

# Controlled Data Users

54 approved projects with access to ICGC Controlled Data. Current as of 30 July 2026. Approvals run for two years and are assessed against the ICGC Policies and Guidelines.

| INSTITUTION                                              | COUNTRY     | PROJECT TITLE                                                                                                                                |
|----------------------------------------------------------|-------------|----------------------------------------------------------------------------------------------------------------------------------------------|
| Taipei Medical University                                | Taiwan      | Clinical Utility of A to I RNA editing landscapes in pediatric and adult brain tumours                                                       |
| Cancer Hospital, Chinese Academy of Medical Sciences     | China       | CCA genome mutation research                                                                                                                 |
| Indian Institute of Science                              | India       | Investigating the role of epigenetic alterations in oral cancer stemness and drug resistance                                                 |
| Rutgers University                                       | USA         | Computational Characterisation of HRD related Molecular and Microenvironmental Features in Pancreatic Ductal Adenocarcinoma                  |
| Fudan University                                         | China       | Bioinformatics discovery of robust melanoma biomarkers for tumour boundary delineation using ICGC controlled multi-omics data                |
| Universite of Vienna                                     | Austria     | Identification of unique variant signature in GEP-NETs and its multiomics interpretation                                                     |
| Hospital Puerta de Hierro                                | Spain       | Anti-HER2 and anti-B7H targeted adoptive cell therapies for gastrointestinal cancer                                                          |
| Sun Yat Sen University                                   | China       | The role of A to I editing on cancer development and progression                                                                             |
| Intelliseq SA                                            | Poland      | Development and validation of proprietary algorithm for the classification of somatic variants according to the 2017 AMP/ASCO/CAP guidelines |
| UCLA                                                     | USA         | Analysis of driver mutations in cancer                                                                                                       |
| University of Applied Sciences, Northwestern Switzerland | Switzerland | Pan cancer re-analysis of cancer specific transcript expression                                                                              |
| Fudan University                                         | China       | A cancer whole genome comparison of early and late onset tumours                                                                             |
| Zhejiang University                                      | China       | Impact of germline DNA repair gene variants on somatic mutational signatures across human cancers                                            |
| University of Gothenburg                                 | Sweden      | Landscape of somatic mutagenesis and selection in cancer                                                                                     |
| VIB                                                      | Belgium     | Non-invasive liquid biopsy assay development for CUP based on cfDNA methylation                                                              |
| INSERM                                                   | France      | Determinants of response to BTK degraders in chronic lymphocytic leukaemia                                                                   |
| Princeton University                                     | USA         | Identifying cancer drivers through integrated analysis of coding and non-coding mutations in molecular and systems contexts                  |
| University of Pittsburgh                                 | USA         | Optimizing phylogeny tools for clinical utility                                                                                              |

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|-------------------------------------------|-------------|-----------------------------------------------------------------------------------------------------------------------------------------------------------------|
| Nanjing University                        | China       | Exploring the relationship between somatic mutations and non B DNA in cancers                                                                                   |
| Imperial College London                   | UK          | Decoding the ALT pathway: Identifying synthetic lethal targets and biomarkers for precision cancer therapy                                                      |
| Dresden University of Technology          | Germany     | Self supervised foundation models for large scale cancer genome analysis                                                                                        |
| Tianjin Medical University                | China       | Pan cancer analysis of functional somatic mutations in non-coding RNA loci and their regulatory impact                                                          |
| Research Institute of Molecular Pathology | Austria     | Prevalence and genomic context of deletion associated vulnerabilities in cancer                                                                                 |
| The University of Texas                   | USA         | Characterising Gene Content on ecDNA in HER2 positive breast cancer using whole genome sequencing                                                               |
| Ospedale San Raffaele                     | Italy       | Esophageal adenocarcinoma based on gene fusion events                                                                                                           |
| Numenos                                   | USA         | Cross indication biomarkers transfer learning to predict therapeutic response                                                                                   |
| University of Ulsan                       | Korea       | Role of ANO9 expression in epithelial-mesenchymal transition and distant metastases in pancreatic ductal adenocarcinoma                                         |
| HUB Organoids / Merck                     | Netherlands | Tumourigenic scoring of cancer patient derived organoids                                                                                                        |
| University of Edinburgh                   | UK          | Molecular defects in gynaecological cancers: Genomic correlations and phenotypic consequences                                                                   |
| PulseLogic Biosciences                    | USA         | Independent external validation of biomarker probability fusion across ICGC cancer Cohorts                                                                      |
| University Health Network                 | Canada      | Genome-wide DNA methylation profiling of follicular lymphoma to inform cell-free DNA biomarker development                                                      |
| TU Dresden                                | Germany     | Genome specificity of mutagenesis                                                                                                                               |
| Yale University                           | USA         | Leveraging genomic variation to understand mutational processes shaping cancer genomics                                                                         |
| Tongji University                         | China       | Longitudinal clinico-genomic analysis of treatment response and resistance in cancer                                                                            |
| Francis Crick Institute                   | UK          | Somatic copy number heterogeneity and structural variants as drivers of tumour progression in clear cell renal cell carcinoma                                   |
| Fred Hutchinson Cancer Centre             | USA         | Epigenetics and risk prediction for esophageal adenocarcinoma                                                                                                   |
| University of Cambridge                   | UK          | Understanding the inherited and acquired genetic changes that influence development of cancers (including myelodysplastic syndrome and acute myeloid leukaemia) |
| Massachusetts General Hospital            | USA         | Homologous recombination deficiency in localised prostate cancer                                                                                                |
| Indian Institute of Technology            | India       | Identifying the key mutational drivers of therapy resistance in cancer                                                                                          |

| INSTITUTION                                            | COUNTRY     | PROJECT TITLE                                                                                                                                             |
|--------------------------------------------------------|-------------|-----------------------------------------------------------------------------------------------------------------------------------------------------------|
| <b>Dana Farber Cancer Institute</b>                    | USA         | Prostate cancer subtype identification                                                                                                                    |
| <b>UPPThERA</b>                                        | Korea       | Integrative analysis of chromatin context and somatic mutation patterns to infer cancer cell of origin                                                    |
| <b>Amsterdam UMC</b>                                   | Netherlands | The microenvironment contributions to cancer stemness and therapy resistance in esophagogastric adenocarcinoma                                            |
| <b>Nationwide Children's Hospital</b>                  | USA         | Meta-analysis, validation and development of osteosarcoma patient stratification methodologies                                                            |
| <b>Imperial College London</b>                         | UK          | Validation of single-cell-derived transcriptional tumour states associated with chemotherapy response in oesophageal adenocarcinoma                       |
| <b>Gustave Roussy</b>                                  | France      | Systemic mutational processes and genetic determinants of internal and skin cancer risk in xeroderma pigmentosum                                          |
| <b>The Children's Hospital of Philadelphia</b>         | USA         | The stability of epigenetic cell identity in cancer                                                                                                       |
| <b>Yonsei University College of Medicine</b>           | Korea       | Analysis of circulating nucleic acid genetic profiles in lymphoma patients                                                                                |
| <b>University of Trento</b>                            | Italy       | Validation of a Novel Transcriptomic Signature for Metastatic Risk in LIRI-JP liver cancer                                                                |
| <b>Blank Bio</b>                                       | USA         | Evaluating RNA foundation model representations for prognostic biomarker discovery and survival prediction across ICGC ARGO and ICGC 25k Oncology cohorts |
| <b>Stanford University</b>                             | USA         | Pan-Cancer Analysis of the relationship between G-Quadruplex Structures and Somatic Mutations                                                             |
| <b>Centre for Excellence in Molecular Cell Science</b> | China       | Dissecting Genetic Variation Effects on RNA Regulation Across Cancers                                                                                     |
| <b>ShanghaiTech University</b>                         | China       | Integrative analysis of transcriptomic markers and histological features in hepatocellular carcinoma                                                      |
| <b>University College London</b>                       | UK          | Developing TCR-T immunotherapy for the treatment of Ewing Sarcoma                                                                                         |
| <b>Universidad Autonoma de Nuevo León</b>              | Mexico      | Genomic Landscape and determinants of somatic mitochondrial DNA integration across human cancers                                                          |

To raise a question about any project listed here, contact DACO at [admin@icgc-argo.org](mailto:admin@icgc-argo.org).