

Brain health throughout cancer survivorship: the impacts of anti-cancer therapy on
cerebrovascular regulation and pathology

by

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B.S., Miami University, 2018
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Department of Kinesiology
College of Health and Human Sciences

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Abstract

Cancer survivors have substantially greater risk of cardiovascular morbidity and mortality compared to the general population, including a 52% greater risk of heart failure and a 22% greater risk of stroke in some reports. The rates of development of chronic disease, even without immediately fatal endpoints, are similarly worrisome. Addressing both “hard” cardiovascular disease events and the incident development or exacerbation of chronic disease remains critical in the care of cancer survivors. This is even more true today with the increasingly rapid pace of progress in oncology – specifically, the introduction of immune checkpoint inhibitors.

One of the primary concerns addressed in the present dissertation is neurotoxicity, experienced by many cancer survivors as a consequence of both the burden of cancer and due to adverse off-target effects of anti-cancer treatment. This neurotoxicity can manifest in a variety of ways, including cognitive decline, cerebral pathologies like encephalitis or reversible cerebral vasoconstriction syndrome, or in severe cases, stroke or intracranial hemorrhage. Despite the serious and harmful nature of these toxicities, investigations into overall brain health in cancer survivors are limited compared to the research dedicated to other organ systems.

Therefore, in this dissertation, we present a series of four studies aimed at investigating cerebral and cerebrovascular health in cancer survivorship. Our first investigation was a systematic review and meta-analysis examining the associations between two local cerebrovascular regulatory functions (cerebrovascular reactivity, cerebral autoregulation) and one systemic vascular characteristic (arterial stiffness) with cerebral small vessel disease. Subsequently, we aimed to determine if there were impairments in cerebrovascular reactivity in cancer survivors compared to cancer-free controls. We then combined evidence from the first two studies to form a base of evidence suggesting that cancer survivors were likely to be at risk

for cerebral small vessel disease. This led to our last two studies focused on a novel class of anti-cancer treatment, called immune checkpoint inhibitors (ICI). Our third study uses Mendelian randomization and human genetic information to explore relationships between exposure to ICI treatment and the risk of developing cerebral small vessel disease. Finally, our fourth study expands on the previous study's findings with single-cell RNA-sequencing of vascular tissue from patients who did or did not receive ICI treatment. This patient tissue-derived information is combined with genomic and epigenetic analyses to investigate biological processes and pathways linking ICI exposure to cerebral small vessel disease, and to subsequently identify possible therapeutic options. It is our hope that this dissertation may provide insight into the cerebrovascular complications that exist in cancer survivorship, as well as their potential causes and consequences.

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Dedication

This dissertation is dedicated to my late grandfather, Ron Scheuermann. I've always been fortunate to be surrounded by a loving immediate and extended family, even as I struggled to find my own path and made mistakes along the way. Before I started my PhD training, Grandpa Scheuermann passed away with a combination of multiple conditions, including cancer and a history of strokes and coronary artery disease. That day, and the continuing memory of his unwavering strength and compassion throughout my entire life, made my path clear moving forward. Every day is a new opportunity to work with my amazing friends and colleagues and change things for the better, the way that Grandpa Scheuermann did for his community.

Preface

Chapter 2 of the present dissertation is a published, peer-reviewed manuscript. All other chapters have been, or will be, submitted to scientific journals similarly. They are therefore written in published or publication-ready format. Chapter 2 has been reproduced with permission from the publisher. The citation is listed below, along with mock citations for the remaining chapters to provide credit for the co-authors and collaborators.

Chapter 2

Scheuermann, B. C., Parr, S. K., Schulze, K. M., Kunkel, O. N., Turpin, V. R. G., Liang, J., & Ade, C. J. (2023). Associations of cerebrovascular regulation and arterial stiffness with cerebral small vessel disease: a systematic review and meta-analysis. *Journal of the American Heart Association*, 12(23), e032616.

Chapter 3

Scheuermann, B., Hammond, S., Parr, S., Turpin, V.R., Kunkel, O., Baranczuk, A., Schulze, K., Bell, T., Smith, A., Edwards, O., Sanders, S., McGatlin, K., Bailey, H., Ade, C. Cerebral Macro- and Microvascular Regulation in Cancer Survivorship. *In Preparation and Submission*.

Chapter 4

Scheuermann, B., Hakeem, H., Amr, B., Radhi, F., Ade, C. The Effects of Breast Cancer and Immune Checkpoint Inhibition on Cerebral Small Vessel Disease Burden: A Mendelian Randomization Analysis. *In Review at Circulation*.

Chapter 5

Scheuermann, B., Ade, C. Circulatory Links between Immune Checkpoint Inhibitors and Cerebral Small Vessel Disease: Integration of Single Cell RNA-Sequencing and Multiomic Mendelian Randomization. *In Preparation and Submission for Circulation Research.*

Chapter 1 - Physiology and Medicine in the Chronic Disease

“I have criticized the present-day teaching of physiology, anatomy, and pathology, but I want now to urge with all the emphasis I can that whatever may be their present shortcomings, the group of preliminary sciences represented by physiology, anatomy, pathology, and pharmacology form the future basis of practical medicine...The medical art which is not grounded on these sciences is bound to become more and more of an anachronism.”

John Scott Haldane, M.D., F.R.S. *The Relation of Physiology to Medicine*.

Edinburgh Medical Journal (1918).

As the quote above suggests, the observations and predictions of J.S. Haldane at the turn of the 20th century extended far beyond his seminal contributions to understanding the roles of gases in physiology.¹ His treatise implored educational institutions to consider adopting the emerging model in the United States, where “...there was everywhere considerable knowledge of, and enthusiastic belief in, scientific methods...”¹ that led to accelerated advances in both basic and clinical investigation. One of the preeminent physician-physiologists of today, Dr. Michael Joyner, recently pointed out that an understanding of coronary physiology was the driving force behind the 60-70% reduction of coronary artery disease mortality in the last half-century.² In the face of concerns regarding stagnating progress or progress plagued by unanticipated challenges³⁻⁵, returning to foundational integrative physiology to guide research and practice may be warranted. In my opinion, nowhere is this more evident than in the context of cardio-oncology – a field of practice and research aimed at understanding the cardiovascular

complications of cancer and anti-cancer treatments with the goal of improving cancer survivorship outcomes.⁶

Cancer Survivorship and Chronic Disease

“As we move from an earlier time when few cancers were treated successfully to the point when virtually all of them will be cured, we are passing through an uncharted middle ground, which in many aspects remains primitive.”

Fitzhugh Mullan, M.D. *Seasons of Survival: Reflections of a Physician with Cancer.*

The New England Journal of Medicine (1985).

There is an estimated new diagnosis of cancer every 15 seconds in the United States⁷; a staggering rate that has resulted in approximately 18.6 million U.S. cancer survivors as of January 1st, 2025.⁸ Thankfully, the increase in the number of survivors is not solely due to more diagnoses. Recent trends suggest that mortality rates of some of the most common forms of cancer are decreasing, including lung cancer (-4.7%/year), colorectal (-2.0%/year)⁹, and breast cancer (-2.0%/year).¹⁰ Improvements in screening and monitoring have contributed to the reduced mortality, but most sources agree that the largest contribution has come from advances in anti-cancer treatment. One of the earliest “success” stories of chemotherapy (after the initial broad testing performed by German scientist Paul Ehrlich¹¹) stemmed from the adaptation of mustard gas used in World War 2 after observation of its profound leukopenic properties.¹² Advances in anti-cancer treatment followed rapidly, including the isolation of doxorubicin from cultures of *Streptomyces peucetius*¹³ and the synthesis of 5-fluorouracil by Charles Heidelberger and his colleagues.¹⁴ The 21st century has been characterized by a tremendous interest in

developing monoclonal antibodies that target specific tumor-associated antigens¹⁵, such as the use of bevacizumab targeting vascular endothelial growth factor (VEGF) in colorectal and breast cancers.¹⁶ However, these strides in chemotherapy have all been plagued by one critical concern: off-target toxicities.

A phrase heard from Dr. Zachary Clayton at several conferences can summarize one of the major fears of cardiologists, oncologists, and physiologists involved in cancer survivorship: “Today’s cancer patient is tomorrow’s cardiovascular patients” [*Personal Communications*]. Cancer survivors have substantially greater risk of cardiovascular morbidity and mortality compared to the general population, including a 52% greater risk of heart failure and a 22% greater risk of stroke in some reports.¹⁷ The rates of development of chronic disease are similarly worrisome. Exposure to ibrutinib, a tyrosine kinase inhibitor, led to new onset hypertension in 47.2% of treated patients.¹⁸ Androgen suppression therapy for men with prostate cancer impaired glycemic control in 22% of patients.¹⁹ Addressing both “hard” cardiovascular disease events and the incident development or exacerbation of chronic disease remains critical in the care of cancer survivors. This is even more true today with the increasingly rapid pace of progress in oncology – specifically, the introduction of immune checkpoint inhibitors.

Novel Anti-Cancer Therapies: Addressing Benefits and Harms

“Over the past decade, cancer drugs have dominated the accelerated approval pathway, accounting for more than 85% of approvals...The clinical implications cannot be overstated: patients receiving some treatments might be exposed to clinical, financial, and time toxic effects without any meaningful improvements in how long they live or how they feel.”

Kristina Jenei, B.S.N., M.Sc.; Christopher Booth, M.D. The Delicate Balancing Act of Accelerated Approval for Cancer Medicines-Speed, Certainty, and Benefit. JAMA Network Open (2025).

The use of immune checkpoint inhibitor (ICI) therapy will likely be touted as one of the greatest successes in oncology in the past two decades, and for good reason. Trials like KEYNOTE-564 in renal cell carcinoma²⁰ and the CheckMate-141 trial in squamous-cell head and neck cancer²¹ have demonstrated 30-40% reductions in mortality compared to traditional chemotherapy regimens. The so-called “new era of immunotherapy survivorship”²² has been ushered in with 11 approved ICI therapies and an estimated 56% of cancer patients eligible to receive ICI treatment.²³ Despite the excitement for this “era”, the notable toxicities associated with ICI administration has not gone unnoticed by the cardio-oncology community. The goal is not to be nay-sayers of incorporating ICI therapies into regimens, but rather to ensure safe and efficacious planning and monitoring of the cancer survivorship phases. In this regard, early reports of ICI-related myocarditis dominated the research into ICI toxicities, but recent investigations have implicated essentially every organ in the human body as potential target.²⁴ Of particular interest for the present dissertation, neurotoxicity seen after ICI treatment can vary widely in its etiology and presentation, but the potentially fatal outcomes make it a critical gap in our current knowledge.

The Goals of the Present Dissertation

In this dissertation, we aimed to investigate cerebrovascular dysfunction (as a mechanism and manifestation of neurotoxicity) in cancer survivorship. Cerebrovascular dysfunction exists in

a myriad of syndromes, necessitating a more focused approach. Therefore, our first investigation was a systematic review and meta-analysis examining the associations between two local cerebrovascular regulatory functions (cerebrovascular reactivity, cerebral autoregulation) and one systemic vascular characteristic (arterial stiffness) with cerebral small vessel disease (Chapter 2). Subsequently, we aimed to determine if there were impairments in cerebrovascular reactivity in cancer survivors compared to cancer-free controls (Chapter 3). We then combined evidence from Chapters 2 and 3 to form a basis suggesting that cancer survivors were likely to be at risk for cerebral small vessel disease. This led to Chapters 4 and 5, which use unique methods to navigate the current challenges to studying ICIs (i.e., the paucity of data, the novelty of the drugs and lack of follow-up data). Chapter 4 uses Mendelian randomization and human genetic information to explore relationships between exposure to ICI treatment and the risk of developing cerebral small vessel disease. Finally, Chapter 5 expands on Chapter 4 with single-cell RNA-sequencing of vascular tissue from patients who did or did not receive ICI treatment. This patient tissue-derived information is combined with genomic and epigenetic analyses to investigate biological processes and pathways linking ICI exposure to cerebral small vessel disease, and to subsequently identify possible therapeutic options.

It is our hope that this dissertation may provide insight into the cerebrovascular complications that exist in cancer survivorship, as well as their potential causes and consequences. These initial investigations of the ICIs, specifically, will hopefully inform future investigations promoting monitoring and mitigation strategies targeting ICI-associated neurotoxicity. Finally, we hope this dissertation captures the efforts of all members of the research team involved, and most importantly, the dedicated time that numerous cancer survivors

spent with us throughout this process. The devotion of these participants and patients cannot be understated.

“A human being is far more than the mere organism with which medicine and surgery are immediately concerned...If, therefore, medicine is to have more science and less rule of thumb, let us see to it also that with the science goes more humanity, and, where possible, a broader general education, not in the mere dry bones of the humanities, but on living humanistic lines.”

John Scott Haldane, M.D., F.R.S. *The Relation of Physiology to Medicine.*

Edinburgh Medical Journal (1918).

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Chapter 2 - Associations of Cerebrovascular Regulation and Arterial Stiffness with Cerebral Small Vessel Disease: A Systematic Review and Meta-Analysis

Abstract

Background: Cerebral small vessel disease (cSVD) is a major contributing factor to ischemic stroke and dementia. However, the vascular etiologies of cSVD remain inconclusive. The aim of this systematic review and meta-analysis was to characterize the associations between cSVD and cerebrovascular reactivity (CVR), cerebral autoregulation (CA), and arterial stiffness (AS). **Methods and Results:** MEDLINE, Web of Science, and Embase were searched from inception to September 2023 for studies reporting CVR, CA, or AS in relation to radiological markers of cSVD. Data were extracted in predefined tables, reviewed, and meta-analyses performed using inverse-variance random effects models to determine pooled odds ratios (OR). A total of 1611 studies were identified; 142 were included in the systematic review, of which 60 had data available for meta-analyses. Systematic review revealed that CVR, CA, and AS were consistently associated with cSVD (80.4%, 78.6%, and 85.4% of studies, respectively). Meta-analysis in 7 studies (536 participants, 32.9% women) revealed a borderline association between impaired CVR and cSVD (OR:2.26, 95%CI:0.99-5.14; P=0.05). In 37 studies (27,952 participants, 53.0% women) increased AS, per SD, was associated with cSVD (OR:1.24, 95%CI: 1.15-1.33; P<0.01). Meta-regression adjusted for comorbidities accounted for one-third of the AS model variance ($R^2=29.4\%$, $P_{\text{moderators}}=0.02$). Subgroup analysis of AS studies demonstrated an association with white matter hyperintensities (OR:1.42, 95%CI:1.18-1.70; P<0.01).

Conclusions: The collective findings of the present systematic review and meta-analyses suggest an association between cSVD and impaired CVR and elevated AS. However, longitudinal investigations into vascular stiffness and regulatory function as possible risk factors for cSVD remain warranted.

Introduction

Cerebral small vessel disease (cSVD) is responsible for roughly one-fifth of ischemic strokes, contributes to 45% of dementias, and is associated with poor outcomes in Alzheimer's disease and cancer, two of the leading causes of death in the United States.¹⁻³ cSVD in itself is a complex pathology affecting the small (40-200 μ m) perforating arterioles that supply blood to the subcortical white matter of the brain, manifesting as lesions observed with advanced neuroimaging as described by the STRIVE criteria.^{4,5} In addition to the elevated risk for cerebrovascular events, cSVD increases the risk for reduced quality of life and mortality, highlighting the critical importance of identifying risk factors for cSVD to better understand its pathophysiology and inform risk management practices.^{6,7} Common risk factors, particularly hypertension, have been the most prominently investigated underlying mechanisms preceding the onset or progression of cSVD.⁸⁻¹⁰ However, combining the most common cardiovascular risk factors (e.g., hypertension, smoking, diabetes, hyperlipidemia, and elevated homocysteine) still only explains ~2% of the variance in cSVD.¹¹

While the underlying pathophysiology of cSVD is not fully delineated, several studies have suggested that patients with cSVD exhibit vascular vulnerabilities independent of hypertension.¹¹⁻¹³ Interestingly, normotensive patients in these studies often had underlying conditions associated with increased arterial stiffness¹⁴⁻¹⁶, a vascular property of critical importance in health and disease.¹⁷ Stiffening of central (aorta) and conduit (extracranial and intracranial) arteries potentiate small vessel injury in the brain as a result of increased transmission of pulsatile energy¹⁸⁻²⁰, which may cause or develop in parallel with disruption of local regulatory mechanisms such as cerebrovascular reactivity or cerebral autoregulation.^{18,21} Importantly, in a comprehensive review, Wardlaw et al.¹² recently proposed that the

development of cSVD may incorporate the loss of these regulatory functions, suggesting that exploring topics like arterial stiffness and local regulatory mechanisms, such as cerebrovascular reactivity or cerebral autoregulation, could significantly advance our comprehension of cSVD pathogenesis. However, interpretation of the current evidence base is complicated by small sample sizes, varied study methodologies, limited longitudinal studies, and different populations of interest. Therefore, we conducted the present systematic review and meta-analyses to provide an overview of the current evidence for cerebrovascular reactivity, cerebral autoregulation, and arterial stiffness as potential local and global vascular mechanisms associated with cSVD.

Methods

The authors declare that all supporting data are available within the article and its online supplementary files. The analysis was carried out and reported following the guidelines outlined in the Preferred Reporting Items for Systematic Reviews and Meta-Analyses (PRISMA) and Cochrane Collaboration. Additionally, it was registered with the International Prospective Register of Systematic Reviews under the ID number 42023448225.

Search Strategy

Three separate systematic searches of the English literature were performed in the MEDLINE, Web of Science, and Embase electronic databases using the search strategies outlined in the supplementary files (Tables S1-S3) in order to evaluate the relationship between cerebral small vessel disease and cerebrovascular reactivity, cerebrovascular autoregulation, or arterial stiffness. Additional studies were identified through manual searches of reference lists in the publications retrieved. The last database search was performed on September 30th, 2023. There were no *a priori* limitations for constraining searches to specific timeframes; thus, searches included studies published from database inception to the date of the final search. Literature searches and selection of studies were performed by three independent reviewers (B.S., V.T., O.K.), and disagreements were resolved by consensus.

Eligibility Criteria

Studies were considered eligible for the systematic review and meta-analysis if they met the following criteria: (1) full-length publication in a peer-reviewed journal, (2) included participants aged ≥ 18 years who had brain imaging for detection of cSVD by magnetic resonance

imaging (MRI) and (3) reported markers of cSVD compared against a valid, quantified measure of cerebrovascular reactivity, cerebrovascular autoregulation, or arterial stiffness. While previous reports have assessed cSVD burden using computed tomography (CT)²²⁻²⁴ and have noted good agreement between CT- and MRI-derived cSVD features, the features detected on CT are limited to only a couple of the full range of markers recommended for quantification by guidelines.^{4,25} Research standards currently recommend MRI due to the higher sensitivity and specificity for determining cSVD load⁴, and therefore, the present review and meta-analyses exclude studies only using CT. Studies including populations with a previous stroke or other cerebrovascular event (prior transient ischemic attack, intracranial arterial stenosis, etc.) were eligible. The nature of the present research question did not preclude the inclusion of specific study designs. Therefore, cross-sectional or longitudinal studies of any quantitative design were eligible for selection. Studies were excluded if the report was not an original research article; the study was performed using cell, animal, or post-mortem subjects; the study used computed tomography to assess cerebral injury; or cerebral atrophy was the only marker reported. The studies remaining at this step were eligible for qualitative synthesis in the systematic review and were further examined for eligibility for inclusion in quantitative meta-analyses. Studies were not eligible for the subsequent meta-analysis if they did not report an odds ratio (OR) or provide values for the presence of cSVD in the study sample that allowed for the calculation of OR from crude event rates²⁶; however, these studies remained eligible for qualitative synthesis in the systematic review.

Exposure Modalities

The primary exposures extracted were local and systemic measures of cerebrovascular reactivity, cerebral autoregulation, and arterial stiffness:

1. Cerebrovascular reactivity is defined as an index of the change in cerebrovascular tone for a given change in the arterial partial pressure of carbon dioxide.^{27,28} The two primary means of assessing cerebrovascular reactivity included in the present analysis evaluated cerebral blood flow/velocity during changes in arterial partial pressure of carbon dioxide. The first approach included the breath-hold index (BHI), which calculates cerebrovascular reactivity as the percent change in cerebral perfusion divided by the length of the breath-hold phase. The second approach uses controlled mixtures of inhaled gases and calculates cerebrovascular reactivity as the change in cerebral perfusion divided by the change in arterial carbon dioxide.²⁹
2. Cerebral autoregulation is the ability of the brain to adapt vascular tone to maintain a constant cerebral perfusion across a range of perfusion pressures.^{30,31} As a non-invasive measurement, cerebral autoregulation is assessed as the change in cerebral perfusion relative to a change in arterial blood pressure. Evaluation of cerebral autoregulation typically examines either spontaneous or induced oscillations in blood pressure and quantification of cerebral autoregulation may include time domain or frequency domain calculations. Frequency domain cerebral autoregulation reports gain and phase values, which estimate the association and time-lag between cerebral perfusion and blood pressure.^{32,33} Time domain cerebral autoregulation instead assesses the correlation between blood pressure and cerebral perfusion, providing a correlation coefficient over time-windows lasting at least 2 min.³⁴

3. Arterial stiffness is defined as the resistance of the arterial walls to deformation. Arterial stiffness can be a local or regional measure, depending on the method of determination.¹⁷ In the present analysis, the most frequent assessment of arterial stiffness was carotid-femoral pulse wave velocity (cfPWV). Calculated as the ratio of the distance between two sites over the transit time for a pulse wave to reach the sites, cfPWV characterizes global arterial health and structure.^{17,20} Two clinically relevant alternative indices of global arterial function (brachial-ankle PWV and Cardio-Ankle Vascular Index) were also reported in the included studies. We also included local (local PWV, β -stiffness index, distensibility coefficient) measures of arterial stiffness in the carotid artery as a conduit vessel along the vascular path in the heart-brain axis. Recent reports of elevated carotid artery stiffness demonstrating an association with cerebral injury justified, including local stiffness measures.³⁵⁻³⁷

Outcomes

The primary outcome of this study is the presence of cSVD, determined in accordance with the standardized STRIVE guidelines as follows⁴:

1. Recent small subcortical infarcts: recent infarction (≤ 20 mm in diameter) in the territory of a perforating arteriole, occurring within the previous few weeks.
2. Lacune: approximately circular, fluid-filled cavity between 3-15 mm in diameter.
3. White matter hyperintensity: hyperintense regions identified on T2-weighted sequences, not located within subcortical grey matter or the brainstem.

4. Perivascular spaces: fluid-filled spaces that follow a typical course of a blood vessel, with a diameter typically less than 3 mm. In the basal ganglia, perivascular spaces may be enlarged (up to 10-20 mm).
5. Cerebral microbleeds: Small (often 2-5 mm in diameter, but may range up to 10 mm) areas of signal void seen on T2*-weighted MRI, but not seen on FLAIR, T1-weighted, or T2-weighted sequences.

Significant inconsistency has been noted with the reporting of cerebral lesions.³⁸ To ensure thorough systematic literature searches, the alternate terminology for each cSVD marker reported by Wardlaw et al. was also incorporated into the search strategies.⁴ We included studies that described ‘silent cerebral infarcts’ due to the common use of this term to describe neuroimaging markers of cSVD³⁸; the cSVD subtype that these studies analyzed was determined by consensus review of the study methods and comparison against the criteria laid out in the STRIVE guidelines.⁴ Brain atrophy alone did not qualify a study for inclusion since cerebral atrophy itself is not a specific marker of cSVD^{4,25} and due to inconsistent reporting.³⁹ Additionally, we omitted ‘cortical superficial siderosis’ as this was more recently incorporated as a marker for cSVD and cerebral amyloid angiopathy and thus has not been extensively investigated or incorporated into summary scoring of cSVD burden.²⁵

Literature Screening and Data Extraction

All search results retrieved from the online databases were downloaded to a commercially available research publication and citation management system (Endnote, Clarivate Analytics). Literature processing began with the removal of duplicates, review articles, conference abstracts, letters to the editor, and case studies. Reviewers (B.S., V.T., O.K.)

independently screened remaining full-text records for eligibility before extracting data from eligible publications. The data extracted from records included factors for study identification (authors, year of publication, journal), study design characteristics (recruitment procedures, study protocols), descriptions of the study samples (sample size, age, sex, past or present cardiovascular or cerebral/cerebrovascular disease, use of medications), details of the exposure or predictor (type of measure, methods of assessment), cerebral small vessel disease markers (along with modality or modalities used for assessment), effect size (OR reported by the study, or calculated from reported crude event rates), and adjustments for covariates. Some studies reported multiple measures of the specific exposure; authors agreed on consensus for extraction in these cases.

Risk of Bias Assessment

The risk of bias was evaluated with the Newcastle-Ottawa Scale⁴⁰, in which the quality of each report is assessed on categories of bias, including selection, comparability, and exposure. Studies were predominantly of cross-sectional or case-control design; therefore, we applied the 9-item scale to assess the risk of bias. No study was excluded on the basis of quality alone.

Statistical Analysis

Primary Analyses

All statistical analyses were performed using GraphPad Prism (version 9.0) and the software R (version 4.1.2) with packages *meta* and *metafor*. Consistent with previous meta-analysis approaches, the cSVD subtypes were first pooled for analysis due to the limited number of studies available with each individual subtype.^{39,41} When possible we performed subgroup

analyses examining individual subtypes of cSVD to account for differences in the pathogenesis processes when feasible, specifically white matter hyperintensities and lacunes.^{5,11,12} Subgroup analyses were also performed by stratifying studies by cerebral region within cSVD subtypes, where feasible, due to variable risk factor contributions depending on location.^{5,42} To further explore a potential source of heterogeneity in the studies reporting arterial stiffness measures, we performed a subgroup analysis including only the studies that assessed arterial stiffness as cfPWV, the gold standard approach.^{17,20} Finally, subgroup analyses were also performed with the arterial stiffness data to examine the possibility of artery-specific relationships by conducting separate analyses on the studies that measured central artery stiffness (cfPWV or MRI-derived aortic PWV) or carotid stiffness (local carotid PWV, carotid distensibility coefficient, or carotid β -stiffness).

Extracted data for each predictor variable were divided into continuous or dichotomous before separate analyses were performed. In order to standardize effect sizes for meta-analyses in which the exposure variable was a continuous measure, OR from each study were adjusted by multiplying the natural-log of the OR by the study-specific standard deviation (i.e., adjusted OR = $\exp[\text{SD} * \ln(\text{OR})]$). If interquartile ranges were provided, standard deviations were calculated as (Quartile 3 – Quartile 1)/1.35, consistent with guidelines.^{43,44} If standard deviations were reported by subgroup, pooled standard deviations were calculated as described in the Cochrane Handbook.⁴³ For arterial stiffness, differences in directionality for the carotid distensibility coefficient (i.e., decreases in carotid distensibility coefficient indicate increases in arterial stiffness, whereas increases in PWV, CAVI, and β -stiffness indicate increases in arterial stiffness) were corrected by taking the inverse of the reported effect sizes as directed by the Cochrane Handbook.⁴³ Studies that reported risk ratios were included in accordance with the

previous consensus that these are roughly equivalent in smaller effect sizes.⁴⁵ For meta-analyses in which the exposure variable was dichotomous, studies that did not directly report an OR but provided sufficient information to generate a 2x2 contingency table were included after calculating the OR as described in the Cochrane Handbook.⁴³ GraphPad Prism version 9.0 was used to calculate the OR and associated confidence intervals. Given the wide variance in methods of assessing each predictor variable, we proceeded with a random-effects model to minimize potential bias.⁴⁶ Heterogeneity was assessed with the Cochran Q test, the Higgin I^2 statistic, and the τ^2 statistic. Forest plots were generated describing the OR, 95% confidence intervals and pooled summary estimates. Effect sizes were considered significant at $P < 0.05$. Certainty of evidence for each meta-analysis performed was assessed using the Grading of Recommendations Assessment, Development, and Evaluation (GRADE) system.^{47,48}

Secondary Analyses

For the investigation of a temporal relationship between the exposure measures and cSVD, we performed secondary analyses incorporating only the reports with longitudinal study designs where possible. Meta-regression analyses were performed to explore the influence of the three most reported vascular risk factors/diseases (hypertension, diabetes mellitus, and hyperlipidemia) on the outcomes derived from primary analyses. For all secondary analyses performed, the effect size was considered significant if $P < 0.05$.

Sensitivity Analyses

The presence of “small study effects” was examined using funnel plots, as described by the test of Egger et al.^{49,50} Sensitivity analyses were conducted using a leave-one-out approach,

in which the pooled treatment effects were iteratively calculated after excluding each study one at a time and recording the pooled OR, confidence interval, and P-value. We performed further sensitivity analysis by re-calculating the pooled effect size using fixed-effects analyses in order to investigate the impact of the number of studies quantitatively synthesized on the precision of τ^2 estimates.⁵⁰

Results

Systematic Review and Qualitative Synthesis

Cerebrovascular Reactivity and Cerebral Small Vessel Disease

Our initial database and manual search of references identified 479 records assessing the relationship between cerebrovascular reactivity and cSVD, which was reduced to 429 preliminary records after excluding duplicates (Figure S1). Abstract screening and exclusion of non-original research, records lacking full-text, or records that did not quantitatively assess a relationship between cerebrovascular reactivity and cSVD resulted in 46 publications for qualitative synthesis in the systematic review. Of the 46 articles, 3 assessed recent small subcortical infarcts⁵¹⁻⁵³, 8 assessed the presence of lacunes⁵⁴⁻⁶¹, 7 assessed enlarged perivascular spaces^{52,57-59,62-64}, 9 assessed cerebral microbleeds^{52,54,56-61,65}, 41 assessed white matter hyperintensities^{51,52,54,56-61,64-95}, and 5 assessed a total cSVD score.^{58,59,65,82,96} The total population across the included reports consisted of healthy/aging individuals with or without vascular risk factors (70% of studies), neurocognitive or neurodegenerative disorders (22%), non-cSVD cerebrovascular disease (20%), and those with prior diagnoses of cSVD (39%). All included studies used only MRI for determining the presence of radiological markers of cSVD. MRI was also the primary modality in the studies included (61% of included studies) for assessing cerebrovascular reactivity, with the remaining studies using transcranial Doppler (39% of included studies). Moreover, diverse techniques were used, including different MRI assessment methods like blood-oxygen level dependent (BOLD MRI) (39% of included studies) and arterial spin labeling (ASL MRI) (13% of included studies), examined various transcranial Doppler target vessels such as the middle cerebral artery and posterior communicating artery, and employed different approaches to induce cerebrovascular hyperemia, such as the CO₂ challenge

(56.5% of included studies), acetazolamide or dipyridamole (13% of included studies), and breath-holds (28% of included studies).^{29,97-99}

Of the included studies, 39 were cross-sectional in design, with 32 reporting a significant association between cerebrovascular reactivity and cSVD.^{51-54,56-59,62,63,65-70,72-77,80-86,91,92,94}

Twenty-one of the cross-sectional studies were case-control studies^{51-53,58,63,65-}

71,75,77,78,80,81,83,86,87,91. The remaining 18 studies were prospective or retrospective cohort

studies.^{54-57,59,62,72-74,76,79,82,84,85,92-95} In 203 leukoaraiosis patients, Bian et al.⁹¹ demonstrated that

patients exhibiting more severe white matter hyperintensities (Fazekas grades II and III) had a

significantly reduced cerebrovascular reactivity compared to those with lower severity. In

another larger cohort study, Staszewski et al.⁵⁸ reported that in 120 subjects, the lowest tertile of

cerebrovascular reactivity had a 19-fold greater likelihood of having cSVD compared to the

highest tertile. This is supported by Silvestrini et al.⁵³, who found that each 0.1 decrease in BHI

was associated with a 2-fold greater risk of cSVD. Contrary to these findings, Bisschops et al.⁵⁵

found that cerebrovascular reactivity had no relationship with radiological markers of cSVD.

This was the only study in the systematic review to focus solely on participants with internal

carotid artery occlusion, which has been previously shown to alter transcranial Doppler

assessments of cerebral hemodynamics.^{100,101}

Of the 7 longitudinal studies^{60,61,64,88-90,96}, only 2^{60,90} did not find an association between cerebrovascular reactivity and progression of cSVD, with follow-up times ranging from 1 to 7

years after the initial assessment of cerebrovascular reactivity. These longitudinal studies

primarily focused on white matter hyperintensities; for example, Liem et al.⁶¹ divided 38

participants into two groups by the median cerebrovascular reactivity and reported that in

participants with a high cerebrovascular reactivity at baseline, the increase in white matter

hyperintensity volume over 7.1 years was 0.37 percent compared to 2.9 percent in those with a low cerebrovascular reactivity. This relationship was supported by Staszewski et al.⁹⁶, who determined in 60 cSVD patients and 20 healthy controls that the participants with a progression of cSVD had a significantly lower cerebrovascular reactivity at baseline. Conversely, Moreton et al.⁶⁰ found no association between baseline cerebrovascular reactivity and development of incident cSVD in 14 subjects over a two-year follow-up. In the work by Smolinski et al.⁹⁰, similar results to Moreton et al.⁶⁰ were found when the measures of cerebrovascular reactivity were compared to cSVD progression in a group of 43 multiple sclerosis patients in remission.

Cerebral Autoregulation and Cerebral Small Vessel Disease

Our initial database and manual search of references identified 254 records assessing the relationship between cerebral autoregulation and cSVD, which was reduced to 202 preliminary records after excluding duplicates (Figure S2). Abstract screening and exclusion of non-original research, records lacking full-text, or records that did not quantitatively assess a relationship between cerebral autoregulation and cSVD resulted in 14 publications for systematic review. Of the 14 articles, 4 assessed recent small subcortical infarcts¹⁰²⁻¹⁰⁵, 1 assessed the presence of lacunes¹⁰⁶, 2 assessed enlarged perivascular spaces^{106,107}, 3 assessed cerebral microbleeds¹⁰⁶⁻¹⁰⁸, 8 assessed white matter hyperintensities^{106,107,109-114}, and 4 assessed the total cSVD score.^{106,107,110,115} All included studies were cross-sectional in design. The total population consisted of healthy/aging individuals with or without vascular risk factors (57% of included studies), previously diagnosed cSVD (36%), cerebrovascular events (36%), and patients undergoing cardiac surgery (7%). All included studies used only MRI for determining the presence of radiological markers of cSVD. Only one included study did not use transcranial

Doppler ultrasound to assess cerebral autoregulation; Meyer et al.¹⁰⁴ calculated blood flow from clearance curves after bolus infusion.

All^{102-104,107-112,114,115} but three^{105,106,113} studies demonstrated a significant association between cerebral autoregulation impairments and greater cSVD burden. Six studies were case-control studies^{102,103,105,107,108,113} and eight studies were prospective or retrospective cohort studies.^{104,106,109-112,114,115} In a study of 346 patients undergoing cardiopulmonary bypass, Nomura et al.¹¹⁰ reported that cSVD was associated with a 3-fold greater odds of impaired cerebral autoregulation. Liu et al.¹⁰⁷ analyzed 113 cSVD patients and 83 cSVD-free controls and similarly found a significantly reduced cerebral autoregulation in the cSVD patients. Multivariate regression models adjusted for age, sex, and heart rate revealed that cerebral autoregulation in the total population was independently associated with individual cSVD markers (except lacunes) and a total cSVD score. Guo et al.¹⁰² extended the findings from the above studies by following up the patients after initial cross-sectional analysis, and demonstrated that the observation of impaired cerebral autoregulation in the cSVD groups was diffuse and persisted for 6 months after the initial lacunar infarction. Contrary to most studies included, both Wu et al.¹⁰⁶ and Xiong et al.¹⁰⁵ reported no association between cerebral autoregulation and any radiological markers of cSVD. However, both studies used approaches to determining cerebral autoregulation that differed from those previously discussed.^{116,117}

Less than half of the studies^{103,106,110-112,114} accounted for vascular risk factors either in baseline comparisons or with statistical methods. Five^{103,110-112,114} of the 6 studies that adjusted for risk factors found that the relationship between cerebral autoregulation and cSVD persisted, while one¹⁰⁶ instead found only a relationship between the vascular risk factors (hypertension and diabetes mellitus) and cSVD.

Arterial Stiffness and Cerebral Small Vessel Disease

Our initial database and manual search of references identified 878 records assessing the relationship between arterial stiffness and cSVD, which was reduced to 694 preliminary records after excluding duplicates (Figure S3). Abstract screening and exclusion of non-original research, records lacking full-text, or records that did not quantitatively assess a relationship between arterial stiffness and cSVD resulted in 82 publications for systematic review. Of the 82 articles, 12 assessed recent small subcortical infarcts¹¹⁸⁻¹²⁹, 24 assessed the presence of lacunes^{21,130-152}, 9 assessed enlarged perivascular spaces^{118,138,144,145,150,152-155}, 23 assessed cerebral microbleeds^{37,118,120,123-127,131-134,138,139,144,145,149,150,152,153,156-158}, 59 assessed white matter hyperintensities^{21,36,118,119,122,123,125-127,130-134,138-142,145,150-152,155,156,159-192}, and 8 assessed the total cSVD score.^{133,138,139,152,193-196} The total population consisted of healthy/aging individuals with or without vascular risk factors (77% of included studies), previously diagnosed cSVD (6%), cerebrovascular events (8%), cognitive decline or complaints (5%), cardiovascular disease including MI and heart failure (13%), and metabolic syndromes or renal disease (11%). All included studies used only MRI for determining the presence of radiological markers of cSVD. Central or large artery stiffness was the primary assessment (69 studies, or 84%); only 13 studies measured conduit artery stiffness. The most frequently used approach was cfPWV (26 studies, 32%), followed by brachial-ankle PWV (20 studies, 24%).

The majority of studies included in the systematic review were cross-sectional in nature; with 86% of the cross-sectional studies reporting a significant association between arterial stiffness and cSVD.^{21,118-121,123-128,130-134,136-145,147,148,150-154,156-158,160,161,163,165-167,169,171-173,176-179,182,183,185-187,190,193-195} Of the 69 cross-sectional studies, 13 were case-control

studies^{118,127,128,155,166,168,171,173,177,179,182,192,195} and 56 were prospective or retrospective cohort studies.^{21,119-121,123-126,130-154,156-158,160-163,165,167,169,172,176,178,181,183,185-188,190,193,194,196} Using the Framingham Heart Study third generation cohort, Pase et al.¹³⁷ demonstrated a significant association between arterial stiffness and white matter hyperintensity volume that was unaffected by adjustment for age, sex, and common vascular risk factors. Van Sloten et al.¹⁴³ extended these findings to other cSVD markers in 2058 older participants (mean age of 79.6 years, 59% women), who reported that a one-standard deviation increase in cfPWV increased the risk of subcortical infarcts, enlarged perivascular spaces, and cerebral microbleeds by 27%, 15%, and 9%, respectively. This concept is supported by the data from 1820 subjects analyzed by Cooper et al.¹²⁰, who showed that not only was cfPWV related to white matter hyperintensities, but also that in mediation analyses, ~41% of the effect of cfPWV on cognitive function was explained by the relationship between cfPWV and cSVD. In contrast, Rundek et al.¹⁴⁶ did not find any association between arterial stiffness and cSVD in a cohort of 1166 participants of the Northern Manhattan Study (NOMAS). The sample from the study by Rundek et al. was older (71 ± 9 years), 40% were on antihypertensive medication, and 53% were current or former smokers.¹⁴⁶

Of the 13 longitudinal studies^{36,37,122,129,159,164,170,174,175,180,184,189,191} included in the systematic review, 11 of the 13 reported significant associations between arterial stiffness and cSVD. The average follow-up time was 7.0 years from baseline (range 2 – 21.5 years). King et al.¹⁸⁴ demonstrated that arterial stiffness was a significant predictor of white matter hyperintensity progression over 7 years in 1270 subjects, such that a 1% increase in aortic arch stiffness was associated with a 0.3% increase in subsequent white matter hyperintensity volume. Using the gold-standard cfPWV, Rosano et al.¹⁷⁰ found that a higher arterial stiffness predicted the presence of cSVD over a 10-year follow-up, even after multivariate adjustment including

vascular risk factors, incident stroke, incident myocardial infarction, and changes in arterial blood pressure. Ding et al.³⁷ analyzed the association between baseline carotid artery stiffness and incident cSVD in a sample of 2512 participants from the Age, Gene/Environment Susceptibility (AGES-Reykjavik) study and demonstrated that the risk of incident cerebral microbleeds was 11% higher per standard deviation decrease in baseline carotid arterial strain. This relationship was not attenuated by adjustment for age, sex, arterial blood pressure and other vascular risk factors. Conversely, the study from Suri et al.¹⁸⁹ was one of two reports to find no association between arterial stiffness and cSVD. Specifically, the authors demonstrated no relationship between cfPWV and the progression of white matter hyperintensity volume. Tsao et al.¹⁹¹ similarly found no association between arterial stiffness and cSVD. Of their 1223 older participants (mean age of 61 years) from the Framingham Heart Study only 28% reported antihypertensive medication use and 9% reported prior diagnoses of diabetes mellitus, both lower than expected age-specific prevalence.^{197,198}

Meta-analyses

Six separate meta-analyses were planned before beginning the literature search to determine if cerebrovascular regulatory functions or properties of arterial stiffness were associated with cSVD. Measures were separated by whether the predictor variable was analyzed as a continuous or dichotomous variable. For dichotomous predictors, the cut-off values varied significantly across studies due to differences in study methodology. For cerebral autoregulation specifically, we only found articles reporting OR or crude event rates with cerebral autoregulation as a dichotomized measure.

Cerebrovascular Reactivity and Cerebral Small Vessel Disease

Of the studies included in the qualitative synthesis and systematic review of the association between cerebrovascular reactivity and cSVD, 10 studies were eligible for inclusion in the quantitative meta-analysis. The analyses of these 10 studies included 4 studies (pooled sample $n=387$, 37.7% women) that utilized a continuous predictor and 7 studies (pooled sample $n=536$, 32.9% women) that utilized a dichotomous predictor; one study presented cerebrovascular reactivity as both a continuous and dichotomous predictor variable (Table 1). A sample size of 4 studies was deemed too low for quantitative synthesis, therefore, the individual results of these studies are presented qualitatively in Figure 1. Of note, all 4 studies reported a significant association between impaired cerebrovascular reactivity and cSVD. For the dichotomous exposure measure of cerebrovascular reactivity, Cochran Q statistics indicated that there was significant heterogeneity in the dichotomous predictor data ($Q=18.62$, $P=0.005$). The Higgin's I^2 value was 67.8% (95% CI: 28.5-85.5%) and τ^2 was 0.82 (95% CI: 0.11-6.44). Shown in Figure 2, meta-analysis of dichotomous cerebrovascular reactivity revealed a borderline significant association between an impaired cerebrovascular reactivity and an increased prevalence of cSVD (Dichotomous Predictor Pooled OR, 2.26; 95% CI: 0.99-5.14, $P=0.05$).

Funnel plots were inappropriate for the cerebral predictors, given that each category had less than 10 studies.¹⁹⁹ The leave-one-out analysis conducted with dichotomous cerebrovascular reactivity measures demonstrated fluctuations in both the effect sizes (OR range: 1.58-2.79; number of studies per run=6) and the P-values (range 0.02-0.14), including reporting significance ($P<0.05$) with the removal of either Bisschops et al.⁵⁵ or Tawfik et al.⁵⁹ In further sensitivity analyses, the fixed-effect model for dichotomous cerebrovascular reactivity

Table 2-1. Cerebrovascular reactivity (CVR) studies presenting odds ratios or crude event rates.

Study	Assessment Modalities for CVR	cSVD Subtype(s)	Sample (n, % women)	Age (years)	Subject Characteristics	Risk of Bias Score (Max of 9)
<i>Continuous Predictors</i>						
Bakker et al. 1999 ⁸⁴	TCD	WMH	73, 26.0%	70.2 ± 8.0	Healthy elderly	7
Lee et al. 2022 ⁸¹	MRI	WMH	62, 67.7%	Controls: 33.8 ± 8.0, Cases: 34.0 ± 8.1	Migraine patients vs. non-migraine controls	7
Molina et al. 1999 ⁵¹	TCD	RSCCI	92, 30.4%	Controls: 58.3 ± 12.0, Cases: 56.6 ± 13.4	Controls vs. first-ever lacunar infarction patients	8
Silvestrini et al. 2006 ⁵³	TCD	RSCCI	160, 35.6%	Controls: 59.8 ± 9.2, Cases: 67.6 ± 8.7	Controls vs. lacunar stroke patients	8
<i>Dichotomous Predictors</i>						
Bakker et al. 1999 ⁸⁴	TCD	WMH	73, 26.0%	70.2 ± 8.0	Healthy elderly	7
Bisschops et al. 2003 ⁵⁵	TCD	Lacunes	70, 27.1%	59, range: (35-71)	Unilateral Occlusion of ICA	7
Deplanque et al. 2013 ⁵²	TCD	RSSCI, WMH, PVS, CMB	162, 27.2%	Controls: 63.2 ± 10.4, Cases: 62.1 ± 11.4	cSVD patients vs. non-cSVD controls	6
Liem et al. 2009 ⁶¹	MRI	RSSCI, WMH, CMB	38, 52.6%	Controls: 36.7 ± 8.0, Cases: 42.2 ± 10.0	Controls vs. NOTCH3 Mutation Carriers	7
Palaiodimou et al. 2023 ⁹³	TCD	WMH	23, 43.0%	51 ± 13	Fabry disease patients	8
Staszewski et al. 2019 ⁵⁸	TCD	Lacunes, WMH, PVS, CMB, cSVD Score	120, 40.0%	Controls: 71.7 ± 3.4, Cases: 71.8 ± 3.4	cSVD patients vs. non-cSVD controls	5
Tawfik et al. 2022 ⁵⁹	TCD	Lacunes, WMH, PVS, CMB, cSVD Score	50, *	*	Lacunar stroke patients	6

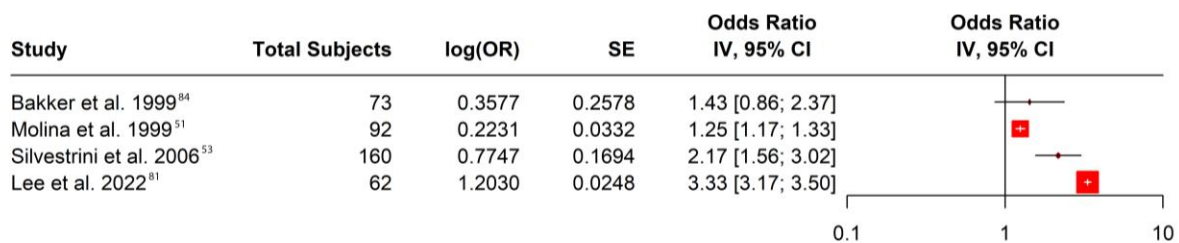


Figure 2-1. Individual study results from studies reporting cerebrovascular reactivity as a continuous exposure measure. Forest plot illustrating the individual effect sizes reported for each study containing continuous cerebrovascular reactivity in relation to cSVD burden. OR, odds ratio; SE, standard error; IV, inverse-variance.

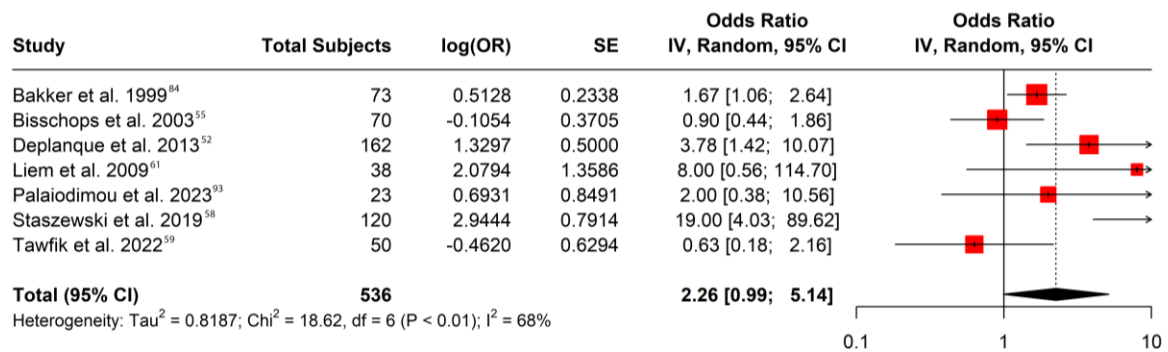


Figure 2-2. Odds ratio results from pooled studies reporting cerebrovascular reactivity as a dichotomous exposure variable. Forest plot illustrating the effect sizes dichotomous cerebrovascular reactivity in relation to cSVD burden. There was a borderline significant association between impaired cerebrovascular reactivity and a greater cSVD burden (OR: 2.26, 95% CI: 0.99-5.14). OR, odds ratio; SE, standard error; IV, inverse-variance.

demonstrated significance (OR: 1.73, 95% CI: 1.25-2.40, $P=0.001$) in contrast to the borderline significant results of the random-effects analysis.

Cerebral Autoregulation and Cerebral Small Vessel Disease

Of the studies included in the qualitative synthesis and systematic review of the association between cerebral autoregulation and cSVD, 3 studies (pooled sample $n=455$, 30.1% women) were eligible for inclusion in the quantitative meta-analysis, with all reporting cerebral autoregulation as a dichotomous variable (Table 2). A sample size of three studies was deemed insufficient for quantitative analysis; therefore, the individual results of the studies are presented qualitatively in Figure 3.

Arterial Stiffness and Cerebral Small Vessel Disease

Of the studies included in the systematic review of the association between arterial stiffness and cSVD, 47 were eligible for inclusion in the meta-analysis. The analyses for studies assessing arterial stiffness included 37 studies (pooled sample $n=27952$, 53.0% women) that used arterial stiffness as a continuous predictor and 13 studies (pooled sample $n=10140$, 53.1% women) that used arterial stiffness as a dichotomous predictor; 4 of these studies presented data for arterial stiffness as both a continuous and a dichotomous predictor variable (Table 3). Both the continuous and dichotomous models demonstrated significant ($P < 0.0001$) heterogeneity assessed as the Q statistic (Continuous: 126.97, Dichotomous: 72.96). In the continuous model, Higgin's I^2 value was 71.6% (95% CI: 60.6-79.6%), and the τ^2 value was 0.024 (95% CI: 0.020-0.22). In the dichotomous model, Higgin's I^2 was 83.6% (95% CI: 73.3-89.9%), and the τ^2 was 0.15 (95% CI: 0.038-0.62). Regardless of whether the arterial stiffness predictor was continuous

Table 2-2. Cerebral autoregulation (CA) studies presenting odds ratios or crude event rates.

Study	Assessment Modalities for CA	cSVD Subtype(s)	Sample (n, % women)	Age (years)	Subject Characteristics	Risk of Bias Score (Max of 9)
<i>Dichotomous Predictors</i>						
Castro et al. 2018 ¹⁰⁹	TCD	WMH	46, 58.7%	73.0 ± 12.0	Ischemic Stroke patients	6
Nomura et al. 2018 ¹¹⁰	TCD	WMH, cSVD Score	346, 29.5%	Controls: 71.2 ± 7.8, Cases: 69.9 ± 8.3	Controls vs. Impaired cerebral autoregulation	7
Wu et al. 2022 ¹⁰⁶	TCD	Lacunes, WMH, PVS, CMB, cSVD Score	63, 12.7%	56.3 ± 9.9	Small artery occlusion patients	7

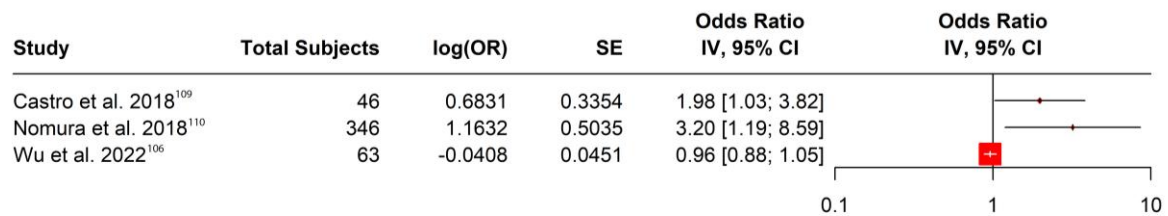


Figure 2-3. Individual study results from studies reporting cerebral autoregulation as a dichotomous exposure measure. Forest plot illustrating the individual effect sizes reported for each study containing dichotomous cerebral autoregulation in relation to cSVD burden. OR, odds ratio; SE, standard error; IV, inverse-variance.

Table 2-3. Arterial stiffness (AS) studies presenting odds ratios or crude event rates.

Study	Assessment Modality for AS	cSVD Subtype(s)	Sample (n, % women)	Age (years)	Subject Characteristics	Risk of Bias Score (Max of 9)
<i>Continuous Predictors</i>						
Amier et al. 2021 ¹¹⁸	MRI; aortic PWV	RSSCI, WMH, PVS, CMB	559, 35.8%	67.9 ± 8.8	Healthy, Cognitive Impairment, CVD	9
Brandts et al. 2009 ¹³⁰	MRI; aortic PWV	RSSCI, WMH	50, 62.0%	49.2 ± 12.7	Hypertensive	9
Brisset et al. 2013 ¹¹⁹	Carotid DC	RSSCI, WMH	1800, 59.9%	72.5 ± 4.1	Healthy	8
Choi et al. 2013 ¹³¹	CAVI	WMH, Lacunes, CMB	484, 35.5%	50 ± 7	Healthy	7
Cooper et al. 2016 ¹²⁰	cfPWV	RSSCI, CMB	1820, 60.0%	80 ± 5	Healthy	9
Coutinho et al. 2011 ¹⁷²	cfPWV	WMH	812, 57.6%	58.4 ± 9.7	Healthy with hypertensive family members	9
Ding et al. 2015 ³⁷	Carotid DC	CMB	2512, 58.5%	74.6	Healthy	9
Gustavsson et al. 2015 ¹⁵⁶	cfPWV	WMH, CMB	208, 59.1%	71.0 ± 4.8	Healthy	8
Hashimoto et al. 2008 ¹²¹	btPWV	RSSCI	351, 71.8%	65 ± 6	Healthy	8
Hashimoto et al. 2018 ¹⁶³	cfPWV	WMH	286, 60.1%	54 ± 13	Patients referred for hypertension, CVD risk	8
Henskens et al. 2008 ¹³²	cfPWV	WMH, Lacunes, CMB	167, 49.1%	51.8 ± 13.1	Patients referred for hypertension	8
Hughes et al. 2013 ¹⁶⁴	cfPWV	WMH	91, 34.1%	86.9 ± 2.8	Healthy elderly	9
Hughes et al. 2018 ¹⁶⁵	cfPWV	WMH	19, *	*	Healthy	9
Jochemsen et al. 2015 ¹²²	Carotid DC	WMH, RSSCI	526, 17.0%	59 ± 10	Healthy	8

Kim et al. 2016 ¹³³	baPWV	WMH, Lacunes, CMB, cSVD Score	1282, 42.3%	67.6 ± 12.2	Ischemic or transient stroke patients	6
Laugesen et al. 2013 ¹⁶⁶	cfPWV	WMH	178, 48.3%	59 ± 10	Type 2 Diabetes	9
Liu et al. 2020 ¹⁹⁴	baPWV	cSVD Score	684, 34.5%	54.0, IQR: 48.0 – 60.0	Healthy	8
Matsumoto et al. 2007 ¹³⁵	baPWV	Lacunes	476, 42.6%	51.5 ± 7.8	Healthy	6
Mitchell et al. 2011 ²¹	cfPWV	RSSCI, WMH	668, 56.6%	75.4 ± 4.0	Healthy	9
Ochi et al. 2010 ¹³⁶	baPWV	Lacunes	500, 61.8%	66.9 ± 8.4	Healthy elderly	8
Ohmine et al. 2008 ¹⁶⁹	baPWV	WMH	144, 62.9%	70.3 ± 9.0	Healthy elderly	9
Pase et al. 2016 ¹³⁷	cfPWV	Lacunes	3207, 53.1%	46 ± 9	Healthy	9
Poels et al. 2012 ¹²³	cfPWV	RSSCI, WMH, CMB	1460, 55.4%	58.2 ± 7.2	Healthy	9
Riba-Llena et al. 2018 ¹³⁸	cfPWV	WMH, Lacunes, PVS, CMB, cSVD Score	782, 49.6%	62.7 ± 5.4	Healthy	9
Robert et al. 2022 ¹³⁹	Carotid PWV	WMH, Lacunes, CMB, cSVD Score	272, 57.7%	75.4 ± 6.8	Healthy	8
Rundek et al. 2017 ¹⁴⁶	Carotid β -stiffness	Lacunes	1166, 60.0%	71 ± 9	Healthy	9
Saji et al. 2012a ¹⁴⁰	baPWV	WMH, Lacunes	240, 49.6%	69 ± 9	Healthy	8
Saji et al. 2012b ¹⁴¹	CAVI	WMH, Lacunes	220, 40.4%	69 ± 10	Healthy	8
Shan et al. 2016 ¹⁴²	MRI; aortic arch PWV	RSSCI, WMH	62, 40.3%	56.8 ± 7.5	Type 2 diabetes patients	8
Shimoyama et al. 2012 ¹⁵⁷	CAVI	CMB	105, 32.4%	70.0, IQR: 68.0-76.5	Cerebral infarct or transient ischemic stroke patients	8
Song et al. 2014 ¹⁵⁸	baPWV	CMB	1137, 37.7%	65 ± 12	Cerebral infarct or transient ischemic stroke patients	8

Tsao et al. 2013 ¹⁴⁷	cfPWV	Lacunes	1587, 55.0%	61 ± 9	Healthy	9
Turk et al. 2016 ¹⁷¹	Carotid PWV	WMH	96, 43.8%	53.8 ± 7.9	Controls vs. WMH-positive patients	5
van Elderen et al. 2010 ¹²⁵	MRI; aortic PWV	RSSCI, WMH, CMB	86, 43.0%	46.9 ± 11.7	Type 1 diabetes patients	8
van Sloten et al. 2016 ¹⁴³	cfPWV	RSSCI	2058, 59.0%	79.6 ± 4.6	Healthy	9
Zhai et al. 2018 ¹⁴⁴	baPWV	Lacunes, PVS, CMB	953, 62.5%	55.7 ± 9.4	Healthy	9
Zhang et al. 2020 ¹⁴⁵	baPWV	WMH, Lacunes, PVS, CMB	904, 55.3%	59.7 ± 3.0	Healthy	7
<i>Dichotomous Predictors</i>						
Bae et al. 2021 ¹⁵³	baPWV	PVS, CMB	854, 48.2%	68.2 ± 12.5	Ischemic or transient stroke patients	9
Chang et al. 2023 ¹⁹⁶	baPWV	cSVD Score	820, 39.9%	68.0, IQR: 59.0 – 78.0	Ischemic Stroke patients	5
Choi et al. 2013 ¹³¹	CAVI	WMH, Lacunes, CMB	484, 35.5%	50 ± 7	Healthy	7
Kinjo et al. 2016 ¹³⁴	baPWV	WMH, Lacunes, CMB	990, 53.6%	53, range: 24-86	Recruited from brain check-ups	8
Liu et al. 2021 ¹⁵²	CAVI	WMH	1176, 51.3%	67.5 ± 13.2	Healthy	7
Palta et al. 2019 ¹²⁶	cfPWV	RSSCI, WMH, CMB	3703, 59.3%	75.2 ± 5.0	Healthy	9
Rosano et al. 2013 ¹⁷⁰	cfPWV	WMH	303, 56.0%	82.9	Healthy	9
Saji et al. 2012a ¹⁴⁰	baPWV	WMH, Lacunes	240, 49.6%	69 ± 9	Healthy	8
Saji et al. 2012b ¹⁴¹	CAVI	WMH, Lacunes	220, 40.4%	69 ± 10	Healthy	8
Shimoyama et al. 2012 ¹⁵⁷	CAVI	CMB	105, 32.4%	70.0, IQR: 68.0-76.5	Cerebral infarct or transient ischemic stroke patients	8
Tabata et al. 2017 ¹²⁴	baPWV	RSSCI, CMB	149, 32.9%	70.8 ± 10.0	Coronary artery disease patients	6
Zijlstra et al. 2020 ¹⁴⁹	MRI; aortic PWV	Lacunes, CMB	85, 34.1%	75.6 ± 6.9	Healthy	4
Zhou et al. 2023 ¹⁴⁸	estimated PWV	Lacunes	1011, 64.5%	64.2 ± 9.1	Healthy	7

(Figure 4) or dichotomized (Figure 5), an increased arterial stiffness was associated with an increased burden of cSVD. Random effects meta-analyses indicated this for both measures (Continuous Predictor Pooled OR, 1.24; 95% CI: 1.15-1.33, $P < 0.0001$) (Dichotomous Predictor Pooled OR, 1.86; 95% CI: 1.41-2.45, $P < 0.0001$).

For specific subtypes of cSVD, only subgroup analyses between continuous arterial stiffness and white matter hyperintensities or lacunes had enough studies to be appropriately powered. Eleven studies^{119,125,132,156,163-166,169,171,172} investigated white matter hyperintensities. The pooled random effects OR was 1.42 (95% CI: 1.18-1.70; number of studies=11), and the heterogeneity was not significant ($I^2=31\%$, $\tau^2=0.023$, $P=0.15$, Figure S5). Thirteen studies^{21,130,135-137,139-144,146,147} investigated lacunes specifically. For this analysis, the pooled random effects OR was 1.28 (95% CI: 1.10-1.49; number of studies=13) with significant heterogeneity ($I^2=70\%$, $\tau^2=0.038$, $P<0.01$) (Figure S5).

Within the subtype of white matter hyperintensities, only 4 studies^{125,130,138,169} reported measures separately for deep white matter hyperintensities and periventricular white matter hyperintensities. Within the subtype of cerebral microbleeds, only 5 studies^{37,123,133,144,158} reported separate effect sizes for strictly lobar cerebral microbleeds and deep cerebral microbleeds. The limited number of studies precluded formal meta-analyses, so the individual results of these studies are presented qualitatively in Figure S6.

Fourteen studies^{21,120,123,132,137,138,143,147,156,163-166,172} specifically assessed arterial stiffness with the gold-standard, cfPWV, as a continuous measure. In this secondary analysis, the pooled random effects OR was 1.23 (95% CI: 1.09-1.39, $P=0.001$; number of studies=14). The model demonstrated significant heterogeneity ($I^2=47.5\%$, $\tau^2=0.021$, $P=0.03$). This model suggests that

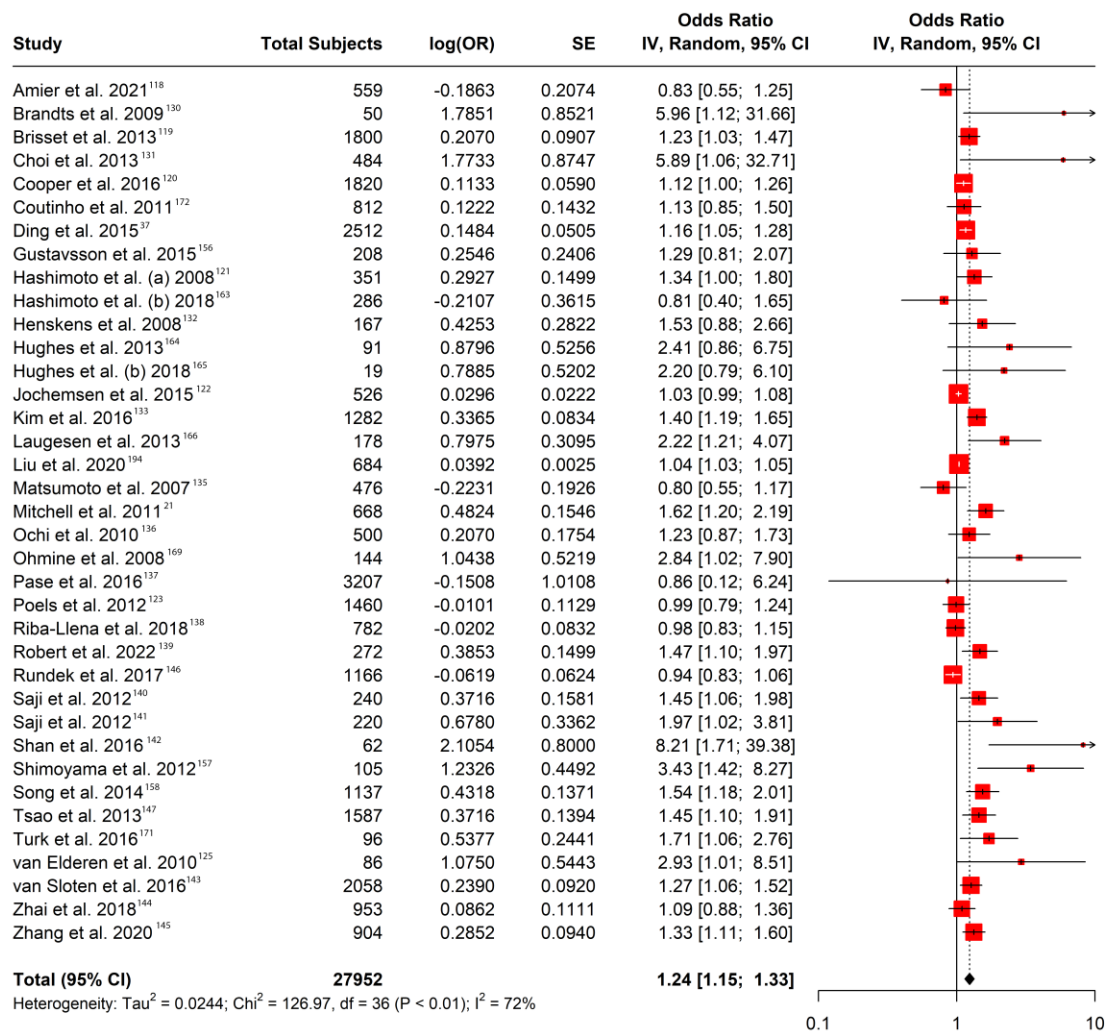


Figure 2-4. Odds ratio results from pooled studies reporting arterial stiffness as a continuous exposure variable. Forest plot illustrating the effect sizes for studies reporting continuous arterial stiffness in relation to cSVD burden. Effect sizes are reported per 1-SD increase. The overall effect favored a greater presence of cSVD as arterial stiffness increases (OR: 1.24, 95% CI: 1.15-1.33). OR, odds ratio; SE, standard error; IV, inverse-variance.

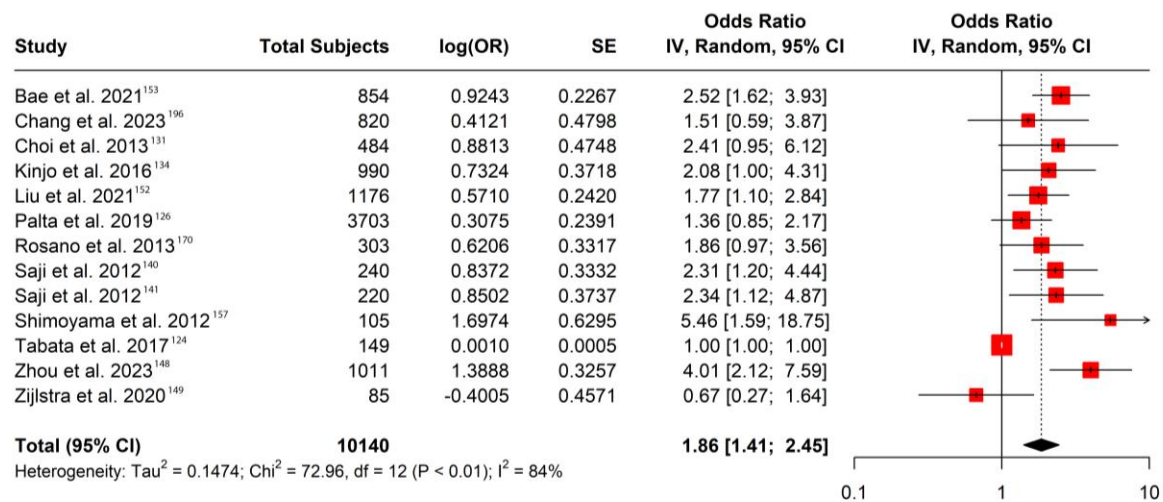


Figure 2-5. Odds ratio results from pooled studies reporting arterial stiffness as a dichotomous exposure variable. Forest plot illustrating the effect sizes for studies reporting dichotomous arterial stiffness in relation to cSVD burden. Effect sizes are reported per 1-SD increase. The overall effect suggested a greater arterial stiffness was associated with a greater presence of cSVD (OR: 1.86, 95% CI: 1.41-2.45). OR, odds ratio; SE, standard error; IV, inverse-variance.

for each standard deviation-increase in the clinically relevant cfPWV, the odds of cSVD increase by 23 percent (Figure S7).

The continuous arterial stiffness measures were analyzed to investigate the differences between central arterial stiffness and conduit (carotid) arterial stiffness. Six studies^{37,119,122,139,146,171} reported measures of carotid arterial stiffness, and 18 studies^{21,118,120,123,125,130,132,137,138,142,143,147,156,163-166,172} reported measures of central arterial stiffness. Both carotid artery assessments (OR: 1.15, 95% CI: 1.00-1.31; number of studies=6) and central artery assessments (OR: 1.26, 95% CI: 1.10-1.44; number of studies=18) were associated with pooled markers of cSVD. Random-effects analysis of subgroup differences did not reveal significant differences ($P=0.34$), suggesting that central and conduit arterial stiffness may be associated with cSVD burden (Figure S8).

Analysis of the funnel plots for continuous and dichotomous arterial stiffness measures (Figures S11 and S12) suggested suspicion of evidence of publication bias. Conducting sensitivity analyses using the leave-one-out approach revealed that the significance in the random effects models for continuous and dichotomous arterial stiffness was maintained throughout the analysis. In further sensitivity analysis, numerical differences but not statistical differences were detected when applying fixed-effects analysis to continuous arterial stiffness (OR: 1.04, 95% CI: 1.04-1.05) or to dichotomous arterial stiffness (OR: 1.001, 95% CI: 1.000-1.002).

Secondary Analyses

Meta-analysis of longitudinal studies from the studies included in quantitative primary statistical analysis was not feasible due to a limited number of studies. One study⁶¹ investigated

the longitudinal relationship between dichotomous cerebrovascular reactivity and cSVD, 3 studies^{37,122,147} investigated longitudinal relationships between continuous measures of arterial stiffness and cSVD, and 1 study¹⁷⁰ investigated the longitudinal relationship between arterial stiffness as a dichotomous exposure and cSVD. The individual results of these studies are presented qualitatively in Figure S4.

The multivariate meta-regression results are presented in the supplementary materials (Table S4). Only the continuous arterial stiffness category of studies was applicable for appropriately powered analysis.^{200,201} Therefore, we conducted multivariate meta-regression with the continuous arterial stiffness model, incorporating the study-level covariates of hypertension, diabetes mellitus, and hyperlipidemia (or medication use targeting these conditions). Twelve studies^{125,130,132,137,142-144,146,147,164,165,171} were removed from the original 37 studies on the basis of incomplete demographic information, leaving 25 studies for meta-regression. The random-effects meta-analysis of the remaining studies remained statistically significant (OR, 1.21; 95% CI: 1.12-1.32, $P < 0.0001$; number of studies=25). In the risk factor-adjusted model, the three risk factors (hypertension, diabetes mellitus, and hyperlipidemia) extracted from study-level data, not individual patient data, accounted for 29.4% of the model heterogeneity. Among the 25 studies analyzed, the majority (20 out of 25, 80%) centered around generally healthy participants with different risk factors, while 7 out of the 12 (58%) not included in the meta-regression focused on healthy populations. Meta-regression results for the model adjusted for each factor individually and for all three risk factors are presented in Table S4. Bubble plots for the individual covariates are presented in supplementary materials (Figures S6-S8).

Risk of Bias Assessment and GRADE Rating of Primary Outcomes

Studies included in quantitative meta-analyses for primary outcomes were assessed for risk of bias using the Newcastle-Ottawa scale. The average risk of bias for studies reporting dichotomous cerebrovascular reactivity was 6.6 ± 1.0 , for studies reporting continuous arterial stiffness measures was 8.2 ± 1.0 , and for studies reporting dichotomous arterial stiffness was 7.3 ± 1.5 . Individual study assessment outcomes are reported in Tables 1 and 3. The GRADE assessment of the certainty of evidence for the primary outcomes is presented in Table S5.

Discussion

The present systematic review and meta-analyses represent the most recent and updated work summarizing the relationship between cerebral autoregulation, cerebrovascular reactivity, and arterial stiffness in relation to cSVD burden. The main findings of the present systematic review are: 1) the majority of studies included in the qualitative systematic review found associations between cSVD and cerebrovascular reactivity (80.4% of studies), cerebral autoregulation (78.6% of studies), and arterial stiffness (85.4% of studies); and 2) in quantitative meta-analyses, cSVD was associated with increases in arterial stiffness and borderline associated with impaired cerebrovascular reactivity. While the vast majority of literature, to date, surrounding the risk of cSVD has focused on traditional vascular risk factors, specifically hypertension, their role as dominant factors in the pathogenesis of cSVD has been challenged.^{12,202,203} Emerging theories propose complex vascular etiologies, including an impaired cerebrovascular function, as important factors mediating cSVD, alongside or independent of hypertension.^{12,18} These relate to the varied complexities of the vascular etiologies proposed for cSVD subtypes, given cerebrovascular regulatory functions are mediated, in part, by local endothelial function^{27,28} and arterial stiffness is, in part, dictated by vascular matrix composition and endothelial dysregulation of vascular smooth muscle tone.^{17,204,205} Importantly, the collective findings of the present systematic review expand our current understanding of the pathogenesis of cSVD by demonstrating associations of increasing cSVD burden with reductions in cerebrovascular reactivity (37 of 46 studies, or 80.4%), impairments in cerebral autoregulation (11 of 14 studies, or 78.6%), and increases in arterial stiffness (70 of 82 studies, or 85.4%) (Figure 6). In addition, our subsequent meta-analysis of eligible studies comprising 27,952 participants (53.0% women) revealed a significant association between

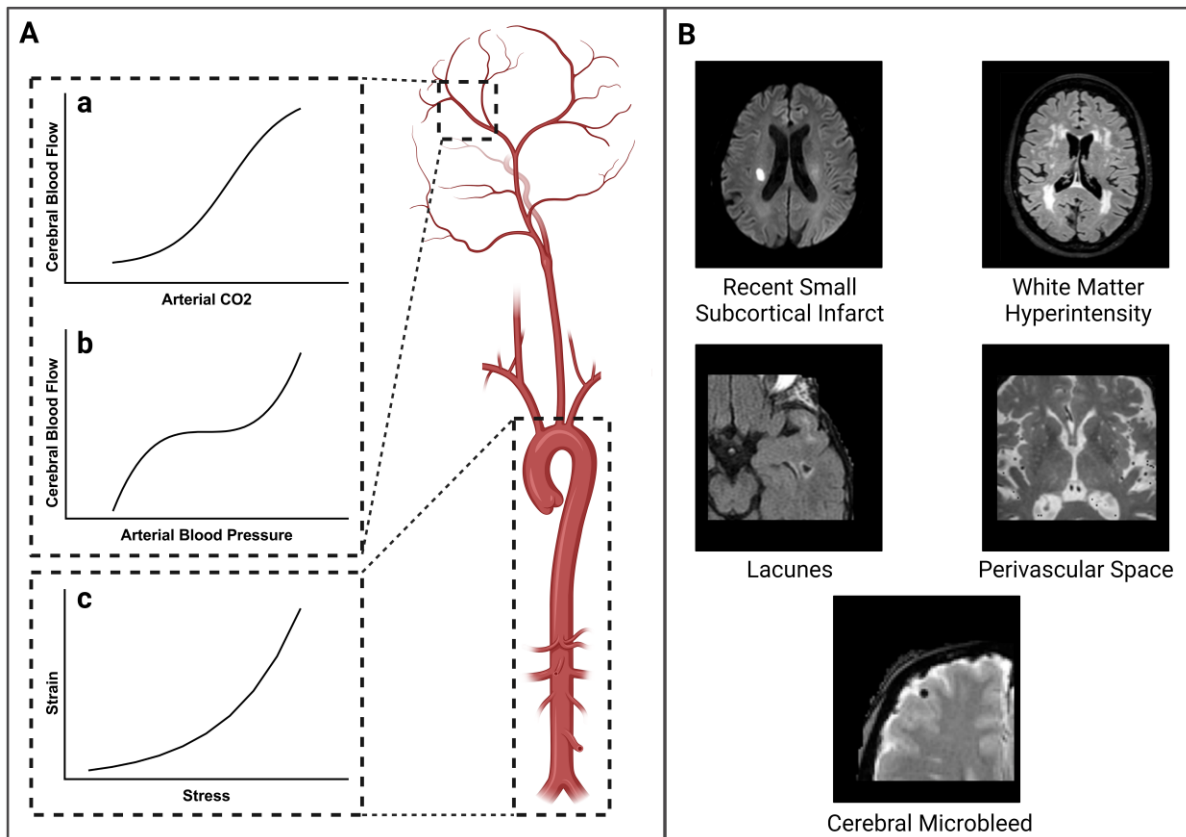


Figure 2-6. Characterization of arterial stiffness and cerebrovascular regulation in relation to cSVD. **A:** a) Cerebrovascular reactivity is an aspect of the chemo-regulation of cerebral blood flow, where a healthy cerebrovascular system should demonstrate a positive relationship between cerebral blood flow and arterial carbon dioxide content (arterial CO₂). b) Cerebral autoregulation is the regulatory process by which the cerebral circulation maintains relatively stable perfusion through a range of arterial blood pressures. c) In-vivo measurements of arterial stiffness capture incremental stress-strain relationships, describing the overall impact that arterial structural and functional components have on arterial elasticity, buffering of pulsatile pressures, etc. **B:** Examples of MRI images depicting the five primary radiological markers of cSVD. Created with BioRender.com. MRI images adapted from Table 1 from Bennett et al.²⁰⁶ used under CC BY 4.0.

increases in arterial stiffness and cSVD. In a limited number of studies however, meta-analysis only revealed a borderline association between cerebrovascular reactivity and cSVD. However, the heterogeneity and limited data result in uncertainty to the strength of these relationships and highlight the need for longitudinal investigations into vascular stiffness and regulatory function as possible risk factors for cSVD.

Cerebrovascular Reactivity

The present study suggests that reduced cerebrovascular reactivity is associated with an increased cSVD burden. As one of the standard measures of cerebrovascular reactivity first used in 1990 by Ratnatunga and Adiseshiah²⁰⁷, the BHI has demonstrated predictive capabilities in patients with asymptomatic carotid artery stenosis for the risk of ischemic stroke events.²⁰⁸ While typically measured in the context of cerebrovascular disease^{29,209}, cerebrovascular reactivity has been previously shown to relate to cardiac arrhythmias²¹⁰, cardiorespiratory fitness²¹¹, and all-cause mortality²¹², which suggests systemic influences. This may be due to the assessment of cerebrovascular reactivity as an indicator of endothelial function, a known predictor of regional and global cardiovascular dysfunction.^{27,28}

While hypertension and other vascular risk factors are often referred to as critical factors in the development and progression of cSVD, more recent evidence suggests that the etiology of cSVD is complex and likely extends beyond arterial blood pressure.^{11,12} The hypothesis that the characterization of cSVD may include reductions in cerebrovascular reactivity alongside other risk factors is supported by Molina et al.⁵¹, who reported that in 92 participants, cerebrovascular reactivity and hypertension were both significantly associated with lacunar infarction.

It is worth noting that the limited number of studies available for meta-analysis coupled with different methods of assessing cerebrovascular reactivity could affect the strength of the relationship between cerebrovascular reactivity and cSVD. The wide variability in approaches may have contributed to the considerable heterogeneity ($I^2=68\%$) observed in the meta-analysis of dichotomous cerebrovascular reactivity. Due to the limited number of studies and inconsistencies in determining cut-off values, it was not possible to explore this possible source of heterogeneity further in the present analyses. Adapting a standard approach in future investigations may help establish cerebrovascular reactivity as a functional assessment of the cerebrovasculature for further investigations. Moreover, of the eligible studies for inclusion in the quantitative meta-analysis, we were only able to pool the results from 7 studies out of the 46 included in the systematic review, highlighting a critical need for expansion of the body of evidence.

Cerebral Autoregulation

Cerebral autoregulation is a regulatory mechanism serving to maintain cerebral perfusion throughout a range of physiological variations in perfusion pressure³². Of the 14 articles extracted for cerebral autoregulation in the systematic analysis, 11 studies suggested a significant association between impaired cerebral autoregulation and greater cSVD. However, numerous methods exist for determining cerebral autoregulation, limiting formal interpretation across studies. One prominent approach uses frequency domain transformations of arterial blood pressure and cerebral artery blood velocity, calculating gain and phase from frequency data.^{32,33} Other approaches incorporate time domain indices, including moving correlation coefficients between blood pressure and cerebral artery blood velocity.³⁴ Work beginning less than a decade

ago has attempted to establish a standardized approach²¹³, but methodological convergence is still progressing.^{34,214} Present qualitative findings suggest the possibility of cerebral autoregulatory impairments as a target for understanding the pathophysiology of cSVD. However, the limited number of studies eligible for meta-analysis demonstrates an avenue for future work to expand on the contributions of impaired cerebral autoregulation to cSVD.

Arterial Stiffness

Central arterial stiffening, which occurs with healthy aging and in many pathological states, leads to a diminished impedance gradient between the proximal aorta, carotid arteries, and cerebral vasculature.¹⁷⁻¹⁹ This reduces wave reflection and enhances the transmission of pulsatile waves deeper into the cerebral vascular bed.^{18,20} Pre-clinical models using transverse aortic constriction surgery²¹⁵ or a genetic model of arterial stiffness²¹⁶ to increase carotid artery pulse pressure have suggested that enhanced cerebrovascular pulsatility impaired endothelium-dependent vasodilation²¹⁶, disrupted blood-brain barrier function, and resulted in cerebral microbleeds.²¹⁵ While our qualitative and quantitative syntheses of studies do not have enough longitudinal information to address the specific underlying pathophysiological mechanisms that precede cSVD development, the significant associations between arterial stiffness, cerebrovascular reactivity, and cSVD demonstrated herein suggest possible mechanisms associated with the presence of cSVD.

Both the continuous arterial stiffness meta-analysis and the dichotomous arterial stiffness meta-analysis displayed significant heterogeneity ($I^2=72\%$ and 84% , respectively). To address this, we performed a sub-analysis analysis using only the studies that measured cfPWV to support this point, which revealed a heterogeneity numerically less than observed in the primary

analysis. Another possible explanation is the challenge of disentangling arterial stiffness from lifestyle factors and comorbidities associated with arterial stiffness and cSVD. Positive lifestyle activities, such as physical activity, have previously been shown to reduce arterial stiffness.^{217,218} It is possible that this may have been a factor in studies such as Amier et al.¹¹⁸ or Hashimoto et al.¹⁶³, where the average cfPWV values of participants were lower than expected for the sample age and blood pressure.²¹⁹ However, physical activity assessments were not commonly reported in presently-included studies, and none incorporated laboratory measurements of gold-standard indices of cardiorespiratory fitness (i.e., VO₂ peak or maximal values) that have been shown to be associated with arterial stiffness.²¹⁷ We performed meta-regression to investigate further sources of heterogeneity associated with three comorbidities (hypertension, diabetes mellitus, and hypercholesterolemia), demonstrating that including these three study-level covariates explained ~30% of the overall model heterogeneity. However, caution with interpretation is warranted – these covariates were extracted from study-level data, not individual patient data. Therefore, extrapolation of this information is dependent on the study samples included. Of relevance, the majority of the studies included (20 of the 25, 80%) focused on generally healthy participants with varying proportions of risk factors. In contrast, only 7 of the remaining 12 studies (58%) not included in the meta-regression focused on healthy populations.

An additional cause of heterogeneity in the present study is the different pathogenic processes of the individual cSVD subtypes. In subgroup analyses between arterial stiffness, white matter hyperintensities, and lacunes, the heterogeneity was not significant in the white matter hyperintensity analysis ($I^2=31\%$, $P=0.15$), while the lacune analysis remained considerably heterogeneous ($I^2=70\%$). These findings may be related to a strong dependence of

lacunes on age¹⁴⁴, whereas white matter hyperintensities have been suggested to be associated with arterial stiffness, vascular injury, and blood-brain barrier dysfunction.^{4,12,220,221}

Implications

The implications of the present work are that impairments in cerebrovascular regulatory functions and increased arterial stiffness are associated with cSVD burden. Assessing these vascular traits may aid in further understanding the vascular etiologies or pathophysiological progression of cSVD. Despite a prevalence of cSVD that has been suggested to be $\geq 90\%$ in aging populations²²², the underlying mechanisms of cSVD are still incompletely understood. Previous literature has established the contributions of high blood pressure and hypertension^{223,224} to cSVD. However, studies using antihypertensive medications targeting reductions in cSVD have been sparse⁸ and demonstrate overall mixed responses²²⁵⁻²²⁸, suggesting that additional contributing factors may interact with or independent of hypertension and other traditional comorbidities. In line with the present study's findings, a recent series of randomized controlled trials, the Lacunar Intervention Trial-1 and Trial-2 (LACI-1 and LACI-2), demonstrated that treatments targeting vascular endothelial function improved cerebrovascular reactivity in cSVD patients²²⁹ and improved outcomes in cSVD patients.²³⁰ Importantly, the results of the present study do not suggest replacing monitoring or treatment of hypertension, but suggest that additional assessments of cerebrovascular autoregulation, cerebrovascular reactivity, and/or arterial stiffness may be useful. When assessed alongside traditional cardiovascular measurements (i.e., blood pressure testing, echocardiography, etc.), incorporating these three measures of vascular structure and function in longitudinal studies or studies focusing on

clinically relevant populations may provide further critical insight into the underlying pathophysiology that contributes to the development or progression of cSVD.

Study Limitations

There were three main limitations in the present study. First, age and hypertension are important cardiovascular risk factors that may contribute to the development or progression of cSVD. These factors also impact the three primary measures incorporated into the present review and meta-analyses.^{137,163,231-233} Although blood pressure or hypertension may be a confounding factor, many studies adjusted for this. However, it is worth noting that we did not have any randomized-controlled trials in our meta-analyses, which may partly explain discrepancies regarding the impact of hypertension on cSVD.^{41,234} Second, there was significant heterogeneity between studies in terms of study population demographics, methods of assessing the primary predictor variable, and the subtype(s) of cSVD used as the outcome. A key possibility that may have affected all three primary exposures is the presence of large or small artery disease, such as arterial stenosis. Stenotic intracranial and extracranial arteries have been associated with an increased burden of cSVD²³⁵ alongside separate associations of arterial stenosis with increased arterial stiffness²³⁶, impaired cerebrovascular reactivity²³⁷, and impaired cerebral autoregulation.²³⁸ As pointed out in a recent consensus statement²³⁹, current measures of arterial stenosis do not provide deeper information into the mechanisms linking stenosis and cSVD. While outside the scope of the present analyses, the findings presented herein suggest that incorporating measures of cerebrovascular regulation and arterial stiffness as mediators of the link between stenosis and cSVD could further our understanding of the pathophysiology. Finally, we acknowledge that there are statistical limitations in using pooled OR as the primary outcome

in that these pooled measures may come from different methodological designs and result in high levels of heterogeneity.

Conclusions

The present systematic review and meta-analyses demonstrate significant associations between impaired cerebrovascular reactivity, increased arterial stiffness and cSVD. Collectively, the current literature suggests that measurements of cerebrovascular regulation and arterial stiffness may provide feasible means of further investigating the mechanisms involved in the development or progression of cSVD. These findings highlight the utility of vascular assessment in furthering our understanding of the underlying pathophysiology of cSVD.

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Chapter 3 - Cerebral Macro- and Microvascular Regulation in Cancer Survivorship

Abstract

Background: Approximately 46% of cancer survivors report cognitive impairments across many types of cancer, which has been associated with anti-cancer therapy and often results in reduced quality of life. Pre-clinical studies suggest that determinants of brain health in chronic disease states, such as cancer survivorship, are likely to involve cerebrovascular dysfunction. We aimed to determine cerebrovascular hemodynamic function (cerebrovascular reactivity to carbon dioxide, cerebrovascular pulsatility) at the macrovascular and microvascular levels in survivors of cancer. We also conducted exploratory assessments of cognitive function in a subset of the cohort. **Methods:** Participants were recruited locally and through the Stormont-Vail Healthcare Network. Testing included resting measurements of cerebral hemodynamics to determine resting blood velocities, microvascular oxygen saturation and concentrations of hemoglobin, and cerebrovascular pulsatility. Then, cerebral blood velocity in the large arteries (middle cerebral artery or MCA) and oxygenated hemoglobin in microcirculation (HbO₂; prefrontal cortex region), blood pressure, and end-tidal CO₂ were collected during a rebreathing task. MAP was used to calculate indices of cerebrovascular conductance. Cerebrovascular reactivity (CVR) was calculated as the change in cerebral blood velocity, HbO₂, or vascular conductance over the change in end-tidal CO₂. Cognitive tests were also administered, which included Dimensional Change Card Sort, Picture Sequence Memory Form A, and Pattern Comparison Processing Speed from the National Institute of Health Toolbox. **Results:** Twenty-four women were recruited (10 healthy controls [HC], 14 survivors of cancer [CS]). Cancer types included

melanoma, lymphoma, and breast cancer. There were no differences in age, body-mass index, or blood pressure resting measurements between groups. At baseline, there were no significant differences in resting MCA mean velocity between groups (HC: 61.4 ± 34.4 cm/s vs. CS: 58.7 ± 29.7 cm/s; $p > 0.9$) or in resting HbO₂ (HC: 25.6 ± 3.0 μ M vs. CS: 24.7 ± 7.5 μ M; $p = 0.69$). However, there was a significantly lower microcirculation pulsatility index in HC (HC: 2.1 ± 0.5 μ M vs. CS: 2.7 ± 0.7 μ M; $p = 0.040$). In the absolute CVR measurements, there were no observed differences between HC and CS in CVR_{MCA} (HC: 0.87 ± 0.37 cm/s/mmHg vs. CS: 0.80 ± 0.50 cm/s/mmHg; $p > 0.70$) or CVR_{HbO₂} (HC: 0.22 ± 0.27 μ M/mmHg vs. CS: 0.11 ± 0.13 μ M/mmHg; $p = 0.37$). Adjusting for changes in MAP by using vascular conductance measures revealed a significantly lower CVR_{HbO₂} in CS (HC: 0.90 ± 1.06 μ M/mmHg/mmHg*10 vs. CS: -0.07 ± 0.22 μ M/mmHg/mmHg*10; $p = 0.040$). There were no differences between HC and CS in the Dimensional Card Change Sort test ($p = 0.51$), the Picture Sequence Memory Form A ($p = 0.64$), or the Pattern Comparison Processing Speed ($p = 0.32$). **Conclusions:** Survivors of cancer had a greater pulsatility and reduced vascular conductance reactivity in the microcirculation of the brain, highlighting the injury present in a region critical for maintaining cerebral functions. These findings highlight the importance of monitoring cerebrovascular function, especially in the cerebral small vessels, in cancer survivors.

Introduction

For the first time in the United States, over 2 million people are expected to be diagnosed with cancer – roughly equivalent to one new diagnosis every 15 seconds.^{1,2} Improvements in cancer detection and treatment have significantly reduced cancer mortality over prior decades, resulting in an estimated 20.3 million cancer survivors in the U.S. by 2026.³ This medical progress has led to awareness of an emerging concern: many cancer survivors experience long-term complications, such as heightened risk for cardiovascular disease or cerebrovascular disease.^{4,5}

Numerous studies have provided evidence that anti-cancer therapies, namely chemotherapy, are primary contributing factors. From the early studies of cardiotoxicity in doxorubicin⁶ to contemporary investigations into immunotherapy-related myocarditis⁷, many of these studies have focused on the timeframe from the beginning of treatment to within a year of the end of treatment. With modern survival rates increasing, attention has shifted to long-term fatal and non-fatal events. A key example is cognitive impairment, which is reportedly experienced by up to 1 in 3 breast cancer survivors.⁸ This cognitive impairment, or “chemo-fog”, remains a poorly understood mediator of reduced quality of life in cancer survivors^{9,10} and a gap in the literature highlighted by the National Cancer Institute.¹¹

One of the leading hypotheses for mechanisms underlying chemo-fog is that neuroinflammation and oxidative stress induced by chemotherapy impair cerebrovascular function. The diminished cerebrovascular regulation results in a mismatch between neuronal metabolism and cerebral blood flow, leading to cognitive decline.^{12,13} Similar hypotheses have been investigated and supported in general population samples¹⁴, multiple sclerosis¹⁵, cerebral

amyloid angiopathy¹⁶, and several other chronic conditions including aging.¹⁷ However, this concept has had limited attention in cancer survivorship.

One study from Downs et al.¹⁸ investigated cerebrovascular reactivity to carbon dioxide (a standard marker of cerebrovascular regulatory function¹⁹) and found that breast cancer survivors had a reduced cerebrovascular reactivity compared to cancer-free controls. The authors suggested that this may have contributed to the lower cognitive scores also observed in the breast cancer survivors. However, the study only assessed blood velocity in the middle cerebral artery (MCA). While the large arteries and pial vessels contribute substantially to the vascular resistance of the brain, the microvasculature remains the site of metabolic exchange between blood and the cerebral parenchyma.²⁰ Assessment of microvascular responses may provide information beyond that of the large vessel reactivity.

Therefore, the aim of the present study was to compare large and small vessel reactivity between cancer survivors and cancer-free controls. We additionally tested a select battery of cognitive function assessments between groups. We hypothesized that cancer survivors would have reduced large and small vessel reactivity, and reduced cognitive function. Furthermore, we hypothesized that the reductions in vascular reactivity would be correlated with cognitive impairment.

Methods

All procedures in this study were conducted in accordance with the Declaration of Helsinki and received institutional ethical approval from Kansas State University and Stormont Vail Health (IRB #11181). The authors declare that all supporting data are available upon reasonable request.

Study Cohort

Males and female cancer survivors (CS) and cancer-free controls (CF) were eligible for participation in the study. Participants were recruited from June 2022 through August 2024 from the Manhattan, Kansas area and surrounding regions through social media campaigns, campus media announcements, and recruitment through the Stormont Vail Health network. Eligibility criteria for CS were: 1) 21 years of age or older, 2) primary non-CNS cancer diagnosis within the previous 15 years, and 3) completion of primary treatment (surgery, radiation, and/or chemotherapy). For CF, criteria were: 1) 21 years of age or older, and 2) no prior diagnoses of any form of cancer. Exclusion criteria for both groups were: 1) younger than 21 years of age, 2) current or previous cerebrovascular, neurodegenerative, and/or pulmonary disease, and 3) unable to provide written and verbal informed consent.

Experimental Design

Experiments were performed in Manhattan, Kansas (altitude of 327 meters above sea level) in a controlled clinical environment (Stormont Vail Health Manhattan Campus) or in a controlled laboratory setting (Lafene Health Center, Kansas State University). Temperature, humidity, and ambient pressure did not differ between locations during testing. Participants were

instructed to refrain from caffeine and strenuous exercise prior to the experimental visit, but to maintain any daily medication and supplement use according to their normal schedule. At the beginning of each visit, informed consent, anthropometric measures, health history information, and medical record release documents were collected. Brachial blood pressure (OMRON Intellisense Pro; OMRON Healthcare, Inc., IL, USA) was assessed as the average of 2 measurements performed after ~10 minutes of quiet rest. Visits lasted 60-90 minutes in total, and started between 7:00am and 6:00pm with no difference in morning or afternoon visit allocation between CF and CS groups.

Cerebral Hemodynamics

All equipment herein was calibrated and checked for quality according to manufacturer recommendations before experiments. Equipment checks and operations were performed throughout all experiments by the same investigators (B.S., C.A.).

Transcranial Doppler Ultrasound

Transcranial doppler (TCD) ultrasonography was used for collection of cerebral hemodynamics. Participants were seated in an upright position while the TCD operator (B.S.) positioned a convex probe connected to a traditional ultrasonography system (General Electric HealthCare Technologies, Inc., Chicago, IL, USA). B-mode and color flow scans were performed to identify the middle cerebral artery (MCA) at a depth of 40-65 mm through the temporal window. Pulse-wave doppler scans assessed minimum, maximum, and mean MCA velocities with an insonation angle less than 15 degrees.²¹

Near-infrared Spectroscopy

Non-invasive measurements of cerebrovascular hemodynamics will be performed serially by cerebral near-infrared spectroscopy (NIRS) using a commercially available frequency-domain system (OxiplexTS, ISS Inc., Champaign, IL, USA). In brief, NIRS devices emit near-infrared light into biological tissue which is absorbed primarily by heme; in cerebral tissue, heme is primarily found circulating as hemoglobin in red blood cells.²² The optical properties of hemoglobin vary if the hemoglobin is bound to oxygen, allowing NIRS to differentiate between oxygenated and deoxygenated hemoglobin (HbO₂ and HHb, respectively).²³ The absolute concentrations of these species, along with their sum (total-Hb) and the oxygen-saturation percent (Tissue Oxygenation Index, or TOI%), provide non-invasive indices of cerebral microvascular hemodynamics.^{24,25} For the present work, we used HbO₂ and total-Hb as our primary measurements in line with previous literature.²⁴⁻²⁶

Assessment of Microvascular Pulsatility

In a subsample of the present study, we determined the pulsatility in the microcirculation using the NIRS. Cerebral microcirculatory data collected via NIRS during a resting period preceding cerebrovascular reactivity testing (described in the following section) was exported at 10Hz and imported into LabChart 8 (ADInstruments Inc., CO, USA). Built-in software algorithms for peak detection were used to identify cardiac cycles, using 2 standard deviations as a threshold criteria to exclude peaks resulting from noise during the refractory window. Within each cycle, the maximum and minimum total-Hb values were used to calculate the amplitude (the maximum minus the minimum). These amplitudes were averaged over ≥ 10 cycles, resulting in a NIRS-derived pulsatility index (PI) in the microcirculation. Consistent with prior work²⁶, the

total-Hb signal was selected to represent the local cerebral blood volume (assuming hematocrit remains constant during the resting period).²⁷

Cerebrovascular Reactivity

To assess MCA and cerebral microcirculation responsiveness to changes in blood gases, a modified rebreathing approach was adopted.²⁸ Participants breathed room air for a 2 minute baseline period before switching to rebreathing from a 6-liter anesthesia bag pre-filled with 4 liters of room air until pre-determined cardiorespiratory endpoints were achieved. End-tidal partial pressures of oxygen ($P_{ET}O_2$) and carbon dioxide ($P_{ET}CO_2$) were collected breath-by-breath with a metabolic cart (Ultima CPX, MGC Diagnostics Corporation, MN, USA) or cardiorespiratory monitor (CardioCap 5, General Electric HealthCare, IL, USA). The final 60 seconds of baseline and the last 10 seconds of rebreathing data were used for analyses. Due to simultaneous changes in both $P_{ET}O_2$ and $P_{ET}CO_2$ that occur during rebreathing, we calculated a previously described stimulus index (SI)²⁹, the ratio of $P_{ET}CO_2$ over $P_{ET}O_2$, as the blood gas stimulus for cerebrovascular responses. To account for changes in blood pressure, vascular conductance indices were calculated as the hemodynamic variable divided by mean arterial pressure (MAP). MAP was calculated as one-third of the difference between systolic blood pressure (SBP) and diastolic blood pressure (DBP) added to DBP. Cerebrovascular reactivity (CVR) was determined as 1) the absolute or relative change in MCA velocity or microcirculatory HbO_2 over the change in SI, and 2) as the absolute or relative change in MCA vascular conductance or in microcirculatory vascular conductance over the change in SI. Equations are provided below:

$$CVR_{X-Abs} = (X_{end} - X_{bsl}) / (SI_{end} - SI_{bsl}) \quad [1]$$

$$CVR_{X-Rel} = [(X_{end} - X_{bsl}) / (X_{bsl}) * 100] / (SI_{end} - SI_{bsl}) \quad [2]$$

$$CVR_{X.VC-Abs} = (VC_{X-end} - VC_{X-bsl}) / (SI_{end} - SI_{bsl}) \quad [3]$$

$$CVR_{X.VC-Rel} = [(VC_{X-end} - VC_{X-bsl}) / (VC_{X-bsl}) * 100] / (SI_{end} - SI_{bsl}) \quad [4]$$

where X represents either MCA velocity or HbO₂, the subscript *end* indicates the measurement during the last 10 seconds of rebreathing, the subscript *bsl* indicates the measurement taken during baseline, and VC_X is the vascular conductance measure for either MCA velocity or HbO₂ obtained by dividing the hemodynamic variable by MAP.

Cognitive Assessments

Participants were comfortably seated at a table in the testing site for cognitive testing. These tests were performed on an iPad (10th generation, Apple Inc., Cupertino, CA, USA) after entering participant age and education level. Tests included Dimensional Change Card Sort, Picture Sequence Memory Form A, and Pattern Comparison Processing Speed from the National Institute of Health Toolbox version 3.10.1.3. Analyses of the cognitive tests were performed by researchers blinded to participant cancer history (T.B., A.S., O.E., S.S.). Demographic-corrected T-scores for the tests are reported by adjusting raw test scores for age, sex and race/ethnicity.

Statistical Analyses

Statistical analyses were performed in GraphPad Prism 10.3.0 (Dotmatics, Boston, MA, USA) or SigmaPlot 13.0 (Systat Software Inc., Chicago, IL, USA). Normality of data was assessed with Shapiro-Wilks tests. Outliers were determined with the ROUT method set at a

standard threshold ($Q=1\%$). Comparisons between groups were assessed as independent t-tests, Mann-Whitney tests if the normality assumption was violated, or t-test with Welch's correction if variances were unequal. Associations between cognitive test outcomes and NIRS-derived microcirculation measures were assessed using the Spearman r coefficient and corresponding p-value. The microcirculatory outcomes were selected for correlational analyses as the cerebral microcirculation is the site of the neurovascular unit, linking cognition to vascular function.³⁰⁻³² Statistical significance was set *a priori* at $p<0.05$. Data in results are presented as means $\pm$ standard deviations unless otherwise noted.

Results

Demographics for the overall study cohort are reported in Table 3-1. Healthy controls (HC) were well matched to survivors of cancer (CS) for age, height, weight, body mass index, systolic and diastolic blood pressure (all $p>0.05$). For all cerebrovascular assessments, all HC and CS participants were women. Due to technical challenges present in cerebrovascular and cognitive testing, some participants had to be excluded from certain tests.

Cerebrovascular Reactivity and Pulsatility

At baseline, there were no significant differences in resting MCA mean velocity between groups (HC: 61.4 ± 34.4 cm/s vs. CS: 58.7 ± 29.7 cm/s; $p>0.9$) or in resting HbO₂ (HC: 25.6 ± 3.0 μ M vs. CS: 24.7 ± 7.5 μ M; $p=0.69$). However, as shown in Figure 3-1, there was a significantly lower microcirculation PI in HC (HC: 2.1 ± 0.5 μ M vs. CS: 2.7 ± 0.7 μ M; $p=0.04$). For cardiopulmonary measures, there were no differences in MAP ($p=0.28$) or SI ($p=0.25$). The change in SI from baseline to end-test was not different between groups (HC: 0.13 ± 0.11 mmHg vs. 0.14 ± 0.11 mmHg; $p>0.9$); however, there was a significantly greater change in MAP from baseline to end-test in CS (HC: 1.1 ± 5.6 mmHg vs. CS: 8.1 ± 8.4 mmHg; $p=0.04$).

In the absolute CVR measurements, there were no observed differences between HC and CS in $CVR_{MCA-Abs}$ (HC: 0.87 ± 0.37 cm/s/mmHg vs. CS: 0.80 ± 0.50 cm/s/mmHg; $p>0.7$) or $CVR_{HbO2-Abs}$ (HC: 0.22 ± 0.27 μ M/mmHg vs. CS: 0.11 ± 0.13 μ M/mmHg; $p=0.37$). The same was true for relative CVR measurements, both in $CVR_{MCA-Rel}$ (HC: 1.95 ± 1.35 %/mmHg vs. CS: 1.47 ± 0.93 %/mmHg; $p=0.39$) and in $CVR_{HbO2-Rel}$ (HC: 1.05 ± 1.28 %/mmHg vs. CS: 0.50 ± 0.50 %/mmHg; $p=0.48$). Results are presented in Figure 3-2.

Table 3-1. Study cohort demographics and comparisons.

	Healthy Controls	Cancer Survivors	P-value for Comparison
Sample Size (n)	10	14	--
Age (yrs)	43.8 ± 16.2	52.9 ± 15.3	0.18
Sex, female (%)	100	100	1
BMI (kg/m ²)	25.7 ± 7.5	29.1 ± 5.9	0.23
SBP (mmHg)	127.6 ± 10.5	126.9 ± 12.4	0.9
DBP (mmHg)	80.6 ± 5.4	84.8 ± 7.4	0.15
MAP (mmHg)	96.2 ± 6.0	98.8 ± 8.7	0.44
PP (mmHg)	47.0 ± 9.6	42.1 ± 7.5	0.19
HR (bpm)	73.6 ± 9.7	76.6 ± 9.5	0.47

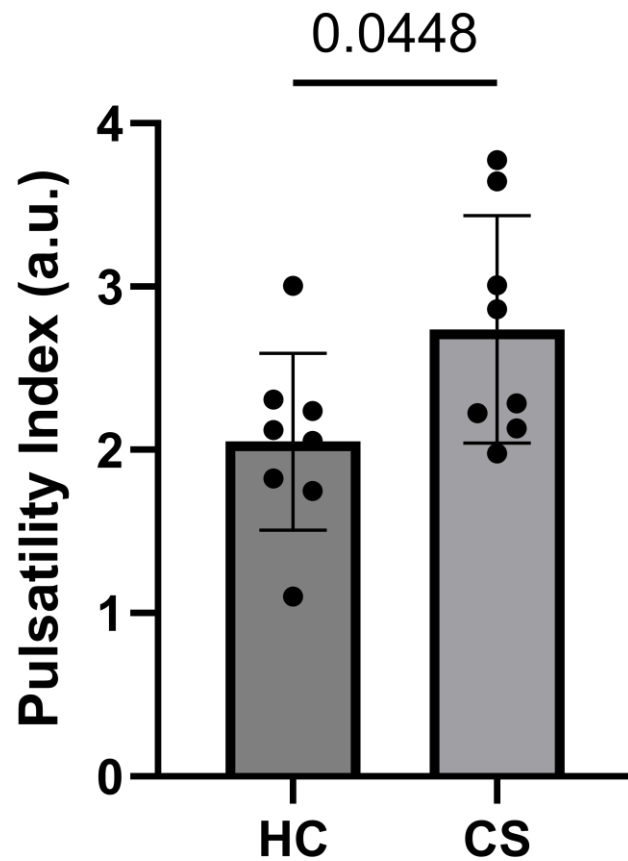


Figure 3-1. A comparison of microvascular pulsatility between cancer-free, healthy controls (HC) and survivors of cancer (CS). The pulsatility index was derived from near-infrared spectroscopy assessments of the prefrontal cortex microcirculation during a resting baseline.

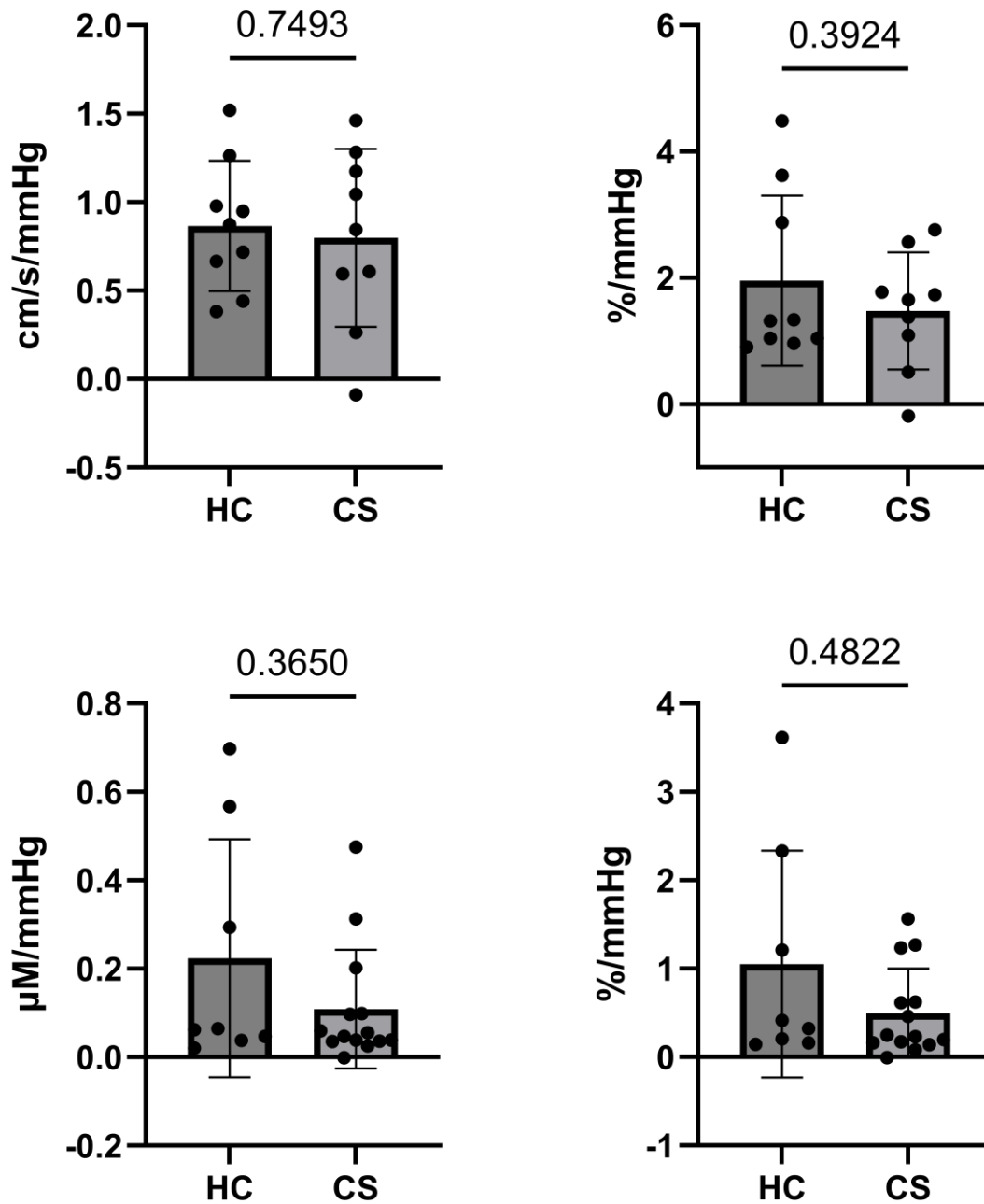


Figure 3-2. (*Top-Left*) Absolute middle cerebral artery cerebrovascular reactivity in response to a rebreathing protocol. (*Top-Right*) Relative middle cerebral artery cerebrovascular reactivity in response to a rebreathing protocol. (*Bottom-Left*) Absolute microcirculatory cerebrovascular reactivity in response to a rebreathing protocol. (*Bottom-Right*) Relative microcirculatory cerebrovascular reactivity in response to a rebreathing protocol. See Methods for details of calculation. HC, healthy controls; CS, cancer survivors.

In contrast, adjusting for changes in MAP by using vascular conductance measures revealed a significantly lower $CVR_{HbO_2.VC-Abs}$ in CS (HC: $0.90 \pm 1.06 \mu M/mmHg/mmHg*10$ vs. CS: $-0.07 \pm 0.22 \mu M/mmHg/mmHg*10$; $p=0.04$). This was consistent with the relative measure, $CVR_{HbO_2.VC-Rel}$ (HC: $0.39 \pm 0.49 \%/mmHg$ vs. CS: $-0.02 \pm 0.11 \%/mmHg$; $p=0.03$). However, there was a lack of significant difference between groups MCA vascular conductance CVR in both absolute and relative terms (both $p>0.1$). Results for vascular conductance CVR outcomes are presented in Figure 3-3.

Cognitive Assessments

There were no differences between HC and CS in the Dimensional Card Change Sort test (HC: 56.4 ± 21.1 vs. CS: 45.1 ± 10.9 ; $p=0.51$), the Picture Sequence Memory Form A (HC: 61.6 ± 16.4 vs. CS: 60.4 ± 7.5 ; $p=0.64$), or the Pattern Comparison Processing Speed (HC: 53.6 ± 13.7 vs. CS: 48.2 ± 9.6 ; $p=0.32$).

In correlational analyses, greater CVR_{HbO_2-Abs} (Spearman r : 0.66, $p<0.05$) and greater CVR_{HbO_2-Rel} (Spearman r : 0.65, $p<0.05$) were associated with higher Picture Sequence Memory Form A scores. However, this correlation was not observed in the vascular conductance CVR measures (both $p>0.05$). There was also a borderline but non-significant association between microcirculatory PI and the Picture Sequence Memory Form A scores ($p=0.05$). None of the CVR measures were correlated with either Dimension Card Change Sort test or Pattern Comparison Processing Speed test performance (all $p>0.05$). Test scores and the correlation matrix are presented in Figure 3-4.

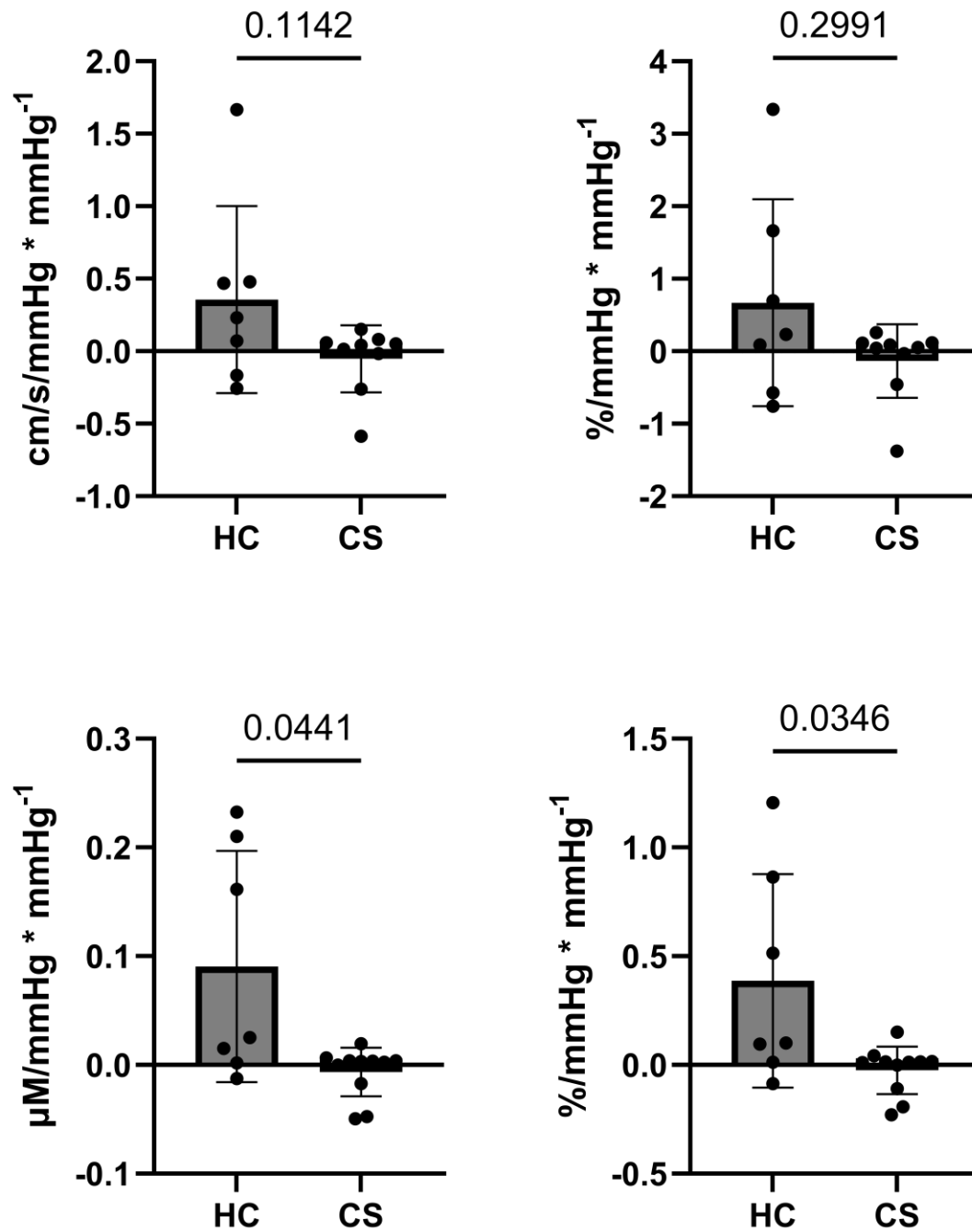


Figure 3-3. (*Top-Left*) Absolute middle cerebral artery vascular conductance in response to a rebreathing protocol. (*Top-Right*) Relative middle cerebral artery vascular conductance in response to a rebreathing protocol. (*Bottom-Left*) Absolute microcirculatory vascular conductance in response to a rebreathing protocol. (*Bottom-Right*) Relative microcirculatory vascular conductance in response to a rebreathing protocol. See Methods for details of calculation. HC, healthy controls; CS, cancer survivors.

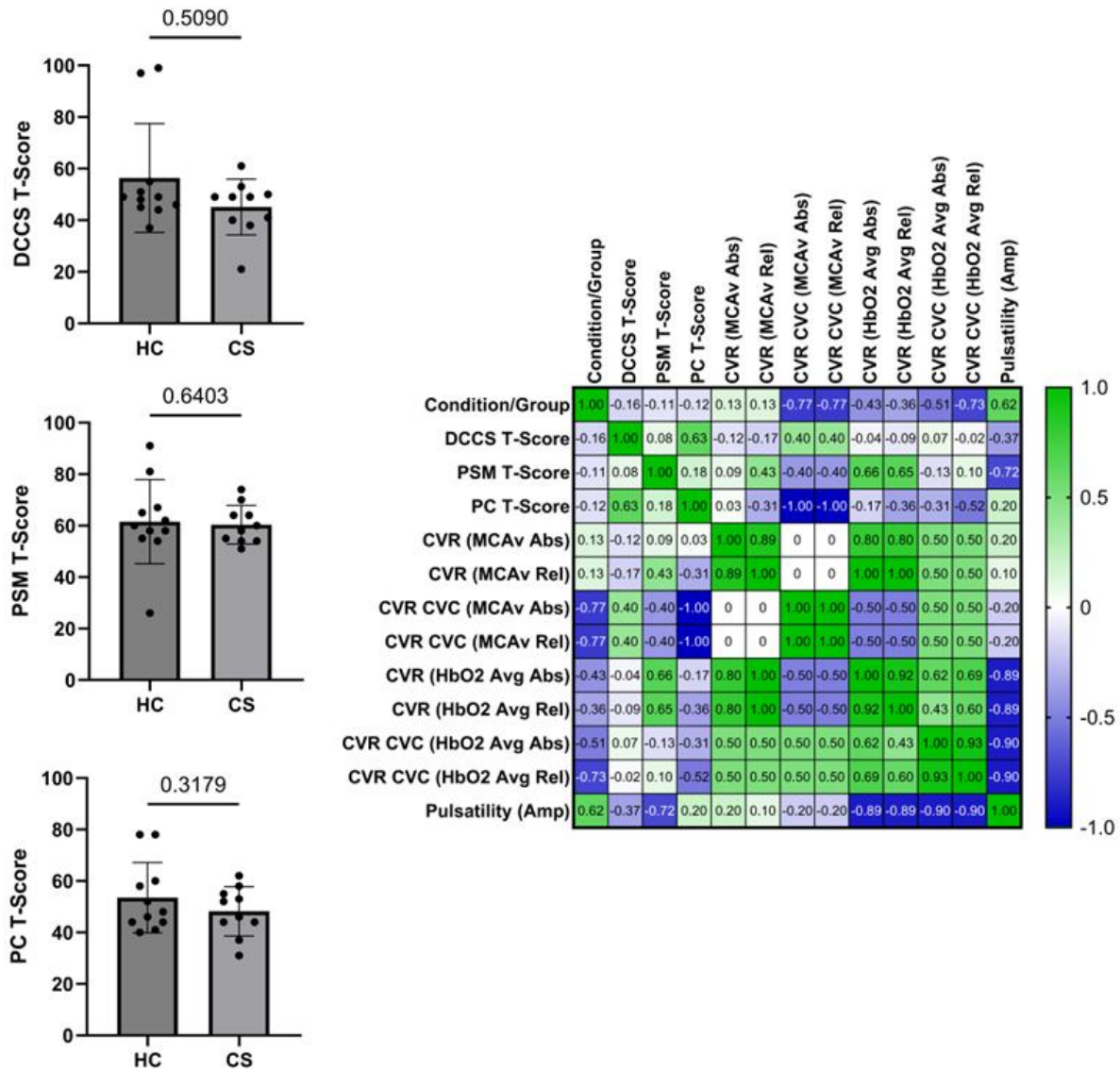


Figure 3-4. (Left) Comparisons between cancer-free, health controls (HC) and survivors of cancer (CS) for three cognitive assessments. DCCS, Dimensional Card Change Sort; PSM, Picture Sequence Memory Form A; PC, Pattern Comparison Processing Speed. Raw scores from the tests were adjusted for participant demographics and reported as T-scores. (Right) Correlation matrix for cognitive assessments and cerebral hemodynamics. CVR, Cerebrovascular reactivity; CVC, Cerebrovascular conductance; HbO₂, oxygenated hemoglobin.

Discussion

The main findings of this study demonstrate a reduced vascular conductance CVR response and a greater pulsatility in the cerebral microcirculation of survivors of cancer, which were suggested to be correlated with cognitive performance on a memory task. However, in contrast to our initial hypothesis, we found no significant differences in large artery (MCA) CVR or reduced cognitive performance in survivors of cancer compared to cancer-free controls. Overall, these findings support a primarily cerebral microvascular dysfunction that may persist throughout cancer survivorship, potentially relating to cognitive impairment over time.

Cerebrovascular Reactivity and Pulsatility

One of the key findings in the present study was that the microcirculatory vascular conductance reactivity was lower by ~110% in CS compared to HC counterparts, suggesting an almost completely reversed direction of the expected hemodynamic response in some participants.^{33,34} Interestingly, this significantly impaired response was only observed when considering changes in MAP over the course of the stimulus. A similar phenomenon was described by Miller et al.³⁵ in a study comparing CVR in the MCA between young and old healthy, physically active individuals. In that work, the authors suggest that this may indicate an age-related reliance on changes in perfusion pressure to augment cerebral blood flow as a compensatory mechanism for reduced cerebral microcirculatory function. We extended on those ideas by non-invasively measuring the large and small cerebral arteries simultaneously, and we found that the perfusion pressure dependent (i.e., vascular conductance) differences between groups were significant only in the microvasculature. It should be noted that the ages were not different between groups in this study; however, cancer and many anti-cancer treatments may

accelerate biological aging that result in survivors presenting with phenotypes and physiological responses characteristic of an older individual.³⁶⁻³⁸ Thus, insight into cerebrovascular regulation in both aging and cancer survivorship may lead to overlapping understanding of the underlying pathology.

It is also likely that other factors may play a role; for example, prior work has suggested an increased chemoreflex response to hypoxia^{39,40} and a reduced CO₂ threshold⁴¹ in older adults. This sympathetic hyperexcitation would drive MAP increases to a greater extent, and excessive sympathetic activity has been well documented in cancer survivors.⁴²⁻⁴⁴ The role of sympathetic activity in CVR to hypercapnia is a topic of debate^{45,46}, but more recent literature provides strong evidence for a role that may vary between health and disease.⁴⁷

We also found a significantly greater pulsatility in the cerebral microcirculation of CS, with an increase of ~30% relative to HC. Generally, conduit arteries between the heart and brain act to dampen the pulsatile energy generated by the left ventricle during contraction in order to prevent transmission of excess force into the vulnerable cerebral microvascular beds.^{48,49} Increased microvascular pulsatility has been linked to impaired endothelium-dependent vasodilation⁵⁰, blood-brain barrier breakdown⁵¹, and development of cerebral small vessel disease.⁵² The findings from the present study (impaired CVR, microvascular pulsatility) - and prior work from our laboratory demonstrating increased arterial stiffness⁵³ - provide strong evidence supporting the likelihood of small vessel disease, given that these physiological processes and functions are associated with the disease in the general population.⁵⁴

Cognitive Function in Cancer Survivorship

Impairments in cognitive function have been demonstrated throughout the continuum of cancer survivorship, from before treatment⁵⁵ to beyond 20 years from the end of treatment.⁵⁶ Our present findings did not suggest any substantial differences in cognitive ability across the domains tested. While this was an opposing finding to our hypothesis, it was also not entirely unexpected given that prevalence rates for detectable cancer- or treatment-related cognitive impairment vary widely, and do not often exceed 40% when using short, standardized cognitive batteries.⁸ A substantial portion of patients and survivors report cognitive complaints, but challenges in methodology and the need for specific tools designed to encompass the multifaceted and heterogeneous forms of cancer-related cognitive impairment may warrant novel approaches.⁵⁷ In a similar vein, incorporation of physiological measures alongside neurocognitive outcomes may reveal insight that extends beyond only using one or the other. Our correlative findings between microcirculatory pulsatility, reactivity, and memory-specific deficits may suggest that survivors who present with cerebrovascular dysfunction may be more predisposed to a certain cognitive phenotype; further work is needed to fill critical gaps in present knowledge.⁵⁸

Limitations

Our study is not without limitations. Our primary limitation was sample size – due to the nature of the study design, larger sample sizes could not be included in the present work. This limits the ability to stratify by duration of cancer survivorship or types of treatment received, key targets for future work. Secondly, our use of a rebreathing test that elicited both hypercapnia and hypoxia prevents isolation of physiological responses specific to CO₂ or oxygen. However, this

method has been previously established²⁹ and aids in interpreting the two changing stimuli simultaneously. Third, we used transcranial doppler ultrasonography to assess cerebral blood velocity in the MCA, which does not account for changes in the cross-sectional area of the vessel. The concept that MCA cross-sectional area remains constant during short rebreathing assessments has been challenged.⁵⁹ It is important to note that in that study, substantially smaller increases in cross-sectional area were observed in older adults (~5% vs. ~12% in younger adults). Thus, in the present study where the average age of the cohort was ~50 years old, vasodilation may have had less of an impact.

Conclusions

Our study demonstrates that cerebral microvascular conductance responses to a rebreathing challenge are impaired in survivors of cancer. Additionally, survivors of cancer demonstrated greater cerebral microvascular pulsatility than cancer-free controls at rest. Future work should examine this effect across a variety of cancer types and chemotherapy regimens to investigate the differential impacts that these may have. Furthermore, the implications of this cerebrovascular dysfunction on cognitive outcomes should be explored with a wider array of neurocognitive assessments.

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Chapter 4 - The Effects of Breast Cancer and Immune Checkpoint Inhibition on Cerebral Small Vessel Disease Burden: A Mendelian Randomization Analysis

Abstract

Importance: Breast cancer survivorship is rapidly increasing in the U.S., largely due to novel anti-cancer treatments such as immune checkpoint inhibitors (ICIs). However, robust evidence investigating adverse effects of ICIs is lacking despite the reported variety of neurotoxicities. Understanding the effects of ICIs on cerebrovascular injury, specifically cerebral small vessel disease (CSVD), may inform monitoring and management strategies. **Objective:** To use genetic instruments for estimating the causal effects of breast cancer or exposure to ICIs on CSVD burden. **Design:** This was a genetic association study using two-sample and drug-target Mendelian randomization methods. Analyses were performed between December 2024 and March 2025. **Setting:** Genetic summary statistics were used, primarily representing a European population. **Participants:** Genetic data for primary analyses were predominantly extracted from the Breast Cancer Association Consortium, UK Biobank, Alzheimer's Disease Neuroimaging Initiative or stroke consortium meta-analysis. **Exposures:** Exposures were: 1) genetically predicted breast cancer, stratified into any breast cancer, estrogen-receptor positive or negative, or triple-negative subtypes; 2) a genetic instrument designed and validated to proxy the effects of ICIs. **Main Outcomes and Measures:** Beta coefficients (β) or odds ratios (OR) and 95% confidence intervals (CI) for four CSVD markers: white matter hyperintensity volume (WMH), perivascular space burden (PVS), cerebral microbleeds (CMB), and small vessel stroke (SVS).

Results: Summary data were available for WMH (n=18381), PVS (n=40095; 9339 cases), CMB (n=25862; 3556 cases) and SVS (n=1614080; 13620 cases). Breast cancer - regardless of type - was not associated with any CSVD marker (all $p > 0.30$). However, the genetically-proxied effect of ICIs was associated with a greater WMH volume (β 0.045, 95%CI:[0.003-0.087], $p=0.034$) and a greater risk of PVS (OR 1.02, 95%CI:[1.00-1.03], $p=0.023$). **Conclusions and Relevance:** Our findings suggest that breast cancer does not have a direct effect on CSVD, but exposure to ICIs may increase CVSD burden – particularly WMH and PVS.

Introduction

Advances in cancer screening and innovative treatments have dramatically improved survival rates for breast cancer, with the number of survivors in the United States projected to exceed 26 million by 2040.¹ One such innovation in treatment is the addition of immune checkpoint inhibitors (ICIs), which have emerged in the last decade as a promising approach to reduce breast cancer-associated mortality, especially in advanced stage breast cancer.² Evidence from clinical trials have demonstrated improved pathologic complete response and overall survival with ICIs compared to chemotherapy alone—successes highlighted in the KEYNOTE-522 (NCT03036488)³ and KEYNOTE-756 (NCT03725059)⁴ clinical trials—underscoring their potential role in shaping the future of breast cancer care. Despite the improvement in cancer-specific outcomes, ICIs are associated with acute and late-developing adverse events - including neurologic and cerebrovascular injury - that can carry severe consequences.⁵⁻⁷ As recently highlighted⁸, we are entering “a new era of immunotherapy survivorship”, with ICI-related long-term complications that are becoming increasingly relevant to clinical care.

The increased risk of cerebrovascular morbidity and mortality in long-term survivorship^{9,10} is potentially due to common pathophysiological mechanisms between cerebrovascular disease and cancer - such as oxidative stress and inflammation^{11,12} – along with the acute and chronic toxicity associated with some cancer treatments, including ICIs.¹³ These complications are suggestive of cerebral small vessel disease (CSVD)^{14,15}, a pathology that primarily develops in regions of vascular endothelial dysfunction^{16,17} and is detected on magnetic resonance imaging (MRI).¹⁸ Notably, evidence suggests that both endothelial dysfunction¹⁹⁻²¹ and markers of CSVD, such as cerebral microbleeds (CMB)²², are associated with conventional

chemotherapy. The burden of CSVD after treatment with ICIs remains critically underexplored despite the severity of these cerebral adverse events.²³

There are obstacles to advancing our knowledge of ICI-related long-term toxicity. As pointed out in a recent *JAMA Oncology* Viewpoint, reporting of adverse events beyond 90 days in ICI clinical trials is incredibly rare⁸, restricting the ability to investigate this phenomenon. The few cancer registries reporting ICI-related adverse events are limited by selection bias, among other biases.²⁴ An innovative approach to circumvent these obstacles is the application of Mendelian randomization (MR), a study design that uses genetic variants as instrumental variables to examine the causal association between an exposure and an outcome.^{25,26} This unique methodology also assesses long-term consequences of an exposure²⁷, thereby addressing a critically understudied window of time in “immunotherapy survivorship”. Taking advantage of MR study design, we aimed to identify the effects of breast cancer and ICIs on MRI-derived measures of CSVD. We hypothesized that immune checkpoint inhibition, but not breast cancer, would be associated with an increased burden of CSVD.

Methods

Overview of Mendelian Randomization

Mendelian randomization (MR) begins with identifying genetic variants associated with a selected exposure trait; these variants are used as a genetic instrumental variable. Using genetic summary statistics for an outcome trait, the association between the selected exposure and the target outcome can be assessed. If the core assumptions of MR are met, then this approach results in an estimate of the causal relationship under investigation.²⁸ There are three core assumptions: 1) relevance – the instrumental variable is associated with the exposure of interest; 2) independence – the instrumental variable is not related to any confounders, and 3) exclusion restriction – the instrumental variable is not related to the outcome measure.²⁹ Further details are provided in the Supplementary Methods (Appendix B).

This study performed two separate sets of two-sample MR analyses, shown in the study design overview (Figure 1). In both analysis stages, exposure and outcome information was derived from genome-wide association studies (GWAS). The first stage of analysis focuses on the direct effects of breast cancer – and breast cancer subtypes – on markers of CSVD. Exposure data for breast cancer and breast cancer subtypes were obtained from the Breast Cancer Association Consortium.³⁰ The primary outcomes were individual imaging markers of CSVD (described further below) assessed from MRI-scans and analyzed in a manner consistent with international guidelines.¹⁸ In the second stage of analysis, genetic variants were used to create an instrument to proxy the effects of ICIs. This exposure was assessed in two-sample MR analyses with the same outcomes (CSVD markers) as in the first stage of analysis.

All methods and reporting conducted herein were performed to be consistent with the Strengthening the Reporting of Observational Studies in Epidemiology Using Mendelian

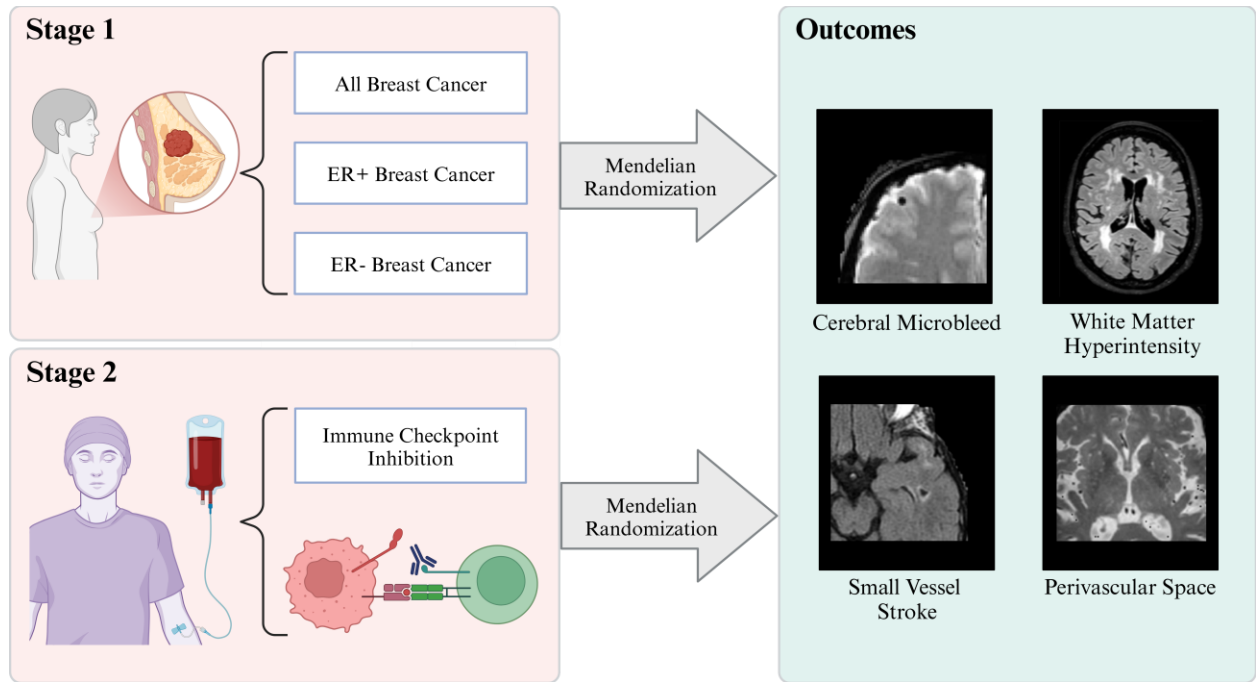


Figure 4-1. An overview of the study design. In stage 1, we used two-sample Mendelian Randomization (MR) to assess the causal associations of all breast cancer types, estrogen receptor positive (ER+) breast cancer, and estrogen receptor negative (ER-) breast cancer with cerebral small vessel disease (CSVD) imaging markers. In stage 2, we identified a genetic instrument designed to mimic the effects of immune checkpoint inhibition, and used this as the exposure for the same outcomes as stage 1. Figure adapted in part from Scheuermann et al.⁷⁸

Randomization (STROBE-MR) recommendations (Appendix B).³¹ All analyses used publicly available GWAS summary statistics from studies that obtained ethical approval and participant informed consent; therefore, approval by local institutional research boards were not required.

Exposure Instrumental Variables

Breast Cancer and Subtypes

GWAS summary level data for breast cancer, estrogen-receptor positive (ER+) breast cancer, and estrogen-receptor negative (ER-) breast cancer were derived from a Breast Cancer Association Consortium³⁰ study. Data for triple-negative (TN) breast cancer was retrieved from a separate meta-analysis of Breast Cancer Association Consortium studies.³² Study characteristics for the published GWAS are provided in Table 4-1. Extracted single nucleotide polymorphism (SNP) variants met standard threshold criteria (significant p-value < 5×10^{-8} , window size = 10,000 kb) to ensure that SNPs were significantly associated with the exposure (i.e., breast cancer and subtypes) and not in linkage disequilibrium with one another ($r^2 < 0.001$). The linkage disequilibrium reference used was the 1000 Genomes reference panel.³³

Genetic Instrument for PD-1/PD-L1 Signaling Inhibition.

To determine a genetic instrument reflecting the effects of ICIs, we first identified drug targets with supported pharmacological action using the DrugBank database.³⁴ Cis-variants (i.e., variants within ± 100 kb of target gene region) significantly associated with the expression of these target genes in whole blood were extracted from the Genotype Tissue Expression (GTEx v10) database³⁵ and combined.³⁶ In contrast to the breast cancer analyses, variants were allowed

Table 4-1. Characteristics of the genome-wide association studies (GWAS) used in the present investigation.

Extracted Variable	Source GWAS	Predominant Ethnicity	Sample Size	Adjustments in Model ^a
Exposures				
Any Breast Cancer, ER+/ER- Breast Cancer	PMID: 29059683	European	106,776 ^c	Study site, first 10 PCs.
Triple-Negative Breast Cancer	PMID: 32424353	European	106,377	Age, first 10 PCs.
<i>PDCD1</i> , <i>CD274</i> eQTL ^b	PMID: 32913098	European	943	Sex, PCs, PEER factors ^d , sequencing platform, sequencing protocol.
Primary Outcomes				
White Matter Hyperintensity	PMID: 32358547	European	18,381	Age, sex, genotyping array, UK Biobank site, first 10 PCs, MRI head motion.
Perivascular Spaces	PMID: 37069360	European	40,095	Age, sex, intracranial volume, study site, PCs.
Cerebral Microbleeds	PMID: 32913026	European	25,862	Age, sex, PCs.
Small Vessel Stroke	PMID: 36180795	European	1,614,080	Age, sex, PCs, study-specific covariates.
Secondary Outcomes ^e				
PD-1, PD-L1 Protein Expression	PMID: 29875488	European	3301	Age, sex, duration between blood draw and processing, first 3 PCs.
Leukocyte Count	PMID: 29892013	European	459,327	Age, age squared, sex, assessment center, genotyping array.
Neutrophil, Lymphocyte, Monocyte Counts	PMID: 32888493	European	562,132	Age, age squared, sex, first 10 PCs, study-specific covariates (i.e., study site).
Interleukin-8 Levels	PMID: 33067605	European	21,758	PCs, study-specific covariates.

^a PCs, principal components used to adjust for population stratification.

^b eQTL, expression quantitative trait loci.

^c Only the oncoarray-based summary statistics were used in the present study.

^d PEER, probabilistic estimation of expression residuals. A method used to identify a set of covariates based on sample size.

^e Secondary outcomes were those used in Mendelian randomization analyses aimed at providing biological evidence supporting the validity of the immune checkpoint inhibition genetic instrument.

to be in weak linkage disequilibrium ($r^2 < 0.4$) to increase statistical power of analyses.³⁶⁻³⁸

Further details on variant selection are provided in Supplementary Methods (Appendix B).

Validation of Genetic Instruments.

For both drug targets and breast cancer, instrument strength for each SNP was assessed using the F-statistic, calculated as $(\beta_{\text{exposure}}^2 / \text{SE}_{\text{exposure}}^2)$ where SE is standard error.³⁹ The overall F-statistic for the genetic instrument was taken as the average of all individual F-statistic values. An F-value > 10 indicates sufficient instrument strength.⁴⁰

For the genetic instrument designed to proxy the effects of ICIs, additional validation steps were conducted. First, the genetic instrument was assessed in two-sample MR to determine the effect on protein expression of programmed death-1 (PD-1) and programmed death ligand-1 (PD-L1) to account for physiological states that may result in differences between predictors of gene and protein expression.^{37,41} Second, biological validation was conducted to establish consistent effects of the genetic instrument compared to the clinical effects of ICIs.³⁷ This was conducted via two-sample MR, estimating the effect of immune checkpoint signaling inhibition on immune cell counts and circulating inflammatory markers, which have been reported before and after ICI exposure in a previous study.⁴²

Primary Outcome Variables

Primary outcomes in the present study for CSVD were white matter hyperintensity (WMH) volume, perivascular spaces burden (PVS), cerebral microbleeds (CMB), and small vessel strokes (SVS). WMH data was obtained from a previously published GWAS⁴³ conducted using the UK Biobank cohort, which has been previously described elsewhere.^{44,45} Genetic

associations with PVS were obtained from a study combining 18 population-based cohorts.⁴⁶ Data for CMB was extracted from an Alzheimer's Disease Neuroimaging Initiative study incorporating 11 population-based studies and 3 case-control or control-only stroke cohorts.⁴⁷ Finally, SVS summary GWAS statistics were derived from a meta-analysis of >1 million individuals of European descent.⁴⁸ Cohort characteristics are presented in Table 4-1, and detailed information CSVD marker assessment methods can be found in the respective publications.^{43,46-}

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Phenome-Wide Associations of Immune Checkpoint Inhibition

We used phenome-wide GWAS results available through a web-based platform, PheWeb⁴⁹, to identify potential phenotypes associated with immune checkpoint inhibition . Specifically, this step of analyses was conducted to identify potential confounding phenotypes that influence the associations between ICI effects and CSVD.⁵⁰ Phenotypes were extracted from the FinnGen study, a genomics initiative that has analyzed over 500,000 Finnish biobank samples and correlated genetic variation with health data to understand disease mechanisms and predispositions.⁵¹ Significant phenotypes were identified at $p < 2.0 \times 10^{-5}$ to account for the 2469 phenotypes listed in PheWeb.

Statistical Analyses

Our primary outcome for MR analyses was the inverse-variance weighted method, which is often considered as the primary approach for two-sample MR.²⁵ We additionally assessed all models in sensitivity analyses using MR-Egger, weighted-median, and MR Pleiotropy RESidual Sum and Outlier (MR-PRESSO) methods. The MR-Egger approach tests for a causal effect but

additionally is used to detect horizontal pleiotropy.⁵² The weighted-median method provides consistent results even when up to 50% of the information comes from invalid SNPs.⁵³ The MR-PRESSO method detects, and corrects for, potential outlier SNPs.⁵⁴ MR-PRESSO models were run with 1000 bootstraps.

Model heterogeneity was assessed with the MR-Egger Q statistic.^{53,55,56} Horizontal pleiotropy was tested with the MR-Egger intercept, where a value significantly different from zero indicates potential horizontal pleiotropy.⁵² Finally, scatter plots were used to visualize the agreement and consistency between the various methods applied.⁵⁵

All analyses were performed in R Studio (v2024.12.0), and figures were created using GraphPad Prism (v10.4.0). MR estimates are presented as beta and 95% confidence intervals (95% CI) for continuous outcomes (WMH), or odds ratio (OR) and 95% CI for binary outcomes (PVS, CMB, SVS). These estimates are given per additional copy of the effect allele, and represent the inverse-variance weighted results unless otherwise stated. Statistical significance was set *a priori* at a 2-sided $p < 0.05$. Results were considered robust when statistical significance was achieved in ≥ 2 methods of assessment.

Results

Effect of Breast Cancer on Cerebral Small Vessel Disease

Instrument strength was sufficient with an average F-statistic value of 78.6 (range 29.8-686.4) for breast cancer, 81.2 (range 30.3-787.2) for ER+, 49.3 (range 31.8-92.1) for ER- exposures, and 67.8 (range 30.3-217.8) for TN breast cancer. None of the methods applied in MR analyses demonstrated a significant relationship between breast cancer and markers of CSVD (all $p > 0.3$; Figure 4-2). There was evidence of heterogeneity in tests for WMH, CMB and SVS ($Q\ p < 0.05$); however, adjusting for outliers with MR-PRESSO did not substantially alter results in any case (all $p > 0.3$). There was no evidence of horizontal pleiotropy. Results were similar for ER+, ER- and TN subtypes (Appendix Table B-1). Visual inspection of scatter plots indicated agreement across the methods applied (Appendix Figures B-1 through B-4).

Effect of Immune Checkpoint Inhibition on Cerebral Small Vessel Disease

Validation of the Genetic Instrument

The genetic instrument for immune checkpoint signaling inhibition comprised 17 variants in cis-regions for the identified gene targets, PD-1 and PD-L1 (Appendix Table B-2), with an average F-statistic of 33.5 (range 13.5-115.4). Results from MR analyses indicated that the instrument was associated with both PD-1 protein expression (β 0.23, 95% CI: [0.12-0.34], $p = 2.4 \times 10^{-5}$) and PD-L1 protein expression (β 0.34, 95% CI: [0.23-0.45], $p = 6.6 \times 10^{-10}$), mirroring the effects of pembrolizumab observed in patients previously.⁵⁷ Subsequent analyses performed for changes in immune cell type distribution and inflammatory biomarkers provided further evidence for the validity of the genetic instrument when compared to observations from a recent trial in responders and non-responders to immunotherapy.⁴² Specifically, both the genetic

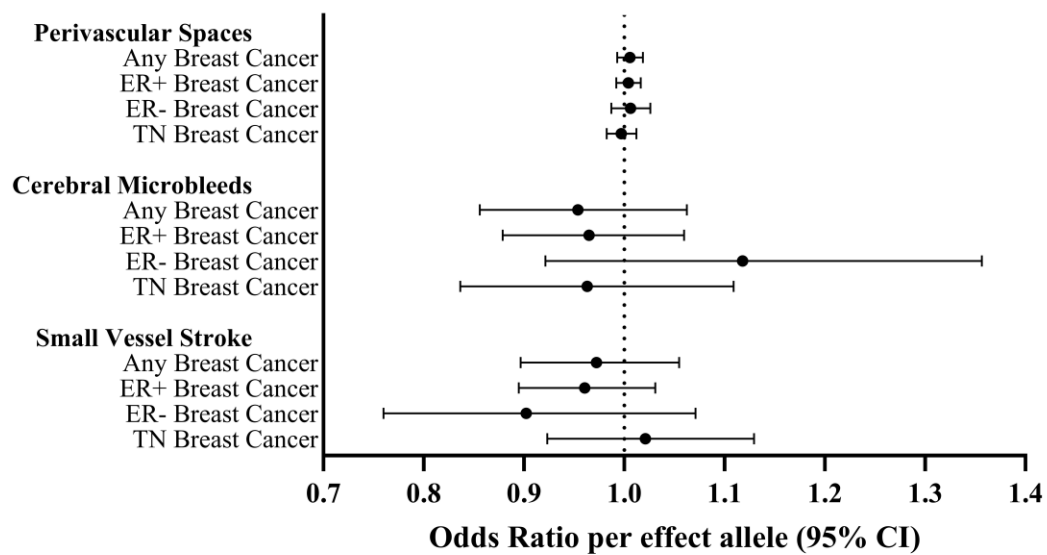
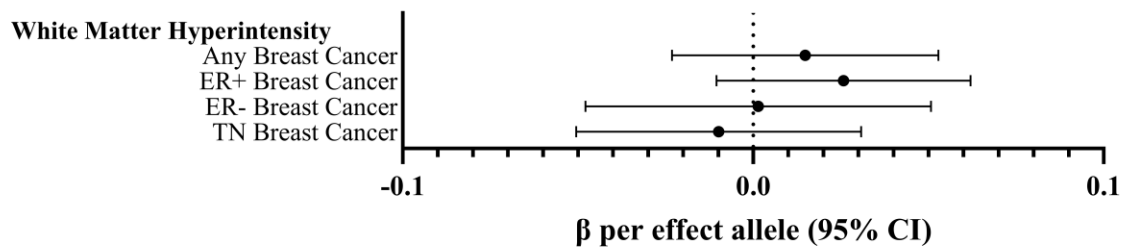


Figure 4-2. Primary inverse-variance weighted (IVW) results of the Mendelian randomization analyses for the effect of any breast cancer type, estrogen-receptor positive (ER+) breast cancer, estrogen-receptor negative (ER-) breast cancer, and triple-negative (TN) breast cancer on the four included markers of cerebral small vessel disease. 95% CI indicates that the plotted error bars show the 95% confidence interval.

instrument and observational data indicated increased lymphocytes and interleukin-8 levels, decreased leukocyte and neutrophils, and no change in monocytes. Evidence supporting biological validity of the genetic instrument is shown in Figure 4-3.

Effect on CSVD Outcomes.

The genetic associations of the effects of ICIs with specific CSVD markers are shown in Figure 4-4. Notably, ICI effects were significantly associated with greater WMH volume (β 0.045, 95% CI: [0.003-0.087], $p=0.034$) and higher risk for more severe PVS burden (OR 1.02, 95% CI: [1.00-1.03], $p=0.023$). Both were considered robust, with significant associations supported by at least one additional method (Appendix Table B-3). ICI effects were not associated with CMBs or the risk of SVS ($p>0.20$). MR-PRESSO detected potential outliers for the SVS model (outlier test $p=0.025$), however, adjusting for outliers did not substantially alter results (outlier-corrected $p=0.37$). Scatter plots indicated generally consistent results across the MR methods applied (Appendix Figure B-5).

Phenome-Wide Associations of Immune Checkpoint Inhibition

Of the genetic variants included in the instrument for ICI effects, 5 unique variants were associated with 9 unique phenotypes (Appendix Table B-4). The phenotypes were primarily categorized into diseases of the digestive system (i.e., inflammatory bowel disease, noninfective enteritis and colitis, ulcerative colitis) or the respiratory disease (i.e., chronic lower respiratory diseases, asthma/COPD). Notably, one variant (rs73399174) was associated with the broad phenotype of autoimmune disease ($p=1.9 \times 10^{-5}$).

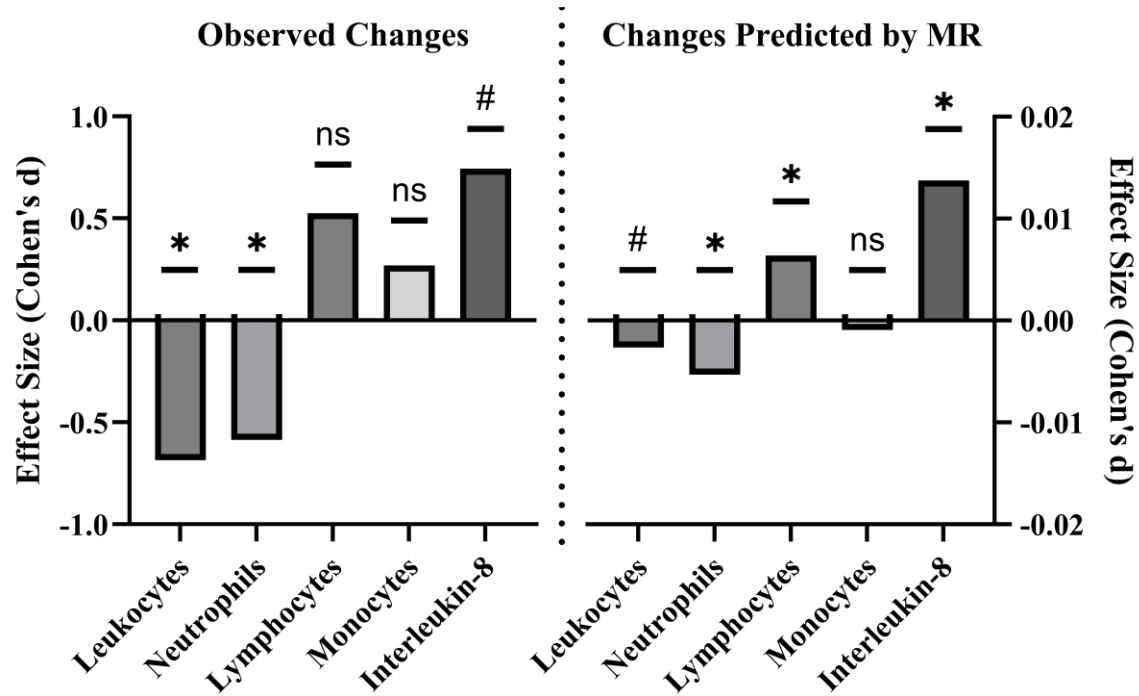


Figure 4-3. The effect of immune checkpoint inhibition on immune and inflammatory circulating markers, compared between clinical data observed in a recent study⁴² and from Mendelian randomization analyses conducted with the genetic instrument designed in the present study. Data reported by Juliá et al.⁴² were estimated from figures using PlotDigitizer (<https://plotdigitizer.com/>). Mendelian randomization results shown were conducted using the inverse-variance weighted (IVW) method. * $p < 0.05$, # $p < 0.10$.

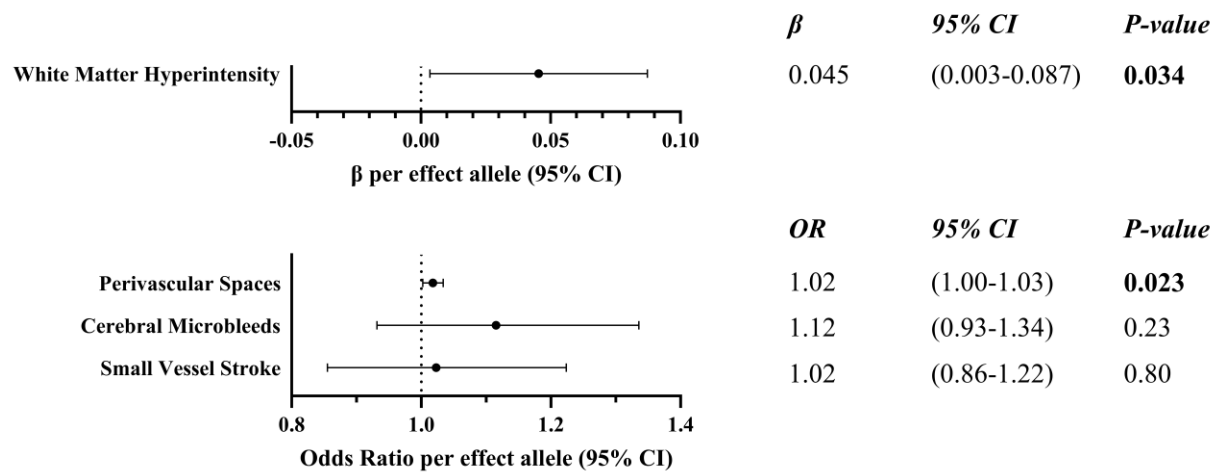


Figure 4-4. Primary inverse-variance weighted (IVW) results of drug-target Mendelian randomization analyses for immune checkpoint inhibition on imaging markers of cerebral small vessel disease (CSVD). 95% CI indicates that the plotted error bars show the 95% confidence interval. Bolded p-values indicate statistically significant results ($p < 0.05$).

Discussion

In the present study, we first used genetic analyses to provide causal estimates of the associations between breast cancer (and breast cancer subtypes) with CSVD. We subsequently identified genetic variants to design a genetic instrument mimicking the effects of immune checkpoint signaling inhibition (i.e., the effects of ICIs), and provided evidence supporting the biological validity of the instrument. This instrument was used in genetic analyses to assess the association between ICI effects and markers of CSVD. Consistent with our hypothesis, our present findings suggested: 1) breast cancer itself is not associated with a greater CSVD burden, but 2) exposure to pharmacological immune checkpoint signaling inhibition is associated with CSVD.

Collectively, these findings may advance our understanding of cerebrovascular health – and its associated consequences – in breast cancer survivors. The presence of pre-treatment, breast cancer-associated decrements in brain health remain controversial. Several studies have reported cognitive deficits in treatment-naïve patients with breast cancer⁵⁸, which has been suggested to attribute to proinflammatory cytokines or cognitive-emotional stress associated with the cancer diagnosis.⁵⁹ The risk of stroke in survivors of cancer is also significantly higher around the time of cancer diagnosis, potentially due to a cancer-induced hypercoagulable state.⁶⁰ However, assessments of CSVD burden in treatment-naïve breast cancer are rare in the literature. One study found that survivors of breast cancer treated with chemotherapy - but not survivors without prior chemotherapy - had impaired white matter integrity compared to cancer-free controls.⁶¹ Conversely, a longitudinal study more recently suggested that patients with breast cancer with or without systemic treatment both demonstrated greater WMH volume compared to cancer-free controls.⁶² The present findings are consistent with the former report, suggesting that

breast cancer is not associated with direct injury to cerebral white matter. Given the paucity of studies investigating CSVD in survivors of any cancer, further studies are warranted.

Detrimental effects of different anti-cancer therapies on cerebral structure and function are more consistently observed in both the human⁶³ and pre-clinical research⁶⁴; however, few studies have investigated the newer class of ICIs in the context of cancer survivorship. One of the largest studies in patients who received ICIs suggested a 4-fold increased risk of ischemic stroke⁶⁵, but this study did not separate stroke outcomes into subtypes that would specifically examine CSVD-related outcomes. Another study⁶⁶ assessed survivors of cancer diagnosed with ICI-induced encephalitis, and found that more than half of those patients with focal encephalitis had abnormal MRI T2/FLAIR hyperintensity (a marker used to determine WMH volume¹⁸) but again, did not directly assess CSVD burden. Remaining evidence largely comes from case reports⁷, which suggest clinical symptoms and cerebrovascular events that are consistent with the known sequelae of CSVD.⁶⁷ Interestingly, administration of pembrolizumab has shown promising results in human JC polyoma virus-induced progressive multifocal leukoencephalopathy (PML).^{68,69} Why our present findings contrast with observations in PML is unknown; however, it is worth noting that treatment with ICIs in PML patients may lead to immune reconstitution inflammatory syndrome (IRIS), which is associated with worsening leukoencephalopathy and severe immune infiltration in the brain.⁷⁰ While some degree of immune-inflammation is necessary to clear the human JC polyoma virus from cerebral tissue, this may explain the adverse cerebrovascular and neurological effects observed in survivors of cancer.

Phenome-wide analyses generally did not indicate confounding phenotypes that may influence the associations between ICI effects and CSVD burden. While asthma has been

reported as related to WMH volume and PVS burden⁷¹, the nature of these relationships remain unclear. Conversely, the association between variant rs73399174 and broad autoimmune disease requires further investigation. It is plausible that autoimmune responses and associated cytokine release⁷² may in part underly ICI-related toxicity.

Strengths and Limitations

Our study has strengths to consider beyond the strengths traditionally discussed in the context of MR analyses.^{28,29} Specifically, investigations into long-term ICI-associated toxicities are hampered by the sparse nature of available data from prospective or retrospective studies.⁸ The key notable strength of our study is the design and validation of a genetic instrument to investigate the effect of immune checkpoint signaling inhibition on cerebrovascular injury (specifically CSVD), which may inform future investigations.

There are a few limitations in our present study. First, the GWAS summary statistics used in this study were primarily conducted in individuals of European descent. Therefore, generalizability to other ethnicities may be limited. Second, the genetic data used to examine breast cancer and subtype exposures did not allow for specific investigations of the effects of breast tumor grade or other tumor characteristics. Third, and related to our second limitation, it should be noted that breast cancer predominantly affects women – this likely leads to an imbalanced distribution of sex in our breast cancer exposure variables versus our CSVD outcome variables. As pointed out in a recent commentary⁷³, this limitation may bias results towards the null due to unknown sex differences in genetic variants associated with CSVD outcomes. Fourth, the gene targets of ICIs selected for this study were specified using the on-target effects derived from DrugBank. However, there are side effects of these drugs and other anti-cancer therapies, such as inflammation and oxidative stress, that could directly impact cerebral tissue⁷⁴⁻⁷⁶ or

predicate damage to regulatory functions that result in cerebral damage.^{77,78} Finally, despite our sensitivity analyses, it remains possible that there is heterogeneity or pleiotropy not accounted for in our results.

Conclusions

The results from the present two-sample MR study, using two separate sets of exposures, suggest that breast cancer does not have a causal effect on CSVD but that ICIs used for some subtypes of breast cancer (and many other cancers) may increase CSVD burden. This work implicates changes in markers of CSVD after ICI exposure as a critical target for future investigation, especially as the clinical use of these antibodies expands rapidly in cancer and other conditions.

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Chapter 5 - Circulatory Links between Immune Checkpoint Inhibitors and Cerebral Small Vessel Disease: Integration of Single Cell RNA-Sequencing and Multiomic Mendelian Randomization

Abstract

Background: Immune checkpoint inhibitor (ICI) exposure is associated with neurotoxic adverse events that vary in incidence rates and severity. Many forms of these neurotoxicities share common traits with cerebral small vessel disease (CSVD), suggesting a possible link between ICI treatment and CSVD burden. However, investigations into this pathway have been limited. **Methods:** We leveraged single-cell RNA-sequencing data obtained from clear cell renal carcinoma patients who were (n=4) or were not (n=3) exposed to ICI treatment. Differentially expressed genes were identified specifically in endothelial cells to target the endothelium as a link between ICI exposure and CSVD. The set of differentially expressed genes were subsequently used to design exposures in multiomic Mendelian randomization analyses with CSVD outcomes. Both gene expression and methylation omics levels were entered as exposures using expression quantitative trait loci and methylation quantitative trait loci. Genes associated with CSVD markers in both levels were subsequently selected to identify potential therapeutics with opposing transcription signatures. **Results:** Single-cell RNA-seq analysis of renal vascular endothelial cells from clear cell carcinoma patients (untreated n=3, ICI-treated n=4) identified 1085 differentially expressed genes (DEGs) after ICI exposure, relating to pathways involving oxidative phosphorylation, protein folding chaperones, and cellular redox homeostasis. Five genes (*Cd55*, *Cltb*, *Htra1*, *Nme4*, *Xrcc6*) were associated with CSVD markers at both genomic

and epigenetic levels in Mendelian randomization analysis, highlighting biological mechanisms including DNA damage repair and complement/coagulation cascades. Finally, pharmacotranscriptomic analyses suggested the strongest therapeutic potential was observed in statins.

Discussion: Our findings from the present study provide multiomic evidence supporting an association between ICI exposure and CSVD. These results were extended to explore potential pharmacological approaches, which identified statins as a strong possibility.

Introduction

Targeting the anti-tumor immune response through administration of immune checkpoint inhibitors (ICI) has provided treatment opportunities for many cancer tumor types, improving cancer control five-fold in some cases.¹ The ever-expanding list of successful trials, such as KEYNOTE-564 (NCT03142334) in renal-cell carcinoma² or the Impower150 trial (NCT02366143) in metastatic non-squamous non-small-cell lung cancer³, underscore their growing contributions across a variety of oncology settings. As the rate of ICI prescription increases⁴, so does the role of immune-vascular oncology research in determining the causes and consequences of ICI-related adverse effects on the cardiovascular system.⁵ As pointed out by Cronin et al earlier this year⁶, we are in “a new era of immunotherapy survivorship” that brings not only the hope of improving cancer outcomes, but also the reminder to consider the integrated physiological consequences of anti-cancer treatment.

One of the most severe adverse side-effects of ICI exposure is neurotoxicity.⁷ While incidences tend to be rare⁸, some reports suggest mortality rates ranging from 8% to 15% mortality rate after severe neurotoxic events.^{9,10} The clinical presentations vary widely, indicating the possibility of multiple etiological mechanisms¹¹; however, emerging case reports^{12,13} and biomarker discovery studies¹⁴⁻¹⁶ have implicated substantial overlaps with cerebral small vessel disease (CSVD). CSVD is a pathology primarily affecting the small penetrating arterioles of the cerebrovasculature detected on magnetic resonance imaging^{17,18}, associated with numerous physiological¹⁹ and clinical sequelae.²⁰ An understanding of CSVD in the neurotoxicity associated with ICI treatment would likely advance monitoring and therapeutic strategies, yet findings remain limited for numerous reasons despite the vital importance.

The same publication that detailed the “new era of immunotherapy survivorship” also discussed several obstacles to studying adverse events in the short and long-term timeframes.⁶ Predominant amongst these obstacles are the restricted adverse event reporting windows in clinical trials (typically ~90 days) and biases inherent to observational or retrospective studies.²¹ Thus, in an effort to guide future prospective or clinical trials in this area, unique approaches are necessary such as using Mendelian randomization^{22,23}. In the present study, we aimed to first identify vascular cell-specific effects of ICI treatment using single-cell RNA-sequencing data collected from patients who were or were not exposed to monoclonal antibodies targeting programmed death 1 (PD-1). Genes that were differentially expressed between ICI conditions were selected as a “gene set” that guided subsequent analyses. The gene set from single-cell RNA-sequencing was integrated with genetic and epigenetic Mendelian randomization analyses to estimate the effects of ICI-related vascular cell alterations on CSVD. Finally, vascular genes supported by robust evidence (i.e., found to be significant in both gene expression and methylation expression Mendelian randomization analyses) were selected for further exploration of potential therapeutic routes that may reverse the vascular effects of ICI treatment. The goals of the present work are two-fold: 1) to provide initial insight into possible mechanisms linking ICI exposure to CSVD through the effects ICIs have on the vasculature, and 2) to inform future investigations focusing on both understanding the etiology of neurotoxicity after ICI use and means to mitigate or treat the neurotoxicity.

Methods

Ethics Statement and Study Overview

The design, execution and reporting of this study were conducted in adherence with the Strengthening the Reporting of Observational studies in Epidemiology – Mendelian Randomization (STROBE-MR) guidelines.²⁴ All data used herein were sourced from published and publicly available databases that obtained ethical approval and participant informed consent; therefore, approval by local institutional research boards at Kansas State University was not required. All data and analyses can be found in this study or by reasonable request to the authors.

In this study, we aimed to identify biological pathways and processes contributing to the risk of CSVD in patients who have received ICI treatments, alongside the identification of possible therapeutic options. A visual schematic overview of the study design is presented in Figure 5-1.

scRNA-seq Analysis of Patient Tissue

Data source.

We used scRNA-seq data from the Zenodo database to evaluate differentially expressed genes (DEGs) between ICI treatment conditions in patients with clear cell carcinoma. Tumor and adjacent non-tumor bulk tissue samples were obtained in the study from Bi et al²⁵ and pre-processed as part of a publicly available dataset from Gondal et al.²⁶ The tissue samples were collected from untreated patients (n=3) and treated patients (n=4); the treated patients received some combination of anti-PD-1 blockade, anti-CTLA-4 blockade, and/or VEGF inhibitors. Patient characteristics are detailed in Table 5-1. Sample collection details can be found in the original publication.²⁵

Table 5-1. Characteristics of patients who contributed tissue samples for the single-cell RNA sequencing data used in the present study. Data originally collected by Bi et al.²⁵

Patient ID	Age (years)	Sex	Cancer Type	AJCC Stage	ICI Type	Response to ICI
<i>No Immune Checkpoint Inhibitors</i>						
P76	68	Female	Clear cell renal carcinoma	IV	N/A	N/A
P90	71	Female	Clear cell renal carcinoma	I	N/A	N/A
P916	61	Male	Clear cell renal carcinoma	IV	N/A	N/A
<i>Treated with Immune Checkpoint Inhibitors</i>						
P55	57	Male	Clear cell renal carcinoma	IV	Anti-PD-1	PR
P912	60	Male	Clear cell renal carcinoma	IV	Anti-PD-1	NE
P913	47	Male	Clear cell renal carcinoma	IV	Anti-PD-1	PR
P915	58	Male	Clear cell renal carcinoma	IV	Anti-PD-1 / Anti-CTLA-4	SD

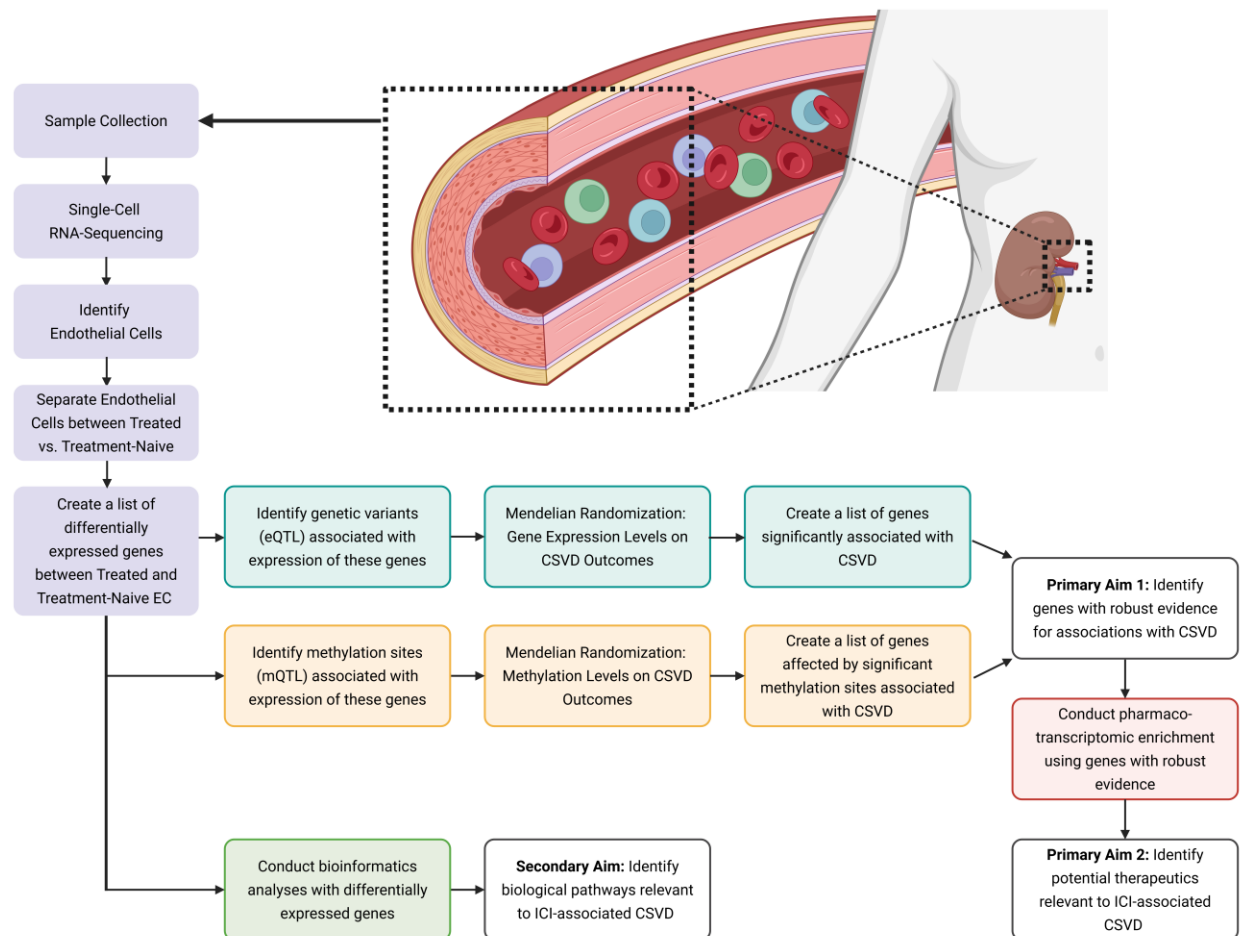


Figure 5-1. An overview schematic of the study design. ICI, immune checkpoint inhibitor; CSVD, cerebral small vessel disease. Figure created with BioRender.

Data processing.

Data processing and analysis were conducted using the *Seurat* package (version 5.2).^{27,28} To ensure data quality, cells with >20% mitochondrial gene content or <5% ribosomal RNA expression were excluded. The *DoubletFinder* algorithm²⁹ was used to remove any doublets (more than one cell per bead). Further filtering removed any non-malignant cell types that had less than 20 cells.²⁶ Subsequently, data were normalized and scaled using the *NormalizeData* and *ScaleData* functions. Dimensionality reduction and Louvain unsupervised clustering were performed using the first 20 principal components. Cell types were identified using cell-specific molecular signatures through the *Vision* algorithm³⁰ alongside CellMarker 2.0.³¹ Using patient clinical metadata, differential expression analyses were performed between treatment-naïve and ICI-treated conditions within cell types. To specifically investigate ICI-induced vascular changes, endothelial cells were selected as the cell-type of primary interest since endothelial cells act as the interface between circulating biological or pharmacological factors and organ tissue.^{32,33} Furthermore, endothelial dysfunction and impaired vascular reactivity are implicated as key factors in the early pathogenesis of CSVD.³⁴ Therefore, the endothelial cell cluster was deemed most relevant to investigating the effects of ICI treatment on the risk of CSVD in the face of limitations of not having cerebral tissue-specific analyses available. Markers used to identify the endothelial cell cluster are provided in Table 5-2.

Statistical analysis

The Wilcoxon rank sum test was used to compare genes between patient samples with or without ICI treatment. Differentially expressed genes within the endothelial cell type were identified at Bonferroni-adjusted P-values <0.05 to account for multiple testing.

Table 5-2. The top 15 markers used to identify the endothelial cell subcluster from the single-cell RNA-sequencing analysis on bulk tumor and non-tumor tissue derived from Bi et al. The “Proportion Expressed” column is the proportion of cells in the endothelial cell cluster that expressed the marker compared to the proportion of all cells in the other clusters that expressed the marker; p-values (adjusted for multiple comparisons) are provided. EC, endothelial cells; OC, other cells; PMID, PubMed identification number.

Marker ID	Marker Name	Proportion Expressed (EC:OC)	Adjusted P-value	Publication Reference PMIDs
EGFL7	EGF like domain multiple 7	0.827 : 0.075	$<1.00 \times 10^{-100}$	30789893, 32483223
VWF	von Willebrand factor	0.755 : 0.007	$<1.00 \times 10^{-100}$	29230012, 35168605, 33936064, 34687145
IGFBP7	insulin like growth factor binding protein 7	0.673 : 0.170	$<1.00 \times 10^{-100}$	34775482
PLVAP	plasmalemma vesicle associated protein	0.664 : 0.005	$<1.00 \times 10^{-100}$	32754283, 30093597
IFITM3	interferon induced transmembrane protein 3	0.659 : 0.360	4.99×10^{-42}	32236824
CRIP2	cysteine rich protein 2	0.600 : 0.091	$<1.00 \times 10^{-100}$	32236824
FLT1	fms related receptor tyrosine kinase 1	0.595 : 0.008	$<1.00 \times 10^{-100}$	34921160, 32754283
RAMP2	receptor activity modifying protein 2	0.568 : 0.003	$<1.00 \times 10^{-100}$	34921160, 30789893
CLDN5	claudin 5	0.527 : 0.005	$<1.00 \times 10^{-100}$	33936064
CDH5	cadherin 5	0.495 : 0.001	$<1.00 \times 10^{-100}$	34843404
VWA1	von Willebrand factor A domain containing 1	0.414 : 0.036	$<1.00 \times 10^{-100}$	33406409
TEK	TEK receptor tyrosine kinase	0.327 : 0.001	$<1.00 \times 10^{-100}$	32107344
TJP1	tight junction protein 1	0.286 : 0.023	$<1.00 \times 10^{-100}$	32236824
NOS3	nitric oxide synthase 3	0.127 : 0.003	$<1.00 \times 10^{-100}$	35168605
ABCG2	ATP binding cassette subfamily G member 2 (JR blood group)	0.086 : 0.002	$<1.00 \times 10^{-100}$	32236824

Pathway Enrichment Analysis of Differentially Expressed Genes

Differentially expressed genes identified as significant from analyses were selected as inputs for bioinformatics analyses. Only genes significant at a Bonferroni-adjusted $p < 0.05$ were selected from scRNA-seq analyses. Protein-protein interaction maps were generated using Cytoscape (version 3.10.3) and the String database plugin (version 10.0). Enriched Gene Ontology (GO) Biological Processes³⁵, Reactome Pathways³⁶, and Kyoto Encyclopedia of Genes and Genomes (KEGG) pathways were identified.³⁷ Pathways were visualized with GeneMania.³⁸ To further facilitate biological interpretation, the functionally related GO pathway terms were clustered using the ClueGO plugin (version 2.5.10) in Cytoscape.³⁹ Only genes with a $\log_2(\text{fold-change}) \geq 2.0$ were imported into ClueGO. Network settings were GO Tree intervals between 3 and 10, the minimum number of genes involved per pathway set at 4, and at least 15% coverage of genes with associated terms. ClueGO cluster significance was adjusted using the Bonferroni step-down correction.

Endothelial Cell-Based Multiomic Associations with CSVD

Gene Expression Exposures

Gene expression quantitative trait loci (eQTL) connect genetic variants to the expression of specific genes across different tissue sites. To investigate gene expressions associated with CSVD, cis-variants (i.e., variants within $\pm 100\text{kb}$ of target gene region) significantly associated with the expression a specific gene in whole blood were extracted from the Genotype Tissue Expression (GTEx v10) database⁴⁰ to form gene-specific eQTL. In sensitivity analysis, eQTL were also created for coronary artery tissue to determine the robustness of associations in another vascular tissue type. Variants were allowed to be in weak linkage disequilibrium ($r^2 < 0.2$, window

10000kb) to increase statistical power of analyses. The linkage disequilibrium reference used in the present study was the 1000 Genomes reference panel.⁴¹ Instrument strength for each exposure was assessed using the F-statistic, calculated as $[F = (R^2 \times (N-2))/(1-R^2)]$, where R^2 is the squared correlation of the exposure relationship and N is the sample size.⁴²⁻⁴⁴ The overall F-statistic for each genetic instrument was taken as the average of all included individual genetic variant F-statistic values. An F-value > 10 indicates sufficient instrument strength. Further details on variant selection in the GTEx database are provided in Supplementary Methods (Appendix C).

Methylation Exposures

Similar to eQTL, methylation quantitative trait loci (mQTL) quantitatively link genetic variants to methylation levels at specific DNA sites. The Accessible Resource for Integrated Epigenomics Studies (ARIES) project⁴⁵ generated epigenetic data on blood samples from 1,018 participants of the Avon Longitudinal Study of Parents and Children (ALSPAC) study.⁴⁶ Cis-variants associated with cytosine guanine dinucleotide (CpG) site methylation levels ($p < 1 \times 10^{-7}$, $r^2 = 0.001$, window 10000kb) were extracted to form methylation site-specific mQTL. Statistical criteria for variants were selected to be consistent with the ARIES study methods. Only cis-variants detected for both sexes were incorporated in current analyses. Instrument strength for each methylation exposure was assessed using the F-statistic, calculated using the same approach as described for gene expression exposures. Further details on variant selection in the ARIES database are provided in Supplementary Methods (Appendix C).

CSVD Outcomes

Imaging markers and clinical consequences of CSVD were selected as the outcome variables for the present study, including white matter hyperintensity (WMH) volume, perivascular spaces burden (PVS), cerebral microbleeds (CMB), and small vessel strokes (SVS). WMH data was obtained from a previously published GWAS⁴⁷ conducted using the UK Biobank cohort, which has been previously described elsewhere.^{48,49} Genetic associations with PVS were obtained from a study combining 18 population-based cohorts.⁵⁰ Data for CMB was extracted from an Alzheimer's Disease Neuroimaging Initiative study incorporating 11 population-based studies and 3 case-control or control-only stroke cohorts.⁵¹ SVS summary GWAS statistics were derived from a meta-analysis of >1 million individuals of European descent.⁵² Cohort characteristics are presented in Table 5-3, and detailed information CSVD marker assessment methods can be found in the respective publications.^{47,50-52}

Mendelian randomization

In brief, MR begins with identifying genetic variants associated with a selected exposure trait; these variants are used as a genetic instrumental variable. Using genetic summary statistics for an outcome trait, the association between the selected exposure and the target outcome can be assessed. If the core assumptions of MR are met, then this approach results in an estimate of the causal relationship under investigation.⁵³ There are three core assumptions: 1) relevance – the instrumental variable is associated with the exposure of interest; 2) independence – the instrumental variable is not related to any confounders, and 3) exclusion restriction – the instrumental variable is not related to the outcome measure.⁵⁴ Further description of MR theory is provided in the Supplementary Methods (Appendix C).

Table 5-3. Characteristics of the genome-wide association studies (GWAS) used in the present investigation.

Extracted Variable	Source GWAS	Predominant Ethnicity	Sample Size	Adjustments in Model ^a
<i>Exposures</i>				
Gene Expression – Whole Blood	PMID: 32913098	European	943	Sex, PCs, PEER ^b factors, sequencing platform, sequencing protocol.
Gene Expression – Coronary Artery	PMID: 32913098	European	943	Sex, PCs, PEER factors, sequencing platform, sequencing protocol.
Methylation – Whole Blood	PMID: 25869828	European	1018	Gestational age, sex, birth weight, parity, maternal age, maternal smoking, child delivery method.
<i>Primary Outcomes</i>				
White Matter Hyperintensity	PMID: 32358547	European	18,381	Age, sex, genotyping array, UK Biobank site, first 10 PCs, MRI head motion.
Perivascular Spaces	PMID: 37069360	European	40,095	Age, sex, intracranial volume, study site, PCs.
Cerebral Microbleeds	PMID: 32913026	European	25,862	Age, sex, PCs.
Small Vessel Stroke	PMID: 36180795	European	1,614,080	Age, sex, PCs, study-specific covariates.

^a PCs, principal components used to adjust for population stratification.

^b PEER, probabilistic estimation of expression residuals. A method used to identify a set of covariates based on sample size.

In the present study, MR was implemented both at the levels of gene expression and methylation. Differentially expressed genes in scRNA-seq analysis of endothelial cells were selected, and both gene expression data and methylation data for those genes were identified if available. The set of differentially expressed genes with gene expression and/or methylation data were entered into MR models with the CSVD markers as outcomes.

MR statistical analysis

Exposure-outcome associations were assessed using inverse-variance weighted methods, or with Wald ratio methods for exposure variables with only 1 genetic variant. To account for multiple testing within each CSVD marker, p-values were adjusted using the Benjamini-Hochberg method with a false discovery rate (FDR) <0.05. Analyses were run in RStudio (version 2024.12.0) using the *TwoSampleMR* package.⁵⁵ Results are presented as beta and 95% confidence intervals (95% CI) for continuous outcomes (WMH), or odds ratio (OR) and 95% CI for binary outcomes (PVS, CMB, SVS). These estimates are given per additional copy of the effect allele.

Identifying Potential Pharmacological Interventions

Differentially expressed genes from scRNA-seq analysis associated with at least one marker of CSVD in both gene expression and methylation MR analyses were selected as inputs for pharmaco-transcriptomics. These genes were queried against the Connectivity Map⁵⁶, a database of perturbation expression signatures based on human cell lines. A reduced statistical threshold (FDR<0.1) was implemented to ensure a sufficient number of differentially expressed genes. A total of 171 perturbation signature classes – grouped by pharmacological or biological

mechanisms of action – were queried. Embedded tests in the Connectivity Map assess each signature class against the input data, resulting in a normalized connectivity score ranging from -1 (reference signature is completely opposite of the input query) to +1 (reference signature completely mirrors the input query).⁵⁶ Connectivity Map analyses were conducted using the web tools (version 1.1.1.43) along with RStudio (version 2024.12.0). Drug classes identified through Connectivity Map query were subsequently described using the online webtool, DrugBank.⁵⁷

Results

ICI-induced Differences in scRNA-seq of Patient Tissue

Overview of patient cohort

As described in detail in Table 5-1, samples were collected from patients either treated with immune checkpoint inhibitors (n=3) or not treated with ICI (n=4) for renal cell carcinoma. Treatment-naïve samples were collected from 1 man and 2 women (66.7 years, range: 61-71 years). Two patients were stage IV and one patient was stage I, based on American Joint Committee on Cancer staging criteria. ICI-treated patient samples were not collected from any individuals who had contributed treatment-naïve samples. ICI-treated patient samples were collected from 4 males (55.5 years, range: 47-60 years) who all had stage IV renal cell carcinoma. All ICI-treated patients contributing tissue had received anti-PD-1 blockade therapy, and samples were collected ~2 months (range: 1-3 months) after cessation of ICIs.

Differentially expressed genes and enriched pathways

Endothelial cells were identified based on cluster cell markers and stratified by treatment exposure, resulting in 74 treatment-naïve endothelial cells and 146 endothelial cells treated with anti-PD-1 (Figure 5-2; Appendix Figure C-1). A total of 1085 differentially expressed genes were identified in endothelial cells with or without ICI treatment, the majority of which were upregulated with exposure to ICIs (Figure 5-3A). Several of the top GO Biological Processes, ranked by FDR, indicated alterations in metabolism (Figure 5-3B). Major genes encoding for cytochrome proteins (*Mt-cyb*, *Mt-co2*) or other portions of the electron transport chain (*Mt-nd1*, *Atp5f1d*, *Ndufb7*) were differentially regulated, resulting in enriched pathways related to oxidative phosphorylation (GOBP:0006119) and cellular respiration (GOBP:00453333). This

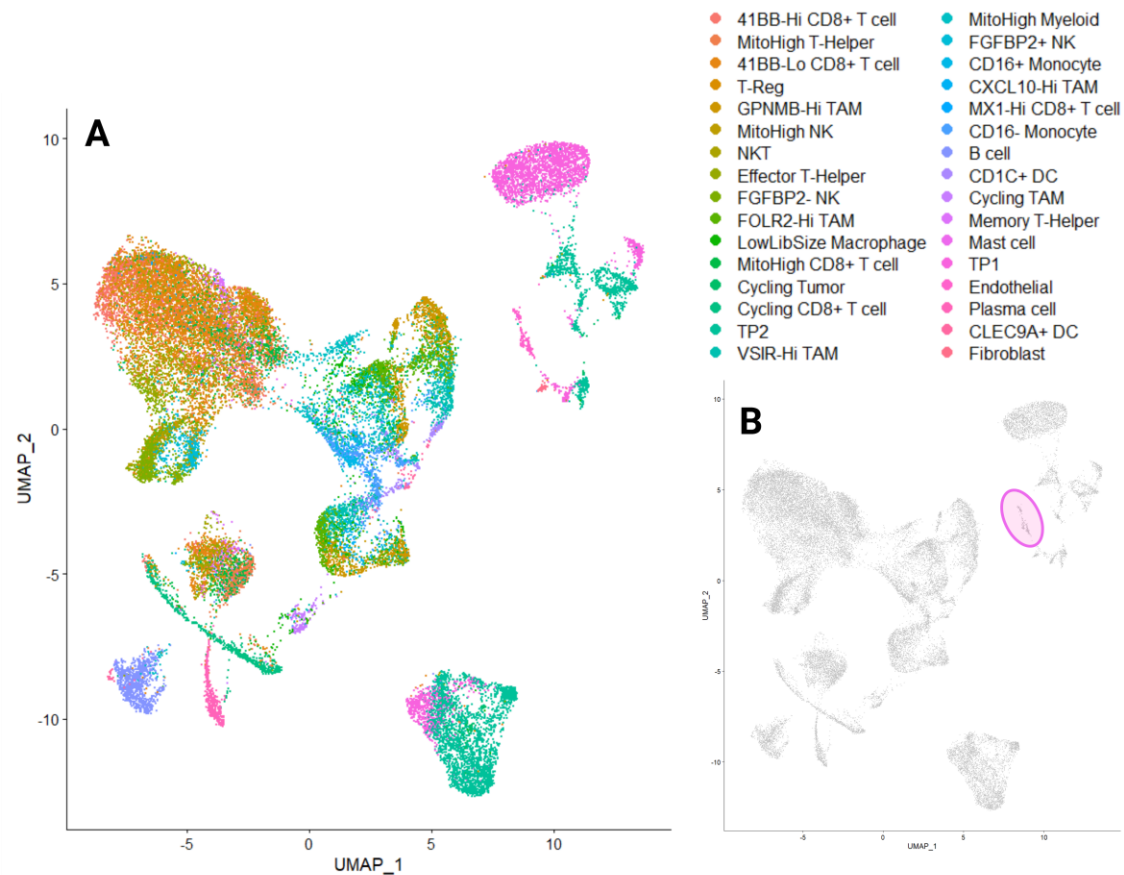


Figure 5-2. Cells from the single-cell RNA-sequencing data were clustered according to standard cell markers. The resulting clusters are presented using a uniform manifold projection and approximation (UMAP) plot (**A**). For clarity, the location of the endothelial cell cluster is highlighted (**B**).

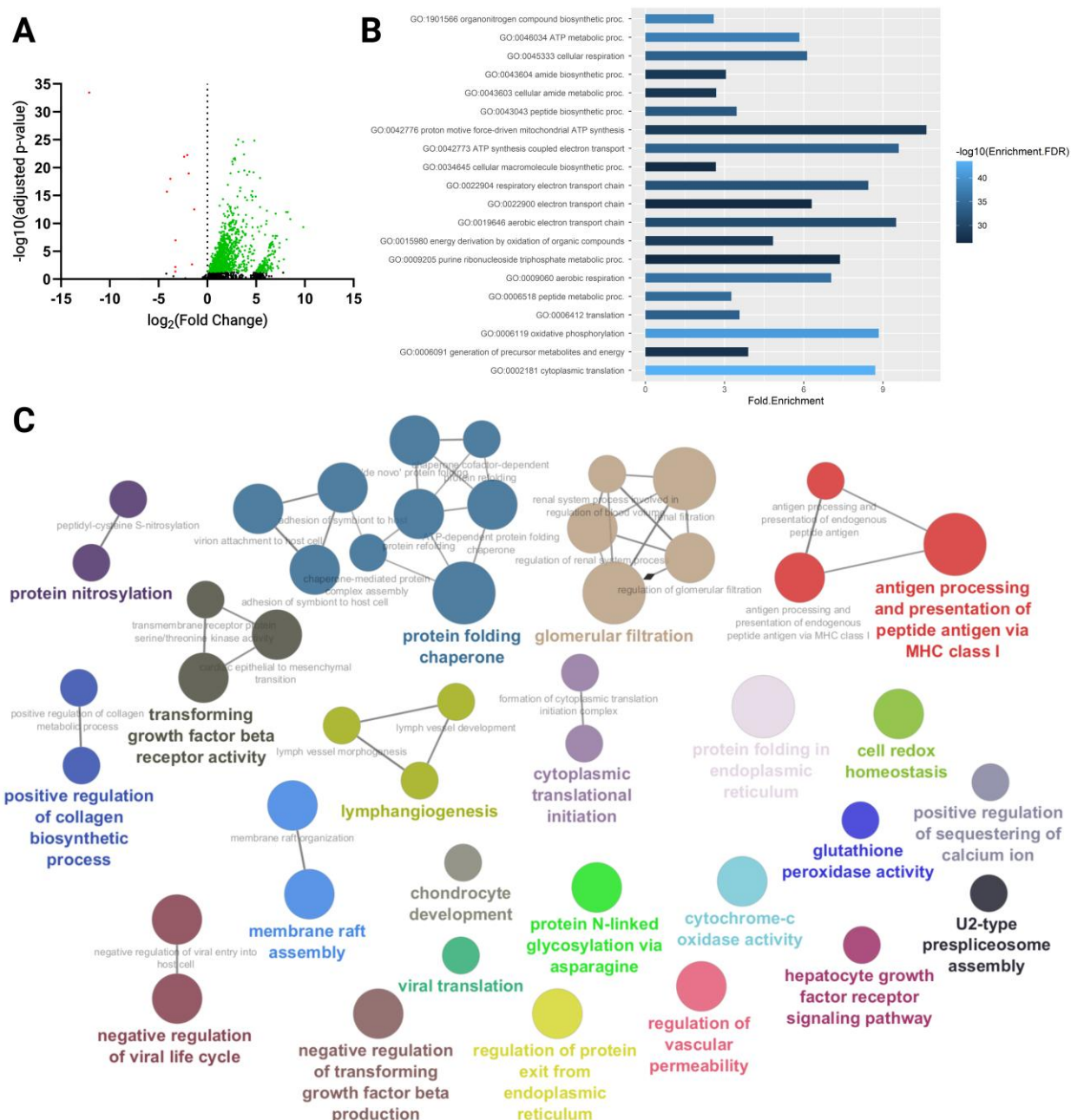


Figure 5-3. (A) Volcano plot depiction of endothelial cell-specific genes that were upregulated (green) or downregulated (red) after immune checkpoint inhibitor exposure. (B) Gene Ontology Biological Process (GOBP) pathways significantly enriched when comparing differentially expressed genes between control and immune checkpoint inhibitor-exposed endothelial cells. (C) Enriched pathways were clustered using the ClueGO software plugin as part of the Cytoscape suite of programs. Significant clusters are shown (C); statistics are reported in Appendix Table C-1.

was supported by enrichment analyses in KEGG and Reactome (Appendix Figures C-2, C-3). Interestingly, pathways related to cerebral diseases, such as Alzheimer's disease or Huntington's disease, were also enriched by the presence of genes implicated in oxidative stress (*Sod1*), cell structure and adhesion (*Tubb*, *Adrm1*) and cell transport processes (*Hspa5*, *Cav1*, *Slc25a5*).

Clustering analyses resulted in 23 distinct clusters that were largely consistent with pathway enrichment analyses. ClueGO analyses indicated that 19.6% of genes were involved in protein folding chaperones, 6.5% in transforming growth factor beta receptor activity, 4.4% in membrane raft assembly, 2.2% in cellular redox homeostasis and 2.2% in cytochrome c oxidase activity (Figure 5-3C; Appendix Table C-1).

Gene Expression Levels Associated with CSVD

Genetic eQTL instruments were analyzed in up to 619 differentially expressed genes identified from patient tissue analyses. All 619 instruments were available for the PVS outcome; in the remaining outcomes, <8% of instruments had to be excluded due to nonmatching genomic summary statistics in the outcome variable (Appendix Tables C-2, C-3). All genetic instruments demonstrated sufficient strength (average F-statistic: 53.5, range: 12.4 – 2282.4).

In MR analyses, a total of 38 unique genes were significantly associated with at least one marker of CSVD (Figure 5-4). Two genes (*Hla-c*, *Hla-drb1*) were associated with multiple CVSD outcomes – both WMH and PVS. Overall, the slight majority of gene-outcome pairs (n=22, 55%) of the significant individual models were positively related to a greater CSVD burden.

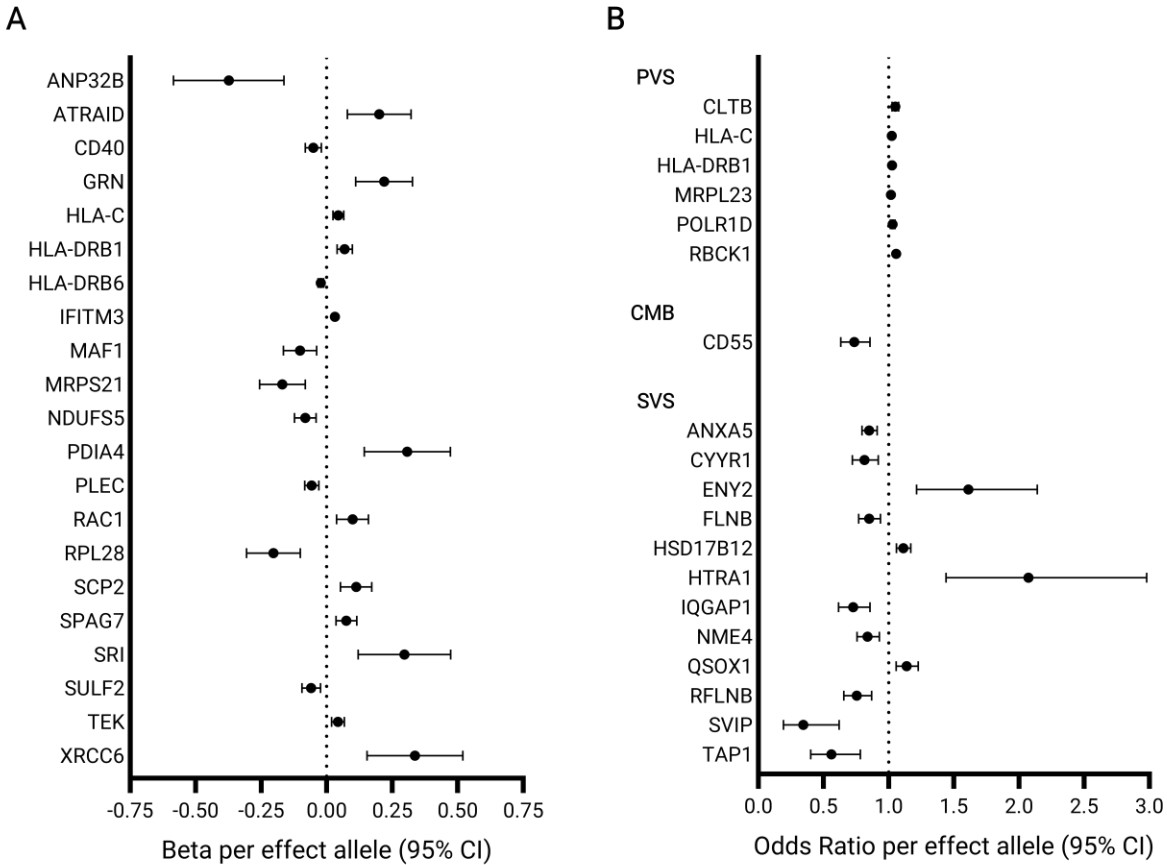


Figure 5-4. Gene expression-level results of Mendelian randomization analyses with imaging markers of cerebral small vessel disease outcomes. Panel **A** depicts results for white matter hyperintensity (WMH) volume. Panel **B** depicts results for perivascular space (PVS) burden, cerebral microbleeds (CMB), and small-vessel stroke (SVS). Results are presented for inverse variance weighted or Wald (if the instrument only had 1 variant) methods. 95% CI indicates that the plotted error bars show the 95% confidence interval.

Sensitivity analyses were conducted using eQTL in coronary artery tissue (instead of whole blood) at a nominal $p < 0.05$. There were notably less significant gene-outcome associations in the coronary artery analyses after adjusting p-values for multiple testing (Supplementary Table C-4); however, the results were largely consistent with our primary findings. Several genes were supported with evidence from both whole blood and coronary artery eQTL, such as *Hla-c*, *Hla-drb1*, *Iqgap1* and *Ndufs5*. Importantly, the direction of effect was consistent across both eQTL analyses in the majority (83.5%) of cases.

Methylation Levels Associated with CSVD

In MR analyses, 531 methylation sites (mQTL) were eligible for testing in WMH; PVS (1.1%), CMB (1.3%) and SVS (4.1%) had some excluded instruments due to nonmatching genomic summary statistics in the outcome variable. This corresponded to 267 unique genes targeted by the methylation (mQTL) sites that were tested for WMH and PVS, 268 for CMB, and 262 for SVS (Appendix Tables C-5, C-6). All exposure instrument variables demonstrated sufficient strength assessed with F-statistics (mean: 146.9, range: 26.7 – 1407.5).

There were a total of 52 methylation sites associated with at least one marker of CSVD, with an even split (50.0%) of associations positively related to CSVD burden (Figure 5-5). Seven methylation sites were associated with ≥ 2 CSVD markers; two sites (*cg16958793*, *cg00472373*) were associated with three markers. A total of 38 unique genes were linked to the significant methylation sites. Six of those genes (*Cmip*, *Htra1*, *Bmpr2*, *Arpc4*, *St6gal1*, *Cdkn1a*) were significantly related to multiple CSVD outcomes.

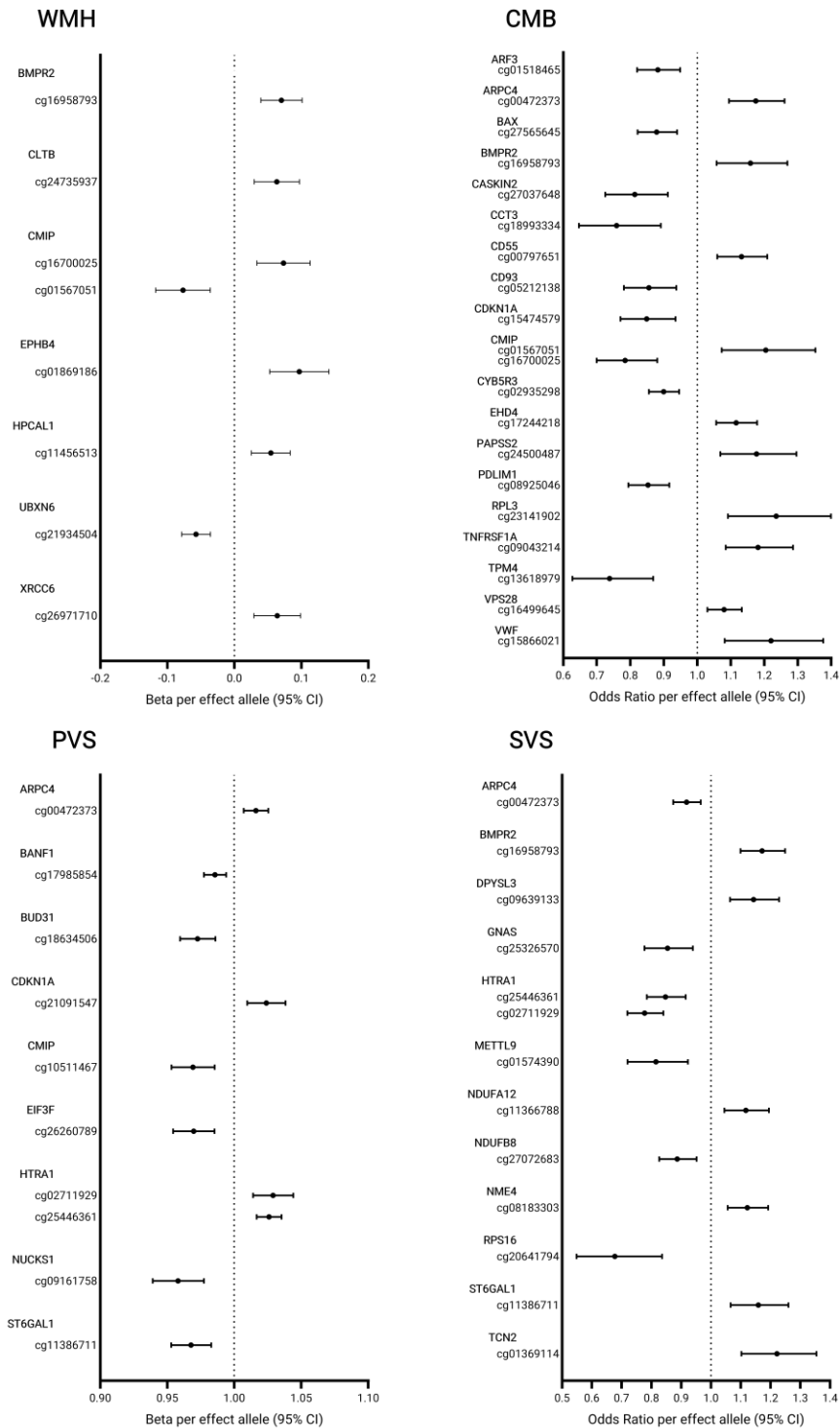


Figure 5-5. Methylation-level results of Mendelian randomization analyses with imaging markers of cerebral small vessel disease outcomes. Results are presented for inverse variance weighted or Wald (if the instrument only had 1 variant) methods. 95% CI indicates that the plotted error bars show the 95% confidence interval. WMH, white matter hyperintensity volume; PVS, perivascular space burden; CMB, cerebral microbleeds; SVS, small vessel stroke.

Integrated Evidence from Multiomic Analyses

Shown in Figure 5-6A, integrating genes from the eQTL and mQTL analyses resulted in five shared, high-priority targets: *Cd55* (cluster of differentiation 55 molecule), *Cltb* (clathrin light chain B), *Htra1* (high temperature requirement A serine peptidase 1), *Nme4* (NME/NM23 nucleoside diphosphate kinase 4), and *Xrcc6* (X-ray repair cross complementing 6). Gene loci and surrounding gene encoding regions are presented in Appendix Figures C-4 through C-8. Pathway enrichment of these genes (allowing for up to 10 additional interacting molecules) predominantly implicated DNA damage repair pathways (GOBP:0006302, FDR $p=9.9 \times 10^{-5}$; GOBP:0006303, FDR $p=3.0 \times 10^{-4}$) and activation of complement and coagulation cascades (GOBP:0006956, FDR $p=0.036$). The complement and coagulation pathways were supported by evidence from KEGG (hsa04610, FDR $p=0.011$) and Reactome (HSA-977606, FDR $p=0.018$) databases. The protein-protein interaction map is presented in Figure 5-6B.

Pharmaco-transcriptomic Enrichment

We used a reduced threshold (FDR $p < 0.10$) to integrate results from MR analysis of eQTL and mQTL for pharmaco-transcriptomic analysis. The 5 genes above (*Cd55*, *Cltb*, *Htra1*, *Nme4*, and *Xrcc6*) were included, as were 8 additional genes (*Arf3*, *Ephb4*, *Ifitm3*, *Mvp*, *Ndufb8*, *Qsox1*, *Scp2*, and *Ssbp4*). This list of 13 genes (all upregulated by ICI treatment in endothelial cells based on scRNA-seq results) were queried in the Connectivity Map database against 2385 combinations of pharmacological classes tested in different human cell lines. We ranked significant results (FDR $p < 0.05$) separately by positive (similar directions of results from this study and reference perturbation) and negative (opposing directions of results from this study and reference perturbation) connectivity score.

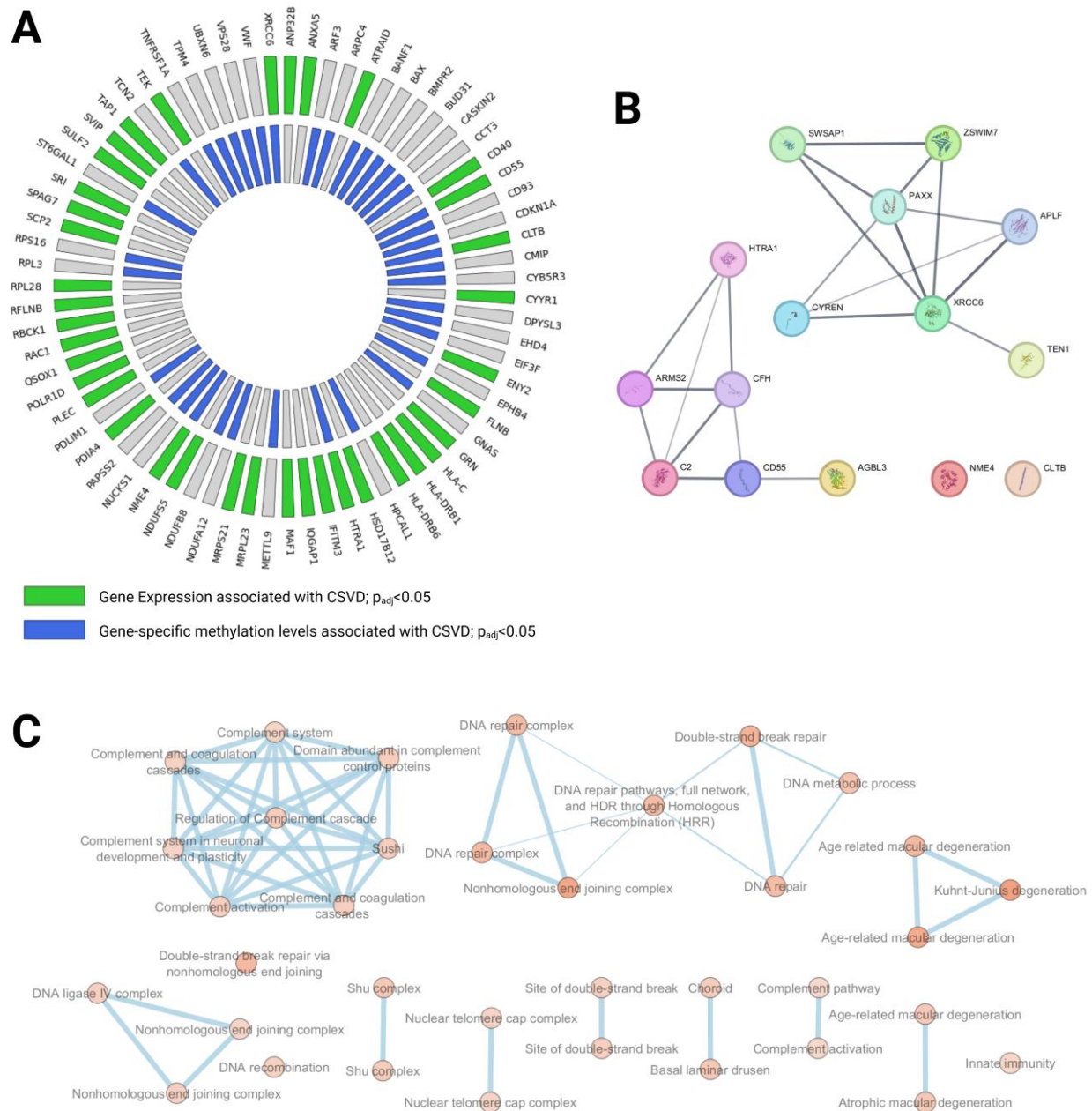


Figure 5-6. Integration of evidence across multiple omics levels. (A) Circle plot depicting genes that were significantly associated with cerebral small vessel disease at the genomic (green) and/or methylomic (blue) levels. (B) Protein-protein interaction mapping of the genes that were significantly associated with cerebral small vessel disease in both omics and were therefore considered “robust”. (C) Pathway enrichment results for the “robust” genes associated with cerebral small vessel disease.

The top 10 significant, opposing results are shown in Table 5-4. Notably, the top hit for negative connectivity scores was a standard pharmaceutical in cardiovascular risk prevention – 3-hydroxy-3-methylglutaryl-CoA reductase (HMGCR) inhibitors, or statins (Connectivity Score: -0.72, FDR $p=2.2 \times 10^{-16}$). Several other classes with negative scores were investigational drugs without regulatory approval (Table 5-3). Pharmacological classes with positive connectivity scores consisted largely of anti-cancer therapeutics (Appendix Table C-7), as well as selective estrogen receptor modulators (FDR $p=0.0042$) and vitamin D receptor agonists (FDR $p=0.046$).

Table 5-4. The top 10 (ranked by connectivity score) pharmacological perturbation signatures opposing the effects of immune checkpoint inhibitor treatment on endothelial cell gene expression in the gene set robustly associated with cerebral small vessel disease.

Pharmacological Class	Cell Types Tested	Raw Connectivity Score	Adjusted P-value	Regulatory Status
HMGR Inhibitors	HEPG2	-0.72	2.2×10^{-16}	FDA-approved
DNA Inhibitors	HEK293	-0.69	0.004	FDA-approved
ATPase Inhibitors	ASC	-0.66	2.2×10^{-16}	Investigational
XIAP Inhibitors	A375	-0.65	0.0011	Investigational
Aurora Kinase Inhibitors	HCC515	-0.63	2.2×10^{-16}	Investigational
GABA Receptor Antagonists	HCC515	-0.57	0.0098	FDA-approved
HSP Inhibitors	HCC515	-0.47	0.021	Investigational
JAK Inhibitors	HA1E	-0.43	0.048	FDA-approved
Protein Synthesis Inhibitors	PC3	-0.36	0.0018	FDA-approved
Ubiquitin-specific Protease Inhibitors	N/A	-0.33	0.037	FDA-approved

Discussion

In the present study, we integrated findings from scRNA-seq, gene expression (eQTL) and methylation (mQTL) analyses to 1) explore links between the effects of ICIs on endothelial cells and the risk of CSVD, and 2) identify potential therapeutic approaches to mitigate ICI-related CSVD. Our results indicated 5 genes that were consistently associated with one or more CSVD markers: *Cd55*, *Cltb*, *Htra1*, *Nme4*, and *Xrcc6*. Furthermore, including these 5 genes and 8 more genes at a less strict statistical threshold in a query targeting pharmacological routes identified possible therapeutic options, such as statins. Taken in sum, our study provides multiomic evidence supporting vascular and circulation-specific pathological links between ICI treatment and CSVD as well as possible means of mitigating this phenomenon.

The gene implicated most frequently across CSVD markers was *Htra1*, which has been demonstrated in several studies to contain mutations that drive a rare familial form of CSVD called cerebral autosomal recessive arteriopathy with subcortical infarcts and leukoencephalopathy (CARASIL).^{58,59} However, emerging evidence suggests that polymorphisms in the *Htra1* gene region may also lead to sporadic, non-familial forms of CSVD.⁶⁰ The HTRA family of proteins act as both chaperones and serine proteases⁶¹ – HTRA1 degrades components of the extracellular matrix such as fibronectin and type II collagen, playing a key role in vascular integrity⁶², inflammation, and immune cell infiltration.⁶³ HTRA1 also mediates transforming growth factor beta (TGF- β) signaling, which is believed to underly HTRA1-specific CSVD.⁶⁴ Interestingly, pre-clinical models of CSVD have suggested that HTRA1 protein expression was increased only in animal models of cerebral amyloid angiopathy, not in models of hypertensive CSVD.⁶⁵ This finding aligns with reports that HTRA1 variants are associated with CSVD independent of hypertension, even in sporadic CSVD.⁶⁰ While not

apparent in the present approach, literature supports an association between *Htra1* mutations and local cerebral arteriosclerosis, regardless of whether the mutations are homozygous or heterozygous.⁶⁶ Further research is needed to better understand the role of *Htra1* in sporadic CSVD.

Three of the five key genes identified (*Htra1*, *Nme4*, *Xrcc6*) have been implicated as contributors to cellular senescence. Levels of HTRA1 protein appear to regulate cell cycle processes; for example, upregulation of HTRA1 is associated with accelerated cellular senescence.⁶⁷ While the exact mechanisms are not fully known, evidence in an HTRA1 loss-of-function model may compromise the function of cell cycle checkpoints as they relate to DNA damage.⁶⁸ This overlaps with senescence-related properties of both the *Nme4* and *Xrcc6* - both have been linked to DNA damage and DNA repair pathways^{69,70}, albeit via different routes. The *Xrcc6* gene encodes Ku70, part of the Ku heterodimer that aids in repairing DNA through non-homologous end joining.⁷¹ Impairment in the *Xrcc6* gene results in cell death characterized by severe telomere shortening⁶⁹, a stereotypical presentation of accelerated cellular aging and cellular senescence.^{72,73} *Nme4* is also implicated in telomere length and cellular senescence. However, as it encodes a mitochondrial protein, reports indicate pathways involving *Nme4* likely include dysregulated metabolism and generation of reactive oxygenation species.⁷⁰ In connection to CSVD, cellular senescence has been linked to injury in the cerebrovasculature and several of the subsequent manifestations in multiple preclinical studies.⁷⁴⁻⁷⁶ However, the potential impacts of these pathophysiological mechanisms remain largely unknown in patients.

In our analysis of endothelial cell gene expression, ICI treatment induced an upregulation in the *Cd55* and *Cltb* genes. This is not necessarily a surprising finding in the context of ICI-induced immune activation. It has previously been established that complement activation results

in an increased CD55 protein expression.⁷⁷ Similarly, CLTB expression is enhanced as part of the lysosome signaling cascades that regulate cell death and autophagy in immune responses.⁷⁸ CLTB is also associated with atherosclerosis - a key factor in the pathogenesis of sporadic CSVD⁷⁹ - through lysosome-mediated lipid metabolism. Low-density lipoprotein receptor (LDLR) endocytosis is mediated through clathrin-associated pathways⁸⁰ in the endothelium, and subsequent release of LDL into the subendothelial space can lead to atherogenesis.⁸¹ This process may be exacerbated in the context of overt immune activation, such as the systemic response to ICI treatment. A previous report provided evidence to support this concept of an immune role by demonstrating that *apoE*^{-/-}/*Cd55*^{-/-} mice had reduced plaque development compared to *apoE*^{-/-} controls.⁸² Their findings in this atherosclerosis-prone preclinical model lacking CD55 were unexpected - the loss of CD55, as an inhibitor of the complement system, was hypothesized to increase atherosclerosis. However, this paradoxical finding has been reproduced in other studies.⁸³ A better understanding of the complement and immune systems in CSVD and atherosclerosis contributions to CSVD is warranted, especially as investigations continue to report accelerated atherosclerotic development after ICI treatment.^{5,84}

Considering the variety of biological pathways implicated in our present findings, a pharmacological therapeutic with established benefits in a variety of conditions - and limited side effects - is ideal. The results of our pharmaco-transcriptomics analysis identified several possibilities; however, the potential repurposing of statins may present a route that satisfies the above criteria and is more feasible from a regulatory viewpoint.⁸⁵ Beyond their lipid-lowering effects, statins have demonstrated beneficial effects on reducing cellular senescence⁸⁶ and atherosclerosis.^{87,88} Indeed, statins are often prescribed on the basis of atherosclerotic cardiovascular disease prevention.⁸⁹ While statins have been described as beneficial to improve

cerebrovascular regulation⁹⁰, which is associated with CSVD¹⁹, few studies have investigated statin use directly for the treatment of CSVD.⁹¹ Nevertheless, their pleiotropic effects and limited adverse effect profile⁹² posits drugs of the statin class as encouraging candidates for reducing cerebrovascular complications, such as CSVD, in ICI-treated patients. American Heart Association calculators that predict 10-year risk of atherosclerotic cardiovascular disease have not yet accounted for the heightened risk that anti-cancer treatments induce, but reports of their validity in general⁹³ and cancer-specific contexts⁹⁴ suggest that this may be adapted for statin prescription in cardio-oncology settings. Research into the links between statin use, immune regulation, and CSVD may provide further insight.⁹⁵

Strengths and Limitations

The primary strength of this study lies in its triangulation of evidence using scRNA-seq data, multiomics data and genetic analyses to provide robust results.⁹⁶ Additionally, our use of combined publicly available data and genetic analyses allows us to address a gap in the literature where current investigations into long-term ICI-associated toxicities are hampered by the sparse nature of available data from prospective or retrospective studies.⁶ However, there are limitations to the present study that are worth noting. First, the GWAS summary statistics used in this study were primarily conducted in individuals of European descent. Therefore, generalizability to other ethnicities may be limited. Second, the summary statistics used in the present work were collected in mixed sex samples, precluding the investigation of sex-specific effects. As suggested recently⁹⁷, this limitation may bias results towards the null due to unknown sex differences in genetic variants associated with CSVD outcomes. Third, the results of scRNA-seq analyses were derived from renal vascular endothelial cells, and not cerebrovascular endothelial cells which

limits generalizability.⁹⁸ While the two vascular beds have several distinct characteristics, both are high-flow, low-impedance regions of the cardiovascular system with unique barrier properties and vascular regulatory mechanisms.^{99,100} The use of renal samples also avoids the substantial challenges making collecting cerebral tissue samples difficult in human patients. Finally, despite our sensitivity analyses, it remains possible that there is heterogeneity or pleiotropy not accounted for in our results.

Conclusions

Findings from our present study suggest that genetically predicted gene expression and methylation levels of 5 genes (*Cd55*, *Ctlb*, *Htra1*, *Nme4*, *Xrcc6*) derived from scRNA-seq analysis of patients with or without ICI treatment are associated with CSVD. Furthermore, integration of multiomic data revealed potential therapeutic options, including statins. Expanded research is needed to elucidate underlying biological mechanisms linking ICI treatment with CSVD and to evaluate mitigation strategies.

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Appendix A - Supplementary Materials for Chapter 2

Supplementary Tables

Appendix Table A-1. Electronic search string for cerebrovascular reactivity and cerebral small vessel disease.

MEDLINE	WEB OF SCIENCE
("cerebrovascular reactivity" OR "cerebral vascular reactivity" OR "cerebral vasoreactivity" OR "CVR" OR "cerebrovascular reserve" OR "cerebral vasomotor reactivity")	ALL = ("cerebrovascular reactivity" OR "cerebral vascular reactivity" OR "cerebral vasoreactivity" OR "CVR" OR "cerebrovascular reserve" OR "cerebral vasomotor reactivity")
AND ("cerebral small vessel disease*" OR "lacun* infarct*" OR "subcortical stroke" OR "microinfarct*" OR "subcortical lesion*" OR "cerebrovascular disorder" OR "perivascular space*" OR "Virchow-Robin space*" OR "leukoaraiosis" OR "white matter lesion*" OR "white matter hyperintens*" OR "cerebral microbleed*" OR "white matter disease*" OR "cerebral atrophy")	AND ALL = ("cerebral small vessel disease*" OR "lacun* infarct*" OR "subcortical stroke" OR "microinfarct*" OR "subcortical lesion*" OR "cerebrovascular disorder" OR "perivascular space*" OR "Virchow-Robin space*" OR "leukoaraiosis" OR "white matter lesion*" OR "white matter hyperintens*" OR "cerebral microbleed*" OR "white matter disease*" OR "cerebral atrophy")
EMBASE	
("cerebrovascular reactivity" OR "cerebral vascular reactivity" OR "cerebral vasoreactivity" OR "CVR" OR "cerebrovascular reserve" OR "cerebral vasomotor reactivity")	
AND ("cerebral small vessel disease*" OR "lacun* infarct*" OR "subcortical stroke" OR "microinfarct*" OR "subcortical lesion*" OR "cerebrovascular disorder" OR "perivascular space*" OR "Virchow-Robin space*" OR "leukoaraiosis" OR "white matter lesion*" OR "white matter hyperintens*" OR "cerebral microbleed*" OR "white matter disease*" OR "cerebral atrophy")	

Appendix Table A-2. Electronic search string for cerebral autoregulation and cerebral small vessel disease.

MEDLINE	WEB OF SCIENCE
("cerebral autoregulation" OR "cerebrovascular autoregulation" OR "cerebral vascular autoregulation")	ALL = ("cerebral autoregulation" OR "cerebrovascular autoregulation" OR "cerebral vascular autoregulation")
AND ("cerebral small vessel disease*" OR "lacun* infarct*" OR "subcortical stroke" OR "microinfarct*" OR "subcortical lesion*" OR "cerebrovascular disorder" OR "perivascular space*" OR "Virchow-Robin space*" OR "leukoaraiosis" OR "white matter lesion*" OR "white matter hyperintens*" OR "cerebral microbleed*" OR "white matter disease*" OR "cerebral atrophy")	AND ALL = ("cerebral small vessel disease*" OR "lacun* infarct*" OR "subcortical stroke" OR "microinfarct*" OR "subcortical lesion*" OR "cerebrovascular disorder" OR "perivascular space*" OR "Virchow-Robin space*" OR "leukoaraiosis" OR "white matter lesion*" OR "white matter hyperintens*" OR "cerebral microbleed*" OR "white matter disease*" OR "cerebral atrophy")
EMBASE	
("cerebral autoregulation" OR "cerebrovascular autoregulation" OR "cerebral vascular autoregulation")	
AND ("cerebral small vessel disease*" OR "lacun* infarct*" OR "subcortical stroke" OR "microinfarct*" OR "subcortical lesion*" OR "cerebrovascular disorder" OR "perivascular space*" OR "Virchow-Robin space*" OR "leukoaraiosis" OR "white matter lesion*" OR "white matter hyperintens*" OR "cerebral microbleed*" OR "white matter disease*" OR "cerebral atrophy")	

Appendix Table A-3. Electronic search string for arterial stiffness and cerebral small vessel disease.

MEDLINE	WEB OF SCIENCE
("arterial stiffness" OR "pulse-wave velocity" OR "PWV" OR "arterial elasticity" OR "aortic stiffness" OR "carotid stiffness")	ALL = ("arterial stiffness" OR "pulse-wave velocity" OR "PWV" OR "arterial elasticity" OR "aortic stiffness" OR "carotid stiffness")
AND ("cerebral small vessel disease*" OR "lacun* infarct*" OR "subcortical stroke" OR "microinfarct*" OR "subcortical lesion*" OR "cerebrovascular disorder" OR "perivascular space*" OR "Virchow-Robin space*" OR "leukoaraiosis" OR "white matter lesion*" OR "white matter hyperintens*" OR "cerebral microbleed*" OR "white matter disease*" OR "cerebral atrophy")	AND ALL = ("cerebral small vessel disease*" OR "lacun* infarct*" OR "subcortical stroke" OR "microinfarct*" OR "subcortical lesion*" OR "cerebrovascular disorder" OR "perivascular space*" OR "Virchow-Robin space*" OR "leukoaraiosis" OR "white matter lesion*" OR "white matter hyperintens*" OR "cerebral microbleed*" OR "white matter disease*" OR "cerebral atrophy")
EMBASE	
("arterial stiffness" OR "pulse-wave velocity" OR "PWV" OR "arterial elasticity" OR "aortic stiffness" OR "carotid stiffness")	
AND ("cerebral small vessel disease*" OR "lacun* infarct*" OR "subcortical stroke" OR "microinfarct*" OR "subcortical lesion*" OR "cerebrovascular disorder" OR "perivascular space*" OR "Virchow-Robin space*" OR "leukoaraiosis" OR "white matter lesion*" OR "white matter hyperintens*" OR "cerebral microbleed*" OR "white matter disease*" OR "cerebral atrophy")	

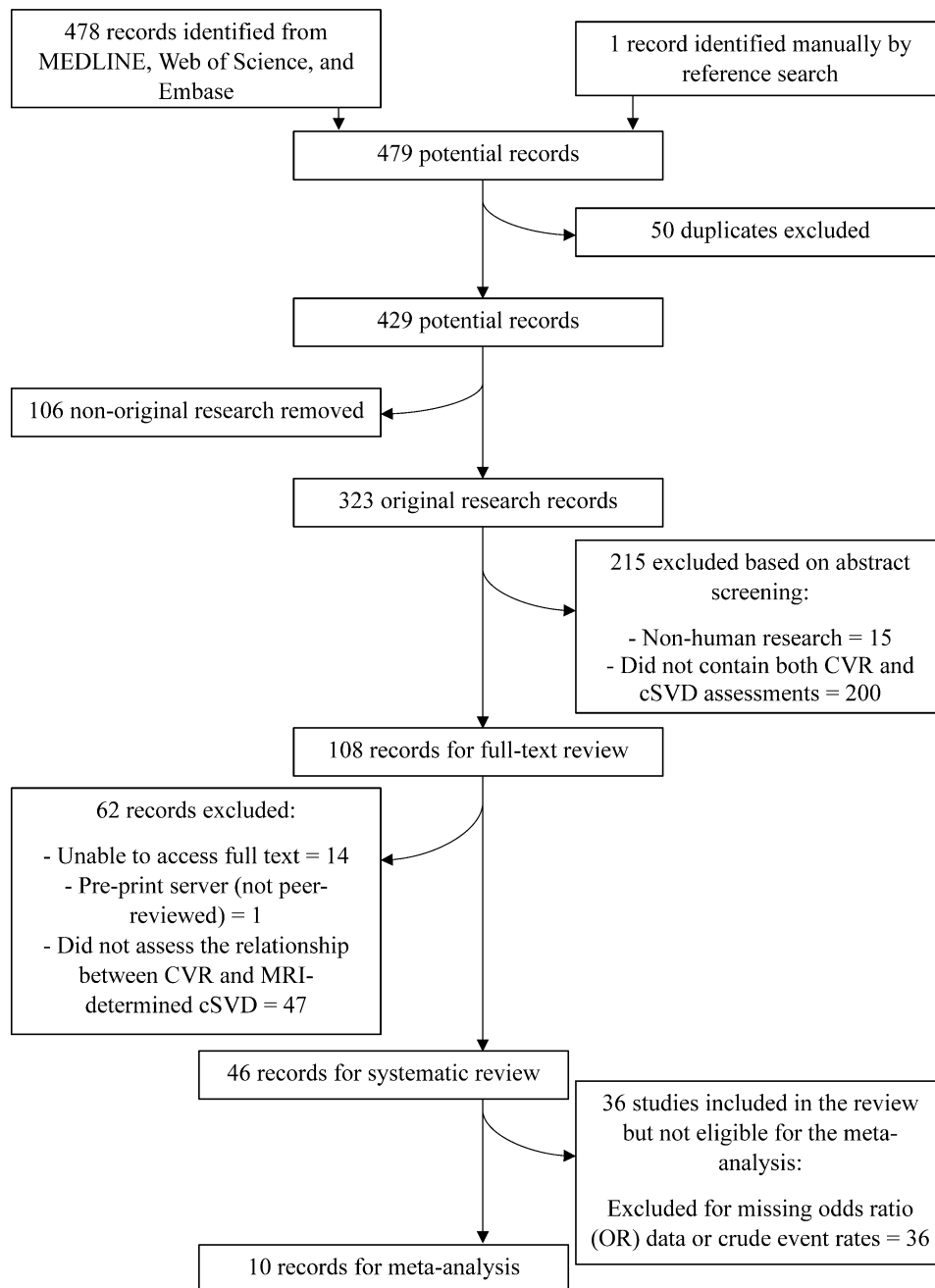
Appendix Table A-4. Results from multivariate meta-regression secondary analysis adjusted for three risk factors (hypertension, diabetes mellitus, and hyperlipidemia).

Predictor	Variable	Point Estimate (95% CI)	P-Value
<i>Continuous Arterial Stiffness</i>			
	Hypertension	0.0026 (-0.0014, 0.0065)	0.2
	Diabetes Mellitus	0.0082 (0.0022, 0.0142)	0.01
	Hyperlipidemia	-0.0026 (-0.0061, 0.0010)	0.16

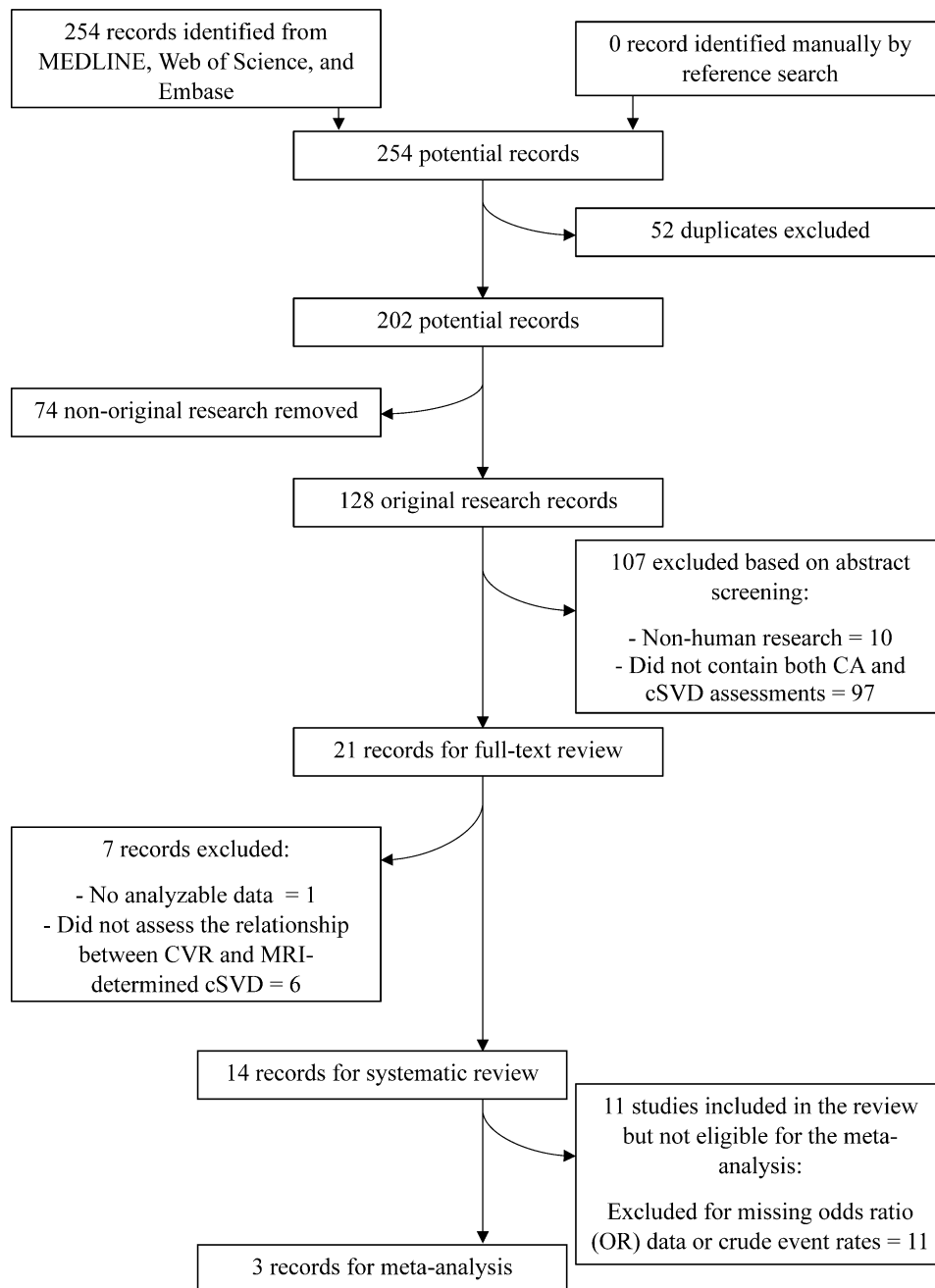
Appendix Table A-5. Grading of Recommendations Assessment, Development, and Evaluation (GRADE) scores for certainty of evidence.

Certainty of Evidence Analyses							Overall Certainty Assessment
No. of Studies	Study Designs	Risk of Bias	Inconsistency	Indirectness	Imprecision	Other Considerations	
Cerebrovascular Reactivity Association with cSVD – Dichotomous Exposure Variable							
7	Observational	Not serious	Serious	Not serious	Not serious	Potential Confounding, Large Effect Size, Small Sample Size	Low
Arterial Stiffness Association with cSVD – Continuous Exposure Variable							
37	Observational	Serious	Serious	Not serious	Not serious	Potential Confounding, Evidence of a Gradient	Low
Arterial Stiffness Association with cSVD – Dichotomous Exposure Variable							
13	Observational	Not serious	Serious	Not serious	Not serious	Potential Confounding	Low

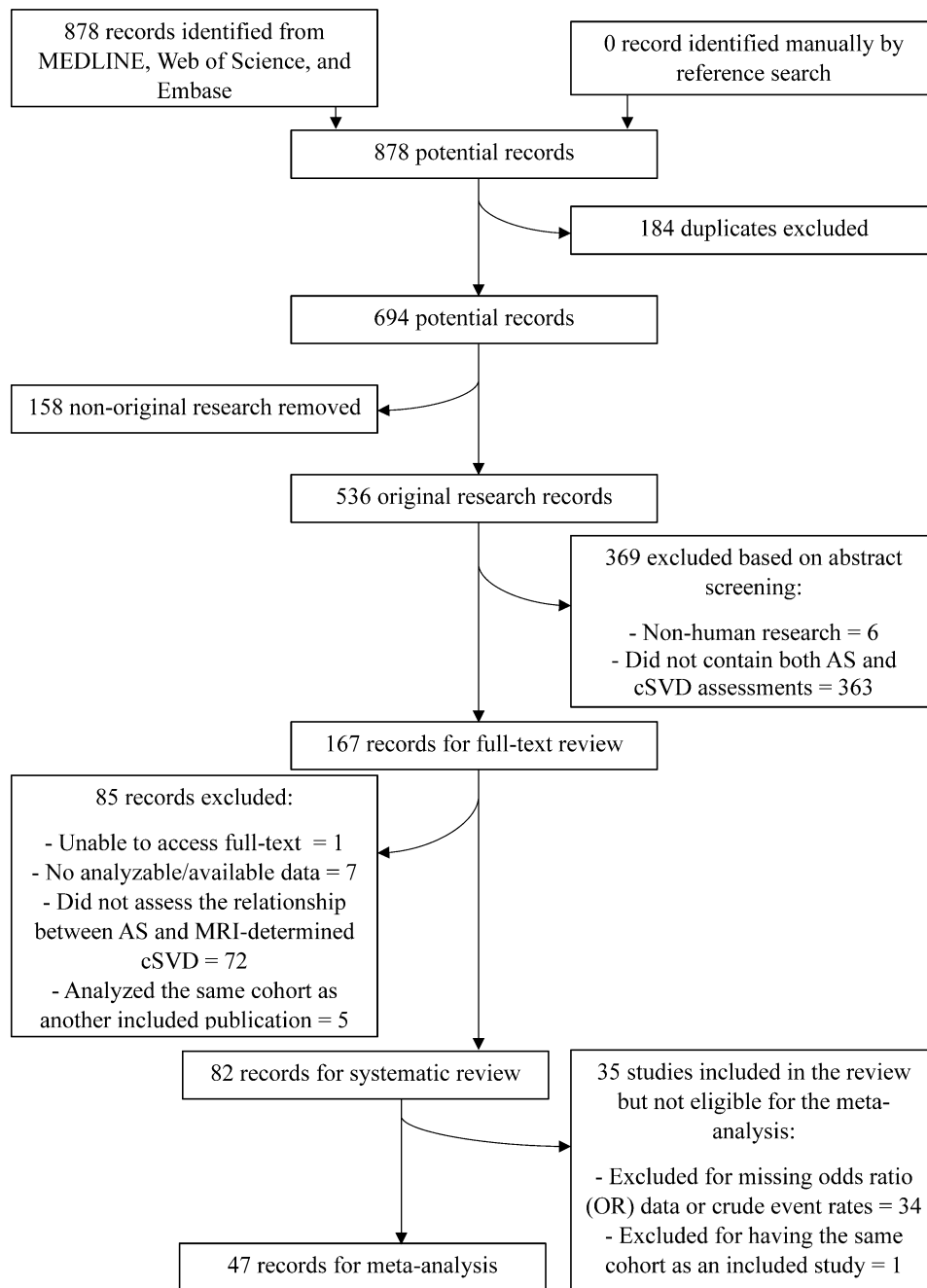
Supplementary Figures



Appendix Figure A-1. Flow chart of the selection process for eligible cerebrovascular reactivity studies. CVR indicates cerebrovascular reactivity.



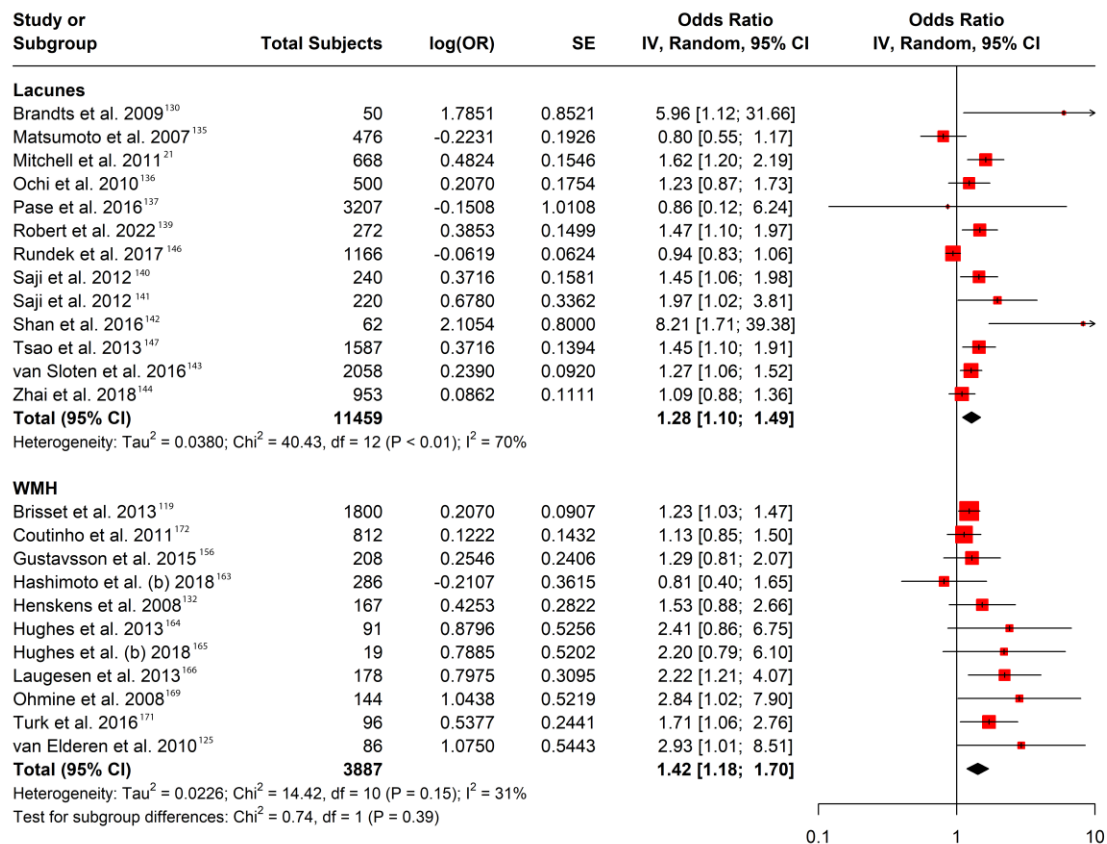
Appendix Figure A-2. Flow chart of the selection process for eligible cerebral autoregulation studies. CA indicates cerebral autoregulation.



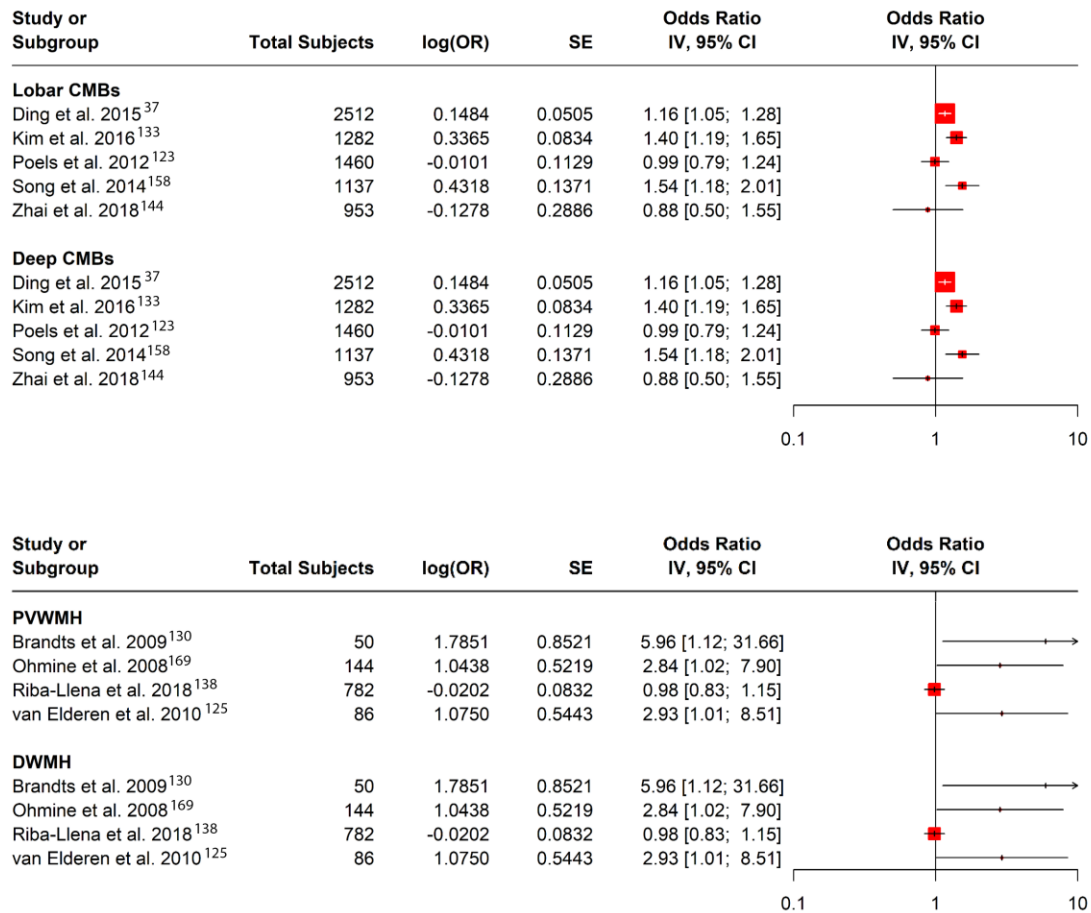
Appendix Figure A-3. Flow chart of the selection process for eligible arterial stiffness studies. AS indicates arterial stiffness.



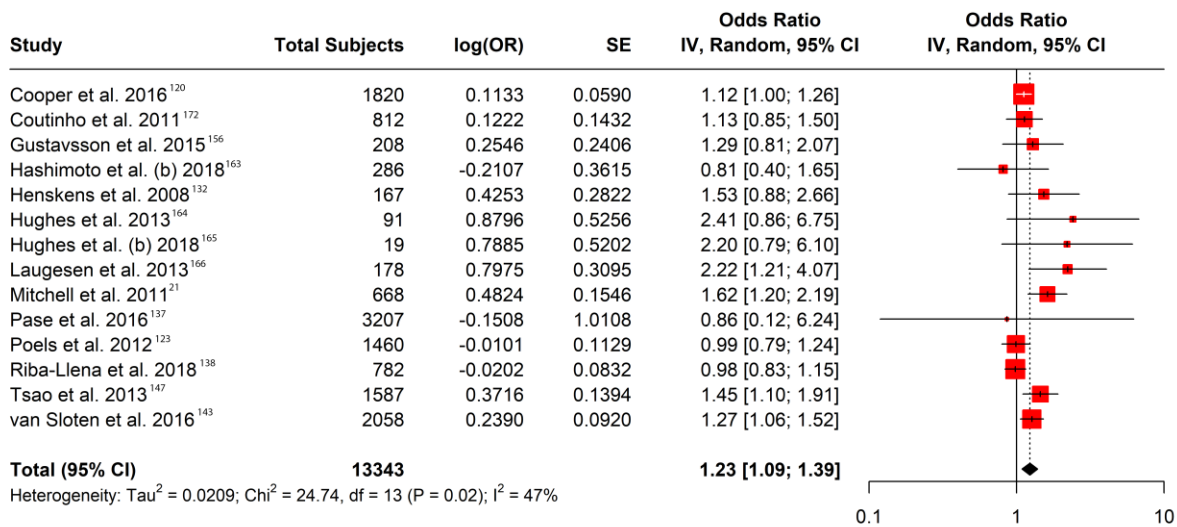
Appendix Figure A-4. Individual study results from longitudinal studies. Forest plot illustrating the individual effect sizes reported for each longitudinal study. Three studies were included for continuous arterial stiffness, while dichotomous cerebrovascular reactivity and dichotomous arterial stiffness only had one longitudinal study each. AS indicates arterial stiffness, while CVR indicates cerebrovascular reactivity.



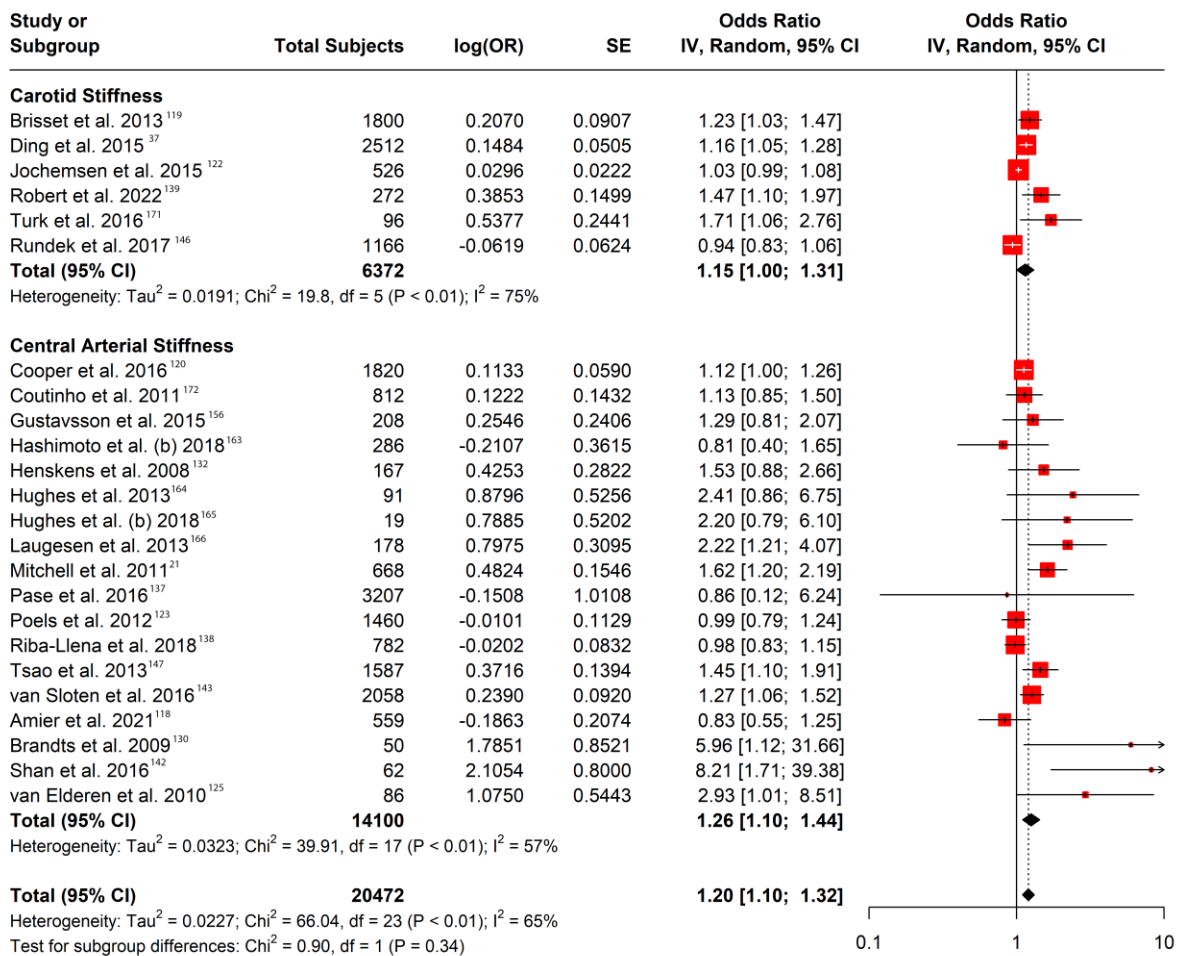
Appendix Figure A-5. Odds ratio results from secondary analyses of studies reporting arterial stiffness as a continuous exposure variable in relation to white matter hyperintensities or lacunes. Forest plot illustrating the effect sizes for studies reporting continuous arterial stiffness in relation to the presence of white matter hyperintensity or lacunes. Effect sizes are reported per 1-SD increase. The separate overall effects suggested an increasing arterial stiffness was associated with a greater presence of lacunes (OR: 1.28, 95% CI: 1.10-1.49) and a greater burden of white matter hyperintensities (OR: 1.42, 95% CI: 1.18-1.70). WMH, white matter hyperintensities; OR, odds ratio; SE, standard error; IV, inverse-variance.



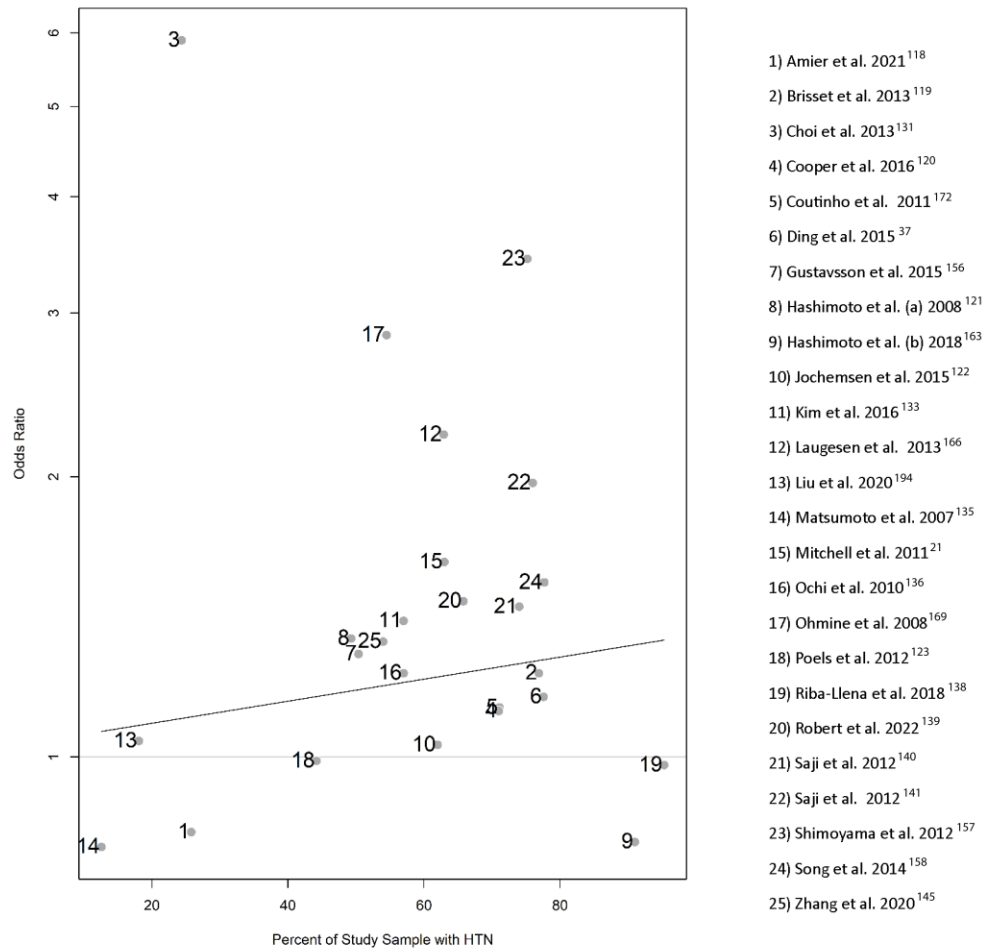
Appendix Figure A-6. Individual study results from continuous arterial stiffness studies that differentiated by region within a cSVD subtype. Forest plot illustrating the individual effect sizes reported for studies that divided the presence of lacunes into strictly lobar or deep lacunes (*top panel*) and studies that divided white matter hyperintensity burden into periventricular regions or deep regions (*bottom panel*). CMBs, cerebral microbleeds; PVWMH, periventricular white matter hyperintensities; DWMH, deep white matter hyperintensities; OR, odds ratio; SE, standard error; IV, inverse-variance.



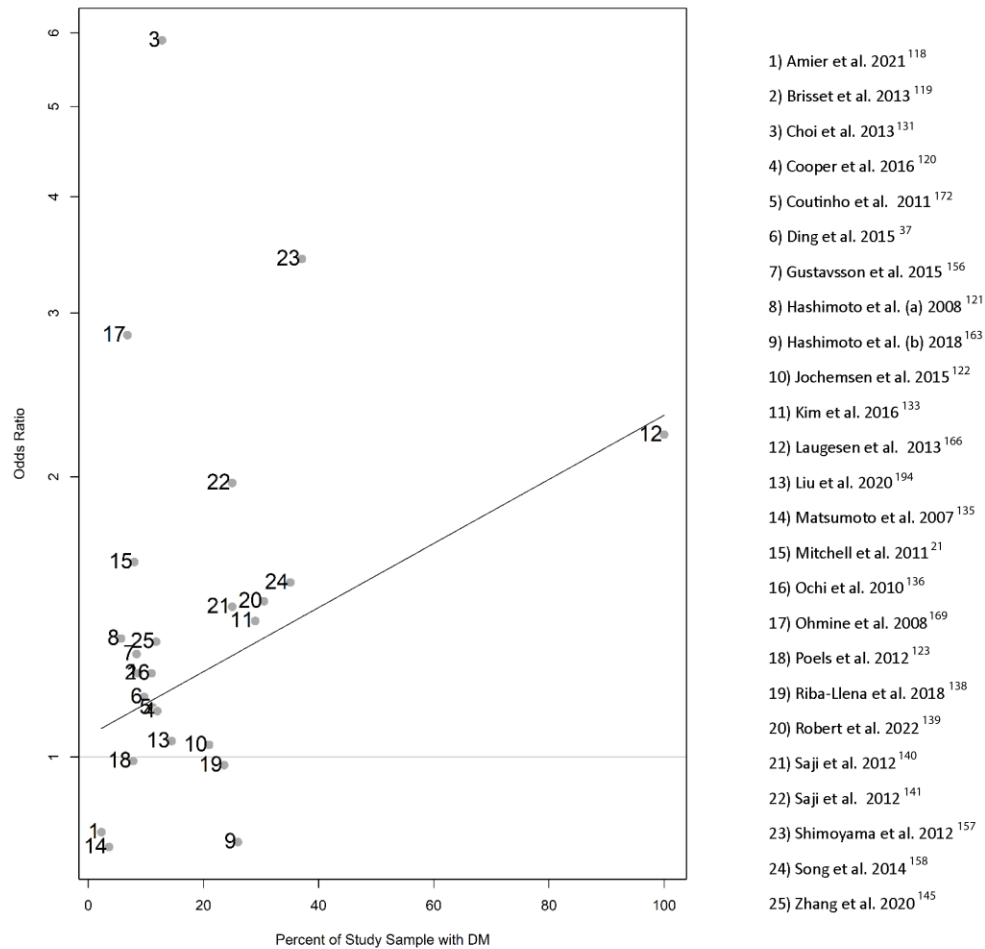
Appendix Figure A-7. Odds ratio results from secondary analyses of only the studies that assessed arterial stiffness as carotid-femoral pulse wave velocity. Forest plot illustrating the effect sizes for studies reporting carotid-femoral pulse wave velocity (cfPWV) in relation to cSVD burden. Effect sizes are reported per 1-SD increase. The separate overall effects suggested an increasing arterial stiffness was associated with a greater presence of cSVD (OR: 1.23, 95% CI: 1.09-1.39). OR, odds ratio; SE, standard error; IV, inverse-variance.



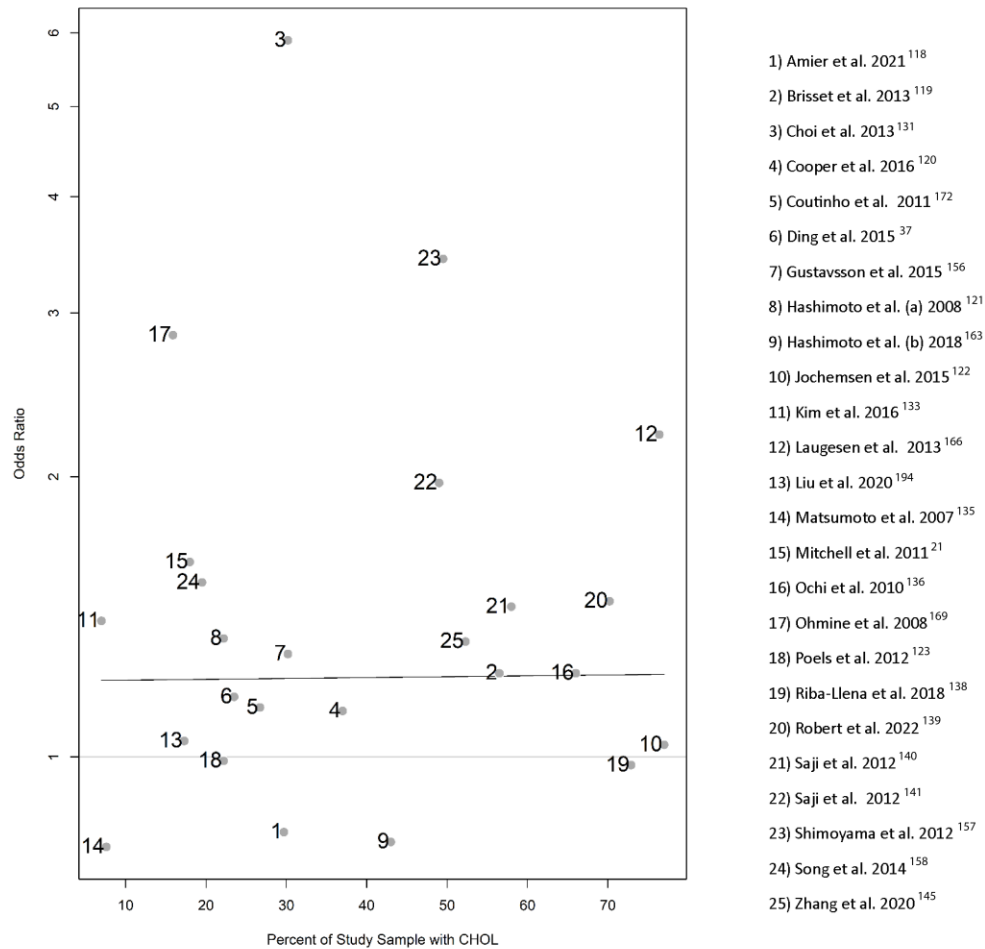
Appendix Figure A-8. Odds ratio results from secondary analyses comparing the studies that assessed central artery stiffness with the studies that assessed carotid artery stiffness. Forest plot illustrating the effect sizes for studies reporting central artery stiffness and for studies reporting carotid artery stiffness. Effect sizes are reported per 1-SD increase. The separate overall effects suggested that both an increasing central arterial stiffness (OR: 1.26, 95% CI: 1.10-1.44) and an increasing carotid artery stiffness (OR: 1.15, 95% CI: 1.00-1.31) were associated with a greater presence of cSVD. No significant differences were observed between central artery stiffness and carotid artery stiffness ($P=0.34$). OR, odds ratio; SE, standard error; IV, inverse-variance.



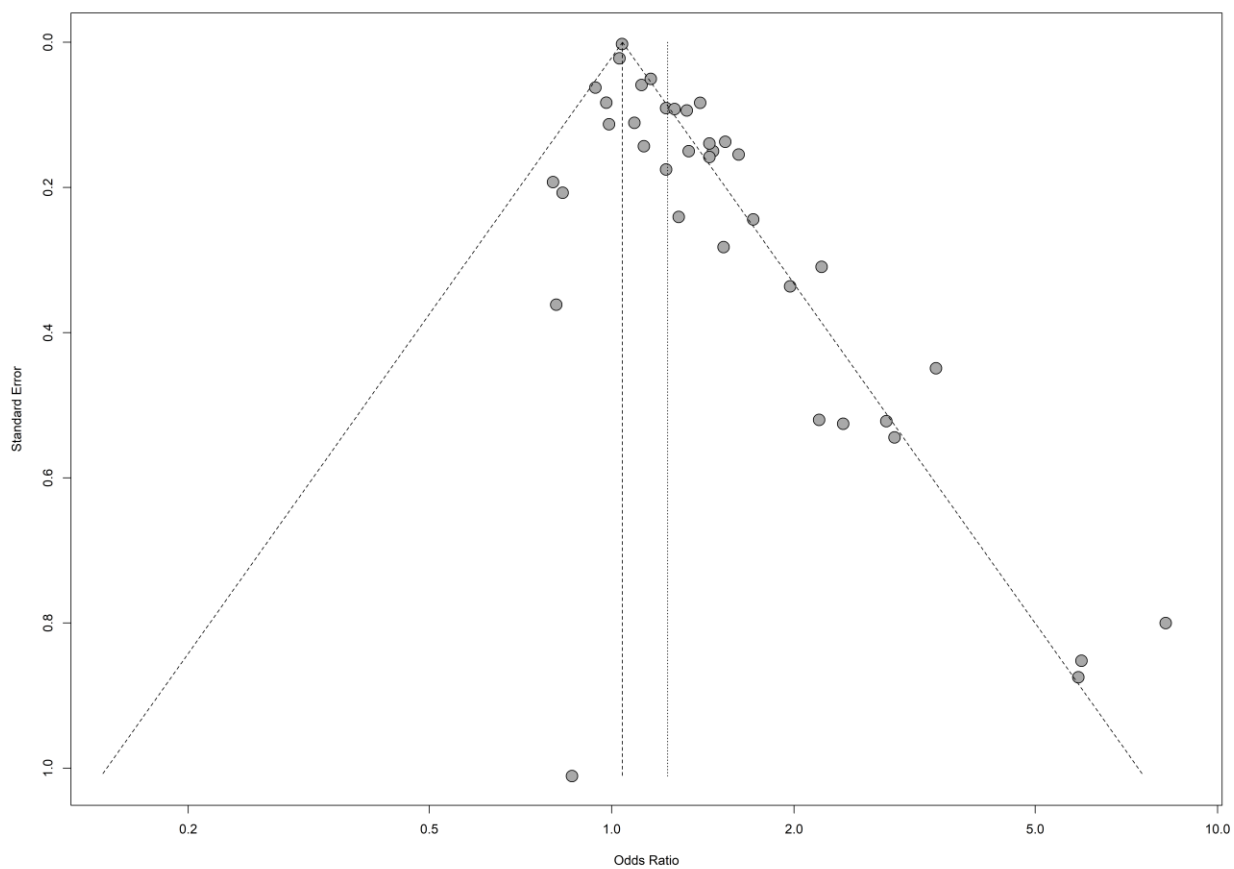
Appendix Figure A-9. Bubble plot from meta-regression showing the study proportion of hypertensive (HTN) participants as a study-level covariate.



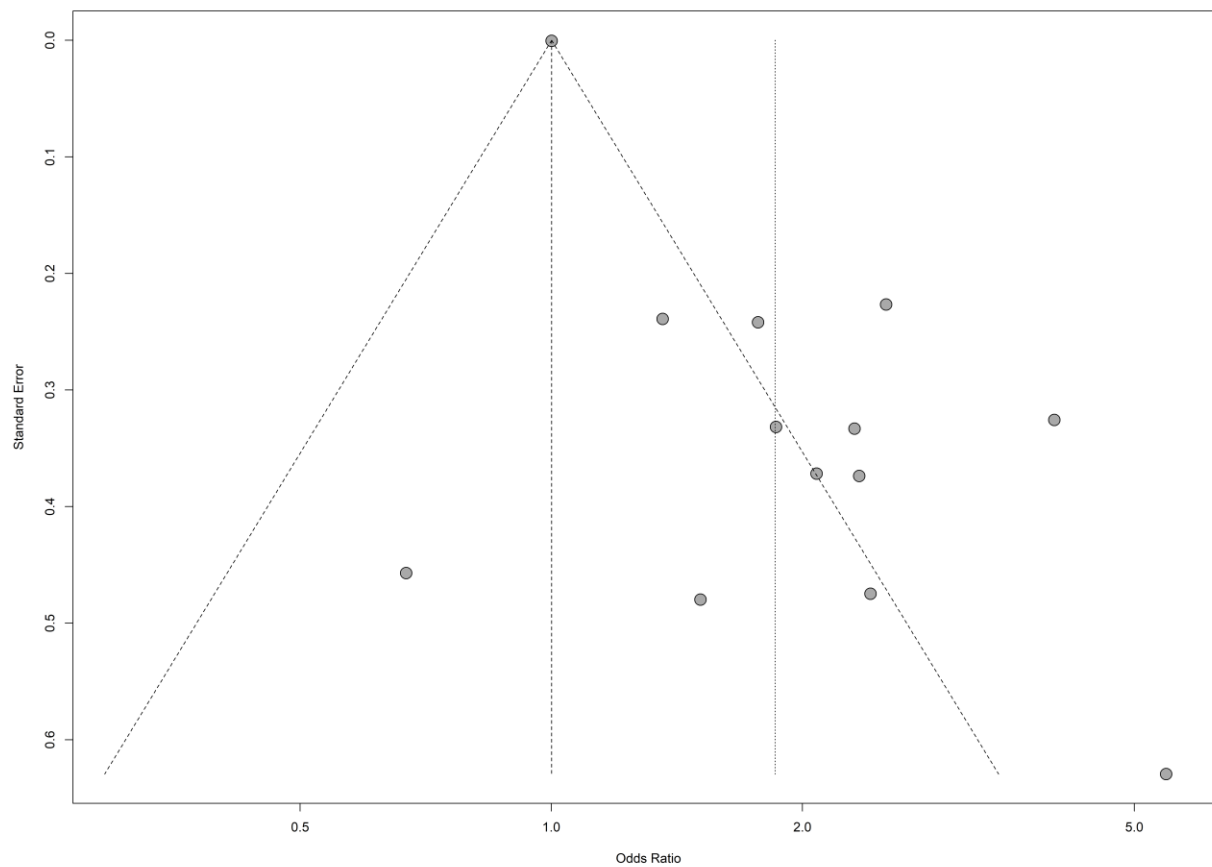
Appendix Figure A-10. Bubble plot from meta-regression showing the study proportion of diabetic (DM) participants as a study-level covariate.



Appendix Figure A-11. Bubble plot from meta-regression showing the study proportion of participants with hypercholesterolemia (HTN) as a study-level covariate.



Appendix Figure A-12. Funnel plot for studies reporting continuous arterial stiffness measures.



Appendix Figure A-13. Funnel plot for studies reporting dichotomous arterial stiffness measures.

Appendix B - Supplementary Materials for Chapter 4

Strengthening Reporting of Observational Studies in Epidemiology –

Mendelian Randomization (STROBE-MR) Guidelines

Item No.	Section	Checklist item	Page No.
1	TITLE and ABSTRACT	Indicate Mendelian randomization (MR) as the study's design in the title and/or the abstract if that is a main purpose of the study	123
	INTRODUCTION		
2	Background	Explain the scientific background and rationale for the reported study. What is the exposure? Is a potential causal relationship between exposure and outcome plausible? Justify why MR is a helpful method to address the study question	125, 126
3	Objectives	State specific objectives clearly, including pre-specified causal hypotheses (if any). State that MR is a method that, under specific assumptions, intends to estimate causal effects	127
	METHODS		
4	Study design and data sources	Present key elements of the study design early in the article. Consider including a table listing sources of data for all phases of the study. For each data source contributing to the analysis, describe the following:	128
	a)	Setting: Describe the study design and the underlying population, if possible. Describe the setting, locations, and relevant dates, including periods of recruitment, exposure, follow-up, and data collection, when available.	129-132
	b)	Participants: Give the eligibility criteria, and the sources and methods of selection of participants. Report the sample size, and whether any power or sample size calculations were carried out prior to the main analysis	129-132
	c)	Describe measurement, quality control and selection of genetic variants	129-132
	d)	For each exposure, outcome, and other relevant variables, describe methods of assessment and diagnostic criteria for diseases	129-132
	e)	Provide details of ethics committee approval and participant informed consent, if relevant	N/A
5	Assumptions	Explicitly state the three core IV assumptions for the main analysis (relevance, independence and exclusion restriction) as well assumptions for any additional or sensitivity analysis	Appendix B
6	Statistical methods: main analysis	Describe statistical methods and statistics used	132-133
	a)	Describe how quantitative variables were handled in the analyses (i.e., scale, units, model)	132-133
	b)	Describe how genetic variants were handled in the analyses and, if applicable, how their weights were selected	132-133
	c)	Describe the MR estimator (e.g. two-stage least squares, Wald ratio) and related statistics. Detail the included covariates and, in case of two-sample MR, whether the same covariate set was used for adjustment in the two samples	132-133
	d)	Explain how missing data were addressed	N/A
	e)	If applicable, indicate how multiple testing was addressed	N/A
7	Assessment of assumptions	Describe any methods or prior knowledge used to assess the assumptions or justify their validity	132-133
8	Sensitivity analyses and additional analyses	Describe any sensitivity analyses or additional analyses performed (e.g. comparison of effect estimates from different approaches, independent replication, bias analytic techniques, validation of instruments, simulations)	132-133
9	Software and pre-registration		

	a)	Name statistical software and package(s), including version and settings used	133
	b)	State whether the study protocol and details were pre-registered (as well as when and where)	N/A
	RESULTS		
10	Descriptive data		
	a)	Report the numbers of individuals at each stage of included studies and reasons for exclusion. Consider use of a flow diagram	N/A
	b)	Report summary statistics for phenotypic exposure(s), outcome(s), and other relevant variables (e.g. means, SDs, proportions)	134-135
	c)	If the data sources include meta-analyses of previous studies, provide the assessments of heterogeneity across these studies	N/A
	d)	For two-sample MR: i. Provide justification of the similarity of the genetic variant-exposure associations between the exposure and outcome samples ii. Provide information on the number of individuals who overlap between the exposure and outcome studies	N/A
11	Main results		
	a)	Report the associations between genetic variant and exposure, and between genetic variant and outcome, preferably on an interpretable scale	136
	b)	Report MR estimates of the relationship between exposure and outcome, and the measures of uncertainty from the MR analysis, on an interpretable scale, such as odds ratio or relative risk per SD difference	136
	c)	If relevant, consider translating estimates of relative risk into absolute risk for a meaningful time period	N/A
	d)	Consider plots to visualize results (e.g. forest plot, scatterplot of associations between genetic variants and outcome versus between genetic variants and exposure)	137-138
12	Assessment of assumptions		
	a)	Report the assessment of the validity of the assumptions	Appendix B
	b)	Report any additional statistics (e.g., assessments of heterogeneity across genetic variants, such as I^2 , Q statistic or E-value)	Appendix B
13	Sensitivity analyses and additional analyses		
	a)	Report any sensitivity analyses to assess the robustness of the main results to violations of the assumptions	136
	b)	Report results from other sensitivity analyses or additional analyses	136
	c)	Report any assessment of direction of causal relationship (e.g., bidirectional MR)	N/A
	d)	When relevant, report and compare with estimates from non-MR analyses	N/A
	e)	Consider additional plots to visualize results (e.g., leave-one-out analyses)	Appendix B
	DISCUSSION		
14	Key results		Summarize key results with reference to study objectives
15	Limitations		Discuss limitations of the study, taking into account the validity of the IV assumptions, other sources of potential bias, and imprecision. Discuss both direction and magnitude of any potential bias and any efforts to address them
16	Interpretation		
	a)	Meaning: Give a cautious overall interpretation of results in the context of their limitations and in comparison with other studies	139-141
	b)	Mechanism: Discuss underlying biological mechanisms that could drive a potential causal relationship between the investigated exposure and the outcome, and whether the gene-environment equivalence assumption is reasonable. Use causal language carefully, clarifying that IV estimates may provide causal effects only under certain assumptions	139-141

	c)	Clinical relevance: Discuss whether the results have clinical or public policy relevance, and to what extent they inform effect sizes of possible interventions	139-141
17	Generalizability	Discuss the generalizability of the study results (a) to other populations, (b) across other exposure periods/timings, and (c) across other levels of exposure	141
	OTHER INFORMATION		
18	Funding	Describe sources of funding and the role of funders in the present study and, if applicable, sources of funding for the databases and original study or studies on which the present study is based	
19	Data and data sharing	Provide the data used to perform all analyses or report where and how the data can be accessed, and reference these sources in the article. Provide the statistical code needed to reproduce the results in the article, or report whether the code is publicly accessible and if so, where	
20	Conflicts of Interest	All authors should declare all potential conflicts of interest	

Supplementary Methods

Core Assumptions of Mendelian Randomization

The core assumptions of two-sample Mendelian randomization studies are as follows: 1) relevance, 2) exchangeability, and 3) exclusion-restriction.¹ The relevance assumption is satisfied by demonstrating that the instrumental variable (the single genetic variant or multiple genetic variants used to proxy the exposure variable) is associated with the actual exposure of interest (Appendix Figure B-6, Panel A). In the scientific methods, this is done by selecting genetic variants that have previously been shown to associate with the exposure of interest at genome-wide standard threshold criteria (usually $p < 5 \times 10^{-8}$).² The exchangeability assumption says that there are no confounding pathways, mechanisms, or phenotypes between the instrumental variable and the outcome of interest that act independently of the exposure of interest (Appendix Figure B-6, Panel B). Genetic variation (aside from somatic mutations) are determined at conception, so many traditional confounding factors do not have an effect in this context. However, genome-specific confounders like population stratification and dynastic effects may play some role. To a degree, these are adjusted for in genome-wide association studies; some degree of confounding is always still possible.^{1,3} Finally, the exclusion-restriction assumption states that the instrumental variable only affects the outcome through the exposure of interest, and there are no other traits that have downstream effects on the outcome variable (Appendix Figure B-6, Panel C). In our methods, this assumption is tested by checking both horizontal pleiotropy in the statistical Mendelian randomization models and by using phenome-wide analyses to identify potential confounding phenotypes.⁴ However, it is important to note

that while sensitivity analyses may help address this third assumption, it cannot be truly and fully confirmed as there is always the possibility of some degree of unmeasured confounding.⁵

Details on Genetic Variant Identification Methods

For identifying and selecting genetic variants to proxy the effects of immune checkpoint inhibition, we followed the analytical and statistical methods of the GTEx consortium.⁶ In brief, the GTEx protocol primarily used FastQTL for processing and analysis.⁷ Variants were considered cis-variants if they were $\pm 1\text{Mb}$ from a gene transcription start site (which we reduced to $\pm 100\text{kb}$), and all variants with a minor allele frequency ≥ 0.01 were incorporated. Genes with at least one eQTL (expression quantitative trait loci) variant were identified at a false discovery rate (FDR) ≤ 0.05 and clustered together as “eGenes”. To then identify cis-variants significantly associated with expression of their target gene, first an empirical genome-wide p-value threshold (p_t) was set based on the empirical p-value of the eGene closest to FDR=0.05. This p_t value was used to establish gene-specific significance thresholds for each eGene. Cis-variants with a nominal p-value less than their target eGene significance threshold were considered statistically significant eQTL and reported as “significant gene-variant pairs”.⁶ These pairs were extracted from GTEx v10 data for present analyses.

Supplementary Tables

Appendix Table B-1. Mendelian randomization primary and sensitivity results for the effects of any breast cancer, estrogen receptor positive (ER+), estrogen receptor negative (ER-), and triple-negative (TN) breast cancer subtypes on cerebral small vessel disease outcomes. Results as reported as beta and 95% confidence interval for white matter hyperintensity (WMH) volume, and as odds ratio and 95% confidence interval for perivascular space (PVS) burden, cerebral microbleeds (CMB), and small vessel stroke (SVS).

		Cerebral Small Vessel Disease Marker			
<i>Exposure</i>	<i>MR Method</i>	<i>WMH</i>	<i>PVS</i>	<i>CMB</i>	<i>SVS</i>
Any Breast Cancer	IVW	0.015 (-0.023-0.053)	1.01 (0.99-1.02)	0.95 (0.86-1.06)	0.97 (0.90-1.05)
	MR-PRESSO	0.015 (-0.023-0.053)	1.01 (0.99-1.02)	0.95 (0.86-1.06)	0.97 (0.90-1.05)
	Weighted Median	0.014 (-0.034-0.061)	1.00 (0.98-1.02)	1.07 (0.92-1.23)	1.00 (0.89-1.11)
	MR-Egger	0.012 (-0.077-0.102)	1.00 (0.97-1.03)	0.94 (0.73-1.22)	1.08 (0.88-1.31)
ER+ Breast Cancer	IVW	0.026 (-0.01-0.062)	1.00 (0.99-1.02)	0.96 (0.88-1.06)	0.96 (0.89-1.03)
	MR-PRESSO	0.026 (-0.01-0.062)	1.00 (0.99-1.02)	0.96 (0.88-1.06)	0.96 (0.89-1.03)
	Weighted Median	0.014 (-0.029-0.058)	1.00 (0.98-1.02)	1.05 (0.93-1.19)	1.00 (0.90-1.10)
	MR-Egger	-0.004 (-0.082-0.074)	1.00 (0.98-1.03)	1.02 (0.83-1.25)	1.04 (0.89-1.21)
ER- Breast Cancer	IVW	0.001 (-0.048-0.051)	1.01 (0.99-1.03)	1.12 (0.92-1.36)	0.90 (0.76-1.07)
	MR-PRESSO	0.019 (-0.127-0.165)	1.01 (0.15-6.71)	1.12 (0.92-1.36)	0.90 (0.76-1.07)
	Weighted Median	-0.008 (-0.071-0.055)	1.01 (0.98-1.03)	1.14 (0.90-1.44)	1.03 (0.85-1.23)

	MR-Egger	-0.065 (-0.227-0.097)	1.03 (0.97-1.1)	1.56 (0.88-2.76)	1.29 (0.84-1.97)
TN Breast Cancer	IVW	-0.01 (-0.050-0.031)	1.00 (0.98-1.01)	0.96 (0.84-1.11)	1.02 (0.92-1.13)
	MR- PRESSO	-0.01 (-0.050-0.031)	1.00 (0.98-1.01)	0.96 (0.84-1.11)	1.02 (0.92-1.13)
	Weighted Median	-0.009 (-0.063-0.045)	1.00 (0.98-1.03)	1.01 (0.84-1.21)	1.00 (0.87-1.13)
	MR-Egger	0.002 (-0.110-0.114)	1.03 (0.99-1.07)	1.26 (0.87-1.83)	1.04 (0.77-1.42)

Appendix Table B-2. Variants included in the genetic instrument designed to proxy the effects of pharmacological immune checkpoint inhibition.

rsID	Gene Name	Variant ID	Distance (kb) ^a	MAF ^b	F-Statistic
rs115775475	<i>PDCDI</i>	chr2_241919740_A_C_b38	60846	0.095	13.6
rs13415837	<i>PDCDI</i>	chr2_241810383_G_C_b38	-48511	0.239	16.4
rs145228326	<i>PDCDI</i>	chr2_241901623_G_A_b38	42729	0.043	26.2
rs34667857	<i>PDCDI</i>	chr2_241808501_C_T_b38	-50393	0.419	42.9
rs3749155	<i>PDCDI</i>	chr2_241814768_C_T_b38	-44126	0.167	14.3
rs4441512	<i>PDCDI</i>	chr2_241822219_G_A_b38	-36675	0.417	32
rs62191180	<i>PDCDI</i>	chr2_241908700_G_A_b38	49806	0.157	13.5
rs62193087	<i>PDCDI</i>	chr2_241808893_A_C_b38	-50001	0.27	16.8
rs73011941	<i>PDCDI</i>	chr2_241777177_C_A_b38	-81717	0.034	14.4
rs74003953	<i>PDCDI</i>	chr2_241928080_C_G_b38	69186	0.549	24.2
rs76356158	<i>PDCDI</i>	chr2_241810882_C_G_b38	-48012	0.504	49.1
rs147055142	<i>CD274</i>	chr9_5476045_C_T_b38	25542	0.126	20.7
rs1970000	<i>CD274</i>	chr9_5465036_C_A_b38	14533	0.506	55.9
rs2890658	<i>CD274</i>	chr9_5465130_C_A_b38	14627	0.101	65.6
rs59906468	<i>CD274</i>	chr9_5466085_A_G_b38	15582	0.236	115.4
rs62560214	<i>CD274</i>	chr9_5471193_T_C_b38	20690	0.046	33.5
rs73399174	<i>CD274</i>	chr9_5487288_G_A_b38	36785	0.05	14.8

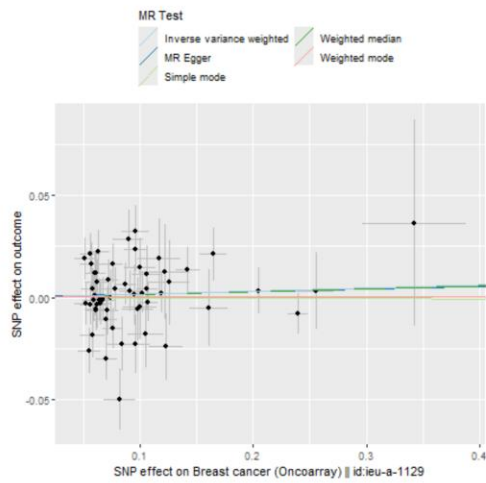
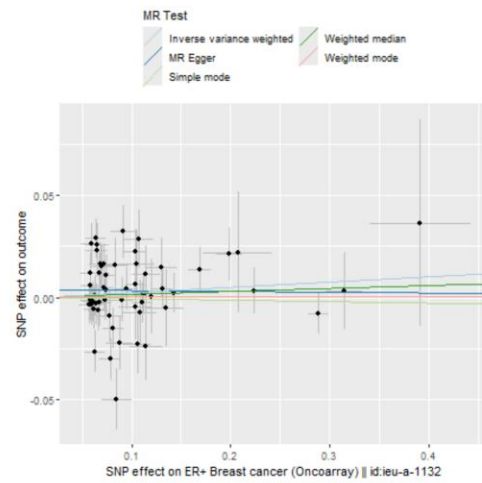
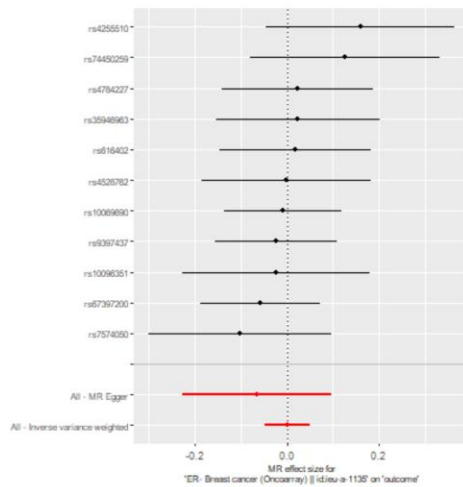
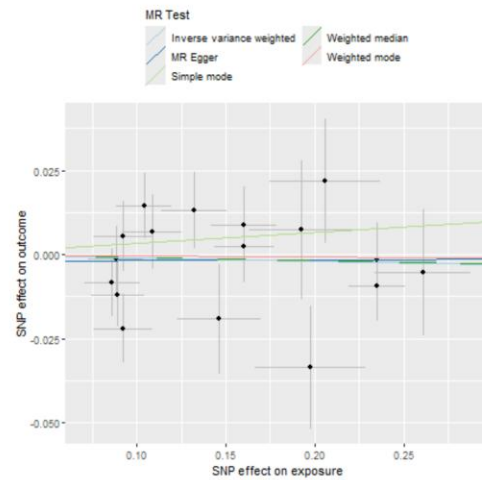
^a Distance from gene-encoding region. A negative value indicates that the variant is upstream of the transcription start site.

^b MAF, minor allele frequency (evaluated in the GTEx study cohort).

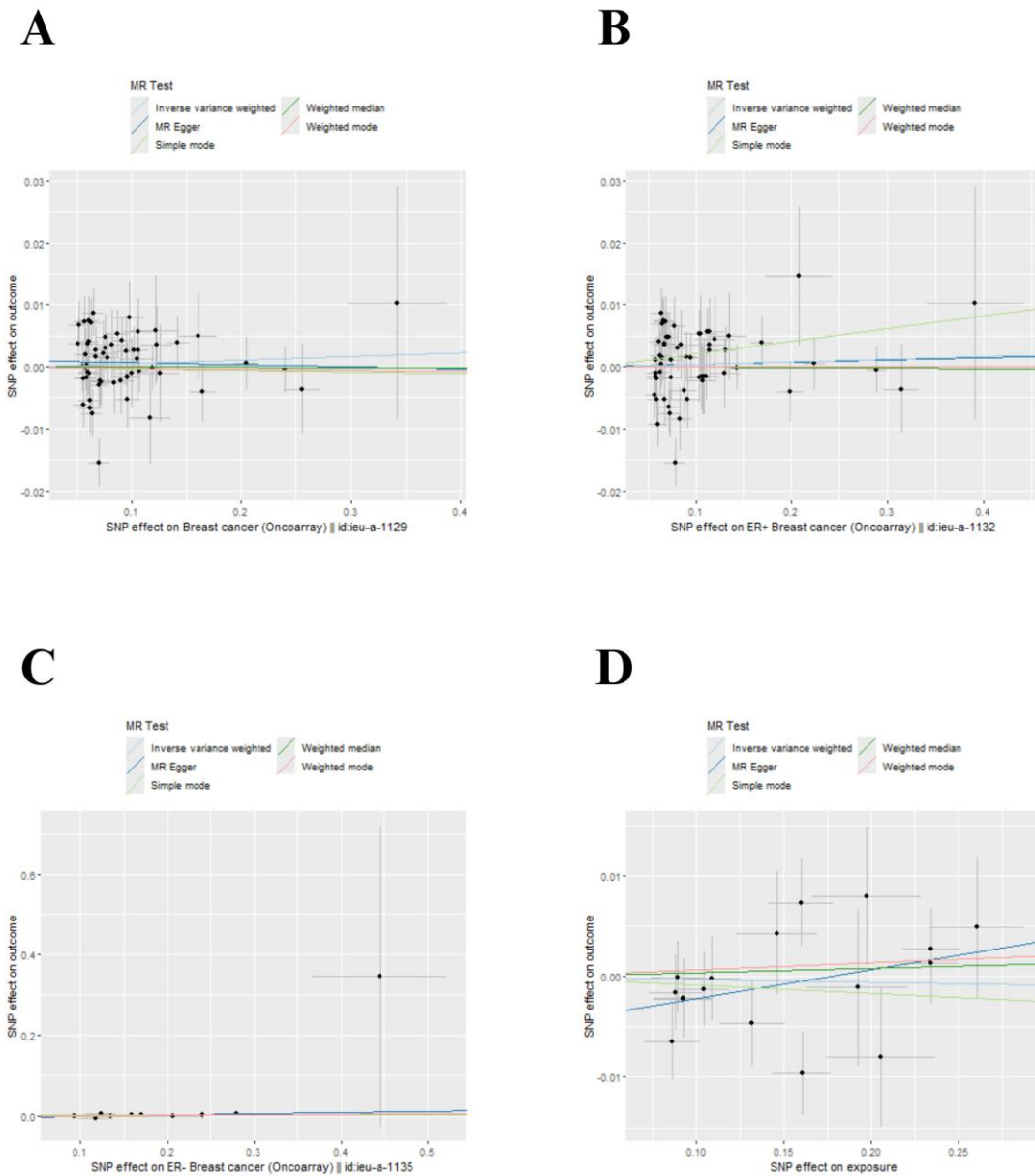
Appendix Table B-3. Mendelian randomization primary and sensitivity results for the effects of immune checkpoint inhibition on cerebral small vessel disease markers. Results as reported as beta and 95% confidence interval for white matter hyperintensity (WMH) volume, and as odds ratio and 95% confidence interval for perivascular space (PVS) burden, cerebral microbleeds (CMB), and small vessel stroke (SVS). Values are bolded for those that achieved significance ($p < 0.05$).

		Cerebral Small Vessel Disease Marker			
<i>Exposure</i>	<i>MR Method</i>	<i>WMH</i>	<i>PVS</i>	<i>CMB</i>	<i>SVS</i>
Immune Checkpoint Inhibition	IVW	0.045 (0.003-0.087)	1.02 (1.00-1.03)	1.12 (0.93-1.34)	1.02 (0.86-1.22)
	MR-PRESSO	0.045 (0.017-0.074)	1.02 (1.00-1.03)	1.12 (1.01-1.23)	1.02 (0.86-1.22)
	Weighted Median	0.021 (-0.037-0.078)	1.02 (1.00-1.05)	1.12 (0.90-1.41)	1.07 (0.90-1.26)
	MR-Egger	-0.034 (-0.164-0.096)	1.01 (0.97-1.06)	1.43 (0.69-2.98)	1.62 (1.01-2.59)

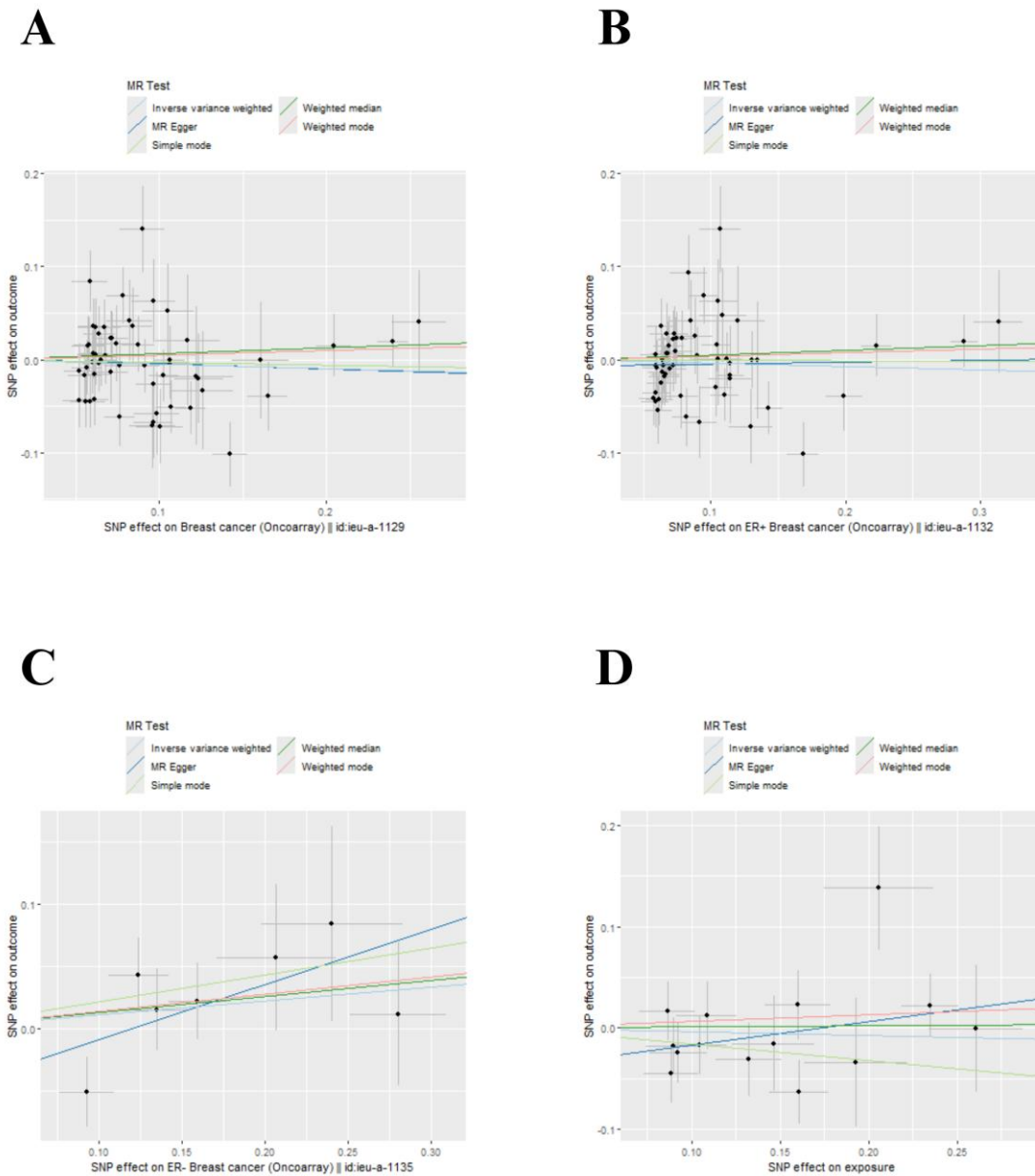
Supplementary Figures

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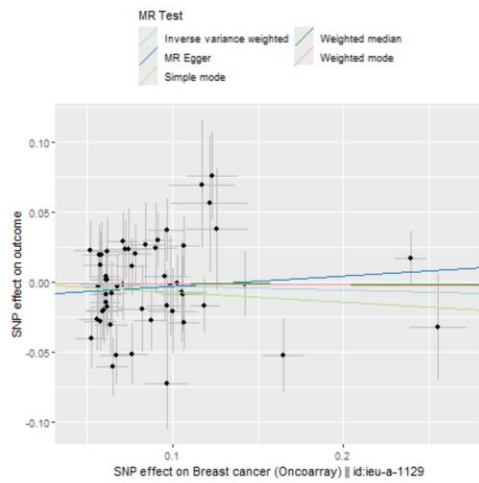
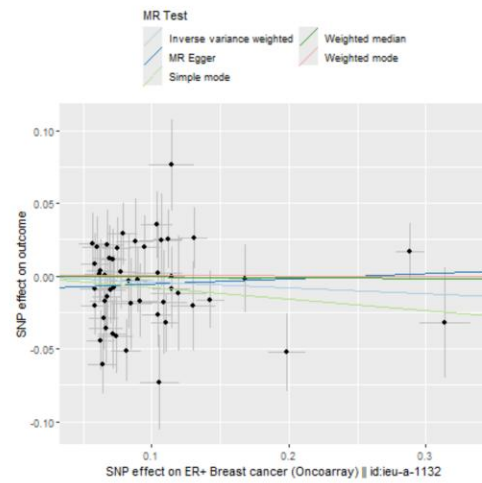
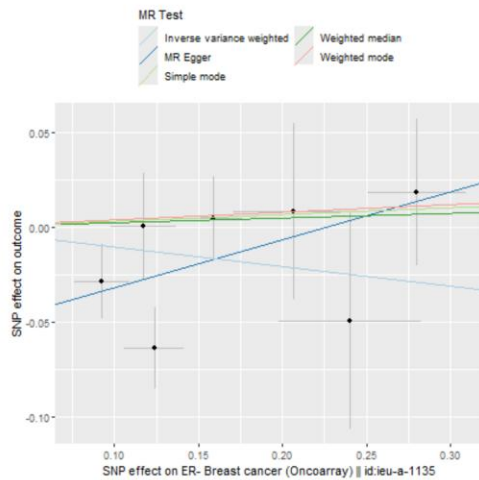
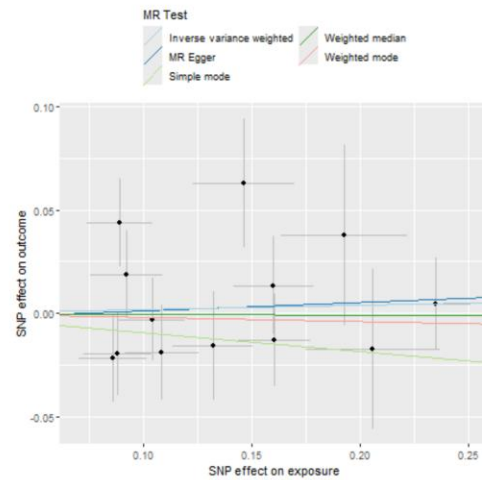
Appendix Figure B-1. Scatter plots depicting the different Mendelian randomization methods applied to assess the relationship between overall breast cancer (A), estrogen-receptor positive breast cancer (B), estrogen-receptor negative breast cancer (C) and triple-negative (TN) breast cancer (D) and white matter hyperintensity volume.



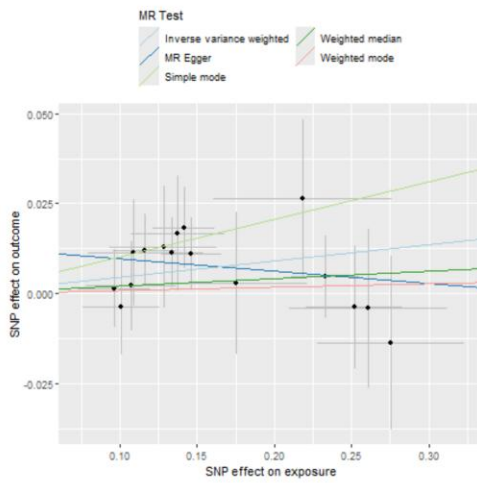
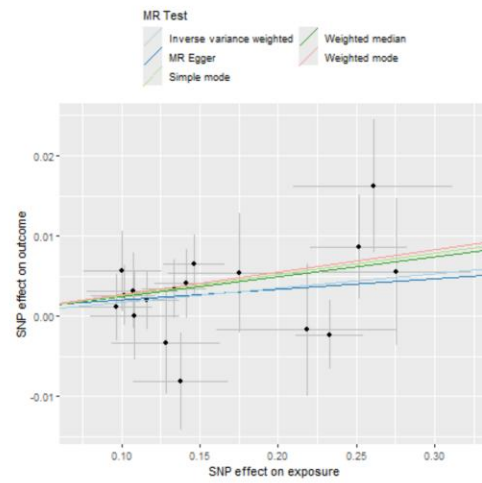
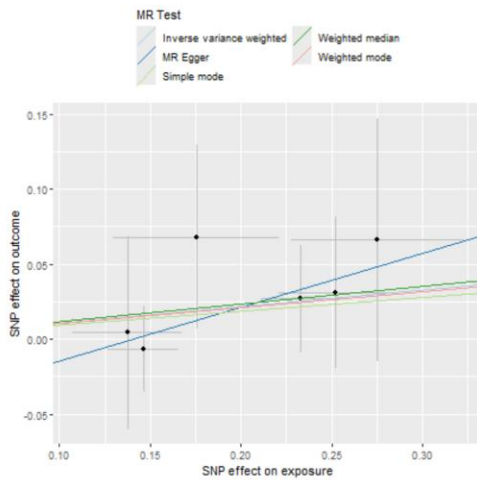
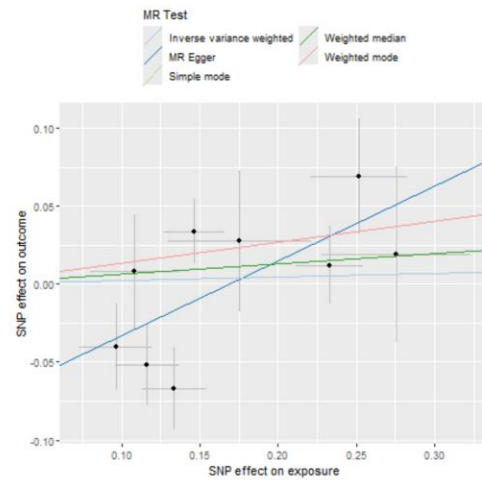
Appendix Figure B-2. Scatter plots depicting the different Mendelian randomization methods applied to assess the relationship between overall breast cancer (A), estrogen-receptor positive breast cancer (B), estrogen-receptor negative breast cancer (C) and triple-negative (TN) breast cancer (D) and perivascular space burden.



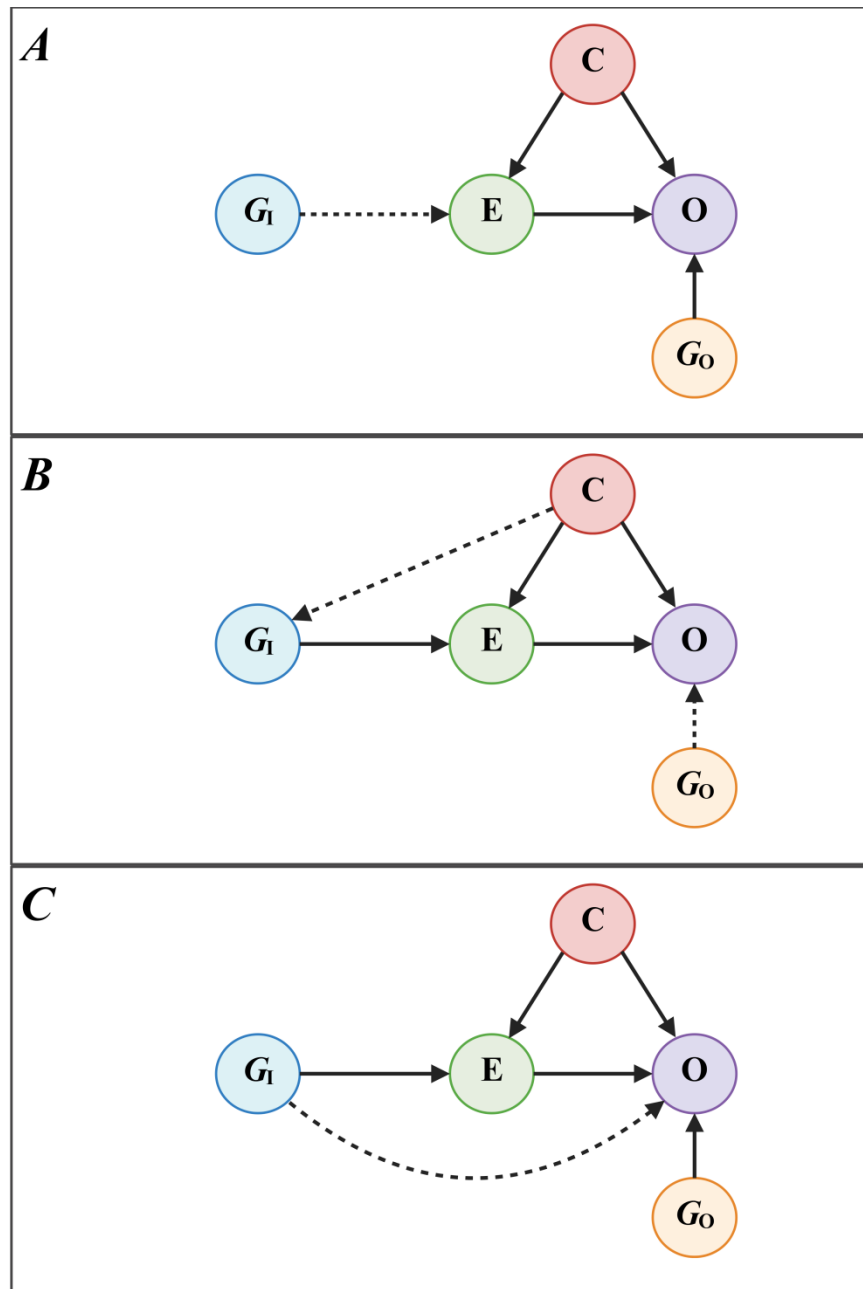
Appendix Figure B-3. Scatter plots depicting the different Mendelian randomization methods applied to assess the relationship between overall breast cancer (A), estrogen-receptor positive breast cancer (B), estrogen-receptor negative breast cancer (C) and triple-negative (TN) breast cancer (D) and cerebral microbleeds.

A**B****C****D**

Appendix Figure B-4. Scatter plots depicting the different Mendelian randomization methods applied to assess the relationship between overall breast cancer (A), estrogen-receptor positive breast cancer (B), estrogen-receptor negative breast cancer (C) and triple-negative (TN) breast cancer (D) and the risk of small vessel stroke.

A**B****C****D**

Appendix Figure B-5. Scatter plots depicting the different Mendelian randomization methods applied to assess the relationship between immune checkpoint inhibition and (A) white matter hyperintensity volume, (B) perivascular space burden, (C) cerebral microbleeds, and (D) the risk of small vessel stroke.



Appendix Figure B-6. Schematic demonstration of Mendelian randomization principles, as well as the core assumptions allowing for causal estimates to be derived. Panel A demonstrates the relevance assumption, Panel B depicts the exchangeability assumption, and Panel C shows the exclusion-restriction assumption. G_1 , genetic variants used as instrumental variables for the exposure; G_0 , genetic variants used as instrumental variables for the outcome; E , exposure variable; O , outcome variable; C , potential unmeasured confounding variables.

Supplementary References

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Appendix C - Supplementary Materials for Chapter 5

Strengthening Reporting of Observational Studies in Epidemiology –

Mendelian Randomization (STROBE-MR) Guidelines

Item No.	Section	Checklist item	Page No.
1	TITLE and ABSTRACT	Indicate Mendelian randomization (MR) as the study's design in the title and/or the abstract if that is a main purpose of the study	154
	INTRODUCTION		
2	Background	Explain the scientific background and rationale for the reported study. What is the exposure? Is a potential causal relationship between exposure and outcome plausible? Justify why MR is a helpful method to address the study question	156-157
3	Objectives	State specific objectives clearly, including pre-specified causal hypotheses (if any). State that MR is a method that, under specific assumptions, intends to estimate causal effects	156-157
	METHODS		157, 160
4	Study design and data sources	Present key elements of the study design early in the article. Consider including a table listing sources of data for all phases of the study. For each data source contributing to the analysis, describe the following:	157, 160
	a)	Setting: Describe the study design and the underlying population, if possible. Describe the setting, locations, and relevant dates, including periods of recruitment, exposure, follow-up, and data collection, when available.	159, 166
	b)	Participants: Give the eligibility criteria, and the sources and methods of selection of participants. Report the sample size, and whether any power or sample size calculations were carried out prior to the main analysis	159, 166
	c)	Describe measurement, quality control and selection of genetic variants	163-164
	d)	For each exposure, outcome, and other relevant variables, describe methods of assessment and diagnostic criteria for diseases	163-165
	e)	Provide details of ethics committee approval and participant informed consent, if relevant	N/A
5	Assumptions	Explicitly state the three core IV assumptions for the main analysis (relevance, independence and exclusion restriction) as well assumptions for any additional or sensitivity analysis	165
6	Statistical methods: main analysis	Describe statistical methods and statistics used	167
	a)	Describe how quantitative variables were handled in the analyses (i.e., scale, units, model)	167
	b)	Describe how genetic variants were handled in the analyses and, if applicable, how their weights were selected	167
	c)	Describe the MR estimator (e.g. two-stage least squares, Wald ratio) and related statistics. Detail the included covariates and, in case of two-sample MR, whether the same covariate set was used for adjustment in the two samples	167
	d)	Explain how missing data were addressed	N/A
	e)	If applicable, indicate how multiple testing was addressed	167
7	Assessment of assumptions	Describe any methods or prior knowledge used to assess the assumptions or justify their validity	167
8	Sensitivity analyses and additional analyses	Describe any sensitivity analyses or additional analyses performed (e.g. comparison of effect estimates from different approaches, independent replication, bias analytic techniques, validation of instruments, simulations)	167

9	Software and pre-registration		
	a)	Name statistical software and package(s), including version and settings used	167
	b)	State whether the study protocol and details were pre-registered (as well as when and where)	N/A
	RESULTS		
10	Descriptive data		
	a)	Report the numbers of individuals at each stage of included studies and reasons for exclusion. Consider use of a flow diagram	159, 166
	b)	Report summary statistics for phenotypic exposure(s), outcome(s), and other relevant variables (e.g. means, SDs, proportions)	166
	c)	If the data sources include meta-analyses of previous studies, provide the assessments of heterogeneity across these studies	N/A
	d)	For two-sample MR: i. Provide justification of the similarity of the genetic variant-exposure associations between the exposure and outcome samples ii. Provide information on the number of individuals who overlap between the exposure and outcome studies	N/A
11	Main results		
	a)	Report the associations between genetic variant and exposure, and between genetic variant and outcome, preferably on an interpretable scale	172, 174
	b)	Report MR estimates of the relationship between exposure and outcome, and the measures of uncertainty from the MR analysis, on an interpretable scale, such as odds ratio or relative risk per SD difference	172-175
	c)	If relevant, consider translating estimates of relative risk into absolute risk for a meaningful time period	N/A
	d)	Consider plots to visualize results (e.g. forest plot, scatterplot of associations between genetic variants and outcome versus between genetic variants and exposure)	173, 175
12	Assessment of assumptions		
	a)	Report the assessment of the validity of the assumptions	N/A
	b)	Report any additional statistics (e.g., assessments of heterogeneity across genetic variants, such as I^2 , Q statistic or E-value)	N/A
13	Sensitivity analyses and additional analyses		
	a)	Report any sensitivity analyses to assess the robustness of the main results to violations of the assumptions	N/A
	b)	Report results from other sensitivity analyses or additional analyses	N/A
	c)	Report any assessment of direction of causal relationship (e.g., bidirectional MR)	N/A
	d)	When relevant, report and compare with estimates from non-MR analyses	N/A
	e)	Consider additional plots to visualize results (e.g., leave-one-out analyses)	N/A
	DISCUSSION		
14	Key results	Summarize key results with reference to study objectives	180-183
15	Limitations	Discuss limitations of the study, taking into account the validity of the IV assumptions, other sources of potential bias, and imprecision. Discuss both direction and magnitude of any potential bias and any efforts to address them	183
16	Interpretation		
	a)	Meaning: Give a cautious overall interpretation of results in the context of their limitations and in comparison with other studies	180-183
	b)	Mechanism: Discuss underlying biological mechanisms that could drive a potential causal relationship between the investigated exposure and the outcome, and whether the gene-environment equivalence assumption is reasonable. Use causal language carefully, clarifying that IV estimates may provide causal effects only under certain assumptions	180-183

	c)	Clinical relevance: Discuss whether the results have clinical or public policy relevance, and to what extent they inform effect sizes of possible interventions	180-183
17	Generalizability	Discuss the generalizability of the study results (a) to other populations, (b) across other exposure periods/timings, and (c) across other levels of exposure	183
	OTHER INFORMATION		
18	Funding	Describe sources of funding and the role of funders in the present study and, if applicable, sources of funding for the databases and original study or studies on which the present study is based	
19	Data and data sharing	Provide the data used to perform all analyses or report where and how the data can be accessed, and reference these sources in the article. Provide the statistical code needed to reproduce the results in the article, or report whether the code is publicly accessible and if so, where	
20	Conflicts of Interest	All authors should declare all potential conflicts of interest	

Supplementary Methods

Details on Genetic Variant Identification Methods

Gene Expression Quantitative Trait Loci. For identifying and selecting genetic variants to proxy the effects of immune checkpoint inhibition, we followed the analytical and statistical methods of the GTEx consortium.¹ In brief, the GTEx protocol primarily used FastQTL for processing and analysis.² Variants were considered cis-variants if they were $\pm 1\text{Mb}$ from a gene transcription start site (which we reduced to $\pm 100\text{kb}$), and all variants with a minor allele frequency ≥ 0.01 were incorporated. Genes with at least one eQTL (expression quantitative trait loci) variant were identified at a false discovery rate (FDR) ≤ 0.05 and clustered together as “eGenes”. To then identify cis-variants significantly associated with expression of their target gene, first an empirical genome-wide p-value threshold (p_t) was set based on the empirical p-value of the eGene closest to FDR=0.05. This p_t value was used to establish gene-specific significance thresholds for each eGene. Cis-variants with a nominal p-value less than their target eGene significance threshold were considered statistically significant eQTL and reported as “significant gene-variant pairs”.¹ These pairs were extracted from GTEx v10 data for present analyses.

Methylation Quantitative Trait Loci. Methylation quantitative trait loci (mQTL) data were retrieved from the ARIES (Accessible Resource for Integrated Epigenomic Studies) data resource.³ ARIES included data from a subset of participants enrolled in the Avon Longitudinal Study of Parents and Children (ALSPAC).⁴ Specifically, 1018 mother-offspring pairs were included based on the availability of samples for DNA analysis. Mothers were analyzed at two separate time points: pregnancy (average age of mother: 29.2 yrs) and at a follow-up point on

average 15.5 years later. Offspring were assessed at three timepoints: birth (average gestational age: 40 weeks), childhood (average age of offspring: 7.5 yrs), and adolescence (average age of offspring: 17.1 yrs). Blood samples were processed, and genome-wide methylation status was analyzed at over 485000 methylation sites using the Illumina 450K system (Illumina Inc., CA, USA). Samples were distributed across arrays semi-randomly to reduce batch effect biases⁵, and quality control metrics were implemented. Genome-wide significance was set at $p < 5 \times 10^{-7}$ to account for the number of methylation sites assessed. Data for mQTLs were extracted using the *MRInstruments* package in R.⁶

Core Assumptions of Mendelian Randomization

The core assumptions of two-sample Mendelian randomization studies are as follows: 1) relevance, 2) exchangeability, and 3) exclusion-restriction.⁷ The relevance assumption is satisfied by demonstrating that the instrumental variable (the single genetic variant or multiple genetic variants used to proxy the exposure variable) is associated with the actual exposure of interest (Supplementary Figure 9, Panel A). In the scientific methods, this is done by selecting genetic variants that have previously been shown to associate with the exposure of interest at genome-wide standard threshold criteria (usually $p < 5 \times 10^{-8}$).⁸ The exchangeability assumption says that there are no confounding pathways, mechanisms, or phenotypes between the instrumental variable and the outcome of interest that act independently of the exposure of interest (Supplementary Figure 9, Panel B). Genetic variation (aside from somatic mutations) are determined at conception, so many traditional confounding factors do not have an effect in this context. However, genome-specific confounders like population stratification and dynastic effects may play some role. To a degree, these are adjusted for in genome-wide association

studies; some degree of confounding is always still possible.^{7,9} Finally, the exclusion-restriction assumption states that the instrumental variable only affects the outcome through the exposure of interest, and there are no other traits that have downstream effects on the outcome variable (Supplementary Figure 9, Panel C). In our methods, this assumption is tested by checking both horizontal pleiotropy in the statistical Mendelian randomization models and by using phenome-wide analyses to identify potential confounding phenotypes.¹⁰ However, it is important to note that while sensitivity analyses may help address this third assumption, it cannot be truly and fully confirmed as there is always the possibility of some degree of unmeasured confounding.¹¹

Supplementary Tables

Appendix Table C-1. Results of clustering analysis performed with endothelial cell-specific differentially expressed genes obtained from single cell RNA-sequencing in samples obtained from patients with or without exposure to immune checkpoint inhibitors.

Cluster Name	Cluster P-Value
Cytochrome-c oxidase activity	3.43E-03
Glutathione peroxidase activity	5.93E-03
Regulation of vascular permeability	5.25E-04
Cell redox homeostasis	1.63E-03
Hepatocyte growth factor receptor signaling pathway	7.13E-03
Positive regulation of sequestering of calcium ion	5.85E-03
Regulation of protein exit from endoplasmic reticulum	3.63E-03
Negative regulation of transforming growth factor beta production	2.75E-03
U2-type prespliceosome assembly	7.61E-03
Chondrocyte development	6.90E-03
Protein N-linked glycosylation via asparagine	3.43E-03
Viral translation	7.13E-03
Protein folding in endoplasmic reticulum	1.11E-04
Protein nitrosylation	6.25E-03
Negative regulation of viral life cycle	5.01E-04
Cytoplasmic translational initiation	4.30E-03
Membrane raft assembly	3.43E-03
Positive regulation of collagen metabolic process	4.41E-03
Transforming growth factor beta receptor activity	5.27E-03
Antigen processing and presentation of endogenous peptide antigen	4.04E-04
Lymphangiogenesis	6.86E-03
Regulation of glomerular filtration	4.63E-04
Protein folding chaperone	1.10E-07

Appendix Table C-2. List of unique genes included as instruments in the Mendelian randomization analyses using gene expression exposures and cerebral small vessel disease outcomes.

ACKR1	ACTR1A	ACTR2	ACTR3	ADAM15	ADH5	AGTRAP	AHNAK	AHR	ALDH2	ANP32B
ANXA2	ANXA5	AP2M1	AP2S1	APLP2	APOL1	APP	APRT	ARF3	ARL6IP1	ARL6IP5
ARPC1B	ARPC2	ARPC3	ARPC4	ASRGL1	ATOX1	ATP1A1	ATP1B3	ATP2B4	ATP5F1A	ATP5F1C
ATP5F1D	ATP5IF1	ATP5MC1	ATP5PD	ATP5PO	ATP6V0B	ATP6V1G ₁	ATRAID	B2M	BANF1	BAX
BCL7B	BLOC1S1	BMPR2	BNIP2	BRD4	BRI3	BRK1	BSG	BTG1	BTG2	BUD31
BZW1	C12orf57	C19orf53	C1QBP	C4orf3	CACYBP	CALCRL	CALM1	CALM3	CALR	CALU
CAMLG	CAPNS1	CARD16	CARHSP ₁	CASKIN2	CAST	CAV2	CAVIN3	CCDC12	CCDC69	CCDC85B
CCT3	CCT4	CCT5	CCT6A	CCT7	CD151	CD320	CD40	CD55	CD59	CD63
CD81	CD93	CDC26	CDC42	CDC42EP ₃	CDIPT	CDK2AP1	CDKN1A	CFL1	CHCHD2	CHD4
CHMP3	CHMP4B	CHSY1	CLDN5	CLEC2B	CLIC1	CLIC4	CLPP	CLTB	CMIP	CNPY2
COL15A1	COL6A2	COMMD6	COPE	COPS6	COX4I1	COX7A2	COX7A2 _L	COX8A	CRIM1	CRIP2
CRTAP	CTNNA1	CTNNAL1	CTSL	CUTA	CYB5R3	CYYR1	DAD1	DAZAP2	DCTN3	DDRGK1
DDX18	DDX24	DECR1	DEGS1	DGUOK	DNAJC1	DNAJC15	DNAJC3	DPP7	DPYSL2	DPYSL3
DSTN	DUSP23	DUT	DYNC1I2	EBPL	ECE1	EEF2	EHD4	EIF3D	EIF3F	EIF3G
EIF4B	EIF4G2	EIF4H	EIF5	EIF5A	EIF6	EMC4	EMC7	EMP1	ENG	ENY2
EPAS1	EPHB4	ERAP2	ERH	ESM1	ETFB	ETS2	F2R	FAM107 _A	FAM167B	FAM177A ₁
FAM43A	FAU	FCGRT	FERMT2	FIBP	FIS1	FKBP1A	FLNB	FLOT1	FLYWCH2	FRG1
FSTL1	FURIN	FXYD5	GANAB	GAS6	GBP4	GDI2	GHITM	GIMAP1	GIMAP4	GIMAP6
GIMAP7	GINM1	GLUD1	GNA11	GNAI2	GNAS	GNG11	GNG5	GNS	GOLGA7	GRAMD1 _A
GRN	GSTK1	GSTO1	GSTP1	GTF3A	GYPC	HEBP2	HEG1	HIGD2A	HINT1	HLA-A
HLA-B	HLA-C	HLA-DRB1	HLA-DRB6	HLA-E	HMGN1	HMGN3	HNRNPM	HPCAL1	HSBP1	HSD17B1 ₂
HSP90B1	HSPA1B	HSPB1	HTRA1	ICAM2	IER3	IER3IP1	IFITM2	IFITM3	IGFBP2	IGFBP4
IGFBP7	IGHG1	IGLC2	IGLC3	IK	IKBIP	INSR	IQGAP1	ISCU	ISG15	ISG20
ITGA2	JAK1	KANK3	KCNE3	KDEL2	KLF10	KRT10	LAMTOR ₁	LAMTOR ₄	LAMTOR5	LAP3
LDHA	LEPROT	LMAN1	LMAN2	LMNA	LMO2	LRP10	LRPAP1	LRRC32	LSM1	LSM2
LSM4	LSM6	LSM7	LSM8	LTC4S	LXN	LY6E	MAF1	MAPK3	MCFD2	MESD
METTL26	METTL9	MFNG	MGST3	MICOS10	MIDN	MLEC	MOB2	MORF4L ₁	MPHOSPH ₈	MRFAP1
MRPL20	MRPL23	MRPL27	MRPL33	MRPL51	MRPL54	MRPS21	MTLN	MTPN	MVP	MYADM
MYL12A	MYL12B	NAA38	NCL	NDUFA1 ₁	NDUFA12	NDUFA2	NDUFA3	NDUFA6	NDUFAB1	NDUFB1
NDUFB10	NDUFB2	NDUFB5	NDUFB8	NDUFB9	NDUFC1	NDUFC2	NDUFS5	NDUFS8	NEAT1	NECTIN2
NENF	NFIC	NME1	NME4	NNMT	NOP10	NOP53	NOP56	NPDC1	NQO1	NRN1
NSA2	NUB1	NUCB1	NUCB2	NUCKS1	OCIAD1	OLA1	OS9	OSTC	PABPC4	PAK2
PAPSS2	PCMTD1	PDAP1	PDCD5	PDGFB	PDIA3	PDIA4	PDIA6	PDLIM1	PET100	PFKL
PGAM1	PHB2	PHPT1	PIM3	PKIG	PKN1	PLEC	PLPP3	PLSCR1	PLXND1	PNKD
PNRC1	POLE4	POLR1D	POLR2E	POLR2J	POLR2L	POMP	PON2	PPA1	PPDPF	PPIA
PPIB	PPIG	PPP1R18	PPP2CA	PPP2CB	PRCP	PRDX1	PRDX2	PRDX5	PRDX6	PRELID1
PRKCSH	PRMT1	PROS1	PRPF6	PSENEN	PSMB1	PSMB3	PSMB5	PSMB8	PSMB9	PSMC1
PSMC3	PSMC5	PSMD8	PSME1	PTPN12	PTPRM	PTTG1IP	PXDN	QSOX1	RAB2A	RAB31

RABAC1	RAC1	RACK1	RALA	RALBP1	RAMP3	RAP1B	RAPGEF1	RASIP1	RBCK1	RBM8A
RBPMS	RCN1	RDX	REEP5	RFLNB	RHOC	RIPOR1	RNASE1	RNF181	RPL11	RPL13
RPL14	RPL18A	RPL27	RPL28	RPL29	RPL3	RPL30	RPL32	RPL36	RPL36AL	RPL8
RPLP0	RPLP2	RPN1	RPS10	RPS13	RPS14	RPS16	RPS18	RPS19	RPS2	RPS20
RPS24	RPS26	RPS28	RPS3	RPS5	RPS6	RPS8	RPS9	RTF1	RTN3	RWDD1
S100A10	S100A11	S100A13	S100A6	SBDS	SCAND1	SCP2	SDF4	SDHC	SEC11A	SELENOK
SELENO M	SELENON	SELENOT	SELP	SEPHS2	SERF2	SERINC1	SERINC3	SERPINB 1	SERPING1	SERPINH 1
SF3B5	SH3BGRL 3	SH3BP5	SHISA5	SIVA1	SLC25A37	SLC44A2	SLIRP	SLU7	SMAD1	SMARCA 4
SNHG5	SNRK	SNRPB	SNRPB2	SNRPC	SNRPD1	SNRPD2	SNRPE	SNRPF	SNTB2	SNX17
SOCS3	SOD1	SPAG7	SPCS1	SPCS2	SPG21	SPTBN1	SPTLC2	SQSTM1	SRI	SRP14
SRP72	SSBP4	SSU72	ST13	ST6GAL1	STAB1	SUGT1	SULF2	SUMO2	SVIP	SYNGR2
TAGLN2	TAP1	TAP2	TAPBP	TAX1BP1	TAX1BP3	TBCA	TBCB	TCIM	TCN2	TEK
TGOLN2	THBD	THRAP3	TIMM13	TKT	TMA7	TMBIM1	TMED2	TMED9	TMEM109	TMEM123
TMEM147	TMEM14 C	TMEM179 B	TMEM20 4	TMEM23 0	TMEM255 B	TMEM25 8	TMEM30 A	TMEM50 A	TMOD3	TMTC1
TNFRSF1 A	TOMM7	TPGS1	TPM3	TPM4	TPST2	TRAM1	TRAPPC1	TRIM28	TRIM8	TRIOBP
TRMT112	TSPAN4	TSPAN9	TSPO	TUBA1A	TUBB	TUFM	TXN	TXNDC1 7	TYROBP	UBE2B
UBE2L3	UBE2L6	UBE2R2	UBXN6	UFC1	UQCR10	URM1	VAMP3	VAMP5	VAT1	VCP
VDAC2	VKORC1	VPS28	VWF	WDR1	XRCC5	XRCC6	YIPF3	YWHAB	YWHAG	YY1
ZC3H13	ZFP36L1	ZNHIT1								

Appendix Table C-3. Genes excluded for each CSVD outcome in the Mendelian randomization analyses using gene expression exposures and cerebral small vessel disease outcomes.

Excluded for WMH	Excluded for PVS	Excluded for CMB	Excluded for SVS
DPP7		ATP2B4	APLP2
NPDC1		BSG	ATP1A1
		CLIC1	ATP2B4
		COL15A1	BUD31
		FAM107A	C12orf57
		FLOT1	CLIC1
		FRG1	COL15A1
		GAS6	CRIM1
		HLA-A	FAM107A
		HLA-C	GSTO1
		HLA-DRB1	HLA-A
		HLA-DRB6	HLA-E
		HLA-E	HNRNPM
		HSPA1B	HSPA1B
		IER3	HSPB1
		IGHG1	IER3
		ISG15	IGHG1
		LSM2	LSM1
		LTC4S	LSM2
		MRPL20	LSM6
		PPP1R18	LTC4S
		PRMT1	MIDN
		PSMC5	MRPL20
		RAP1B	MRPL33
		RBM8A	MTLN
		RPL18A	OSTC
		RPS13	PDAP1
		S100A6	PPP1R18
		SBDS	PRCP
		SELENON	PRMT1
		TPGS1	PSMC5
		TUBB	PTPRM
		UBE2B	RAP1B
			RBM8A
			RPL18A
			RPL29
			RPL36
			RPS13
			SELENON
			SERINC3
			TMEM179B
			TRAPPC1
			TUBB
			UBE2B
			YY1

Appendix Table C-4. Sensitivity analyses performed using coronary artery-specific gene expression exposures and cerebral small vessel disease outcomes. Genes listed were associated with the respective cerebral small vessel disease marker at a nominal $p < 0.05$; bolded genes were also significant after correction for multiple testing.

Associated with WMH	Associated with PVS	Associated with CMB	Associated with SVS
HLA-DRB6	HLA-C	CCT3	HSD17B12
HLA-C	RBCK1	SPG21	IQGAP1
NDUFS5	HLA-DRB6	TRIOBP	ERAP2
CALCRL	NUCKS1	DDX18	ANXA5
MRPS21	MRPL32	NDUFA3	NME4
PDCD5	NRP2	CAVIN3	SPG21
ANXA5	MRPL23	MRPS21	ACTR3
HLA-B	RCN1	MRPL32	LRPAP1
DYNC1I2	NEAT1	CARHSP1	IKBIP
LRPAP1	LAMTOR4	MRPL23	TCN2
PPA1	RPS9	ATRAID	PRDX1
RPS18	METTL26	PSMB9	PLEC
SPAG7	BANF1	CAMLG	SIVA1
PLEC	MRPS21	SPARC	CDK2AP1
HLA-DRB1	MCFD2	CD59	NSA2
CARHSP1	URM1		EBPL
ARL6IP5	LTC4S		ATRAID
RPL28	QSOX1		MRPL32
ATP5PO	GAS6		ACTR2
LSM2	POLR1D		CD59
PPP1R18	VPS28		PSMB5
FAM107A	RPS24		
ATRAID	C7orf50		
ARHGDIB	IKBIP		
GSTK1	FIS1		
SPG21	RPS18		
	HLA-A		
	CAVIN3		
	TUFM		
	MOB2		

Appendix Table C-5. List of unique methylation sites included as instruments in the Mendelian randomization analyses using gene expression exposures and cerebral small vessel disease outcomes.

cg00061031	cg00166216	cg00323915	cg00347643	cg00348858	cg00356499	cg00375581	cg00395296	cg00423487	cg00431565	cg00472373
cg00524220	cg00551647	cg00581603	cg00684283	cg00685014	cg00726046	cg00785193	cg00797651	cg00836007	cg00836091	cg00854314
cg00883689	cg00900524	cg00923807	cg00935119	cg00962304	cg01054402	cg01091099	cg01114900	cg01284415	cg01284869	cg01285435
cg01286133	cg01299997	cg01328473	cg01359822	cg01369114	cg01422274	cg01439670	cg01459453	cg01514075	cg01517384	cg01518465
cg01529207	cg01567051	cg01574390	cg01591881	cg01629329	cg01667702	cg01741836	cg01758539	cg01770362	cg01827781	cg01869186
cg02065750	cg02072170	cg02075820	cg02101833	cg02152968	cg02183531	cg02232751	cg02276665	cg02338345	cg02427764	cg02573566
cg02652597	cg02711929	cg02792877	cg02799643	cg02814118	cg02871659	cg02935298	cg03038418	cg03043406	cg03063057	cg03079761
cg03110633	cg03141158	cg03183936	cg03309967	cg03355213	cg03394764	cg03437912	cg03480605	cg03589001	cg03633268	cg03714916
cg03853587	cg03861347	cg03863486	cg03864128	cg03870261	cg03888447	cg03957109	cg04053108	cg04059188	cg04070771	cg04188351
cg04226276	cg04351776	cg04506190	cg04552852	cg04614290	cg04633683	cg04663916	cg04696780	cg04728402	cg04731861	cg04833034
cg04865442	cg05046996	cg05083128	cg05147525	cg05163057	cg05212138	cg05231098	cg05232215	cg05236720	cg05241015	cg05380558
cg05498726	cg05532239	cg05587400	cg05638426	cg05638821	cg05834899	cg05868183	cg05965490	cg05977523	cg06018095	cg06046490
cg06070002	cg06151968	cg06285241	cg06355652	cg06409856	cg06419659	cg06422947	cg06463313	cg06483076	cg06521852	cg06524039
cg06532880	cg06599209	cg06627532	cg06644488	cg06809298	cg06958537	cg06961122	cg07066907	cg07069934	cg07093324	cg07119830
cg07202214	cg07202353	cg07248242	cg07337602	cg07341220	cg07388493	cg07480608	cg07578618	cg07621169	cg07639376	cg07718808
cg07844572	cg07850221	cg07898899	cg07915634	cg07915730	cg07955126	cg07964163	cg07985890	cg07992500	cg08006309	cg08038054
cg08179530	cg08182193	cg08183303	cg08216808	cg08297640	cg08314408	cg08380311	cg08446038	cg08521989	cg08523029	cg08550242
cg08596817	cg08627380	cg08742833	cg08831277	cg08859206	cg08925046	cg08925882	cg08946161	cg09043214	cg09056317	cg09161758
cg09313745	cg09330427	cg09411730	cg09505809	cg09553581	cg09554856	cg09571603	cg09580214	cg09622203	cg09639133	cg09685472
cg09687322	cg09699787	cg09757087	cg09757250	cg09986316	cg10075906	cg10148591	cg10189774	cg10219093	cg10409680	cg10465839
cg10487521	cg10511467	cg10551016	cg10573932	cg10636054	cg10652351	cg10797197	cg10816922	cg10921709	cg10980102	cg11108890
cg11124915	cg11343894	cg11350520	cg11366788	cg11374355	cg11375102	cg11386711	cg11401558	cg11405475	cg11453585	cg11456513
cg11569329	cg11718162	cg11781344	cg11875119	cg11938718	cg11961138	cg11964810	cg12017722	cg12037947	cg12046793	cg12075498
cg12143168	cg12150039	cg12311132	cg12379720	cg12394014	cg12441358	cg12444076	cg12488111	cg12514734	cg12555334	cg12614667
cg12619504	cg12640109	cg12930392	cg12933162	cg13012653	cg13104938	cg13142374	cg13249591	cg13313836	cg13375538	cg13385210
cg13431342	cg13445177	cg13485230	cg13618979	cg13620110	cg13634151	cg13655250	cg13683864	cg13720395	cg13787135	cg13835894
cg13985198	cg14236602	cg14284257	cg14391907	cg14465207	cg14554217	cg14656441	cg14714391	cg14729962	cg14788334	cg14792002
cg14800883	cg14833160	cg14844236	cg14883993	cg14976592	cg15001636	cg15091337	cg15432367	cg15474579	cg15481791	cg15570293
cg15700009	cg15716373	cg15773148	cg15778232	cg15822222	cg15866021	cg15892280	cg15928398	cg16073427	cg16230307	cg16246488
cg16274678	cg16285447	cg16416158	cg16499645	cg16509239	cg16511795	cg16553119	cg16577123	cg16672223	cg16673712	cg16700025
cg16714654	cg16719560	cg16734191	cg16751098	cg16833797	cg16839921	cg16847315	cg16894138	cg16909084	cg16958793	cg17041152
cg17052170	cg17073323	cg17181653	cg17244218	cg17338821	cg17388039	cg17448192	cg17453456	cg17480554	cg17490089	cg17518825
cg17755386	cg17801352	cg17965690	cg17982102	cg17985854	cg18039042	cg18079499	cg18087520	cg18114828	cg18145911	cg18158419
cg18279742	cg18322321	cg18390683	cg18456459	cg18474885	cg18634506	cg18670235	cg18829411	cg18872420	cg18969008	cg18993334
cg19009305	cg19087104	cg19096034	cg19114214	cg19114543	cg19145710	cg19238380	cg19265998	cg19303748	cg19378537	cg19383211
cg19392998	cg19404215	cg19495714	cg19513321	cg19525717	cg19553910	cg19574915	cg19733740	cg19757176	cg19788250	cg19811118
cg19859729	cg19875535	cg19905587	cg20167074	cg20267732	cg20322193	cg20388165	cg20399252	cg20533899	cg20641794	cg20727362
cg20752233	cg20755353	cg20950843	cg21016503	cg21039874	cg21052403	cg21091547	cg21098323	cg21103987	cg21104449	cg21154227

cg21160842	cg21364723	cg21404906	cg21537187	cg21601405	cg21663431	cg21790991	cg21824733	cg21934504	cg22041417	cg22045942
cg22138327	cg22141781	cg22215678	cg22237777	cg22339338	cg22360649	cg22383121	cg22532475	cg22614203	cg22703724	cg22712983
cg22821355	cg22830091	cg22854549	cg22857356	cg22977317	cg22979368	cg23003085	cg23044884	cg23050437	cg23102026	cg23139584
cg23141902	cg23189044	cg23325242	cg23398173	cg23473904	cg23486701	cg23541619	cg23569941	cg23702046	cg23725454	cg23902361
cg23991482	cg24082795	cg24114444	cg24129977	cg24152080	cg24251862	cg24254196	cg24342717	cg24406162	cg24441185	cg24500487
cg24586039	cg24637417	cg24731702	cg24733384	cg24735937	cg24760922	cg24795825	cg24869272	cg24897127	cg25090051	cg25135322
cg25302646	cg25326570	cg25369027	cg25404088	cg25408620	cg25446361	cg25467652	cg25595793	cg25603927	cg25630910	cg25635139
cg25649188	cg25676471	cg25694790	cg25848158	cg25866895	cg25882345	cg25902939	cg25960063	cg25974617	cg26071135	cg26102819
cg26104986	cg26149485	cg26201815	cg26230275	cg26260789	cg26371346	cg26440467	cg26489057	cg26529300	cg26548293	cg26581729
cg26594335	cg26758857	cg26786924	cg26844104	cg26971710	cg27031448	cg27037648	cg27047750	cg27072683	cg27104695	cg27149555
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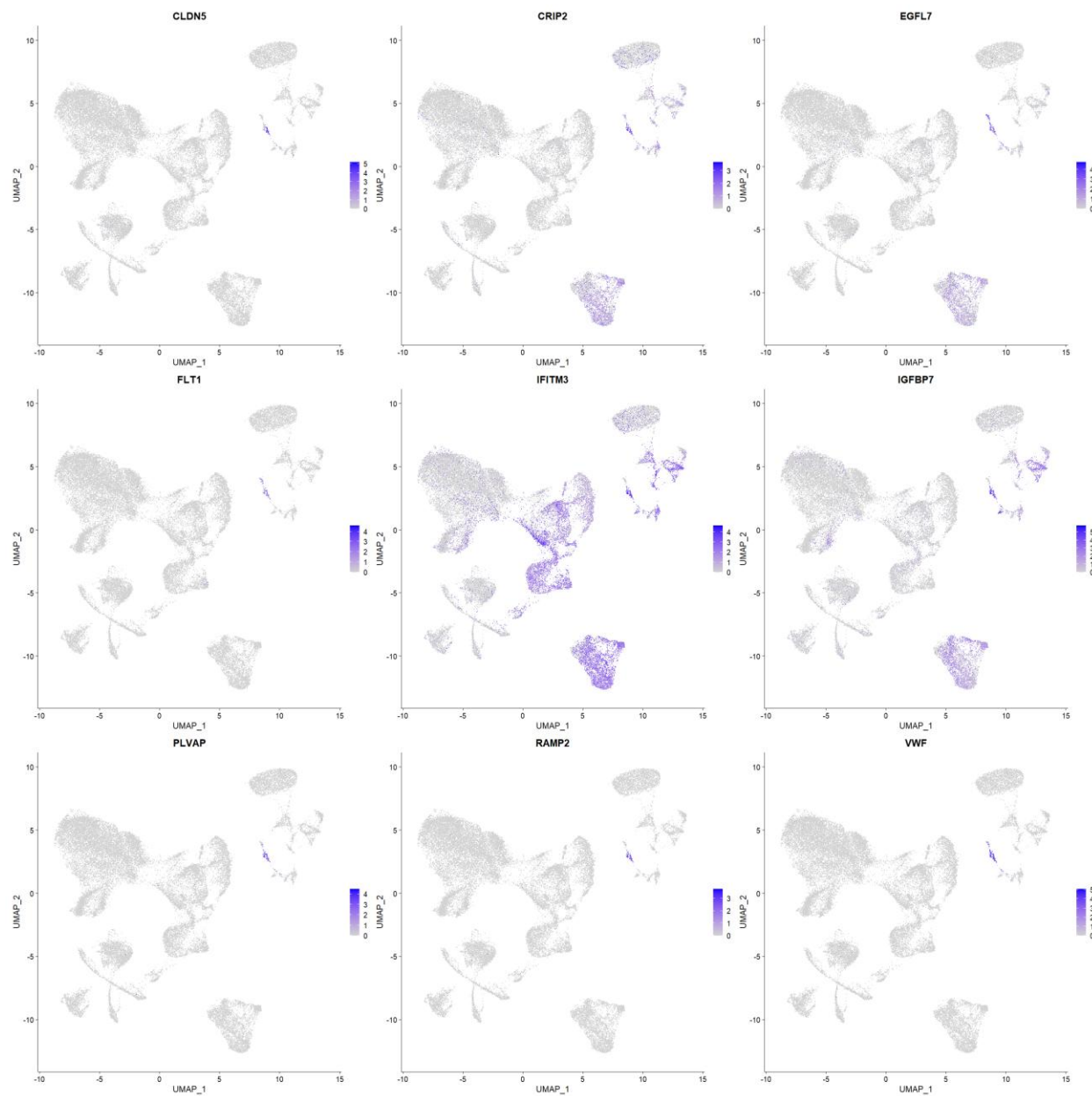
Appendix Table C-6. Genes excluded for each CSVD outcome in the Mendelian randomization analyses using methylation site exposures and cerebral small vessel disease outcomes.

Excluded for WMH	Excluded for PVS	Excluded for CMB	Excluded for SVS
ANXA5	ANXA5	CDKN1A	ANP32B
DNAJC15	CDKN1A	CRIP2	ANXA5
FIS1	CRIP2	FIS1	ARPC2
HLA-C	DNAJC15	GNA11	BUD31
NPDC1	GNA11	HLA-B	CDKN1A
TRIOBP	HLA-C	HLA-DRB6	CRIP2
	KANK3	IGFBP4	DNAJC15
	PHB2	PHB2	FIS1
	PNKD	PNKD	GNA11
	TRIOBP	SQSTM1	HLA-C
	TSPAN4	TSPAN4	HLA-DRB6
	VPS28	VPS28	IGFBP4
			KANK3
			LRPAP1
			PFKL
			PHB2
			PIM3
			PNKD
			PXDN
			RNASE1
			S100A13
			SQSTM1
			SSU72
			ST13
			TRIOBP
			TSPAN4
			VPS28

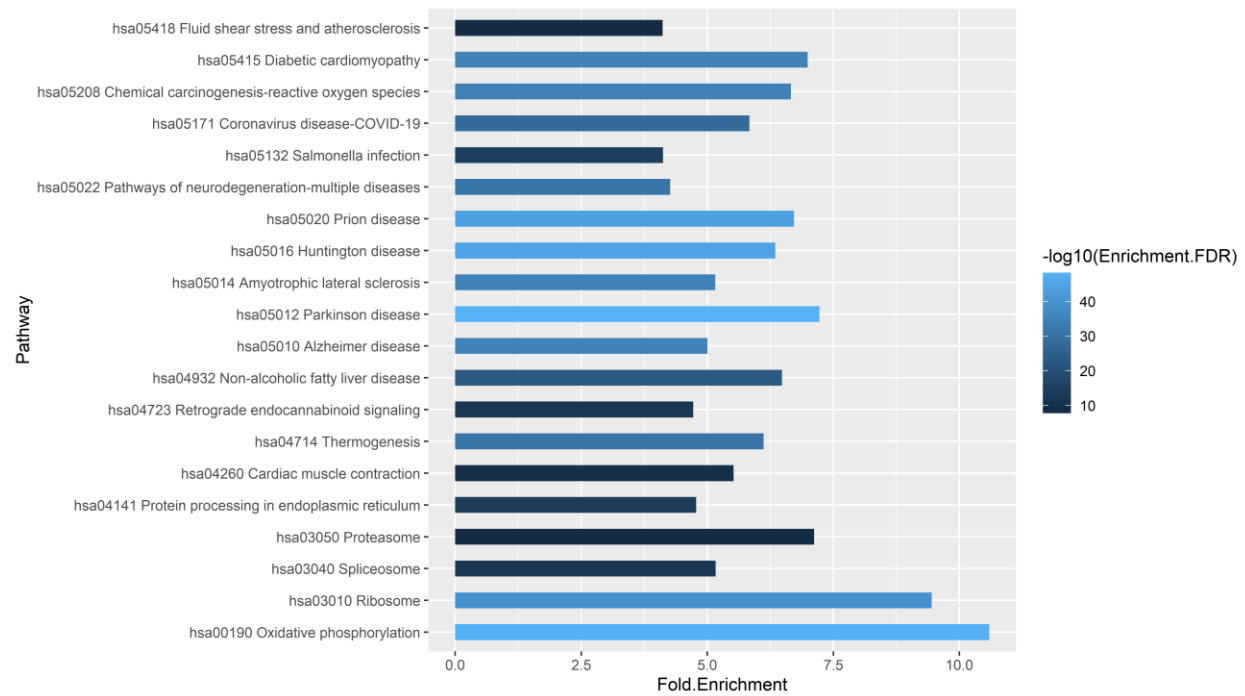
Appendix Table C-7. The top 10 (ranked by connectivity scores) pharmacological perturbation signatures in the same direction as the effects of immune checkpoint inhibitor treatment on endothelial cell gene expression in the gene set robustly associated with cerebral small vessel disease.

Pharmacological Class	Cell Types Tested	Raw Connectivity Score	Adjusted P-value	Regulatory Status
Selective Estrogen Receptor Modulators	MCF7	0.81	0.0042	FDA-approved
ALK Tyrosine Kinase Receptor Inhibitors	MCF10A	0.81	0.046	FDA-approved
Vitamin D Receptor Agonists	MCF10A	0.76	0.046	FDA-approved
Dihydrofolate Reductase Inhibitors	HA1E	0.74	0.0052	FDA-approved
MEK Inhibitors	MCF10A	0.7	0.0036	FDA-approved
BCR-ABL Kinase Inhibitors	HT29	0.69	0.0039	FDA-approved
DNA Methyltransferase Inhibitors	HA1E	0.66	0.046	FDA-approved
RET Tyrosine Kinase Inhibitors	YAPC	0.66	0.035	FDA-approved
RAF Inhibitors	HT29	0.65	0.0024	FDA-approved
FLT3 Inhibitors	HT29	0.59	0.0029	FDA-approved

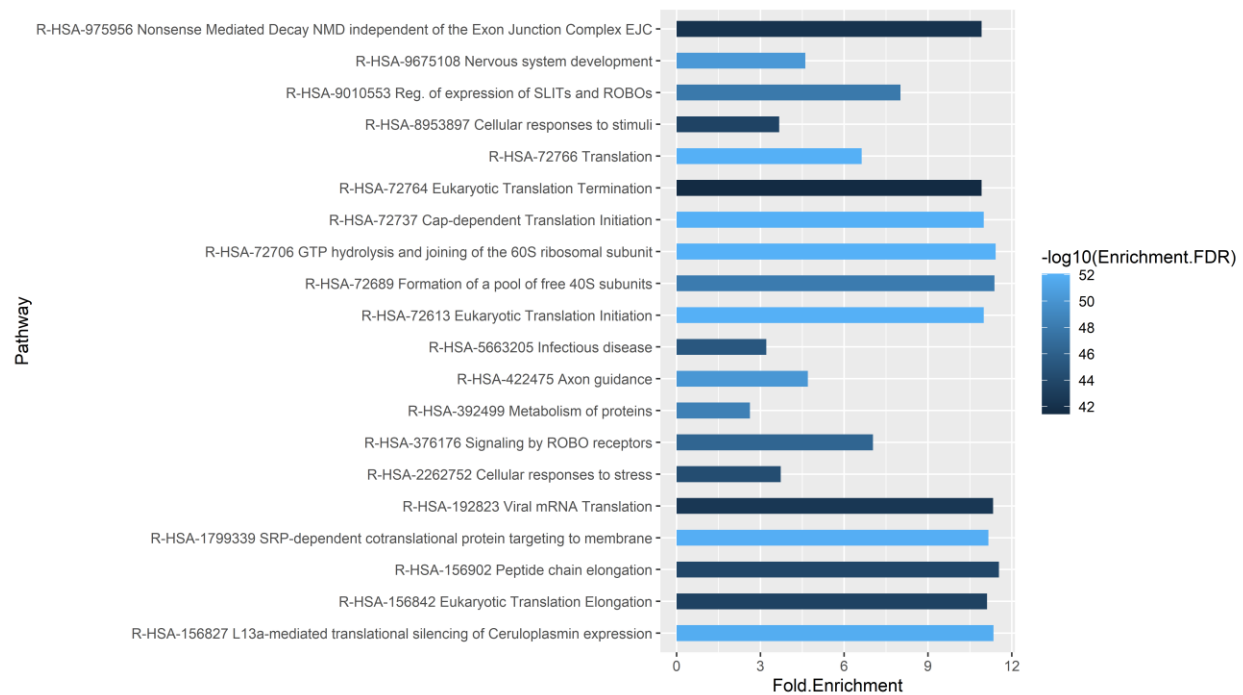
Supplementary Figures



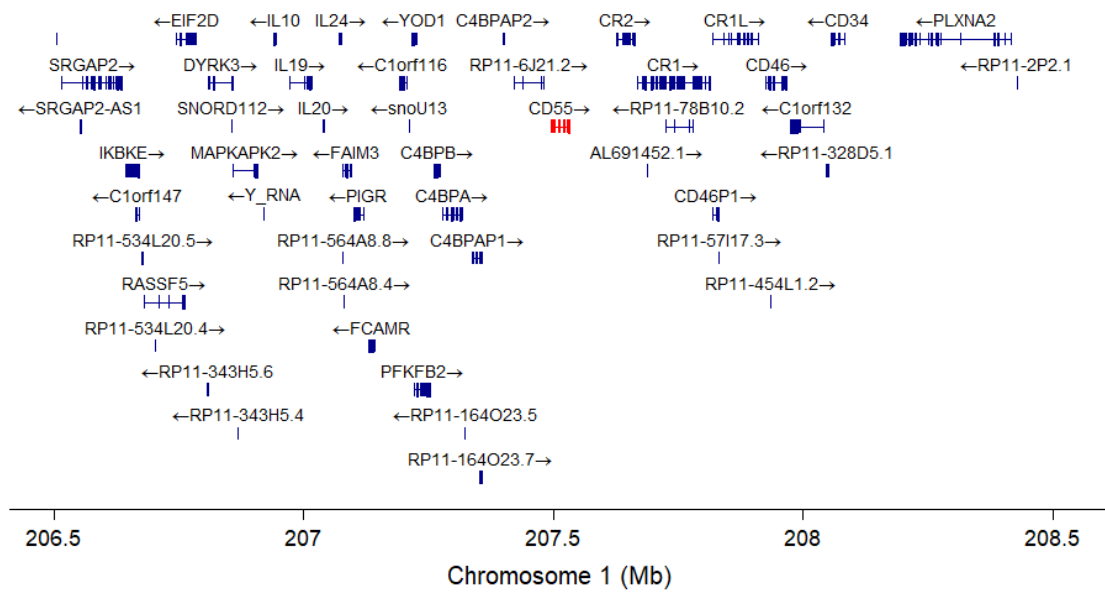
Appendix Figure C-1. Uniform manifold approximation and projection (UMAP) plots for 9 of the top markers used to identify the cluster of endothelial cells from single-cell RNA-sequencing data collected in clear cell renal carcinoma patients.



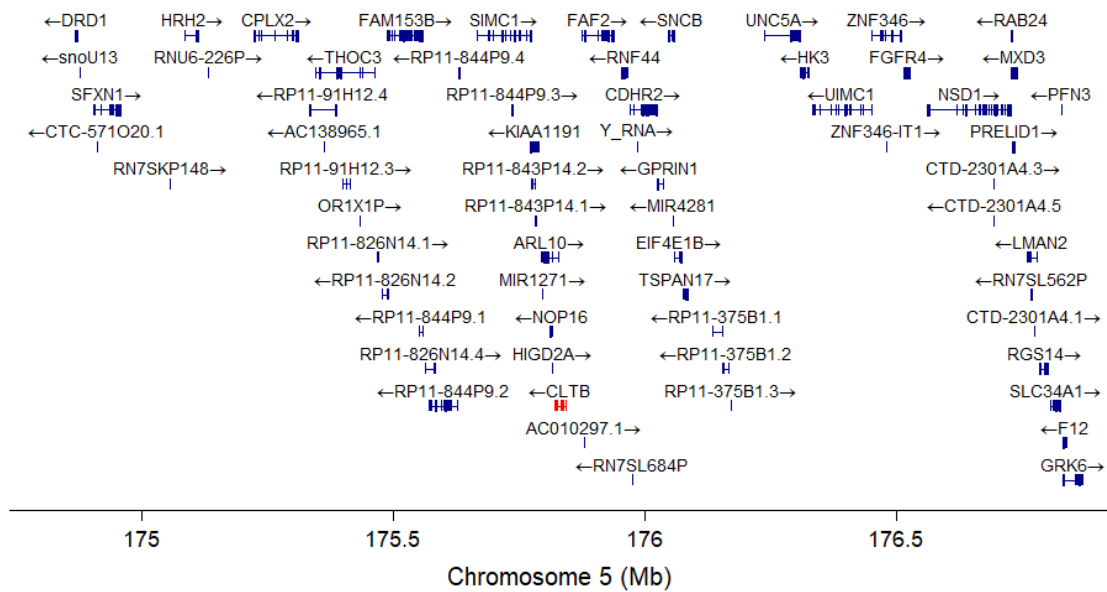
Appendix Figure C-2. Kyoto Encyclopedia of Genes and Genomes (KEGG) pathways significantly enriched when comparing differentially expressed genes between control and immune checkpoint inhibitor-exposed endothelial cells.



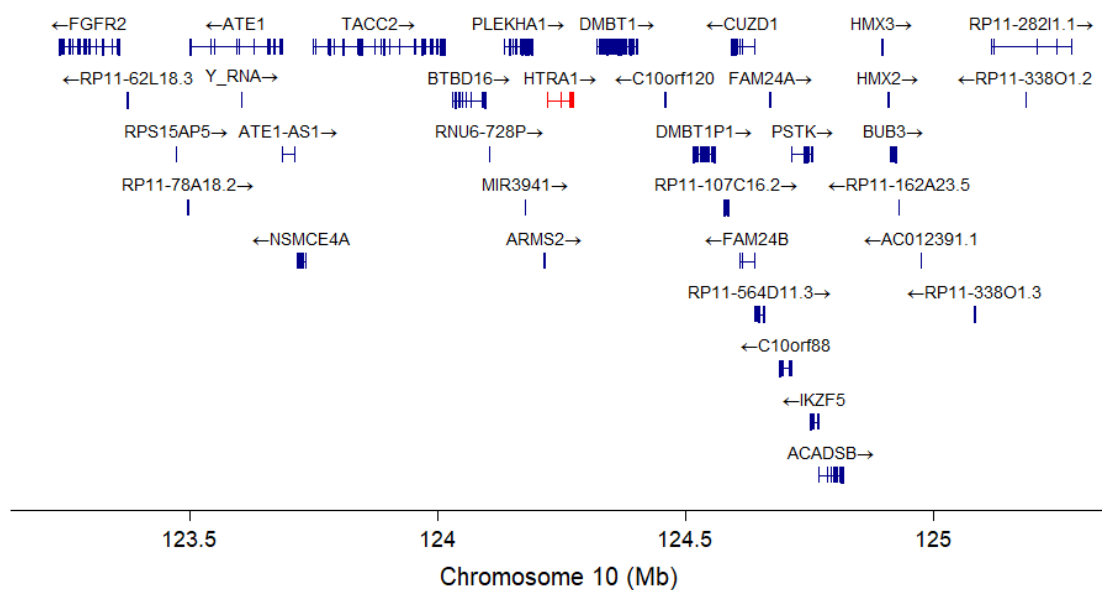
Appendix Figure C-3. Reactome pathways significantly enriched when comparing differentially expressed genes between control and immune checkpoint inhibitor-exposed endothelial cells.



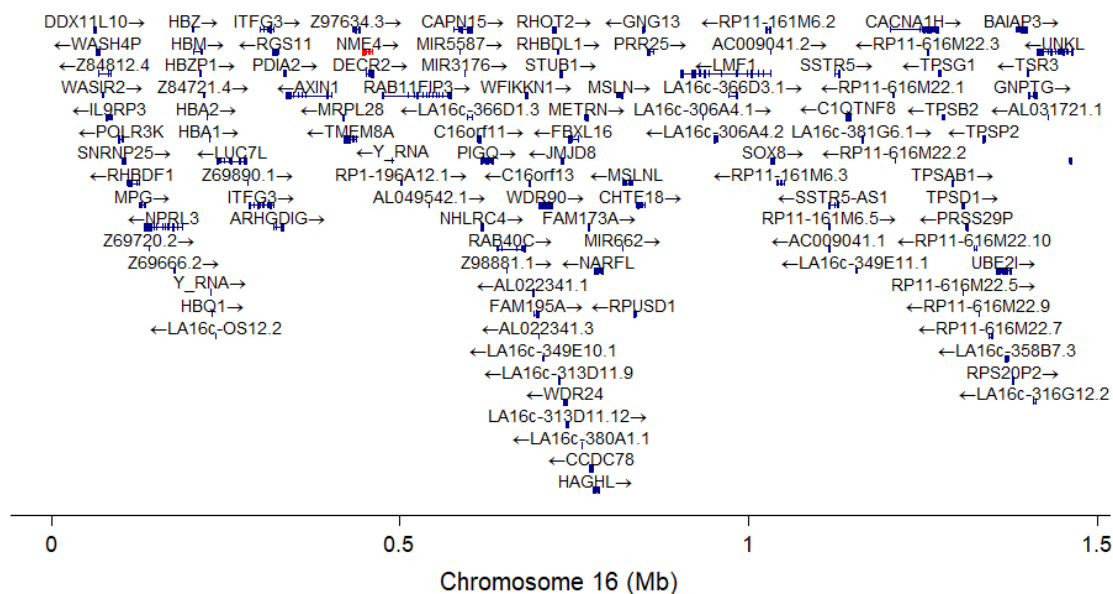
Appendix Figure C-4. Gene track depicting the location of the *Cd55* gene.



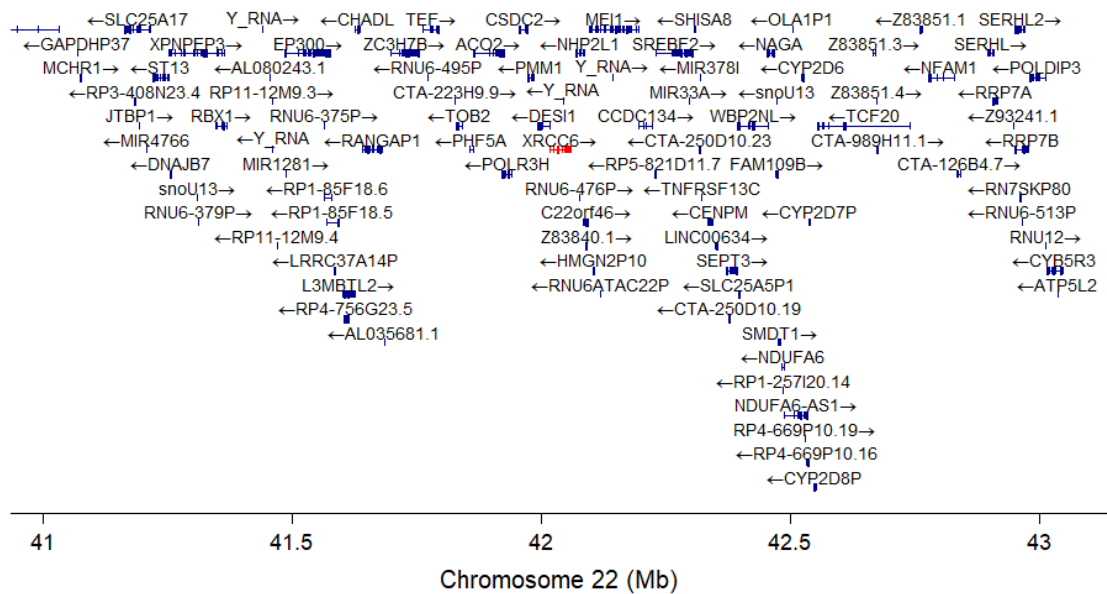
Appendix Figure C-5. Gene track depicting the location of the *Cltb* gene.



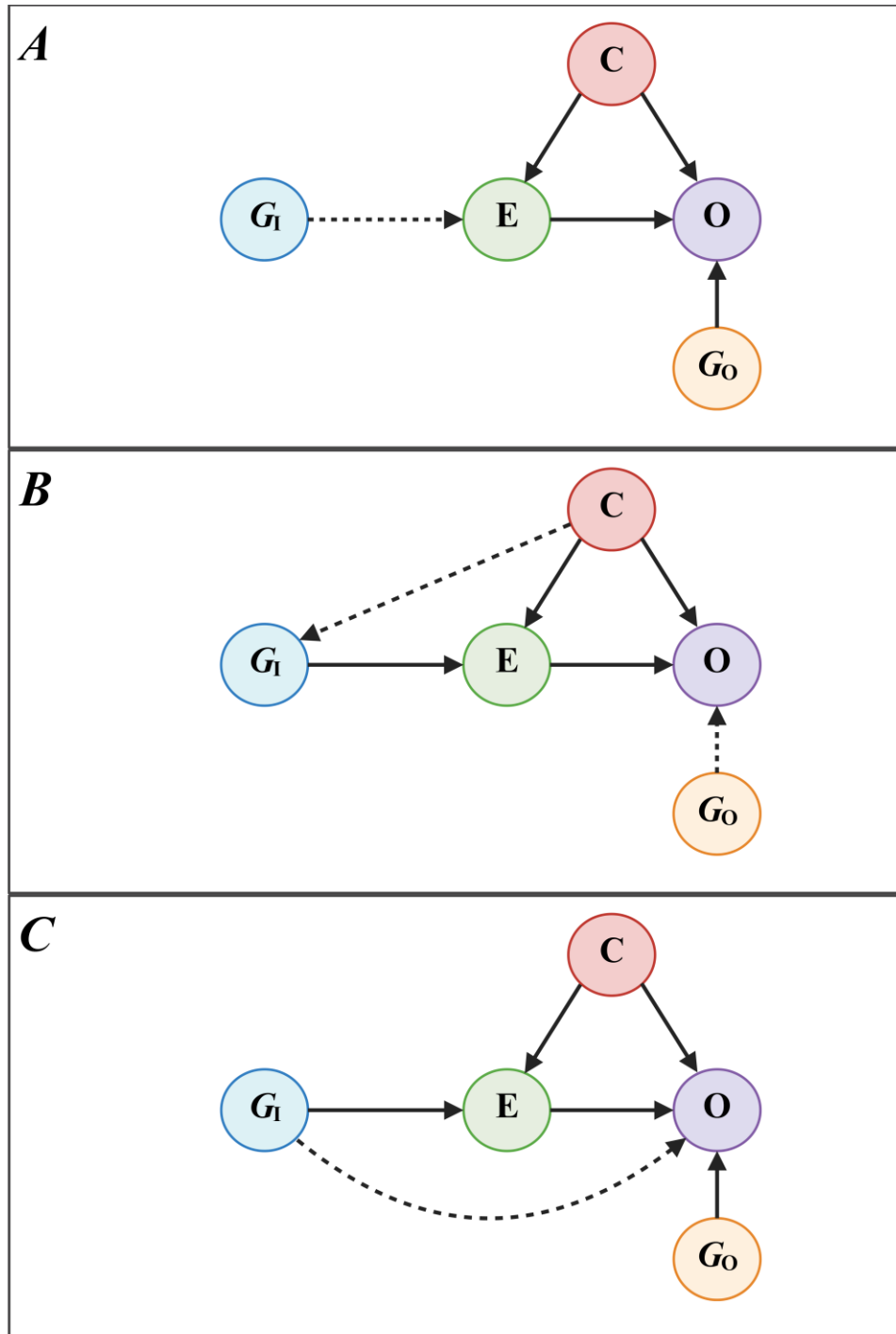
Appendix Figure C-6. Gene track depicting the location of the *Htral* gene.



Appendix Figure C-7. Gene track depicting the location of the *Nme4* gene.



Appendix Figure C-8. Gene track depicting the location of the *Xrcc6* gene.



Appendix Figure C-9. Schematic demonstration of Mendelian randomization principles, as well as the core assumptions allowing for causal estimates to be derived. Panel A demonstrates the relevance assumption, Panel B depicts the exchangeability assumption, and Panel C shows the exclusion-restriction assumption. G_1 , genetic variants used as instrumental variables for the exposure; G_0 , genetic variants used as instrumental variables for the outcome; E , exposure variable; O , outcome variable; C , potential unmeasured confounding variables.

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