

# Masahiro Kanai

## Curriculum Vitae

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## Education

**Harvard University** **Boston, USA**  
Bioinformatics and Integrative Genomics PhD Program, Harvard Medical School Aug. 2017–present

**Keio University** **Yokohama, Japan**  
B.S. in Bioinformatics, Department of Biosciences and Informatics Apr. 2013–Mar. 2017

## Research Experience

**Keio University** **Yokohama, Japan**  
Undergraduate Researcher, Laboratory for Bioinformatics Apr. 2016–Mar. 2017

**Advisor:** Dr. Yasubumi Sakakibara

**Bachelor thesis:** Integrative multi-omics analysis of renal cell carcinoma

**RIKEN Center for Integrative Medical Sciences** **Yokohama, Japan**  
Research Assistant, Laboratory for Statistical Analysis May 2015–present

**Advisor:** Drs. Yoichiro Kamatani & Yukinori Okada

**Research theme:**

- Genome-wide association study (GWAS) of ~200,000 individuals in the BioBank Japan Project.
- Interpretation of GWAS polygenic signals using epigenomic data.
- Population genetics analysis of 1,037 Japanese whole-genome sequences.

**Tokyo Medical and Dental University** **Tokyo, Japan**  
Technical Assistant, Department of Human Genetics and Disease Diversity Apr. 2014–Mar. 2016

**Advisor:** Drs. Yukinori Okada & Toshihiro Tanaka

**Research theme:**

- Empirical estimation of genome-wide significance thresholds based on GWAS simulations.
- HLA imputation analysis using the Japanese-specific reference panel.

## Certification

**The Certification for Bioinformatics Engineers**  
certificated by the Japanese Society of Bioinformatics 2015

## Awards and Fellowships

**The Nakajima Foundation Scholarship** **Tokyo, Japan**  
which covers tuition: up to JPY3,000,000/year and stipend: JPY200,000/month. 2017–2019+

**The 3rd place, Worldwide Finals** **New York, USA**  
Microsoft Imagine Cup 2011 Windows 7 Touch Challenge 2011

**The 1st place, National Finals & Worldwide Finalist** **Japan & Poland**  
Microsoft Imagine Cup 2010 Software Design Competition 2010

## Technical Skills

**Programming Language:** C/C++, C#, Python, R, Java, Matlab, Unix shell, sed/awk

**Analysis:** GWAS, Genotype Imputation, HLA Imputation, Polygenic analysis using GCTA and LDSC

## Publications

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1. Sudo, T., Okada, Y., Ozaki, K., Urayama, K., **Kanai, M.**, Kobayashi, H., Gokyu, M., Izumi, Y. & Tanaka, T. Association of NOD2 Mutations with Aggressive Periodontitis. *Journal of Dental Research* **96**, 1100–1105 (2017).
2. Okada, Y., Suzuki, A., Ikari, K., Terao, C., Kochi, Y., Ohmura, K., Higasa, K., Akiyama, M., Ashikawa, K., **Kanai, M.**, Hirata, J., Suita, N., Teo, Y.-Y., Xu, H., Bae, S.-C., Takahashi, A., Momozawa, Y., Matsuda, K., Momohara, S., Taniguchi, A., Yamada, R., Mimori, T., Kubo, M., Brown, M. A., Raychaudhuri, S., Matsuda, F., Yamanaka, H., Kamatani, Y. & Yamamoto, K. Contribution of a Non-classical HLA Gene, HLA-DOA, to the Risk of Rheumatoid Arthritis. *The American Journal of Human Genetics* **99**, 366–374 (2016).
3. **Kanai, M.**, Tanaka, T. & Okada, Y. Empirical estimation of genome-wide significance thresholds based on the 1000 Genomes Project data set. *Journal of Human Genetics* **61**, 861–866 (2016).
4. Okada, Y., Muramatsu, T., Suita, N., **Kanai, M.**, Kawakami, E., Lotchkova, V., Soranzo, N., Inazawa, J. & Tanaka, T. Significant impact of miRNA–target gene networks on genetics of human complex traits. *Scientific Reports* **6**, 22223 (2016).
5. Okada, Y., Momozawa, Y., Ashikawa, K., **Kanai, M.**, Matsuda, K., Kamatani, Y., Takahashi, A. & Kubo, M. Construction of a population-specific HLA imputation reference panel and its application to Graves' disease risk in Japanese. *Nature Genetics* **47**, 798–802 (2015).

## Reviews (in Japanese)

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1. **Kanai, M.** & Okada, Y. HLA imputation: construction of a population-specific reference panel in Japanese. *Journal of Clinical and Experimental Medicine (IGAKU NO AYUMI)* **257**, 939–940 (2016).

## Presentations

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### International Conference

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1. **Kanai, M.**, Akiyama, M., Okada, Y., Ikeda, M., Iwata, N., Kubo, M. & Kamatani, Y. Trans-ethnic comparison of partitioned heritability reveals shared cell-type specific enrichment between East Asian and European genome-wide association studies. *The 66th Annual Meeting of the American Society of Human Genetics, Poster Session* (2016).
2. Akiyama, M., **Kanai, M.**, Okada, Y., Takahashi, A., Momozawa, Y., Ikeda, M., Iwata, N., Ikegawa, S., Hirata, M., Matsuda, K., Yamaji, T., Iwasaki, M., Sobue, K., Yamamoto, M., Kubo, M. & Kamatani, Y. Genetic study of body mass index in 173,430 Japanese identifies 76 new loci and highlights shared heritability with broad spectrum of complex diseases. *The 66th Annual Meeting of the American Society of Human Genetics, Oral Session* (2016).
3. **Kanai, M.**, Tanaka, T. & Okada, Y. Empirical estimation of genome-wide significance thresholds based on the 1000 Genomes Project. *The 13th International Congress of Human Genetics, Oral Session* (2016).
4. **Kanai, M.**, Okada, Y., Muramatsu, T., Suita, N., Kawakami, E., Lotchkova, V., Soranzo, N., Inazawa, J. & Tanaka, T. Significant impact of miRNA–target gene networks on genetics of human complex traits. *The 13th International Congress of Human Genetics, Oral Session* (2016).

### Domestic Conference (in Japan)

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1. **Kanai, M.**, Tanaka, T. & Okada, Y. Empirical estimation of a genome-wide significance threshold based on the 1000 Genomes Project. *The 60th Annual Meeting of the Japan Society of Human Genetics, Oral Session* (2015).
2. Suita, N., **Kanai, M.**, Higuchi, C., Tanaka, T. & Okada, Y. Comprehensive pathway analysis for 23 large-scale genome-wide association studies. *The 60th Annual Meeting of the Japan Society of Human Genetics, Poster Session* (2015).

3. **Kanai, M.**, Yamane, K., Higuchi, C., Tanaka, T. & Okada, Y. Performance evaluation of PLINK v.1.90: a next version of a tool set for genome-wide association study. *The 59th Annual Meeting of the Japan Society of Human Genetics, Poster Session* (2014).

Last updated: September 1, 2017.