

## **Project financed by the SCOR Foundation for Science (2023-2025)**

**Final report - December 2025**

### **Aligning competitive morbidities and causes of early onset deaths**

#### **Project coordinators**

**CUSSENOT Olivier** (MD, PhD) and **CANCEL-TASSIN Géraldine** (PhD)

CeRePP, Paris, France

#### **Partners**

Professor Freddy Hamdy (MD PhD), Nuffield Department of Surgical Sciences, University of Oxford, Oxford, UK.

Professor Antoine Chambaz (PhD), Mathématiques appliquées, MAP5 (736-O), Université Paris Cité, France

#### **General context and objectives of the project**

In France, age-related diseases, particularly prostate pathologies—prostate cancer (PCa) and benign prostatic hyperplasia (BPH), the most frequent benign tumour in men—represent a major public health and medical-economic burden. Cancers and cardiovascular diseases alone account for more than half of all deaths nationwide, with marked regional disparities in mortality rates and in the proportion of deaths considered preventable through primary prevention. Each year, around 400,000 men are treated for prostate disorders, including 90,000 surgical procedures, and approximately 8,500 deaths from prostate cancer are recorded. The management and prevention of prostate diseases are complicated by the high prevalence of competing age-related comorbidities, mainly cardiovascular and degenerative disorders (dementia, Parkinson's disease). These conditions are closely linked to common and potentially modifiable risk factors such as hypertension, dyslipidemia, obesity, diabetes, and sleep apnea, which affect a substantial proportion of the male population.

Evidence guiding prevention and screening policies largely relies on observational epidemiological studies, due to ethical constraints or difficulties in performing randomized clinical trials in this area. However, such studies are particularly prone to bias and contradictory findings<sup>1</sup>, especially concerning prostate diseases. Many factors related to lifestyle, metabolism, medications, and anthropometric parameters exhibit paradoxical associations, appearing protective and harmful depending on the study design and endpoints. For example, obesity, physical activity, diabetes, statins, metformin, aspirin, and antihypertensive treatments have all been associated with conflicting risks of BPH, prostate cancer progression or mortality<sup>2-19</sup>. Prostate cancer treatments, especially hormonal therapies, can themselves exacerbate metabolic syndrome and cardiovascular risk, thus increasing competitive mortality<sup>20,21</sup>.

Over the past decade, large cohorts and biobanks have enabled genome-wide association studies on multifactorial diseases and causal inference approaches, improving understanding of genetic susceptibility, metabolic disorders, and longevity<sup>22-41</sup>. However, long-term male cohorts remain rare in France. The PROGENE cohort, active since 1995, is unique in its focus on prostate diseases<sup>42-45</sup>. In parallel, national health databases (French National Health Data System, SNDS) and the Health Data Hub now offer unprecedented opportunities for large-scale, real-world analyses. Anticipating this development, the OBSERVAPUR study extracted nationwide data from the SNDS to capture all medical and surgical treatments for prostate diseases since 2006<sup>46-48</sup>, thus providing a powerful analytical framework for studying the interactions between prostate pathologies, comorbidities, and their treatments at a national level.

This project, led by Olivier Cussenot, Professor of Urology. had the following objectives:

- To integrate genetic markers in the estimation of competitive morbidity and mortality using data from cohorts of men followed for twenty years and define subsets of genetic markers and predictive algorithms useful for personalized screening, and interventional prevention.
- To define strategies useful for causal inference in prostate diseases.

## Achievements and results

**Article 1 : Cussenot O**, Taille Y, Portal JJ, **Cancel-Tassin G**, Roupret M, de la Taille A, Ploussard G, Mathieu R, Hamdy FC, Vicaut E. [A Comprehensive National Survey of Prostate-specific Antigen Testing and Prostate Cancer Management in France: Uncovering Regional and Temporal Disparities](#). Eur Urol Oncol. 2024 Oct;7(5):978-981.

This nationwide population-based study provides a comprehensive overview of prostate-specific antigen (PSA) testing and prostate cancer (PCa) management in France, using real-life data from the French National Health Insurance database (OBSERVAPUR study) between 2006 and 2018. The analysis included 4 936 750 men, among whom 692 516 were diagnosed with PCa and 3 899 509 served as controls without PCa, with more than 37 million PSA tests recorded.

The study highlights that PSA testing in France is both frequent and late. Although half of men underwent at least five PSA tests, the first test was most often performed between 65 and 75 years of age. This late initiation of testing is associated with delayed diagnosis, reduced access to curative treatments, and increased mortality. Regional disparities were observed, with earlier PSA testing and higher detection rates in overseas territories (Martinique and Guadeloupe) compared with mainland France.

Regarding disease characteristics and management, 28% of PCa cases were detected at the first PSA test, and among men aged 50–70 years, nearly one-quarter already had locally advanced or metastatic disease at diagnosis. Radical prostatectomy remained the most frequent first-line treatment in this age group, whereas the use of systemic therapies (androgen deprivation therapy and chemotherapy or new hormonal agents) increased steadily over time, suggesting a rising burden of metastatic disease at diagnosis. In contrast, active surveillance and watchful waiting remained underutilised and stable over the study period ( $\approx 12\%$ ), despite evidence supporting their safety in selected patients.

Mortality analyses showed an excess risk of death in men with PCa across all age groups, including the elderly, with significant regional variations. However, these results should be interpreted cautiously due to competing comorbidities and differences in life expectancy between regions. Overall, this study reveals substantial temporal and geographical heterogeneity in PSA testing and PCa management in France, underscoring the need for clearer national guidelines on PSA testing, better support for primary care physicians, earlier risk-adapted detection strategies, and wider adoption of active surveillance to reduce overtreatment and improve outcomes.

**Articles 2: Cussenot O**, Fromont G, **Cancel-Tassin G**, **Hamdy FC**, Martin RM. [Endemic statistical paradoxes in epidemiologic studies distort knowledge on prostate cancer: mitigation and caution of fallacies in prostate cancer causal epidemiological studies](#). Curr Opin Urol. 2023 Nov 1;33(6):421-427. Supplement (1) - Supplement (2)

This review analyses why epidemiological studies on prostate cancer (PCa) frequently produce contradictory or misleading conclusions, focusing on endemic statistical paradoxes driven by the use of prostate-specific antigen (PSA) as a diagnostic and stratification tool. Because PCa case–control definitions often rely on PSA thresholds rather than true disease prevalence, observed associations between exposures and PCa risk may reflect changes in the predictive performance of PSA rather than genuine causal effects.

This underlines that PSA is not a neutral classifier: its blood levels are biologically influenced by multiple endogenous and exogenous factors, including prostate volume, body mass index (BMI), ancestry, medications, hormonal status, and genetic variants. When an exposure modifies PSA levels, it alters test sensitivity or specificity, thereby changing the posterior probability of PCa detection without affecting the underlying prevalence. This mechanism explains major biases such as collider (Berkson's) bias and the Will Rogers paradox, which can reverse or inflate associations between risk factors and PCa outcomes.

The review shows that even advanced causal inference methods, such as Mendelian randomization, cannot fully correct these biases if selection into studies depends on PSA level. Through conceptual models and a detailed case study using the PROGENE cohort, we demonstrate that factors influencing PSA (e.g. BMI, height, prostate volume) show directionally unstable associations with PCa depending on control selection, whereas true causal factors (family history, established genetic susceptibility variants) remain consistent.

To mitigate these biases, methodological strategies were proposed: avoiding PSA-based stratification when it is linked to the exposure; testing independence between exposures and PSA; deliberately using multiple control selection modalities within the same study; and incorporating positive and negative genetic controls. In conclusion, a deeper understanding and exploitation of selection mechanisms, combined with robust genetic instruments, are essential to distinguish real causal factors from spurious ones, and to improve the validity of epidemiological evidence guiding PCa prevention and clinical decision-making.

**Article 3: Cussenot O, Rouprêt M, Shariat SF. [Time to Refine Prostate Cancer Epidemiology: Defining New Endpoints for Effective Screening and Causal Epidemiological Studies](#). Eur Urol Oncol. 2025 Feb;8(1):7-8.**

This editorial argues that prostate cancer (PCa) epidemiology must be urgently modernized to reflect current knowledge of disease biology, diagnostic tools, and screening practices. We highlighted how confusion between population-level recommendations against systematic PSA screening and urologists' endorsement of individualized screening has led to widespread misuse of PSA testing. In countries such as France, PSA testing is often initiated too late (median age ~69 years), when early detection and curative treatment have limited impact on mortality, as demonstrated by major randomized trials.

We emphasize that PSA-based epidemiological studies are profoundly affected by selection and collider biases. PSA levels are influenced by numerous biological and external factors (eg, obesity, medications, hormonal status), which can distort associations between exposures and prostate cancer risk or prognosis. As a result, changes in PSA performance are frequently misinterpreted as true causal effects. These biases persist even in sophisticated designs, including Mendelian randomization, if PSA is used as a stratification or selection variable without verifying its independence from the exposure of interest.

We further argue that current epidemiological indicators largely reflect diagnostic intensity rather than the true incidence of clinically significant PCa. Autopsy studies suggest that histological PCa is extremely common, whereas many detected cancers—particularly International Society of Urological Pathology grade group 1 (GG1)—have minimal metastatic or lethal potential and are best managed with active surveillance. These findings support ongoing discussions about excluding GG1 disease from the clinical definition of “cancer” for epidemiological purposes and call for updates to disease classification systems to distinguish indolent from clinically significant PCa.

Mortality remains a key endpoint, but PCa-specific mortality is difficult to measure reliably in real-world data. Incorporating endpoints such as metastatic castration-resistant PCa could better capture clinically meaningful outcomes. Finally, the rising incidence of metastatic PCa at diagnosis is discussed, noting that it reflects both delayed detection due to inadequate screening strategies and stage migration driven by increasingly sensitive imaging technologies.

In conclusion, this editorial warns that, without redefining endpoints, refining control selection, and aligning epidemiological frameworks with contemporary diagnostic and pathological understanding, prostate cancer research risks missing a critical opportunity to reassess and optimize screening strategies.

**Article 4: Cussenot O**, Taille Y, Portal JJ, **Cancel-Tassin G**, Rouprêt M, de la Taille A, Ploussard G, Mathieu R, Vicaut E. [Eliciting the Impact of Metformin and Statins on Prostate Cancer Outcomes from a Real-life National Database Analysis](#). *Eur Urol Oncol*. 2025 Aug;8(4):871-874.

This report evaluates the impact of statins and metformin, prescribed for metabolic syndrome and type 2 diabetes, on survival outcomes in men with prostate cancer (PCa), using French nationwide real-life health data (Observapur study) collected between 2006 and 2018. The study included 521 052 men diagnosed with PCa and 1 827 345 men without PCa as controls, making it one of the largest observational analyses addressing this question. Previous studies have reported conflicting results regarding the effects of these drugs on PCa prognosis, partly due to selection bias and confounding by comorbidities.

Overall mortality was highest among men with PCa exposed to both statins and metformin, reflecting the heavy burden of cardiovascular and metabolic comorbidities in this group. When analyses were stratified by first-line PCa treatment, which served as a proxy for disease aggressiveness and life expectancy at diagnosis, contrasting effects emerged. In men initially treated with radical prostatectomy, exposure to statins and/or metformin was associated with worse survival, likely reflecting underlying comorbid conditions rather than a detrimental drug effect.

In contrast, among patients whose first-line treatment was androgen deprivation therapy (ADT), statin use was associated with a significant survival benefit. Compared with non-users, statin exposure alone and combined statin–metformin exposure were associated with reduced mortality, whereas metformin alone was associated with higher mortality. Statin users receiving ADT also experienced a delayed progression to second-line chemotherapy, although this may partly reflect more cautious use of chemotherapy in patients with cardiovascular disease.

To strengthen causal interpretation, a Bayesian network causal modelling was applied, which confirmed a modest protective effect of statins on early mortality, while metformin showed no protective effect. This analysis was further supported by semantic causal elicitation using generative artificial intelligence integrating published biomedical knowledge.

The study concludes that statins may confer a selective survival benefit in men with advanced PCa treated with ADT, potentially through cardiovascular risk mitigation or biological interactions with androgen signalling. In contrast, metformin does not appear to improve PCa outcomes. These findings argue against a universal protective role of metabolic drugs in PCa and support a more nuanced, context-dependent interpretation of observational data.

#### **Article 5 in preparation:**

Evaluation of the “low-pass” whole genome sequencing (lpWGS) on germline DNA, which corresponds to next-generation sequencing at low-depth coverage (4X), to simultaneously identify genetic variants associated with the risk of prostate diseases and their comorbidities.

The primary objective of this study was to evaluate whether low-pass whole genome sequencing, combined with genotype imputation, could reliably identify genetic variants associated with prostate disease susceptibility and related comorbidities in a previously genotyped cohort.

The secondary objective was to compare variant detection performance between lpWGS and a prior SNP array–based genotyping platform, in order to determine the suitability of lpWGS for comprehensive genetic profiling in the PROGENE cohort.

A subset of 180 patients was selected from the PROGENE study cohort. These individuals had previously undergone germline genotyping using a high-density microarray covering approximately 300,000 single nucleotide polymorphisms (SNPs). The selected patients were

representative of the broader study population in terms of clinical and demographic characteristics. Genomic DNA was previously extracted from peripheral blood samples using standardized extraction protocols. DNA concentration and purity were assessed using spectrophotometric and fluorometric quantification methods. Only samples meeting predefined quality criteria were included in sequencing analyses. Low-pass whole genome sequencing was performed at a mean depth of coverage of approximately 4X. Library preparation was carried out using validated protocols. Paired-end sequencing was conducted to ensure uniform genome-wide representation. Sequencing reads were aligned to the human reference genome using a standard alignment algorithm. Post-alignment processing included duplicate marking, base quality recalibration, and variant calling using established bioinformatics pipelines optimized for low-depth sequencing data. Given the low sequencing depth, genotype likelihoods were first computed at all observed loci. Direct genotype calls from lpWGS were considered preliminary due to limited coverage at individual positions. Genotype imputation was subsequently performed using high-quality population-based reference panels (GLIMPSE 2.0). The imputation pipeline included: phasing of genotype likelihoods, imputation of unobserved and low-confidence variants and calculation of posterior genotype probabilities and imputation quality metrics. Variants were filtered according to predefined thresholds for imputation quality, call rate, and minor allele frequency. Only variants meeting quality control criteria were retained for downstream comparison. The comparator dataset consisted of approximately 300,000 SNPs previously genotyped using a microarray-based platform. Standard quality control procedures had been applied to this dataset, including filtering for call rate, Hardy–Weinberg equilibrium, and minor allele frequency. The SNP array dataset served as the reference for concordance analysis and variant recovery assessment. To evaluate technical agreement between platforms, overlapping variants present in both datasets were identified. Concordance was assessed by per-variant genotype concordance rate. Overall concordance between lpWGS-imputed genotypes and SNP array genotypes was high, indicating robust performance of the low-pass sequencing approach when combined with imputation. A predefined list of genetic variants of interest was established prior to analysis: variants identified in genome-wide association studies (GWAS) as associated with prostate cancer risk; variants associated with relevant comorbid conditions, and pathogenic or likely pathogenic variants in established cancer predisposition genes. Recovery of these variants was specifically evaluated in the lpWGS dataset. Although a substantial proportion of common GWAS-associated variants were successfully identified and imputed with acceptable quality metrics, not all variants of interest were captured. In particular, rare variants and certain clinically relevant mutations in cancer predisposition genes were not reliably detected at 4x depth. Despite demonstrating strong overall concordance with array-based genotyping, low-pass whole genome sequencing at 4x coverage did not provide exhaustive identification of all clinically and biologically relevant variants required for comprehensive risk stratification. The limitations observed were mainly attributable to reduced sensitivity for rare variants (mutations) and the dependence of imputation accuracy on the composition of the reference panel and the performed genome alignment. In light of these findings, the study strategy is being revised to use next-generation genotyping arrays specifically designed to analyse all variants identified through large-scale GWAS in prostate cancer and some of its comorbidities, as well as known pathogenic mutations in cancer predisposition genes. These arrays offer optimized content, tailored to disease-relevant loci, while ensuring high genotype accuracy and cost-efficiency for large cohorts.

## **Conclusions and perspectives**

This project demonstrates that prostate cancer (PCa) epidemiology and prevention strategies must be fundamentally rethought by integrating genetic information, competing morbidities, and refined causal inference frameworks. Using large-scale real-world data and complementary genetic and experimental approaches, the study shows that many established associations in

PCa epidemiology are distorted by selection biases related to PSA testing and by failure to account for competing causes of mortality. PSA is not a neutral marker, and its biological and genetic determinants profoundly influence disease detection, risk assessment, and prognosis. By combining population-level analyses, methodological work on causal inference, and mechanistic genetic studies, this project provides a coherent framework for distinguishing true causal factors from artefactual associations. The results support moving beyond PSA-centric definitions of disease towards endpoints that better capture clinically significant PCa, such as metastatic and lethal forms, while also integrating genetic markers to personalize screening and prevention.

Future perspectives include the development of genetically informed risk-adapted screening strategies, the improvement of the alignment of PCa outcomes to competitive comorbidities, and the refinement of epidemiological databases to reflect disease biology rather than diagnostic intensity. This approach lays the groundwork for more accurate, equitable, and causally robust strategies for PCa prevention and management.

## References

1. Griffith GJ, Morris TT, Tudball MJ, Herbert A, Mancano G, Pike L, Sharp GC, Sterne J, Palmer TM, Davey Smith G, Tilling K, Zuccolo L, Davies NM, Hemani G. Collider bias undermines our understanding of COVID-19 disease risk and severity. *Nat Commun.* 2020 Nov 12;11(1):5749.
2. Lauby-Secretan B, Scoccianti C, Loomis D, Grosse Y, Bianchini F, Straif K International Agency for Research on Cancer Handbook Working Group. Body Fatness and Cancer--Viewpoint of the IARC Working Group. *N Engl J Med.* 2016 Aug 25;375(8):794-8.
3. Wallner LP, Morgenstern H, McGree ME, Jacobson DJ, St Sauver JL, Jacobsen SJ, Sarma AV. The effects of body mass index on changes in prostate-specific antigen levels and prostate volume over 15 years of follow-up: implications for prostate cancer detection. *Cancer Epidemiol Biomarkers Prev.* 2011 Mar 20(3):501-8.
4. Davies NM, Gaunt TR, Lewis SJ, Holly J, Donovan JL, Hamdy FC, Kemp JP, Eeles R, Easton D, Kote-Jarai Z, Al Olama AA, Benlloch S, Muir K, Giles GG, Wiklund F, Gronberg H, Haiman CA, Schleutker J, Nordestgaard BG, Travis RC, Neal D, Pashayan N, Khaw KT, Stanford JL, Blot WJ, Thibodeau S, Maier C, Kibel AS, Cybulski C, Cannon-Albright L, Brenner H, Park J, Kaneva R, Batra J, Teixeira MR, Pandha H PRACTICAL consortium, Lathrop M, Smith GD, Martin RM. The effects of height and BMI on prostate cancer incidence and mortality: a Mendelian randomization study in 20,848 cases and 20,214 controls from the PRACTICAL consortium. *Cancer Causes Control.* 2015 Nov;26(11):1603-16.
5. Hammarsten J, Högstedt B. Clinical, haemodynamic, anthropometric, metabolic and insulin profile of men with high-stage and high-grade clinical prostate cancer. *Blood Press.* 2004;13(1):47-55.
6. Saint-Maurice PF, Coughlan D, Kelly SP, Keadle SK, Cook MB, Carlson SA, Fulton JE, Matthews CE. Association of Leisure-Time Physical Activity Across the Adult Life Course With All-Cause and Cause-Specific Mortality. *JAMA Netw Open.* 2019 Mar 12(3):e190355.
7. Burke JP, Jacobson DJ, McGree ME, Roberts RO, Girman CJ, Lieber MM, Jacobsen SJ. Diabetes and benign prostatic hyperplasia progression in Olmsted County, Minnesota. *Urology.* 2006 Jan;67(1):22-5.
8. Laukkanen JA, Laaksonen DE, Niskanen L, Pukkala E, Hakkarainen A, Salonen JT. Metabolic syndrome and the risk of prostate cancer in Finnish men: a population-based study. *Cancer Epidemiol Biomarkers Prev.* 2004 Oct;13(10):1646-50.
9. Tande AJ, Platz EA, Folsom AR. The metabolic syndrome is associated with reduced risk of prostate cancer. *Am J Epidemiol.* 2006 Dec 1;164(11):1094-102.
10. Lund Håheim L, Wisløff TF, Holme I, Nafstad P. Metabolic syndrome predicts prostate cancer in a cohort of middle-aged Norwegian men followed for 27 years. *Am J Epidemiol.* 2006 Oct 15;164(8):769-74.

11. Beebe-Dimmer JL, Nock NL, Neslund-Dudas C, Rundle A, Bock CH, Tang D, Jankowski M, Rybicki BA. Racial differences in risk of prostate cancer associated with metabolic syndrome. *Urology*. 2009 Jul;74(1):185-90.
12. Sauver JL, Jacobsen SJ, Sarma AV. The effects of metabolic conditions on prostate cancer incidence over 15 years of follow-up: results from the Olmsted County Study. *BJU Int*. 2011 Mar;107(6):929-35.
13. Lawrence YR, Morag O, Benderly M, Boyko V, Novikov I, Dicker AP, Goldbourt U, Behar S, Barchana M, Wolf I. Association between metabolic syndrome, diabetes mellitus and prostate cancer risk. *Prostate Cancer Prostatic Dis*. 2013 Jun;16(2):181-6.
14. Polesel J, Gini A, Dal Maso L, Stocco C, Birri S, Taborelli M, Serraino D, Zucchetto A. The impact of diabetes and other metabolic disorders on prostate cancer prognosis. *J Diabetes Complications*. 2016 May-Jun;30(4):591-6.
15. Wang CH, Huang CW, Nguyen PA, Lin MC, Yeh CY, Islam MM, Rahmanti AR, Yang HC. Chemopreventive Effects of Concomitant or Individual Use of Statins, Aspirin, Metformin, and Angiotensin Drugs: A Study Using Claims Data of 23 Million Individuals. *Cancers (Basel)*. 2022 Feb 25;14(5):1211.
16. Longo J, Freedland SJ, Penn LZ, Hamilton RJ. Statins and prostate cancer-hype or hope? The biological perspective. *Prostate Cancer Prostatic Dis*. 2022 Apr;25(4):650-656.
17. Skuli SJ, Alomari S, Gaitsch H, Bakayoko A, Skuli N, Tyler BM. Metformin and Cancer, an Ambiguous Relationship. *Pharmaceuticals (Basel)*. 2022 May 19;15(5):626.
18. Elwood PC, Morgan G, Delon C, Prottly M, Galante J, Pickering J, Watkins J, Weightman A, Morris D. Aspirin and cancer survival: a systematic review and meta-analyses of 118 observational studies of aspirin and 18 cancers. *Ecancelmedicalscience*. 2021 Jul 2;15:1258.
19. Wallner LP, Morgenstern H, McGree ME, Jacobson DJ, St Sauver JL, Jacobsen SJ, Sarma AV. The effects of type 2 diabetes and hypertension on changes in serum prostate specific antigen levels: results from the Olmsted County study. *Urology*. 2011 Jan;77(1):137-41.
20. Li JR, Wang SS, Chen CS, Cheng CL, Hung SC, Lin CH, Chiu KY. Conventional androgen deprivation therapy is associated with an increased risk of cardiovascular disease in advanced prostate cancer, a nationwide population-based study. *PLoS One*. 2022 Jun 28;17(6):e0270292.
21. Wallander M, Axelsson KF, Lundh D, Lorentzon M. Patients with prostate cancer and androgen deprivation therapy have increased risk of fractures-a study from the fractures and fall injuries in the elderly cohort (FRAILCO). *steoporos Int*. 2019 Jan;30(1):115-125.
22. Ciampa J, Yeager M, Amundadottir L, Jacobs K, Kraft P, Chung C, Wacholder S, Yu K, Wheeler W, Thun MJ, Divers WR, Gapstur S, Albanes D, Virtamo J, Weinstein S, Giovannucci E, Willett WC, Cancel-Tassin G, Cussenot O, Valeri A, Hunter D, Hoover R, Thomas G, Chanock S, Chatterjee N. Large-scale exploration of gene-gene interactions in prostate cancer using a multistage genome-wide association study. *Cancer Res*. 2011 May 1;71(9):3287-95.
23. Locke AE, Kahali B, Berndt SI, Justice AE, Pers TH, Day FR, Powell C, Vedantam S, Buchkovich ML, Yang J, Croteau-Chonka DC, Esko T, Fall T, Ferreira T, Gustafsson S, Kutalik Z, Luan J, Mägi R, Randall JC, Winkler TW, Wood AR, Workalemahu T, Faul JD, Smith JA, Zhao JH, Zhao W, Chen J, Fehrmann R, Hedman ÅK, Karjalainen J, Schmidt EM, Absher D, Amin N, Anderson D, Beekman M, Bolton JL, Bragg-Gresham JL, Buyske S, Demirkan A, Deng G, Ehret GB, Feenstra B, Feitosa MF, Fischer K, Goel A, Gong J, Jackson AU, Kanoni S, Kleber ME, Kristiansson K, Lim U, Lotay V, Mangino M, Leach IM, Medina-Gomez C, Medland SE, Nalls MA, Palmer CD, Pasko D, Pechlivanis S, Peters MJ, Prokopenko I, Shungin D, Stančáková A, Strawbridge RJ, Sung YJ, Tanaka T, Teumer A, Trompet S, van der Laan SW, van Setten J, Van Vliet-Ostaptchouk JV, Wang Z, Yengo L, Zhang W, Isaacs A, Albrecht E, Ärnlöv J, Arscott GM, Attwood AP, Bandinelli S, Barrett A, Bas IN, Bellis C, Bennett AJ, Berne C, Blagieva R, Blüher M, Böhringer S, Bonnycastle LL, Böttcher Y, Boyd HA, Bruinenberg M, Caspersen IH, Chen YI, Clarke R, Daw EW, de Craen AJM, Delgado G, Dimitriou M, Doney ASF, Eklund N, Estrada K, Eury E, Folkersen L, Fraser RM, Garcia ME, Geller F, Giedraitis V, Gigante B, Go AS, Golay A, Goodall AH, Gordon

SD, Gorski M, Grabe HJ, Grallert H, Grammer TB, Gräßler J, Grönberg H, Groves CJ, Gusto G, Haessler J, Hall P, Haller T, Hallmans G, Hartman CA, Hassinen M, Hayward C, Heard-Costa NL, Helmer Q, Hengstenberg C, Holmen O, Hottenga JJ, James AL, Jeff JM, Johansson Å, Jolley J, Juliusdottir T, Kinnunen L, Koenig W, Koskenvuo M, Kratzer W, Laitinen J, Lamina C, Leander K, Lee NR, Lichtner P, Lind L, Lindström J, Lo KS, Lobbens S, Lorbeer R, Lu Y, Mach F, Magnusson PKE, Mahajan A, McArdle WL, McLachlan S, Menni C, Merger S, Mihailov E, Milani L, Moayyeri A, Monda KL, Morken MA, Mulas A, Müller G, Müller-Nurasyid M, Musk AW, Nagaraja R, Nöthen MM, Nolte IM, Pilz S, Rayner NW, Renstrom F, Rettig R, Ried JS, Ripke S, Robertson NR, Rose LM, Sanna S, Scharnagl H, Scholtens S, Schumacher FR, Scott WR, Seufferlein T, Shi J, Smith AV, Smolonska J, Stanton AV, Steinthorsdottir V, Stirrups K, Stringham HM, Sundström J, Swertz MA, Swift AJ, Syvänen AC, Tan ST, Tayo BO, Thorand B, Thorleifsson G, Tyrer JP, Uh HW, Vandenput L, Verhulst FC, Vermeulen SH, Verweij N, Vonk JM, Waite LL, Warren HR, Waterworth D, Weedon MN, Wilkens LR, Willenborg C, Wilsgaard T, Wojczynski MK, Wong A, Wright AF, Zhang Q; LifeLines Cohort Study; Brennan EP, Choi M, Dastani Z, Drong AW, Eriksson P, Franco-Cereceda A, Gådin JR, Gharavi AG, Goddard ME, Handsaker RE, Huang J, Karpe F, Kathiresan S, Keildson S, Kiryluk K, Kubo M, Lee JY, Liang L, Lifton RP, Ma B, McCarroll SA, McKnight AJ, Min JL, Moffatt MF, Montgomery GW, Murabito JM, Nicholson G, Nyholt DR, Okada Y, Perry JRB, Dorajoo R, Reinmaa E, Salem RM, Sandholm N, Scott RA, Stolk L, Takahashi A, Tanaka T, van 't Hooft FM, Vinkhuyzen AAE, Westra HJ, Zheng W, Zondervan KT; ADIPOGen Consortium; AGEN-BMI Working Group; CARDIOGRAMplusC4D Consortium; CKDGen Consortium; GLGC; ICBP; MAGIC Investigators; MuTHER Consortium; MIGen Consortium; PAGE Consortium; ReproGen Consortium; GENIE Consortium; International Endogene Consortium; Heath AC, Arveiler D, Bakker SJL, Beilby J, Bergman RN, Blangero J, Bovet P, Campbell H, Caulfield MJ, Cesana G, Chakravarti A, Chasman DI, Chines PS, Collins FS, Crawford DC, Cupples LA, Cusi D, Danesh J, de Faire U, den Ruijter HM, Dominiczak AF, Erbel R, Erdmann J, Eriksson JG, Farrall M, Felix SB, Ferrannini E, Ferrières J, Ford I, Forouhi NG, Forrester T, Franco OH, Gansevoort RT, Gejman PV, Gieger C, Gottesman O, Gudnason V, Gyllensten U, Hall AS, Harris TB, Hattersley AT, Hicks AA, Hindorf LA, Hingorani AD, Hofman A, Homuth G, Hovingh GK, Humphries SE, Hunt SC, Hyppönen E, Illig T, Jacobs KB, Jarvelin MR, Jöckel KH, Johansen B, Jousilahti P, Jukema JW, Jula AM, Kaprio J, Kastelein JJP, Keinänen-Kiukaanniemi SM, Kiemeny LA, Knekt P, Kooner JS, Kooperberg C, Kovacs P, Kraja AT, Kumari M, Kuusisto J, Lakka TA, Langenberg C, Marchand LL, Lehtimäki T, Lysenko V, Männistö S, Marette A, Matise TC, McKenzie CA, McKnight B, Moll FL, Morris AD, Morris AP, Murray JC, Nelis M, Ohlsson C, Oldehinkel AJ, Ong KK, Madden PAF, Pasterkamp G, Peden JF, Peters A, Postma DS, Pramstaller PP, Price JF, Qi L, Raitakari OT, Rankinen T, Rao DC, Rice TK, Ridker PM, Rioux JD, Ritchie MD, Rudan I, Salomaa V, Samani NJ, Saramies J, Sarzynski MA, Schunkert H, Schwarz PEH, Sever P, Shuldiner AR, Sinisalo J, Stolk RP, Strauch K, Tönjes A, Trégouët DA, Tremblay A, Tremoli E, Virtamo J, Vohl MC, Völker U, Waeber G, Willemsen G, Witteman JC, Zillikens MC, Adair LS, Amouyel P, Asselbergs FW, Assimes TL, Bochud M, Boehm BO, Boerwinkle E, Bornstein SR, Bottinger EP, Bouchard C, Cauchi S, Chambers JC, Chanock SJ, Cooper RS, de Bakker PIW, Dedoussis G, Ferrucci L, Franks PW, Froguel P, Groop LC, Haiman CA, Hamsten A, Hui J, Hunter DJ, Hveem K, Kaplan RC, Kivimäki M, Kuh D, Laakso M, Liu Y, Martin NG, März W, Melbye M, Metspalu A, Moebus S, Munroe PB, Njølstad I, Oostra BA, Palmer CNA, Pedersen NL, Perola M, Pérusse L, Peters U, Power C, Quertermous T, Rauramaa R, Rivadeneira F, Saaristo TE, Saleheen D, Sattar N, Schadt EE, Schlessinger D, Slagboom PE, Snieder H, Spector TD, Thorsteinsdottir U, Stumvoll M, Tuomilehto J, Uitterlinden AG, Uusitupa M, van der Harst P, Walker M, Wallaschofski H, Wareham NJ, Watkins H, Weir DR, Wichmann HE, Wilson JF, Zanen P, Borecki IB, Deloukas P, Fox CS, Heid IM, O'Connell JR, Strachan DP, Stefansson K, van Duijn CM, Abecasis GR, Franke L, Frayling TM, McCarthy MI, Visscher PM, Scherag A, Willer CJ, Boehnke M, Mohlke KL, Lindgren CM, Beckmann JS, Barroso I, North KE, Ingelsson E, Hirschhorn JN, Loos RJF,

Speliotes EK. Genetic studies of body mass index yield new insights for obesity biology. *Nature*. 2015 Feb 12;518(7538):197-206.

24. Shungin D, Winkler TW, Croteau-Chonka DC, Ferreira T, Locke AE, Mägi R, Strawbridge RJ, Pers TH, Fischer K, Justice AE, Workalemahu T, Wu JMW, Buchkovich ML, Heard-Costa NL, Roman TS, Drong AW, Song C, Gustafsson S, Day FR, Esko T, Fall T, Kutalik Z, Luan J, Randall JC, Scherag A, Vedantam S, Wood AR, Chen J, Fehrmann R, Karjalainen J, Kahali B, Liu CT, Schmidt EM, Absher D, Amin N, Anderson D, Beekman M, Bragg-Gresham JL, Buyske S, Demirkan A, Ehret GB, Feitosa MF, Goel A, Jackson AU, Johnson T, Kleber ME, Kristiansson K, Mangino M, Leach IM, Medina-Gomez C, Palmer CD, Pasko D, Pechlivanis S, Peters MJ, Prokopenko I, Stančáková A, Sung YJ, Tanaka T, Teumer A, Van Vliet-Ostaptchouk JV, Yengo L, Zhang W, Albrecht E, Ärnlöv J, Arscott GM, Bandinelli S, Barrett A, Bellis C, Bennett AJ, Berne C, Blüher M, Böhringer S, Bonnet F, Böttcher Y, Bruinenberg M, Carba DB, Caspersen IH, Clarke R, Daw EW, Deelen J, Deelman E, Delgado G, Doney AS, Eklund N, Erdos MR, Estrada K, Eury E, Friedrich N, Garcia ME, Giedraitis V, Gigante B, Go AS, Golay A, Grallert H, Grammer TB, Gräßler J, Grewal J, Groves CJ, Haller T, Hallmans G, Hartman CA, Hassinen M, Hayward C, Heikkilä K, Herzig KH, Helmer Q, Hillege HL, Holmen O, Hunt SC, Isaacs A, Ittermann T, James AL, Johansson I, Juliusdottir T, Kalafati IP, Kinnunen L, Koenig W, Kooner IK, Kratzer W, Lamina C, Leander K, Lee NR, Lichtner P, Lind L, Lindström J, Lobbens S, Lorentzon M, Mach F, Magnusson PK, Mahajan A, McArdle WL, Menni C, Merger S, Mihailov E, Milani L, Mills R, Moayyeri A, Monda KL, Mooijaart SP, Mühleisen TW, Mulas A, Müller G, Müller-Nurasyid M, Nagaraja R, Nalls MA, Narisu N, Glorioso N, Nolte IM, Olden M, Rayner NW, Renstrom F, Ried JS, Robertson NR, Rose LM, Sanna S, Scharnagl H, Scholtens S, Sennblad B, Seufferlein T, Sitlani CM, Smith AV, Stirrups K, Stringham HM, Sundström J, Swertz MA, Swift AJ, Syvänen AC, Tayo BO, Thorand B, Thorleifsson G, Tomaschitz A, Troffa C, van Oort FV, Verweij N, Vonk JM, Waite LL, Wennauer R, Wilsgaard T, Wojczynski MK, Wong A, Zhang Q, Zhao JH, Brennan EP, Choi M, Eriksson P, Folkersen L, Franco-Cereceda A, Gharavi AG, Hedman ÅK, Hivert MF, Huang J, Kanoni S, Karpe F, Keildson S, Kiryluk K, Liang L, Lifton RP, Ma B, McKnight AJ, McPherson R, Metspalu A, Min JL, Moffatt MF, Montgomery GW, Murabito JM, Nicholson G, Nyholt DR, Olsson C, Perry JR, Reinmaa E, Salem RM, Sandholm N, Schadt EE, Scott RA, Stolk L, Vallejo EE, Westra HJ, Zondervan KT; ADIPOGen Consortium; CARDIOGRAMplusC4D Consortium; CKDGen Consortium; GEFOS Consortium; GENIE Consortium; GLGC; ICBP; International Endogene Consortium; LifeLines Cohort Study; MAGIC Investigators; MuTHER Consortium; PAGE Consortium; ReproGen Consortium; Amouyel P, Arveiler D, Bakker SJ, Beilby J, Bergman RN, Blangero J, Brown MJ, Burnier M, Campbell H, Chakravarti A, Chines PS, Claudi-Boehm S, Collins FS, Crawford DC, Danesh J, de Faire U, de Geus EJ, Dörr M, Erbel R, Eriksson JG, Farrall M, Ferrannini E, Ferrières J, Forouhi NG, Forrester T, Franco OH, Gansevoort RT, Gieger C, Gudnason V, Haiman CA, Harris TB, Hattersley AT, Heliövaara M, Hicks AA, Hingorani AD, Hoffmann W, Hofman A, Homuth G, Humphries SE, Hyppönen E, Illig T, Jarvelin MR, Johansen B, Jousilahti P, Jula AM, Kaprio J, Kee F, Keinänen-Kiukkaanniemi SM, Kooner JS, Kooperberg C, Kovacs P, Kraja AT, Kumari M, Kuulasmaa K, Kuusisto J, Lakka TA, Langenberg C, Le Marchand L, Lehtimäki T, Lyssenko V, Männistö S, Marette A, Matise TC, McKenzie CA, McKnight B, Musk AW, Möhlenkamp S, Morris AD, Nelis M, Ohlsson C, Oldehinkel AJ, Ong KK, Palmer LJ, Penninx BW, Peters A, Pramstaller PP, Raitakari OT, Rankinen T, Rao DC, Rice TK, Ridker PM, Ritchie MD, Rudan I, Salomaa V, Samani NJ, Saramies J, Sarzynski MA, Schwarz PE, Shuldiner AR, Staessen JA, Steinthorsdottir V, Stolk RP, Strauch K, Tönjes A, Tremblay A, Tremoli E, Vohl MC, Völker U, Vollenweider P, Wilson JF, Wittman JC, Adair LS, Bochud M, Boehm BO, Bornstein SR, Bouchard C, Cauchi S, Caulfield MJ, Chambers JC, Chasman DI, Cooper RS, Dedoussis G, Ferrucci L, Froguel P, Grabe HJ, Hamsten A, Hui J, Hveem K, Jöckel KH, Kivimäki M, Kuh D, Laakso M, Liu Y, März W, Munroe PB, Njølstad I, Oostra BA, Palmer CN, Pedersen NL, Perola M, Pérusse L, Peters U, Power C, Quertermous T, Rauramaa R, Rivadeneira F, Saaristo TE, Saleheen D, Sinisalo J, Slagboom PE, Snieder H, Spector TD, Stefansson K, Stumvoll M, Tuomilehto J, Uitterlinden AG, Uusitupa

- M, van der Harst P, Veronesi G, Walker M, Wareham NJ, Watkins H, Wichmann HE, Abecasis GR, Assimes TL, Berndt SI, Boehnke M, Borecki IB, Deloukas P, Franke L, Frayling TM, Groop LC, Hunter DJ, Kaplan RC, O'Connell JR, Qi L, Schlessinger D, Strachan DP, Thorsteinsdottir U, van Duijn CM, Willer CJ, Visscher PM, Yang J, Hirschhorn JN, Zillikens MC, McCarthy MI, Speliotes EK, North KE, Fox CS, Barroso I, Franks PW, Ingelsson E, Heid IM, Loos RJ, Cupples LA, Morris AP, Lindgren CM, Mohlke KL. New genetic loci link adipose and insulin biology to body fat distribution. *Nature*. 2015 Feb 12;518(7538):187-196.
25. Helfand BT, Roehl KA, Cooper PR, McGuire BB, Fitzgerald LM, Cancel-Tassin G, Cornu JN, Bauer S, Van Blarigan EL, Chen X, Duggan D, Ostrander EA, Gwo-Shu M, Zhang ZF, Chang SC, Jeong S, Fontham ET, Smith G, Mohler JL, Berndt SI, McDonnell SK, Kittles R, Rybicki BA, Freedman M, Kantoff PW, Pomerantz M, Breyer JP, Smith JR, Rebbeck TR, Mercola D, Isaacs WB, Wiklund F, Cussenot O, Thibodeau SN, Schaid DJ, Cannon-Albright L, Cooney KA, Chanock SJ, Stanford JL, Chan JM, Witte J, Xu J, Bensen JT, Taylor JA, Catalona WJ. Associations of prostate cancer risk variants with disease aggressiveness: results of the NCI-SPORE Genetics Working Group analysis of 18,343 cases. *Hum Genet*. 2015 Apr;134(4):439-50.
  26. Hackshaw-McGeagh LE, Penfold CM, Walsh E, Donovan JL, Hamdy FC, Neal DE, Jeffreys M, Martin RM, Lane JA; ProtecT Study Group. Physical activity, alcohol consumption, BMI and smoking status before and after prostate cancer diagnosis in the ProtecT trial: opportunities for lifestyle modification. *Int J Cancer*. 2015 Sep 15;137(6):1509-15.
  27. Gaulton KJ, Ferreira T, Lee Y, Raimondo A, Mägi R, Reschen ME, Mahajan A, Locke A, Rayner NW, Robertson N, Scott RA, Prokopenko I, Scott LJ, Green T, Sparso T, Thuillier D, Yengo L, Grallert H, Wahl S, Frånberg M, Strawbridge RJ, Kestler H, Chheda H, Eisele L, Gustafsson S, Steinthorsdottir V, Thorleifsson G, Qi L, Karssen LC, van Leeuwen EM, Willems SM, Li M, Chen H, Fuchsberger C, Kwan P, Ma C, Linderman M, Lu Y, Thomsen SK, Rundle JK, Beer NL, van de Bunt M, Chalisey A, Kang HM, Voight BF, Abecasis GR, Almgren P, Baldassarre D, Balkau B, Benediktsson R, Blüher M, Boeing H, Bonnycastle LL, Bottinger EP, Burtt NP, Carey J, Charpentier G, Chines PS, Cornelis MC, Couper DJ, Crenshaw AT, van Dam RM, Doney AS, Dorkhan M, Edkins S, Eriksson JG, Esko T, Eury E, Fadista J, Flannick J, Fontanillas P, Fox C, Franks PW, Gertow K, Gieger C, Gigante B, Gottesman O, Grant GB, Grarup N, Groves CJ, Hassinen M, Have CT, Herder C, Holmen OL, Hreidarsson AB, Humphries SE, Hunter DJ, Jackson AU, Jonsson A, Jørgensen ME, Jørgensen T, Kao WH, Kerrison ND, Kinnunen L, Klopp N, Kong A, Kovacs P, Kraft P, Kravic J, Langford C, Leander K, Liang L, Lichtner P, Lindgren CM, Lindholm E, Linneberg A, Liu CT, Lobbens S, Luan J, Lyssenko V, Männistö S, McLeod O, Meyer J, Mihailov E, Mirza G, Mühleisen TW, Müller-Nurasyid M, Navarro C, Nöthen MM, Oskolkov NN, Owen KR, Palli D, Pechlivanis S, Peltonen L, Perry JR, Platou CG, Roden M, Ruderfer D, Rybin D, van der Schouw YT, Sennblad B, Sigurdsson G, Stančáková A, Steinbach G, Storm P, Strauch K, Stringham HM, Sun Q, Thorand B, Tikkanen E, Tonjes A, Trakalo J, Tremoli E, Tuomi T, Wennauer R, Wiltshire S, Wood AR, Zeggini E, Dunham I, Birney E, Pasquali L, Ferrer J, Loos RJ, Dupuis J, Florez JC, Boerwinkle E, Pankow JS, van Duijn C, Sijbrands E, Meigs JB, Hu FB, Thorsteinsdottir U, Stefansson K, Lakka TA, Rauramaa R, Stumvoll M, Pedersen NL, Lind L, Keinänen-Kiukaanniemi SM, Korpi-Hyövälti E, Saaristo TE, Saltevo J, Kuusisto J, Laakso M, Metspalu A, Erbel R, Jöcke KH, Moebus S, Ripatti S, Salomaa V, Ingelsson E, Boehm BO, Bergman RN, Collins FS, Mohlke KL, Koistinen H, Tuomilehto J, Hveem K, Njølstad I, Deloukas P, Donnelly PJ, Frayling TM, Hattersley AT, de Faire U, Hamsten A, Illig T, Peters A, Cauchi S, Sladek R, Froguel P, Hansen T, Pedersen O, Morris AD, Palmer CN, Kathiresan S, Melander O, Nilsson PM, Groop LC, Barroso I, Langenberg C, Wareham NJ, O'Callaghan CA, Gloyn AL, Altshuler D, Boehnke M, Teslovich TM, McCarthy MI, Morris AP; DIAbetes Genetics Replication And Meta-analysis (DIAGRAM) Consortium. Genetic fine mapping and genomic annotation defines causal mechanisms at type 2 diabetes susceptibility loci. *Nat Genet*. 2015 Dec;47(12):1415-25.
  28. Dale CE, Fatemifar G, Palmer TM, White J, Prieto-Merino D, Zabaneh D, Engmann JEL, Shah T, Wong A, Warren HR, McLachlan S, Trompet S, Moldovan M, Morris RW, Sofat R, Kumari M,

- Hyppönen E, Jefferis BJ, Gaunt TR, Ben-Shlomo Y, Zhou A, Gentry-Maharaj A, Ryan A UCLEB Consortium METASTROKE Consortium, Mutsert R, Noordam R, Caulfield MJ, Jukema JW, Worrall BB, Munroe PB, Menon U, Power C, Kuh D, Lawlor DA, Humphries SE, Mook-Kanamori DO, Sattar N, Kivimaki M, Price JF, Davey Smith G, Dudbridge F, Hingorani AD, Holmes MV, Casas JP. Causal Associations of Adiposity and Body Fat Distribution With Coronary Heart Disease, Stroke Subtypes, and Type 2 Diabetes Mellitus: A Mendelian Randomization Analysis. *Circulation*. 2017 Jun 13;135(24):2373-2388.
29. Dadaev T, Saunders EJ, Newcombe PJ, Anokian E, Leongamornlert DA, Brook MN, Cieza-Borrella C, Mijuskovic M, Wakerell S, Olama AAA, Schumacher FR, Berndt SI, Benlloch S, Ahmed M, Goh C, Sheng X, Zhang Z, Muir K, Govindasami K, Lophatananon A, Stevens VL, Gapstur SM, Carter BD, Tangen CM, Goodman P, Thompson IM Jr, Batra J, Chambers S, Moya L, Clements J, Horvath L, Tilley W, Risbridger G, Gronberg H, Aly M, Nordström T, Pharoah P, Pashayan N, Schleutker J, Tammela TLJ, Sipeky C, Auvinen A, Albanes D, Weinstein S, Wolk A, Hakansson N, West C, Dunning AM, Burnet N, Mucci L, Giovannucci E, Andriole G, Cussenot O, Cancel-Tassin G, Koutros S, Freeman LEB, Sorensen KD, Orntoft TF, Borre M, Maehle L, Grindedal EM, Neal DE, Donovan JL, Hamdy FC, Martin RM, Travis RC, Key TJ, Hamilton RJ, Fleshner NE, Finelli A, Ingles SA, Stern MC, Rosenstein B, Kerns S, Ostrer H, Lu YJ, Zhang HW, Feng N, Mao X, Guo X, Wang G, Sun Z, Giles GG, Southey MC, MacInnis RJ, FitzGerald LM, Kibel AS, Drake BF, Vega A, Gómez-Caamaño A, Fachal L, Szulkin R, Eklund M, Kogevinas M, Llorca J, Castaño-Vinyals G, Penney KL, Stampfer M, Park JY, Sellers TA, Lin HY, Stanford JL, Cybulski C, Wokolorczyk D, Lubinski J, Ostrander EA, Geybels MS, Nordestgaard BG, Nielsen SF, Weisher M, Bisbjerg R, Røder MA, Iversen P, Brenner H, Cuk K, Holleccek B, Maier C, Luedeke M, Schnoeller T, Kim J, Logothetis CJ, John EM, Teixeira MR, Paulo P, Cardoso M, Neuhausen SL, Steele L, Ding YC, De Ruyck K, De Meerleer G, Ost P, Razack A, Lim J, Teo SH, Lin DW, Newcomb LF, Lessel D, Gamulin M, Kulis T, Kaneva R, Usmani N, Slavov C, Mitev V, Parliament M, Singhal S, Claessens F, Joniau S, Van den Broeck T, Larkin S, Townsend PA, Aukim-Hastie C, Gago-Dominguez M, Castelao JE, Martinez ME, Roobol MJ, Jenster G, van Schaik RHN, Menegaux F, Truong T, Koudou YA, Xu J, Khaw KT, Cannon-Albright L, Pandha H, Michael A, Kierzek A, Thibodeau SN, McDonnell SK, Schaid DJ, Lindstrom S, Turman C, Ma J, Hunter DJ, Riboli E, Siddiq A, Canzian F, Kolonel LN, Le Marchand L, Hoover RN, Machiela MJ, Kraft P PRACTICAL (Prostate Cancer Association Group to Investigate Cancer-Associated Alterations in the Genome) Consortium, Freedman M, Wiklund F, Chanock S, Henderson BE, Easton DF, Haiman CA, Eeles RA, Conti DV, Kote-Jarai Z. Fine-mapping of prostate cancer susceptibility loci in a large meta-analysis identifies candidate causal variants. *Nat Commun*. 2018 Jun 11;9(1):2256.
30. Matejic M, Saunders EJ, Dadaev T, Brook MN, Wang K, Sheng X, Olama AAA, Schumacher FR, Ingles SA, Govindasami K, Benlloch S, Berndt SI, Albanes D, Koutros S, Muir K, Stevens VL, Gapstur SM, Tangen CM, Batra J, Clements J, Gronberg H, Pashayan N, Schleutker J, Wolk A, West C, Mucci L, Kraft P, Cancel-Tassin G, Sorensen KD, Maehle L, Grindedal EM, Strom SS, Neal DE, Hamdy FC, Donovan JL, Travis RC, Hamilton RJ, Rosenstein B, Lu YJ, Giles GG, Kibel AS, Vega A, Bensen JT, Kogevinas M, Penney KL, Park JY, Stanford JL, Cybulski C, Nordestgaard BG, Brenner H, Maier C, Kim J, Teixeira MR, Neuhausen SL, De Ruyck K, Razack A, Newcomb LF, Lessel D, Kaneva R, Usmani N, Claessens F, Townsend PA, Gago-Dominguez M, Roobol MJ, Menegaux F, Khaw KT, Cannon-Albright LA, Pandha H, Thibodeau SN, Schaid DJ PRACTICAL (Prostate Cancer Association Group to Investigate Cancer-Associated Alterations in the Genome) Consortium, Wiklund F, Chanock SJ, Easton DF, Eeles RA, Kote-Jarai Z, Conti DV, Haiman CA. Germline variation at 8q24 and prostate cancer risk in men of European ancestry. *Nat Commun*. 2018 Nov 5;9(1):4616.
31. Zenin A, Tsepilov Y, Sharapov S, Getmantsev E, Menshikov LI, Fedichev PO, Aulchenko Y. Identification of 12 genetic loci associated with human healthspan. *Commun Biol*. 2019 Jan 30;2:41.

32. Timmers PR, Mounier N, Lall K, Fischer K, Ning Z, Feng X, Bretherick AD, Clark DW; eQTLGen Consortium; Shen X, Esko T, Kutalik Z, Wilson JF, Joshi PK. Genomics of 1 million parent lifespans implicates novel pathways and common diseases and distinguishes survival chances. *Elife*. 2019 Jan 15;8:e39856.
33. Johansson M, Carreras-Torres R, Scelo G, Purdue MP, Mariosa D, Muller DC, Timpson NJ, Haycock PC, Brown KM, Wang Z, Ye Y, Hofmann JN, Foll M, Gaborieau V, Machiela MJ, Colli LM, Li P, Garnier JG, Blanche H, Boland A, Burdette L, Prokhortchouk E, Skryabin KG, Yeager M, Radojevic-Skodric S, Ognjanovic S, Foretova L, Holcatova I, Janout V, Mates D, Mukeriya A, Rascu S, Zaridze D, Bencko V, Cybulski C, Fabianova E, Jinga V, Lissowska J, Lubinski J, Navratilova M, Rudnai P, Benhamou S, Cancel-Tassin G, Cussenot O, Weiderpass E, Ljungberg B, Tumkur Sitaram R, Häggström C, Bruinsma F, Jordan SJ, Severi G, Winship I, Hveem K, Vatten LJ, Fletcher T, Larsson SC, Wolk A, Banks RE, Selby PJ, Easton DF, Andreotti G, Beane Freeman LE, Koutros S, Männistö S, Weinstein S, Clark PE, Edwards TL, Lipworth L, Gapstur SM, Stevens VL, Carol H, Freedman ML, Pomerantz MM, Cho E, Wilson KM, Gaziano JM, Sesso HD, Freedman ND, Parker AS, Eckel-Passow JE, Huang WY, Kahnoski RJ, Lane BR, Noyes SL, Petillo D, Teh BT, Peters U, White E, Anderson GL, Johnson L, Luo J, Buring J, Lee IM, Chow WH, Moore LE, Eisen T, Henrion M, Larkin J, Barman P, Leibovich BC, Choueiri TK, Lathrop GM, Deleuze JF, Gunter M, McKay JD, Wu X, Houlston RS, Chanock SJ, Relton C, Richards JB, Martin RM, Davey Smith G, Brennan P. The influence of obesity-related factors in the etiology of renal cell carcinoma-A mendelian randomization study. *PLoS Med*. 2019 Jan 3;16(1):e1002724.
34. Adams CD, Richmond R, Ferreira DLS, Spiller W, Tan V, Zheng J, Würtz P, Donovan J, Hamdy F, Neal D, Lane JA, Smith GD, Relton C, Eeles RA, Haiman CA, Kote-Jarai Z, Schumacher FR, Olama AAA, Benlloch S, Muir K, Berndt SI, Conti DV, Wiklund F, Chanock SJ, Gapstur S, Stevens VL, Tangen CM, Batra J, Clements JA, Gronberg H, Pashayan N, Schleutker J, Albanes D, Wolk A, West CML, Mucci LA, Cancel-Tassin G, Koutros S, Sorensen KD, Maehle L, Travis RC, Hamilton RJ, Ingles SA, Rosenstein BS, Lu YJ, Giles GG, Kibel AS, Vega A, Kogevinas M, Penney KL, Park JY, Stanford JL, Cybulski C, Nordestgaard BG, Brenner H, Maier C, Kim J, John EM, Teixeira MR, Neuhausen SL, De Ruyck K, Razack A, Newcomb LF, Lessel D, Kaneva RP, Usmani N, Claessens F, Townsend PA, Dominguez MG, Roobol MJ, Menegaux F, Khaw KT, Cannon-Albright LA, Pandha H, Thibodeau SN, Martin RM; PRACTICAL consortium. Circulating Metabolic Biomarkers of Screen-Detected Prostate Cancer in the ProtecT Study. *Cancer Epidemiol Biomarkers Prev*. 2019 Jan;28(1):208-216.
35. Wright KM, Rand KA, Kermany A, Noto K, Curtis D, Garrigan D, Slinkov D, Dorfman I, Granka JM, Byrnes J, Myres N, Ball CA, Ruby JG. A Prospective Analysis of Genetic Variants Associated with Human Lifespan. *G3 (Bethesda)*. 2019 Sep 4;9(9):2863-2878.
36. Huynh-Le MP, Fan CC, Karunamuni R, Walsh EI, Turner EL, Lane JA, Martin RM, Neal DE, Donovan JL, Hamdy FC, Parsons JK, Eeles RA, Easton DF, Kote-Jarai Z, Amin Al Olama A, Benlloch Garcia S, Muir K, Grönberg H, Wiklund F, Aly M, Schleutker J, Sipeky C, Tammela TL, Nordestgaard BG, Key TJ, Travis RC, Pharoah PDP, Pashayan N, Khaw KT, Thibodeau SN, McDonnell SK, Schaid DJ, Maier C, Vogel W, Luedeke M, Herkommer K, Kibel AS, Cybulski C, Wokolorczyk D, Kluzniak W, Cannon-Albright LA, Brenner H, Schöttker B, Holleczeck B, Park JY, Sellers TA, Lin HY, Slavov CK, Kaneva RP, Mitev VI, Batra J, Clements JA, Spurdle AB, Teixeira MR, Paulo P, Maia S, Pandha H, Michael A, Mills IG, Andreassen OA, Dale AM, Seibert TM Australian Prostate Cancer BioResource (APCB) PRACTICAL Consortium. A Genetic Risk Score to Personalize Prostate Cancer Screening, Applied to Population Data. *Cancer Epidemiol Biomarkers Prev*. 2020 Sep;29(9):1731-1738.
37. Wendeu-Foyet MG, Cénée S, Koudou Y, Trétarre B, Rébillard X, Cancel-Tassin G, Cussenot O, Boland A, Olaso R, Deleuze JF, Blanché H, Lamy PJ, Mulot C, Laurent-Puig P, Truong T, Menegaux F. Circadian genes polymorphisms, night work and prostate cancer risk: Findings from the EPICAP study. *Int J Cancer*. 2020 Dec 1;147(11):3119-3129.

38. Gu D, Tang M, Wang Y, Cui H, Zhang M, Bai Y, Zeng Z, Tan Y, Wang X, Zhang B. The Causal Relationships Between Extrinsic Exposures and Risk of Prostate Cancer: A Phenome-Wide Mendelian Randomization Study. *Front Oncol*. 2022 Feb 14;12:829248.
39. Li HQ, Feng YW, Yang YX, Leng XY, Zhang PC, Chen SD, Kuo K, Huang SY, Zhang XQ, Dong Y, Han X, Cheng X, Cui M, Tan L, Dong Q, Yu JT. Causal Relations between Exposome and Stroke: A Mendelian Randomization Study. *J Stroke*. 2022 May;24(2):236-244.
40. Li C, Liu J, Lin J, Shang H. COVID-19 and risk of neurodegenerative disorders: A Mendelian randomization study. *Transl Psychiatry*. 2022 Jul 14;12(1):283.
41. Li J, Zhao L, Ding X, Cui X, Qi L, Chen Y. Obstructive sleep apnea and the risk of Alzheimer's disease and Parkinson disease: A Mendelian randomization study OSA, Alzheimer's disease and Parkinson disease. *Sleep Med*. 2022 Sep;97:55-63.
42. Valeri A, Berthon P, Fournier G, Buzzi JC, Briollais L, Meria P, Blanche H, Bellanne-Chantelot C, Teillac P, Demenais F, Mangin P, Cohen N, Le Duc A, Cussenot O. Etude PROGENE, project français d'analyse génétique du cancer de la prostate familial: recrutement et analyse [The PROGENE study, the French project of genetic analysis of familial prostatic cancer: recruitment and analysis]. *Prog Urol*. 1996 Apr;6(2):226-35.
43. Yeager M, Orr N, Hayes RB, Jacobs KB, Kraft P, Wacholder S, Minichiello MJ, Fearnhead P, Yu K, Chatterjee N, Wang Z, Welch R, Staats BJ, Calle EE, Feigelson HS, Thun MJ, Rodriguez C, Albanes D, Virtamo J, Weinstein S, Schumacher FR, Giovannucci E, Willett WC, Cancel-Tassin G, Cussenot O, Valeri A, Andriole GL, Gelmann EP, Tucker M, Gerhard DS, Fraumeni JF Jr, Hoover R, Hunter DJ, Chanock SJ, Thomas G. Genome-wide association study of prostate cancer identifies a second risk locus at 8q24. *Nat Genet*. 2007 May;39(5):645-9.
44. Prokunina-Olsson L, Fu YP, Tang W, Jacobs KB, Hayes RB, Kraft P, Berndt SI, Wacholder S, Yu K, Hutchinson A, Spencer Feigelson H, Thun MJ, Diver WR, Albanes D, Virtamo J, Weinstein S, Schumacher FR, Cancel-Tassin G, Cussenot O, Valeri A, Andriole GL, Crawford ED, Haiman CA, Henderson BE, Kolonel L, Le Marchand L, Siddiq A, Riboli E, Travis R, Kaaks R, Isaacs WB, Isaacs SD, Grönberg H, Wiklund F, Xu J, Vatten LJ, Hveem K, Kumle M, Tucker M, Hoover RN, Fraumeni JF Jr, Hunter DJ, Thomas G, Chatterjee N, Chanock SJ, Yeager M. Refining the prostate cancer genetic association within the JAZF1 gene on chromosome 7p15.2. *Cancer Epidemiol Biomarkers Prev*. 2010 May;19(5):1349-55.
45. Abdi B, Basset N, Perrot E, Benderra MA, Khalil A, Oudard S, Blanchet P, Brureau L, Coulet F, Cussenot O, Cancel-Tassin G. DNA damage repair gene germline profiling for metastatic prostate cancer patients of different ancestries. *Prostate*. 2022 Sep;82(12):1196-1201.
46. Cornu JN, Cussenot O, Haab F, Lukacs B. A widespread population study of actual medical management of lower urinary tract symptoms related to benign prostatic hyperplasia across Europe and beyond official clinical guidelines. *Eur Urol*. 2010 Sep;58(3):450-6.
47. Lukacs B, Cornu JN, Aout M, Tessier N, Hodée C, Haab F, Cussenot O, Merlière Y, Moysan V, Vicaud E. Management of lower urinary tract symptoms related to benign prostatic hyperplasia in real-life practice in France: a comprehensive population study. *Eur Urol*. 2013 Sep;64(3):493-501.
48. Tuppin P, Samson S, Fagot-Campagna A, Lukacs B, Alla F CNAMTS scientific board members, Paccaud F, Thalabard JC, Vicaud E, Vidaud M, Millat B. Prostate cancer outcomes in France: treatments, adverse effects and two-year mortality. *BMC Urol*. 2014 Jun 13;14:48.