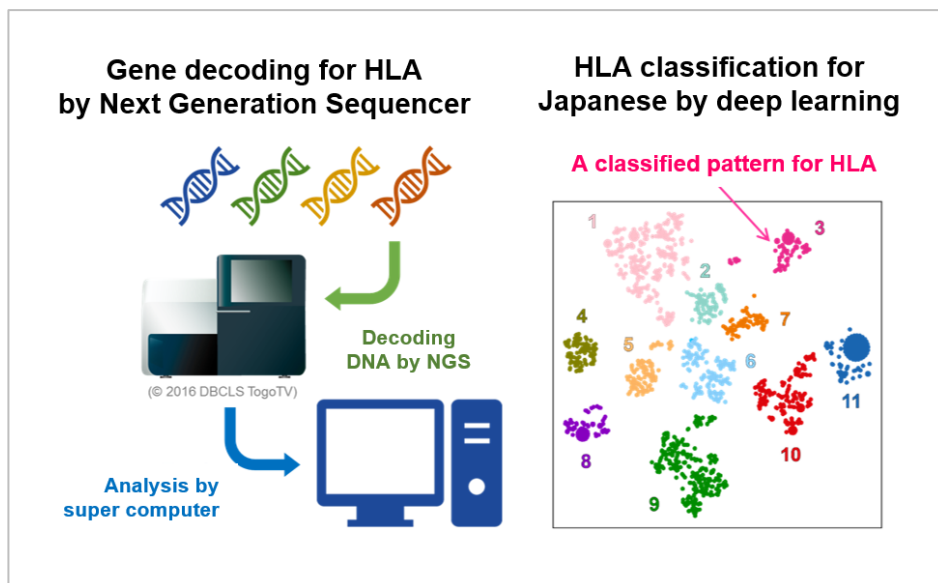


# Genetic and phenotypic landscape of the MHC region in the Japanese population

Keywords: deep machine learning, Next Generation Sequence (NGS), HLA, individualized medicine

To perform detailed fine-mapping of the major histocompatibility complex (MHC) region, Yukinori Okada (IFReC/Graduate School of Medicine, Osaka University) and the research group conducted NGS-based typing of the 33 human leukocyte antigen (HLA) genes of 1,120 Japanese, providing high resolution allele catalogue and linkage disequilibrium (LD) structure of both classical and non-classical HLA genes. Together with population-specific deep whole-genome sequencing (WGS) data (n = 1,276), they conducted NGS-based HLA, SNV, and indel imputation of large-scale genome-wide association (GWAS) data of 166,190 Japanese. A phenome-wide association study (PheWAS) assessing 106 clinical phenotypes identified abundant significant genotype-phenotype associations across 52 phenotypes. Fine-mapping highlighted multiple association patterns conferring independent risks from the classical HLA genes. Region-wide heritability estimates and genetic correlation network analysis elucidated polygenic architecture shared across the phenotypes.



**Journal:** *Nature Genetics* (Jan. 28, 2019 online).

**Title:** "Genetic and phenotypic landscape of the MHC region in the Japanese population."

**Authors:** Jun Hirata, Kazuyoshi Hosomichi, Saori Sakaue, Masahiro Kanai, Hirofumi Nakaoka, Kazuyoshi Ishigaki, Ken Suzuki, Masato Akiyama, Toshihiro Kishikawa, Kotaro Ogawa, Tatsuo Masuda, Kenichi Yamamoto, Makoto Hirata, Koichi Matsuda, Yukihide Momozawa, Ituro Inoue, Michiaki Kubo, Yoichiro Kamatani, Yukinori Okada.

(\* corresponding author)