Shinichi Namba
Graduate School of Medicine, the University of Tokyo

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 medical faculty of the University of Tokyo in 2018. After two years of junior residency, he joined the laboratory of Prof. Yukinori Okada at Osaka University Graduate School of Medicine as a Ph.D. student. He completed his Ph.D. in September 2023 and 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.

[Job]

Nov 2024 – Invited Faculty, Laboratory for Systems Genetics, RIKEN Center for Integrative Medical Sciences

Oct 2024 – Assistant Professor, Department of Genome Informatics, Graduate School of Medicine, The University of Tokyo

Oct 2024 – Invited Faculty, Department of Statistical Genetics, Osaka University Graduate School of Medicine

Apr 2018 – Mar 2020 Japan Red Cross Medical Center (Junior Resident)

[Education]

Apr 2020 – Sep 2023 Ph.D. (Medicine), Department of Statistical Genetics, Osaka University Graduate School of Medicine

Apr 2012 – Mar 2018 The University of Tokyo (B.S.[Medicine], M.D.)

[Grants and Fellowships]

Jun 2024 – Japan Foundation for Applied Enzymology, Grants related to Cardiovascular Innovative Conference

Jul 2024 – Japan Agency for Medical Research and Development (AMED) GRIFIN, “A trans-disciplinary and trans-omics study of gene–environment interactions towards genomics-driven personalized medicine”

Apr 2020 – Mar 2024 – Takeda Science Foundation Scholarship

[Selected Publications] (*, co-first author; $, co-corresponding author)

1. Namba S$, Akiyama M, Hamanoue H, Kato K, Kawashima M, Kushima I, Matsuda K, Nakatochi M, Ogishima S, Sonehara K, Suzuki K, Takata A, Tamiya G, Tanikawa C, Yamamoto K, Yamamoto N, The BioBank Japan Project, Ozaki N, Okada Y$. Inconsistent embryo selection across polygenic score methods. *Nat. Hum. Behav.* 2024, 8, 2264–2267.

2. **Namba S**, Saito Y, Kogure Y, Masuda T, Bondy ML, Gharahkhani P, Gockel I, Heider D, Hillmer A, Jankowski J, MacGregor S, Maj C, Melin B, Ostrom QT, Palles C, Schumacher J, Tomlinson I, Whiteman DC, Okada Y, Kataoka K. Common Germline Risk Variants Impact Somatic Alterations and Clinical Features across Cancers. *Cancer Res.* 2023, 83, 20–27.

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

4. Mishra A*, Malik R*, Hachiya T*, Jürgenson T*, **Namba S***, Posner DC*, (569 authors), Dichgans M, Debette S. Stroke genetics informs drug discovery and risk prediction across ancestries. *Nature* 2022, 611, 115–123.

5. **Namba S**, Ueno T, Kojima S, Kobayashi K, Kawase K, Tanaka Y, Inoue S, Kishigami F, Kawashima S, Maeda N, Ogawa T, Hazama S, Togashi Y, Ando M, Shiraishi Y, Mano H, Kawazu M. Transcript-targeted analysis reveals isoform alterations and double-hop fusions in breast cancer. *Commun. Biol.* 2021, 4, 1320.

6. **Namba S**, Sato K, Kojima S, Ueno T, Yamamoto Y, Tanaka Y, Inoue S, Nagae G, Iinuma H, Hazama S, Ishihara S, Aburatani H, Mano H, Kawazu M. Differential regulation of CpG island methylation within divergent and unidirectional promoters in colorectal cancer. *Cancer Sci.* 2019, 110, 1096–1104.