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

Contact Details

Name: Kyuto Sonehara
Address: Wellcome Sanger Institute
Wellcome Genome Campus, Hinxton, Cambridge, UK
E-mail: ks37@sanger.ac.uk / sonehara-tky@umin.ac.jp
Web: https://plaza.umin.ac.jp/sonehara/en-gb/

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)

(* = corresponding author)

1. **Sonehara K***, Watanabe R, Matsumura Y, Mitsui Y, Ogawa Y, Odomari K, Sakaue S, Namba S, Komuro M, Edamoto M, Watanabe J, Hirota T, Arase N, Nakamura Y, Nakajima K, Okamoto T, Nishikawa R, Yamamoto K, Suzuki K, Kishikawa T, Edahiro R, Shirai Y, Naito T, Sasa N, Ishitsuka Y, Furuta J, Kunimoto K, Kajihara I, Fukushima S, Miyachi H, Matsue H, Kamata M, Momose M, Miyagawa I, Tanaka H, Ueno M, Bito T, Nagai H, Ikeda T, Horikawa T, Adachi A, Matsubara T, Nishida E, Matsuda K, Shojima N, Nakagawa I, Asano Y, Sato S, Imafuku S, Tada Y, Nishigori C, Jinnin M, Ihn H, Asahina A, Saeki H, Yamauchi T, Kadowaki T, Kawamura T, Shimada S, Katayama I, Higasa K, Noguchi E, Sano S, Tanaka Y, Matsuda F, Kumanogoh A, Tamari M, Satoh T, Fujimoto M, Morita A, Okada Y*. (2025) Whole-genome sequencing reveals rare and structural variants contributing to psoriasis and identifies CERCAM as a risk gene. ***Cell Genomics*** 100978. doi:10.1016/j.xgen.2025.100978

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. **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

4. 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

5. 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

6. 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

7. **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

8. 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

9. 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

10. **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

11. 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

12. 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

13. **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. **Sonehara K***, Watanabe R, Matsumura Y, Mitsui Y, Ogawa Y, Odomari K, Sakaue S, Namba S, Komuro M, Edamoto M, Watanabe J, Hirota T, Arase N, Nakamura Y, Nakajima K, Okamoto T, Nishikawa R, Yamamoto K, Suzuki K, Kishikawa T, Edahiro R, Shirai Y, Naito T, Sasa N, Ishitsuka Y, Furuta J, Kunimoto K, Kajihara I, Fukushima S, Miyachi H, Matsue H, Kamata M, Momose M, Miyagawa I, Tanaka H, Ueno M, Bito T, Nagai H, Ikeda T, Horikawa T, Adachi A, Matsubara T, Nishida E, Matsuda K, Shojima N, Nakagawa I, Asano Y, Sato S, Imafuku S, Tada Y, Nishigori C, Jinnin M, Ihn H, Asahina A, Saeki H, Yamauchi T, Kadowaki T, Kawamura T, Shimada S, Katayama I, Higasa K, Noguchi E, Sano S, Tanaka Y, Matsuda F, Kumanogoh A, Tamari M, Satoh T, Fujimoto M, Morita A, Okada Y*. (2025) Whole-genome sequencing reveals rare and structural variants contributing to psoriasis and identifies CERCAM as a risk gene. ***Cell Genomics*** 100978. doi:10.1016/j.xgen.2025.100978

2. Edahiro R, Sato G, Naito T, Shirai Y, Saiki R, **Sonehara K**, Tomofuji Y, Yamamoto K, Namba S, Sasa N, Nagao G, Wang QS, Takahashi Y, Hasegawa T, Kishikawa T, Suzuki K, Liu Y-C, Motooka D, Takuwa A, Tanaka H, Azekawa S, Namkoong H, Koike R, Kimura A, Imoto S, Miyano S, Kanai T, Fukunaga K, Uemura M, Morita T, Kato Y, Hirata H, Takeda Y, Doki Y, Eguchi H, Okuzaki D, Sakakibara S, Ogawa S, Kumanogoh A, Okada Y. (2025) Deciphering state-dependent immune features from multi-layer omics data at single-cell resolution. ***Nat Genet*** 57:1905–1921. doi:10.1038/s41588-025-02266-3

3. 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

4. **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

5. 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

6. 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

7. 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

8. 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

9. 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

10. 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
11. 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
12. 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
13. 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
14. 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
15. 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
16. 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
17. 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 W-Y, Yamamoto K, Hon C-C, 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*** 4:100625. doi:10.1016/j.xgen.2024.100625
18. 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:e034180. doi:10.1161/JAHA.123.034180

19. **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
20. 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.*** doi:10.1007/s11060-024-04727-x
21. Ojima T, Namba S, Suzuki K, Yamamoto K, **Sonehara K**, Narita A, Kamatani Y, Tamiya G, Yamamoto M, Yamauchi T, Kadowaki T, Okada Y. (2024) Body mass index stratification optimizes polygenic prediction of type 2 diabetes in cross-biobank analyses. ***Nat Genet*** 56:1100–1109. doi:10.1038/s41588-024-01782-y
22. Ishikawa T, Masuda T, Hachiya T, Dina C, Simonet F, Nagata Y, Tanck MWT, **Sonehara K**, Glinge C, Tadros R, Khongphatthanayothin A, Lu T-P, Higuchi C, Nakajima T, Hayashi K, Aizawa Y, Nakano Y, Nogami A, Morita H, Ohno S, Aiba T, Juárez CK, Mauleekoonphairoj J, Poovorawan Y, Gourraud J-B, Shimizu W, Probst V, Horie M, Wilde AAM, Redon R, Juang J-MJ, Nademanee K, Bezzina CR, Barc J, Tanaka T, Okada Y, Schott J-J, Makita N. (2024) Brugada syndrome in Japan and Europe: a genome-wide association study reveals shared genetic architecture and new risk loci. ***European Heart Journal*** ehae251. doi:10.1093/eurheartj/ehae251
23. Suzuki K, Hatzikotoulas K, Southam L, Taylor HJ, Yin X, Lorenz KM, Mandla R, Huerta-Chagoya A, Melloni GEM, Kanoni S, Rayner NW, Bocher O, Arruda AL, **Sonehara K**, Namba S, Lee SSK, Preuss MH, Petty LE, Schroeder P, Vanderwerff B, Kals M, Bragg F, Lin K, Guo X, Zhang W, Yao J, Kim YJ, Graff M, Takeuchi F, Nano J, Lamri A, Nakatochi M, Moon S, Scott RA, Cook JP, Lee J-J, Pan I, Taliun D, Parra EJ, Chai J-F, Bielak LF, Tabara Y, Hai Y, Thorleifsson G, Grarup N, Sofer T, Wuttke M, Sarnowski C, Gieger C, Nousome D, Trompet S, Kwak S-H, Long J, Sun M, Tong L, Chen W-M, Nongmaithem SS, Noordam R, Lim VJY, Tam CHT, Joo YY, Chen C-H, Raffield LM, Prins BP, Nicolas A, Yanek LR, Chen G, Brody JA, Kabagambe E, An P, Xiang AH, Choi HS, Cade BE, Tan J, Broadaway KA, Williamson A, Kamali Z, Cui J, Thangam M, Adair LS, Adeyemo A, Aguilar-Salinas CA, Ahluwalia TS, Anand SS, Bertoni A, Bork-Jensen J, Brandslund I, Buchanan TA, Burant CF, Butterworth AS, Canouil M, Chan JCN, Chang L-C, Chee M-L, Chen J, Chen S-H, Chen Y-T, Chen Z, Chuang L-M, Cushman M, Danesh J, Das SK, de Silva HJ, Dedoussis G, Dimitrov L, Doumatey AP, Du S, Duan Q, Eckardt K-U, Emery LS, Evans DS, Evans MK, Fischer K, Floyd JS, Ford I, Franco OH, Frayling TM, Freedman BI, Genter P, Gerstein HC, Giedraitis V, González-Villalpando C, González-Villalpando ME, Gordon-Larsen P, Gross M, Guare LA, Hackinger S, Hakaste L, Han S, Hattersley AT, Herder C, Horikoshi M, Howard A-G, Hsueh W, Huang M, Huang W, Hung Y-J, Hwang MY, Hwu C-M, Ichihara S, Ikram MA, Ingelsson M, Islam MT, Isono M, Jang H-M, Jasmine F, Jiang G, Jonas JB, Jørgensen T, Kamanu FK, Kandeel FR, Kasturiratne A, Katsuya T, Kaur V, Kawaguchi T, Keaton JM, Kho AN, Khor C-C, Kibriya MG, Kim D-H, Kronenberg F, Kuusisto J, Läll K, Lange LA, Lee KM, Lee M-S, Lee NR, Leong A, Li L, Li Y, Li-Gao R, Ligthart S, Lindgren CM, Linneberg A, Liu C-T, Liu J, Locke AE, Louie T, Luan J, Luk AO, Luo X, Lv J, Lynch JA, Lyssenko V, Maeda S, Mamakou V, Mansuri SR, Matsuda K, Meitinger T, Melander O, Metspalu A, Mo H, Morris AD, Moura FA, Nadler JL, Nalls MA, Nayak U, Ntalla I, Okada Y, Orozco L, Patel SR, Patil S, Pei P, Pereira MA, Peters A, Pirie FJ, Polikowsky HG, Porneala B, Prasad G, Rasmussen-Torvik LJ, Reiner AP, Roden M, Rohde R, Roll K,

Sabanayagam C, Sandow K, Sankareswaran A, Sattar N, Schönherr S, Shahriar M, Shen B, Shi J, Shin DM, Shojima N, Smith JA, So WY, Stančáková A, Steinthorsdottir V, Stilp AM, Strauch K, Taylor KD, Thorand B, Thorsteinsdottir U, Tomlinson B, Tran TC, Tsai F-J, Tuomilehto J, Tusie-Luna T, Udler MS, Valladares-Salgado A, van Dam RM, van Klinken JB, Varma R, Wacher-Rodarte N, Wheeler E, Wickremasinghe AR, van Dijk KW, Witte DR, Yajnik CS, Yamamoto K, Yamamoto Kenichi, Yoon K, Yu C, Yuan J-M, Yusuf S, Zawistowski M, Zhang L, Zheng W, Raffel LJ, Igase M, Ipp E, Redline S, Cho YS, Lind L, Province MA, Fornage M, Hanis CL, Ingelsson E, Zonderman AB, Psaty BM, Wang Y-X, Rotimi CN, Becker DM, Matsuda F, Liu Y, Yokota M, Kardia SLR, Peyser PA, Pankow JS, Engert JC, Bonnefond A, Froguel P, Wilson JG, Sheu WHH, Wu J-Y, Hayes MG, Ma RCW, Wong T-Y, Mook-Kanamori DO, Tuomi T, Chandak GR, Collins FS, Bharadwaj D, Paré G, Sale MM, Ahsan H, Motala AA, Shu X-O, Park K-S, Jukema JW, Cruz M, Chen Y-DI, Rich SS, McKean-Cowdin R, Grallert H, Cheng C-Y, Ghanbari M, Tai E-S, Dupuis J, Kato N, Laakso M, Köttgen A, Koh W-P, Bowden DW, Palmer CNA, Kooner JS, Kooperberg C, Liu S, North KE, Saleheen D, Hansen T, Pedersen O, Wareham NJ, Lee J, Kim B-J, Millwood IY, Walters RG, Stefansson K, Ahlqvist E, Goodarzi MO, Mohlke KL, Langenberg C, Haiman CA, Loos RJF, Florez JC, Rader DJ, Ritchie MD, Zöllner S, Mägi R, Marston NA, Ruff CT, van Heel DA, Finer S, Denny JC, Yamauchi T, Kadowaki T, Chambers JC, Ng MCY, Sim X, Below JE, Tsao PS, Chang K-M, McCarthy MI, Meigs JB, Mahajan A, Spracklen CN, Mercader JM, Boehnke M, Rotter JI, Vujkovic M, Voight BF, Morris AP, Zeggini E. (2024) Genetic drivers of heterogeneity in type 2 diabetes pathophysiology. ***Nature*** 1–11. doi:10.1038/s41586-024-07019-6

24. 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. ***Annals of the Rheumatic Diseases*** 83:242–252. doi:10.1136/ard-2023-224537

25. 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 Reports*** 42:113324. doi:10.1016/j.celrep.2023.113324

26. 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

27. 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

28. 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 Genomics and Bioinformatics*** 5:lqad090. doi:10.1093/nargab/lqad090

29. Sato G, Shirai Y, Namba S, Edahiro R, **Sonehara K**, Hata T, Uemura M, Matsuda K, Doki Y, Eguchi H, Okada Y. (2023) Pan-cancer and cross-population genome-wide association studies

dissect shared genetic backgrounds underlying carcinogenesis. ***Nat Commun*** 14:3671. doi:10.1038/s41467-023-39136-7

30. 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
31. Edahiro R, Shirai Y, Takeshima Y, Sakakibara S, Yamaguchi Y, Murakami T, Morita T, Kato Y, Liu Y-C, Motooka D, Naito Y, Takuwa A, Sugihara F, Tanaka K, Wing JB, **Sonehara K**, Tomofuji Y, Namkoong H, Tanaka H, Lee H, Fukunaga K, Hirata H, Takeda Y, Okuzaki D, Kumanogoh A, Okada Y. (2023) Single-cell analyses and host genetics highlight the role of innate immune cells in COVID-19 severity. ***Nat Genet*** 1–15. doi:10.1038/s41588-023-01375-1
32. Naito T, Inoue K, **Sonehara K**, Baba R, Kodama T, Otagaki Y, Okada A, Itcho K, Kobuke K, Kishimoto S, Yamamoto K, BioBank Japan, Morisaki T, Higashi Y, Hinata N, Arihiro K, Hattori N, Okada Y, Oki K. (2023) Genetic Risk of Primary Aldosteronism and Its Contribution to Hypertension: A Cross-Ancestry Meta-Analysis of Genome-Wide Association Study. ***Circulation*** doi:10.1161/CIRCULATIONAHA.122.062349
33. Morii W, Kasai K, Nakamura T, Hayashi D, Hara M, Naito T, **Sonehara K**, Fukuie T, Saito-Abe M, Yang L, Yamamoto-Hanada K, Narita M, Maruo K, Okada Y, Noguchi E, Ohya Y. (2023) A genomewide association study for allergen component sensitizations identifies allergen component-specific and allergen protein group-specific associations. ***J Allergy Clin Immunol: Global*** doi:10.1016/j.jacig.2023.100086
34. Yoshioka W, Iida A, **Sonehara K**, Yamamoto K, Oya Y, Mori-Yoshimura M, Kurashige T, Okubo M, Ogawa M, Matsuda F, Higasa K, Hayashi S, Nakamura H, Sekijima M, Okada Y, Noguchi S, Nishino I. (2022) Multidimensional analyses of the pathomechanism caused by the non-catalytic GNE variant, c.620A>T, in patients with GNE myopathy. ***Sci Rep*** 12:21806. doi:10.1038/s41598-022-26419-0
35. Tomofuji Y, Kishikawa T, Maeda Y, Ogawa K, Otake-Kasamoto Y, Kawabata S, Nii T, Okuno T, Oguro-Igashira E, Kinoshita M, Takagaki M, Oyama N, Todo K, Yamamoto K, **Sonehara K**, Yagita M, Hosokawa A, Motooka D, Matsumoto Y, Matsuoka H, Yoshimura M, Ohshima S, Shinzaki S, Nakamura S, Iijima H, Inohara H, Kishima H, Takehara T, Mochizuki H, Takeda K, Kumanogoh A, Okada Y. (2022) Prokaryotic and viral genomes recovered from 787 Japanese gut metagenomes revealed microbial features linked to diets, populations, and diseases. ***Cell Genomics*** 100219. doi:10.1016/j.xgen.2022.100219
36. Ishigaki K, Sakaue S, Terao C, Luo Y, **Sonehara K**, Yamaguchi K, Amariuta T, Too CL, Laufer VA, Scott IC, Viatte S, Takahashi M, Ohmura K, Murasawa A, Hashimoto M, Ito H, Hammoudeh M, Emadi SA, Masri BK, Halabi H, Badsha H, Uthman IW, Wu X, Lin L, Li T, Plant D, Barton A, Orozco G, Verstappen SMM, Bowes J, MacGregor AJ, Honda S, Koido M, Tomizuka K, Kamatani Y, Tanaka H, Tanaka E, Suzuki A, Maeda Y, Yamamoto K, Miyawaki S, Xie G, Zhang J, Amos CI, Keystone E, Wolbink G, van der Horst-Bruinsma I, Cui J, Liao KP, Carroll RJ, Lee H-S, Bang S-Y, Siminovitch KA, de Vries N, Alfredsson L, Rantapää-Dahlqvist S, Karlson EW, Bae S-C, Kimberly RP, Edberg JC, Mariette X, Huizinga T, Dieudé P, Schneider M, Kerick M, Denny JC, Matsuda K, Matsuo K, Mimori T, Matsuda F, Fujio K, Tanaka Y, Kumanogoh A, Traylor M, Lewis CM, Eyre S, Xu H, Saxena R, Arayssi T, Kochi Y, Ikari K, Harigai M, Gregersen PK, Yamamoto Kazuhiko, Louis

Bridges S, Padyukov L, Martin J, Klareskog L, Okada Y, Raychaudhuri S. (2022) Multi-ancestry genome-wide association analyses identify novel genetic mechanisms in rheumatoid arthritis. ***Nat Genet*** 54:1640–1651. doi:10.1038/s41588-022-01213-w

37. 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

38. 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

39. Wang QS, Edahiro R, Namkoong H, Hasegawa T, Shirai Y, **Sonehara K**, Tanaka H, Lee H, Saiki R, Hyugaji T, Shimizu E, Katayama K, Kanai M, Naito T, Sasa N, Yamamoto K, Kato Y, Morita T, Takahashi K, Harada N, Naito Toshio, Hiki M, Matsushita Y, Takagi H, Ichikawa M, Nakamura A, Harada S, Sandhu Y, 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 H, 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, Shiroyama 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, Tomono K, Kato K, 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, Koji S, 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 M, 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, Takano T, Katayama Kazuhiko, Ai M, 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) The whole blood transcriptional regulation landscape in 465 COVID-19 infected samples from Japan COVID-19 Task Force. ***Nat Commun*** 13:4830. doi:10.1038/s41467-022-32276-2

40. **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

41. Shirai Y, Nakanishi Y, Suzuki A, Konaka H, Nishikawa R, **Sonehara K**, Namba S, Tanaka H, Masuda T, Yaga M, Satoh S, Izumi M, Mizuno Y, Jo T, Maeda Y, Nii T, Oguro-Igashira E, Project TBJ, Morisaki T, Kamatani Y, Nakayamada S, Nishigori C, Tanaka Y, Takeda Y, Yamamoto K, Kumanogoh A, Okada Y. (2022) Multi-trait and cross-population genome-wide association studies across autoimmune and allergic diseases identify shared and distinct genetic component. ***Ann Rheum Dis*** doi:10.1136/annrheumdis-2022-222460

42. 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

43. **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

44. Tomofuji Y, Kishikawa T, Maeda Y, Ogawa K, Nii T, Okuno T, Oguro-Igashira E, Kinoshita M, Yamamoto K, **Sonehara K**, Yagita M, Hosokawa A, Motooka D, Matsumoto Y, Matsuoka H, Yoshimura M, Ohshima S, Nakamura S, Inohara H, Mochizuki H, Takeda K, Kumanogoh A, Okada Y. (2022) Whole gut virome analysis of 476 Japanese revealed a link between phage and autoimmune disease. ***Ann Rheum Dis*** 81:278–288. doi:10.1136/annrheumdis-2021-221267
45. Tomofuji Y, Maeda Y, Oguro-Igashira E, Kishikawa T, Yamamoto K, **Sonehara K**, Motooka D, Matsumoto Y, Matsuoka H, Yoshimura M, Yagita M, Nii T, Ohshima S, Nakamura S, Inohara H, Takeda K, Kumanogoh A, Okada Y. (2021) Metagenome-wide association study revealed disease-specific landscape of the gut microbiome of systemic lupus erythematosus in Japanese. ***Ann Rheum Dis*** 80:1575–1583. doi:10.1136/annrheumdis-2021-220687
46. 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
47. Inoue M, Noguchi S, **Sonehara K**, Nakamura-Shindo K, Taniguchi A, Kajikawa H, Nakamura H, Ishikawa K, Ogawa M, Hayashi S, Okada Y, Kuru S, Iida A, Nishino I. (2021) A recurrent homozygous ACTN2 variant associated with core myopathy. ***Acta Neuropathol*** 142:785–788. doi:10.1007/s00401-021-02363-7
48. **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
49. Sakaue S, Yamaguchi E, Inoue Y, Takahashi M, Hirata J, Suzuki K, Ito S, Arai T, Hirose M, Tanino Y, Nikaido T, Ichiwata T, Ohkouchi S, Hirano T, Takada T, Miyawaki S, Dofuku S, Maeda Y, Nii T, Kishikawa T, Ogawa K, Masuda T, Yamamoto K, **Sonehara K**, 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, Watanabe M, Inoue H, Imaizumi K, Goto Y, Kida H, Fujisawa T, Suda T, Yamada T, Satake Y, Ibata H, Hizawa N, Mochizuki H, Kumanogoh A, Matsuda F, Nakata K, Hirota T, Tamari M, Okada Y. (2021) Genetic determinants of risk in autoimmune pulmonary alveolar proteinosis. ***Nat Commun*** 12:1032. doi:10.1038/s41467-021-21011-y
50. Yamato A, Soda M, Ueno T, Kojima S, **Sonehara K**, Kawazu M, Sai E, Yamashita Y, Nagase T, Mano H. (2015) Oncogenic activity of BIRC2 and BIRC3 mutants independent of nuclear factor-κB-activating potential. ***Cancer Sci*** 106:1137–1142. doi:10.1111/cas.12726

Reviews

51. **Sonehara K,** Okada Y. (2025) Leveraging genome-wide association studies to better understand the etiology of cancers. ***Cancer Science*** 116:288–296. doi:10.1111/cas.16402
52. **Sonehara K**, Okada Y. (2021) Genomics-driven drug discovery based on disease-susceptibility genes. ***Inflamm Regen*** 41:8. doi:10.1186/s41232-021-00158-7

Presentations

International Conference

- **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

- **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 risk HLA variants. ***Human Genetics Asia 2023***, Poster Session, 2023
- **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 14th International Workshop on Advanced Genomics***, Poster Session, 2023
- **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. Genome-wide association study of intracranial germ cell tumors: a common deletion at BAK1 attenuates the enhancer activity and confers risk for the rare disease. ***The American Society of Human Genetics Annual Meeting***, Poster Session, 2022
- **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
- **Sonehara K**, Okada Y. Obelisc: an identical-by-descent mapping tool based on SNP streak. ***The American Society of Human Genetics Annual Meeting***, Poster Session, 2020

Domestic Conference (in Japan)

- **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. Genome-wide association study provides insights into the etiology and epidemiology of intracranial germ cell tumors. ***The 82nd Annual Meeting of the Japanese Cancer Association***, Symposium, 2023
- **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. A common deletion at BAK1 attenuates the enhancer activity and confers risk in intracranial germ cell tumors. ***The 67th Annual Meeting of the Japan Society of Human Genetics***, Oral Session, 2022
- **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. A common deletion at BAK1 attenuates the enhancer activity and confers risk in intracranial germ cell tumors. ***The 81st Annual Meeting of the Japanese Cancer Association***, Oral Session, 2022
- **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 links. ***The 66th Annual Meeting of the Japan Society of Human Genetics***, Oral Session, 2021