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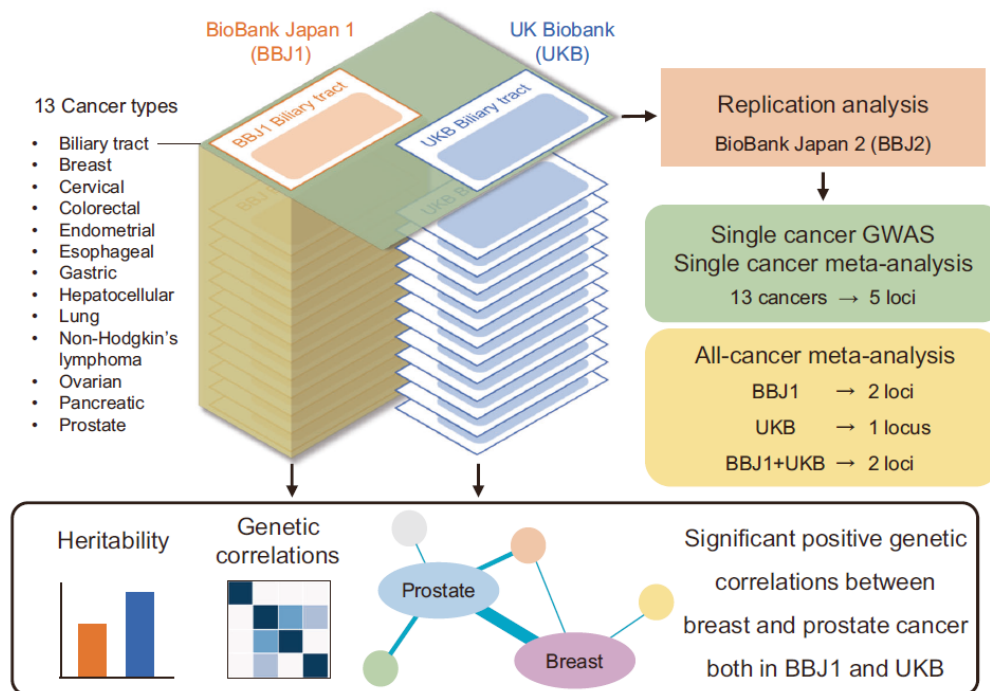 Pan-cancer and cross-population genome wide association studies dissect shared genetic backgrounds underlying carcinogenesis

Yukinori Okada (Graduate School of Medicine, Osaka University/Statistical Immunology, IFReC/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.

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