SCIENTIFIC REPORTS

Received: 27 September 2016 Accepted: 30 March 2017 Published online: 19 June 2017

OPEN A genome-wide association study of anorexia nervosa suggests a risk locus implicated in dysregulated leptin signaling

Dong Li¹, Xiao Chang¹, John J. Connolly¹, Lifeng Tian¹, Yichuan Liu¹, Elizabeth J. Bhoj¹, Nora Robinson¹, Debra Abrams¹, Yun R. Li¹, Jonathan P. Bradfield¹, Cecilia E. Kim¹, Jin Li¹, Fengxiang Wang¹, James Snyder¹, Maria Lemma¹, Cuiping Hou¹, Zhi Wei¹, Yiran Guo ¹, Haijun Qiu¹, Frank D. Mentch¹, Kelly A. Thomas¹, Rosetta M. Chiavacci¹, Roger Cone^{2,5}, Bingshan Li², Patrick A. Sleiman¹, Eating Disorders Working Group of the Psychiatric Genomics Consortium, Price Foundation Collaborative Group & Hakon Hakonarson^{1,3,4}

We conducted a genome-wide association study (GWAS) of anorexia nervosa (AN) using a stringently defined phenotype. Analysis of phenotypic variability led to the identification of a specific genetic risk factor that approached genome-wide significance (rs929626 in EBF1 (Early B-Cell Factor 1); $P = 2.04 \times 10^{-7}$; OR = 0.7; 95% confidence interval (CI) = 0.61–0.8) with independent replication (P=0.04), suggesting a variant-mediated dysregulation of leptin signaling may play a role in AN. Multiple SNPs in LD with the variant support the nominal association. This demonstrates that although the clinical and etiologic heterogeneity of AN is universally recognized, further careful sub-typing of cases may provide more precise genomic signals. In this study, through a refinement of the phenotype spectrum of AN, we present a replicable GWAS signal that is nominally associated with AN, highlighting a potentially important candidate locus for further investigation.

Anorexia nervosa (AN) is a complex and often chronic eating disorder characterized by inability to maintain a normal healthy body weight and a persistent fear of weight gain, resulting in extreme emaciation and even death in some cases¹. Previous genetic and epidemiological studies have indicated a multifactorial etiology, where both genetic and environmental factors contribute to disease risk²⁻⁷.

As sample sizes have increased, genome-wide association studies (GWASs) of AN have begun to identify risk variants⁸⁻¹⁰. To further elucidate the genetic architecture of AN, we performed a GWAS using data from our previously published study⁸ consisting of 1,033 AN cases by excluding 212 patients with AN who experienced diagnostic crossover during the course of their illness. Specifically, we excluded patients who migrated from or to binge-eating disorder (BED) or bulimia nervosa (BN) as assessed with the Structured Interview for Anorexic and Bulimic Disorders¹¹). Although a previous study indicated women with BN were rarely to cross over to AN¹², we observed ~43% of AN/BN crossover cases falls into this category in our cohort, suggestive of a confounding factor. We hypothesized that this reduction in phenotypic heterogeneity, despite the fact that AN and BN may share some genetic risk factors¹³, would enhance gene discovery.

¹Center for Applied Genomics, Children's Hospital of Philadelphia, Philadelphia, PA, USA. ²Department of Molecular Physiology and Biophysics, Vanderbilt University, Nashville, TN, USA. ³Department of Human Genetics, Children's Hospital of Philadelphia, Philadelphia, PA, USA. ⁴Department of Pediatrics, The Perelman School of Medicine, University of Pennsylvania, Philadelphia, PA, USA. ⁵Present address: Department of Molecular and Integrative Physiology, University of Michigan, Ann Arbor, MI, USA. Dong Li and Xiao Chang contributed equally to this work. A comprehensive list of consortium members appears at the end of the paper. Correspondence and requests for materials should be addressed to D.L. (email: lid2@email.chop.edu) or H.H. (email: hakonarson@email.chop.edu)

Results

Our discovery cohort included a total of 692 female AN cases of non-Hispanic European (NHE) descent. Cases were included if they were diagnosed with restricting type and binge eating/purging type of AN as defined by DSM-IV. Both types are characterized by below-normal weight and restricted food intake. Individuals diagnosed as restricting type do not experience binge-eating episodes and do not engage in purging, such as vomiting or use of laxatives. Standard quality controls measures were applied, specifically, excluding potential cryptic relatedness and checking for population stratification (details described elsewhere⁸). The average age of onset of the case subjects was 16.3 years with a standard deviation (SD) of 3 years (Interquartile Range; IQR = 16(14–18)). The control group included 3,570 female matched healthy adolescents of NHE ancestry that had an average age of 18.3 years at the time of data analysis (SD = 5.7; IQR = 19(13–23)) (Supplementary Table 1). Associations were assessed with 507,999 SNPs genotyped on either Illumina HumanHap550 or Human610-Quad BeadChips in an additive model using logistic regression analyses with principal components adjustment, based on the principal component analysis of cases and controls (Supplementary Figure 1), resulting in significantly low level of genomic control inflation factor of 1.03 (Supplementary Figure 2). The analysis yielded one SNP (rs929626) with a *P* value of 2.04×10^{-7} and 4 other SNPs with marginally larger *P* values that are in strong linkage disequilibrium $(r^2 > 0.8)$; these SNPs were selected for further analysis (Supplementary Figure 3; Supplementary Table 2).

Using imputation analysis based on data from the 1000 Genomes Project (Phase I integrated variant set, v2, March 2012), we subsequently tested associations with SNPs (imputed info > 0.5, minor allele frequency (MAF) > 0.05) located in a 200-kb window centered on the SNP rs929626. We observed association with a series of markers around this region, of which 34 SNPs supported suggestive associations ($P < 1.0 \times 10^{-6}$) with both imputed and genotyped SNPs, which were in high LD with AN (Fig. 1; Supplementary Table 3). This suggests that the single markers demonstrating nominal association in the GWAS are likely to be true positives.

We further explored this finding using the meta-analysis results from 15 previously reported AN cohorts¹⁰. Interestingly, two SNPs were also nominally significant (rs929626 with P = 0.037 and rs17543752 with P = 0.05) in the same direction as in the GWAS (Table 1). Meta-analysis results in a P value of 1.52×10^{-7} .

We next used the ENCODE project¹⁴ data to predict possible functional effect of the SNPs identified in this study. The top SNP, rs929626, and other significant markers located in the 6th intron of the *EBF1* gene (Early B-Cell Factor 1), as well as two SNPs (rs113252656 and rs1081071) flanking the top SNP rs929626 at $r^2 > 0.5$ function as binding sites for EBF1 itself (HaploReg v4.1; ref. 15). This suggests that these genetic variants may modulate the expression of *EBF1*. Indeed, we observed a positive correlation with the rs929626 C allele carriers compared with TT homozygotes on the *EBF1* expression level in nine independent subjects (the FPKM value for TT homozygotes (3 subjects) versus C allele carriers (6 individuals) is 5.0 versus 6.4) with both whole genome sequencing data of blood and corresponding RNA-Seq data of heart right ventricle selected from the Pediatric Cardiac Genomics Consortium cohort (dbGaP Study Accession: phs000571.v3.p2). By using the Genotype-Tissue Expression Portal database (http://www.gtexportal.org), we also observed nominally significant expression quantitative trait loci (eQTLs) association (P = 0.0024, tested in 97 samples) in the putamen for rs929626 in the same direction. A few comorbid psychiatric disorders have been linked with the function of the putamen, such as anxiety, obsessive-compulsive disorder and attention deficit-hyperactivity disorder¹⁶⁻¹⁸. Taken together, these suggest the minor allele C carriers have relatively higher *EBF1* expression.

Discussion

EBF1 encodes a transcription factor that originally thought to function as necessary for the development of the immune system¹⁹, but it has since been shown to regulate the development of both osteoblast and adipocyte lineages^{20–22}. Two *EBF1* variants, rs11953630-T and rs9313772-T, showed significant association at genome-wide level ($P < 5 \times 10^{-10}$) in a study testing blood pressure in European whites^{23, 24}. In addition, rs17056278-C was also identified as a metabolic risk allele, interacting with psychosocial stress to contribute to increased hip circumference ($P = 3 \times 10^{-8}$)²⁵. However none of these is in LD with any markers in our identified locus. In animal studies, *Ebf1*-/- mice showed increased adipose tissue within marrow, whereas peripheral white adipose tissue was severely reduced. Circulating levels of leptin, a hormone released by adipocytes and one of the major players in food intake regulation, were also decreased in *Ebf1*-/- mice compared with controls²⁶. This concurs with the reported generalized loss of accumulation of subcutaneous and visceral adipose accompanied by significant increases in yellow marrow in AN patients^{27,28}. Also notable is the finding that circulating levels of leptin are very low in AN patients^{29,30} and a decline in levels of circulating leptin can lead to changes in brain activity in areas involved in regulatory, emotional, and cognitive control of appetite⁵.

Understanding the genetics of AN is currently a major within-field initiative, in parallel to other neuropsychiatric/neurodevelopmental disorders such as schizophrenia, bipolar disorder, and autism spectrum disorders. Although the clinical and etiologic heterogeneity is universally recognized, in practice, many studies still failed to account for sample heterogeneity. In this study, by focusing on individuals with AN who have not crossed over to BN or BED, we have identified a marginally replicating GWAS signal that approached genome-wide significance. One limitation of our study is that all participants may not yet have experienced the full course of their eating disorder (The average duration of follow-up was 8.6 years with a SD of 7.0 years in the discovery cohort, while the average crossover time was 2.8 years with a SD of 2.6 years for the excluded AN patients), and a portion of the sample may develop BN or BED at later stages of illness. This would represent a conservative bias and underscores the importance of further investigation of this locus in the future focusing on individuals with lifetime AN who have never crossed over to other eating disorder presentations.

Methods

Discovery data set and quality control. We conducted a GWAS using data from our previously published study⁸ consisting of 1,033 AN cases by excluding 212 patients with AN who experienced diagnostic

Plotted SNPs

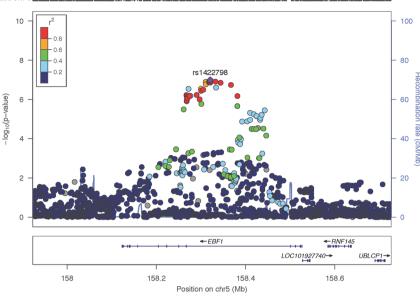


Figure 1. Region of genome-wide nominal association at 5q33.3. Regional plot of the *EBF1*-associated interval for the imputation analysis. Foreground shows scatter plot of the $-\log_{10} P$ values plotted against physical position of human reference hg19. Background shows estimated recombination rates plotted to reflect the local LD structure. The color of the dots represents the strength of LD between the top SNP (rs929626) and its proxies (red, $r^2 \ge 0.8$; orange, $0.8 > r^2 \ge 0.6$; green, $0.6 > r^2 \ge 0.4$; blue and navy, $r^2 < 0.4$). Genes, position of exons, and direction of transcription from UCSC genome browser (http://genome.ucsc.edu) are noted.

SNP	Study	MA	OR	SE	L95	U95	Р
rs929626	CHOP	С	0.7004	0.06855	0.6123	0.8011	2.04E-07
	PGC-ED	С	0.938252	0.027953	0.883465	0.996437	0.037887

Table 1. Association results for the lead genotyped SNP. Abbreviations: MA, minor allele; OR, odds ratio; SE, standard error; L95, lower 95% confidence interval; U95, upper 95% confidence interval; P, P-value.

crossover during the course of their illness (i.e. migrated from or to binge-eating disorder (BED) or bulimia nervosa (BN) as assessed with the Structured Interview for Anorexic and Bulimic Disorders¹¹) plus 100 patients without such information. A total of 692 female AN cases and 3,570 female matched controls that were carefully selected from Center for Applied Genomics (CAG) database were included in the analysis after Standard quality controls, namely, excluding potential cryptic relatedness and checking for population stratification by using the PLINK software³¹ version 1.90a. The Research Ethics Board of CHOP and other participating centers approved the study. Informed consent was obtained from all adult participants and from a parent or legal guardian in the case of children and all work followed was in accordance with an IRB-approved protocol.

Association tests. For the genome-wide association analysis for SNPs, we utilized the PLINK software³¹ version 1.90a, through Cochran–Armitage trend test.

Expression studies. The extended locus around associated SNP was then defined by identification of all SNPs showing $r^2 > 0.5$. Linkage disequilibrium (LD) was defined with the HaploReg v4.1 (ref. 15) based on Phase I of the 1000 Genomes project. Variants showing evidence of LD with associated AN variants were explored for impact on gene function via regulatory function (including eQTLs) by HaploReg v4.1, which both collate data from the Encyclopedia of DNA Elements (ENCODE)¹⁴. We also referred to the Genotype-Tissue Expression Portal database (http://www.gtexportal.org) for eQTLs analysis.

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Acknowledgements

We gratefully thank all the patients and their families who were enrolled in this study, as well as all the control subjects who donated blood samples to The Children's Hospital of Philadelphia (CHOP) for genetic studies. Dong Li is funded in part by 2012–2015 Davis Foundation Postdoctoral Fellowship Program in Eating Disorders Research Award. Bingshan Li was partially supported by Klarman Family Foundation for eating disorders. All genome-wide genotyping for controls was funded by an Institute Development Award to Center for Applied Genomics from CHOP. We thank the Eating Disorders Working Group of the Psychiatric Genomics Consortium (PGC-ED) for providing summary results data for the replication analysis.

Author Contributions

D.L. and H.H. were leading contributions in the design, analysis and writing; D.L., X.C., Y.L., J.P.B. and P.S contributed to data analysis. J.J.C., L.T., N.R., D.A., Y.R.L. contributed samples and phenotypes. C.E.K., J.L., F.W., J.S., M.L., C.H., Z.W., Y.G., H.Q., F.M., K.T., R.C., B.L., and R.C. provided assistance with samples and data processing. Eating Disorders Working Group of the Psychiatric Genomics Consortium and Price Foundation Collaborative Group provided data for the replication and helped with the discussion; D.L. drafted the manuscript. D.L., J.J.C., E.J.B. and H.H. revised the manuscript. All authors approved final version of manuscript.

Additional Information

Supplementary information accompanies this paper at doi:10.1038/s41598-017-01674-8

Competing Interests: The authors declare that they have no competing interests.

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Consortia

Eating Disorders Working Group of the Psychiatric Genomics Consortium (PGC-ED)

Vesna Boraska Perica^{6,7}, Christopher S. Franklin⁶, James A. B. Floyd^{6,8}, Laura M. Thornton⁹, Laura M. Huckins⁶, Lorraine Southam⁶, N. William Rayner^{6,10,11}, Ioanna Tachmazidou⁶, Kelly L. Klump¹², Janet Treasure¹³, Ulrike Schmidt¹³, Federica Tozzi⁹, Kirsty Kiezebrink¹⁴, Johannes Hebebrand¹⁵, Philip Gorwood^{16,17}, Roger A. H. Adan^{18,19}, Martien J. H. Kas¹⁸, Angela Favaro²⁰, Paolo Santonastaso²⁰, Fernando Fernánde-Aranda^{21,22}, Monica Gratacos^{23,24,25,26}, Filip Rybakowski²⁷, Monika Dmitrzak-Weglarz²⁸, Jaakko Kaprio^{29,30,31}, Anna Keski-Rahkonen²⁹, Anu Raevuori-Helkamaa^{29,32}, Eric F. Van Furth^{33,34}, Margarita C. T. Slof-Op't Landt^{33,35}, James I. Hudson³⁶, Ted Reichborn-Kjennerud^{39,38}, Gun Peggy S. Knudsen³⁷, Palmiero Monteleone^{39,40}, Allan S. Kaplan^{41,42}, Andreas Karwautz⁴³, Wade H. Berrettini⁴⁴, Nicholas J. Schork⁴⁵, Tetsuya Ando⁴⁶, Hidetoshi Inoko⁴⁷, Tõnu Esko⁴⁸, Krista Fischer⁴⁸, Katrin Männik^{49,50}, Andres Metspalu^{48,49}, Jessica H. Baker⁹, Janiece E. DeSocio⁵¹, Christopher E. Hilliard⁹, Julie K. O'Toole⁵², Jacques Pantel⁵³, Jin P. Szatkiewicz⁵⁴, Stephanie Zerwas⁹, Oliver S. P. Davis^{55,56}, Sietske Helder⁵⁴, Katharina Bühren⁵⁷, Roland Burghardt⁵⁸, Martina de Zwaan^{59,60}, Karin Egberts⁶¹, Stefan Ehrlich^{62,63}, Beate Herpertz-Dahlmann⁶⁴, Wolfgang Herzog⁶⁵, Hartmut Imgart⁶⁶, André Scherag⁶⁷, Stephan Zipfel⁶⁸, Claudette Boni¹⁶, Nicolas Ramoz¹⁶, Audrey Versini¹⁶, Unna N. Danner¹⁹, Judith Hendriks¹⁸, Bobby P. C. Koeleman⁶⁹, Roel A. Ophoff^{70,71}, Eric Strengman⁶⁹, Annemarie A. van Elburg^{19,72}, Alice Bruson⁷³, Maurizio Clementi⁷³, Daniela Degortes²⁰, Monica Forzan⁷³, Elena Tenconi²⁰, Elisa Docampo^{23,24,25,26}, Geòrgia Escaramís^{23,24,25,26}, Susana Jiménez-Murcia^{21,22}, Jolanta Lissowska⁷⁴, Andrzej Rajewski⁷⁵, Neonila Szeszenia-Dabrowska⁷⁵, Agnieszka Slopien²⁸, Joanna Hauser²⁸, Leila Karhunen⁷⁶, Ingrid Meulenbelt³⁵, P. Eline Slagboom^{35,77}, Alfonso Tortorella³⁹, Mario Maj³⁹, George Dedoussis⁷⁸, Dimitris Dikeos⁷⁹, Fragiskos Gonidakis⁸⁰, Konstantinos Tziouvas⁷⁸, Artemis Tsitsika⁸¹, Hana Papezova⁸², Lenka Slachtova⁸³, Debora Martaskova⁸², James L. Kennedy^{41,42}, Robert D. Levitan^{41,42}, Zeynep Yilmaz^{9,41}, Julia Huemer⁴³, Doris Koubek⁴³, Elisabeth Merl⁴³, Gudrun Wagner⁴³, Paul Lichtenstein⁸⁴, Gerome Breen⁵⁴, Sarah Cohen-Woods⁵⁴, Anne Farmer⁵⁴, Peter McGuffin⁵⁴, Sven Cichon^{85,86,87}, Ina Giegling⁸⁸, Stefan Herms^{85,87}, Dan Rujescu⁸⁸, Stefan Schreiber⁸⁹, H-Erich Wichmann^{90,91}, Christian Dina⁹², Rob Sladek⁹³, Giovanni Gambaro⁹⁴, Nicole Soranzo⁶, Antonio Julia⁹⁵, Sara Marsal⁹⁵, Raquel Rabionet^{23,24,25,26}, Valerie Gaborieau⁹⁶, Danielle M. Dick⁹⁷, Aarno Palotie^{6,98,99}, Samuli Ripatti^{98,100}, Elisabeth Widén^{98,100}, Ole A. Andreassen¹⁰¹, Thomas Espeseth^{101,102}, Astri Lundervold^{103,104,105}, Ivar Reinvanq¹⁰², Vidar M. Steen^{106,107}, Stephanie Le Hellard^{106,107}, Morten Mattingsdal¹⁰¹, Ioanna Ntalla⁷⁸, Vladimir Bencko¹⁰⁸, Lenka Foretova¹⁰⁹, Vladimir Janout¹¹⁰, Marie Navratilova¹⁰⁹, Steven Gallinger¹¹¹, Dalila Pinto¹¹², Stephen W. Scherer¹¹³, Harald Aschauer¹¹⁴, Laura Carlberg¹¹⁴, Alexandra Schosser¹¹⁴, Lars Alfredsson¹¹⁵, Bo Ding¹¹⁵, Lars Klareskog¹¹⁶, Leonid Padyukov¹¹⁶, Chris Finan⁶, Gursharan Kalsi⁵⁵, Marion Roberts⁵⁵, Jeff C Barrett⁶, Xavier Estivill^{23,24,25,26}, Anke Hinney¹⁵, Patrick F. Sullivan^{9,117}, Eleftheria Zeggini⁶ & Cynthia M. Bulik^{9,117}

⁶Wellcome Trust Sanger Institute, Wellcome Trust Genome Campus, Hinxton, Cambridge, UK

⁷University of Split School of Medicine, Split, Croatia

⁸William Harvey Research Institute, Barts and The London School of Medicine and Dentistry, Queen Mary University of London, John Vane Science Centre, Charterhouse Square, London, UK

⁹Department of Psychiatry, University of North Carolina at Chapel Hill, Chapel Hill, NC, USA

¹⁰Wellcome Trust Centre for Human Genetics (WTCHG), University of Oxford, Oxford, UK

 $^{11}\mbox{Oxford}$ Centre for Diabetes, Endocrinology and Metabolism (OCDEM), Oxford, UK

¹²Department of Psychology, Michigan State University, East Lansing, MI, USA

¹³Section of Eating Disorders, Institute of Psychiatry, King's College London, London, UK

¹⁴Health Services Research Unit, University of Aberdeen, Aberdeen, UK

¹⁵Department of Child and Adolescent Psychiatry, Psychosomatics and Psychotherapy, Universitätsklinikum Essen, University of Duisburg-Essen, Essen, Germany

¹⁶INSERM U894, Centre of Psychiatry and Neuroscience, Paris, France

¹⁷Sainte-Anne Hospital (CMME), University of Paris-Descartes, Paris, France

¹⁸Brain Center Rudolf Magnus, Department of Translational Neuroscience, University Medical Center Utrecht, Utrecht, The Netherlands

¹⁹Altrecht Eating Disorders Rintveld, Zeist, The Netherlands

²⁰Department of Neurosciences, University of Padova, Padova, Italy

²¹Department of Psychiatry and CIBERON, University Hospital of Bellvitge-IDIBELL, Barcelona, Spain

²²Department of Clinical Sciences, School of Medicine, University of Barcelona, Barcelona, Spain

²³Genomics and Disease Group, Centre for Genomic Regulation (CRG), Barcelona, Spain

²⁴Universitat Pompeu Fabra (UPF), Barcelona, Spain

²⁵Centro de Investigación Biomédica en Red en Epidemiología y Salud Pública (CIBERESP), Barcelona, Spain
²⁶Hospital del Mar Medical Research Institute (IMIM), Barcelona, Spain

²⁷Department of Child and Adolescent Psychiatry, Institute of Psychiatry and Neurology, Warsaw, Poland

²⁸Department of Child and Adolescent Psychiatry, Department of Psychiatry, Poznan University of Medical Sciences, Poznan, Poland

²⁹Hjelt Institute, University of Helsinki, Helsinki, Finland

³⁰Institute of Molecular Medicine, University of Helsinki, Helsinki, Finland

³¹Department of Mental Health and Substance Abuse Services, National Institute for Health and Welfare, Helsinki, Finland

³²Department of Adolescent Psychiatry, Helsinki University Central Hospital, Helsinki, Finland

³³Center for Eating Disorders Ursula, Leiden, The Netherlands

³⁴Leiden University Medical Centre, Department of Psychiatry, Leiden, The Netherlands

³⁵Leiden University Medical Centre, Molecular Epidemiology Section (Department of Medical Statistics), Leiden, The Netherlands

³⁶Department of Psychiatry, McLean Hospital/Harvard Medical School, Belmont, MA, USA

³⁷Department of Genetics, Environment and Mental Health, Norwegian Institute of Public Health, Oslo, Norway

³⁸Institute of Clinical Medicine, University of Oslo, Oslo, Norway

³⁹Department of Psychiatry, University of Naples SUN, Naples, Italy

⁴⁰Chair of Psychiatry, University of Salerno, Salerno, Italy

⁴¹Centre for Addiction and Mental Health, University of Toronto, Toronto, Canada

⁴²Department of Psychiatry, University of Toronto, Toronto, Canada

⁴³Eating Disorders Unit, Department of Child and Adolescent Psychiatry, Medical University of Vienna, Vienna, Austria

⁴⁴Department of Psychiatry, University of Pennsylvania, Philadelphia, PA, USA

⁴⁵Department of Molecular and Experimental Medicine and The Scripps Translational Science Institute, The Scripps Research Institute, La Jolla, CA, USA

⁴⁶Department of Psychosomatic Research, National Institute of Mental Health, NCNP, Tokyo, Japan

⁴⁷Department of Molecular Life Sciences, Tokai University School of Medicine, Kanagawa, Japan

⁴⁸Estonian Genome Center, University of Tartu, Tartu, Estonia

⁴⁹Institute of Molecular and Cell Biology, University of Tartu, Tartu, Estonia

⁵⁰Center for Integrative Genomics, University of Lausanne, Lausanne, Switzerland

⁵¹Seattle University College of Nursing, Seattle, WA, USA

⁵²Kartini Clinic, Portland, OR, USA

⁵³Centre de Psychiatrie et Neurosciences – Inserm U894, Paris, France

⁵⁴Department of Genetics, The University of North Carolina at Chapel Hill, Chapel Hill, NC, USA

⁵⁵Social, Genetic and Developmental Psychiatry Centre, Institute of Psychiatry, King's College London, London, UK
⁵⁶UCL Genetics Institute, Department of Genetics, Evolution and Environment, University College London, London,

UK

⁵⁷Department of Child and Adolescent Psychiatry, Psychosomatics and Psychotherapy, University Clinics RWTH Aachen, Aachen, Germany

⁵⁸Department of Child and Adolescent Psychiatry, Psychosomatics and Psychotherapy, Charité, Berlin, Germany

⁵⁹Department of Psychosomatic Medicine and Psychotherapy, Hannover Medical School, Hannover, Germany

⁶⁰Department of Psychosomatic Medicine and Psychotherapy, University of Erlangen-Nuremberg, Erlangen, Germany

⁶¹Department of Child and Adolescent Psychiatry, Psychosomatics and Psychotherapy, University Würzburg, Würzburg, Germany

⁶²Department of Child and Adolescent Psychiatry, University Hospital Carl Gustav Carus, Dresden University of Technology, Dresden, Germany

⁶³Massachusetts General Hospital/Harvard Medical School, Athinoula A. Martinos Center for Biomedical Imaging, Psychiatric Neuroimaging Research Program, Charlestown, MA, USA

⁶⁴Department of Child and Adolescent Psychiatry, Psychosomatics and Psychotherapy, University Clinics RWTH Aachen, Aachen, Germany

⁶⁵Departments of Psychosocial and Internal Medicine, Heidelberg University, Heidelberg, Germany

⁶⁶Parklandklinik, Bad Wildungen, Germany

⁶⁷Institute for Medical Informatics, Biometry and Epidemiology, Universitätsklinikum Essen, University of Duisburg-Essen, Essen, Germany

⁶⁸Department of Internal Medicine VI, Psychosomatic Medicine and Psychotherapy, University Medical Hospital Tübingen, Tübingen, Germany

⁶⁹Department of Medical Genetics, University Medical Center Utrecht, Utrecht, The Netherlands

⁷⁰Center for Neurobehavioral Genetics, University of California, Los Angeles, Los Angeles, CA, USA

⁷¹Brain Center Rudolf Magnus, Department of Psychiatry, University Medical Center Utrecht, The Netherlands ⁷²Department of Social Sciences, Utrecht University, Utrecht, The Netherlands

⁷³Clinical Genetics Unit, Department of Woman and Child Health, University of Padova, Padova, Italy
⁷⁴M. Sklodowska-Curie Cancer Center and Institute of Oncology, Warsaw, Poland

⁷⁵Department of Epidemiology, Institute of Occupational Medicine, Department of Epidemiology, Lodz, Poland

⁷⁶Department of Clinical Nutrition, Institute of Public Health and Clinical Nutrition, University of Eastern Finland, Kuopio, Finland

⁷⁷Netherlands Consortium for Healthy Ageing, Leiden University Medical Center, The Netherlands ⁷⁸Department of Nutrition and Dietetics, Harokopio University, Athens, Greece ⁷⁹1st Department of Psychiatry, Athens University Medical School, Athens, Greece

⁸⁰Eating Disorders Unit, 1st Department of Psychiatry, Athens University Medical School, Athens, Greece

⁸¹Adolescent Health Unit (AHU), 2nd Department of Pediatrics – Medical School, University of Athens 'P & A Kyriakou' Children's Hospital, Athens, Greece

⁸²Department of Psychiatry, 1st Faculty of Medicine, Charles University, Prague, Czech Republic

⁸³Department of Pediatrics, 1st Faculty of Medicine, Charles University, Prague, Czech Republic

⁸⁴Department of Medical Epidemiology and Biostatistics, Karolinska Institutet, Stockholm, Sweden

⁸⁵Institute of Human Genetics, Department of Genomics, Life & Brain Center, University of Bonn, Bonn, Germany
⁸⁶Institute of Neuroscience and Medicine (INM-1), Research Center Jülich, Jülich, Germany

⁸⁷Division of Medical Genetics, Department of Biomedicine, University of Basel, Basel, Switzerland

⁸⁸Martin-Luther-Universität Halle-Wittenberg, Klinikum der Medizinischen Fakultät, Halle/Saale, Germany
 ⁸⁹Institute of Clinical Molecular Biology, University of Kiel, Kiel, Germany

⁹⁰Institute of Epidemiology, Helmholtz Zentrum München, German Research Center for Environmental Health, Neuherberg, Germany

⁹¹Institute of Medical Informatics, Biometry and Epidemiology, Ludwig-Maximilians-University, Munich, Germany
⁹²CNRS 8090-Institute of Biology, Pasteur Institute, Lille, France

⁹³McGill University and Genome Quebec Innovation Centre, Montreal, QC, Canada

⁹⁴Division of Nephrology, Department of Internal Medicine and Medical Specialties, Columbus-Gemelly Hospitals, Catholic University, Rome, Italy

⁹⁵Unitat de Recerca de Reumatologia (URR), Institut de Recerca Hospital Universitari Vall d'Hebron, Barcelona, Spain
⁹⁶Genetic Epidemiology Group, International Agency for Research on Cancer (IARC), Lyon, France

⁹⁷Virginia Institute for Psychiatric and Behavioral Genetics, Department of Psychiatry, Virginia Commonwealth University, Virginia, VA, USA

⁹⁸The Finnish Institute of Molecular Medicine Finland (FIMM), University of Helsinki, Helsinki, Finland

⁹⁹The Program for Human and Population Genetics, The Broad Institute of MIT and Harvard, Cambridge, MA, USA ¹⁰⁰Finnish Institute of Occupational Health, Province of Southern Finland, Helsinki, Finland

¹⁰¹NORMENT, KG Jebsen Centre for Psychosis Research, Division of Mental Health and Addiction, Oslo University Hospital & Institute of Clinical Medicine, University of Oslo, Oslo, Norway

¹⁰²Department of Psychology, University of Oslo, Oslo, Norway

¹⁰³Department of Biological and Medical Psychology, University of Bergen, Bergen, Norway

¹⁰⁴Kavli Research Centre for Aging and Dementia, Haraldsplass Deaconess Hospital, Bergen, Norway

¹⁰⁵K.G. Jebsen Centre for Research on Neuropsychiatric Disorders, University of Bergen, Bergen, Norway

¹⁰⁶KG Jebsen Centre for Psychosis Research, Norwegian Centre For Mental Disorders Research (NORMENT), Department of Clinical Science, University of Bergen, Bergen, Norway

¹⁰⁷Dr. Einar Martens Research Group for Biological Psychiatry, Center for Medical Genetics and Molecular Medicine, Haukeland University Hospital, Bergen, Norway

¹⁰⁸Institute of Hygiene and Epidemiology, 1st Faculty of Medicine, Charles University, Prague, Czech Republic ¹⁰⁹Department of Cancer Epidemiology and Genetics, Masaryk Memorial Cancer Institute, Brno, Czech Republic

¹¹⁰Palacky University, Olomouc, Czech Republic

¹¹¹University Health Network and Mount Sinai Hospital, Toronto General Hospital, and Samuel Lunenfeld Research Institute, Toronto, ON, Canada

¹¹²Departments of Psychiatry, and Genetics and Genomic Sciences, Seaver Autism Center, and the Mindich Child Health and Development Institute, Mount Sinai School of Medicine, New York, NY, USA

¹¹³The Centre for Applied Genomics and Program in Genetics and Genome Biology, The Hospital for Sick Children, Toronto, ON, Canada

¹¹⁴Department of Psychiatry and Psychotherapy, Medical University Vienna, Vienna, Austria

¹¹⁵The Institute of Environmental Medicine, Karolinska Institutet, Stockholm, Sweden

 116 Rheumatology Unit, Department of Medicine at the Karolinska University Hospital, Solna, Sweden

¹¹⁷Department of Nutrition, The University of North Carolina at Chapel Hill, Chapel Hill, NC, USA

The Price Foundation Collaborative Group

Harry Brandt¹¹⁸, Steve Crawford¹¹⁸, Scott Crow¹¹⁹, Manfred M. Fichter^{120,121}, Katherine A. Halmi¹²², Craig Johnson¹²³, Allan S. Kaplan^{124,125}, Maria C. La Via⁹, James Mitchell^{126,127}, Michael Strober¹²⁸, Alessandro Rotondo¹²⁹, Janet Treasure¹³⁰, D. Blake Woodside^{42,124,125}, Cynthia M. Bulik⁹, Pamela K. Keel¹³¹, Kelly L. Klump¹², Lisa Lilenfeld¹³², Laura M. Thornton⁹, Andrew W. Bergen¹³³, Wade Berrettini¹³⁴, Walter Kaye¹³⁵ & Pierre Magistretti¹³⁶

¹¹⁸Department of Psychiatry, University of Maryland School of Medicine, Baltimore, MD, USA

¹¹⁹Department of Psychiatry, University of Minnesota, Minneapolis, MN, USA

¹²⁰Roseneck Hospital for Behavioral Medicine, Prien, Germany

¹²¹Department of Psychiatry, University of Munich (LMU), Munich, Germany

¹²²New York Presbyterian Hospital, Westchester Division, Weill Medical College of Cornell University, White Plains, NY, USA

¹²³Laureate Psychiatric Clinic and Hospital, Tulsa, OK, USA

¹²⁴Center for Addiction and Mental Health, Toronto, Canada

¹²⁵Department of Psychiatry, Toronto General Hospital, University Health Network, Toronto, Canada

¹²⁶Neuropsychiatric Research Institute, Fargo, ND, USA

- ¹²⁷Department of Clinical Neuroscience, University of North Dakota School of Medicine and Health Sciences, Grand Forks, ND, USA
- ¹²⁸Department of Psychiatry and Biobehavioral Sciences, David Geffen School of Medicine, University of California at Los Angeles, Los Angeles, CA, USA
- ¹²⁹Neuropsychiatric Research Biotechnologies, University of Pisa, Pisa, Italy
- ¹³⁰Eating Disorders Section, Institute of Psychiatry, King's College, University of London, London, England
- ¹³¹Department of Psychology, Florida State University, Tallahassee, FL, USA
- ¹³²Department of Psychology, Georgia State University, Atlanta, GA, USA
- ¹³³Center for Health Sciences, SRI International, Menlo Park, CA, USA
- ¹³⁴Department of Psychiatry, University of Pennsylvania, Philadelphia, PA, USA
- ¹³⁵Department of Psychiatry, University of California at San Diego, San Diego, CA, USA
- ¹³⁶Department of Psychiatry, Brain Mind Institute EPFL—Lausanne, Center for Psychiatric Neuroscience, University of Lausanne Medical School, Lausanne, Switzerland