Curriculum Vitae
Kyuto Sonehara, M.D., Ph.D.

Contact Details

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Education

2019–2022 **Ph.D. in Medicine**
Osaka University Graduate School of Medicine, Suita, Japan
Doctoral thesis: Genetic architecture of microRNA expression and its link to complex diseases in the Japanese population (mentored by Prof. Yukinori Okada)

2011–2017 **M.D.**
Faculty of Medicine, the University of Tokyo, Tokyo, Japan

Research Experiences

2024–Present Wellcome Sanger Institute, Cambridge, UK
Postdoctoral Fellow, Human Genetics Programme
Supervisor: Dr. Gosia Trynka
Research themes:
- Functional genomics of immune cells
- Functional annotation of disease risk genetic variants

2022–2024 Graduate School of Medicine, the University of Tokyo, Tokyo, Japan
Assistant Professor, Department of Genome Informatics
Supervisor: Prof. Yukinori Okada
Research themes:
- Population genetic analysis of human complex diseases
- Functional annotation of disease risk genetic variants

2019–2022 Osaka University Graduate School of Medicine, Suita, Japan
Graduate Student, Department of Statistical Genetics
Supervisor: Prof. Yukinori Okada

Research themes:

- Population genetic analysis of human complex diseases
- Functional annotation of disease risk genetic variants
- Development of a computational tool for linkage analysis

2014–2017 Faculty of Medicine, the University of Tokyo, Tokyo, Japan
Undergraduate Student, Department of Cellular Signaling
Supervisor: Prof. Hiroyuki Mano
Research theme: Functional analysis of oncogenic driver mutations of lung carcinoma using next-generation sequencing

Clinical Residency

2018–2019 Resident, the University of Tokyo Hospital, Tokyo, Japan
2017–2018 Resident, Japanese Red Cross Medical Center, Tokyo, Japan

Research Interests

Genetics of human complex diseases, statistical genetics, functional genomics

Personal Statement

My primary research interests are elucidating molecular etiology and pathophysiology of human complex diseases, which stemmed from my background as a physician-scientist. I believe population genetics research based on human clinical data and specimens should serve as a promising approach to unraveling unknown disease mechanisms and identifying novel therapeutic targets. I have experience in statistical genetic analysis including genome-wide association study (Akiyama Y. and Sonehara K. ***Cell Rep Med*** 2023; Sonehara K. ***Nat Commun*** 2022; Dofuku S. and Sonehara K. ***Transl Stroke Res*** 2022), functional genomic analysis including expression quantitative trait locus (eQTL) mapping (Sonehara K. ***Hum Mol Genet*** 2022), structural mutation analyses in the human genome (Sonehara K. ***Cell Genomics*** 2025; Sonehara K. ***Nat Commun*** 2024), and developing novel bioinformatics analysis tools (Sonehara K. ***Bioinformatics*** 2021). I am recently interested in the functional population genomics field to translate disease risk variants into underlying molecular mechanisms regarding transcriptome and epigenome regulation, especially those observed in context-dependent manners.

Teaching Experiences

- A seminar course, Biochemistry, 2022–2024, Graduate School of Medicine, the University of Tokyo, Japan

- A practical course, Biochemistry, 2022–2024, Graduate School of Medicine, the University of Tokyo, Japan
- A lecture course, Genome Informatics, 2024, Graduate School of Medicine, the University of Tokyo

Awards

- Ohbu Research Incentive Award, RIKEN, 2025
- Incentive Award, the Japan Society of Human Genetics, 2024
- Best Oral Presentation Award, the Japan Society of Human Genetics, 2022
- ASHG 2022 Annual Meeting Travel Award, the Japan Society of Human Genetics, 2022
- Reviewers' Choice Abstract Award, the American Society of Human Genetics 2022 Annual Meeting, 2022

Fundings

- Grant-in-Aid for Early-Career Scientists from Japan Society for the Promotion of Science (JSPS) KAKENHI, FY2025–
- Overseas Research Fellowship from the Promotion of Science (JSPS), FY2024–
- Grant-in-Aid for Early-Career Scientists from Japan Society for the Promotion of Science (JSPS) KAKENHI, FY2023–2025
- Institute for Open and Transdisciplinary Research Initiatives (OTRI) Research promotion grant (Internal grant at Osaka University), FY2020
- The Takeda Science Foundation Scholarship for Ph.D. study, FY2019–2022

Selected Publications

(† = co-first authorship)

1. **Sonehara K**, Uwamino Y, Saiki R, Takeshita M, Namba S, Uno S, Nakanishi T, Nishimura T, Naito T, Sato G, Kanai M, Liu A, Uchida S, Kurafuji T, Tanabe A, Arai T, Ohno A, Shibata A, Tanaka S, Wakui M, Kashimura S, Tomi C, Hara A, Yoshikawa S, Gotanda K, Misawa K, Tanaka H, Azekawa S, Wang QS, Edahiro R, Shirai Y, Yamamoto K, Nagao G, Suzuki T, Kiyoshi M, Ishii-Watabe A, Higashiue S, Kobayashi S, Yamaguchi H, Okazaki Y, Matsumoto N, Masumoto A, Koga H, Kanai A, Oda Y, Suzuki Y, Matsuda K, Kitagawa Y, Koike R, Kimura A, Kumanogoh A, Yoshimura A, Imoto S, Miyano S, Kanai T, Fukunaga K, Hasegawa N, Murata M, Matsushita H, Ogawa S, Okada Y, Namkoong H. (2025) Germline variants and mosaic chromosomal alterations affect COVID-19 vaccine immunogenicity. ***Cell Genomics*** 100783. doi:10.1016/j.xgen.2025.100783
2. **Sonehara K**, Yano Y, Naito T, Goto S, Yoshihara H, Otani T, Ozawa F, Kitaori T, 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. doi:10.1038/s41467-024-49993-5

3. COVID-19 Host Genetics Initiative. (2023) A second update on mapping the human genetic architecture of COVID-19. ***Nature*** 621:E7–E26. doi:10.1038/s41586-023-06355-3

4. Akiyama Y†, **Sonehara K†**, Maeda D, Katoh H, Naito T, Yamamoto K, the Biobank Japan Project, Morisaki T, Ishikawa S, Ushiku T, Kume H, Homma Y, Okada Y. (2023) Genome-wide association study identifies risk loci within the major histocompatibility complex region for Hunner-type interstitial cystitis. ***Cell Rep Med*** 4:101114. doi:10.1016/j.xcrm.2023.101114

5. Tomofuji Y, **Sonehara K**, Kishikawa T, Maeda Y, Ogawa K, Kawabata S, Nii T, Okuno T, Oguro-Igashira E, Kinoshita M, Takagaki M, Yamamoto K, Kurakawa T, Yagita-Sakamaki M, Hosokawa A, Motooka D, Matsumoto Y, Matsuoka H, Yoshimura M, Ohshima S, Nakamura S, Inohara H, Kishima H, Mochizuki H, Takeda K, Kumanogoh A, Okada Y. (2023) Reconstruction of the personal information from human genome reads in gut metagenome sequencing data. ***Nat Microbiol*** 8:1079–1094. doi:10.1038/s41564-023-01381-3

6. **Sonehara K**, Kimura Y, Nakano Y, Ozawa T, Takahashi M, Suzuki K, Fujii T, Matsushita Y, Tomiyama A, Kishikawa T, Yamamoto K, Naito T, Suzuki T, Yamaguchi S, Miwa T, Sasaki H, Kitagawa M, Ohe N, Fukai J, Ogiwara H, Kawamura A, Miyawaki S, Matsuda F, Kiyokawa N, Ichimura K, Nishikawa R, Okada Y, Terashima K. (2022) A common deletion at BAK1 reduces enhancer activity and confers risk of intracranial germ cell tumors. ***Nat Commun*** 13:4478. doi:10.1038/s41467-022-32005-9

7. Yamamoto K, **Sonehara K**, Namba S, Konuma T, Masuko H, Miyawaki S, Kamatani Y, Hizawa N, Ozono K, Yengo L, Okada Y. (2022) Genetic footprints of assortative mating in the Japanese population. ***Nat Hum Behav*** 7:65–73. doi:10.1038/s41562-022-01438-z

8. Dofuku S†, **Sonehara K†**, Miyawaki S, Sakaue S, Imai H, Shimizu M, Hongo H, Shinya Y, Ohara K, Teranishi Y, Okano A, Ono H, Nakatomi H, Teraoka A, Yamamoto K, Maeda Y, Nii T, Kishikawa T, Suzuki K, Hirata J, Takahashi M, Matsuda K, Kumanogoh A, Matsuda F, Okada Y, Saito N. (2022) Genome-Wide Association Study of Intracranial Artery Stenosis Followed by Phenome-Wide Association Study. ***Transl Stroke Res*** doi:10.1007/s12975-022-01049-w

9. **Sonehara K**, Sakaue S, Maeda Y, Hirata J, Kishikawa T, Yamamoto K, Matsuoka H, Yoshimura M, Nii T, Ohshima S, Kumanogoh A, Okada Y. (2022) Genetic architecture of microRNA expression and its link to complex diseases in the Japanese population. ***Hum Mol Genet*** 31:1806–1820. doi:10.1093/hmg/ddab361

10. Namkoong H, Edahiro R, Takano T, Nishihara H, Shirai Y, **Sonehara K,** Tanaka H, Azekawa S, Mikami Y, Lee H, Hasegawa T, Okudela K, Okuzaki D, Motooka D, Kanai M, Naito T, Yamamoto K, Wang QS, Saiki R, Ishihara R, Matsubara Y, Hamamoto J, Hayashi H, Yoshimura Y, Tachikawa N, Yanagita E, Hyugaji T, Shimizu E, Katayama K, Kato Y, Morita T, Takahashi K, Harada N, Naito Toshio, Hiki M, Matsushita Y, Takagi H, Aoki R, Nakamura A, Harada S, Sasano H, Kabata H, Masaki K, Kamata H, Ikemura S, Chubachi S, Okamori S, Terai H, Morita A, Asakura T, Sasaki J, Morisaki H, Uwamino Y, Nanki K, Uchida S, Uno S, Nishimura T, Ishiguro T, Isono T, Shibata S, Matsui Y, Hosoda C, Takano K, Nishida T, Kobayashi Y, Takaku Y, Takayanagi N, Ueda S, Tada A, Miyawaki M, Yamamoto M, Yoshida E, Hayashi R, Nagasaka T, Arai S, Kaneko Y, Sasaki K, Tagaya E, Kawana M, Arimura K, Takahashi Kunihiko, Anzai T, Ito S, Endo A, Uchimura Y, Miyazaki Y, Honda T, Tateishi T, Tohda S, Ichimura N, Sonobe K, Sassa CT, Nakajima J, Nakano Y, Nakajima Y, Anan R, Arai R, Kurihara Y, Harada Y, Nishio K, Ueda T, Azuma M, Saito R, Sado T, Miyazaki Yoshimune, Sato R, Haruta Y, Nagasaki T, Yasui Y, Hasegawa Y, Mutoh Y, Kimura T, Sato T, Takei R, Hagimoto S, Noguchi Y, Yamano Y, Sasano Hajime, Ota S, Nakamori Y, Yoshiya K, Saito F, Yoshihara T, Wada D, Iwamura H, Kanayama S, Maruyama S, Yoshiyama T, Ohta K,

Kokuto H, Ogata H, Tanaka Y, Arakawa K, Shimoda M, Osawa T, Tateno H, Hase I, Yoshida S, Suzuki S, Kawada M, Horinouchi H, Saito Fumitake, Mitamura K, Hagihara M, Ochi J, Uchida T, Baba R, Arai D, Ogura T, Takahashi H, Hagiwara S, Nagao G, Konishi S, Nakachi I, Murakami K, Yamada M, Sugiura H, Sano H, Matsumoto S, Kimura N, Ono Y, Baba H, Suzuki Y, Nakayama S, Masuzawa K, Namba S, Suzuki K, Naito Y, Liu Y-C, Takuwa A, Sugihara F, Wing JB, Sakakibara S, Hizawa N, Shiroyama T, Miyawaki S, Kawamura Y, Nakayama A, Matsuo H, Maeda Y, Nii T, Noda Y, Niitsu T, Adachi Y, Enomoto T, Amiya S, Hara R, Yamaguchi Y, Murakami T, Kuge T, Matsumoto K, Yamamoto Y, Yamamoto Makoto, Yoneda M, Kishikawa T, Yamada S, Kawabata S, Kijima N, Takagaki M, Sasa N, Ueno Y, Suzuki M, Takemoto N, Eguchi H, Fukusumi T, Imai T, Fukushima M, Kishima H, Inohara H, Tomono K, Kato K, Takahashi M, Matsuda F, Hirata H, Takeda Y, Koh H, Manabe T, Funatsu Y, Ito F, Fukui T, Shinozuka K, Kohashi S, Miyazaki M, Shoko T, Kojima M, Adachi T, Ishikawa M, Takahashi Kenichiro, Inoue T, Hirano T, Kobayashi K, Takaoka H, Watanabe K, Miyazawa N, Kimura Y, Sado R, Sugimoto H, Kamiya A, Kuwahara N, Fujiwara A, Matsunaga T, Sato Y, Okada T, Hirai Y, Kawashima H, Narita A, Niwa K, Sekikawa Y, Nishi K, Nishitsuji M, Tani M, Suzuki J, Nakatsumi H, Ogura Takashi, Kitamura H, Hagiwara E, Murohashi K, Okabayashi H, Mochimaru T, Nukaga S, Satomi R, Oyamada Y, Mori N, Baba T, Fukui Y, Odate M, Mashimo S, Makino Y, Yagi K, Hashiguchi M, Kagyo J, Shiomi T, Fuke S, Saito H, Tsuchida T, Fujitani S, Takita M, Morikawa D, Yoshida T, Izumo T, Inomata M, Kuse N, Awano N, Tone M, Ito A, Nakamura Y, Hoshino K, Maruyama J, Ishikura H, Takata T, Odani T, Amishima M, Hattori T, Shichinohe Y, Kagaya T, Kita T, Ohta Kazuhide, Sakagami S, Koshida K, Hayashi K, Shimizu T, Kozu Y, Hiranuma H, Gon Y, Izumi N, Nagata K, Ueda K, Taki R, Hanada S, Kawamura K, Ichikado K, Nishiyama K, Muranaka H, Nakamura K, Hashimoto N, Wakahara K, Sakamoto K, Omote N, Ando A, Kodama N, Kaneyama Y, Maeda S, Kuraki T, Matsumoto T, Yokote K, Nakada T-A, Abe R, Oshima T, Shimada T, Harada M, Takahashi T, Ono H, Sakurai T, Shibusawa T, Kimizuka Y, Kawana A, Sano T, Watanabe C, Suematsu R, Sageshima H, Yoshifuji A, Ito K, Takahashi S, Ishioka K, Nakamura M, Masuda M, Wakabayashi A, Watanabe H, Ueda Suguru, Nishikawa M, Chihara Y, Takeuchi M, Onoi K, Shinozuka J, Sueyoshi A, Nagasaki Y, Okamoto M, Ishihara S, Shimo M, Tokunaga Y, Kusaka Y, Ohba T, Isogai S, Ogawa A, Inoue Takuya, Fukuyama S, Eriguchi Y, Yonekawa A, Kan-o K, Matsumoto Koichiro, Kanaoka K, Ihara S, Komuta K, Inoue Y, Chiba S, Yamagata K, Hiramatsu Y, Kai H, Asano K, Oguma T, Ito Y, Hashimoto S, Yamasaki M, Kasamatsu Y, Komase Y, Hida N, Tsuburai T, Oyama B, Takada M, Kanda H, Kitagawa Y, Fukuta T, Miyake T, Yoshida Shozo, Ogura S, Abe S, Kono Y, Togashi Y, Takoi H, Kikuchi R, Ogawa S, Ogata T, Ishihara Shoichiro, Kanehiro A, Ozaki S, Fuchimoto Y, Wada S, Fujimoto N, Nishiyama Kei, Terashima M, Beppu S, Yoshida K, Narumoto O, Nagai H, Ooshima N, Motegi M, Umeda A, Miyagawa K, Shimada H, Endo M, Ohira Y, Watanabe M, Inoue S, Igarashi A, Sato M, Sagara H, Tanaka A, Ohta S, Kimura Tomoyuki, Shibata Y, Tanino Y, Nikaido T, Minemura H, Sato Yuki, Yamada Y, Hashino T, Shinoki M, Iwagoe H, Takahashi Hiroshi, Fujii K, Kishi H, Kanai Masayuki, Imamura T, Yamashita T, Yatomi M, Maeno T, Hayashi S, Takahashi Mai, Kuramochi M, Kamimaki I, Tominaga Y, Ishii T, Utsugi M, Ono A, Tanaka T, Kashiwada T, Fujita K, Saito Y, Seike M, Watanabe Hiroko, Matsuse H, Kodaka N, Nakano C, Oshio T, Hirouchi T, Makino S, Egi M, Omae Y, Nannya Y, Ueno T, Katayama Kazuhiko, Ai M, Fukui Yoshinori, Kumanogoh A, Sato Toshiro, Hasegawa N, Tokunaga K, Ishii M, Koike R, Kitagawa Yuko, Kimura A, Imoto S, Miyano S, Ogawa Seishi, Kanai T, Fukunaga K, Okada Y. (2022) DOCK2 is involved in the host genetics and biology of severe COVID-19. ***Nature*** 609:754–760. doi:10.1038/s41586-022-05163-5

11. COVID-19 Host Genetics Initiative. (2021) Mapping the human genetic architecture of COVID-19. ***Nature*** 600:472–477. doi:10.1038/s41586-021-03767-x

12. **Sonehara K**, Okada Y. (2021) Obelisc: an identical-by-descent mapping tool based on SNP streak. ***Bioinformatics*** 36:5567–5570. doi:10.1093/bioinformatics/btaa940

Full Publications

Articles

1. Yamamoto Y, Shirai Y, **Sonehara K**, Namba S, Ojima T, Yamamoto K, Edahiro R, Suzuki K, Kanai A, Oda Y, Yutaka Suzuki, Morisaki T, Narita A, Takeda Y, Tamiya G, Yamamoto M, Matsuda K, Kumanogoh A, Yamauchi T, Kadowaki T, Okada Y. (2025) Dissecting cross-population polygenic heterogeneity across respiratory and cardiometabolic diseases. ***Nat Commun*** 16:3765. doi:10.1038/s41467-025-58149-y

2. **Sonehara K**, Uwamino Y, Saiki R, Takeshita M, Namba S, Uno S, Nakanishi T, Nishimura T, Naito T, Sato G, Kanai M, Liu A, Uchida S, Kurafuji T, Tanabe A, Arai T, Ohno A, Shibata A, Tanaka S, Wakui M, Kashimura S, Tomi C, Hara A, Yoshikawa S, Gotanda K, Misawa K, Tanaka H, Azekawa S, Wang QS, Edahiro R, Shirai Y, Yamamoto K, Nagao G, Suzuki T, Kiyoshi M, Ishii-Watabe A, Higashiue S, Kobayashi S, Yamaguchi H, Okazaki Y, Matsumoto N, Masumoto A, Koga H, Kanai A, Oda Y, Suzuki Y, Matsuda K, Kitagawa Y, Koike R, Kimura A, Kumanogoh A, Yoshimura A, Imoto S, Miyano S, Kanai T, Fukunaga K, Hasegawa N, Murata M, Matsushita H, Ogawa S, Okada Y, Namkoong H. (2025) Germline variants and mosaic chromosomal alterations affect COVID-19 vaccine immunogenicity. ***Cell Genomics*** 100783. doi:10.1016/j.xgen.2025.100783

3. Yata T, Sato G, Ogawa K, Naito T, **Sonehara K**, Saiki R, Edahiro R, Namba S, Watanabe M, Shirai Y, Yamamoto K, NamKoong H, Nakanishi T, Yamamoto Y, Hosokawa A, Yamamoto M, Oguro-Igashira E, Nii T, Maeda Y, Nakajima K, Nishikawa R, Tanaka H, Nakayamada S, Matsuda K, Nishigori C, Sano S, Kinoshita M, Koike R, Kimura A, Imoto S, Miyano S, Fukunaga K, Mihara M, Shimizu Y, Kawachi I, Miyamoto K, Tanaka Y, Kumanogoh A, Niino M, Nakatsuji Y, Ogawa S, Matsushita T, Kira J, Mochizuki H, Isobe N, Okuno T, Okada Y. (2025) Contribution of germline and somatic mutations to risk of neuromyelitis optica spectrum disorder. ***Cell Genomics*** 100776. doi:10.1016/j.xgen.2025.100776

4. Funaguma S, Iida A, Saito Y, Tanboon J, De Los Reyes FV, **Sonehara K**, Goto Y, Okada Y, Hayashi S, Nishino I. (2025) Retrotrans-genomics identifies aberrant THE1B endogenous retrovirus fusion transcripts in the pathogenesis of sarcoidosis. ***Nat Commun*** 16:1318. doi:10.1038/s41467-025-56567-6

5. Sasa N, Kojima S, Koide R, Hasegawa T, Namkoong H, Hirota T, Watanabe R, Nakamura Y, Oguro-Igashira E, Ogawa K, Yata T, **Sonehara K**, Yamamoto K, Kishikawa T, Sakaue S, Edahiro R, Shirai Y, Maeda Y, Nii T, Chubachi S, Tanaka H, Yabukami H, Suzuki A, Nakajima K, Arase N, Okamoto T, Nishikawa R, Namba S, Naito T, Miyagawa I, Tanaka Hiroaki, Ueno M, Ishitsuka Y, Furuta J, Kunimoto K, Kajihara I, Fukushima S, Miyachi H, Matsue H, Kamata M, Momose M, Bito T, Nagai H, Ikeda T, Horikawa T, Adachi A, Matsubara T, Ikumi K, Nishida E, Nakagawa I, Yagita-Sakamaki M, Yoshimura M, Ohshima S, Kinoshita M, Ito S, Arai T, Hirose M, Tanino Y, Nikaido T, Ichiwata T, Ohkouchi S, Hirano T, Takada T, Tazawa R, Morimoto K, Takaki M, Konno S, Suzuki M, Tomii K, Nakagawa A, Handa T, Tanizawa K, Ishii H, Ishida M, Kato T, Takeda N, Yokomura K, Matsui T, Uchida A, Inoue H, Imaizumi K, Goto Y, Kida H, Fujisawa T, Suda T, Yamada T, Satake Y, Ibata H, Saigusa M, Shirai T, Hizawa N, Nakata K, Japan COVID-19 Task Force, Imafuku S, Tada Y, Asano Y, Sato S, Nishigori C, Jinnin M, Ihn H, Asahina A, Saeki H, Kawamura T, Shimada S, Katayama I, Poisner HM, Mack TM, Bick AG, Higasa K, Okuno T, Mochizuki H, Ishii M, Koike R,

Kimura A, Noguchi E, Sano S, Inohara H, Fujimoto M, Inoue Y, Yamaguchi E, Ogawa S, Kanai T, Morita A, Matsuda F, Tamari M, Kumanogoh A, Tanaka Y, Ohmura K, Fukunaga K, Imoto S, Miyano S, Parrish NF, Okada Y. (2025) Blood DNA virome associates with autoimmune diseases and COVID-19. ***Nat Genet*** 57:65–79. doi:10.1038/s41588-024-02022-z

6. Guccione C, Patel L, Tomofuji Y, McDonald D, Gonzalez A, Sepich-Poore GD, **Sonehara K**, Zakeri M, Chen Y, Dilmore AH, Damle N, Baranzini SE, Hightower G, Nakatsuji T, Gallo RL, Langmead B, Okada Y, Curtius K, Knight R. (2025) Incomplete human reference genomes can drive false sex biases and expose patient-identifying information in metagenomic data. ***Nat Commun*** 16:825. doi:10.1038/s41467-025-56077-5

7. 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 C-C, Choi M, Park J-E, Ishigaki K, Okamura T, Fujio K, Okada Y, Park W-Y, 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. doi:10.1038/s41588-024-02019-8

8. 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*** S0091-6749(24)01285–5. doi:10.1016/j.jaci.2024.11.033

9. 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, BioBank Japan Project, Ozaki N, Okada Y. (2024a) Inconsistent embryo selection across polygenic score methods. ***Nat Hum Behav*** 8:2264–2267. doi:10.1038/s41562-024-02019-y

10. 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. doi:10.1038/s41467-024-54052-0

11. Kamide Y, **Sonehara K**, Sekiya K, Ueki S, Nakamura Y, Okada Y, Taniguchi M. (2024) Bioactive Mediator Profile of Mepolizumab-Treated Eosinophilic Granulomatosis With Polyangiitis. ***Allergy***. doi:10.1111/all.16395

12. 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, Norio Ozaki, Okada Y. (2024b) Inconsistent embryo selection across polygenic score methods. ***Nat Hum Behav*** 1–4. doi:10.1038/s41562-024-02019-y

13. Wang QS, Hasegawa T, Namkoong H, Saiki R, Edahiro R, **Sonehara K**, Tanaka Hiromu, Azekawa S, Chubachi S, Takahashi Y, Sakaue S, Namba S, Yamamoto K, Shiraishi Y, Chiba K, Tanaka Hiroko, 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, Japan COVID-19 Task Force. (2024) Statistically and functionally fine-mapped blood eQTLs and pQTLs from 1,405 humans reveal distinct regulation patterns and disease relevance. ***Nat Genet*** 56:2054–2067. doi:10.1038/s41588-024-01896-3

14. 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. doi:10.1038/s43856-024-00596-7

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- **Sonehara K**, Akiyama Y, Maeda D, Katoh H, Naito T, Yamamoto K, the Biobank Japan Project, Morisaki T, Ishikawa S, Ushiku T, Kume H, Homma Y, Okada Y. Genome-wide association and HLA fine-mapping analysis of Hunner-type interstitial cystitis identify predisposing class II HLA variants. ***The American Society of Human Genetics Annual Meeting***, Poster Session, 2023

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- **Sonehara K**, Sakaue S, Maeda Y, Hirata J, Kishikawa T, Yamamoto K, Matsuoka H, Yoshimura M, Nii T, Ohshima S, Kumanogoh A, Okada Y. Whole-genome and small RNA sequencing-based microRNA-eQTL mapping in Japanese elucidates variant-microRNA-disease connections. ***The American Society of Human Genetics Annual Meeting***, Poster Session, 2021

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