Shinichi Namba, M.D., Ph.D.

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Research Interests

Statistical Genetics / Population Genomics / Computational Biology / Cancer / Precision medicine / Drug discovery

Personal Statements

Dr. Shinichi Namba is an assistant professor at the Department of Genome Informatics, Graduate School of Medicine, the University of Tokyo. He received his medical degree from the University of Tokyo in 2018. After two years of junior residency, he joined Prof. Yukinori Okada's group at Osaka University Graduate School of Medicine, where he earned his Ph.D. in 2023. He has been in his current position since October 2023. He specializes in the genetics of complex traits and is studying genome-wide associations of complex traits and their clinical implications. He has contributed to many international collaborations on genome-wide association studies and whole-genome sequencing. In particular, he has led a working group within an international biobank collaboration and developed and validated a genomics-driven drug discovery framework integrating disease genetics with multi-omics data. He also contributes to genomic data management and analysis at BioBank Japan. His interdisciplinary research spans a pan-cancer analysis of the relationship between genetic cancer risk and somatic alterations, as well as investigations into the technical and ethical challenges of the clinical application of polygenic risk scores.

Academic Appointments

Nov 2023 –	Invited Faculty, Laboratory for Systems Genetics, RIKEN Center for Integrative Medical Sciences, Yokohama, Japan
Oct 2023 –	Assistant Professor, Department of Genome Informatics, Graduate School of Medicine, The University of Tokyo, Tokyo, Japan
Oct 2023 – Mar 2025	Invited Faculty, Department of Statistical Genetics, Graduate School of Medicine, The University of Osaka, Osaka, Japan

Clinical Training

Apr 2018 – Mar 2020	Junior Resident, Japan Red Cross Medical Center, Tokyo, Japan

Education

Apr 2020 – Sep 2023	Ph.D. (Medicine), Department of Statistical Genetics, Graduate School of Medicine, The University of Osaka, Osaka, Japan Advisor: Yukinori Okada
Apr 2012 – Mar 2018	M.D., Faculty of Medicine, The University of Tokyo, Tokyo, Japan

Honors and Awards

Feb 4, 2026	Inoue Research Award for Young Scientists, Inoue Foundation for Science
Dec 19, 2025	Best Oral Presentation Award, 70th Annual Meeting, Japanese Society of Human Genetics
Oct 10, 2024	Travel Award, ESHG Annual Meeting 2024, Japanese Society of Human Genetics
Mar 31, 2024	Outstanding Doctoral Student Award, Graduate School of Medicine, The University of Osaka
Oct 27, 2020	Reviewer's Choice Abstract, American Society of Human Genetics Annual Meeting 2020

Research Funding

Apr 2026 –	Japan Society for the Promotion of Science (JSPS), Grant-in-Aid for Early-Career Scientists, "Deep learning-based elucidation of the genetic architecture of human lipid metabolism" (PI)
Apr 2026 –	The University of Tokyo Pandemic Preparedness, Infection, and Advanced Research Center (UTOPIA), Grant in Aid for Young Scientists, "Implementation of genome-based drug discovery targeting severe and prolonged infectious diseases" (PI)
Oct 2025 –	Japan Agency for Medical Research and Development (AMED), Practical Research Project for Rare/Intractable Diseases, "All-Japan Cardiomyopathy Genome Omics Digital Cohort Study" (Co-I)
Oct 2025 –	Japan Agency for Medical Research and Development (AMED), Genome-based Drug Discovery Program, "Establishment of drug candidates through integrative analysis of the functional spectrum of genetic mutations and interdisciplinary collaboration of next-generation drug discovery fields" (PI)
Oct 2025 –	Japan Agency for Medical Research and Development (AMED), Medical Research Support Program, "Elucidating the pathophysiology of cardiometabolic diseases through genetic analyses and omics integration" (PI)
Jul 2024 –	Japan Agency for Medical Research and Development (AMED), Advanced Genome Research and Bioinformatics Study to Facilitate Medical Innovation, "A trans-disciplinary and trans-omics study of gene–environment interactions towards genomics-driven personalized medicine" (PI)
Jun 2024 –	Japan Foundation for Applied Enzymology, Grants related to Cardiovascular Innovative Conference, "Genomics-driven personalized medicine and drug discovery by elucidating gene –environment interactions for cardiovascular diseases" (PI)
Dec 2023 – Mar 2026	Japan Agency for Medical Research and Development (AMED), Research and Development Program for Bridging Genomic Research to Drug Discovery and Other Outcomes, "Elucidating the Trajectory of Cerebrovascular Disorders through Integrated Genomic Analysis and Hemodynamic Simulation for Clinical Applications" (Co-I)
Dec 2023 – Mar 2026	Japan Agency for Medical Research and Development (AMED), Research and Development Program for Bridging Genomic Research to Drug Discovery and Other Outcomes, "Digital omics to elucidate mechanisms of stress responses in heart failure for precision medicine" (Co-I)

Fellowships

Apr 2020 – Sep 2023	Scholarship Grant for Ph.D. Program in Medicine, Takeda Science Foundation

Teaching Experience

Apr 2026 –	Introduction to Medicine, Faculty of Medicine, The University of Tokyo
Apr 2025 –	Biochemistry (Lecture), Faculty of Medicine, The University of Tokyo
Apr 2024 –	Advanced Genome Informatics, Graduate School of Medicine, The University of Tokyo
Oct 2023 –	Biochemistry (Laboratory Course), Faculty of Medicine, The University of Tokyo
Apr 2020 – Sep 2023	Clinical Genetics, Teaching Assistant, Faculty of Medicine, The University of Osaka

Selected Publications

* equal contribution; ♯ (co-)corresponding author · Selected 6 of 47 peer-reviewed publications; the complete list is at the end of this CV.

1. **Namba S♯**, Sonehara K, Koyanagi YN, Kikuchi T, Ojima T, Edahiro R *et al.* A cross-population compendium of gene–environment interactions. *Nature* 688–697 (2026).
2. Caro I*, Western D*, **Namba S***, Sun N, Kawaguchi S, He Y *et al.* Proteogenomics in cerebrospinal fluid and plasma reveals new biological fingerprint of cerebral small vessel disease. *Nature Aging* 2514–2531 (2025).

3. **Namba S♯**, Akiyama M, Hamanoue H, Kato K, Kawashima M, Kushima I *et al.* Inconsistent embryo selection across polygenic score methods. *Nature Human Behaviour* 2264–2267 (2024).
4. **Namba S***, Saito Y*, Kogure Y, Masuda T, Bondy ML, Gharahkhani P *et al.* Common germline risk variants impact somatic alterations and clinical features across cancers. *Cancer Research* **83,** 20–27 (2022).
5. **Namba S***, Konuma T*, Wu KH, Zhou W & Okada Y. A practical guideline of genomics-driven drug discovery in the era of global biobank meta-analysis. *Cell Genomics* **2,** 100190 (2022).
6. Mishra A*, Malik R*, Hachiya T*, Jürgenson T*, **Namba S***, Posner DC* *et al.* Stroke genetics informs drug discovery and risk prediction across ancestries. *Nature* **611,** 115–123 (2022).

Publications

* equal contribution; ♯ (co-)corresponding author

Preprints

1. Wang C, Wu H, **Namba S**, Park JY, Matsuda K, Okada Y *et al.* Beyond point estimates: quantifying predictive uncertainty reveals hidden dimensions of biological age acceleration and improves risk interpretation. *bioRxiv* (2026).
2. Palmer DS, Hill B, Hodgson S, Jõeloo M, Kalantzis G, ..., **Namba S** *et al.* The Biobank Rare Variant consortium powers the discovery of rare genetic associations through global collaboration. *medRxiv* (2026).
3. Kyosaka T, Narita A, Kulski JK, Minn AKK, Miyake A, ..., **Namba S** *et al.* Genome-wide association and Mendelian randomization analyses link *Helicobacter pylori* infection to Human Leukocyte Antigen polymorphisms and autoimmune diseases. *medRxiv* (2026).
4. Verma S, Guare L, Das J, Caruth L, Rajagopalan A, ..., **Namba S** *et al.* Expanding the genetic landscape of endometriosis: Integrative -omics analyses implicate key genes and pathways in a multi-ancestry study of over one million women. *Res Sq* (2025).
5. Yang C, **Namba S**, Matsuda K, Okada Y, Moran L, Vincent A & Marques FZ. Acetate, a fibre-derived gut metabolite, is associated with reduced cardiovascular disease risk in females with early menopause. *medRxiv* (2026).
6. Uffelmann E, Wightman DP, Bahrami S, Shadrin AA, Fominykh V, ..., **Namba S** *et al.* Genomic analyses reveal new insights into Alzheimer's disease. *medRxiv* (2025).
7. Shiraishi Y, Ochi Y, Sugawa M, Sakamoto Y, Kimura K, ..., **Namba S** *et al.* Rare k-mers reveal centromere haplogroups underlying human diversity and cancer translocations. *bioRxiv* (2025).

Peer-Reviewed Publications

1. Taguchi M, Sato S, Nannya Y, Mishima H, Horai M, ..., **Namba S** *et al.* Clonal hematopoiesis related to ionizing radiation in atomic bomb survivors. *Leukemia* (2026).
2. Liu S, Zheng H, Gu Y, Yang Z, Zhen J, ..., **Namba S** *et al.* Genome-wide association analyses of gestational phenotypes identify context-specific genetic effects. *Nature Genetics* **58,** 1845–1854 (2026).
3. Liou L, García-González J, Wu HM, **Namba S**, Vaura F, Okada Y *et al.* Polygenic Prediction of Nongoal Response to Statin Therapy. *Circulation: Genomic and Precision Medicine* (2026).
4. Chaya R, Taguchi K, Hashimoto Y, Shirai Y, Edahiro R, ..., **Namba S** *et al.* Cross-Species Comparison between Mouse Kidney Multi-Omics and Human Genome-Wide Association Studies Highlights Molecular Features Associated with Oxalate Nephropathy. *Kidney360* (2026).
5. Lassen FH, Kalantzis G, Eoli A, Hill B, Sonehara K, **Namba S** *et al.* Meta-analysis across six global biobanks identifies recessive coding associations with complex traits and diseases. *The American Journal of Human Genetics* **113,** 1330–1346 (2026).
6. Hirano Y, Miyawaki S, Sonehara K, **Namba S**, Inoue H, Shirai Y *et al.* Integrative GWAS and snRNA-seq Reveal a Mesenchymal-Like Endothelial Signature in Moyamoya Disease. *Stroke* **57,** 1336–1348 (2026).
7. Ueda H, Kubota T, Goto R, Suzuki A, Ojima T, ..., **Namba S** *et al.* Elucidating genetic backgrounds of myasthenia gravis in Japanese by genome-wide association studies and multi-omics analyses of thymoma. *Nature Communications* **17,** (2026).

8. Sato G, Yamamoto Y, Sonehara K, Saiki R, Ojima T, ..., **Namba S** *et al.* Genetic regulation across germline and somatic variation on the Y chromosome contributes to type 2 diabetes. *Nature Medicine* 894–905 (2026).
9. Ishigami D*, **Namba S***, Miyawaki S, Mitsui J, Imai H, Shimizu M *et al.* Delineating the Genetic Basis of RNF213-related vasculopathies: The association of PKHD1 variants with bilateral cerebral vasculopathy. *European Journal of Human Genetics* 788–795 (2026).
10. White SL, Brasher MS, Pattee J, Zhou W, Chapman S, ..., **Namba S** *et al.* Global multi-ancestry genome-wide analyses identify genes and biological pathways associated with thyroid cancer and benign thyroid diseases. *Nature Genetics* **58,** 307–316 (2026).
11. **Namba S**♯, Sonehara K, Koyanagi YN, Kikuchi T, Ojima T, Edahiro R *et al.* A cross-population compendium of gene–environment interactions. *Nature* 688–697 (2026).
12. Caro I*, Western D*, **Namba S***, Sun N, Kawaguchi S, He Y *et al.* Proteogenomics in cerebrospinal fluid and plasma reveals new biological fingerprint of cerebral small vessel disease. *Nature Aging* 2514–2531 (2025).
13. Edahiro R, Sato G, Naito T, Shirai Y, Saiki R, ..., **Namba S** *et al.* Deciphering state-dependent immune features from multi-layer omics data at single-cell resolution. *Nature Genetics* **57,** 1905–1921 (2025).
14. Sonehara K, Watanabe R, Matsumura Y, Mitsui Y, Ogawa Y, ..., **Namba S** *et al.* Whole-genome sequencing reveals rare and structural variants contributing to psoriasis and identifies CERCAM as a risk gene. *Cell Genomics* **5,** 100978 (2025).
15. Yamamoto Y, Shirai Y, Sonehara K, **Namba S**, Ojima T, Yamamoto K *et al.* Dissecting cross-population polygenic heterogeneity across respiratory and cardiometabolic diseases. *Nature Communications* **16,** 3765 (2025).
16. Yata T, Sato G, Ogawa K, Naito T, Sonehara K, ..., **Namba S** *et al.* Contribution of germline and somatic mutations to risk of neuromyelitis optica spectrum disorder. *Cell Genomics* **5,** 100776 (2025).
17. Sonehara K, Uwamino Y, Saiki R, Takeshita M, **Namba S**, Uno S *et al.* Germline variants and mosaic chromosomal alterations affect COVID-19 vaccine immunogenicity. *Cell Genomics* **5,** 100783 (2025).
18. Sasa N, Kojima S, Koide R, Hasegawa T, Namkoong H, ..., **Namba S** *et al.* Blood DNA virome associates with autoimmune diseases and COVID-19. *Nature Genetics* **57,** 65–79 (2025).
19. Kato C, Morimoto S, Takahashi S, **Namba S**, Wang QS, Okada Y & Okano H. Spinal cord motor neuron phenotypes and polygenic risk scores in sporadic amyotrophic lateral sclerosis: deciphering the disease pathology and therapeutic potential of ropinirole hydrochloride. *Journal of Neurology, Neurosurgery & Psychiatry* **96,** 199–201 (2025).
20. Yamamoto K, **Namba S**, Sonehara K, Suzuki K, Sakaue S, Cooke NP *et al.* Genetic legacy of ancient hunter-gatherer Jomon in Japanese populations. *Nature Communications* **15,** 9780 (2024).
21. **Namba S**♯, Akiyama M, Hamanoue H, Kato K, Kawashima M, Kushima I *et al.* Inconsistent embryo selection across polygenic score methods. *Nature Human Behaviour* 2264–2267 (2024).
22. Wang QS, Hasegawa T, Namkoong H, Saiki R, Edahiro R, ..., **Namba S** *et al.* Statistically and functionally fine-mapped blood eQTLs and pQTLs from 1,405 humans reveal distinct regulation patterns and disease relevance. *Nature Genetics* 2054–2067 (2024).
23. Naito T, Inoue K, **Namba S**, Sonehara K, Suzuki K, Matsuda K *et al.* Machine learning reveals heterogeneous associations between environmental factors and cardiometabolic diseases across polygenic risk scores. *Communications Medicine* **4,** 181 (2024).
24. Tomofuji Y, Edahiro R, Sonehara K, Shirai Y, Kock KH, ..., **Namba S** *et al.* Quantification of escape from X chromosome inactivation with single-cell omics data reveals heterogeneity across cell types and tissues. *Cell Genomics* **4,** 100625 (2024).
25. Ojima T, **Namba S**, Suzuki K, Yamamoto K, Sonehara K, Narita A *et al.* Body mass index stratification optimizes polygenic prediction of type 2 diabetes in cross-biobank analyses. *Nature Genetics* **56,** 1100–1109 (2024).
26. De Vincentis A, Tavaglione F, **Namba S**, Kanai M, Okada Y, Kamatani Y *et al.* 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).

27. Lo Faro V, Bhattacharya A, Zhou W, Zhou D, Wang Y, ..., **Namba S** *et al.* Novel ancestry-specific primary open-angle glaucoma loci and shared biology with vascular mechanisms and cell proliferation. *Cell Reports Medicine* **5,** 101430 (2024).

28. Suzuki K, Hatzikotoulas K, Southam L, Taylor HJ, Yin X, ..., **Namba S** *et al.* Genetic drivers of heterogeneity in type 2 diabetes pathophysiology. *Nature* **627,** 347–357 (2024).

29. Koyanagi YN, Nakatochi M, **Namba S**, Oze I, Charvat H, Narita A *et al.* Genetic architecture of alcohol consumption identified by a genotype-stratified GWAS and impact on esophageal cancer risk in Japanese people. *Science Advances* **10,** eade2780 (2024).

30. Campos AI, **Namba S**, Lin SC, Nam K, Sidorenko J, Wang H *et al.* Boosting the power of genome-wide association studies within and across ancestries by using polygenic scores. *Nature Genetics* **55,** 1769–1776 (2023).

31. Sato G, Shirai Y, **Namba S**, Edahiro R, Sonehara K, Hata T *et al.* Pan-cancer and cross-population genome-wide association studies dissect shared genetic backgrounds underlying carcinogenesis. *Nature Communications* **14,** 3671 (2023).

32. Tanaka H, Okada Y, Nakayamada S, Miyazaki Y, Sonehara K, **Namba S** *et al.* Extracting immunological and clinical heterogeneity across autoimmune rheumatic diseases by cohort-wide immunophenotyping. *Annals of the Rheumatic Diseases* **83,** 242–252 (2023).

33. Sekita A, Kawasaki H, Fukushima-Nomura A, Yashiro K, Tanese K, ..., **Namba S** *et al.* Multifaceted analysis of cross-tissue transcriptomes reveals phenotype–endotype associations in atopic dermatitis. *Nature Communications* **14,** 6133 (2023).

34. Edahiro R, Shirai Y, Takeshima Y, Sakakibara S, Yamaguchi Y, ..., **Namba S** *et al.* Single-cell analyses and host genetics highlight the role of innate immune cells in COVID-19 severity. *Nature Genetics* **55,** 753–767 (2023).

35. Wang Y, **Namba S**, Lopera E, Kerminen S, Tsuo K, Läll K *et al.* Global Biobank analyses provide lessons for developing polygenic risk scores across diverse cohorts. *Cell Genomics* **3,** 100241 (2023).

36. Tsuo K, Zhou W, Wang Y, Kanai M, **Namba S**, Gupta R *et al.* Multi-ancestry meta-analysis of asthma identifies novel associations and highlights the value of increased power and diversity. *Cell Genomics* **2,** 100212 (2022).

37. **Namba S***, Saito Y*, Kogure Y, Masuda T, Bondy ML, Gharahkhani P *et al.* Common germline risk variants impact somatic alterations and clinical features across cancers. *Cancer Research* **83,** 20–27 (2022).

38. Zhou W, Kanai M, Wu KHH, Rasheed H, Tsuo K, ..., **Namba S** *et al.* Global Biobank Meta-analysis Initiative: Powering genetic discovery across human disease. *Cell Genomics* **2,** 100192 (2022).

39. **Namba S***, Konuma T*, Wu KH, Zhou W & Okada Y. A practical guideline of genomics-driven drug discovery in the era of global biobank meta-analysis. *Cell Genomics* **2,** 100190 (2022).

40. Mishra A*, Malik R*, Hachiya T*, Jürgenson T*, **Namba S***, Posner DC* *et al.* Stroke genetics informs drug discovery and risk prediction across ancestries. *Nature* **611,** 115–123 (2022).

41. Yamamoto K, Sonehara K, **Namba S**, Konuma T, Masuko H, Miyawaki S *et al.* Genetic footprints of assortative mating in the Japanese population. *Nature human behaviour* **7,** 65–73 (2022).

42. Wang QS, Edahiro R, Namkoong H, Hasegawa T, Shirai Y, ..., **Namba S** *et al.* The whole blood transcriptional regulation landscape in 465 COVID-19 infected samples from Japan COVID-19 Task Force. *Nature communications* **13,** 4830 (2022).

43. Namkoong H, Edahiro R, Takano T, Nishihara H, Shirai Y, ..., **Namba S** *et al.* DOCK2 is involved in the host genetics and biology of severe COVID-19. *Nature* **609,** 754–760 (2022).

44. Shirai Y, Nakanishi Y, Suzuki A, Konaka H, Nishikawa R, ..., **Namba S** *et al.* Multi-trait and cross-population genome-wide association studies across autoimmune and allergic diseases identify shared and distinct genetic component. *Annals of the rheumatic diseases* **81,** 1301–1312 (2022).

45. Ho WK, Tai MC, Dennis J, Shu X, Li J, ..., **Namba S** *et al.* Polygenic risk scores for prediction of breast cancer risk in Asian populations. *Genetics in medicine* **24,** 586–600 (2022).

46. **Namba S**, Ueno T, Kojima S, Kobayashi K, Kawase K, Tanaka Y *et al.* Transcript-targeted analysis reveals isoform alterations and double-hop fusions in breast cancer. *Communications biology* **4,** 1320 (2021).

47. **Namba S**, Sato K, Kojima S, Ueno T, Yamamoto Y, Tanaka Y *et al.* Differential regulation of CpG island methylation within divergent and unidirectional promoters in colorectal cancer. *Cancer science* **110,** 1096–1104 (2019).

Reviews (in Japanese)

1. **Namba S** & Okada Y. [CURRENT PIPELINES FOR WHOLE-GENOME SEQUENCING ANALYSES]. *Arerugi* **72,** 1110–1112 (2023).
2. **Namba S** & Okada Y. [UTILIZING GENOMIC INFORMATION FOR BIOMARKER IDENTIFICATION AND GENOMIC DRUG DISCOVERY]. *Arerugi* **69,** 952–957 (2020).

Invited Conference Talks

Jan 29, 2026	"Gene–environment interactions underlying the dynamics of genetic architecture", The 6th SCARDA Joint Symposium of the Support Institutions at Kyoto University, RIKEN, and the University of Tokyo, Japan
Nov 5, 2025	"Cross-biobank studies", 2025 East Asia Biobank Symposium, China
Sep 3, 2025	"Biobank Japan", FinnGen Face-to-Face Helsinki 2025, Finnland
Jul 2, 2025	"Gene–environment interactions underlying the dynamics of genetic architecture", The 15th International Workshop on Advanced Genomics, Japan
Oct 17, 2024	"Genome and omics data with rich disease phenotypes in BioBank Japan provide insights into disease biology and personalized medicine", World Congress of Psychiatric Genetics 2024, Singapore
Oct 12, 2024	"Integrative analyses of germline variants, somatic mutations, and gene–environment interactions", Japanese Society of Human Genetics 2024, Japan
Oct 12, 2023	"Polygenic germline effects on cancer somatic alterations", Japanese Society of Human Genetics 2023, Japan

Invited Research Seminars

Apr 29, 2026	"A Cross-population Compendium of Gene–Environment Interactions", Psychiatric Genetics Consortium Cross-population Working Group, Virtual
Feb 17, 2026	"Gene–environment interactions underlying the dynamics of genetic architecture", Department of Diabetes and Metabolic Diseases, The University of Tokyo Hospital, Japan (virtual)
Jan 13, 2026	"Gene–environment interactions underlying the dynamics of genetic architecture", Department of Nephrology, The University of Tokyo Hospital, Japan
Dec 19, 2023	"A cross-population atlas of genome-wide gene-environment interactions between the East Asian and European populations", Prof. Alisa Manning Lab, Massachusetts General Hospital and Broad Institute, US (virtual)

Public Profiles

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