Masahiro Kanai, Ph.D.

Curriculum Vitae

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Education

Harvard University — **Boston, USA**
Ph.D. in Biomedical Informatics — *Aug. 2017–May 2022*
Bioinformatics and Integrative Genomics Ph.D. Program, Harvard Medical School

Keio University — **Yokohama, Japan**
B.S. in Bioinformatics, Department of Biosciences and Informatics — *Apr. 2013–Mar. 2017*

Research Experience

Massachusetts General Hospital & Broad Institute of MIT and Harvard — **Boston, USA**
Instructor in Medicine, Center for Computational and Integrative Biology — *July 2025–present*
Research Fellow, Center for Computational and Integrative Biology — *Aug. 2022–June 2025*
Advisor: Dr. Ramnik Xavier
Research themes:

- Functional characterization of causal genetic variants
- Integration of multi-omics data for variant Interpretation

Massachusetts General Hospital & Broad Institute of MIT and Harvard — **Boston, USA**
Graduate Student, Analytic and Translational Genetics Unit — *Jan. 2018–May 2022*
Advisors: Drs. Mark Daly & Hilary Finucane
Ph.D. thesis: Fine-mapping complex traits in large-scale biobanks across diverse populations

Osaka University Graduate School of Medicine — **Osaka, Japan**
Visiting Faculty, Department of Statistical Genetics — *July 2022–Mar. 2025*
Research Student, Department of Statistical Genetics — *Apr. 2017–June 2022*
Advisor: Dr. Yukinori Okada
Research themes:

- Genetic analysis of complex human diseases and traits in the Japanese population
- Efficient visualization of high-dimentional multi-omics data

RIKEN Center for Integrative Medical Sciences — **Yokohama, Japan**
Research Assistant, Laboratory for Statistical Analysis — *May 2015–Jul. 2019*
Advisors: Drs. Yoichiro Kamatani & Yukinori Okada
Research themes:

- Genome-wide association study (GWAS) of ~200,000 individuals in the BioBank Japan Project
- Interpretation of GWAS polygenic signals using epigenomic data
- Population genetics analysis of 1,037 Japanese whole-genome sequences

Keio University — **Yokohama, Japan**
Undergraduate Researcher, Laboratory for Bioinformatics — *Apr. 2016–Mar. 2017*
Advisor: Dr. Yasubumi Sakakibara
Bachelor thesis: Integrative multi-omics analysis of renal cell carcinoma

Tokyo Medical and Dental University **Tokyo, Japan**
Technical Assistant, Department of Human Genetics and Disease Diversity *Apr. 2014–Mar. 2016*
Advisors: Drs. Yukinori Okada & Toshihiro Tanaka
Research themes:

- Empirical estimation of genome-wide significance thresholds based on GWAS simulations
- HLA imputation analysis using the Japanese-specific reference panel

Certification

The Certification for Bioinformatics Engineers
certificated by *the Japanese Society of Bioinformatics* *2015*

Awards and Fellowships

Reviewers' Choice Abstract Award **Boston, USA**
The American Society of Human Genetics 2025 Annual Meeting *2025*

Innovators Under 35 Japan **Tokyo, Japan**
MIT Technology Review *2024*

Reviewers' Choice Abstract Award **Los Angeles, USA**
The American Society of Human Genetics 2022 Annual Meeting *2022*

Reviewers' Choice Abstract Award **USA**
The American Society of Human Genetics 2021 Virtual Meeting *2021*

Charles J. Epstein Trainee Awards for Excellence in Human Genetics Research **USA**
Finalist (Predoctoral), *The American Society of Human Genetics 2020 Virtual Meeting* *2020*

Reviewers' Choice Abstract Award **Houston, USA**
The American Society of Human Genetics 2019 Annual Meeting *2019*

Masason Foundation Fellowship **Tokyo, Japan**
Research grant for cross-population analysis of complex human diseases and traits. *2018–2023*

Nakajima Foundation Fellowship **Tokyo, Japan**
Predoctoral fellowship which covers up to ~$50,000/year for tuition and stipend. *2017–2022*

The 3rd place, Worldwide Finals **New York, USA**
Microsoft Imagine Cup 2011 Windows 7 Touch Challenge *2011*

The 1st place, National Finals & Worldwide Finalist **Japan & Poland**
Microsoft Imagine Cup 2010 Software Design Competition *2010*

Publications

Selected Publications and Preprints

(* = co-first)

1. **Kanai, M.**, Delorey, T. M., Honkanen, J., Rodosthenous, R. S., Juvila, J., ..., Partanen, J., Palotie, A., Graham, D. B., Daly, M. J. & Xavier, R. J. Population-scale multiome immune cell atlas reveals complex disease drivers. ***medRxiv*** (2025).
2. *Karczewski, K. J., *Gupta, R., ***Kanai, M.**, Lu, W., Tsuo, K., ..., Finucane, H. K., Daly, M. J., Neale, B. M., Atkinson, E. G. & Martin, A. R. Pan-UK Biobank GWAS improves discovery, analysis of genetic architecture, and resolution into ancestry-enriched effects. ***Nature Genetics*** **57,** 2408–2417 (2025).

3. **Kanai, M.**, Elzur, R., Zhou, W., Global Biobank Meta-analysis Initiative, Daly, M. J. & Finucane, H. K. Meta-analysis fine-mapping is often miscalibrated at single-variant resolution. ***Cell Genomics*** **2,** 100210 (2022).
4. *Weissbrod, O., ****Kanai, M.**, *Shi, H., Gazal, S., Peyrot, W. J., ..., Okada, Y., The Biobank Japan Project, Martin, A. R., Finucane, H. K. & Price, A. L. Leveraging fine-mapping and multipopulation training data to improve cross-population polygenic risk scores. ***Nature Genetics*** **54,** 450–458 (2022).
5. **Kanai, M.**, Ulirsch, J. C., Karjalainen, J., Kurki, M., Karczewski, K. J., ..., Tewhey, R., Sabeti, P. C., Okada, Y., Daly, M. J. & Finucane, H. K. Insights from complex trait fine-mapping across diverse populations. ***medRxiv*** (2021).
6. *Sakaue, S., ****Kanai, M.**, Tanigawa, Y., Karjalainen, J., Kurki, M., ..., Palotie, A., Rivas, M. A., Daly, M. J., Matsuda, K. & Okada, Y. A cross-population atlas of genetic associations for 220 human phenotypes. ***Nature Genetics*** **53,** 1415–1424 (2021).
7. The COVID-19 Host Genetics Initiative. Mapping the human genetic architecture of COVID-19. ***Nature*** **600,** 472–477 (2021).
8. *Sakaue, S., ****Kanai, M.**, Karjalainen, J., Akiyama, M., Kurki, M., ..., Matsuda, K., Murakami, Y., Daly, M. J., Kamatani, Y. & Okada, Y. Trans-biobank analysis with 676,000 individuals elucidates the association of polygenic risk scores of complex traits with human lifespan. ***Nature Medicine*** **26,** 542–548 (2020).
9. Martin, A. R., **Kanai, M.**, Kamatani, Y., Okada, Y., Neale, B. M. & Daly, M. J. Clinical use of current polygenic risk scores may exacerbate health disparities. ***Nature Genetics*** **51,** 584–591 (2019).
10. **Kanai, M.**, Akiyama, M., Takahashi, A., Matoba, N., Momozawa, Y., ..., Hirata, M., Matsuda, K., Kubo, M., Okada, Y. & Kamatani, Y. Genetic analysis of quantitative traits in the Japanese population links cell types to complex human diseases. ***Nature Genetics*** **50,** 390–400 (2018).

Other Preprints

11. Liu, K., Rasmussen, A., Han, W., Gong, Q., Bohley, S., ..., **Kanai, M.**, ..., Ashenberg, O., Daly, M. J., Chen, F., Graham, D. B. & Xavier, R. J. Sensitive Transcriptomics and Genotyping reveals function of genetic variants in immunity. ***bioRxiv*** (2025).
12. Finucane, H. K., Parsa, S., Guez, J., **Kanai, M.**, Satterstrom, F. K., Nkambule, L. L., Daly, M. J., Seed, C. & Karczewski, K. J. Variant scoring performance across selection regimes depends on variant-to-gene and gene-to-disease components. ***bioRxiv*** (2024).
13. Zhou, W., Cuomo, A., Xue, A., **Kanai, M.**, Chau, G., ..., Xavier, R. J., MacArthur, D. G., Powell, J. E., Daly, M. J. & Neale, B. M. Efficient and accurate mixed model association tool for single-cell eQTL analysis. ***medRxiv*** (2024).
14. Koskela, J. T., Happola, P., Liu, A., FinnGen, Partanen, J., ..., **Kanai, M.**, ..., Ganna, A., Palotie, A., Laitinen, T., Myllarniemi, M. & Daly, M. J. Genetic variant in SPDL1 reveals novel mechanism linking pulmonary fibrosis risk and cancer protection. ***medRxiv*** (2021).
15. Turley, P., Martin, A. R., Goldman, G., Li, H., **Kanai, M.**, ..., Meyer, M. N., Cesarini, D., Daly, M., Benjamin, D. J. & Neale, B. M. Multi-Ancestry Meta-Analysis yields novel genetic discoveries and ancestry-specific associations. ***bioRxiv*** (2021).

Other Publications

16. Reeve, M. P., **Kanai, M.**, Graham, D. B., Karjalainen, J., Luo, S., ..., Pirinen, M., Kero, J., Xavier, R. J., Daly, M. J. & Ripatti, S. Genome-wide association analyses of autoimmune hypothyroidism reveal autoimmune and thyroid-specific contributions and an inverse relationship with cancer risk. ***Nature Genetics*** (2026).

17. Siraj, L., Castro, R. I., Dewey, H. B., Kales, S., Butts, J. C., ..., **Kanai, M.**, ..., Sabeti, P. C., Finucane, H. K., Reilly, S. K., Ulirsch, J. C. & Tewhey, R. Functional dissection of complex trait variants at single-nucleotide resolution. ***Nature*** (2026).
18. Sato, G., Yamamoto, Y., Sonehara, K., Saiki, R., Ojima, T., **Kanai, M.**, ..., Matsuda, K., Ogawa, S., Yamauchi, T., Kadowaki, T. & Okada, Y. Genetic regulation across germline and somatic variation on the Y chromosome contributes to type 2 diabetes. ***Nature Medicine*** (2026).
19. Rossen, J., Shi, H., Strober, B. J., Zhang, M. J., **Kanai, M.**, McCaw, Z. R., Liang, L., Weissbrod, O. & Price, A. L. MultiSuSiE improves multi-ancestry fine-mapping in All of Us whole-genome sequencing data. ***Nature Genetics*** **58,** 67–76 (2026).
20. Jacobs, H. N., Gorissen, B. L., Guez, J., **Kanai, M.**, Gupta, K., Finucane, H. K., Karczewski, K. J. & Burge, C. B. Widespread naturally variable human exons aid genetic interpretation. ***Nature Communications*** **16,** 11345 (2025).
21. Smit, R. A. J., Wade, K. H., Hui, Q., Arias, J. D., Yin, X., ..., **Kanai, M.**, ..., Timpson, N. J., Hirschhorn, J. N., Sun, Y. V., Berndt, S. I. & Loos, R. J. F. Polygenic prediction of body mass index and obesity through the life course and across ancestries. ***Nature Medicine*** **31,** 3151–3168 (2025).
22. Lammi, V., Nakanishi, T., Jones, S. E., Andrews, S. J., Karjalainen, J., ..., **Kanai, M.**, ..., Richards, J. B., Ludwig, K. U., Marks-Hultström, M., Zeberg, H. & Ollila, H. M. Genome-wide association study of long COVID. ***Nature Genetics*** **57,** 1402–1417 (2025).
23. Sonehara, K., Uwamino, Y., Saiki, R., Takeshita, M., Namba, S., ..., **Kanai, M.**, ..., Murata, M., Matsushita, H., Ogawa, S., Okada, Y. & Namkoong, H. Germline variants and mosaic chromosomal alterations affect COVID-19 vaccine immunogenicity. ***Cell Genomics*** **5,** 100783 (2025).
24. Adams, M. J., Streit, F., Meng, X., Awasthi, S., Adey, B. N., ..., **Kanai, M.**, ..., Kuchenbaecker, K., Wray, N. R., Ripke, S., Lewis, C. M. & McIntosh, A. M. Trans-ancestry genome-wide study of depression identifies 697 associations implicating cell types and pharmacotherapies. ***Cell*** **188,** 640–652.e9 (2025).
25. Pozarickij, A., Gan, W., Lin, K., Clarke, R., Fairhurst-Hunter, Z., ..., **Kanai, M.**, ..., Li, L., Chen, Z., Millwood, I. Y., Walters, R. G. & China Kadoorie Biobank Collaborative Group. Causal relevance of different blood pressure traits on risk of cardiovascular diseases: GWAS and Mendelian randomisation in 100,000 Chinese adults. ***Nature Communications*** **15,** 6265 (2024).
26. Carey, C. E., Shafee, R., Wedow, R., Elliott, A., Palmer, D. S., ..., **Kanai, M.**, ..., King, D., Davey Smith, G., Neale, B. M., Walters, R. K. & Robinson, E. B. Principled distillation of UK Biobank phenotype data reveals underlying structure in human variation. ***Nature Human Behaviour*** **8,** 1599–1615 (2024).
27. Trsan, T., Peng, V., Krishna, C., Ohara, T. E., Beatty, W. L., ..., **Kanai, M.**, ..., Jaiswal, A., Stappenbeck, T. S., Daly, M. J., Xavier, R. J. & Colonna, M. The centrosomal protein FGFR1OP controls myosin function in murine intestinal epithelial cells. ***Developmental Cell*** **59,** 2460–2476 (2024).
28. Jermy, B., Läll, K., Wolford, B. N., Wang, Y., Zguro, K., ..., **Kanai, M.**, ..., Palotie, A., Heyne, H., Mars, N., Ganna, A. & Ripatti, S. A unified framework for estimating country-specific cumulative incidence for 18 diseases stratified by polygenic risk. ***Nature Communications*** **15,** 5007 (2024).
29. Sakaue, S., Weinand, K., Isaac, S., Dey, K. K., Jagadeesh, K., **Kanai, M.**, ..., McDavid, A., Donlin, L. T., Wei, K., Price, A. L. & Raychaudhuri, S. Tissue-specific enhancer–gene maps from multimodal single-cell data identify causal disease alleles. ***Nature Genetics*** **56,** 615–626 (2024).
30. De Vincentis, A., Tavaglione, F., Namba, S., **Kanai, M.**, Okada, Y., ..., Pedone, C., Antonelli Incalzi, R., Valenti, L., Romeo, S. & Vespasiani-Gentilucci, U. Poor accuracy and sustainability of the first-step FIB4 EASL pathway for stratifying steatotic liver disease risk in the general population. ***Alimentary Pharmacology & Therapeutics*** **59,** 1402–1412 (2024).

31. Lo Faro, V., Bhattacharya, A., Zhou, W., Zhou, D., Wang, Y., ..., **Kanai, M.**, ..., Gamazon, E. R., Jansonius, N. M., Joos, K., Cox, N. J. & Hirbo, J. Novel ancestry-specific primary open-angle glaucoma loci and shared biology with vascular mechanisms and cell proliferation. ***Cell Reports Medicine*** **5,** 101430 (2024).
32. Scholz, M., Horn, K., Pott, J., Wuttke, M., Kühnapfel, A., ..., **Kanai, M.**, ..., Franceschini, N., Parsa, A., Köttgen, A., Schlosser, P. & Pattaro, C. X-chromosome and kidney function: evidence from a multi-trait genetic analysis of 908,697 individuals reveals sex-specific and sex-differential findings in genes regulated by androgen response elements. ***Nature Communications*** **15,** 586 (2024).
33. Meng, X., Navoly, G., Giannakopoulou, O., Levey, D. F., Koller, D., ..., **Kanai, M.**, ..., Dunn, E. C., Stein, M. B., Gelernter, J., Lewis, C. M. & Kuchenbaecker, K. Multi-ancestry genome-wide association study of major depression aids locus discovery, fine mapping, gene prioritization and causal inference. ***Nature Genetics*** **56,** 222–233 (2024).
34. Chen, S., Francioli, L. C., Goodrich, J. K., Collins, R. L., **Kanai, M.**, ..., Daly, M. J., Tiao, G., Neale, B. M., MacArthur, D. G. & Karczewski, K. J. A genomic mutational constraint map using variation in 76,156 human genomes. ***Nature*** **625,** 92–100 (2024).
35. Cui, R., Elzur, R. A., **Kanai, M.**, Ulirsch, J. C., Weissbrod, O., Daly, M. J., Neale, B. M., Fan, Z. & Finucane, H. K. Improving fine-mapping by modeling infinitesimal effects. ***Nature Genetics*** **56,** 162–169 (2024).
36. Kerimov, N., Tambets, R., Hayhurst, J. D., Rahu, I., Kolberg, P., ..., **Kanai, M.**, ..., Finucane, H., Peterson, H., Mosaku, A., Parkinson, H. & Alasoo, K. eQTL Catalogue 2023: New datasets, X chromosome QTLs, and improved detection and visualisation of transcript-level QTLs. ***PLoS Genetics*** **19,** e1010932 (2023).
37. Wang, Y., **Kanai, M.**, Tan, T., Kamariza, M., Tsuo, K., ..., BioBank Japan Project, Huang, H., Turley, P., Atkinson, E. G. & Martin, A. R. Polygenic prediction across populations is influenced by ancestry, genetic architecture, and methodology. ***Cell Genomics*** **3,** 100408 (2023).
38. The COVID-19 Host Genetics Initiative. A second update on mapping the human genetic architecture of COVID-19. ***Nature*** **621,** E7–E26 (2023).
39. International League Against Epilepsy Consortium on Complex Epilepsies. GWAS meta-analysis of over 29,000 people with epilepsy identifies 26 risk loci and subtype-specific genetic architecture. ***Nature Genetics*** **55,** 1471–1482 (2023).
40. Gupta, R., **Kanai, M.**, Durham, T. J., Tsuo, K., McCoy, J. G., ..., Chinnery, P. F., Karczewski, K. J., Calvo, S. E., Neale, B. M. & Mootha, V. K. Nuclear genetic control of mtDNA copy number and heteroplasmy in humans. ***Nature*** **620,** 839–848 (2023).
41. **Kanai, M.** Leveraging fine-scale population structures for precision healthcare. ***Nature Medicine*** **29,** 1611–1612 (2023).
42. Weeks, E. M., Ulirsch, J. C., Cheng, N. Y., Trippe, B. L., Fine, R. S., ..., **Kanai, M.**, ..., Ardlie, K. G., Hirschhorn, J. N., Lander, E. S., Engreitz, J. M. & Finucane, H. K. Leveraging polygenic enrichments of gene features to predict genes underlying complex traits and diseases. ***Nature Genetics*** **55,** 1267–1276 (2023).
43. Palmer, D. S., Zhou, W., Abbott, L., Wigdor, E. M., Baya, N., ..., Poterba, T., King, D., **Kanai, M.**, Bloemendal, A. & Neale, B. M. Analysis of genetic dominance in the UK Biobank. ***Science*** **379,** 1341–1348 (2023).
44. Ogawa, K., Tsoi, L. C., Tanaka, H., **Kanai, M.**, Stuart, P. E., Nair, R. P., Tanaka, Y., Mochizuki, H., Elder, J. T. & Okada, Y. A cross-trait genetic correlation study identified eight diseases and traits associated with psoriasis. ***Journal of Investigative Dermatology*** **143,** 1813–1816.e2 (2023).

45. Rämö, J. T., Kiiskinen, T., Seist, R., Krebs, K., **Kanai, M.**, ..., Milani, L., Stankovic, K. M., Mäkitie, A., Daly, M. J. & Palotie, A. Genome-wide screen of otosclerosis in population biobanks: 27 loci and shared associations with skeletal structure. ***Nature Communications*** **14,** 157 (2023).

46. Kurki, M. I., Karjalainen, J., Palta, P., Sipilä, T. P., Kristiansson, K., ..., **Kanai, M.**, ..., Plenge, R., McCarthy, M., Runz, H., Daly, M. J. & Palotie, A. FinnGen provides genetic insights from a well-phenotyped isolated population. ***Nature*** **613,** 508–518 (2023).

47. Wang, Y., Namba, S., Lopera, E., Kerminen, S., Tsuo, K., ..., **Kanai, M.**, ..., Cox, N. J., Surakka, I., Okada, Y., Martin, A. R. & Hirbo, J. Global Biobank analyses provide lessons for developing polygenic risk scores across diverse cohorts. ***Cell Genomics*** **3,** 100241 (2023).

48. Kanoni, S., Graham, S. E., Wang, Y., Surakka, I., Ramdas, S., ..., **Kanai, M.**, ..., Natarajan, P., Deloukas, P., Willer, C. J., Assimes, T. L. & Peloso, G. M. Implicating genes, pleiotropy, and sexual dimorphism at blood lipid loci through multi-ancestry meta-analysis. ***Genome Biology*** **23,** 268 (2022).

49. Tsuo, K., Zhou, W., Wang, Y., **Kanai, M.**, Namba, S., ..., Okada, Y., Neale, B. M., Global Biobank Meta-analysis Initiative, Daly, M. J. & Martin, A. R. Multi-ancestry meta-analysis of asthma identifies novel associations and highlights the value of increased power and diversity. ***Cell Genomics*** **2,** 100212 (2022).

50. Zhou, W., **Kanai, M.**, Wu, K.-H. H., Rasheed, H., Tsuo, K., ..., Zöllner, S., Martin, A. R., Willer, C. J., Daly, M. J. & Neale, B. M. Global Biobank Meta-analysis Initiative: Powering genetic discovery across human disease. ***Cell Genomics*** **2,** 100192 (2022).

51. Bhattacharya, A., Hirbo, J. B., Zhou, D., Zhou, W., Zheng, J., **Kanai, M.**, The Global Biobank Meta-analysis Initiative, Pasaniuc, B., Gamazon, E. R. & Cox, N. J. Best practices for multi-ancestry, meta-analytic transcriptome-wide association studies: Lessons from the Global Biobank Meta-analysis Initiative. ***Cell Genomics*** **2,** 100180 (2022).

52. Yengo, L., Vedantam, S., Marouli, E., Sidorenko, J., Bartell, E., ..., **Kanai, M.**, ..., Frayling, T. M., Okada, Y., Wood, A. R., Visscher, P. M. & Hirschhorn, J. N. A saturated map of common genetic variants associated with human height. ***Nature*** **610,** 704–712 (2022).

53. Wang, Q. S., Edahiro, R., Namkoong, H., Hasegawa, T., Shirai, Y., ..., **Kanai, M.**, ..., Miyano, S., Ogawa, S., Kanai, T., Fukunaga, K. & Okada, Y. The whole blood transcriptional regulation landscape in 465 COVID-19 infected samples from Japan COVID-19 Task Force. ***Nature Communications*** **13,** 4830 (2022).

54. Ruotsalainen, S. E., Surakka, I., Mars, N., Karjalainen, J., Kurki, M., **Kanai, M.**, ..., Okada, Y., Palotie, A., Widen, E., Daly, M. J. & Ripatti, S. Inframe insertion and splice site variants in MFGE8 associate with protection against coronary atherosclerosis. ***Communications Biology*** **5,** 802 (2022).

55. Namkoong, H., Edahiro, R., Takano, T., Nishihara, H., Shirai, Y., ..., **Kanai, M.**, ..., Miyano, S., Ogawa, S., Kanai, T., Fukunaga, K. & Okada, Y. DOCK2 is involved in the host genetics and biology of severe COVID-19. ***Nature*** **609,** 754–760 (2022).

56. Ramdas, S., Judd, J., Graham, S. E., Kanoni, S., Wang, Y., ..., **Kanai, M.**, ..., Peloso, G., Assimes, T. L., Willer, C. J., Zhu, X. & Brown, C. D. A multi-layer functional genomic analysis to understand noncoding genetic variation in lipids. ***The American Journal of Human Genetics*** **109,** 1366–1387 (2022).

57. The COVID-19 Host Genetics Initiative. A first update on mapping the human genetic architecture of COVID-19. ***Nature*** **608,** E1–E10 (2022).

58. Winkler, T. W., Rasheed, H., Teumer, A., Gorski, M., Rowan, B. X., ..., **Kanai, M.**, ..., Hung, A. M., Kronenberg, F., Köttgen, A., Pattaro, C. & Heid, I. M. Differential and shared genetic effects on kidney function between diabetic and non-diabetic individuals. ***Communications Biology*** **5,** 580 (2022).

59. Wang, Y., Tsuo, K., **Kanai, M.**, Neale, B. M. & Martin, A. R. Challenges and Opportunities for Developing More Generalizable Polygenic Risk Scores. ***Annual Review of Biomedical Data Science*** **5,** 293–320 (2022).

60. Mars, N., Kerminen, S., Feng, Y.-C. A., **Kanai, M.**, Läll, K., ..., Pirinen, M., Palotie, A., Ganna, A., Martin, A. R. & Ripatti, S. Genome-wide risk prediction of common diseases across ancestries in one million people. ***Cell Genomics*** **2,** 100118 (2022).

61. Zheng, J., Zhang, Y., Rasheed, H., Walker, V., Sugawara, Y., ..., **Kanai, M.**, ..., Barbour, S., Yu, C., Åsvold, B. O., Zhang, H. & Gaunt, T. R. Trans-ethnic Mendelian-randomization study reveals causal relationships between cardiometabolic factors and chronic kidney disease. ***International Journal of Epidemiology*** **50,** 1995–2010 (2022).

62. Graham, S. E., Clarke, S. L., Wu, K.-H. H., Kanoni, S., Zajac, G. J. M., ..., **Kanai, M.**, ..., Morris, A. P., Assimes, T. L., Deloukas, P., Sun, Y. V. & Willer, C. J. The power of genetic diversity in genome-wide association studies of lipids. ***Nature*** **600,** 675–679 (2021).

63. Polygenic Risk Score Task Force of the International Common Disease Alliance. Responsible use of polygenic risk scores in the clinic: potential benefits, risks and gaps. ***Nature Medicine*** **27,** 1876–1884 (2021).

64. Luo, Y., **Kanai, M.**, Choi, W., Li, X., Sakaue, S., ..., Esko, T., Okada, Y., Han, B., McLaren, P. J. & Raychaudhuri, S. A high-resolution HLA reference panel capturing global population diversity enables multi-ancestry fine-mapping in HIV host response. ***Nature Genetics*** **53,** 1504–1516 (2021).

65. Griesemer, D., Xue, J. R., Reilly, S. K., Ulirsch, J. C., Kukreja, K., ..., **Kanai, M.**, ..., Montgomery, S. B., Finucane, H. K., Novina, C. D., Tewhey, R. & Sabeti, P. C. Genome-wide functional screen of 3'UTR variants uncovers causal variants for human disease and evolution. ***Cell*** **184,** 5247–5260.e19 (2021).

66. Reilly, S. K., Gosai, S. J., Guiterrez, A., Ulirsch, J. C., **Kanai, M.**, ..., Butler, G. B., Gladden-Young, A., Finucane, H. K., Sabeti, P. C. & Tewhey, R. Direct characterization of cis-regulatory elements and functional dissection of complex genetic associations using HCR–FlowFISH. ***Nature Genetics*** **53,** 1166–1176 (2021).

67. Wang, Q. S., Kelley, D. R., Ulirsch, J., **Kanai, M.**, Sadhuka, S., ..., Okada, Y., Aguet, F., Ardlie, K. G., MacArthur, D. G. & Finucane, H. K. Leveraging supervised learning for functionally informed fine-mapping of cis-eQTLs identifies an additional 20,913 putative causal eQTLs. ***Nature Communications*** **12,** 3394 (2021).

68. Nakatochi, M., Toyoda, Y., **Kanai, M.**, Nakayama, A., Kawamura, Y., ..., Yokota, M., Wakai, K., Okada, Y., Matsuo, H. & Japan Uric Acid Genomics Consortium (Japan Urate). An X chromosome-wide meta-analysis based on Japanese cohorts revealed that non-autosomal variations are associated with serum urate. ***Rheumatology*** **60,** 4430–4432 (2021).

69. Pirastu, N., Cordioli, M., Nandakumar, P., Mignogna, G., Abdellaoui, A., ..., **Kanai, M.**, ..., Neale, B. M., Walters, R. K., Nivard, M. G., Perry, J. R. B. & Ganna, A. Genetic analyses identify widespread sex-differential participation bias. ***Nature Genetics*** **53,** 663–671 (2021).

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