Supplementary text and figures

1. Supplementary figures

   S1 - Liability-scale heritability explained vs chromosome size.
   S2 – SNP beta estimate comparison for the 156 LOY loci in discovery analyses including or excluding cancer cases
   S3 – The impact of sample size and Y chromosome PAR1 / Non-PAR ratio on PAR-LOY power over mLRR-Y
   S4 - Cell and tissue type enrichment estimated using LDSC-SEG
   S5 - Differential expression of the TCL1A gene in B-lymphocytes with and without the Y chromosome within individual subjects

2. Consortium authorship

3. Acknowledgements
Figure S1 | Liability-scale heritability explained vs chromosome size.
Figure S2 | SNP beta estimate comparison for the 156 LOY loci in discovery analyses including or excluding cancer cases

$R^2 = 0.9963$
Figure S3 | The impact of sample size and Y chromosome PAR1 / Non-PAR ratio on PAR-LOY power over mLRR-Y.
Figure S4 | Cell and tissue type enrichment estimated using LDSC-SEG

[Bar chart showing cell and tissue type enrichment]
Supplementary Figure 5. Differential expression of the TCL1A gene in B-lymphocytes with and without the Y chromosome within individual subjects. Error bars indicate the 95% confidence interval of the mean normalized expression of TCL1A within each group. To avoid stochastic effects that might occur in estimations using a small number of cells, results are shown for individuals with LOY in at least 10% of the B-lymphocytes and with LOY in more than five individual B-lymphocytes. Within each of the seven individuals (S1-S7) meeting this criteria, TCL1A showed a higher expression in the LOY cells compared to normal cells. This suggests that the observed TCL1A overexpression in B-lymphocytes without a Y chromosome is independent from the individual genotypes at the lead GWAS-SNP (rs2887399).
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53. Institute for Advanced Research, Wenzhou Medical University, Wenzhou, Zhejiang 325027, China
3. Acknowledgements

We thank the 23andMe research participants who contributed to this study.

K. Ström is acknowledged for collection of samples for the single cell project. This work was supported by grants from the European Research Council ERC Starting Grant, the Swedish Research Council, and Kjell och Märta Beijers Stiftelse to L.A.F and by the Hjärnfonden, Swedish Cancer Society, the Swedish Research Council, Alzheimerfonden and the Foundation for Polish Science under the International Research Agendas Programme to J.P.D. Sequencing was performed by the SNP&SEQ Technology Platform in Uppsala. The facility is part of the National Genomics Infrastructure (NGI) Sweden and Science for Life Laboratory. The SNP&SEQ Platform is also supported by the Swedish Research Council and the Knut and Alice Wallenberg Foundation.

Stephen J Chanock is supported by the NIH Intramural Research Program. Rong Li is supported by the National Institute of Health (R35-GM118172).

Po-Ru Loh is supported by NIH grant DP2-ES030554, a Burroughs Wellcome Fund Career Award at the Scientific Interfaces, a Glenn Foundation for Medical Research and AFAR Grants for Junior Faculty award, and the Next Generation Fund at the Broad Institute of MIT and Harvard.

J.C.U. is supported by a National Institutes of Health training grant (5T32 GM007226-43). J.C.U acknowledges analytical help and advice from Christian Benner, Liam Abbott, Masahiro Kanai, Erik Bao, Caleb Lareau.

Work in the Houlston Laboratory is supported by grants from Cancer Research UK (C1298/A8362) and Bloodwise (LRF05001, LRF06002 and LRF13044).

Lung Cancer Consortium

Transdisciplinary Research for Cancer in Lung (TRICL) of the International Lung Cancer Consortium (ILCCO) was supported by grants U19-CA148127 and CA148127S1. ILCCO data harmonization is supported by the Cancer Care Ontario Research Chair of Population Studies to R.J.H. and the Lunenfeld-Tanenbaum Research Institute, Sinai Health System. The TRICL-ILCCO OncoArray was supported by in-kind genotyping by the Centre for Inherited Disease Research (26820120008-0-26800068-1). IARC acknowledges and thanks V. Gaborieau, M. Foll, L. Fernandez-Cuesta, P. Chopard, T. Delhomme and A. Chabrier for their technical assistance in this project. The authors would like to thank the staff at the Respiratory Health Network Tissue Bank of the FRQS for their valuable assistance with the lung eQTL data set at Laval University. The lung eQTL study at Laval University was supported by the Fondation de l’Institut Universitaire de Cardiologie et de Pneumologie de Québec, the Respiratory Health Network of the FRQS and the Canadian Institutes of Health Research (MOP-123369).

The CAPUA study was supported by FIS-FEDER/Spain grant numbers FIS-01/310, FIS-PI03-0365, and FIS-07-BI060604, FICYT/Asturias grant numbers FICYT PB02-67 and FICYT IB09-133, and the University Institute of Oncology (IUOPA), of the University of Oviedo and the Ciber de Epidemiologia y Salud Pública. CIBERESP, SPAIN.
The work performed in the CARET study was supported by the National Institute of Health / National Cancer Institute: UM1 CA167462 (PI: Goodman), National Institute of Health UO1-CA6367307 (PIs Omen, Goodman); National Institute of Health R01 CA111703 (PI Chen), National Institute of Health 5R01CA151989-01A1(PI Doherty).

The Liverpool Lung project is supported by the Roy Castle Lung Cancer Foundation.

The Harvard Lung Cancer Study was supported by the NIH (National Cancer Institute) grants CA092824, CA090578, CA074386.

The Multiethnic Cohort Study was partially supported by NIH Grants CA164973, CA033619, CA63464 and CA148127.

The work performed in MSH-PMH study was supported by The Canadian Cancer Society Research Institute (020214), Ontario Institute of Cancer and Cancer Care Ontario Chair Award to R.J.H. and G.L. and the Alan Brown Chair and Lusi Wong Programs at the Princess Margaret Hospital Foundation.

NJLCS was funded by the State Key Program of National Natural Science of China (81230067), the National Key Basic Research Program Grant (2011CB503805), the Major Program of the National Natural Science Foundation of China (81390543).

The Norway study was supported by Norwegian Cancer Society, Norwegian Research Council.

The Shanghai Cohort Study (SCS) was supported by National Institutes of Health R01 CA144034 (PI: Yuan) and UM1 CA182876 (PI: Yuan).

The Singapore Chinese Health Study (SCHS) was supported by National Institutes of Health R01 CA144034 (PI: Yuan) and UM1 CA182876 (PI: Yuan).

The work in TLC study has been supported in part the James & Esther King Biomedical Research Program (09KN-15), National Institutes of Health Specialized Programs of Research Excellence (SPORE) Grant (P50 CA119997), and by a Cancer Center Support Grant (CCSG) at the H. Lee Moffitt Cancer Center and Research Institute, an NCI designated Comprehensive Cancer Center (grant number P30-CA76292).

The Vanderbilt Lung Cancer Study – BioVU dataset used for the analyses described was obtained from Vanderbilt University Medical Center’s BioVU, which is supported by institutional funding, the 1S10RR025141-01 instrumentation award, and by the Vanderbilt CTSA grant UL1TR000445 from NCATS/NIH. Dr. Aldrich was supported by NIH/National Cancer Institute K07CA172294 (PI:Aldrich).

The Copenhagen General Population Study (CGPS) was supported by the Chief Physician Johan Boserup and Lise Boserup Fund, the Danish Medical Research Council and Herlev Hospital.
The NELCS study: Grant Number P20RR018787 from the National Center for Research Resources (NCRR), a component of the National Institutes of Health (NIH).

The Kentucky Lung Cancer Research Initiative was supported by the Department of Defense [Congressionally Directed Medical Research Program, U.S. Army Medical Research and Materiel Command Program] under award number: 10153006 (W81XWH-11-1-0781). Views and opinions of, and endorsements by the author(s) do not reflect those of the US Army or the Department of Defense. This research was also supported by unrestricted infrastructure funds from the UK Center for Clinical and Translational Science, NIH grant UL1TR000117 and Markey Cancer Center NCI Cancer Center Support Grant (P30 CA177558) Shared Resource Facilities: Cancer Research Informatics, Biospecimen and Tissue Procurement, and Biostatistics and Bioinformatics.

The M.D. Anderson Cancer Center study was supported in part by grants from the NIH (P50 CA070907, R01 CA176568) (to X. Wu), Cancer Prevention & Research Institute of Texas (RP130502) (to X. Wu), and The University of Texas MD Anderson Cancer Center institutional support for the Center for Translational and Public Health Genomics.

The study in Lodz center was partially funded by Nofer Institute of Occupational Medicine, under task NIOM 10.13: Predictors of mortality from non-small cell lung cancer - field study.

Genetic sharing analysis was funded by NIH grant CA194393

The work to assemble the FTND GWAS meta-analysis was supported by the National Institutes of Health (NIH), National Institute on Drug Abuse (NIDA) grant number R01 DA035825 (Principal Investigator [PI]: DBH). The study populations included COGEND (dbGaP phs000092.v1.p1 and phs000404.v1.p1), COPDGene (dbGaP phs000179.v3.p2), deCODE Genetics, EAGLE (dbGaP phs000093.vs.p2), and SAGE. dbGaP phs000092.v1.p1).

The PRACTICAL Consortium

Genotyping of the OncoArray was funded by the US National Institutes of Health (NIH) [U19 CA 148537 for ELucidating Loci Involved Prostate cancer SuscEptibility (ELLIPSE) project and X01HG007492 to the Center for Inherited Disease Research (CIDR) under contract number HHSN268201200008I]. Additional analytic support was provided by NIH NCI U01 CA188392 (PI: Schumacher). The PRACTICAL consortium was supported by Cancer Research UK Grants C5047/A7357, C1287/A10118, C1287/A16563, C5047/A3354, C5047/A10692, C16913/A6135, European Commission's Seventh Framework Programme grant agreement n° 223175 (HEALTH-F2-2009-223175), and The National Institute of Health (NIH) Cancer Post-Cancer GWAS initiative grant: No. 1 U19 CA 148537-01 (the GAME-ON initiative). We would also like to thank the following for funding support: The Institute of Cancer Research and The Everyman Campaign, The Prostate Cancer Research Foundation, Prostate Research Campaign UK (now Prostate Action), The Orchid Cancer Appeal, The National Cancer
Research Network UK, The National Cancer Research Institute (NCRI) UK. We are grateful for support of NIHR funding to the NIHR Biomedical Research Centre at The Institute of Cancer Research and The Royal Marsden NHS Foundation Trust.

The Breast Cancer Association Consortium

The breast cancer genome-wide association analyses were supported by the Government of Canada through Genome Canada and the Canadian Institutes of Health Research, the ‘Ministère de l’Économie, de la Science et de l’Innovation du Québec’ through Genome Québec and grant PSR-SIIRI-701, The National Institutes of Health (U19 CA148065, X01HG007492), Cancer Research UK (C1287/A10118, C1287/A16563, C1287/A10710) and The European Union (HEALTH-F2-2009-223175 and H2020 633784 and 634935). All studies and funders are listed Michailidou et al (2017) [PMID 29059683].

Consortium of Investigators of Modifiers of BRCA1/2 (CIMBA)

The CIMBA data management and data analysis were supported by Cancer Research – UK grants C12292/A20861, C12292/A11174. ACA is a Cancer Research -UK Senior Cancer Research Fellow. GCT and ABS are NHMRC Research Fellows. iCOGS: the European Community's Seventh Framework Programme under grant agreement n° 223175 (HEALTH-F2-2009-223175) (COGS), Cancer Research UK (C1287/A10118, C1287/A 10710, C12292/A11174, C1281/A12014, C5047/A8384, C5047/A15007, C5047/A10692, C8197/A16565), the National Institutes of Health (CA128978) and Post-Cancer GWAS initiative (1U19 CA148537, 1U19 CA148065 and 1U19 CA148112 - the GAME-ON initiative), the Department of Defence (W81XWH-10-1-0341), the Canadian Institutes of Health Research (CIHR) for the CIHR Team Familial Risks of Breast Cancer (CRN-87521), and the Ministry of Economic Development, Innovation and Export Trade (PSR-SIIRI-701), Komen Foundation for the Cure, the Breast Cancer Research Foundation, and the Ovarian Cancer Research Fund. The PERSPECTIVE project was supported by the Government of Canada through Genome Canada and the Canadian Institutes of Health Research, the Ministry of Economy, Science and Innovation through Genome Québec, and The Quebec Breast Cancer Foundation.

Colorectal Cancer UK GWAS

At the Institute of Cancer Research, this work was supported by Cancer Research UK (C1298/A25514). Additional support was provided by the National Cancer Research Network. The COIN and COIN-B trials were funded by Cancer Research UK and the Medical Research Council and were conducted with the support of the National Institute of Health Research Cancer Research Network. COIN and COIN-B translational studies were supported by the Bobby Moore Fund from Cancer Research UK, Tenovus, the Kidani Trust, Cancer Research Wales and the National Institute for Social Care and Health Research Cancer Genetics Biomedical Research Unit (2011–2014). For control sample genotypes, we
acknowledge the PRACTICAL consortium support from Cancer Research UK Grants C5047/A7357, C1287/A10118, C1287/A16563, C5047/A3354, C5047/A10692, C16913/A6135, European Commission's Seventh Framework Programme grant agreement n° 223175 (HEALTH-F2-2009-223175), and The National Institute of Health (NIH) Cancer Post-Cancer GWAS initiative grant: No. 1 U19 CA 148537-01 (the GAME-ON initiative).

In Birmingham, funding was provided by Cancer Research UK (C6199/A16459). In Oxford additional funding was provided by the Oxford Comprehensive Biomedical Research Centre and the EU FP7 CHIBCHA grant. Core infrastructure support to the Wellcome Trust Centre for Human Genetics, Oxford was provided by grant (090532/Z/09/Z). We are grateful to many colleagues within UK Clinical Genetics Departments (for CORGI) and to many collaborators who participated in the VICTOR, QUASAR2 and SCOT trials. We acknowledge use of genotype data from the British 1958 Birth Cohort DNA collection, which was funded by the Medical Research Council Grant G0000934 and the Wellcome Trust Grant 068545/Z/02. A full list of the investigators who contributed to the generation of the data is available from http://www.wtccc.org.uk.

In Edinburgh, the work was supported by Programme Grant funding from Cancer Research UK (C348/A18927) and by MRC Centre Grant funding (U127527202 and U127527198 from 1/4/18) to the MRC Human Genetics Unit. Infrastructure and staffing funding is acknowledged from the Edinburgh CRUK Cancer Research Centre grant. The Lothian Birth Cohort studies are funded by Age UK (Disconnected Mind project) and the Biotechnology and Biological Sciences Research Council (grant no. BB/F019394/1). Genotyping of the GS:SFHS samples was carried out by the Edinburgh Clinical Research Facility, University of Edinburgh, and was funded by the Medical Research Council UK and the Wellcome Trust (Wellcome Trust Strategic Award ‘STratifying Resilience and Depression Longitudinally’ (STRADL), Reference 104036/Z/14/Z). GS:SFHS received core support from the Scottish Executive Health Department, Chief Scientist Office, grant number CZD/16/6. The MRC provides core funding to the QTL in Health and Disease research program at the MRC HGU, IGMM, University of Edinburgh. The inclusion of UK Biobank cases and controls was conducted under the UK Biobank Resource Application Number 7441.

The Endometrial Cancer Association Consortium

The authors thank the many individuals who participated in this study and the numerous institutions and their staff who supported recruitment.

The iCOGS and OncoArray endometrial cancer analysis were supported by NHMRC project grants [ID#1031333 & ID#1109286] Funding for the iCOGS infrastructure came from: the European Community's Seventh Framework Programme under grant agreement no 223175 [HEALTH-F2-2009-223175] [COGS], Cancer Research UK [C1287/A10118, C1287/A 10710, C12292/A11174, C1281/A12014, C5047/A8384, C5047/A15007, C5047/A10692, C8197/A16565], the National Institutes of Health [CA128978] and Post-Cancer GWAS
initiative [1U19 CA148537, 1U19 CA148065 and 1U19 CA148112 - the GAME-ON initiative], the Department of Defence [W81XWH-10-1-0341], the Canadian Institutes of Health Research [CIHR] for the CIHR Team in Familial Risks of Breast Cancer, Komen Foundation for the Cure, the Breast Cancer Research Foundation, and the Ovarian Cancer Research Fund. OncoArray genotyping of ECAC cases was performed with the generous assistance of the Ovarian Cancer Association Consortium (OCAC). We particularly thank the efforts of Cathy Phelan. The OCAC OncoArray genotyping project was funded through grants from the US National Institutes of Health (CA1X01HG007491-01, U19-CA148112, R01-CA149429 and R01-CA058598); Canadian Institutes of Health Research (MOP-86727); and the Ovarian Cancer Research Fund. CDR genotyping for the Oncoarray was conducted under contract 268201200008I. OncoArray genotyping of the BCAC controls was funded by Genome Canada Grant GPH-129344, NIH Grant U19 CA148065, and Cancer UK Grant C1287/A16563.

Stage 1 and stage 2 case genotyping was supported by the NHMRC [ID#552402, ID#1031333]. Control data were generated by the Wellcome Trust Case Control Consortium (WTCCC), and a full list of the investigators who contributed to the generation of the data is available from the WTCCC website. We acknowledge use of DNA from the British 1958 Birth Cohort collection, funded by the Medical Research Council grant G0000934 and the Wellcome Trust grant 068545/Z/02 - funding for this project was provided by the Wellcome Trust under award 085475. NSECG was supported by the EU FP7 CHIBCHA grant, Wellcome Trust Centre for Human Genetics Core Grant 090532/Z/09Z, and CORGI was funded by Cancer Research UK. We thank Nick Martin, Dale Nyholt and Anjali Henders for access to GWAS data from QIMR Controls. Recruitment of the QIMR controls was supported by the NHMRC. The University of Newcastle, the Gladys M Brawn Senior Research Fellowship scheme, The Vincent Fairfax Family Foundation, the Hunter Medical Research Institute and the Hunter Area Pathology Service all contributed towards the costs of establishing the Hunter Community Study. The WHI program is funded by the National Heart, Lung, and Blood Institute, the US National Institutes of Health and the US Department of Health and Human Services (HHSN268201100046C, HHSN268201100001C, HHSN268201100002C, HHSN268201100003C, HHSN268201100004C and HHSN271201100004C). This work was also funded by NCI U19 CA148065-01. This research has been conducted using the UK Biobank Resource under applications 5122 and 9797.

ANECS recruitment was supported by project grants from the NHMRC [ID#339435], The Cancer Council Queensland [ID#4196615] and Cancer Council Tasmania [ID#403031 and ID#457636]. SEARCH recruitment was funded by a programme grant from Cancer Research UK [C490/A10124]. The Bavarian Endometrial Cancer Study (BECS) was partly funded by the ELAN fund of the University of Erlangen. The Hannover-Jena Endometrial Cancer Study was partly supported by the Rudolf Bartling Foundation. The Leuven Endometrium Study (LES) was supported by the Verelst Foundation for endometrial cancer. The Mayo Endometrial Cancer Study (MECS) and Mayo controls (MAY) were supported by grants from the National Cancer Institute of United States Public Health Service [R01 CA122443, P30 CA15083, P50
CA136393, and GAME-ON the NCI Cancer Post-GWAS Initiative U19 CA148112], the Fred C and Katherine B Andersen Foundation, the Mayo Foundation, and the Ovarian Cancer Research Fund with support of the Smith family, in memory of Kathryn Sladek Smith. MoMaTEC received financial support from a Helse Vest Grant, the University of Bergen, Melzer Foundation, The Norwegian Cancer Society (Harald Andersens legat), The Research Council of Norway and Haukeland University Hospital. The Newcastle Endometrial Cancer Study (NECS) acknowledges contributions from the University of Newcastle, The NBN Children’s Cancer Research Group, Ms Jennie Thomas and the Hunter Medical Research Institute. RENDOCAS was supported through the regional agreement on medical training and clinical research (ALF) between Stockholm County Council and Karolinska Institutet [numbers: 20110222, 20110483, 20110141 and DF 07015], The Swedish Labor Market Insurance [number 100069] and The Swedish Cancer Society [number 11 0439]. The Cancer Hormone Replacement Epidemiology in Sweden Study (CAHRES, formerly called The Singapore and Swedish Breast/Endometrial Cancer Study; SASBAC) was supported by funding from the Agency for Science, Technology and Research of Singapore (A*STAR), the US National Institutes of Health and the Susan G. Komen Breast Cancer Foundation.

The Nurses’ Health Study (NHS) is supported by the NCI, NIH Grants Number UM1 CA186107, P01 CA087969, R01 CA49449, 1R01 CA134958, and 2R01 CA082838. The authors thank the participants and staff of the Nurses’ Health Study for their valuable contributions as well as the following state cancer registries for their help: AL, AZ, AR, CA, CO, CT, DE, FL, GA, ID, IL, IN, IA, KY, LA, ME, MD, MA, MI, NE, NH, NJ, NY, NC, ND, OH, OK, OR, PA, RI, SC, TN, TX, VA, WA, WY. The authors assume full responsibility for analyses and interpretation of these data. The authors also thank Channing Division of Network Medicine, Department of Medicine, Brigham and Women’s Hospital and Harvard Medical School. Finally, the authors also acknowledge Pati Soule and Hardeep Ranu for their laboratory assistance. The Connecticut Endometrial Cancer Study was supported by NCI, NIH Grant Number RO1CA98346. The Fred Hutchinson Cancer Research Center (FHCRC) is supported by NCI, NIH Grant Number NIH R01 CA105212, RO1 CA 87538, RO1 CA75977, R03 CA80636, NO1 HD23166, R35 CA39779, K05 CA92002 and funds from the Fred Hutchinson Cancer Research Center. The Multiethnic Cohort Study (MEC) is supported by the NCI, NHI Grants Number CA54281, CA128008 and 2R01 CA082838. The California Teachers Study (CTS) is supported by NCI, NIH Grant Number 2R01 CA082838, R01 CA91019 and R01 CA77398, and contract 97-10500 from the California Breast Cancer Research Fund. The Polish Endometrial Cancer Study (PECS) is supported by the Intramural Research Program of the NCI. The Prostate, Lung, Colorectal, and Ovarian Cancer Screening Trial (PLCO) is supported by the Extramural and the Intramural Research Programs of the NCI.

**Testicular Germ Cell Tumour GWAS**

We thank the subjects with TGCT and the clinicians involved in their care for participation in this work. We thank the patients and all clinicians forming part of the UK Testicular Cancer
Collaboration (UKTCC) for their participation in this work. This work makes use of data generated by the Wellcome Trust Case Control Consortium 2 (WTCCC2). We acknowledge the contribution of E. Rapley, M. Stratton and K. Litchfield to the generation of the GWAS data. This study was supported by the Movember Foundation and the Institute of Cancer Research. Additional support was provided as follows: genotyping of the OncoArray was funded by the US National Institutes of Health (NIH) [U19 CA 148537 for ELucidating Loci Involved in Prostate cancer SuscEptibility (ELLIPSE) project and X01HG007492 to the Center for Inherited Disease Research (CIDR) under contract number HHSN268201200008I]; additional analytic support was provided by NIH NCI U01 CA188392 (PI: Schumacher); the PRACTICAL consortium was supported by Cancer Research UK Grants C5047/A7357, C1287/A10118, C1287/A16563, C5047/A3354, C5047/A10692, C16913/A6135, European Commission's Seventh Framework Programme grant agreement n° 223175 (HEALTH-F2-2009-223175), and The National Institute of Health (NIH) Cancer Post-Cancer GWAS initiative grant: No. 1 U19 CA 148537-01 (the GAME-ON initiative).

**Glioma GWAS**

We are grateful to all of the patients and individuals for their participation, and we would also like to thank the clinicians and other hospital staff members, cancer registries and the study staff members in the respective centers who contributed to the blood sample and data collection.

The GICC was supported by grants from the US National Institutes of Health (NIH) (R01CA139020, R01CA52689, R01CA52689 and P30CA125123. Additional support was provided by the McNair Medical Institute and the Population Sciences Biorepository at Baylor College of Medicine.

In Sweden, work was additionally supported by Acta Oncologica through the Royal Swedish Academy of Science and by the Swedish Research Council and the Swedish Cancer Foundation. We are grateful to the National Clinical Brain Tumor Group and to all of the clinicians and research nurses throughout Sweden who identified all of the cases.

In the UK, funding was provided by Cancer Research UK (C1298/A8362 supported by the Bobby Moore Fund, the Wellcome Trust and the DJ Fielding Medical Research Trust. The National Brain Tumor Study is supported by the National Cancer Research Network, and we acknowledge all clinicians and healthcare professionals who contributed to this initiative. The UK INTERPHONE study was supported by the European Union Fifth Framework Program 'Quality of Life and Management of Living Resources' (QLK4-CT-1999-01563) and the International Union against Cancer (UICC). The UICC received funds from the Mobile Manufacturers' Forum and the GSM Association. Provision of funds via the UICC was
governed by agreements that guaranteed INTERPHONE's scientific independence
(http://www.iarc.fr/ENG/Units/RCAd.html), and the views expressed in the paper are not
necessarily those of the funders. The UK centers were also supported by the Mobile
Telecommunications and Health Research (MTHR) Programme, and the Northern UK Centre
was supported by the Health and Safety Executive, Department of Health and Safety
Executive and the UK Network Operators.

In France, funding was provided by the Ligue Nationale Contre le Cancer, the Fondation
ARC, the Institut National du Cancer (INCa; PL046), the French Ministry of Higher Education
and Research and the program “Investissements d’avenir” ANR-10-IAIHU-06. This study was
additionally supported by a grant from Génome Québec, le Ministère de l'Enseignement
supérieur, de la Recherche, de la Science et de la Technologie (MESRST) Québec and McGill
University.

In Germany, funding was provided by the Deutsche Forschungsgemeinschaft (Si552,
Schr285), the Deutsche Krebshilfe (70-2385-Wi2, 70-3163-Wi3, 10-6262) and BONFOR.
Funding for the WTCCC was provided by the Wellcome Trust (076113 and 085475). The
KORA Ausburg studies are supported by grants from the German Federal Ministry of
Education and Research (BMBF) and were mainly financed by the Helmholtz Zentrum
München, German Research Center for Environmental Health, Neuherberg. This work was
financed by the German National Genome Research Network (NGFN) and supported within
the Munich Center of Health Sciences (MC Health) as part of LMUinnovativ. Generation of
the German control data was partially supported by a grant of the German Federal Ministry
of Education and Research (BMBF) through the Integrated Network IntegraMent (Integrated
Understanding of Causes and Mechanisms in Mental Disorders), under the auspices of the
e:Med research and funding concept (01ZX1314A).

For the UK GWAS, we acknowledge the funders, organizations and individuals who
contributed to the blood sample and data collection as listed in Hepworth et al. (PMID:
16428250). MD Anderson acknowledges the work of P. Adatto, F. Morice, H. Zhang, V. Levin,
the Brain and Spine Center for the MDA GWAS. For the French study, we are indebted to A.
Rahimian (Onconeurotek), A.M. Lekieffre and M. Brandel for help in collecting data and to Y.
Marie for database support. For the German study, we are indebted to B. Harzheim (Bonn),
S. Ott and A. Müller-Erkwoh (Bonn) for help with the acquisition of clinical data and to R.
Mahlberg (Bonn), who provided technical support. The UK study made use of control
genotyping data generated by the Wellcome Trust Case–Control Consortium. A full list of
the investigators who contributed to the generation of the data is available
from http://www.wtccc.org.uk. The MDA GWAS made use of control genotypes from the
CGEMS prostate and breast cancer studies. A full list of the investigators who contributed to
the generation of the data is available from http://cgems.cancer.gov/. French controls were
taken from the SU.VI.MAX study. The German GWAS made use of genotyping data from
three population control sources: KORA-gen39, the Heinz-Nixdorf RECALL study and
POPGEN. The HNR cohort was established with the support of the Heinz-Nixdorf
Foundation. F.D. received support from the BONFOR Programme of the University of Bonn,
Germany.
The UCSF Adult Glioma Study was supported by the NIH (grant numbers R01CA52689, P50CA097257, R01CA126831 and R01CA139020), the Loglio Collective, the National Brain Tumor Foundation, the Stanley D. Lewis and Virginia S. Lewis Endowed Chair in Brain Tumor Research, the Robert Magnin Newman Endowed Chair in Neuro-oncology and by donations from the families and friends of J. Berardi, H. Glaser, E. Olsen, R.E. Cooper and W. Martinusen. This project also was supported by the National Center for Research Resources and the National Center for Advancing Translational Sciences, NIH, through UCSF–CTSI grant UL1 RR024131 (UCSF CTSI). The contents of this work are solely the responsibility of the authors and do not necessarily represent the official views of the NIH. The collection of cancer incidence data used in this study was supported by the California Department of Public Health as part of the statewide cancer reporting program mandated by California Health and Safety Code section 103885, the National Cancer Institute's Surveillance, Epidemiology and End Results Program under contract HHSN261201000140C (awarded to the Cancer Prevention Institute of California), contract HHSN261201000035C (awarded to the University of Southern California) and contract HHSN261201000034C (awarded to the Public Health Institute), and the Centers for Disease Control and Prevention's National Program of Cancer Registries under agreement # U58DP003862-01 (awarded to the California Department of Public Health). The ideas and opinions expressed herein are those of the author(s), and endorsement by the State of California Department of Public Health, the National Cancer Institute and the Centers for Disease Control and Prevention, or their contractors and subcontractors, is not intended nor should be inferred. Other significant contributors for the UCSF Adult Glioma Study include M. Berger, P. Bracci, S. Chang, J. Clarke, A. Molinaro, A. Perry, M. Pezmecki, M. Prados, I. Smirnov, T. Tihan, K. Walsh, J. Wiemels and S. Zheng.