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Publication appendix

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Full publication list based on archive at google scholar.

- H-index: **63**
- i10-index: **124**

1. Howe, L., Nivard, M., Morris, T., Hansen, A., Rasheed, H., Cho, Y., et al. Within-sibship genome-wide association analyses decrease bias in estimates of direct genetic effects. Nature genetics (2022).
2. Battram, T., Yousefi, P., Crawford, G., Prince, C., Babaei, M., Sharp, G., et al. The EWAS catalog: A database of epigenome-wide association studies. Wellcome open research (2022).
3. Zhao, H., Rasheed, H., Nøst, T., Cho, Y., Liu, Y., et al. Proteome-wide mendelian randomization in global biobank meta-analysis reveals multi-ancestry drug targets for common diseases. Cell genomics (2022).
4. Speyer, L., Neaves, S., Hall, H., Hemani, G., Lombardo, M., Murray, A., et al. Polygenic risks for joint developmental trajectories of internalizing and externalizing problems: Findings from the ALSPAC cohort. Journal of Child Psychology and Psychiatry (2022).
5. Borges, M., Haycock, P., Zheng, J., Hemani, G., Holmes, M., et al. Role of circulating polyunsaturated fatty acids on cardiovascular diseases risk: Analysis using mendelian randomization and fatty acid genetic association data from over 114 …. BMC medicine (2022).
6. Woolf, B., Cara, N., Moreno-Stokoe, C., Whitesell, V., Drax, K., Higgins, J., et al. Investigating the transparency of reporting in two-sample summary data mendelian randomization studies using the MR-base platform. International journal of epidemiology (2022).
7. Lee, M., Huan, T., McCartney, D., Chittoor, G., Vries, M., Lahousse, L., et al. Pulmonary function and blood DNA methylation: A multiancestry epigenome-wide association meta-analysis. American Journal of Respiratory and Critical Care Medicine (2022).
8. Howe, L., Evans, D., Hemani, G., Smith, G. & Davies, N. Evaluating indirect genetic effects of siblings using singletons. PLoS genetics (2022).
9. Shen, X., Caramaschi, D., Adams, M., Walker, R., Min, J., Kwong, A., et al. DNA methylome-wide association study of genetic risk for depression implicates antigen processing and immune responses. Genome medicine (2022).
10. Mitchell, D., Stone, E., Andrews, O., Bamber, J., Bingham, R., Browse, J., et al. The bristol CMIP6 data hackathon. Weather (2022).
11. Fitzsimons, E., Moulton, V., Hughes, D., Neaves, S., Ho, K., Hemani, G., et al. Collection of genetic data at scale for a nationally representative population: The UK millennium cohort study. Longitudinal and Life Course Studies (2022).
12. Wade, K., Yarmolinsky, J., Giovannucci, E., Lewis, S., Millwood, I., et al. Applying mendelian randomization to appraise causality in relationships between nutrition and cancer. Cancer Causes & Control (2022).
13. Robinson, J., Hemani, G., Babaei, M., Huang, Y., Baird, D., Tsai, E., et al. An efficient and robust tool for colocalisation: Pair-wise conditional and colocalisation (PWCoCo). bioRxiv (2022).

14. Corfield, E., Frei, O., Shadrin, A., Rahman, Z., Lin, A., Athanasiu, L., et al. The norwegian mother, father, and child cohort study (MoBa) genotyping data resource: MoBaPsychGen pipeline v. 1. BioRxiv (2022).

15. Borges, M., Haycock, P., Zheng, J., Hemani, G., Howe, L., Schmidt, A., et al. The impact of fatty acids biosynthesis on the risk of cardiovascular diseases in europeans and east asians: A mendelian randomization study. Human Molecular Genetics (2022).

16. Walters, R., Fairhurst-Hunter, Z., Lin, K., Millwood, I., Pozarickij, A., Chen, T., et al. Trans-ancestry meta-analysis improves performance of genetic scores for multiple adiposity-related traits in east asian populations. (2022).

17. Hemani, G. Meta-analysis in genetic association studies. Systematic Reviews in Health Research: Meta-Analysis in Context (2022).

18. Hemani, G., Tilling, K. & Smith, G. Collider bias from selecting disease samples distorts causal inferences. Genetic Epidemiology (2022).

19. Forde, A., Hemani, G. & Ferguson, J. Review and further developments in statistical corrections for winner's curse in genetic association studies. bioRxiv (2022).

20. Fairhurst-Hunter, Z., Lin, K., Millwood, I., Pozarickij, A., Chen, T., Torres, J., et al. Trans-ancestry meta-analysis improves performance of genetic scores for multiple adiposity-related traits in east asian populations. medRxiv (2022).

21. Battram, T., Gaunt, T., Relton, C., Timpson, N. & Hemani, G. A comparison of the genes and genesets identified by EWAS and GWAS of fourteen complex traits. medRxiv (2022).

22. Watkins, S., Suderman, M., Hemani, G., Burrows, K., Lawlor, D., West, J., et al. DNA co-methylation has a stable structure and is related to specific aspects of genome regulation. bioRxiv (2022).

23. Robinson, J., Battram, T., Baird, D., Haycock, P., Zheng, J., Hemani, G., et al. Evaluating the potential benefits and pitfalls of combining protein and expression quantitative trait loci in evidencing drug targets. bioRxiv (2022).

24. Võsa, U., Claringbould, A., Westra, H., Bonder, M., Deelen, P., Zeng, B., et al. Large-scale cis-and trans-eQTL analyses identify thousands of genetic loci and polygenic scores that regulate blood gene expression. Nature genetics (2021).

25. Min, J., Hemani, G., Hannon, E., Dekkers, K., Castillo-Fernandez, J., Luijk, R., et al. Genomic and phenotypic insights from an atlas of genetic effects on DNA methylation. Nature genetics (2021).

26. Brooks-Pollock, E., Christensen, H., Trickey, A., Hemani, G., Nixon, E., et al. High COVID-19 transmission potential associated with re-opening universities can be mitigated with layered interventions. Nature communications (2021).

27. Lyon, M., Andrews, S., Elsworth, B., Gaunt, T., Hemani, G. & Marcora, E. The variant call format provides efficient and robust storage of GWAS summary statistics. Genome biology (2021).

28. McCartney, D., Min, J., Richmond, R., Lu, A., Sobczyk, M., Davies, G., et al. Genome-wide association studies identify 137 genetic loci for DNA methylation biomarkers of aging. Genome biology (2021).

29. Sanderson, E., Richardson, T., Hemani, G. & Smith, G. The use of negative control outcomes in mendelian randomization to detect potential population stratification. International journal of epidemiology (2021).

30. Wang, J., Zhao, Q., Bowden, J., Hemani, G., Smith, G., Small, D., et al. Causal inference for heritable phenotypic risk factors using heterogeneous genetic instruments. PLoS genetics (2021).

31. Simcoe, M., Valdes, A., Liu, F., Furlotte, N., Evans, D., et al. Genome-wide association study in almost 195,000 individuals identifies 50 previously unidentified genetic loci for eye color. Science advances (2021).
32. Nixon, E., Trickey, A., Christensen, H., Finn, A., Thomas, A., Relton, C., et al. Contacts and behaviours of university students during the COVID-19 pandemic at the start of the 2020/2021 academic year. Scientific reports (2021).
33. Anderson, E., Richmond, R., Jones, S., Hemani, G., Wade, K., Dashti, H., et al. Is disrupted sleep a risk factor for alzheimer's disease? Evidence from a two-sample mendelian randomization analysis. International journal of epidemiology (2021).
34. Baird, D., Liu, J., Zheng, J., Sieberts, S., Perumal, T., Elsworth, B., et al. Identifying drug targets for neurological and psychiatric disease via genetics and the brain transcriptome. PLoS genetics (2021).
35. Liu, Y., Elsworth, B., Erola, P., Haberland, V., Hemani, G., et al. EpiGraphDB: A database and data mining platform for health data science. Bioinformatics (2021).
36. Dongen, J., Gordon, S., McRae, A., Odintsova, V., Mbarek, H., et al. Identical twins carry a persistent epigenetic signature of early genome programming. Nature communications (2021).
37. Sadreev, I., Elsworth, B., Mitchell, R., Paternoster, L., Sanderson, E., et al. Navigating sample overlap, winner's curse and weak instrument bias in mendelian randomization studies using the UK biobank. medRxiv (2021).
38. Russell, A., Hemani, G., Jones, H., Ford, T., Gunnell, D., et al. An exploration of the genetic epidemiology of non-suicidal self-harm and suicide attempt. BMC psychiatry (2021).
39. Schlosser, P., Tin, A., Matias-Garcia, P., Thio, C., Joehanes, R., Liu, H., et al. Meta-analyses identify DNA methylation associated with kidney function and damage. Nature communications (2021).
40. Bonilla, C., Bertoni, B., Min, J., Hemani, G., et al. Investigating DNA methylation as a potential mediator between pigmentation genes, pigmentary traits and skin cancer. Pigment cell & melanoma research (2021).
41. Hemani, G., Powell, J., Wang, H., Shakhbazov, K., Westra, H., Esko, T., et al. Phantom epistasis between unlinked loci. Nature (2021).
42. Fang, S., Hemani, G., Richardson, T., Gaunt, T. & Smith, G. Evaluating and implementing block jackknife resampling mendelian randomization to mitigate bias induced by overlapping samples. medRxiv (2021).
43. Korologou-Linden, R., Xu, B., Coulthard, E., Walton, E., Wearn, A., Hemani, G., et al. The bidirectional causal effects of brain morphology across the life course and risk of alzheimer's disease: A cross-cohort comparison and mendelian randomization meta-analysis. medRxiv (2021).
44. Higbee, D., Granell, R., Hemani, G., Smith, G. & Dodd, J. Lung function, COPD and cognitive function: A multivariable and two sample mendelian randomization study. BMC pulmonary medicine (2021).
45. Howe, L., Battram, T., Morris, T., Hartwig, F., Hemani, G., Davies, N., et al. Assortative mating and within-spouse pair comparisons. PLoS genetics (2021).
46. Hemani, G., Thomas, A., Walker, J., Trickey, A., Nixon, E., Ellis, D., et al. Modelling pooling strategies for SARS-CoV-2 testing in a university setting. medRxiv (2021).
47. Tin, A., Schlosser, P., Matias-Garcia, P., Thio, C., Joehanes, R., et al. Epigenome-wide association study of serum urate reveals insights into urate co-regulation and the SLC2A9 locus. Nature communications (2021).

48. Thomas, A., Danon, L., Christensen, H., Northstone, K., Smith, D., Nixon, E., et al. Limits of lockdown: Characterising essential contacts during strict physical distancing. medRxiv (2021).

49. Trickey, A., Nixon, E., Christensen, H., Finn, A., Thomas, A., Relton, C., et al. University students and staff able to maintain low daily contact numbers during various COVID-19 guideline periods. Epidemiology & Infection (2021).

50. Trickey, A., Nixon, E., Christensen, H., Finn, A., Thomas, A., Relton, C., et al. Contact patterns before and during the UK's autumn 2020 COVID-19 lockdown among university students and staff. (2021).

51. Chong, A., Mitchell, R., Hemani, G., Smith, G., Yolken, R., et al. Genetic analyses of common infections in the avon longitudinal study of parents and children cohort. Frontiers in immunology (2021).

52. Robinson, J., Hemani, G., Gaunt, T. & Zheng, J. An efficient and robust tool for genetic colocalization: Pair-wise conditional and colocalization (PWCoCo). GENETIC EPIDEMIOLOGY (2021).

53. Hemani, G., Shakhbazov, K., Westra, H., Esko, T., Henders, A., McRae, A., et al. Retraction note: Detection and replication of epistasis influencing transcription in humans. Nature (2021).

54. Simcoe, M., Evans, D., Hemani, G., Ring, S., Smith, G. & Hysi, P. Genome-wide association study in almost 195,000 individuals identifies 50 previously unidentified genetic loci for eye color. Science Advances (2021).

55. Liu, Y., Elsworth, B., Erola, P., Haberland, V., Hemani, G., et al. EpiGraphDB: A database and data mining platform for health data science (nov, 10.1093/bioinformatics/btaa961, 2020). BIOINFORMATICS (2021).

56. Liu, Y., Elsworth, B., Erola, P., Haberland, V., Hemani, G., et al. Erratum to: EpiGraphDB: A database and data mining platform for health data science. Bioinformatics (2021).

57. Nixon, E., Thomas, A., Stocks, D., Barreaux, A., Hemani, G., Trickey, A., et al. Impacts of vaccination and asymptomatic testing on SARS-CoV-2 transmission dynamics in a university setting (preprint). (2021).

58. Nixon, E., Thomas, A., Stocks, D., Barreaux, A., Hemani, G., Trickey, A., et al. Impacts of vaccination and asymptomatic testing on SARS-CoV-2 transmission dynamics in a university setting. medRxiv (2021).

59. Hatcher, C., Hemani, G., Rodriguez, S., Gaunt, T., Lawson, D., Min, J., et al. Evidence of positive and negative selection associated with DNA methylation. bioRxiv (2021).

60. Woolf, B., Cara, N., Moreno-Stokoe, C., Skrivankova, V., Drax, K., et al. Investigating the transparency of reporting in two-sample summary data mendelian randomization studies. medRxiv (2021).

61. Griffith, G., Morris, T., Tudball, M., Herbert, A., Mancano, G., Pike, L., et al. Collider bias undermines our understanding of COVID-19 disease risk and severity. Nature communications (2020).

62. Zhao, Q., Wang, J., Hemani, G., Bowden, J. & Small, D. Statistical inference in two-sample summary-data mendelian randomization using robust adjusted profile score. The Annals of Statistics (2020).

63. Wootton, R., Richmond, R., Stuijfzand, B., Lawn, R., Sallis, H., et al. Evidence for causal effects of lifetime smoking on risk for depression and schizophrenia: A mendelian randomisation study. Psychological medicine (2020).

64. Brumpton, B., Sanderson, E., Heilbron, K., Hartwig, F., Harrison, S., Vie, G., et al. Avoiding dynastic, assortative mating, and population stratification biases in mendelian randomization through within-family analyses. Nature communications (2020).

65. Zheng, J., Haberland, V., Baird, D., Walker, V., Haycock, P., Hurle, M., et al. Phenome-wide mendelian randomization mapping the influence of the plasma proteome on complex diseases. Nature genetics (2020).

66. Elsworth, B., Lyon, M., Alexander, T., Liu, Y., Matthews, P., et al. The MRC IEU OpenGWAS data infrastructure. BioRxiv (2020).

67. Morris, T., Davies, N., Hemani, G. & Smith, G. Population phenomena inflate genetic associations of complex social traits. Science advances (2020).

68. Anderson, E., Howe, L., Wade, K., Ben-Shlomo, Y., Hill, W., Deary, I., et al. Education, intelligence and alzheimer's disease: Evidence from a multivariable two-sample mendelian randomization study. International journal of epidemiology (2020).

69. Lawson, D., Davies, N., Haworth, S., Ashraf, B., Howe, L., Crawford, A., et al. Is population structure in the genetic biobank era irrelevant, a challenge, or an opportunity? Human Genetics (2020).

70. Richardson, T., Hemani, G., Gaunt, T., Relton, C. & Smith, G. A transcriptome-wide mendelian randomization study to uncover tissue-dependent regulatory mechanisms across the human phenome. Nature communications (2020).

71. Cho, Y., Haycock, P., Sanderson, E., Gaunt, T., Zheng, J., Morris, A., et al. Exploiting horizontal pleiotropy to search for causal pathways within a mendelian randomization framework. Nature communications (2020).

72. Banos, D., McCartney, D., Patxot, M., Anchieri, L., Battram, T., et al. Bayesian reassessment of the epigenetic architecture of complex traits. Nature communications (2020).

73. Zheng, J., Brion, M., Kemp, J., Warrington, N., Borges, M., Hemani, G., et al. The effect of plasma lipids and lipid-lowering interventions on bone mineral density: A mendelian randomization study. Journal of Bone and Mineral Research (2020).

74. Neumeyer, S., Hemani, G. & Zeggini, E. Strengthening causal inference for complex disease using molecular quantitative trait loci. Trends in molecular medicine (2020).

75. Reed, Z., Suderman, M., Relton, C., Davis, O. & Hemani, G. The association of DNA methylation with body mass index: Distinguishing between predictors and biomarkers. Clinical epigenetics (2020).

76. Christensen, H., Turner, K., Trickey, A., Booton, R., Hemani, G., Nixon, E., et al. COVID-19 transmission in a university setting: A rapid review of modelling studies. MedRxiv (2020).

77. Hammerschlag, A., Byrne, E., Agbessi, M., Ahsan, H., Alves, I., Andiappan, A., et al. Refining attention-deficit/hyperactivity disorder and autism spectrum disorder genetic loci by integrating summary data from genome-wide association, gene expression, and DNA …. Biological Psychiatry (2020).

78. Herbert, A., Griffith, G., Hemani, G. & Zuccolo, L. The spectre of berkson's paradox: Collider bias in covid-19 research. Significance (2020).

79. McCartney, D., Min, J., Richmond, R., Lu, A., Sobczyk, M., Davies, G., et al. Genome-wide association studies identify 137 loci for DNA methylation biomarkers of ageing. BioRxiv (2020).

80. Russell, A., Ford, T., Gunnell, D., Heron, J., Joinson, C., et al. Investigating evidence for a causal association between inflammation and self-harm: A multivariable mendelian randomisation study. Brain, behavior, and immunity (2020).

81. Sanderson, E., Richardson, T., Hemani, G. & Smith, G. The use of negative control outcomes in mendelian randomisation to detect potential population stratification or selection bias. bioRxiv (2020).

82. Howe, L., Hemani, G., Lesseur, C., Gaborieau, V., Ludwig, K., Mangold, E., et al. Evaluating shared genetic influences on nonsyndromic cleft lip/palate and oropharyngeal neoplasms. Genetic epidemiology (2020).

83. Fitzsimons, E., Moulton, V., Hughes, D., Neaves, S., Ho, K., Hemani, G., et al. Collection of DNA samples and genetic data at scale in the UK millennium cohort study. London, UK, UCL Institute of Education (2020).

84. Griffith, G., Sterne, J., Hemani, G., Herbert, A., Tudball, M., Sharp, G., et al. We should be cautious about associations of patient characteristics with COVID-19 outcomes that are identified in hospitalised patients. (2020).

85. Battram, T., Gaunt, T., Speed, D., Timpson, N. & Hemani, G. Exploring the variance in complex traits captured by DNA methylation assays. bioRxiv (2020).

86. Davies, N., Mancano, G., Herbert, A., Tudball, M., Morris, T., Griffith, G., et al. Implications of selection bias for the COVID symptom tracker study. Science (2020).

87. Lawson, D., Davies, N., Haworth, S., Ashraf, B., Howe, L., Crawford, A., et al. Is population structure in the genetic biobank era irrelevant, a challenge, or an opportunity?(vol 138, pg 2321, 2019). HUMAN GENETICS (2020).

88. Dooley, H., Lee, K., Freidin, M., Hemani, G., Roberts, A., Cadet, Jl., et al. ACE inhibitors, ARBs and other anti-hypertensive drugs and novel COVID-19: An association study from the COVID symptom tracker apin 2,215,386 individuals. (2020).

89. Howard, D., Adams, M., Clarke, T., Hafferty, J., Gibson, J., Shirali, M., et al. Genome-wide meta-analysis of depression identifies 102 independent variants and highlights the importance of the prefrontal brain regions. Nature neuroscience (2019).

90. Linnér, R., Biroli, P., Kong, E., Meddens, S., Wedow, R., et al. Genome-wide association analyses of risk tolerance and risky behaviors in over 1 million individuals identify hundreds of loci and shared genetic influences. Nature genetics (2019).

91. Warrington, N., Beaumont, R., Horikoshi, M., Day, F., Helgeland, Ø., et al. Maternal and fetal genetic effects on birth weight and their relevance to cardio-metabolic risk factors. Nature genetics (2019).

92. Haworth, S., Mitchell, R., Corbin, L., Wade, K., Dudding, T., Budu-Aggrey, A., et al. Apparent latent structure within the UK biobank sample has implications for epidemiological analysis. Nature communications (2019).

93. Richardson, T., Harrison, S., Hemani, G. & Smith, G. An atlas of polygenic risk score associations to highlight putative causal relationships across the human phenome. Elife (2019).

94. Carter, A., Gill, D., Davies, N., Taylor, A., Tillmann, T., Vaucher, J., et al. Understanding the consequences of education inequality on cardiovascular disease: Mendelian randomisation study. bmj (2019).

95. Bandres-Ciga, S., Noyce, A., Hemani, G., Nicolas, A., Calvo, A., Mora, G., et al. Shared polygenic risk and causal inferences in amyotrophic lateral sclerosis. Annals of neurology (2019).

96. Morris, A., Le, T., Wu, H., Akbarov, A., Most, P., Hemani, G., et al. Trans-ethnic kidney function association study reveals putative causal genes and effects on kidney-specific disease aetiologies. Nature communications (2019).

97. Kraja, A., Liu, C., Fetterman, J., Graff, M., Have, C., et al. Associations of mitochondrial and nuclear mitochondrial variants and genes with seven metabolic traits. The American Journal of Human Genetics (2019).

98. Taylor, D., Jackson, A., Narisu, N., Hemani, G., Erdos, M., Chines, P., et al. Integrative analysis of gene expression, DNA methylation, physiological traits, and genetic variation in human skeletal muscle. Proceedings of the National Academy of Sciences (2019).

99. Walker, V., Davies, N., Hemani, G., Zheng, J., Haycock, P., Gaunt, T., et al. Using the MR-base platform to investigate risk factors and drug targets for thousands of phenotypes. Wellcome open research (2019).

100. Noyce, A., Bandres-Ciga, S., Kim, J., Heilbron, K., Kia, D., et al. The parkinson's disease mendelian randomization research portal. Movement Disorders (2019).

101. Howe, L., Lawson, D., Davies, N., Pourcain, B., Lewis, S., et al. Genetic evidence for assortative mating on alcohol consumption in the UK biobank. Nature communications (2019).

102. Battram, T., Richmond, R., Baglietto, L., Haycock, P., Perduca, V., et al. Appraising the causal relevance of DNA methylation for risk of lung cancer. International journal of epidemiology (2019).

103. Periyasamy, S., John, S., Padmavati, R., Rajendren, P., Thirunavukkarasu, P., et al. Association of schizophrenia risk with disordered niacin metabolism in an indian genome-wide association study. JAMA psychiatry (2019).

104. Lawlor, D., Wade, K., Borges, M., Palmer, T., Hartwig, F., Hemani, G., et al. A mendelian randomization dictionary: Useful definitions and descriptions for undertaking, understanding and interpreting mendelian randomization studies. OSF Preprints (2019).

105. Moen, G., Hemani, G., Warrington, N. & Evans, D. Calculating power to detect maternal and offspring genetic effects in genetic association studies. Behavior Genetics (2019).

106. Langdon, R., Richmond, R., Hemani, G., Zheng, J., Wade, K., et al. A phenome-wide mendelian randomization study of pancreatic cancer using summary genetic DataMR-PheWAS of pancreatic cancer using summary genetic data. Cancer Epidemiology, Biomarkers & Prevention (2019).

107. Howe, L., Richardson, T., Arathimos, R., Alvizi, L., Passos-Bueno, M., et al. Evidence for DNA methylation mediating genetic liability to non-syndromic cleft lip/palate. Epigenomics (2019).

108. Russell, A., Heron, J., Gunnell, D., Ford, T., Hemani, G., et al. Pathways between early-life adversity and adolescent self-harm: The mediating role of inflammation in the avon longitudinal study of parents and children. Journal of child psychology and psychiatry (2019).

109. Howe, L., Sharp, G., Hemani, G., Zuccolo, L., Richmond, S. & Lewis, S. Prenatal alcohol exposure and facial morphology in a UK cohort. Drug and Alcohol Dependence (2019).

110. Ward-Caviness, C., Vries, P., Wiggins, K., Huffman, J., Yanek, L., et al. Mendelian randomization evaluation of causal effects of fibrinogen on incident coronary heart disease. PloS one (2019).

111. Richardson, T., Richmond, R., North, T., Hemani, G., Smith, G., et al. An integrative approach to detect epigenetic mechanisms that putatively mediate the influence of lifestyle exposures on disease susceptibility. International journal of epidemiology (2019).

112. Speed, D., Hemani, G., Speed, M., Børglum, A. & Østergaard, S. Investigating the causal relationship between neuroticism and depression via mendelian randomization. Acta psychiatrica Scandinavica (2019).

113. North, T., Davies, N., Harrison, S., Carter, A., Hemani, G., Sanderson, E., et al. Using genetic instruments to estimate interactions in mendelian randomization studies. Epidemiology (2019).

114. Lawn, R., Sallis, H., Taylor, A., Wootton, R., Smith, G., Davies, N., et al. Schizophrenia risk and reproductive success: A mendelian randomization study. Royal Society open science (2019).

115. Reed, Z., Jones, H., Hemani, G., Zammit, S. & Davis, O. Schizophrenia liability shares common molecular genetic risk factors with sleep duration and nightmares in childhood. Wellcome Open Research (2019).

116. Howe, L., Lawson, D., Davies, N., Pourcain, B., Lewis, S., Smith, G., et al. Alcohol consumption and mate choice in UK biobank: Comparing observational and mendelian randomization estimates. bioRxiv (2019).

117. Lawn, R., Sallis, H., Taylor, A., Wootton, R., Smith, G., Davies, N., et al. Comment on the relationship between common variant schizophrenia liability and number of offspring in the UK biobank. American Journal of Psychiatry (2019).

118. Hysi, P., Valdes, A., Liu, F., Furlotte, N., Evans, D., et al. Publisher correction: Genome-wide association meta-analysis of individuals of european ancestry identifies new loci explaining a substantial fraction of hair color variation …. Nature Genetics (2019).

119. Hysi, P., Valdes, A., Liu, F., Furlotte, N., Evans, D., et al. Publisher correction: Genome-wide association meta-analysis of individuals of european ancestry identifies new loci explaining a substantial fraction of hair color variation …. (2019).

120. Hemani, G., Zheng, J., Elsworth, B., Wade, K., Haberland, V., Baird, D., et al. The MR-base platform supports systematic causal inference across the human phenome. elife (2018).

121. Hemani, G., Bowden, J. & Smith, G. Evaluating the potential role of pleiotropy in mendelian randomization studies. Human molecular genetics (2018).

122. Xue, A., Wu, Y., Zhu, Z., Zhang, F., Kemper, K., et al. Genome-wide association analyses identify 143 risk variants and putative regulatory mechanisms for type 2 diabetes. Nature communications (2018).

123. Võsa, U., Claringbould, A., Westra, H., Bonder, M., Deelen, P., Zeng, B., et al. Unraveling the polygenic architecture of complex traits using blood eQTL metaanalysis. BioRxiv (2018).

124. Min, J., Hemani, G., Smith, G., Relton, C. & Suderman, M. Meffil: Efficient normalization and analysis of very large DNA methylation datasets. Bioinformatics (2018).

125. Bowden, J., Hemani, G. & Smith, G. Invited commentary: Detecting individual and global horizontal pleiotropy in mendelian randomization—a job for the humble heterogeneity statistic? American journal of epidemiology (2018).

126. Hysi, P., Valdes, A., Liu, F., Furlotte, N., Evans, D., et al. Genome-wide association meta-analysis of individuals of european ancestry identifies new loci explaining a substantial fraction of hair color variation and heritability. Nature genetics (2018).

127. Haas, M., Aragam, K., Emdin, C., Bick, A., Hemani, G., Smith, G., et al. Genetic association of albuminuria with cardiometabolic disease and blood pressure. The American Journal of Human Genetics (2018).

128. Richardson, T., Haycock, P., Zheng, J., Timpson, N., Gaunt, T., et al. Systematic mendelian randomization framework elucidates hundreds of CpG sites which may mediate the influence of genetic variants on disease. Human molecular genetics (2018).

129. Wootton, R., Richmond, R., Stuijfzand, B., Lawn, R., Sallis, H., et al. Causal effects of lifetime smoking on risk for depression and schizophrenia: Evidence from a mendelian randomisation study. Biorxiv (2018).

130. Warrington, N., Shevroja, E., Hemani, G., Hysi, P., Jiang, Y., Auton, A., et al. Genome-wide association study identifies nine novel loci for 2D:4D finger ratio, a putative retrospective biomarker of testosterone exposure in utero. Human molecular genetics (2018).

131. Zheng, J., Richardson, T., Millard, L., Hemani, G., Elsworth, B., et al. PhenoSpD: An integrated toolkit for phenotypic correlation estimation and multiple testing correction using GWAS summary statistics. Gigascience (2018).

132. Howe, L., Lee, M., Sharp, G., Smith, G., Pourcain, B., Shaffer, J., et al. Investigating the shared genetics of non-syndromic cleft lip/palate and facial morphology. PLoS genetics (2018).

133. Haworth, S., Mitchell, R., Corbin, L., Wade, K., Dudding, T., Budu-Aggrey, A., et al. Common genetic variants and health outcomes appear geographically structured in the UK biobank sample: Old concerns returning and their implications. BioRxiv (2018).

134. Ye, J., Richardson, T., McArdle, W., Relton, C., Gillespie, K., Suderman, M., et al. Identification of loci where DNA methylation potentially mediates genetic risk of type 1 diabetes. Journal of Autoimmunity (2018).

135. Partida, G., Laurin, C., Ring, S., Gaunt, T., McRae, A., Visscher, P., et al. Genome-wide survey of parent-of-origin effects on DNA methylation identifies candidate imprinted loci in humans. Human molecular genetics (2018).

136. Laurin, C., Cuellar-Partida, G., Hemani, G., Smith, G., Yang, J. & Evans, D. Partitioning phenotypic variance due to parent-of-origin effects using genomic relatedness matrices. Behavior genetics (2018).

137. Walton, E., Hemani, G., Dehghan, A., Relton, C. & Smith, G. Systematic evaluation of the causal relationship between DNA methylation and c-reactive protein. bioRxiv (2018).

138. Noyce, A., Kia, D., Heilbron, K., Jepson, J., Hemani, G., Hinds, D., et al. Tendency towards being a 'morning person' increases risk of parkinson's disease: Evidence from mendelian randomisation. BioRxiv (2018).

139. Carter, A., Gill, D., Davies, N., Taylor, A., Tillmann, T., Vaucher, J., et al. What explains the effect of education on cardiovascular disease? Applying mendelian randomization to identify the consequences of education inequality. bioRxiv (2018).

140. Howe, L., Richardson, T., Arathimos, R., Alvizi, L., Passos-Bueno, M., et al. DNA methylation mediates genetic liability to non-syndromic cleft lip/palate. bioRxiv (2018).

141. Morris, A., Le, T., Wu, H., Akbarov, A., Most, Pj., Hemani, G., et al. Trans-ethnic genome-wide association study of kidney function provides novel insight into effector genes and causal effects on kidney-specific disease aetiologies. bioRxiv (2018).

142. Zheng, J., Erzurumluoglu, A., Elsworth, B., Kemp, J., Howe, L., Haycock, P., et al. LD hub: A centralized database and web interface to perform LD score regression that maximizes the potential of summary level GWAS data for SNP heritability and genetic …. Bioinformatics (2017).

143. Hemani, G., Tilling, K. & Smith, G. Orienting the causal relationship between imprecisely measured traits using GWAS summary data. PLoS genetics (2017).

144. Haycock, P., Burgess, S., Nounu, A., Zheng, J., Okoli, G., Bowden, J., et al. Association between telomere length and risk of cancer and non-neoplastic diseases: A mendelian randomization study. JAMA oncology (2017).

145. Zheng, J., Baird, D., Borges, M., Bowden, J., Hemani, G., Haycock, P., et al. Recent developments in mendelian randomization studies. Current epidemiology reports (2017).

146. Noyce, A., Kia, D., Hemani, G., Nicolas, A., Price, T., Pablo-Fernandez, E., et al. Estimating the causal influence of body mass index on risk of parkinson disease: A mendelian randomisation study. PLoS medicine (2017).

147. Zheng, J., Erzurumluoglu, A., Elsworth, B., Kemp, J., Howe, L., Haycock, P., et al. Early genetics and lifecourse epidemiology (EAGLE) eczema consortium. LD hub: A centralized database and web interface to perform LD score regression that maximizes the …. Bioinformatics (2017).

148. Hemani, G., Bowden, J., Haycock, P., Zheng, J., Davis, O., et al. Automating mendelian randomization through machine learning to construct a putative causal map of the human phenome. BioRxiv (2017).

149. Richardson, T., Zheng, J., Smith, G., Timpson, N., Gaunt, T., Relton, C., et al. Mendelian randomization analysis identifies CpG sites as putative mediators for genetic influences on cardiovascular disease risk. The American Journal of Human Genetics (2017).

150. Xu, L., Borges, M., Hemani, G. & Lawlor, D. The role of glycaemic and lipid risk factors in mediating the effect of BMI on coronary heart disease: A two-step, two-sample mendelian randomisation study. Diabetologia (2017).

151. Mitchell, R., Hemani, G., Dudding, T. & Paternoster, L. UK biobank genetic data: Mrc-ieu quality control, version 1. University of Bristol (2017).

152. Elsworth, B., Mitchell, R., Raistrick, C., Paternoster, L., Hemani, G. & Gaunt, T. MRC IEU UK biobank GWAS pipeline version 1. Bristol, UK: University of Bristol (2017).

153. Lukowski, S., Lloyd-Jones, L., Holloway, A., Kirsten, H., Hemani, G., Yang, J., et al. Genetic correlations reveal the shared genetic architecture of transcription in human peripheral blood. Nature communications (2017).

154. Richmond, R., Wade, K., Corbin, L., Bowden, J., Hemani, G., Timpson, N., et al. Investigating the role of insulin in increased adiposity: Bi-directional mendelian randomization study. BioRxiv (2017).

155. Haycock, P., Hemani, G. & Aviv, A. Telomere length and risk of cancer and non-neoplastic diseases: Is survivin the ariadne's thread?—reply. JAMA oncology (2017).

156. Richardson, T., Zheng, J., Smith, G., Timpson, N., Gaunt, T., Relton, C., et al. Causal epigenome-wide association study identifies CpG sites that influence cardiovascular disease risk. bioRxiv (2017).

157. Noyce, A., Kia, D., Hemani, G., Nicolas, A., Price, T., et al. Increased BMI may protect against parkinson's disease: Evidence from mendelian randomisation study. MOVEMENT DISORDERS (2017).

158. Gaunt, T., Shihab, H., Hemani, G., Min, J., Woodward, G., Lyttleton, O., et al. Systematic identification of genetic influences on methylation across the human life course. Genome biology (2016).

159. Horikoshi, M., Beaumont, R., Day, F., Warrington, N., Kooijman, M., et al. Genome-wide associations for birth weight and correlations with adult disease. Nature (2016).

160. Hartwig, F., Davies, N., Hemani, G. & Smith, G. Two-sample mendelian randomization: Avoiding the downsides of a powerful, widely applicable but potentially fallible technique. International journal of epidemiology (2016).

161. Simpkin, A., Hemani, G., Suderman, M., Gaunt, T., Lyttleton, O., Mcardle, W., et al. Prenatal and early life influences on epigenetic age in children: A study of mother–offspring pairs from two cohort studies. Human molecular genetics (2016).

162. White, J., Sofat, R., Hemani, G., Shah, T., Engmann, J., et al. Plasma urate concentration and risk of coronary heart disease: A mendelian randomisation analysis. The lancet Diabetes & endocrinology (2016).

163. Richmond, R., Hemani, G., Tilling, K., Smith, G. & Relton, C. Challenges and novel approaches for investigating molecular mediation. Human molecular genetics (2016).

164. Chen, J., Bacanu, S., Yu, H., Zhao, Z., Jia, P., et al. Genetic relationship between schizophrenia and nicotine dependence. Scientific reports (2016).

165. Powell, J., Fung, J., Shakhbazov, K., Sapkota, Y., Cloonan, N., Hemani, G., et al. Endometriosis risk alleles at 1p36. 12 act through inverse regulation of CDC42 and LINC00339. Human molecular genetics (2016).

166. Ware, J., Chen, X., Vink, J., Loukola, A., Minica, C., et al. Genome-wide meta-analysis of cotinine levels in cigarette smokers identifies locus at 4q13. 2. Scientific reports (2016).

167. Mehta, D., Tropf, F., Gratten, J., Bakshi, A., Zhu, Z., et al. Evidence for genetic overlap between schizophrenia and age at first birth in women. JAMA psychiatry (2016).

168. Shakhbazov, K., Powell, J., Hemani, G., Henders, A., Martin, N., et al. Shared genetic control of expression and methylation in peripheral blood. BMC genomics (2016).

169. Richardson, T., Shihab, H., Hemani, G., Zheng, J., Hannon, E., Mill, J., et al. Collapsed methylation quantitative trait loci analysis for low frequency and rare variants. Human molecular genetics (2016).

170. Zheng, J., Haycock, P., Hemani, G., Elsworth, B., Shihab, H., Laurin, C., et al. LD hub and MR-base: Online platforms for preforming LD score regression and mendelian randomization analysis using GWAS summary data. Behavior Genetics (2016).

171. Warrington, N., Hemani, G., Hysi, P., Mangino, M., McMahon, G., Hickey, M., et al. Genome-wide association study of 6,939 individuals identifies five novel loci and suggests that prenatal exposure to testosterone is not a major determinant of individual …. Behavior Genetics (2016).

172. Laurin, C., Hemani, G. & Evans, D. Detecting parent of origin effects using GREML of transmitted genotypes. Behavior Genetics (2016).

173. Richmond, R., Suderman, M., Haycock, P., Hemani, G., Relton, C. & Smith, G. Investigating DNA methylation as a marker for historical smoke exposure and a mediator of disease risk. GENETIC EPIDEMIOLOGY (2016).

174. Yang, J., Bakshi, A., Zhu, Z., Hemani, G., Vinkhuyzen, A., Lee, S., et al. Genetic variance estimation with imputed variants finds negligible missing heritability for human height and body mass index. Nature genetics (2015).

175. Robinson, M., Hemani, G., Medina-Gomez, C., Mezzavilla, M., Esko, T., et al. Population genetic differentiation of height and body mass index across europe. Nature genetics (2015).

176. Zhu, Z., Bakshi, A., Vinkhuyzen, A., Hemani, G., Lee, S., Nolte, I., et al. Dominance genetic variation contributes little to the missing heritability for human complex traits. The American Journal of Human Genetics (2015).

177. Joshi, P., Esko, T., Mattsson, H., Eklund, N., Gandin, I., et al. Directional dominance on stature and cognition in diverse human populations. Nature (2015).

178. Peyrot, W., Lee, S., Milaneschi, Y., Abdellaoui, A., Byrne, E., Esko, T., et al. The association between lower educational attainment and depression owing to shared genetic effects? Results in 25 000 subjects. Molecular psychiatry (2015).

179. Yang, J., Bakshi, A., Zhu, Z., Hemani, G., Vinkhuyzen, A., Nolte, I., et al. Genome-wide genetic homogeneity between sexes and populations for human height and body mass index. Human molecular genetics (2015).

180. Warrington, N., Zhu, G., Dy, V., Heath, A., Madden, P., Hemani, G., et al. Genome-wide association study of blood lead shows multiple associations near ALAD. Human molecular genetics (2015).

181. Davies, N., Hemani, G., Timpson, N., Windmeijer, F. & Smith, G. The role of common genetic variation in educational attainment and income: Evidence from the national child development study. Scientific Reports (2015).

182. Wood, A., Esko, T., Yang, J., Vedantam, S., Pers, T., et al. Defining the role of common variation in the genomic and biological architecture of adult human height. Nature genetics (2014).

183. Smith, G. & Hemani, G. Mendelian randomization: Genetic anchors for causal inference in epidemiological studies. Human molecular genetics (2014).

184. Wei, W., Hemani, G. & Haley, C. Detecting epistasis in human complex traits. Nature Reviews Genetics (2014).

185. Visscher, P., Hemani, G., Vinkhuyzen, A., Chen, G., Lee, S., Wray, N., et al. Statistical power to detect genetic (co) variance of complex traits using SNP data in unrelated samples. PLoS genetics (2014).

186. McRae, A., Powell, J., Henders, A., Bowdler, L., Hemani, G., Shah, S., et al. Contribution of genetic variation to transgenerational inheritance of DNA methylation. Genome biology (2014).

187. Hemani, G., Shakhbazov, K., Westra, H., Esko, T., Henders, A., McRae, A., et al. Retracted article: Detection and replication of epistasis influencing transcription in humans. Nature (2014).

188. Jiang, L., Yin, J., Ye, L., Yang, J., Hemani, G., et al. Novel risk loci for rheumatoid arthritis in han chinese and congruence with risk variants in europeans. Arthritis & rheumatology (2014).

189. Hemani, G., Shakhbazov, K., Westra, H., Esko, T., Henders, A., McRae, A., et al. Hemani et al. reply. Nature (2014).

190. Hemani, G., Shakhbazov, K., Westra, H., Esko, T., Henders, A., McRae, A., et al. Another explanation for apparent epistasis. Nature (2014).

191. Visscher, P., Hemani, G., Vinkhuyzen, A., Chen, G. & Lee, S. Statistical power to detect genetic (co) variance of complex traits using SNP. (2014).

192. Hemani, G., Knott, S. & Haley, C. An evolutionary perspective on epistasis and the missing heritability. PLoS genetics (2013).

193. Hemani, G., Yang, J., Vinkhuyzen, A., Powell, J., Willemsen, G., Hottenga, J., et al. Inference of the genetic architecture underlying BMI and height with the use of 20,240 sibling pairs. The American Journal of Human Genetics (2013).

194. Powell, J., Henders, A., McRae, A., Kim, J., Hemani, G., Martin, N., et al. Congruence of additive and non-additive effects on gene expression estimated from pedigree and SNP data. PLoS genetics (2013).

195. Speed, D., Hemani, G., Johnson, M. & Balding, D. Response to lee et al.: SNP-based heritability analysis with dense data. The American Journal of Human Genetics (2013).

196. Speed, D., Hemani, G., Johnson, M. & Balding, D. Improved heritability estimation from genome-wide SNPs. The American Journal of Human Genetics (2012).

197. French, A., Ogden, R., Eland, C., Hemani, G., Pong-Wong, R., Corcoran, B., et al. Genome-wide analysis of mitral valve disease in cavalier king charles spaniels. The veterinary journal (2012).

198. Wei, W., Hemani, G., Gyenesei, A., Vitart, V., Navarro, P., Hayward, C., et al. Genome-wide analysis of epistasis in body mass index using multiple human populations. European Journal of Human Genetics (2012).

199. Hemani, G. Dissecting genetic interactions in complex traits. The University of Edinburgh (2012).

200. Hemani, G., Theocharidis, A., Wei, W. & Haley, C. EpiGPU: Exhaustive pairwise epistasis scans parallelized on consumer level graphics cards. Bioinformatics (2011).

201. Wei, W., Hemani, G., Hicks, A., Vitart, V., Cabrera-Cardenas, C., Navarro, P., et al. Characterisation of genome-wide association epistasis signals for serum uric acid in human population isolates. PLoS One (2011).

202. French, A., Ogden, R., Eland, C., Hemani, G., Corcoran, B. & Summers, K. Use of non-invasive methods to collect DNA for genome wide analysis from companion animals. Advances in Animal Biosciences (2011).

203. Theocharidis, A., Hemani, G., Kargas, M. & Freeman, T. A comparison of CPU and OpenCL parallelization methods for correlation and graph layout algorithms used in the network analysis of high dimensional data. (2011).

204. Hadjipavlou, G., Hemani, G., Leach, R., Louro, B., Nadaf, J., Rowe, S., et al. Extensive QTL and association analyses of the QTLMAS2009 data. BMC proceedings (2010).

205. Haycock, P., Burgess, S., Nounu, A., Zheng, J., Okoli, G., Bowden, J., et al. Association between telomere length and risk of cancer and non-neoplastic diseases. JAMA Oncol.

206. Knapp, M., Stergiakouli, E., Pourcain, B., Smith, G., Sandy, J., Relton, C., et al. DNA methylation mediates genetic liability to non-syndromic cleft lip/palate.