

# Curriculum Vitae

## Contact Details:

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2-2 Yamadaoka, Suita, Osaka 565-0871, Japan

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## Present Position:

Professor, Department of Genome Informatics, Graduate School of Medicine, the University of Tokyo.

Professor, Department of Statistical Genetics, Osaka University Graduate School of Medicine.

Team Leader, Laboratory for Systems Genetics, RIKEN Center for Integrative Medical Sciences.

## Education:

1999-2005 MD, the University of Tokyo, Tokyo, Japan

2007-2011 PhD of Medicine, Graduate School of Medicine, the University of Tokyo, Tokyo, Japan

## Doctor thesis:

Identification of RA susceptible genetic factors through a GWAS and an analysis in the MHC region (mentored by Prof. Kazuhiko Yamamoto)

## Clinical Residencies:

2005-2006 Resident, Fujieda Municipal Hospital, Shizuoka, Japan

2006-2007 Resident, the University of Tokyo Hospital, Tokyo, Japan

## Academic Appointments:

2010-2012 Postdoctoral Fellow of the Japan Society for the Promotion of Science

2012-2013 Postdoctoral Fellow for Research Abroad of the Japan Society for the Promotion of Science

2012-2013 Research Fellow, Division of Rheumatology, Immunology, and Allergy, Brigham and Women's Hospital, and Postdoctoral Fellow, the Broad Institute

2013-2016 Tenure Track Junior Associate Professor, Tokyo Medical and Dental University

2016- Professor, Osaka University

2021- Team Leader, RIKEN Center for Integrative Medical Sciences

2022- Professor, the University of Tokyo

## Major Research Interests:

Genetics of human complex traits, statistical genetics, bioinformatics, drug discovery, personalized medicine

## Personal Statements:

My research theme is the elucidation of mechanism where genetic variants in the populations affect clinical phenotypes of individuals, especially for autoimmune diseases and clinical biomarkers. One of my strengths is multiple professional backgrounds as a rheumatologist, a statistician, and a bioinformatician. Through active collaborative partnerships among the researchers in the field of human genetics, I have enormously conducted genome-wide association studies (GWAS) of human complex traits and identified >15,000 novel genetic risk loci (Okada Y. *Nat Genet* 2012a/2012b/2012c, Okada Y. *Nature* 2014, Kanai M. *Nat Genet* 2018, Sakaue S. *Nat Genet* 2021, Ishigaki K. *Nat Genet* 2021, NamKoong H. *Nature* 2022, Yengo L. *Nature* 2022, Sato G. *Nat Commun* 2023). I also have experiences for analyzing genetic variants in the major histocompatibility complex (MHC) region including human leukocyte antigen (HLA) genes and killer immunoglobulin receptor (KIR) region, which have substantial impacts on disease genetics and can act as clinical biomarkers (Okada Y. *Nat Genet* 2015, Hirata. *Nat Genet* 2019, Naito. *Nat Commun* 2021, Sakaue. *Cell Genom* 2022, Sonehara K. *Nat Commun* 2022, *Cell Rep Med* 2023, *Nat Commun* 2024). My interests are now moving towards genetic and bioinformatics analysis using multi-modal human omics data generated by technologies in the post-GWAS era, and its application to novel drug discovery and drug repositioning (Sakaue S. *Nucleic Acids Res* 2018, Sakaue S. *Bioinformatics* 2019, Namba S. *Cell Genom* 2022), trans-omics analysis (Tomofuji Y. *Ann Rheum Dis* 2021/2022, *Cell Genom* 2022, *Nat Microbiol* 2023, *Cell Rep* 2023), single cell sequencing (Eda Hiro R. *Nat Genet* 2023, Tomofuji Y. *Cell Genom* 2024, Sasa N. *Nat Genet* 2024), human evolution and population genetics (Okada Y. *Nat Commun* 2018, Sakaue S. *Nat Commun* 2020, Yasumizu Y. *Mol Biol Evol* 2020, Yamamoto K. *Nat Hum Behav* 2023, Yamamoto K. *Nat Commun* 2024), and personalized medicine (Sakaue S. *Nat Med* 2020, Namba S. *Can Res* 2023, Sekita A. *Nat Commun* 2023, Tanaka H. *Ann Rheum Dis* 2023, Ojima T. *Nat Genet* 2024, Namba S. *Nat Hum Behav* 2024).

## Teaching Experiences:

A course lecture, Super Science High School Program, 2013-2014, Graduate School of Medical and Dental Sciences, Tokyo Medical and Dental University, Tokyo, Japan

A course lecture, Genetics and Diversity, 2014-2017, Graduate School of Medical and Dental Sciences, Tokyo Medical and Dental University, Tokyo, Japan

A course lecture, Genetics and Bioinformatics, 2016-, Osaka University Graduate School of Medicine, Osaka, Japan

A practical course, Genetics and Bioinformatics, 2020-, Osaka University Graduate School of Medicine, Osaka, Japan

A course lecture, Biochemistry, 2022-, Graduate School of Medicine, the University of Tokyo, Tokyo, Japan

A practical course, Biochemistry, 2022-, Graduate School of Medicine, the University of Tokyo, Tokyo, Japan

## Journal Editorial Activities:

Associate Editor, *Genes & Genetic Systems*, 2019-

Associate Editor, *Human Genome Variations*, 2018-

Advisory Editor, *Arthritis & Rheumatology*, 2017-2019

## Selected Publications (with correspondence):

- Sasa N et al. Blood DNA virome associates with autoimmune diseases and COVID-19. *Nat Genet* In Press.
- Yamamoto K et al. (2024) Genetic legacy of ancient hunter-gatherer Jomon in Japanese populations. *Nat Commun* 15:9780.
- Namba S et al. Inconsistent embryo selection across polygenic score methods. *Nat Hum Behav* 8:2264-2267.
- Wang QS et al. Statistically and functionally fine-mapped blood e/pQTLs from 1,405 humans reveal their distinct regulation patterns and disease relevance. *Nat Genet* 56:2054-2067.
- Sonehara K et al. (2024) Common and rare genetic variants predisposing females to unexplained recurrent pregnancy loss. *Nat Commun* 15:5744.
- Tomofuji Y et al. (2024) Quantification of escape from X chromosome inactivation with single-cell omics data

- reveals heterogeneity across cell types and tissues. *Cell Genom* 100625.
- Ojima T et al. Body mass index stratification optimizes polygenic prediction of type 2 diabetes in trans-biobank analysis. *Nat Genet* 56:1100-1109.
  - Tanaka H et al. (2024) Extracting immunological and clinical heterogeneity across autoimmune rheumatic diseases by cohort-wide immunophenotyping. *Ann Rheum Dis* 83:242-252.
  - Tomofuji Y et al. (2023) Analysis of gut microbiome, host genetics, and plasma metabolites reveals gut microbiome-host interactions in the Japanese population. *Cell Rep* 42:113324.
  - Sato G et al. (2023) Pan-cancer and cross-population genome-wide association studies dissect shared genetic backgrounds underlying carcinogenesis. *Nat Commun* 14:3671.
  - Tomofuji Y et al. (2023) Reconstruction of the personal information from human genome reads in gut metagenome sequencing data. *Nat Microbiol* 8:1079-1094.
  - Eda Hiro R et al. (2023) Biological and host genetic involvement of innate immune cells in COVID-19 severity. *Nat Genet* 55:753-767.
  - Sekita A et al. (2023) Multifaceted analysis of cross-tissue transcriptomes reveals phenotype-endotype associations in atopic dermatitis. *Nat Commun* 14:6133.
  - Namba S et al. (2023) Common germline risk variants impact somatic alterations and clinical features across cancers. *Cancer Res* 83:20-27.
  - Yamamoto K et al. (2023) Genetic footprints of assortative mating in the Japanese population. *Nat Hum Behav* 7:65-73.
  - Tomofuji Y et al. (2022) Prokaryotic and viral genomes recovered from 787 Japanese gut metagenomes revealed microbial features linked to diets, populations, and diseases. *Cell Genom* 2:100219.
  - Ishigaki K et al. (2022) Multi-ancestry genome-wide association analyses identify novel genetic mechanisms in rheumatoid arthritis. *Nat Genet* 54:1640-1651.
  - Namba S et al. A practical guideline of genomics-driven drug discovery in the era of global biobank meta-analysis. (2022) *Cell Genom* 2:100190.
  - Yengo L et al. (2022) A saturated map of common genetic variants associated with human height. *Nature* 610:704-712.
  - Wang QS et al. (2022) The whole blood transcriptional regulation landscape in 465 COVID-19 infected samples from Japan COVID-19 Task Force. *Nat Commun* 13:4830.
  - Namkoong H et al. DOCK2 is involved in genetics and biology of severe COVID-19. *Nature* 609:754-760.
  - Sonehara K et al. (2022) A common deletion at BAK1 reduces enhancer activity and confers risk of intracranial germ cell tumors. *Nat Commun* 13:4478.
  - Shirai Y et al. (2022) Multi-trait and cross-population genome-wide association studies across autoimmune and allergic diseases identify shared and distinct genetic components. *Ann Rheum Dis* 81:1301-1312.
  - **Okada Y.** (2022) An evolving hypothesis in autoimmune disease genetics. *Nat Rev Genet* 23:458-459.
  - Sakaue S et al. (2022) Decoding the diversity of killer immunoglobulin-like receptors by deep sequencing and a high-resolution imputation method. Decoding the diversity of killer immunoglobulin-like receptors by deep sequencing and a high-resolution imputation method. *Cell Genomics* 2:100101.
  - Tomofuji Y et al. (2022) Whole gut virome analysis of 476 Japanese revealed a link between phage and autoimmune disease. *Ann Rheum Dis* 81:278-288.
  - Sakaue S et al. (2021) A cross-population atlas of genetic associations for 220 human phenotypes. *Nat Genet* 53:1415-1424.
  - **Okada Y** et al. (2021) A massive effort links protein-coding gene variants to health. *Nature* 599:561-563.
  - Tomofuji Y et al. (2021) A metagenome-wide association study revealed disease-specific landscape of the gut microbiome of systemic lupus erythematosus in Japanese. *Ann Rheum Dis* 80:1575-1583.
  - Naito T et al. (2020) A deep learning method for HLA imputation and trans-ethnic MHC fine-mapping of type 1 diabetes. *Nat Commun* 12:1639.
  - Sakaue S et al. (2021) Genetic determinants of risk in autoimmune pulmonary alveolar proteinosis. *Nat Commun* 12:1032.
  - Shirai Y et al. (2020) Association of the RPA3-UMAD1 locus with interstitial lung diseases complicated with

rheumatoid arthritis in Japanese. *Ann Rheum Dis* 79:1305-1309.

- Sakaue S et al. (2020) Trans-biobank analysis with 676,000 individuals elucidates the association of polygenic risk scores of complex traits with human lifespan. *Nat Med* 26:542-548.
- Sakaue S et al. (2020) Dimensionality reduction reveals fine-scale structure in the Japanese population with consequences for polygenic risk prediction. *Nat Commun* 11:1569.
- Matoba N et al. (2020) GWAS of 165,084 Japanese individuals identified nine loci associated with dietary habits. *Nat Hum Behav* 4:308-316.
- Kishikawa T et al. (2020) A metagenome-wide association study of gut microbiome revealed novel etiology of rheumatoid arthritis in the Japanese population. *Ann Rheum Dis* 79:103-111.
- Hirata J et al. (2019) Genetic and phenotypic landscape of the MHC region in the Japanese population. *Nat Genet* 51:470-480.
- Sakaue S et al. (2018) Integration of genetics and miRNA-target gene network identified disease biology implicated in tissue specificity. *Nucleic Acids Res* 46:11898-11909.
- Kanai M et al. (2018) Genetic analysis of quantitative traits in the Japanese population links cell types to complex human diseases. *Nat Genet* 50:390-400.
- Okada Y et al. (2018) Deep whole-genome sequencing reveals recent selection signatures linked to evolution and disease risk of Japanese. *Nat Commun* 9:1631.
- Okada Y et al. (2015) Construction of a population-specific HLA imputation reference panel and its application to Graves' disease risk in Japanese. *Nat Genet* 47:798-802.
- Okada Y et al. (2014) Genetics of rheumatoid arthritis contributes to biology and drug discovery. *Nature* 506:376-381.
- Okada Y et al. (2012) Meta-analysis identifies multiple loci associated with kidney function-related traits in east Asian populations. *Nat Genet* 44:904-909.
- Okada Y et al. (2012) Meta-analysis identifies nine new loci associated with rheumatoid arthritis in the Japanese population. *Nat Genet* 44:511-516.
- Okada Y et al. (2012) Common variants at CDKAL1 and KLF9 are associated with body mass index in east Asian populations. *Nat Genet* 44:302-306.

## Publications:

(†: Corresponding author, \*: Equal contribution.)

### Articles and Letters

- Sasa N, Kojima S, Koide S, Hasegawa T, Namkoong H, ..., Fukunaga K, Imoto S, Miyano S, Parrish NF†, **Okada Y†**. Blood DNA virome associates with autoimmune diseases and COVID-19. *Nat Genet* In Press.
- Nakamura J, Yamamoto T†, Takabatake Y, Namba-Hamano T, Takahashi A, Matsuda J, Minami S, Sakai S, Yonishi H, Maeda S, Matsui S, Kawai H, Matsui I, Yamamuro T, Edahiro R, Takashima S, Takasawa A, **Okada Y**, Yoshimori T, Ballabio A, Isaka Y. (2024) Age-related TFEB downregulation in proximal tubules causes systemic metabolic disorders and occasional apolipoprotein A4-related amyloidosis. *JCI Insight* doi:10.1172/jci.insight.184451.
- Noguchi E†, Morii W, Kitazawa H, Hirota T, Sonehara K, Masuko H, **Okada Y**, Hizawa N. (2024) A genome-wide meta-analysis reveals shared and population-specific variants for allergic sensitization. *J Allergy Clin Immunol* doi:10.1016/j.jaci.2024.11.033.
- Tian C, Zhang Y, Tong Y, Kock KH, Sim DY, Liu F, Dong J, Jing Z, Wang W, Gao J, Tan LM, Han KY, Tomofuji Y, Nakano M, Buyamin EV, Sonthalia R, Ando Y, Hatano H, Sonehara K; Asian Immune Diversity Atlas Network; Jin X, Loh M, Chambers J, Hon CC, Choi M, Park JE, Ishigaki K, Okamura T, Fujio K, **Okada Y**, Park WY, Shin JW, Roca X, Prabhakar S, Liu B†. (2024) Single-cell RNA sequencing of peripheral blood links cell-type-specific regulation of splicing to autoimmune and inflammatory diseases. *Nat Genet* 56:2739-2752.
- Yamamoto K, Namba S, Sonehara K, Suzuki K, Sakaue S, Cooke NP, Higashiue S, Kobayashi S, Afuso H, Matsuura K, Mitsumoto Y, Fujita Y, Tokuda T, Biobank Japan Project, Matsuda K, Gakuhari T, Yamauchi T, Kadowaki T, Nakagome S†, **Okada Y†**. (2024) Genetic legacy of ancient hunter-gatherer Jomon in Japanese populations. *Nat Commun* 15:9780.
- Major TJ, Takei R, Matsuo H, Leask MP, Sumpter NA, Topless RK, Shirai Y, Wang W, Cadzow MJ, Phipps-Green AJ, Li Z, Ji A, Merriman ME, Morice E, Kelley EE, Wei WH, McCormick SPA, Bixley MJ, Reynolds RJ, Saag KG, Fadason T, Golovina E, O'Sullivan JM, Stamp LK, Dalbeth N, Abhishek A, Doherty M, Roddy E, Jacobsson LTH, Kapetanovic MC, Melander O, Andrés M, Pérez-Ruiz F, Torres RJ, Radstake T, Jansen TL, Janssen M, Joosten LAB, Liu R, Gaal OI, Crişan TO, Rednic S, Kurreeman F, Huizinga TWJ, Toes R, Lioté F, Richette P, Bardin T, Ea HK, Pascart T, McCarthy GM, Helbert L, Stibůrková B, Tausche AK, Uhlig T, Vitart V, Boutin TS, Hayward C, Riches PL, Ralston SH, Campbell A, MacDonald TM; FAST Study Group; Nakayama A, Takada T, Nakatochi M, Shimizu S, Kawamura Y, Toyoda Y, Nakaoka H, Yamamoto K, Matsuo K, Shinomiya N, Ichida K; Japan Gout Genomics Consortium; Lee C; Asia Pacific Gout Consortium; Bradbury LA, Brown MA, Robinson PC, Buchanan RRC, Hill CL, Lester S, Smith MD, Rischmueller M, Choi HK, Stahl EA, Miner JN, Solomon DH, Cui J, Giacomini KM, Brackman DJ, Jorgenson EM; GlobalGout Genetics Consortium; Liu H, Susztak K; 23andMe Research Team; Shringarpure S, So A, **Okada Y**, Li C, Shi Y, Merriman TR†. (2024) A genome-wide association analysis reveals new pathogenic pathways in gout. *Nat Genet* 56:2392-2406.
- Namba S†, Akiyama M, Hamanoue H, Kato K, Kawashima M, Kushima I, Matsuda K, Nakatochi M, Ogishima S, Sonehara K, Suzuki K, Takata S, Tamiya G, Tanikawa C, Yamamoto K, Yamamoto N, Ozaki N, **Okada Y†**. (2024) Inconsistent embryo selection across polygenic score methods. *Nat Hum Behav* 8:2264-2267.
- Tanaka H, Toya E, Chubachi S†, Namkoong H, Asakura T, Azekawa S, Otake S, Nakagawara K, Fukushima T, Watase M, Sakurai K, Masaki K, Kamata H, Ishii M, Hasegawa N, **Okada Y**, Koike R, Kitagawa Y, Kimura A, Imoto S, Miyano S, Ogawa S, Kanai T, Fukunaga K. (2024) Combined use of serum ferritin and KL-6 levels as biomarkers for predicting COVID-19 severity. *Respir Investig* 62:1132-1136.
- Wang QS†, Hasegawa T, Namkoong H†, Saiki R, Edahiro R, Sonehara K, Tanaka H, Azekawa S, Chubachi S, Takahashi Y, Sakaue S, Namba S, Yamamoto K, Shiraiishi Y, Chiba K, Tanaka H, Makishima H, Nannya Y, Zhang Z, Tsujikawa R, Koike R, Takano T, Ishii M, Kimura A, Inoue F, Kanai T, Fukunaga K, Ogawa S, Imoto S, Miyano S, **Okada Y†**. (2024) Statistically and functionally fine-mapped blood e/pQTLs from 1,405 humans reveal their distinct regulation patterns and disease relevance. *Nat Genet* 56:2054-2067.
- Yamamoto K†, Lee Y, Masuda T, Ozono K, Iwatani Y, Watanabe M, **Okada Y**, Sakai N†. (2024) Functional landscape of genome-wide postzygotic somatic mutations between monozygotic twins. *DNA Res* 31:dsae028.
- Naito T†, Inoue K, Namba S, Sonehara K, Suzuki K, BioBank Japan, Matsuda K, Kondo N, Toda T, Yamauchi T, Kadowaki T, **Okada Y†**. (2024) Machine learning reveals heterogeneous associations between environmental factors and cardiometabolic diseases across polygenic risk scores. *Commun Med* 4:181.

- Yanagawa K, Kuma A, Hamasaki M, Kita S, Yamamuro T, Nishino K, Nakamura S, Omori H, Kaminishi T, Oikawa S, Kato Y, Edahiro R, Kawagoe R, Taniguchi T, Tanaka Y, Shima T, Tabata K, Iwatani M, Bekku N, Hanayama R, **Okada Y**, Akimoto T, Kosako H, Takahashi A, Shimomura I, Sakata Y, Yoshimori T†. (2024) The Rubicon-WIPI axis regulates exosome biogenesis during ageing. **Nat Cell Biol** 26:1558-1570.
- Inoue K†, Naito T, Fuji R, Sonehara K, Yamamoto K, Baba R, Kodama T, Otagaki Y, Okada A, Itcho K, Kobuke K, Ohno H, BioBank Japan, Morisaki T, Hattori N, Goto A, Nishikawa T, Oki K, **Okada Y†**. (2024) Primary Aldosteronism and Risk of Cardiovascular Outcomes: Genome-Wide Association and Mendelian Randomization Study. **J Am Heart Assoc** 13:e03418.
- Tomofuji Y†, Edahiro R, Sonehara K, Shirai Y, Kock KH, Wang QS, Namba S, Moody J, Ando Y, Suzuki A, Yata T, Ogawa K, Naito T, Namkoong H, Xuan Lin QX, Buyamin EV, Tan LM, Sonthalia R, Han KY, Tanaka H, Lee H; Asian Immune Diversity Atlas Network, Japan COVID-19 Task Force, The BioBank Japan Project; Okuno T, Liu B, Matsuda K, Fukunaga K, Mochizuki H, Park WY, Yamamoto K, Hon CC, Shin JW, Prabhakar S, Kumanogoh A, **Okada Y†**. (2024) Quantification of escape from X chromosome inactivation with single-cell omics data reveals heterogeneity across cell types and tissues. **Cell Genom** 100625.
- Pozarickij A, Gan W, Lin K, Clarke R, Fairhurst-Hunter Z, Koido M, Kanai M, **Okada Y**, Kamatani Y, Bennett D, Du H, Chen Y, Yang L, Avery D, Guo Y, Yu M, Yu C, Schmidt Valle D, Lv J, Chen J, Peto R, Collins R, Li L†, Chen Z, Millwood IY, Walters RG†, China Kadoorie Biobank Collaborative Group. (2024) Causal relevance of different blood pressure traits on risk of cardiovascular diseases: GWAS and Mendelian randomisation in 100,000 Chinese adults. **Nat Commun** 15:6265.
- Sonehara K, Yano Y, Naito T, Goto S, Yoshihara H, Otani T, Ozawa F, Kitaori T, Biobank Japan Project, Matsuda K, Nishiyama T, **Okada Y†**, Sugiura-Ogasawara M†. (2024) Common and rare genetic variants predisposing females to unexplained recurrent pregnancy loss. **Nat Commun** 15:5744.
- Yamada S, Umehara T, Sonehara K, Kijima N†, Kawabata S, Takano K, Kidani T, Hirayama R, Arita H, Okita Y, Kinoshita M, Kagawa N, Fujinaka T, Fujita T, Wakayama A, Biobank Japan Project, Matsuda K, **Okada Y**, Kishima H. (2024) Genome-wide association study on meningioma risk in Japan: a multicenter prospective study. **J Neurooncol** 169:281-286.
- Bridges SL†, Shapira R, Aksentijevich I, Mack SJ, Merriman TR, Klein CJ, Bowen BM, Klein TE, **ClinGen Rheumatologic Autoimmune Disease Clinical Domain Working Group**. (2024) Curating Genetic Associations with Rheumatologic Autoimmune Diseases to Improve Patient Outcomes. **Arthritis Rheumatol** 76:1577-1581.
- Jermy B, Läll K, Wolford BN, Wang Y, Zguro K, Cheng Y, Kanai M, Kanoni S, Yang Z, Hartonen T, Monti R, Wanner J, Youssef O, Estonian Biobank research team, FinnGen, Lippert C, van Heel D, **Okada Y**, McCartney DL, Hayward C, Marioni RE, Furini S, Renieri A, Martin AR, Neale BM, Hveem K, Mägi R, Palotie A, Heyne H, Mars N, Ganna A†, Ripatti S†. (2024) A unified framework for estimating country-specific cumulative incidence for 18 diseases stratified by polygenic risk. **Nat Commun** 15:5007.
- Ojima T, Namba S, Suzuki K, Yamamoto K, Sonehara K, Narita A, Kamatani Y, Tamiya G, Yamamoto M, Yamauchi T, Kadowaki T, **Okada Y†**. Body mass index stratification optimizes polygenic prediction of type 2 diabetes in trans-biobank analysis. **Nat Genet** 56:1100-1109.
- Tanaka H\*, **Okada Y\*†**, Nakayamada S, Miyazaki Y, Sonehara K, Namba S, Honda S, Shirai Y, Yamamoto K, Kubo S, Ikari K, Harigai M, Sonomoto K, Tanaka Y†. (2024) Extracting immunological and clinical heterogeneity across autoimmune rheumatic diseases by cohort-wide immunophenotyping. **Ann Rheum Dis** 83:242-252.
- Tomofuji Y†, Kishikawa T, Sonehara K, Maeda Y, Ogawa K, Kawabata S, Oguro-Igashira E, Okuno T, Nii T, Kinoshita M, Takagaki M, Yamamoto K, Arase N, Yagita-Sakamaki M, Hosokawa A, Motooka D, Matsumoto Y, Matsuoka H, Yoshimura M, Ohshima S, Nakamura S, Fujimoto M, Inohara H, Kishima H, Mochizuki H, Takeda K, Kumanogoh A, **Okada Y†**. (2023) Analysis of gut microbiome, host genetics, and plasma metabolites reveals gut microbiome-host interactions in the Japanese population. **Cell Rep** 42:113324.
- Sakurai K, Chubachi S, Asakura T, Namkoong H, Tanaka H, Azekawa S, Shimada T, Otake S, Nakagawara K, Fukushima T, Lee H, Watase M, Kusumoto T, Masaki K, Kamata H, Ishii M, Hasegawa N, **Okada Y**, Koike R, Kitagawa Y, Kimura A, Imoto S, Miyano S, Ogawa S, Kanai T, Fukunaga K. (2024) Prognostic significance of hypertension history and blood pressure on admission in Japanese patients with coronavirus disease 2019: integrative analysis from the Japan COVID-19 Task Force. **Hypertens Res** 47:639-64.
- Fukushima T, Maetani T, Chubachi S†, Tanabe N†, Asakura T, Namkoong H, Tanaka H, Shimada T, Azekawa S, Otake S, Nakagawara K, Watase M, Shiraishi Y, Terai H, Sasaki M, Ueda S, Kato Y, Harada N, Suzuki S, Yoshida S, Tateno H, Yamada Y, Jinzaki M, Hirai T, **Okada Y**, Koike R, Ishii M, Kimura A, Imoto S, Miyano S, Ogawa S, Kanai T, Fukunaga K. (2023) Epicardial adipose tissue measured from analysis of adipose tissue

- area using chest CT imaging is the best potential predictor of COVID-19 severity. *Metabolism* 150:155715.
- Wang QS†, Edahiro R, Namkoong H, Hasegawa T, Shirai Y, Sonehara K; Japan COVID-19 Task Force; Kumanogoh A, Ishii M, Koike R, Kimura A, Imoto S, Miyano S, Ogawa S, Kanai T, Fukunaga K, **Okada Y†**. (2023) Estimating gene-level false discovery probability improves eQTL statistical fine-mapping precision. *NAR Genom Bioinform* 5:lqad090.
  - Hangai M, Kawaguchi T, Takagi M, Matsuo K, Jeon S, Chiang CWK, Dewan AT, De Smith AJ, Imamura T, Okamoto Y, Saito AM, Deguchi T, Kubo M, Tanaka Y, Ayukawa Y, Hori T, Ohki K, Kiyokawa N, Inukai T, Arakawa Y, Mori M, Hasegawa D, Tomizawa D, Fukushima H, Yuza Y, Noguchi Y, Taneyama Y, Ota S, Goto H, Yanagimachi M, Keino D, Koike K, Toyama D, Nakazawa Y, Nakamura K, Moriwaki K, Sekinaka Y, Morita D, Hirabayashi S, Hosoya Y, Yoshimoto Y, Yoshihara H, Ozawa M, Kobayashi S, Morisaki N, Gyeltshen T, Takahashi O, **Okada Y**, Matsuda M, Tanaka T, Inazawa J, Takita J, Ishida Y, Ohara A, Metayer C, Wiemels JL, Ma X, Mizutani S, Koh K, Momozawa Y, Horibe K, Matsuda F, Kato M, Manabe A, Urayama KY†. (2023) Genome-wide assessment of genetic risk loci for childhood acute lymphoblastic leukemia in Japanese patients. *Haematologica* 109:1247-12524.
  - Wang Y, Kanai M, Tan T, Kamariza M, Tsuo K, Yuan K, Zhou W, **Okada Y**, BioBank Japan Project; Huang H, Turley P, Atkinson EG, Martin AR†. (2023) Polygenic prediction across populations is influenced by ancestry, genetic architecture, and methodology. *Cell Genom* 3:100408.
  - Nishide M, Nishimura K, Matsushita H, Edahiro R, Inukai S, Shimagami H, Kawada S, Kato Y, Kawasaki T, Tsujimoto K, Kamon H, Omiya R, **Okada Y** Hattori K, Narazaki M, Kumanogoh A†. (2023) Single-cell multi-omics analysis identifies two distinct phenotypes of newly-onset microscopic polyangiitis. *Nat Commun* 14:5789.
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