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RESEARCH ARTICLE

Implementation of the precision oncology program in catalonia's public health system: results, lessons learned, and future prospects

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Abstract

Purpose The Precision Oncology Program (POP) in Catalonia aims to provide equitable access to molecular testing for individuals with cancer, integrating Next-Generation Sequencing (NGS) into clinical practice to inform diagnosis, prognosis, and treatment decisions for both adult and pediatric patients with solid and hematologic malignancies, including somatic and germline alterations. This study evaluates the program's outcomes and impact.

Methods This evaluation covers the period from the program's implementation in July 2021 through December 2023, with a more detailed analysis focusing on 2022–2023. The program involved 12 reference centers utilizing NGS technology for cancer genetic analysis, coordinated by CatSalut, the regional public health service payer. Data collected from each reference laboratory included the number of tests performed, types of tumor panels used, clinical indications, and associated outcomes.

Results Between July 2021 and December 2023, a total of 23,135 molecular tests were performed on 22,501 patients. The most frequently analyzed panels were for solid tumors (38.1%), hematologic cancers (17.3%), and germline mutations (42.2%). Pediatric patients accounted for 2.4% of the total. Notably, 24.7% of patients underwent a change in clinical management, contributing to more targeted treatment strategies, particularly in solid tumors (58.7%). Reports were delivered within an average of four weeks, meeting program benchmarks and facilitating timely decision-making. Sample submission compliance was high, reaching 98.5%.

Conclusions This POP successfully addressed operational, financial, and logistic challenges, ensuring equitable access to molecular testing. This program led to more efficient and personalized clinical management, with growing impact on cancer care and patient outcomes.

Keywords Precision oncology · Next-generation sequencing · Personalized therapies · Molecular testing · Implementation · CatSalut

Abbreviations

NGS	Next-generation sequencing
SISCAT	Sistema de Información de Salud de Cataluña
CatSalut	Servei Català de la Salut
PMI	Precision medicine initiative
ISCIII	Instituto de Salud Carlos III
IMPaCT	Infraestructura de Medicina de Precisión asociada a la Ciencia y la Tecnología
MTB	Molecular tumor board
POP	Precision oncology program
GDPR	General data protection regulation
SD	Standard deviation
IQR	Interquartile range

Introduction

Precision medicine represents a transformative approach in healthcare, particularly in oncology, by leveraging molecular and genetic information to enable tailored diagnostic, prognostic, and therapeutic interventions [1]. Globally, major initiatives, such as the US Precision Medicine Initiative (PMI) now known as *All of Us* research program [2, 3] and the UK 100,000 Genomes Project, have set benchmarks for integrating genomic profiling into routine

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care, demonstrating significant improvements in patient outcomes [4]. In France, Plan for Genomic Medicine 2025 has emerged as a notable example, establishing 12 pilot platforms for whole-genome sequencing and creating a framework to ensure equitable access to genomic testing nationwide [5, 6]. These initiatives illustrate how precision medicine can enhance clinical decision-making while addressing structural and systemic challenges to implementation [7–9].

At a national level, Spain has made efforts to advance personalized medicine through the National Strategy for Personalized Medicine [10], spearheaded by the Carlos III Health Institute (ISCIII), which includes the *Infraestructura de Medicina de Precisión asociada a la Ciencia y la Tecnología* (IMPaCT) project [11]. While this strategy sets the stage for broader integration of precision medicine into public healthcare, the deployment of precision oncology within the Spanish health system remains fragmented and inconsistent. This variability stems, in part, from the decentralized nature of Spain's public health system, where regional governments independently manage their healthcare policies and budgets [12].

The introduction of molecular test has often been driven by hospital-specific research programs, collaborations with the pharmaceutical industry, or within the framework of research projects, rather than through unified, strategic approach ensuring quality. As a result, genetic alterations with established clinical utility are analyzed inconsistently, with only a limited number of centers conducting these tests, usually without standardized criteria for analysis or interpretation. Compounding this issue, the absence of dedicated funding for genetic testing has created disparities in access to pharmacological treatments, particularly targeted therapies, across the National Health System. This fragmentation has resulted in inconsistencies in quality standards and inequities in access to molecular testing.

To address these disparities and advance the integration of precision medicine into the public health system, the POP in Catalonia was established under Instruction 03/2021 of the Servei Català de la Salut (CatSalut) [13]. This program seeks to eliminate inequities and ensure equitable access to molecular testing for all eligible cancer patients in Catalonia, following the principles outlined in Table 1.

This study presents the outcomes of the implementation process of the POP from its inception in July 2021 through the end of 2023.

Methods

Healthcare setting

This study was conducted in Catalonia, Spain (population: 8 million), which operates under a National Health Service model with a purchaser-provider split. The public agency CatSalut plays a central role in contracting healthcare services from hospitals. Within Catalonia's integrated healthcare system (SISCAT), 68 publicly funded centers provide hospital care, with varying levels of involvement in cancer care.

Organizational model

To implement the POP, a robust organizational model was developed to integrate NGS technology into clinical practice across the Catalan public health system (Fig. 1).

The program combines strategic governance through multidisciplinary committees, a network of specialized reference centers, and standardized procedures for genetic analysis and data management (see Instruction 03/2021, www.catsalut.gencat.cat for more details). Key components include:

1. Executive Board and Scientific Committee: The program is overseen by an Executive Board responsible for approving operational criteria, securing funding, and evaluating program performance. Chaired by the Director of the Health Care Planning Unit of the Catalonian Health Service, the board includes representatives from each hospital with a reference laboratory, the Agency for Health Quality and Assessment in Catalonia, the Catalonian Cancer Strategy, and the chair of the Scientific Committee. Complementing this board, a scientific committee provides expert guidance on gene panels, clinical reporting, and the establishment of quality standards to ensure the program's scientific rigor and clinical relevance. This committee comprises 12 experts across various disciplines, including medical oncology, pathol-

Table 1 Core values of the Precision Oncology Program in Catalonia

1. Guaranteeing equitable access to molecular testing for all cancer patients who meet the established inclusion criteria
2. Identifying genetic alterations based on scientific evidence and/or regulatory agency guidelines, with testing conducted at designated reference centers
3. Developing a centralized platform that complies with data protection regulations to track clinical outcomes, facilitate the interpretation of Next-Generation Sequencing (NGS) data, and enhance health outcomes
4. Continuously monitoring program outcomes to ensure equitable access and comprehensive population coverage

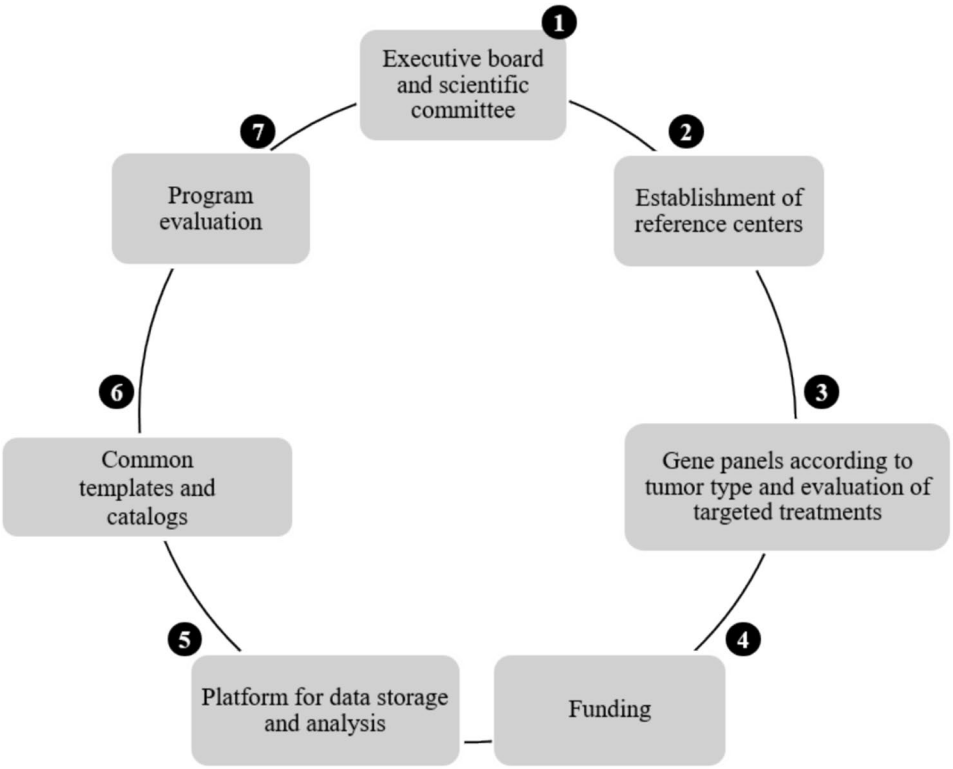


Fig. 1 Operational model defined in Catalonia for the Precision Oncology Program

ogy, clinical hematology, genetics, pediatric oncology, molecular biology, health technology assessment, epidemiology, and radiation oncology.

2. Network of reference centers: The program includes 12 specialized hospitals acting as reference centers. Additionally, the remaining healthcare centers send samples to these designated reference centers. They focus on specific tumor types based on their expertise, multidisciplinary teams, and research projects: hereditary cancer (8 centers), solid tumors (6 centers), hematological cancers (5 centers), and pediatric cancers (2 centers). A multidisciplinary tumor molecular committee (molecular tumor board, MTB) discusses complex cases and their genetic variants to decide on the clinical management of the patient. The MTB should have their discussions and recommendations included in the clinical record of the patient. The referring hospital clinician is invited to the discussion.
3. Technology and molecular markers: Four specialized working groups, organized by tumor type (solid tumors, hematologic malignancies, pediatric oncology, and hereditary cancer), assess and update the molecular and genetic mutations included in the NGS-based gene panels for each area. These updates are reviewed annually, validated by the scientific committee, and submitted to the Executive Board for final approval before immediate implementation. The selection of genes informed for each pathology is consistent across reference centers and is based on clinical evidence, regulatory status, and funding criteria set by CatSalut. Any new drug approved with a companion biomarker is reported to the Scientific Advisory Board, which could propose its immediate inclusion in the NGS panels.
4. Funding allocation: CatSalut allocates specific annual budgets for each type of gene panel (solid tumors, hematological tumors, childhood tumors, and germline mutations) through contracts with the reference centers.
5. Data platform: A centralized platform ensures the secure storage and analysis of NGS data, complying with general data protection regulations (GDPR). Bioinformatics tools and software are developed to support data analysis and interpretation.
6. Standardization of data: The program promotes standardization across genetic and clinical data, creating templates and catalogs aligned with the scientific committee's guidelines, which are applied throughout the Catalan health system.
7. Program evaluation: The effectiveness of the program is evaluated using process measures performance, including the number of cases analyzed per reference center and gene panel, report delivery timelines, and, in the immediate future, the clinical benefits for cancer patients.

Registry of the activity

Patient data included in the program were collected using a Secure File Transfer Protocol (SFTP) to ensure data protection and security. Reference centers submitted data quarterly. During the first year of the program (July–December 2021), the total number of cases sequenced by each gene panel was reported. From 2022 onwards, additional variables, such as panel type, diagnosis, clinical indication, request date, NGS results, and the date of the final report, were also collected.

Data analysis

Phenotype-associated pathogenic variants were defined as pathogenic or likely pathogenic variants located in genes that have been consistently linked to a specific pathology, in accordance with CatSalut's genetic profile determination guidelines, which are based on clinical indications (link). These variants were evaluated using data reported by the reference centers. Additionally, the estimated time to complete the genetic study was calculated as the interval between the test request date and the date on which the genetic report was finalized. Sample referral compliance was defined as adherence to the established workflows, whereby healthcare centers send samples to the designated reference center based on territorial assignment.

Statistical analyses were conducted using R statistical software (v4.4.1, R Foundation for Statistical Computing, Vienna, Austria). Assumptions of normality and homoscedasticity were tested for all continuous variables. Time-to-result delivery was analyzed by calculating mean, standard deviation (SD), median, and interquartile range (IQR). Comparisons between groups were analyzed using parametric tests, such as the Spearman t test and ANOVA. Differences in frequencies were assessed using the proportional test and Fisher's exact test. All statistical tests were two-sided, and the differences were considered statistically significant when the p value was < 0.05.

Results

Activity results

Between July 2021 and December 2023, a total of 22,501 patients (23,135 samples) were included in the POP with their cases sequenced across the reference centers. The distribution of sequenced cases by panel type was as follows: 38.1% for solid tumors, 17.3% for hematologic cancers, 2.4% for pediatric cancers, and 42.2% for hereditary cancer.

The volume of panel testing increased significantly between 2022 and 2023, with 10,438 panels performed in 2023, reflecting a 17.8% increase compared to 2022 (Fig. 2).

The mean percentage of panels performed relative to cancer incidence in Catalonia highlights significant variations across tumor types (Fig. 2b). In 2023, for solid tumors in adults, 10.1% of incident cases underwent sequencing, while for hematological cancer, the percentage was much higher, at 61.7%. Germline testing in adults was performed in 9.4% of cancer cases. Among pediatric patients, solid and hematological tumors showed the highest proportion of sequencing, with an average of 94.9% of cases tested, while pediatric germline testing was performed in 29.5% of cases (Table 2). These panels were selected based on clinical indications with the majority performed for diagnostic, prognostic and therapeutic purposes. The number of patients tested by panel and cancer type is detailed in Supplementary Table 1.

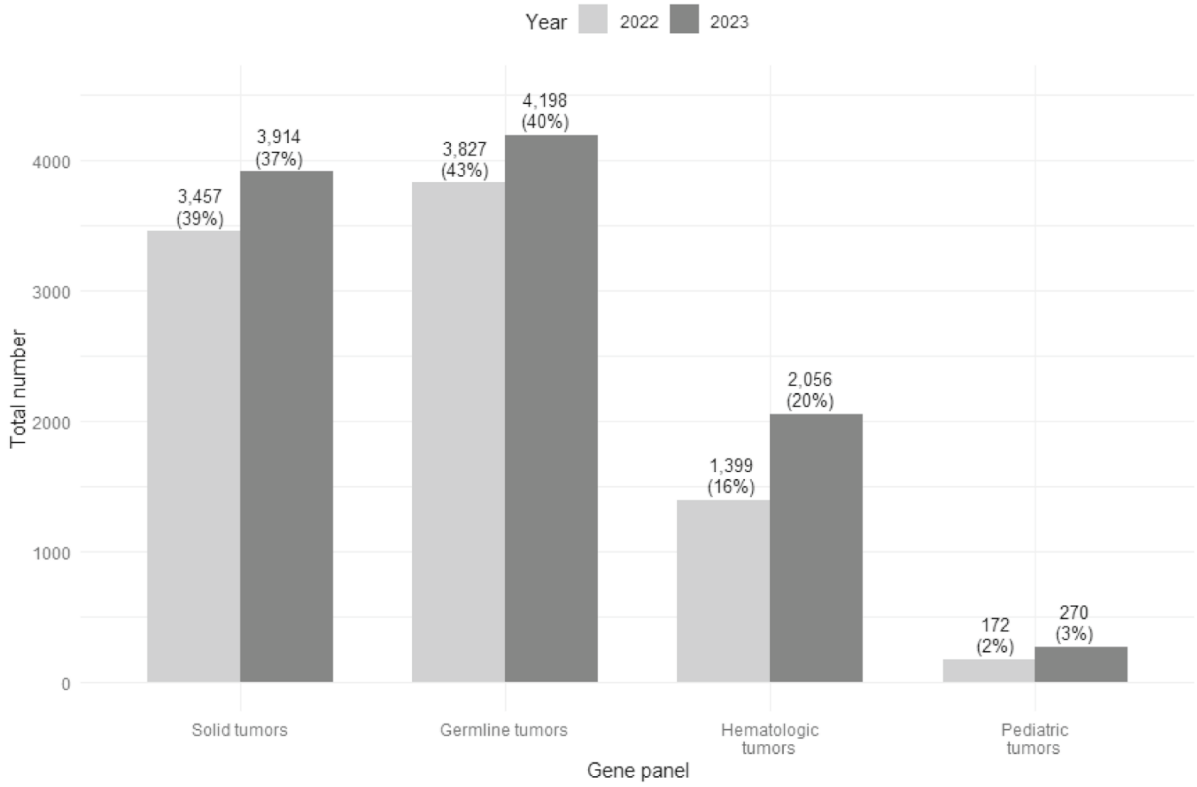
According to the reported data, pathogenic variants probably associated to diagnosis, prognosis or treatment were most frequently identified in solid (68.9%) and hematological tumors (66.0%), while germline mutations had a much lower proportion (10.6%). Pediatric tumors showed 48.4% of cases harboring pathogenic variants. In addition, when focusing on phenotype-associated variants, the percentages decreased across all cancer types (Table 2 and Supplementary Table 1). In solid tumors, the highest proportion of pathogenic variants was observed in lung cancer (54.0%), and central nervous system tumors (18.2%). For hematological tumors, myelodysplastic neoplasms and acute myeloid leukemia showed a high variant identification rate (36% and 25%, respectively). In germline tumors, familial breast and ovarian cancer accounts for a substantial 58.4% of pathogenic variants, followed by familial non-polyposis colorectal cancer (18%) (Supplementary Table 1).

Furthermore, reports were delivered with an average time of 4 weeks (1.6–7.0) in line with the program's goals to provide timely results. Molecular findings drove patient clinical management in a significant proportion of patients (24.7%), which contributed to more predicted targeted treatment strategies in 58.7% of patients with solid tumors. Patients diagnosed with lung, colorectal cancers, and melanoma have the most targeted therapies available (Table 3 and Supplementary Table 2). Moreover, sample referral compliance was high across all cancer types with an overall fulfillment rate of 98.5% (Table 2).

Discussion

Despite advancements in NGS integration in oncology across Europe, disparities in accessibility remain a significant challenge [14]. The POP was designed to ensure equitable access to molecular testing for eligible patients across all healthcare centers in Catalonia. A territorial sectorization optimized resource allocation and established clear coordination between regional health areas, reference centers, and

a



b

Cancer Type	Incidence		Nº patients (%)		Increase (%)
	2022	2023	2022	2023	(2022-2023)
Solid tumors in adult [1]	34,629	38,781	3,457 (10)	3,914 (10.1)	457 (13.2)
Hematological cancers in adult [1]	3,107	3,330	1,399 (45.0)	2,056 (61.7)	657 (47.0)
Germline tumors in adult [2,3]	37,736	42,111	3,607 (9.6)	3,975 (9.4)	368 (9.7)
Solid and hematological tumors in pediatric [4]	180	217	158 (87.8)	206 (94.9)	48 (30.4)
Germline tumors in pediatric [4]	180	217	14 (7.8)	64 (29.5)	50 (357.1)
Total			**8,635**	**10,215**	**1,580 (17.8)**

Fig. 2 **a** Patients included in the Precision Oncology Program of Catalonia (2022–2023) for each gene panel testing. **b** Molecular testing performed in patients relative to cancer incidence in Catalonia. 1. Cancer incidence estimates for the population of Catalonia were extrapolated based on actual data from the Girona and Tarragona cancer registries. 2. Incidence considering solid and hematological tumors. 3. Healthy person with family history of cancer were excluded ($n=443$). 4. Data for ages 0 to 14 are based on actual records from the Spanish Registry of Childhood Tumors; data for ages 15 to 18 are estimates derived from incidence rates and population by age from IDESCAT (Statistical Institute of Catalonia)

sample-sending centers. This was supported by standardized protocols and the identification of key interlocutors. These organizational measures facilitated the seamless integration of NGS technology into clinical practice, ensuring timely result delivery and effective clinical decision-making.

Careful initial planning and clear organization were critical to achieving these outcomes, aligning with experiences in other regions, such as France's Plan Médecine Génomique 2025 and the UK's 100,000 Genomes Project, where governance and structured workflows improved the

Table 2 Description of the percentage of pathogenic variants, turnaround time for results, clinical indications, and sample referral compliance by gene panel (2022 and 2023 activity)

	Solid tumors (N = 7,371)	Hereditary cancer (N = 8,025)	Hematological tumors (N = 3,455)	Pediatric tumors (N = 442)	Overall (N = 19,293)	P value
Alterations identified						
Pathogenic variants	5,081 (68.9%)	847 (10.6%)	2,280 (66.0%)	214 (48.4%)	8,422 (43.7%)	< 0.001
Phenotype-associated variants	2,198 (29.8%)	668 (8.3%)	1,748 (50.6%)	148 (33.5%)	4,762 (24.7%)	
Not assessable	272 (3.7%)	68 (0.8%)	369 (10.7%)	27 (6.1%)	736 (3.8%)	
Time (weeks)						
Mean (SD)	2.0 (1.4)	7.1 (2.7)	3.8 (2.7)	3.8 (2.9)	4.4 (3.2)	< 0.001
Median [IQR]	1.7 [1.0-2.6]	7.3 [5.3–8.9]	3.0 [1.7–5.3]	3.3 [1.7–5.4]	3.4 [1.6–7.0]	
Sample referral compliance						
Fulfillment	7,122 (96.6%)	8,015 (99.9%)	3,419 (99.0%)	439 (99.3%)	18,995 (98.5%)	< 0.001
Non-compliance	249 (3.4%)	10 (0.1%)	36 (1.0%)	3 (0.7%)	298 (1.5%)	

Table 3 Frequency of predicted treatment-associated biomarkers in solid tumors by cancer type

Cancer type	Predicted treatment-associated biomarker (%)
Lung cancer	3,368 (77.87)
Colorectal cancer	641 (14.82)
Melanoma	122 (2.82)
Gastrointestinal stroma tumors	74 (1.71)
Breast cancer	44 (1.01)
Central nervous system tumors	37 (0.85)
Thyroid cancer	17 (0.39)
Ovarian cancer	14 (0.32)
Others	5 (0.16)
Endometrial cancer	2 (0.05)
Sarcoma	1 (0.02)
Total	4,325 (58.68)

Percentage calculated as the number of cases with predicted treatment-associated biomarkers for each diagnosis relative to the total number of patients with possible targeted treatment

efficiency and equity [4, 6, 8, 15–17]. Moreover, ensuring continuous funding and effectively allocating resources were key to the program's sustainability. By establishing annual budgets for genetic panels (approximately 5 million €) and supporting operational needs of reference centers with specific reimbursement for each NGS panel done, Catalonia maintained and scaled the program efficiently. Despite the cost of the program plus the costs derived from targeted therapies, other studies demonstrated long-term cost-savings by reducing unnecessary interventions and enabling better treatment allocation [16]. A cost-effectiveness evaluation of the program will be considered once it has matured further.

The active involvement of reference centers, hospitals, and governance bodies created a cohesive approach to precision oncology, while consensus among stakeholders ensured adherence to clinical guidelines and ethical standards [18], further enhancing the program's ability to deliver personalized care. This led to the creation of virtual MTBs, convening experts in oncology, pharmacology, genetics and clinical trials from the referring and reference institutions to discuss the best options for individual patients based on the genomic alterations present in their tumors. This collaborative effort laid the foundation for continuous improvement and innovation in clinical management.

Continuous evaluation using predefined metrics has driven iterative improvements by tracking test numbers, genetic results, protocol adherence and clinical impact. As a result, the program's impact on clinical management has been significant, with over 22,000 patients benefiting from molecular testing. The 17% increase in activity between 2022 and 2023 highlights its expanding reach. The integration of NGS panels into clinical practice allowed for the identification of diagnostic and/or potentially actionable findings useful across a range of cancers. Clinically relevant pathogenic variants were identified in 29.8% of solid tumors, 50.6% of hematological malignancies, and 8.3% of hereditary cancer, similar to those reported in France's Plan Médecine Génomique 2025 (25–35% in solid tumors, up to 50% in hematological malignancies) [6, 21], the UK's 100,000 Genomes Project (25–35% in solid tumors), and large hereditary cancer series (8–15%) [22, 23]. The median turnaround time in POP was 1.7 weeks for solid tumors, aligning with ESMO recommendations (10–28 days) [1] and faster than the 4–6 weeks reported in France and the UK, which focused on whole-genome sequencing [4, 6]. In contrast, the median turnaround for hereditary cancer testing was 7.3 weeks, reflecting the additional validation steps and the need for genetic counseling. This distinction highlights the urgency of timely somatic NGS results to guide treatment decisions.

Molecular findings influenced clinical management in 24.7% of patients and predicted targeted therapies in 58.7% of solid tumor cases, results comparable to the proportion of actionable alterations reported in other large-scale initiatives (30–40%) [1, 24]. High compliance rates in sample submission further demonstrate the program's success in optimizing operational workflows, ensuring timely access to molecular testing. These results facilitated prevention, accurate diagnosis and prognosis, and personalized treatment strategies, which improved the precision of cancer management, in line with other programs [25, 26]. The multidisciplinary approach, by means of MTBs, was essential to the success of the precision medicine programs [27], and its impact will be evaluated in future studies. Ultimately, this approach will lead to improved quality of life and higher survival rates for patients, as well as increased access to clinical trials [28].

The experience in Catalonia demonstrates that the key elements of successful precision oncology programs, centralized planning and governance, sustained financial investment, integration of multidisciplinary teams, standardized protocols, and continuous evaluation, also present in other models, represent transferable strategies that can be successfully adapted to decentralized health systems [13].

However, some limitations should be considered. The program only evaluates cases where NGS has been performed, making it difficult to assess how many eligible patients do not undergo testing. Additionally, it does not track sample failure rates, which could impact test efficiency, nor systematically monitor patient outcomes or integrate with drug data. This limits the assessment of treatment effectiveness, survival impact, and the real-world use of targeted therapies. Finally, the full deployment of the centralized data platform, which compiles all sequencing and clinical data, will further enhance program evaluation, provide timely results to clinicians, and support future research through an anonymized, GDPR-compliant repository for international collaboration.

This integrated model, which has proven effective in precision oncology [13], could also be adapted to other conditions, such as rare genetic diseases or chronic disorders, where molecular testing and personalized care could significantly improve clinical outcomes. A promising avenue is the incorporation of emerging methodologies, such as liquid biopsy, which could enhance early detection and monitoring diseases [29]. This would further advance precision medicine and its application to diverse health needs. Additionally, the program's platform, particularly its data storage and genomic analysis capabilities, could serve as a foundation for broader applications, including multi-omics approaches, which provide deeper insights into disease mechanisms and enable more precise diagnostics and therapies [30]. Likewise, its connection with other centralized platforms and relevant data, such as medical imaging, clinical data, treatments, demographic data, and lifestyle habits, will facilitate the implementation of precision medicine, enabling a more comprehensive and personalized approach to healthcare.

In conclusion, the Precision Oncology Program in Catalonia demonstrates the importance of robust planning, sustained financial investment, multidisciplinary collaboration, and continuous evaluation for successful precision medicine implementation. These lessons learned from this program have not only transformed patient care but also provide a model for other territories looking to incorporate precision medicine into their healthcare systems.

Supplementary Information The online version contains supplementary material available at https://doi.org/10.1007/s12094-025-04022-9.

Declarations

Conflict of interest JT reports personal financial interest in form of scientific consultancy role for Accent Therapeutics, Alentis Therapeutics, AstraZeneca, Boehringer Ingelheim, Chugai, Daiichi Sankyo, F. Hoffmann-La Roche Ltd, Genentech Inc, Lilly, Menarini, Merus, MSD, Novartis, Ono Pharma USA, Peptomyc, Pfizer, Pierre Fabre, Quantro Therapeutics, Scandion Oncology, Scorpion Therapeutics, Servier, Sotio Biotech, Taiho, Takeda Oncology and Tolremo Therapeutics, and stocks from Oniria Therapeutics, Alentis Therapeutics, Pangaea Oncology and 1TRIALSP. RS reports personal financial interest in form of Consultant or Advisory Role (including Steering Committees, DSMBs): Laboratorios Esteve, Sanofi Genzyme; and speaking/teaching activities: Sanofi-Aventis, GlaxoSmithKline and WNT Pharma. Co-owner of SACE Medhealth, commercial medical education company, until April 2022; subsequently owned by spouse until December 2023. DC has received honoraria from AstraZeneca, Novartis, Incyte, Sophia genetics and Thermofisher for speaking/teaching at educational activities: Sanofi-Aventis, GlaxoSmithKline. AP reports grants from AstraZeneca, Novartis, Daiichi Sankyo, Pfizer, Reveal Genomics, and WNTRoche and personal fees from Roche, AstraZeneca, Novartis, Daiichi Sankyo, Pfizer, Ona Therapeutics, Peptomyc, Reveal Genomics; in addition, AP reports patents for HER2DX, and DNADX issued and licensed to Reveal Genomics. LM is past member of data monitoring committees for clinical trials sponsored by Novartis, Shionogi and Incyte; had a consulting role for Novartis, Norgine, Boehringer, Ymabs, Merck, Roche, Bayer and Shionogi; participated in educational activities organized by Bayer and Eusa Pharma and received travel expenses from Eusa Pharma; is President of SIOPEN (European neuroblastoma research cooperative group), an organization which receives royalties for the sales of dinutuximab beta. J-M.R., reports consulting/advisory roles at Incyte, Pfizer, Bristol Myers Squibb, Novartis, and Takeda; and research funding from Amgen. JA has received consulting, advisory or speaker fees from Roche, Pfizer, MSD, Gilead, Menarini, Lilly, Novartis and AstraZeneca Daiichi-Sankyo; research funding or grant support trials by Roche, Pfizer, Amgen, Novartis, MSD, Lilly, AstraZeneca Daiichi-Sankyo; and travel and accommodation support from Gilead and AstraZeneca Daiichi-Sankyo. Holds a patent on LCOR, EGFR ECD (licensed) and stock options in Inbiomotion. BB received honoraria for speaker, consultancy or advisory role from Astra-Zeneca, Janssen, Merck-Serono, Novartis, Roche, Thermo Fisher, Pfizer, BMS, and research grants from Astra-Zeneca, Thermo Fisher, Roche Diagnostics, Roche Farma. X. M.-G.; Lectures and associated travel expenses: Roche Farma, Qiagen, Ferrer Internacional, Novartis, Menarini, Biocartis, Agilent-Dako, Leyca, Reig Jofre, Sysmex, MSD, Astra-Zeneca, BMS, GSK, Clovis. Eisai; Advisory Boards: Astra-Zeneca, Lilly, Amgen, GSK, Janssen, Illumina, MiMark Diagnostics,

MSD, Daiichi Sankyo, Inc, Abbvie. FB reports financial interest in form of consultancy role and speaking/teaching activities for Johnson & Johnson, Abbvie, Novartis, F. Hoffmann-La Roche Ltd, Genentech Inc, Lilly, Beigene, Ascentage, AstraZeneca, Boehringer Ingelheim, MSD, Allogene, Takeda, Kite, Gilead. JMB received honoraria for speaker from Roche, Abbvie, and MSD.

Ethical approval The program is part of the standard of care in Catalonia's public healthcare system. The current study adheres to ethical standards established by the Bioethics Committee of Catalonia and complies with the principles of the Declaration of Helsinki.

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