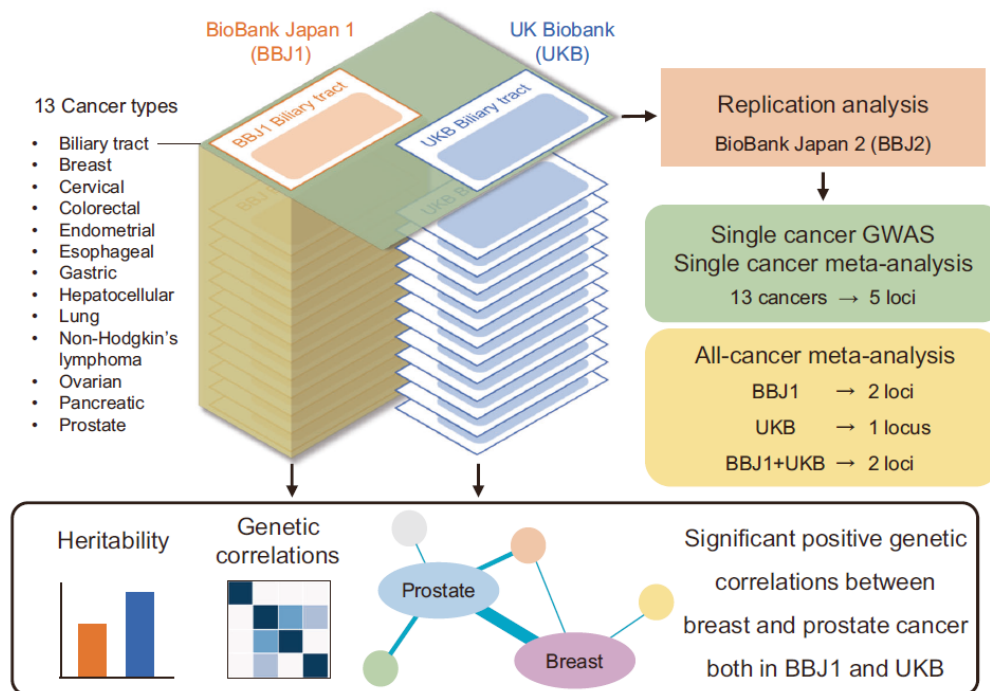


Pan-cancer and cross-population genome wide association studies dissect shared genetic backgrounds underlying carcinogenesis

Keywords: cancer, human genome. bioinformatics

Yukinori Okada (Graduate School of Medicine, Osaka University/Statistical Immunology, IFRcC/University of Tokyo/RIKEN) and his research group studied a large-scale genome analysis using information from 1.18 million human genomes. In this study, they conducted a cross-species analysis of 13 cancer types: biliary tract cancer, breast cancer, cervical cancer, colorectal cancer, uterine cancer, esophageal cancer, stomach cancer, liver cancer, lung cancer, non-Hodgkin's lymphoma, ovarian cancer, pancreatic cancer, and prostate cancer (Figure). Based on genome-wide association analysis (GWAS) using genomic data from Japanese and Western populations, they identified ten new genetic polymorphisms affecting "genetic predisposition" in cancer.



Article

Journal: *Nature Communications* (June 20, 2023 online)

Title: "Pan-cancer and cross-population genome-wide association studies dissect shared genetic backgrounds underlying carcinogenesis"

Authors: Go Sato, Yuya Shirai, Shinichi Namba, Ryuya Edahiro, Kyuto Sonehara, Tsuyoshi Hata, Mamoru Uemura, the Biobank Japan Project, Koichi Matsuda, Yuichiro Doki, Hidetoshi Eguchi, Yukinori Okada.