

Curriculum Vitae

そねはら きゅうと
曾根原 究人



連絡先

氏名: 曾根原 究人
住所: Wellcome Sanger Institute
Wellcome Genome Campus, Hinxton, Cambridge, UK
E-mail: ks37@sanger.ac.uk / sonehara-ky@umin.ac.jp
Web: <https://plaza.umin.ac.jp/sonehara/>

職歴・研究歴

2014–2017 東京大学 医学部 細胞情報学 学部生
指導教員: 間野 博行 教授
2017–2018 日本赤十字社医療センター 初期研修医
2018–2019 東京大学医学部附属病院 初期研修医
2019–2022 大阪大学 大学院医学系研究科 遺伝統計学 大学院生
指導教員: 岡田 随象 教授
2022–2024 東京大学 大学院医学系研究科 遺伝情報学 助教
指導教員: 岡田 随象 教授
2024–現在 ウェルカム・サンガー研究所 博士研究員 (Postdoctoral Fellow)
指導教員: Dr. Gosia Trynka

学歴

2008–2011 開成高等学校 卒業
2011–2017 東京大学 医学部医学科 卒業, 学士 (医学) ・ 医師免許取得
2019–2022 大阪大学 大学院医学系研究科 医学専攻 修了 (早期修了), 博士 (医学) 取得
博士論文: Genetic architecture of microRNA expression and its link to complex diseases in the Japanese population (日本人におけるマイクロ RNA 発現の遺伝的構造及びその疾患との関連の解明)
指導教員: 岡田 随象 教授

教育歴

2022–2024 生化学実習 (東京大学 医学部)

- 2022–2024 生化学ゼミナール (東京大学 医学部)
 2024 遺伝情報学各論 (東京大学 医学系研究科)

賞罰

- 2025 理化学研究所 桜舞賞 (研究奨励賞)
- 2024 日本人類遺伝学会 奨励賞
- 2022 日本人類遺伝学会第 67 回大会 大会賞 (最優秀口演賞)
- 2022 アメリカ人類遺伝学会 2022 Annual meeting トラベルアワード, 日本人類遺伝学会
- 2022 Reviewers' Choice Abstract Award at the American Society of Human Genetics

競争的資金

- 2025– 日本学術振興会 科学研究費助成事業 若手研究
- 2024– 日本学術振興会 海外特別研究員
- 2023–2025 日本学術振興会 科学研究費助成事業 若手研究
- 2020 大阪大学先導の学際研究機構 生命医科学融合フロンティア研究部門 研究費
- 2019–2022 武田科学振興財団医学部博士課程奨学助成

主要論文

(† = 共同第一著者)

(* = 責任著者)

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](https://doi.org/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](https://doi.org/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](https://doi.org/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](https://doi.org/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](https://doi.org/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](https://doi.org/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](https://doi.org/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](https://doi.org/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](https://doi.org/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](https://doi.org/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 Kunihiro, 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](https://doi.org/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](https://doi.org/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](https://doi.org/10.1093/bioinformatics/btaa940)

発表論文一覧

査読付原著論文

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](https://doi.org/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](https://doi.org/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](https://doi.org/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](https://doi.org/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](https://doi.org/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](https://doi.org/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, Poinsner 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](https://doi.org/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](https://doi.org/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](https://doi.org/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](https://doi.org/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](https://doi.org/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](https://doi.org/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](https://doi.org/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](https://doi.org/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](https://doi.org/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](https://doi.org/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](https://doi.org/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](https://doi.org/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](https://doi.org/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](https://doi.org/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](https://doi.org/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](https://doi.org/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, Nounsime 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, Udder MS, Valladares-Salgado A, van Dam RM, van Klinken JB, Varma R, Wachter-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 RJJ, Florez JC, Rader DJ, Ritchie MD, Zöllner S, Mägi R, Marston NA, Ruff CT, van Heel DA, Finan 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](https://doi.org/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](https://doi.org/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](https://doi.org/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](https://doi.org/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](https://doi.org/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](https://doi.org/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](https://doi.org/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](https://doi.org/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](https://doi.org/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](https://doi.org/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](https://doi.org/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](https://doi.org/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](https://doi.org/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](https://doi.org/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](https://doi.org/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 Kunihiro, 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](https://doi.org/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](https://doi.org/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](https://doi.org/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](https://doi.org/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](https://doi.org/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](https://doi.org/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](https://doi.org/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](https://doi.org/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](https://doi.org/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](https://doi.org/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](https://doi.org/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, Ichihata 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](https://doi.org/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- κ B-activating potential. *Cancer Sci* 106:1137–1142. doi:[10.1111/cas.12726](https://doi.org/10.1111/cas.12726)

査読付総説論文

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](https://doi.org/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](https://doi.org/10.1186/s41232-021-00158-7)

主要な口頭発表

国際学会

- **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

日本国内学会

- **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