**Figure S1 | Association of the 43 identified loci on NEB and childlessness.** The direction of effect has been reversed for childless to show a risk increasing odds-ratio for easier interpretation of effect magnitude.



**Figure S2 | Candidate genes in the 43 NEB and childlessness associated loci.** Information for 54 genes prioritized in loci identified by GWAS for number of children ever born (NEB) and/or childlessness (CLN) that are located within 1 million bp of lead SNPs. Blue and orange indicate transitions from one locus to the next. From left to right, panels indicate: 1) if the locus was identified for NEB and/or CLN; 2) which bioinformatic approaches highlighted the gene as a candidate; 3) the cell types in brain, glands, female reproductive organs, and male reproductive organs in which the genes are expressed at a low, moderate or high level (small, medium and large circles) based on data from the Human Protein Atlas; 4) gene functions as extracted from Entrez, Uniprot and GeneCards; 5) which phenotypes were observed in mutant

**Figure S3 | Change in polygenic risk score (PGS) for NEB by birth year in the HRS study**. Polygenic risk score scaled to have a mean of 0 and standard deviation of 1.



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**NESDA: The Netherlands Study of Depression and Anxiety**

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**NHS: The Nurses’ Health Study**

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**NTR: Netherlands Twin Register**

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**RPGEH: Research Program on Genes, Environment and Health/Genetic Epidemiology Research on Aging (RPGEH/GERA)**

Data used in this study were provided by the Kaiser Permanente Research Program on Genes, Environment, and Health (RPGEH): Genetic Epidemiology Research on Adult Health and Aging (GERA), funded by the National Institutes of Health [RC2 AG036607 (Schaefer and Risch)], the Robert Wood Johnson Foundation, the Wayne and Gladys Valley Foundation, The Ellison Medical Foundation, and the Kaiser Permanente Community Benefits Program. Access to RPGEH data used in this study may be obtained by application via the RPGEH Research portal: https://rpgehportal.kaiser.org. A subset of the GERA cohort consented for public use can be found at NIH/dbGaP: phs000674.v1.p1.

**RS-I (Rotterdam Study Baseline), RS-II (Rotterdam Study Extension of Baseline) and RS-III (Rotterdam Study Young)**

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**SHIP: Study of Health in Pomerania**

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**STR: Swedish Twin Registry**

The Jan Wallander and Tom Hedelius Foundation (P2015-0001:1), the Ragnar Soderberg Foundation (E9/11, E42/15), The Swedish Research Council (421-2013-1061). STR is financially supported by Karolinska Institutet. Researchers interested in using STR data must obtain approval from a Swedish Ethical Review Board and from the Steering Committee of the Swedish Twin Registry. Researchers using the data are required to follow the terms of an Assistance Agreement containing a number of clauses designed to ensure protection of privacy and compliance with relevant laws. For further information, contact Patrik Magnusson (Patrik.magnusson@ki.se). C.A. Rietveld gratefully acknowledges funding from the Netherlands Organization for Scientific Research (NWO Veni grant 016.165.004).

**TwinsUK: St Thomas’ UK Adult Twin Registry**

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**UK Biobank**

This research has also been conducted using the UK Biobank Resource under Application Numbers 11425, 12514 and 9797. Informed consent was obtained from UK Biobank subjects.

**UKHLS: Understanding Society – The UK Household Longitudinal Study**

The UK Household Longitudinal Study, led by the Institute for Social and Economic Research at the University of Essex is funded by the Economic and Social Research Council (Grant Number: ES/M008592/1). Data were collected by NatCen and the genome wide scan data were analysed by the Wellcome Trust Sanger Institute. Access the data at <https://www.understandingsociety.ac.uk/>

**WGHS: Women’s Genome Health Study**

The WGHS is supported by the National Heart, Lung, and Blood Institute (HL043851,

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**WLS: Wisconsin Longitudinal Study**

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**QIMR: Queensland Institute of Medical Research**

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