

| SG10K_Health approved studies- updated as of 01 Jul 2025 |   |                    |  |                  |
|--|---|--------------------|--|------------------|
| No.  | Title of research   | Lead Investigator  | Institution  | Date of approval |
| 1  | SV landscape in the three diverse Asian populations   | Nicolas Bertin     | c-BIG / Genome Institute of Singapore, Agency for Science, Technology and Research (A*STAR), Singapore   | 26 May 2020      |
| 2  | The Asian Clinical Variome  | Weng Khong Lim     | 1) SingHealth Duke-NUS Institute of Precision Medicine (PRISM), Duke-NUS Medical School<br>2) Cancer & Stem Cell Biology Program, Duke-NUS Medical School, Singapore | 26 May 2020      |
| 3  | Post-call quality control and population structure in SG10K_Health for downstream analyses        | Xueling Sim        | Epidemiology, Saw Swee Hock Sch of Public Health, National University of Singapore, Singapore  | 29 May 2020      |
| 4  | To evaluate various algorithms for calling Short Tandem Repeat (STR) markers using the SG10K data | Jian Jun Liu       | Genome Institute of Singapore, Agency for Science, Technology and Research (A*STAR), Singapore   | 13 Aug 2020      |
| 5  | Performance of Polygenic Score in SG10K_Health  | Marie Loh          | Lee Kong Chian School of Medicine, Nanyang Technological University, Singapore   | 18 Aug 2020      |
| 6  | Ageing in Asians  | Brian Kennedy      | NUS Medicine Healthy Longevity Research Programme, National University of Singapore, Singapore   | 16 Oct 2020      |
| 7  | Annotation of unmapped reads from the SG10K dataset   | Jian Jun Liu       | Genome Institute of Singapore, Agency for Science, Technology and Research (A*STAR), Singapore   | 16 Oct 2020      |
| 8  | Microbial signatures in blood from WGS data for SG10K   | Niranjan Nagarajan | Genome Institute of Singapore, Agency for Science, Technology and Research (A*STAR), Singapore   | 16 Oct 2020      |

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| 9  | Variant Landscape of CYP2D6 Pharmacogene in a Multi-Ethnic Population in Singapore   | Nicolas Bertin | c-BIG / Genome Institute of Singapore, Agency for Science, Technology and Research (A*STAR), Singapore  | 24 Feb 2021 |
| 10 | Trusted Research/ Real world-data Utilisation and Sharing Tech ("TRUST") Platform Phase 1 development                        | Mingshi Koh    | Chief Health Scientist Office, Ministry of Health, Singapore  | 26 Feb 2021 |
| 11 | SNPdrug3D – variant annotation with 3D structure drug proximity  | Chandra Verma  | Bioinformatics Institute, Agency for Science, Technology and Research (A*STAR), Singapore   | 16 Mar 2021 |
| 12 | CHORUS variant browser to assist aggregated SG10K_Health variants frequency query  | Eleanor Wong   | Precision Medicine Office, Agency for Science, Technology and Research, (A*STAR), Singapore   | 16 Mar 2021 |
| 13 | Exploring genetics and non-genetics relationships of methylation in SG10K_Health   | John Chambers  | Lee Kong Chian School of Medicine, Nanyang Technological University, Singapore  | 19 Apr 2021 |
| 14 | NPM Phase II- Pre-competitive Industry Consortium (PCC) Teaser sandbox   | Nicolas Bertin | Centre for Big Data and Integrative Genomics (c-BIG), Genome Institute of Singapore (GIS), Agency for Science Technology and Research (A*STAR), Singapore | 19 Apr 2021 |
| 15 | Resource Utilisation Study on the use of Next Generation Sequencing (NGS) Technologies in Familial Hypercholesterolemia (FH) | Wee Hwee Lin   | Saw Swee Hock School of Public Health, National University of Singapore, Singapore  | 19 Apr 2021 |
| 16 | Generating phenotypes from electronic health records to enable accurate clinical variant classification in Singaporeans      | Weng Khong Lim | 1) SingHealth Duke-NUS Institute of Precision Medicine (PRISM)<br>2) Cancer & Stem Cell Biology Program, Duke-NUS Medical School, Singapore               | 19 Apr 2021 |
| 17 | SNPdrug3D web service  | Chandra Verma  | Bioinformatics Institute, Agency for Science Technology and Research (A*STAR), Singapore  | 24 May 2021 |

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| 18 | Imputation web service for the National Precision Medicine Program (Phase 1A)  | Richard Tai Ling Chiat        | Computer Intelligence-Institute of High Performance Computing, Agency for Science Technology and Research (A*STAR), Singapore | 24 May 2021 |
| 19 | Polygenic risk scores and lifestyle choices on chronic disease risk  | Marie Loh                     | Lee Kong Chian School of Medicine, Nanyang Technological University, Singapore  | 24 May 2021 |
| 20 | CHORUS SG10K_Health aggregated variant query webservices   | Nicolas Bertin                | Centre for Big Data and Integrative Genomics (c-BIG), Genome Institute of Singapore (GIS), Agency                             | 24 May 2021 |
| 21 | Natural splicing variations in Singaporeans: from human genomics to disease susceptibility   | Francesc Xavier Roca Castella | School of Biological Sciences, Nanyang Technological University, Singapore  | 20 Jun 2021 |
| 22 | Design, Development, Validation and Implementation of a Robust, Comprehensive and Adequately Customized Clinical Pharmacogenomics Testing Panel in Singapore | Folefac Aminkeng              | Department of Medicine, National University of Singapore  | 5 Nov 2021  |
| 23 | Genetic variants and methylation signatures of neurocognitive diseases in Singapore: From discovery to clinical applications                                 | Kok Pin Ng                    | National Neuroscience Institute   | 7 Mar 2022  |
| 24 | Evaluating the use of the SG10K_Health dataset to increase statistical power of disease-based association studies in Singapore.                              | Zheng Li                      | Genome Institute of Singapore, Agency for Science, Technology and Research (A*STAR), Singapore                                | 22 Mar 2022 |
| 25 | Re-imputation of Southeast Asian samples using SG10K Health reference panel  | Jing Mei Li                   | Genome Institute of Singapore, Agency for Science, Technology and Research (A*STAR), Singapore                                | 18 Apr 2022 |
| 26 | Understanding the genomic modifiers of cancer risk in Singapore  | Joanne Ngeow                  | Lee Kong Chian School of Medicine, Nanyang Technological University   | 19 May 2022 |

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| 27 | Whole-genome Sequencing Based Blood Group Antigen Automated Typing   | JiaHai Shi       | Synthetic Biology Translational Research Program, Yong Loo Lin School of Medicine, National University of Singapore                         | 21 Jun 2022  |
| 28 | Candidate gene analysis of Fuch's endothelial corneal dystrophy in a Singapore Population                              | Chiea Chuen Khor | Genome Institute of Singapore, Agency for Science, Technology and Research (A*STAR), Singapore  | 25 Jul 2022  |
| 29 | Imputation of PRS markers using a multi-ethnic reference panel derived from the Singapore population                   | Nicolas Bertin   | Genome Institute of Singapore, Agency for Science, Technology and Research (A*STAR), Singapore  | 25 Jul 2022  |
| 30 | Health and Economic Impact of Next Generation Sequencing in Primary Glomerular Diseases in Singapore                   | Kar Hui Ng       | Department of Paediatrics, Yong Loo Lin School of Medicine, National University of Singapore  | 16 Aug 2022  |
| 31 | Construction of an Asian STR database using the SG10K WGS dataset  | Jian Jun Liu     | Genome Institute of Singapore, Agency for Science, Technology and Research (A*STAR), Singapore  | 15 Sept 2022 |
| 32 | Imputation of large-scale local GWAS datasets with ancestry matched SG10K Health reference panels                      | Rajkumar Dorajoo | Genome Institute of Singapore, Agency for Science, Technology and Research (A*STAR), Singapore  | 15 Sept 2022 |
| 33 | Application of Artificial Intelligence (AI) tools for the prediction of the effect of genetic variants in SG10K_Health | Weng Khong Lim   | 1) SingHealth Duke-NUS Institute of Precision Medicine (PRISM)<br>2) Cancer & Stem Cell Biology Program, Duke-NUS Medical School, Singapore | 15 Oct 2022  |
| 34 | Identification of novel genetic variants in Singaporean patients with Autism Spectrum Disorders                        | Jinyue Liu       | Genome Institute of Singapore, Agency for Science, Technology and Research (A*STAR), Singapore  | 15 Oct 2022  |
| 35 | The genetic basis of autosomal recessive inherited retinal diseases in Singapore                                       | Beau Fenner      | Singapore National Eye Centre, Singapore  | 15 Nov 2022  |

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| 36 | Evaluation of HLA haplotype frequency of Singapore population for iPSC biobanking   | Jonathan Yui-Han LOH | Institute of Molecular and Cell Biology, Agency for Science, Technology and Research (A*STAR), Singapore | 15 Nov 2022 |
| 37 | Role of Genomics in Covid-19 Pandemic   | Kelvin Bryan Tan     | Programme for Research in Epidemic Preparedness and REsponse (PREPARE), MOH                              | 15 Nov 2022 |
| 38 | Prevalence of Genetic Variants Predicting Disease Onset in our Singapore Population   | Mien Lin Justina Tan | SingHealth Duke-NUS Institute, Singapore   | 16 Dec 2022 |
| 39 | Improved identification of pathogenic missense variants using state-of-the-art computational predictors and deep mutational scanning data | Joanne Ngeow         | Lee Kong Chian School of Medicine, Nanyang Technological University, Singapore                           | 16 Dec 2022 |
| 40 | CHORUS 3.0 - SG10K_Health federated aggregated variant browser webservice   | Nicolas Bertin       | Genome Institute of Singapore, Agency for Science, Technology and Research (A*STAR), Singapore           | 4 Dec 2023  |
| 41 | Identifying the Functional Consequences of Genetic Variation in Type 2 Diabetes Mellitus Susceptibility in Asia                           | John Greally         | Albert Einstein College of Medicine, USA   | 26 Jan 2024 |
| 42 | Investigating potential disease-related rare genetic variants in Parkinson's disease patients of South East Asian ancestry in Malaysia    | Azlina Ahmad Annuar  | University of Malaya   | 26 Feb 2024 |
| 43 | ALDH2 Polymorphism in NAFLD-HCC   | Hui Min Tan          | Institute of Molecular and Cell Biology, Agency for Science, Technology and Research (A*STAR), Singapore | 19 Apr 2024 |
| 44 | Analysing the prevalence of severe paediatric and highly penetrant genomic variants in the Singaporean population                         | Yasmin Bylstra       | SingHealth Duke-NUS Institute of Precision Medicine, Singapore   | 15 May 2024 |

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| 45 | Functional characterisation of haplotype blocks containing cardiac-specific cis-regulatory regions in a multi-ethnic South-East Asian Cohort | Roger Foo                | Cardiovascular Metabolic Translational Research Program, Yong Loo Lin School of Medicine, National University of Singapore | 15 Jul 2024 |
| 46 | Enhancing GWAS Data Imputation with Foundation Models  | Hengtong Li              | Department of Ophthalmology, Centre for Innovation and Precision Eye Health, National University of Singapore              | 15 Oct 2024 |
| 47 | Ethnic-Specific Systems Ageing Heterogeneity   | Ives Lim Yubin           | Bioinformatics Institute, Agency for Science, Technology and Research (A*STAR), Singapore                                  | 15 Oct 2024 |
| 48 | Cancer cell clonal tracing in CML using long-read single-cell sequencing   | Elaine Cao Yiqun         | Genome Institute of Singapore, Agency for Science, Technology and Research (A*STAR), Singapore                             | 22 Nov 2024 |
| 49 | Ancestry matched imputation of Singapore Immuno-Oncology Pharmacogenomics Project (SIOPP) GWAS dataset                                       | Yiqing Huang             | National University Cancer Institute, Singapore  | 15 Apr 2025 |
| 50 | Development of DNA Microarrays for the Inference of Extended Blood Types   | Xiangxi Gao              | National University of Singapore, Singapore  | 15 Jun 2025 |
| 51 | DNA methylation surrogates and biomarkers of age-related disease in Asian population   | Feng Lei                 | National University of Singapore, Singapore  | 15 Jun 2025 |
| 52 | Benchmarking a quantum transformer using Asian population genomes and epigenomes   | Petretto Enrico Giuseppe | Duke-NUS Medical School, Singapore   | 15 Jun 2025 |
| 53 | Development of HLA and EBV risk variant-based assays and model for Nasopharyngeal Carcinoma risk prediction in Southeast Asia                | Jianjun Liu              | Genome Institute of Singapore, Agency for Science, Technology and Research (A*STAR), Singapore                             | 15 Jun 2025 |