| SG10K_Health approved studies- updated as of 6 February 2024 | | | | |
|---|---|---|---|---|
| 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 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 |

| 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) 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 |

| 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 associarion 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 |

| 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 Sep 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 Sep 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) 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 |

| 36 | Evaluation of HLA haplotype frequency of Singapore population for iPSC biobanking | Jonathan Yuin-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 PredictingDisease 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 |