

CGI-500genomes - Open Call for Sequencing

Guidelines for applicants

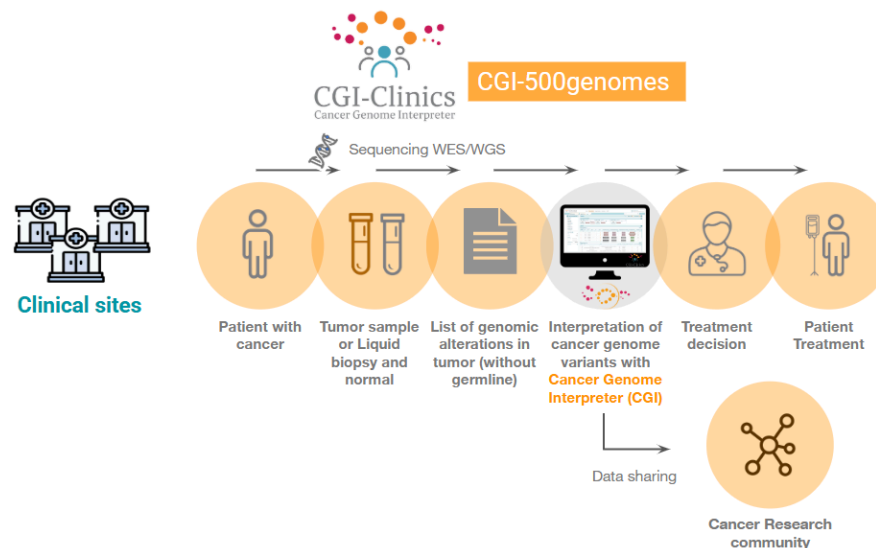
Background:

The CGI-Clinics project is a community-driven project that aims to advance precision medicine in oncology by optimising genomic data interpretation. It currently brings together 17 project partners from five countries, including 10 clinical partners, patient associations, and cancer researchers.

Scope:

The CGI-Clinics consortium is launching the CGI-500genomes initiative, a collaborative effort to sequence 500 tumor samples and establish a comprehensive database including genomic and associated clinical data to advance cancer research. To support this effort, the CGI-Clinics project will cover the cost of sequencing whole genomes (WGS) or whole exomes (WES) of clinically and scientifically relevant patient samples. A total of 150 samples are currently being sequenced as part of the initiative, and **350 samples (WGS or WES)** will be sequenced as part of this open call to complete the 500 WGS/WES objective. In addition, data analysis and advanced genomic interpretation via the new Cancer Genome Interpreter (CGI) will be provided, alongside personalised support throughout the entire process, including data deposition in a controlled-access repository.

The primary goal of this initiative is to demonstrate how tumour genomic data from clinical settings can be shared with the broader research community to improve cancer care. A second goal is to support the integration of new hospitals into the CGI-Clinics network while testing a complete end-to-end workflow, from sample sequencing to mutation interpretation and reporting, as illustrated below.



Key Dates:

- **Submission Open:** April 15, 2026
- **Application Deadline:** May 21, 2026
 - Submit your application form to cgi500genomes@irbbarcelona.org
- **Notification of prioritisation:** End of June 2026
- **Legal agreements in place and samples ready to ship:**
 - **Retrospective cohorts:** July 2026
 - **Prospective cohorts:** February 2027

Application Details:

1. Eligibility:

This Open Call for the CGI-500genomes initiative invites institutions in Europe to submit scientific-clinical cohorts facing complex interpretation challenges for analysis using advanced genomic sequencing and interpretation resources.

Participants must request the CGI License (provided free of charge) and the Data Processing Agreement (DPA) from the CGI-Clinics team at cgi500genomes@irbbarcelona.org before the application deadline. All legal documentation must be finalized and signed before samples are shipped. Please note that CGI is the platform used for analysing the CGI-500genomes cohort.

By submitting a proposal, applicants commit to adhering to the EGA Data Sharing Policy as data providers. Accordingly, patients whose samples are included in the proposal must have given their consent for their data to be shared for research purposes, following evaluation by a Data Access Committee. Please note that cohorts must be submitted for ethical approval at the time of application. While all high-quality studies that are ethically-compliant for research and long-term storage will be considered, this call will prioritize prospective studies.

To ensure timely processing, proposals from institutions whose legal documentation is not finalized by the start of the sequencing period may be deprioritised for sequencing.

2. Offered Sequencing:

Successful applicants will have the cost of sequencing, Whole Genome Sequencing (WGS) or Whole Exome Sequencing (WES), covered for their selected cohort samples, including both tumor and matched normal samples from each patient, as proposed and scientifically justified in their application. Please note that the inclusion of matched normal samples is an absolute requirement for the effective discrimination of germline variants.

The choice between WGS and WES must be supported by a clear scientific and/or clinical impact rationale. Sequencing is scheduled to begin in July 2026. To ensure timely progress, retrospective cohort proposals without finalized legal documentation or shipping-ready samples by October 2026 will lose priority status. For prospective studies,

the deadline is February 2027.

The successful candidates should cover the costs for shipping the samples.

3. Data Analysis:

Sequencing data analysis will also be provided, together with mutation interpretation using the newly developed CGI Platform. In addition, data produced within this initiative will be used to improve CGI's automatic learning platform, thus contributing to the advancement of cancer genome interpretation for future patients. The National Center for Genomic Analysis (CNAG) in Barcelona will receive the samples, carry out the sequencing, and provide the raw sequenced data to each successful applicant, along with the data interpreted through the CGI platform, ready for clinical interpretation and exploration.

4. Associated Clinical Data

To ensure the genomic data is meaningful and can be effectively used for research, accompanying metadata and clinical information are essential. For the CGI-500genomes cohort, we request that at a minimum the following types of data be provided:

- Basic clinical information (e.g., age at diagnosis, sex)
- Tumor type
- Treatment details
- Other relevant molecular and clinical data
- *Optional but valuable:* Follow-up data (e.g., response to treatment, progression)

5. Data Sharing Policy:

Successful applicants are contributing to the CGI-500genomes cohort, a community effort from patients, clinicians and scientists. To that aim, it is obliged to deposit the generated genomic data (pseudonymized/anonymized where appropriate) with associated clinical data into the European Genome-Phenome Archive (EGA) repository or equivalent platform. The details for data deposition can be consulted in EGA: <https://ega-archive.org/submission/data/file-preparation/crypt4gh/>

6. Application Process:

To apply, please complete the attached application form and submit it via email to cgi500genomes@irbbarcelona.org by May 21st. Along with the application, please include the registration documentation for your cohort as submitted to your ethics committee for approval.

7. Application Content:

Applicants will be asked to indicate the scientific relevance and characteristics of the proposed samples, as well as confirm their legal and logistical capacity to carry out the project. The application form will require concise responses on the following points:

- **Scientific and Clinical Interest of the Cohort:** Provide a brief description of the scientific and clinical relevance of the proposed cohort in the context of advancing precision medicine in oncology.

- **Type of Cancer and Samples:**
 - Specify the type(s) of malignancies represented in the cohort.
 - Indicate the type(s) of samples to be sequenced (e.g. frozen tissue, FFPE)
 - Confirm that paired normal samples (e.g., blood) are available and indicate the type of sample to be sequenced as normal.
 - Provide both the minimum and the maximum number of samples that could be included in the proposed cohort.
 - Indicate if it is a prospective or retrospective cohort.
 - Indicate if the samples correspond to patients that consented its use for research studies and their data can be deposited into the European Genome-Phenome Archive (EGA) repository or equivalent platform.
- **Proposed Sequencing (WGS/WES) and Justification:** Clearly indicate whether WGS or WES is proposed for your cohort, along with a brief scientific justification for your choice. Please note that WGS is preferred over WES for the CGI-500genomes cohort.
- **Associated Clinical data:** Indicate the type of of clinical data that could be provided along with the genomic data (age at diagnosis, sex, tumor type, treatment details, response to treatment etc)
- **Project readiness and feasibility:** Indicate the project ethical, legal and logistics readiness of the project by engaging with the CGI-Clinics initiative

8. Selection Process & Committee:

A CGI-Clinics Scientific Committee, composed of members of the CGI-Clinics Consortium, will evaluate all eligible submissions.

In this Open Call, up to a total of 350 samples will be sequenced. Tentatively, between 6 and 10 projects will be selected for sequencing. Sample allocation across the selected projects will be determined based on the proposed minimum and maximum number of samples of the study by the applicant and the evaluation conducted by the Selection Committee.