INSIGHTS-JOURNAL OF
HEALTH AND REHABILITATION

INSIGHTS-JHR
INSIGHTS-JOURNAL OF HEALTH AND REHABILITATION

DESCRIPTIVE STUDY ON GENETIC MUTATIONS AND THEIR ASSOCIATION WITH CANCER DEVELOPMENT AMONG PATIENTS IN TERTIARY CARE HOSPITALS

Original Research

Roshana Nawaz[1]*, Humera Usman[2], Sibgha Mubeen[3], Sapna Sapna[4], Touseef Abid[5], Zar Saman Habib[6], Eman Aslam[7], Sadaf Moeez[8]

[1]Department of Zoology, Government College Women University, Faisalabad, Pakistan.
[2]Assistant Professor, Department of Biochemistry, Fazaia Medical College, Air University, Islamabad, Pakistan.
[3]MPhil Genetics, Bahauddin Zakariya University, Multan, Pakistan.
[4]Assistant Professor, Government Girls Degree College, Gambat, Khairpur, Pakistan.
[5]BS Allied Health Sciences in Medical Laboratory Technology, National Institute of Health, Islamabad, Pakistan.
[6]MPhil, Gomal University, Dera Ismail Khan, Pakistan.
[7]MBBS Final Year, Wah Medical College, Islamabad, Pakistan.
[8]Assistant Professor, Department of Biological Sciences, International Islamic University, Islamabad, Pakistan.

Corresponding Author: Roshana Nawaz, Department of Zoology, Government College Women University, Faisalabad, Pakistan, roshana.nawaz589@gmail.com

Acknowledgement: The authors thank all participating institutions for their support.

Conflict of Interest: None

Grant Support & Financial Support: None

ABSTRACT

Background: Cancer is a genetically heterogeneous disease, with various mutations contributing to tumor initiation and progression. Understanding the distribution of genetic mutations across different cancer types can enhance diagnosis and treatment personalization, especially in underrepresented regions like South Punjab.

Objective: To describe patterns of genetic mutations and evaluate their association with different cancer types among affected patients in tertiary care hospitals.

Methods: A descriptive, observational study was conducted over eight months in tertiary care hospitals across South Punjab. A total of 384 adult cancer patients who underwent molecular genetic testing were included. Patient records were reviewed to extract demographic, clinical, and genetic data. Mutation types, frequencies, and their associations with specific cancers were analyzed using descriptive statistics and chi-square tests in SPSS version 26, with a significance threshold of $p < 0.05$.

Results: The mean age of patients was 52.3 ± 11.8 years, with a slight male predominance (54.2%). Breast cancer was the most common malignancy (26.6%), followed by lung (20.3%) and colorectal cancers (16.1%). TP53 mutations were the most frequent (25.0%), followed by BRCA1 (14.1%), BRCA2 (9.9%), KRAS (9.4%), and EGFR (8.3%). TP53 was significantly associated with breast cancer, while BRCA1/2 were prevalent in breast and ovarian cancers. KRAS and EGFR were primarily linked to lung and colorectal cancers. Statistically significant associations were observed between specific gene mutations and cancer types.

Conclusion: This study highlights distinct genetic mutation profiles among cancer patients in South Punjab, reinforcing the value of molecular testing in regional oncology practice. The findings support efforts to personalize cancer care based on genomic insights.

Keywords: BRCA1 Protein, Colorectal Neoplasms, EGFR Mutations, Genetic Testing, KRAS Mutations, Lung Neoplasms, Neoplasms, Precision Medicine, TP53 Tumor Suppressor Protein.

INTRODUCTION

Cancer remains one of the most significant health challenges of the modern era, characterized not only by its widespread impact but also by its complex and multifactorial origins (1). While environmental and lifestyle factors undeniably play a role in oncogenesis, a growing body of evidence points to the critical role of genetic mutations in the initiation, progression, and heterogeneity of various malignancies. In recent years, advances in molecular biology and genetic sequencing have enabled researchers and clinicians to delve deeper into the genomic underpinnings of cancer, revealing an intricate landscape of mutations that vary widely between individuals and tumor types (2). This growing understanding has transformed cancer from a single disease to a collection of genetically distinct disorders, each with its own biological signature and clinical behavior. As researchers continue to uncover the mechanisms by which genetic alterations drive tumor development, it has become evident that certain mutations confer increased susceptibility to specific cancer types (3). For instance, mutations in the BRCA1 and BRCA2 genes are well-established markers for hereditary breast and ovarian cancers, while KRAS, EGFR, and TP53 mutations have been frequently implicated in colorectal, lung, and multiple other malignancies. These discoveries have not only enhanced diagnostic accuracy but also opened the door to targeted therapies that aim to disrupt the molecular pathways activated by such mutations. Despite these advancements, significant gaps remain in the comprehensive understanding of mutation patterns across diverse patient populations, particularly in developing regions where genomic studies are relatively scarce (4).

In many tertiary care hospitals, particularly those serving heterogeneous populations, cancer patients present with varied clinical histories and genetic backgrounds (5). This diversity offers a valuable opportunity to explore the prevalence and distribution of specific genetic mutations across different types of cancer. However, there is a lack of systematic documentation and analysis of these patterns, which limits the ability to draw broader conclusions that could inform clinical decision-making (6). The absence of such localized genetic profiling means that treatment approaches often rely on general guidelines that may not fully align with the patient's individual molecular profile, potentially compromising outcomes. Moreover, the evolving nature of cancer genetics requires continuous research to keep pace with emerging discoveries (7). Every cancer genome holds a story — a sequence of events encoded within DNA that can explain how normal cells transformed into malignant ones. Understanding these stories not only improves diagnostic precision but also holds the potential to personalize therapy, avoid unnecessary treatments, and identify high-risk individuals before cancer manifests clinically. Yet, the translation of this knowledge into routine clinical practice demands a foundational step: descriptive studies that map mutation patterns in real-world clinical settings (8).

Such studies serve as the bedrock for larger, more hypothesis-driven research by establishing baseline data and identifying trends worthy of deeper exploration (9). They also contribute to the global cancer genomics database, particularly when originating from underrepresented populations. This is crucial, as most existing genomic data stems from high-income countries, potentially overlooking mutation patterns that may be unique or more prevalent in other regions (10). Including a broader spectrum of genetic information can enrich global understanding and foster more inclusive therapeutic development. Against this backdrop, the current study aims to provide a descriptive overview of genetic mutations identified among cancer patients in tertiary care hospitals (11). By evaluating the types and frequencies of mutations observed and examining their associations with specific cancer types, the study seeks to generate insights that may inform future research, contribute to precision medicine initiatives, and ultimately support more tailored patient care (12). The objective is thus to describe patterns of genetic mutations and evaluate their association with different cancer types in affected patients, thereby addressing a critical gap in the contextual understanding of cancer genetics within a real-world clinical environment.

METHODS

This descriptive study was conducted over a duration of eight months in tertiary care hospitals located in South Punjab, with the objective of identifying patterns of genetic mutations and evaluating their association with various cancer types among diagnosed patients. The study design was observational, employing a non-interventional approach focused on capturing and analyzing existing clinical and genetic data from cancer patients who had undergone molecular testing as part of their diagnostic workup.

INSIGHTS-JHR
INSIGHTS-JOURNAL OF HEALTH AND REHABILITATION

A calculated sample size of 384 patients was determined using the Cochran formula for descriptive studies, assuming a 95% confidence interval, a 5% margin of error, and an estimated 50% prevalence of genetic mutations among cancer patients to ensure maximum variability and adequate representation. Patients of all genders aged 18 years and above, with a confirmed diagnosis of cancer and documented results of genetic testing (including either targeted gene panels or next-generation sequencing), were included in the study. Patients were excluded if they lacked complete medical records, had not undergone genetic testing, or if their reports were inconclusive or unrelated to the study's target parameters.

Data collection involved retrospective review of patient files, laboratory genetic reports, and hospital oncology registries. Demographic data including age, gender, and clinical diagnosis were recorded alongside genetic information such as the type of mutation, gene involved, mutation classification (e.g., missense, nonsense, insertion, deletion), and pathogenicity status (pathogenic, likely pathogenic, variant of uncertain significance). Cancer types were classified according to the primary organ system and histopathological diagnosis. Genetic mutation data were primarily extracted from molecular pathology reports based on standardized testing protocols using validated platforms such as next-generation sequencing (NGS), Sanger sequencing, and polymerase chain reaction (PCR)-based panels, depending on the hospital's available resources.

Outcome measurement was focused on the descriptive categorization of mutation types and their frequency distribution across different cancer types. Mutations were further grouped according to their functional impact, and cross-tabulated with the cancer diagnosis to explore potential associations. All data were entered into a secure database and coded to ensure patient confidentiality.

Data analysis was performed using IBM SPSS Statistics version 26. Continuous variables such as age were expressed as mean and standard deviation, while categorical variables including mutation type and cancer classification were presented as frequencies and percentages. Given that the data followed a normal distribution, as assessed by the Kolmogorov-Smirnov test, the chi-square test was applied to assess associations between specific genetic mutations and cancer types. A p-value of less than 0.05 was considered statistically significant.

This methodological approach allowed for a comprehensive overview of genetic mutation trends among cancer patients in a diverse clinical setting, thereby offering valuable insights into potential genotype-phenotype correlations relevant to regional cancer care.

RESULTS

A total of 384 patients with confirmed cancer diagnoses were included in the study. The mean age of the participants was 52.3 years (±11.8), with a slightly higher proportion of males (54.2%) compared to females (45.8%). Breast cancer emerged as the most prevalent malignancy, affecting 26.6% of the cohort, followed by lung cancer (20.3%), colorectal cancer (16.1%), ovarian cancer (12.5%), prostate cancer (9.9%), lymphoma (7.3%), and various other malignancies accounting for the remaining 7.3% of cases (Table 2, Figure 1).

Genetic analysis revealed that TP53 was the most frequently mutated gene, identified in 25.0% of patients. This was followed by BRCA1 (14.1%), BRCA2 (9.9%), KRAS (9.4%), EGFR (8.3%), and PIK3CA (7.8%). Collectively, these accounted for a significant portion of the detected mutations, while other less common or rare mutations made up 25.5% of the total findings (Table 3, Figure 2).

When stratified by cancer type, distinct mutation patterns were observed. TP53 mutations were predominantly associated with breast (n=32), lung (n=18), and colorectal cancers (n=16), while BRCA1 mutations were mostly seen in breast (n=41) and ovarian cancers (n=13). BRCA2 alterations were also notable in breast (n=24) and ovarian cancers (n=9). KRAS mutations were primarily identified in colorectal (n=14) and lung cancers (n=10), whereas EGFR mutations were most commonly linked with lung cancer (n=19). A small proportion of these mutations appeared in other cancer types with lower frequencies (Table 4).

The chi-square test showed statistically significant associations between specific gene mutations and cancer types ($p < 0.05$). For instance, BRCA1 mutations showed a strong association with breast and ovarian cancers, while KRAS and EGFR mutations were more commonly linked to lung and colorectal cancers. TP53 mutations, while more widespread, were still significantly more frequent in breast cancer compared to other malignancies.

Overall, the study demonstrated that certain genetic mutations tend to cluster with specific cancer types, with notable variation in prevalence and distribution. These findings suggest potential genotype-phenotype relationships that may inform future diagnostic and therapeutic strategies tailored to the genetic profile of patients in this region.

INSIGHTS-JHR
INSIGHTS-JOURNAL OF HEALTH AND REHABILITATION

Table 1: Demographic Characteristics of Participants

Variable	Value
Total Participants	384
Mean Age (±SD)	52.3 ± 11.8
Gender - Male	208 (54.2%)
Gender - Female	176 (45.8%)

Table 2: Distribution of Cancer Types

Cancer Type	Frequency (n)	Percentage (%)
Breast	102	26.6
Lung	78	20.3
Colorectal	62	16.1
Ovarian	48	12.5
Prostate	38	9.9
Lymphoma	28	7.3
Others	28	7.3

Table 3: Most Common Genetic Mutations Identified

Gene	Frequency (n)	Percentage (%)
TP53	96	25.0
BRCA1	54	14.1
BRCA2	38	9.9
KRAS	36	9.4
EGFR	32	8.3
PIK3CA	30	7.8
Others	98	25.5

Table 4: Mutation Type by Cancer Type

Gene	Breast	Lung	Colorectal	Ovarian	Others
TP53	32	18	16	12	18
BRCA1	41	0	0	13	0
BRCA2	24	0	0	9	5
KRAS	2	10	14	1	9
EGFR	3	19	5	0	5

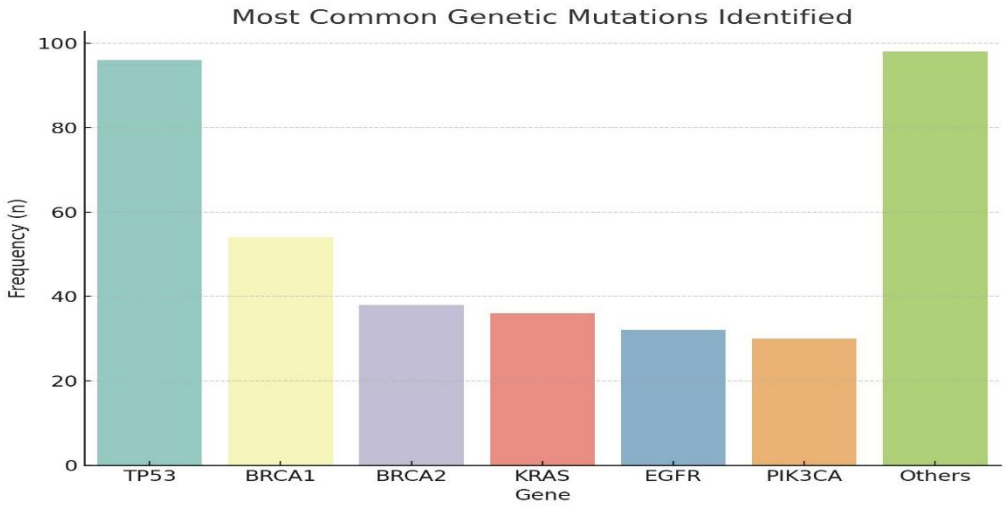

Figure 1 Most Common Genetic Mutations Identified

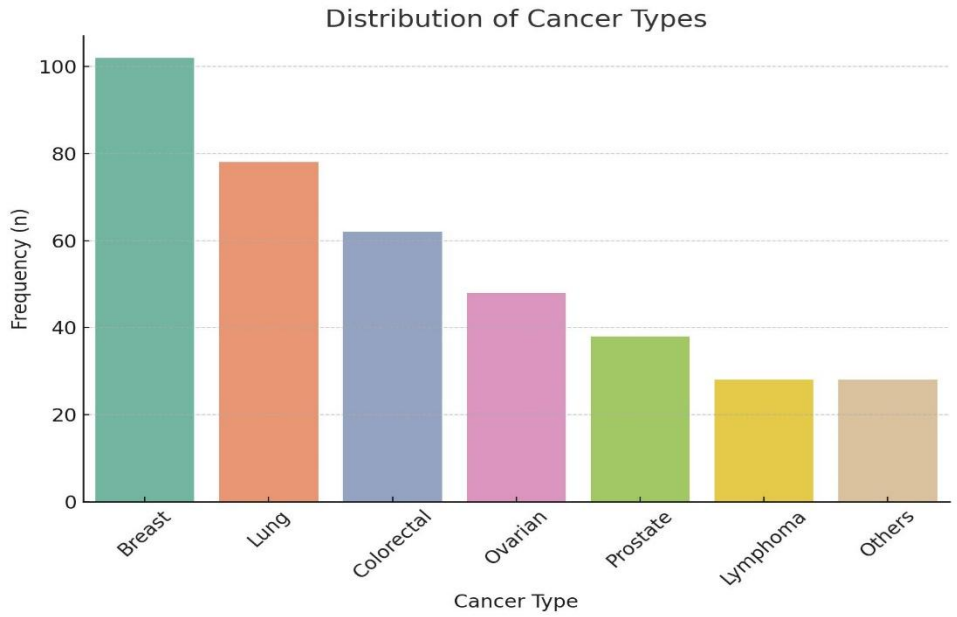

Figure 2 Distribution of Cancer Type

DISCUSSION

The findings of this descriptive study highlighted distinct patterns of genetic mutations across various cancer types in a diverse patient population from South Punjab. By mapping the frequency and distribution of key oncogenic mutations, the study contributed valuable regional insight into the molecular landscape of cancer, with direct relevance to diagnostic precision, prognostication, and future development of targeted treatment strategies (13). The high prevalence of mutations in genes such as TP53, BRCA1, BRCA2, KRAS, and EGFR mirrored broader global trends, suggesting that, despite geographical and demographic differences, certain genetic alterations maintain a consistent role in carcinogenesis. Among the most notable results was the predominance of TP53 mutations across multiple cancer types, with a particularly high frequency in breast cancer cases. This finding aligned with the gene's well-established role as a critical tumor suppressor frequently disrupted in a wide array of malignancies. BRCA1 and BRCA2 mutations were heavily concentrated in breast and ovarian cancer patients, consistent with their roles in hereditary cancer syndromes and DNA repair pathways. These patterns further supported the clinical rationale for including BRCA screening in high-risk patients and

INSIGHTS-JHR
INSIGHTS-JOURNAL OF HEALTH AND REHABILITATION

emphasized the need for genetic counseling as part of oncology care in tertiary settings. KRAS and EGFR mutations were primarily associated with lung and colorectal cancers, reaffirming their recognized status as oncogenic drivers in these tumor types. The relatively high detection rates of these mutations also underscored their potential utility as therapeutic targets in precision oncology. Notably, EGFR mutations showed a strong affinity for lung cancer, supporting the integration of tyrosine kinase inhibitors in treatment regimens. The diversity of mutation types and their distributions illustrated the molecular heterogeneity of cancer and suggested that individualized molecular profiling could play a critical role in improving clinical outcomes, especially in regions with emerging cancer care infrastructure (14).

One of the strengths of this study lay in its real-world clinical setting, capturing data from a representative cohort of patients undergoing active treatment in tertiary care hospitals. This enhanced the external validity of the findings and offered practical relevance for healthcare providers. Furthermore, the use of established molecular testing platforms such as next-generation sequencing and PCR-based panels ensured reliability and accuracy of mutation detection. The inclusion of a broad range of cancer types also allowed for comparative insights across different malignancies, enriching the scope of the study (15). However, several limitations must be acknowledged. The retrospective nature of the study relied on pre-existing data, which may have introduced selection bias or information gaps due to inconsistent documentation. Genetic testing was not uniform across all cases, as resource availability varied between institutions, potentially affecting the comprehensiveness of mutation detection. Variants of uncertain significance were not analyzed in depth, which may have limited the interpretive power of certain findings. Additionally, due to the descriptive design, causality could not be established, and functional implications of the mutations were not explored beyond their frequency and distribution. Another consideration was the absence of long-term clinical outcome data, such as survival or response to targeted therapies, which could have strengthened the association between specific mutations and prognostic significance. The sample, although sufficiently powered, represented only a fraction of the broader cancer population, and future studies with larger, multicenter cohorts would be beneficial to confirm these patterns. Furthermore, ethnic and environmental influences on mutation prevalence, which may be particularly relevant in this region, were not captured and remain areas for further investigation (16).

Despite these limitations, the study underscored the importance of integrating molecular profiling into routine oncology practice, even in resource-constrained settings. The results provided a foundation for more focused genomic research in the region and emphasized the value of establishing local genetic databases to guide treatment protocols (17). As the field of oncology moves toward personalized medicine, understanding regional mutation trends becomes imperative for optimizing therapy and improving outcomes. Future research should aim to incorporate prospective designs with standardized testing protocols and follow-up data to explore how genetic profiles influence treatment response and survival. Studies examining the socio-economic and biological factors influencing mutation patterns could also provide deeper insight into disparities in cancer incidence and outcomes. Expanding the range of genes tested and integrating multi-omics approaches could further unravel the complexity of tumor biology in this population. In conclusion, the study offered a meaningful contribution to the understanding of cancer genomics in a developing regional context. The documentation of mutation trends among cancer patients in South Punjab provided essential groundwork for future translational efforts in cancer care, paving the way for more personalized, genetics-driven clinical management (18).

CONCLUSION

This study identified distinct patterns of genetic mutations associated with specific cancer types among patients in tertiary care hospitals of South Punjab. The findings emphasize the relevance of molecular profiling in guiding targeted cancer therapies and support the integration of genetic testing into routine oncology practice. By providing region-specific genomic data, the study contributes to the foundation for personalized cancer care and highlights the need for continued research in diverse clinical populations.

INSIGHTS-JHR
INSIGHTS-JOURNAL OF HEALTH AND REHABILITATION

AUTHOR CONTRIBUTION

Author	Contribution
Roshana Nawaz*	Substantial Contribution to study design, analysis, acquisition of Data Manuscript Writing Has given Final Approval of the version to be published
Humera Usman	Substantial Contribution to study design, acquisition and interpretation of Data Critical Review and Manuscript Writing Has given Final Approval of the version to be published
Sibgha Mubeen	Substantial Contribution to acquisition and interpretation of Data Has given Final Approval of the version to be published
Sapna Sapna	Contributed to Data Collection and Analysis Has given Final Approval of the version to be published
Touseef Abid	Contributed to Data Collection and Analysis Has given Final Approval of the version to be published
Zar Saman Habib	Substantial Contribution to study design and Data Analysis Has given Final Approval of the version to be published
Eman Aslam	Contributed to study concept and Data collection Has given Final Approval of the version to be published
Sadaf Moeez	Writing - Review & Editing, Assistance with Data Curation

REFERENCES

1. Aleissa M, Ekram SJOR. A comprehensive framework for the management of hereditary breast cancers: guiding light in precision medicine. 2025;19:1633387.

2. Farhat J, Alzyoud L, AlWahsh M, Acharjee A, Al-Omari BJCM. Advancing Precision Medicine: The Role of Genetic Testing and Sequencing Technologies in Identifying Biological Markers for Rare Cancers. 2025;14(8):e70853.

3. Rajkhowa S, Zeenat S, Agarwal M, Zaheen A, Zaki ME, Sinha S. From genes to recovery: precision medicine and its influence on multidrug resistant breast cancer. Breast Cancer Genetics, Immunology, and Immunotherapy: An Interdisciplinary Approach: Springer; 2024. p. 187-235.

4. Rituraj, Pal RS, Wahlang J, Pal Y, Chaitanya M, Saxena SJMO. Precision oncology: transforming cancer care through personalized medicine. 2025;42(7):246.

5. Bonetti G, Madeo G, Michelini S, Ricci M, Cestari M, Gadler M, et al. Omics sciences and precision medicine in breast and ovarian cancer. 2023;174(6).

6. Dalal H. Precision Medicine in Breast Cancer: A Molecular Genomics and Diagnostics Approach: Lund University; 2024.

7. Dalghi EJIJoBS. Bridging Genomics and Oncology: Molecular Approaches to Personalized Medicine. 2023;2(2):281-90.

8. Malgerud L. Advancing precision medicine in pancreatic cancer through bioinformatics-assisted genomic profiling and clinical stratification: Karolinska Institutet; 2025.

9. Basu M, Singh R, Bharadwaj H, Ray S, Choughule A, Prabhash K, et al. Empowering precision medicine in rural India by establishment of a molecular genetics laboratory in Bihar: A prospective observational study. 2024;7(4):410-20.

10. Tripathi D, Davies NM, Rajinikanth PS, Pandey PJCGT. Advancements in Targeted Therapies and Pharmacogenomics for Personalized Breast Cancer Treatment: The Role of Gene SNPs in Treatment Resistance. 2025.

11. Walsh RJ, Ong R, Cheo SW, Low PQ, Jayagopal A, Lee M, et al. Molecular profiling of metastatic breast cancer and target-based therapeutic matching in an Asian tertiary phase I oncology unit. 2024;14:1342346.

12. Torres-Narvaez ES, Mendivelso-Gonzalez DF, Artunduaga-Alvarado JA, Ortega-Recalde OJFiO. Cancer genomics and bioinformatics in Latin American countries: applications, challenges, and perspectives. 2025;15:1584178.

13. Taj J, Ajmal MN, Arshad T, Dawood A, Abbas A, Hafeez M, et al. Integrative Molecular Profiling of Oncogenic Pathways and Genetic Mutations in Cancer Progression and Therapeutic Response. 2025;6:738-50.

14. Sharma P. Clinical Applications of Cancer Genetic Testing: CRC Press; 2025.

15. Mir MA. p53 in Breast Cancer: Molecular Mechanisms, Clinical Implications, and Therapeutic Targets: CRC Press; 2024.

16. Jha P, Mishra R, Joshi A, Sharma N, Shah M, Babu G, et al. Circulating tumor DNA profiling for non-invasive genomic analysis in Indian lung cancer patients: A real-world experience. 2025:100300.

17. Sharma R, Kamireddy AP, Hussaini SM, Chatterjee S, Hasan Q, Jain JJFiG. The landscape of actionable genomic alterations in lung adenocarcinomas in India. 2023;14:1256756.

18. Philips AO, Panda SS, Cyriac S, Moharana L, Kilaru S, Kolluri S, et al. Real-World Experiences of Next-Generation Sequencing in Oncology: From an Indian Multicenter Registry and Collaborative Centers. 2024.