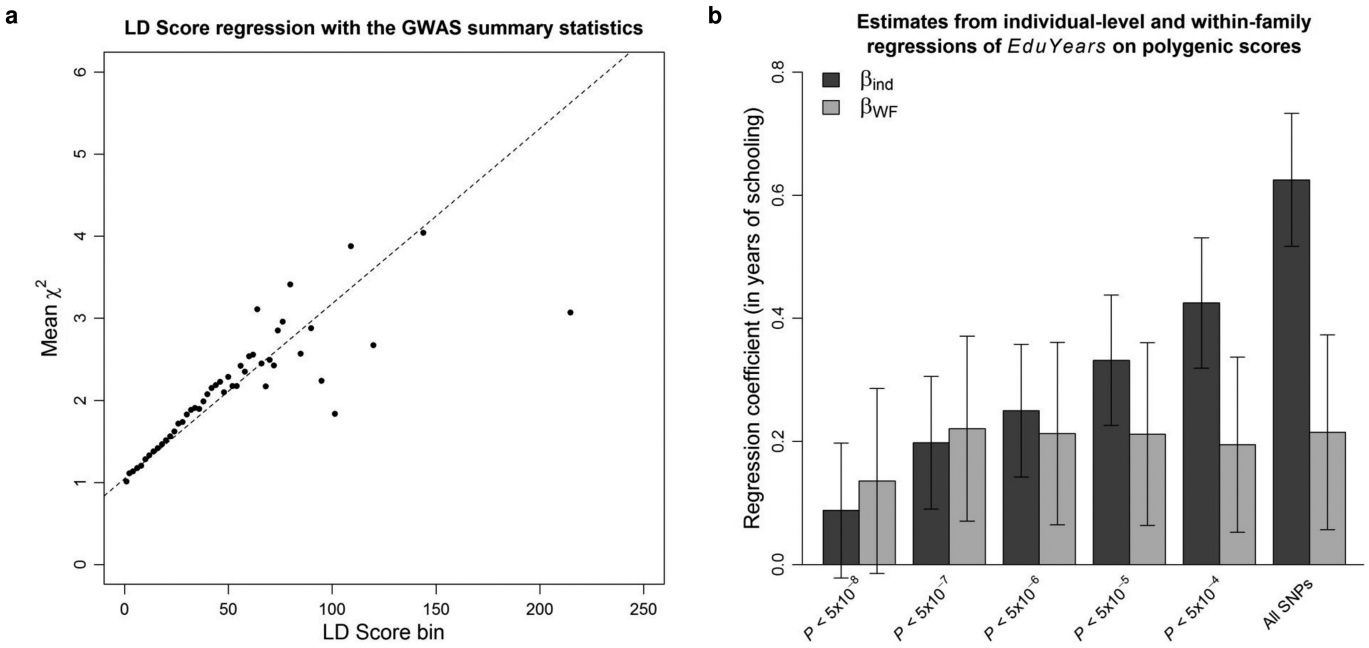
Medical Center Groningen, University of Groningen, Groningen, 9700 RB, The Netherlands. [74]Institute of Epidemiology and Social Medicine, University of Münster, Münster 48149, Germany. [75]Divisions of Genetics and Rheumatology, Department of Medicine, Brigham and Women's Hospital, Harvard Medical School, Boston, Massachusetts 02115, USA. [76]Partners Center for Personalized Genetic Medicine, Boston, Massachusetts 02115, USA. [77]Rush Alzheimer's Disease Center, Rush University Medical Center, Chicago, Illinois 60612, USA. [78]Department of Neurological Sciences, Rush University Medical Center, Chicago, Illinois 60612, USA. [79]Department of Epidemiology, University of Michigan, Ann Arbor, Michigan 48109, USA. [80]Department of Gastroenterology and Hepatology, University of Groningen, University Medical Center Groningen, Groningen, 9713 GZ, The Netherlands. [81]Institute of Epidemiology and Preventive Medicine, University of Regensburg, Regensburg D-93053, Germany. [82]Institute of Molecular Genetics, National Research Council of Italy, Pavia 27100, Italy. [83]Department of Behavioral Sciences, Rush University Medical Center, Chicago, Illinois 60612, USA. [84]Warwick Medical School, University of Warwick, Coventry CV4 7AL, UK. [85]Department of Psychology, University of Edinburgh, Edinburgh EH8 9JZ, UK. [86]Saïd Business School, University of Oxford, Oxford OX1 1HP, UK. [87]William Harvey Research Institute, Barts and The London School of Medicine and Dentistry, Queen Mary University of London, London EC1M 6BQ, UK. [88]Princess Al-Jawhara Al-Brahim Centre of Excellence in Research of Hereditary Disorders (PACER-HD), King Abdulaziz University, Jeddah 21589, Saudi Arabia. [89]The Berlin Aging Study II; Research Group on Geriatrics, Charité – Universitätsmedizin Berlin, Germany, Berlin 13347, Germany. [90]Institute of Medical and Human Genetics, Charité-Universitätsmedizin, Berlin, Berlin 13353, Germany. [91]German Socio- Economic Panel Study, DIW Berlin, Berlin 10117, Germany. [92]Health Economics Research Centre, Nuffield Department of Population Health, University of Oxford, Oxford OX3 7LF, UK. [93]The University of Queensland Diamantina Institute, The Translational Research Institute, Brisbane, QLD 4102, Australia. [94]Survey Research Center, Institute for Social Research, University of Michigan, Ann Arbor, Michigan 48109, USA. [95]Department of Genetics, Division of Statistical Genomics, Washington University School of Medicine, St. Louis, Missouri 63018, USA. [96]Institute of Human Genetics, University of Bonn, Bonn 53127, Germany. [97]Department of Genomics, Life and Brain Center, University of Bonn, Bonn 53127, Germany. [98]Institute of Biomedical and Neural Engineering, School of Science and Engineering, Reykjavik University, Reykjavik 101, Iceland. [99]Laboratory of Epidemiology, Demography, National Institute on Aging, National Institutes of Health, Bethesda, Maryland 20892-9205, USA. [100]Department of Psychiatry, Washington University School of Medicine, St. Louis, Missouri 63110, USA. [101]Division of Applied Health Sciences, University of Aberdeen, Aberdeen AB25 2ZD, UK. [102]Interfaculty Institute for Genetics and Functional Genomics, University Medicine Greifswald, Greifswald 17475, Germany. [103]Manchester Medical School, The University of Manchester, Manchester M13 9PT, UK. [104]Program in Translational NeuroPsychiatric Genomics, Departments of Neurology & Psychiatry, Brigham and Women's Hospital, Boston, Massachusetts 02115, USA. [105]Harvard Medical School, Boston, Massachusetts 02115, USA. [106]Department of Genes and Environment, Norwegian Institute of Public Health, N-0403 Oslo, Norway. [107]Department of Genomics of Common Disease, Imperial College London, London, W12 0NN, UK. [108]Department of Clinical Physiology, Tampere University Hospital, 33521 Tampere, Finland. [109]Department of Clinical Physiology, University of Tampere, School of Medicine, 33014 Tampere, Finland. [110]Public Health, Medical School, University of Split, 21000 Split, Croatia. [111]Institute of Social and Preventive Medicine, Lausanne University Hospital (CHUV), Lausanne 1010, Switzerland. [112]Neuroepidemiology Section, National Institute on Aging, National Institutes of Health, Bethesda, Maryland 20892-9205, USA. [113]Amsterdam Brain and Cognition Center, University of Amsterdam, Amsterdam, 1018 XA, The Netherlands. [114]Department of Psychiatry and Behavioral Sciences, Stanford University, Stanford, California 94305-5797, USA. [115]Institute of Human Genetics, Helmholtz Zentrum München, German Research Center for Environmental Health, Neuherberg 85764, Germany. [116]Medical Genetics Section, Centre for Genomic and Experimental Medicine, Institute of Genetics and Molecular Medicine, University of Edinburgh, Edinburgh, EH4 2XU, UK. [117]Department of Internal Medicine, Internal Medicine, Lausanne University Hospital (CHUV), Lausanne 1011, Switzerland. [118]Tema BV, Hoofddorp, 2131 HE, The Netherlands. [119]Molecular Epidemiology, QIMR Berghofer Medical Research Institute, Brisbane, QLD 4029, Australia. [120]Institute of Health and Biomedical Innovation, Queensland Institute of Technology, Brisbane, QLD 4059, Australia. [121]Analytic and Translational Genetics Unit, Department of Medicine, Massachusetts General Hospital, Boston, Massachusetts 02114, USA. [122]The Stanley Center for Psychiatric Research, Broad Institute of MIT and Harvard, Cambridge, Massachusetts 02142, USA. [123]Psychiatric & Neurodevelopmental Genetics Unit, Department of Psychiatry, Massachusetts General Hospital, Boston, Massachusetts 02114, USA. [124]Institute for Molecular Medicine Finland (FIMM), University of Helsinki, Helsinki 00014, Finland. [125]Department of Neurology, Massachusetts General Hospital, Boston, Massachusetts 02114, USA. [126]Medical Genetics, Institute for Maternal and Child Health IRCCS "Burlo Garofolo", Trieste 34100, Italy. [127]Social Impact, Arlington, Virginia 22201, USA. [128]Department of Economics, University of Minnesota Twin Cities, Minneapolis, Minnesota 55455, USA. [129]Department of Psychiatry and Behavioral Sciences, NorthShore University HealthSystem, Evanston, Illinois 60201-3137, USA. [130]Department of Psychiatry and Behavioral Neuroscience, University of Chicago, Chicago, Illinois 60637, USA. [131]Public Health Genomics Unit, National Institute for Health and Welfare, 00300 Helsinki, Finland. [132]Research Unit for Genetic Epidemiology, Institute of Molecular Biology and Biochemistry, Center of Molecular Medicine, General Hospital and Medical University, Graz, Graz 8010, Austria. [133]Information Based Medicine Stream, Hunter Medical Research Institute, New Lambton, NSW 2305, Australia. [134]Medical Research Institute, University of Dundee, Dundee DD1 9SY, UK. [135]Research Unit Hypertension and Cardiovascular Epidemiology, Department of Cardiovascular Science, University of Leuven, Leuven 3000, Belgium. [136]R&D VitaK Group, Maastricht University, Maastricht, 6229 EV, The Netherlands. [137]Institute of Genetic Epidemiology, Helmholtz Zentrum München, German Research Center for Environmental Health, Neuherberg 85764, Germany. [138]Institute of Medical Informatics, Biometry and Epidemiology, Chair of Genetic Epidemiology, Ludwig Maximilians-Universität, Munich 81377, Germany. [139]Department of Geriatrics, Florida State University College of Medicine, Tallahassee, Florida 32306, USA. [140]Department of Health Sciences and Genetics, University of Leicester, Leicester LE1 7RH, UK. [141]Department of Internal Medicine, Erasmus Medical Center, Rotterdam, 3015 GE, The Netherlands. [142]Research Center for Group Dynamics, Institute for Social Research, University of Michigan, Ann Arbor, Michigan 48104, USA. [143]Platform for Genome Analytics, Institutes of Neurogenetics & Integrative and Experimental Genomics, University of Lübeck, Lübeck 23562, Germany. [144]Neuroepidemiology and Ageing Research Unit, School of Public Health, Faculty of Medicine, Imperial College of Science, Technology and Medicine, London SW7 2AZ, UK. [145]Department of Health Sciences, Community & Occupational Medicine, University of Groningen, University Medical Center Groningen, Groningen, 9713 AV, The Netherlands. [146]Department of Psychology, Union College, Schenectady, New York 12308, USA. [147]Istituto di Ricerca Genetica e Biomedica (IRGB), Consiglio Nazionale delle Ricerche, c/o Cittadella Universitaria di Monserrato, Monserrato, Cagliari 9042, Italy. [148]Institute of Biomedical Technologies, Italian National Research Council, Segrate (Milano) 20090, Italy. [149]Department of General Practice and Primary Health Care, University of Helsinki, 00014 Helsinki, Finland. [150]Departments of Human Genetics and Psychiatry, Donders Centre for Neuroscience, Nijmegen, 6500 HB, The Netherlands. [151]Department of Genetics, University Medical Center Groningen, University of Groningen, Groningen, 9700 RB, The Netherlands. [152]Sidra, Experimental Genetics Division, Sidra, Doha 26999, Qatar. [153]Department of Psychiatry and Psychotherapy, University Medicine Greifswald, Greifswald 17475, Germany. [154]Department of Psychiatry and Psychotherapy, HELIOS-Hospital Stralsund, Stralsund 18437, Germany. [155]Econometric Institute, Erasmus School of Economics, Erasmus University Rotterdam, Rotterdam, 3062 PA, The Netherlands. [156]Durrer Center for Cardiogenetic Research, ICIN-Netherlands Heart Institute, Utrecht, 1105 AZ, The Netherlands. [157]Generation Scotland, Centre for Genomics and Experimental Medicine, Institute of Genetics and Molecular Medicine, University of Edinburgh, Edinburgh EH4 2XU, UK. [158]Centre for Population Health Research, School of Health Sciences and Sansom Institute, University of South Australia, Adelaide, SA 5000, Australia. [159]South Australian Health and Medical Research Institute, Adelaide, SA 5000, Australia. [160]Population, Policy and Practice, UCL Institute of Child Health, London WC1N 1EH, UK. [161]Department of Epidemiology and Biostatistics, MRC-PHE Centre for Environment & Health, School of Public Health, Imperial College London, London W2 1PG, UK. [162]Center for Life Course Epidemiology, Faculty of Medicine, University of Oulu, 90014 Oulu, Finland. [163]Unit of Primary Care, Oulu University Hospital, 90029 Oulu, Finland. [164]Biocenter Oulu, University of Oulu, 90014 Oulu, Finland. [165]Fimlab Laboratories, 33520 Tampere, Finland. [166]Department of Clinical Chemistry, University of Tampere, School of Medicine, 33014 Tampere, Finland. [167]Economics, NYU Shanghai, 200122 Pudong, China. [168]Policy Studies, Queen's University, Kingston, Ontario K7L 3N6, Canada. [169]Genetic Epidemiology, QIMR Berghofer Medical Research Institute, Brisbane, QLD 4029, Australia. [170]Institute of Molecular and Cell Biology, University of Tartu, Tartu 51010, Estonia. [171]Centre for Clinical and Cognitive Neuroscience, Institute Brain Behaviour and Mental Health, Salford Royal Hospital, Manchester M6 8HD, UK. [172]Manchester Institute for Collaborative Research in Ageing, University of Manchester, Manchester M13 9PL, UK. [173]Faculty of Medicine, University of Split, Split 21000, Croatia. [174]Department of Clinical Genetics, VU Medical Centre, Amsterdam, 1081 HV, The Netherlands. [175]Institute of Preventive Medicine. Bispebjerg and Frederiksberg Hospitals, The Capital Region, Frederiksberg 2000, Denmark. [176]Montpellier Business School, Montpellier 34080, France. [177]Panteia, Zoetermeer, 2715 CA, The Netherlands. [178]Department of Psychiatry, Erasmus Medical Center, Rotterdam, 3015 GE, The Netherlands. [179]Department of Child and Adolescent Psychiatry, Erasmus Medical Center, Rotterdam, 3015 GE, The Netherlands. [180]Department of Internal Medicine, Erasmus Medical Center, Rotterdam, 3015 GE, The Netherlands. [181]Department of Sociology, New York University, New York, New York 10012, USA. [182]School of Medicine, New York University, New York, New York 10016, USA. [183]Bioethics Program, Union Graduate College – Icahn School of Medicine at Mount Sinai, Schenectady, New York 12308, USA. [184]Department of Economics, Stockholm School of Economics, Stockholm 113 83, Sweden. [185]Department of Genetics, Harvard Medical School, Boston, Massachusetts 02115, USA. [186]Research Institute for Industrial Economics, Stockholm 10215, Sweden.
*These authors contributed equally to this work.
§These authors jointly supervised this work.
†A list of participants and affiliations appears in the Supplementary Information.



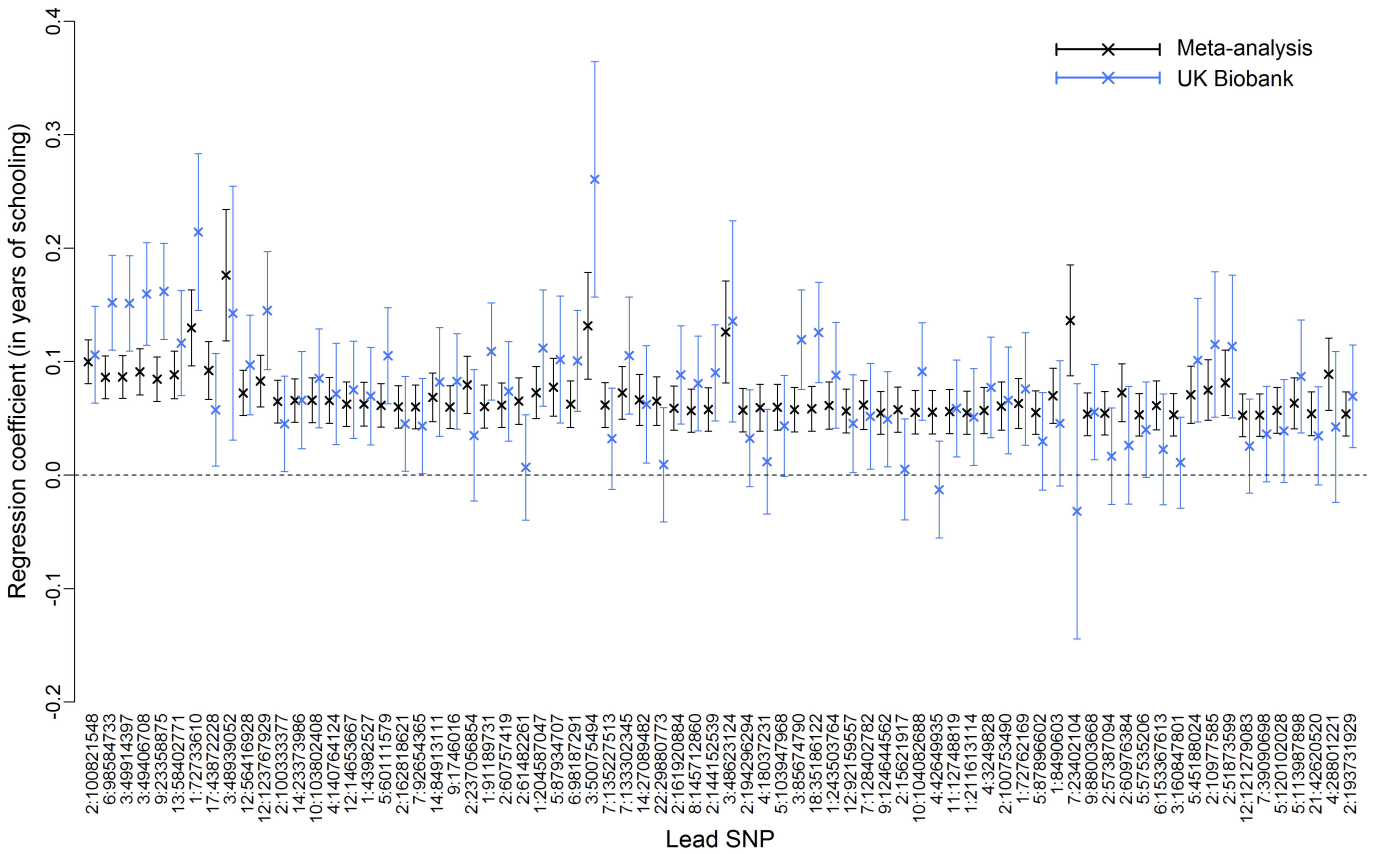
Extended Data Figure 1 | Q–Q plot of the genome-wide association meta-analysis of 64 EduYears results files ($n = 293{,}723$). Observed and expected P values are on a $-\log_{10}$ scale (two-tailed). The grey region depicts the 95% confidence interval under the null hypothesis of a uniform P value distribution. The observed λ_{GC} is 1.28. (As reported in Supplementary Information section 1.5.4, the unweighted mean λ_{GC} is 1.02, the unweighted median is 1.01, and the range across cohorts is 0.95–1.15.)



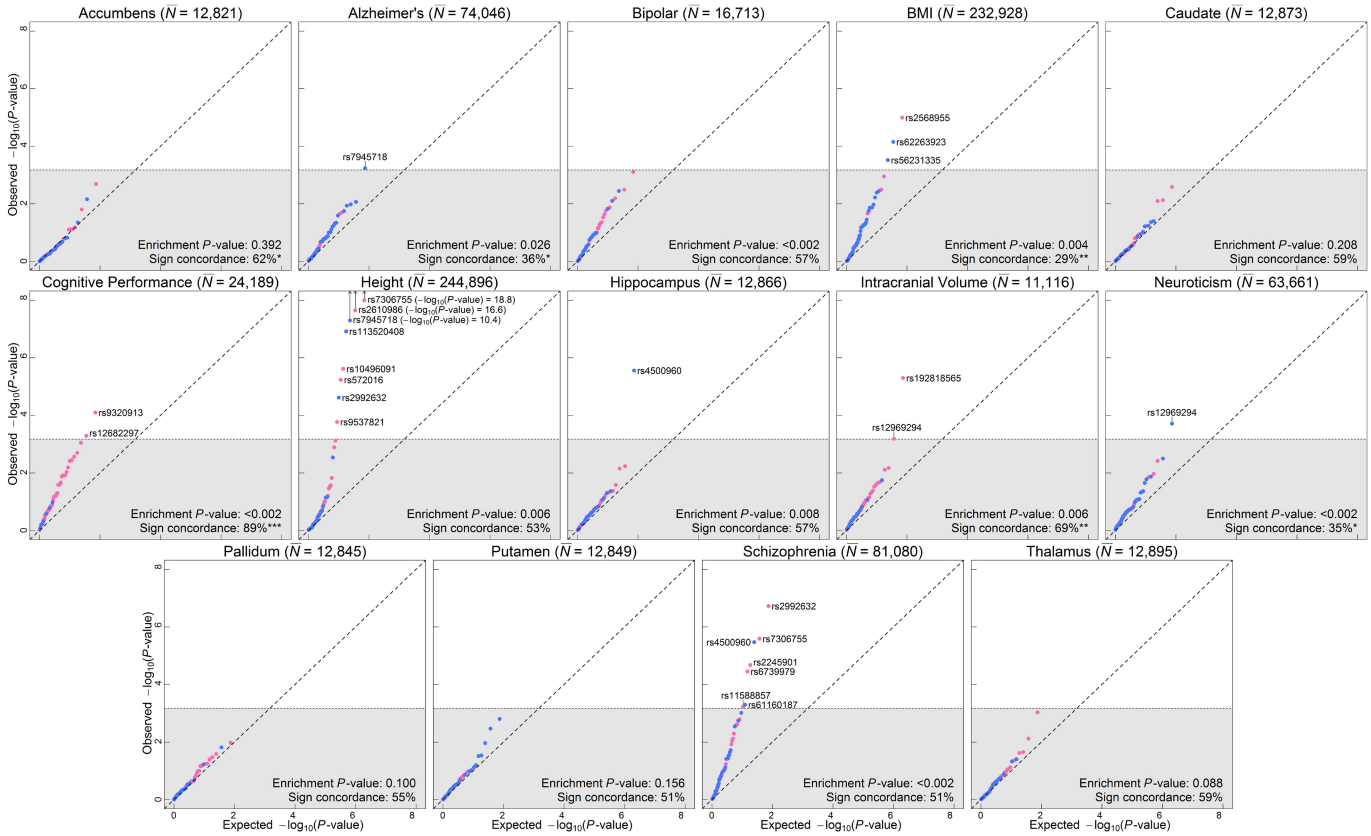
Extended Data Figure 2 | The distribution of effect sizes of the 74 lead SNPs. a, SNPs ordered by absolute value of the standardized effect of one more copy of the education-increasing allele, with 95% confidence intervals. **b**, SNPs ordered by R^2. Effects on EduYears are benchmarked against the top 74 genome-wide significant hits identified in the largest GWAS conducted to date of height and body mass index (BMI), and the 48 associations reported for waist-to-hip ratio adjusted for BMI (WHR). These results are based on the GIANT consortium's publicly available results for pooled analyses restricted to European-ancestry individuals: https://www.broadinstitute.org/collaboration/giant/index.php/GIANT_consortium.



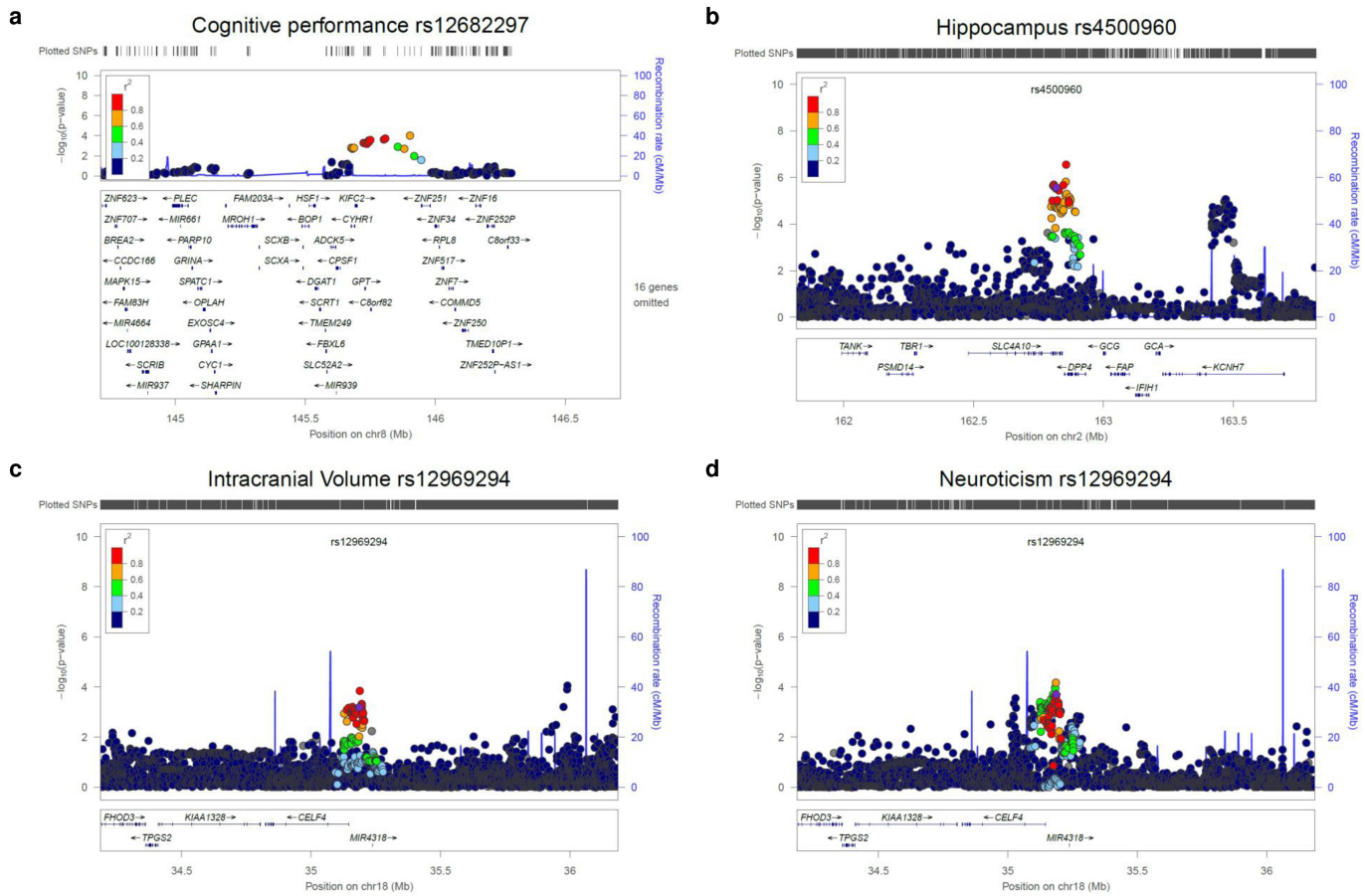
Extended Data Figure 3 | Assessing the extent to which population stratification affects the estimates from the GWAS. a, LD score regression plot with the summary statistics from the GWAS. Each point represents an LD score quantile for a chromosome (the *x* and *y* coordinates of the point are the mean LD score and the mean χ^2 statistic of variants in that quantile). That the intercept is close to 1 and that the χ^2 statistics increase linearly with the LD scores suggest that the bulk of the inflation in the χ^2 statistics is due to true polygenic signal and not to population stratification. **b**, Estimates and 95% confidence intervals from individual-level and within-family regressions of EduYears on polygenic scores, for scores constructed with sets of SNPs meeting different *P* value thresholds. In addition to the analyses shown here, we conduct a sign concordance test, and we decompose the variance of the polygenic score. Overall, these analyses suggest that population stratification is unlikely to be a major concern for our 74 lead SNPs. See Supplementary Information section 3 for additional details.



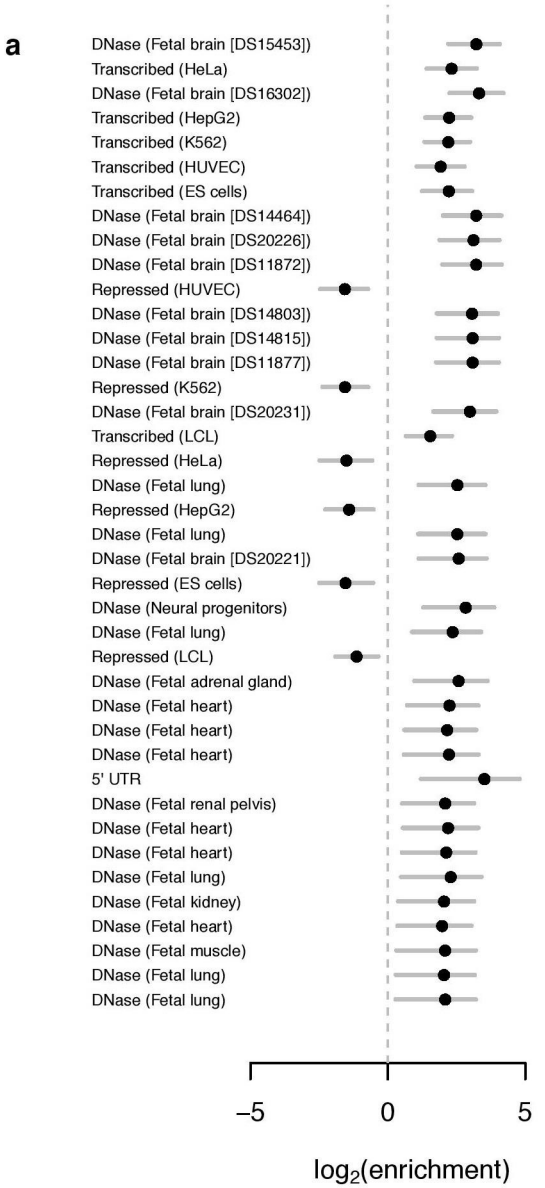
Extended Data Figure 4 | Replication of 74 lead SNPs in the UK Biobank data. Estimated effect sizes (in years of schooling) and 95% confidence intervals of the 74 lead SNPs in the meta-analysis sample ($n = 293{,}723$) and the UK Biobank replication sample ($n = 111{,}349$). The reference allele is the allele associated with higher values of EduYears in the meta-analysis sample. SNPs are in descending order of R^2 in the meta-analysis sample. Of the 74 lead SNPs, 72 have the anticipated sign in the replication sample, 52 replicate at the 0.05 significance level, and 7 replicate at the 5×10^{-8} significance level.

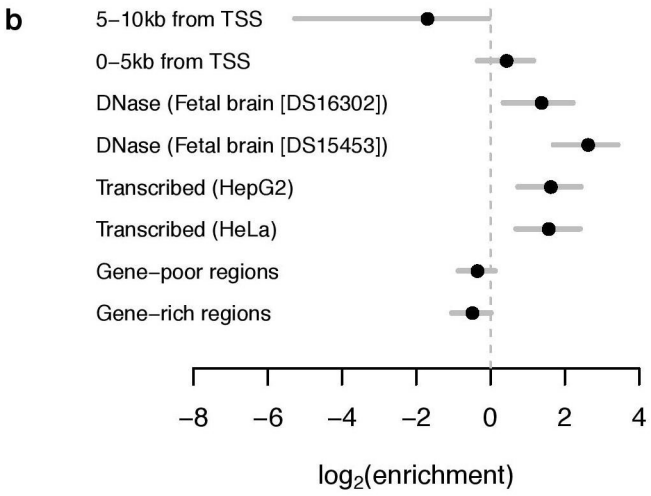


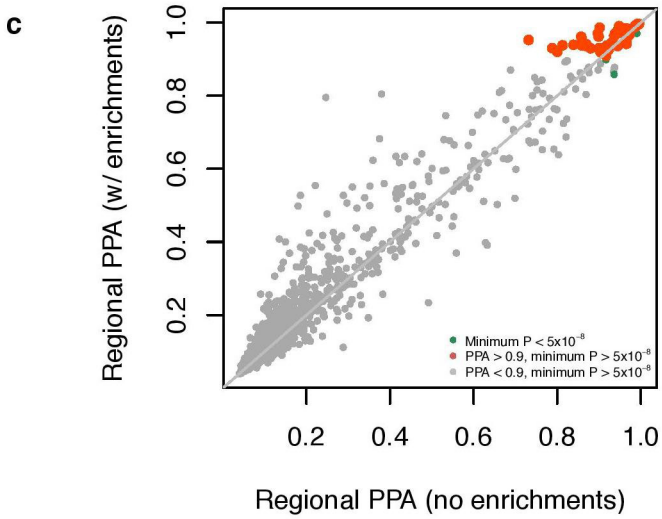
Extended Data Figure 5 | Q–Q plots for the 74 lead EduYears SNPs (or LD proxies) in published GWAS of other phenotypes. SNPs with concordant effects on both phenotypes are pink, and SNPs with discordant effects are blue. SNPs outside the grey area pass Bonferroni-corrected significance thresholds that correct for the total number of SNPs we tested ($P < 0.05/74 = 6.8 \times 10^{-4}$) and are labelled with their rs numbers. Observed and expected P values are on a $-\log_{10}$ scale. For the sign concordance test: $^{*}P < 0.05$, $^{**}P < 0.01$ and $^{***}P < 0.001$.



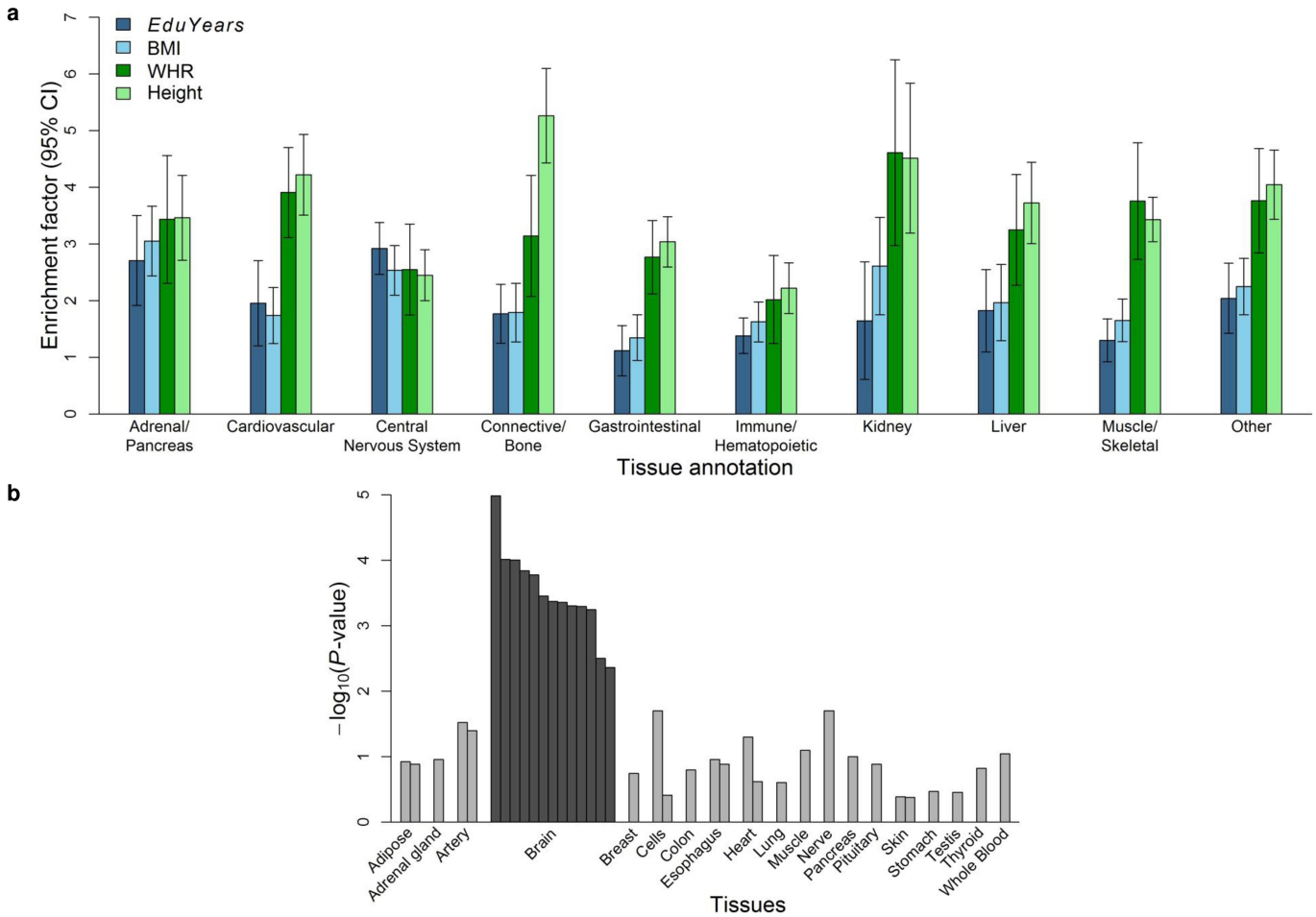
Extended Data Figure 6 | Regional association plots for four of the ten prioritized SNPs for mental health, brain anatomy, and anthropometric phenotypes identified using EduYears as a proxy phenotype. **a**, Cognitive performance; **b**, hippocampus; **c**, intracranial volume; **d**, neuroticism. The four were selected because very few genome-wide significant SNPs have been previously reported for these traits. Data sources and methods are described in Supplementary Information section 3. The R^2 values are from the hg19 / 1000 Genomes Nov 2014 EUR references samples. The figures were created with LocusZoom (http://csg.sph.umich.edu/locuszoom/). Mb, megabases.



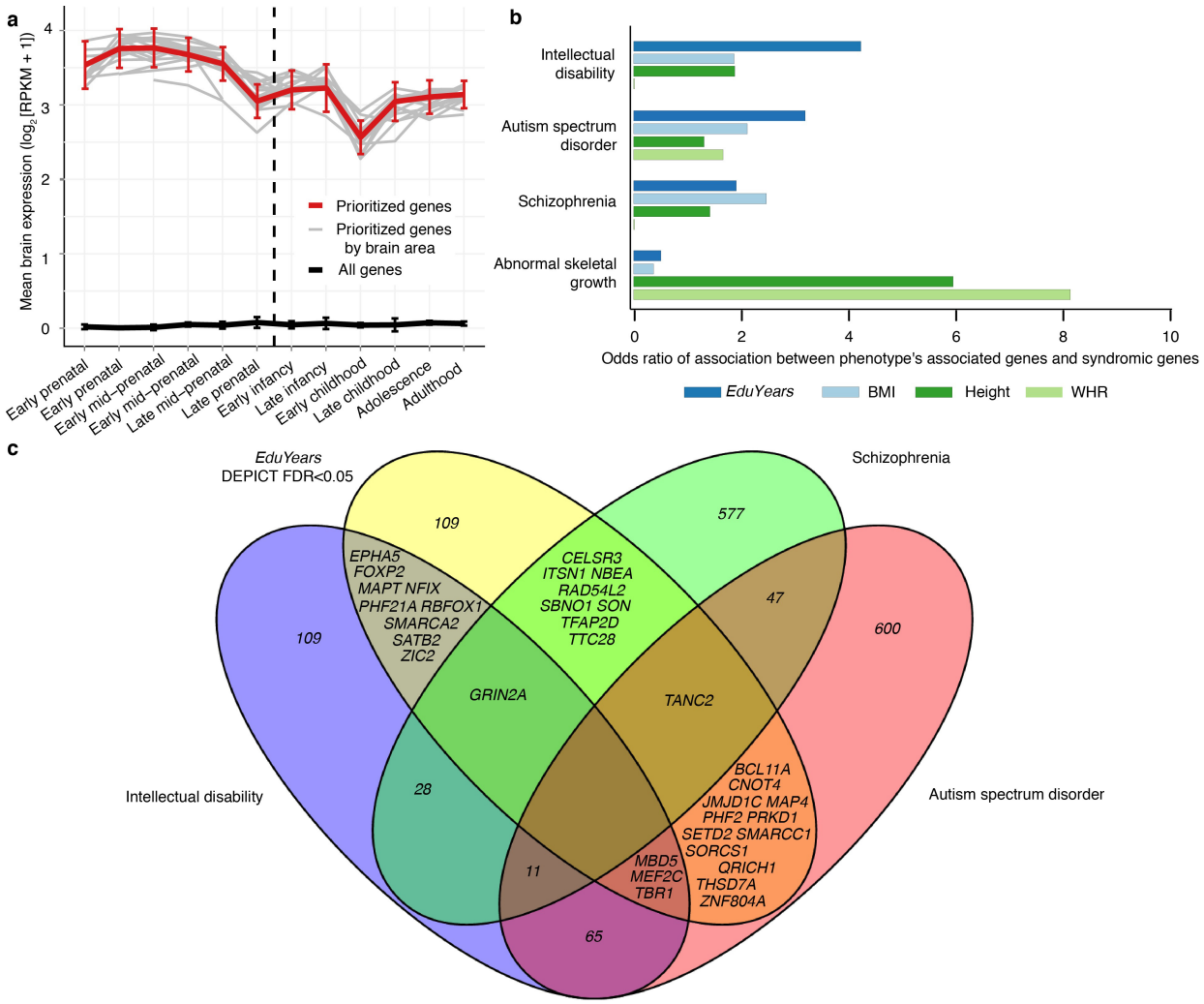




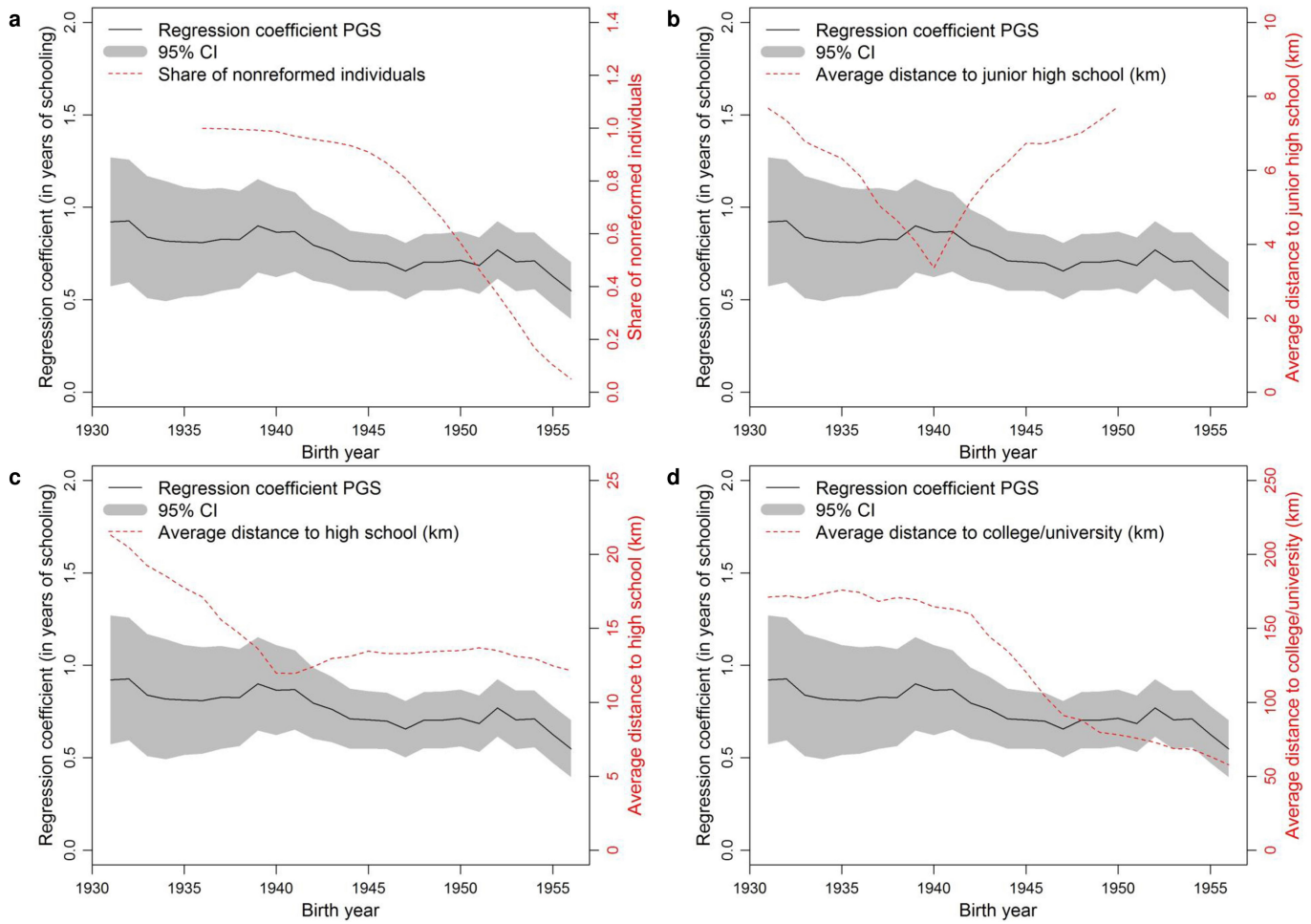
Extended Data Figure 7 | Application of fgwas to EduYears. See Supplementary Information section 4.2 for further details. **a**, The results of single-annotation models. 'Enrichment' refers to the factor by which the prior odds of association at an LD-defined region must be multiplied if the region bears the given annotation; this factor is estimated using an empirical Bayes method applied to all SNPs in the GWAS meta-analysis regardless of statistical significance. Annotations were derived from ENCODE and a number of other data sources. Plotted are the base 2 logarithms of the enrichments and their 95% confidence intervals. Multiple instances of the same annotation correspond to independent replicates of the same experiment. **b**, The results of combining multiple annotations and applying model selection and cross-validation. Although the maximum-likelihood estimates are plotted, model selection was performed with penalized likelihood. **c**, Reweighting of GWAS loci. Each point represents an LD-defined region of the genome, and shown are the regional posterior probabilities of association (PPAs). The *x* axis gives the PPA calculated from the GWAS summary statistics alone, whereas the *y* axis gives the PPA upon reweighting on the basis of the annotations in **b**. The orange points represent genomic regions where the PPA is equivalent to the standard GWAS significance threshold only upon reweighting.



Extended Data Figure 8 | Tissue-level biological annotation. a, The enrichment factor for a given tissue type is the ratio of variance explained by SNPs in that group to the overall fraction of SNPs in that group. To benchmark the estimates for EduYears, we compare the enrichment factors to those obtained when we use the largest GWAS conducted to date on BMI, height, and waist-to-hip ratio adjusted for BMI. The estimates were produced with the LDSC Python software, using the LD scores and functional annotations introduced in ref. 17 and the HapMap3 SNPs with minor allele frequency >0.05. Each of the ten enrichment calculations for a particular cell type is performed independently, while each controlling for the 52 functional annotation categories in the full baseline model. The error bars show the 95% confidence intervals. **b**, We took measurements of gene expression by the Genotype-Tissue Expression (GTEx) Consortium and determined whether the genes overlapping EduYears-associated loci are significantly overexpressed (relative to genes in random sets of loci matched by gene density) in each of 37 tissue types. These types are grouped in the panel by organ. The dark bars correspond to tissues where there is significant overexpression. The *y* axis is the significance on a $-\log_{10}$ scale.



Extended Data Figure 9 | Gene-level biological annotation. a, The DEPICT-prioritized genes for EduYears measured in the BrainSpan Developmental Transcriptome data (red curve) are more strongly expressed in the brain prenatally rather than postnatally. The DEPICT-prioritized genes exhibit similar gene expression levels across different brain regions (grey lines). Analyses were based on $\log_2$-transformed RNA-seq data. Error bars represent 95% confidence intervals. **b**, For each phenotype and disorder, we calculated the overlap between the phenotype's DEPICT-prioritized genes and genes believed to harbour *de novo* mutations causing the disorder. The bars correspond to odds ratios. **c**, DEPICT-prioritized genes in EduYears-associated loci exhibit substantial overlap with genes previously reported to harbour sites where mutations increase risk of intellectual disability and autism spectrum disorder (Supplementary Table 4.6.1).



Extended Data Figure 10 | The predictive power of a polygenic score (PGS) varies in Sweden by birth cohort. Five-year rolling regressions of years of education on the PGS (left axis in all four panels), share of individuals not affected by the comprehensive school reform (**a**, right axis), and average distance to nearest junior high school (**b**, right axis), nearest high school (**c**, right axis) and nearest college/university (**d**, right axis). The shaded area displays the 95% confidence intervals for the PGS effect.