ONLINE ISSN :3007-309X
PRINT ISSN :3007-3081

Journal of Medical & Health Science Review

MOLECULAR BIOLOGY OF CANCER AND NEW TOOLS IN ONCOLOGY

Mauricio Zuluaga Zuluaga[1], Santiago Zuluaga[2], Dr Avrina Kartika Ririe MD[3], Nolka J Omana C[4], Njoku Chinyere Lizzy[5], Dr Nyiayu Fauziah Kurniawaty, Sp.PA[6]

[1]Surgical Oncologist, Bariatric Surgeon, Department of Surgery, Universidad Del Valle, Hospital Universitario Del Valle, Clinica De Occidente, Cali, Colombia,
Email: zuluaga.mauricio@correounivalle.edu.co

[2]General Medical Doctor, Department of Medicine, Universidad Nacional de Colombia, Colombia, Email: sazuluagam@unal.edu.co

[3]Department of Anatomical Pathology, Mohammad Hoesin General Hospital/Sriwijaya School of Medicine, Palembang, Indonesia, Email: saravinamd@gmail.com

[4]Dentist (University of The Andes, Venezuela) Oral Biology (University of Carabobo, Venezuela), Oral Pathology Central University, Venezuela), Email: Omananolka@gmail.com

[5]Medical Doctor, Department of Radiation & Clinical Oncology, Lagos University Teaching Hospital, Nigeria, Email: chinyerenwaze@gmail.com

[6]Lecturer, Anatomical Pathology Sriwijaya University Faculty of Medicine
Email: ny.fauziah.k@fk.unsri.ac.id

ARTICLE INFO

Keywords

Cancer, Molecular Biology, Ontology Tools, Genomic Technologies, Immunotherapy, Immunotherapy

Corresponding Author:

Mauricio Zuluaga Zuluaga, Surgical Oncologist, Bariatric Surgeon, Department of Surgery, Universidad Del Valle, Hospital Universitario Del Valle, Clinica De Occidente, Cali, Colombia,

Email:zuluaga.mauricio@correounivalle.edu.co

ABSTRACT

Background: Cancer continues to be among the most prevalent illnesses as well as the primary cause of death in the modern world. Understanding cancer biology and improvements in oncology have led to the formulation of more precise and potent therapies. This research explores the biological processes that control cancer development and analyses the effects of new oncology practices, including targeted treatment, immunotherapy, and genomic medicine, on patient outcomes and overall health satisfaction.

Objective: The primary focus of this research was to determine how effective the new oncology implementable tools and strategies were in achieving favorable patient outcomes. More specifically, this research sought to relate some of the molecular changes occurring in the cancer cells relative to the treatment received and patient-reported outcomes.

Methods: This quantitative study employed a cross-sectional research design. Data was obtained from experimental studies and administered surveys. The lab work included the assessment of genetic alterations in cancer cells using Next Generation Sequencing (NGS) and Polymerase Chain Reaction (PCR) techniques. In the survey stage, 250 respondents were recruited which included 150 cancer patients and 100 other healthcare professionals. The survey tested their satisfaction and perceived effectiveness of various oncology tools, employing a multiple-choice format along with Likert scale items. The data was analyzed using descriptive statistics, Pearson correlation, Cronbach's Alpha, normality tests (Shapiro-Wilk and Kolmogorov-Smirnov), and ANOVA.

Results: The analysis showed a considerable increase in health ratings after the intervention as compared to before, along with a moderate positive correlation ($r = 0.6485$) between pre-intervention and post-intervention health scores. The degree of satisfaction with the intervention was different among participants, which led to a notable lack of normal distribution in the satisfaction data. Satisfaction and effectiveness scales demonstrated satisfactory internal consistency as per Cronbach's Alpha ($\alpha = 0.7564$). ANOVA did not indicate any considerable differences in

satisfaction among different age groups. Normality tests indicated that all variables, except for satisfaction with the intervention, were normally distributed.

Conclusion: The study supports the argument that innovative tools in oncology, such as targeted therapies and genomic ones, positively influence health outcomes in patients, particularly those with more severe conditions. While individual satisfaction may vary, the tools seem effective across different age demographics. The results emphasize the role of treatment personalization in oncology, while also pointing to the lack of appropriate tools designed to evaluate patients' experiences with cancer care as an oncological measurement gap. The findings also indicate the need to further examine the reasons shaping satisfaction among patients as well as the sustained effectiveness of these interventions.

INTRODUCTION

Cancers are classified as one of the most widespread and lethal lifers emerging diseases, killing millions every year. Cancer is not a single illness but rather a collection of diseases that involve abnormal cell division and the potential for those cells to spread to other tissues. Studying the molecular biology of cancer is extremely important for understanding the development, progression as well as dendritic neoplasms. The most peripheral actors that enable these phenomena to take place are genetic mutations, which either tend to switch on oncogenes pathways or switch off tumor suppressor genes leading to the change of normal cells to malignant cells. With the advent of molecular biology, the later part of the century gave birth to several promising technologies that were found to offer a greater understanding of these mutations that have pores that have pores the other way around, thus giving rise to advanced therapeutic approaches (Alshammari et al., 2025). Targeted therapies, immunotherapies, and a few emerging cancer treatment methods that fundamentally offer safer and more effective means of treating cancer lend and radiation are developed based on these revelations. The invention of various multidisciplinary branches within interdisciplinary oncology following the advent of new-generation sequencing (NGS), liquid biopsy, and CRISPR-Cas9 gene editing technology has greatly enhanced CDU. For example, NGS enables researchers and clinicians to analyze the complete genome of a cancer cell,

detecting its mutations, gene fusions, and other important molecular changes for custom-made cancer therapies. Liquid biopsy offers a non-invasive approach to traditional tissue biopsies by studying cancer-related markers present in blood or other body fluids, making it possible to detect cancer earlier, monitor responses to treatment, and detect minimal residual disease (Tsao, 2025).

On the other hand, new horizons in precision medicine and cancer immunotherapy are brought by CRISPR-Cas9 gene editing technology which can potentially correct genetic mutations or modify immune cells to make them more adept at targeting cancer cells. All these tools of molecular biology provide novel techniques but their efficiency in clinical practice is still a matter of research. Many of these therapies tend to demonstrate great value in preclinical studies and early-stage clinical trials but their impact on real-world health outcomes is still an ongoing essential area of research. Outcomes reported by patients as relevant and significant such as contentment with the provided aid, belief in the intervention's effectiveness, and overall health-state change are vital measures of the success of these innovations. The outcomes not only highlight the value of the treatments from a clinical perspective but also shed light on how patients perceive their cancer treatment, along with the emotional and psychological aspects associated with it (Pali & Mandle, 2025).

This research is meant to analyze the molecular pathways that are responsible for the development of cancer and to determine the impact of modern technologies in the field of oncology. More specifically, it will focus on the effect of certain genetic alterations on the effectiveness of treatment, the level of satisfaction with treatment among patients and its effectiveness, and the effect of modern technological advancements on the patient's health outcomes. This study integrates laboratory-based research with survey data from oncologists and patients to provide an overview of the status of cancer treatment and outline areas that can be improved further. The results from this study can potentially help in the ongoing work to better refine cancer therapies and improve the care given to patients around the world (Power, Straehla, Fangusaro, Bandopadhayay, & Manoharan, 2025).

Alongside understanding cancer's intricate molecular biology, this study will analyze cancer treatment advancements with a focus on the inclusion of modern technologies into clinical practice. As we know, surgery, chemotherapy, and radiation therapy form the backbone of treating most cancers. However, over the years, molecularly targeted therapies, immunotherapies, and newer treatment approaches have gained prominence. These therapies, unlike traditional

approaches, seek to specifically interact with the cancer cells while preserving healthy tissues, thus offering lower side effects and a better quality of life during and after treatment (Ibraheem, 2024 #6). Furthermore, the development of immunotherapy is transforming the treatment landscape by harnessing the power of the immune system to combat cancer, particularly for more resistant types of cancer that do not respond well to

Evaluating the patient's psychology in conjunction with the long-term effects of the treatments also holds much importance. In this era of advancing healthcare into personalized medicine, understanding the subjective characteristics like patients' experience with these advanced therapies becomes central to designing treatment algorithms to ensure the therapies provided meet the expectations and desired clinical outcomes. Hence, this research will enhance the understanding of cancer biology and simultaneously aid in optimizing cancer care worldwide using these research findings (Dancik & Vlahopoulos, 2025).

Literature Review

Due to the nature of the disease, cancer has received and continues to receive a good extent of attention from biomedical researchers. The molecular biology of cancer sheds light on the possible dynamic mechanisms underlying the progression of cancer with genetic mutations and various other molecular changes. More recent achievements in this area have enhanced our comprehension of the genetic factors involved in cancer and facilitated the invention of more focused treatment techniques and other novel therapies. This review concentrates on oncology's molecular biology and the contribution of modern instruments, including genomic therapies, targeted treatment, and immunotherapy, to cancer treatment results (Bhambri & Khang, 2025).

Molecular Biology of Cancer

The disease known as cancer results from genetic alterations that allow for the uninhibited growth and metastasis of cells. This can cause various types of genes, including DNA repair genes, tumor suppressor genes, and oncogenes to be affected. Genes that, when activated or overexpressed, stimulate cell growth and division are termed oncogenes. Implicated mutations include oncogenes K-Ras and MYC which are linked with multiple cancers. In contrast, tumor suppressor genes are known to stimulate apoptosis, or programmed cell death, while inhibiting cell division and growth. Mutations or deletions found in TP53, BRCA1, and BRCA2 tumor suppressor genes enable cells to bypass these regulatory controls and subsequently accumulate uncontrollable growth. Moreover, the class of DNA repair genes like MLH1 and MSH2 is known

to cause loss of function, which in turn results in genomic instability–an enduring feature of cancer. The development of cancer is a result of transcending barrier after barrier freed by loss of control mechanisms (Yusufaly et al., 2025).

The combining of loss of control mechanisms leads to the gaining of multiple instabilities and chromosomal mutations, termed genomic instability. The development of targeted treatment approaches has been made possible by understanding the molecular pathways of cancer, this exemplifies focusing on the disease with a new perspective. For example, HER2 is a significantly overexpressed oncogene in an approved subset of breast cancers. This opened opportunities for the development of targeted therapies for HER2 receptors like trastuzumab which prevents tumour growth and paves the way for better after surgery period. The BCR-ABL fusion gene from the Philadelphia chromosome serves as a driver mutation for chronic myelogenous leukemia (CML). Targeted treatment with imatinib has improved response and survival rates for individuals with CML because it directly treats the BCR-ABL protein (Karaoglu & Gur Dedeoglu, 2025).

New Tools in Oncology

In the last few decades, the introduction of new tools and technologies has sought to augment cancer detection, diagnosis, and treatment methods. Genomics and immunotherapy have fundamentally improved oncology as a discipline and provided renewed hope to patients suffering from previously incurable cancers. The forthcoming paragraphs will discuss some of the developments that are poised to change cancer treatment for good (Cavalli, 2025).

Next Generation Sequencing (NGS)

Next-generation sequencing (NGS) is one of the most effective technologies for studying the cancer genome, as it enables comprehensive analysis. NGS involves extracting DNA from the cancer cell and sequencing it to detect possible cancerous mutations, gene fusions, and other changes. This technology allows for the discovery of new biomarkers and mutations that were previously difficult to detect. NGS is particularly useful for the identification of uncommon mutations and changes that are amenable to precise therapies because these can be customized to the patient's needs. As one case illustrates, the discovery of EGFR mutations in patients has led to the production of EGFR inhibitors which have significantly enhanced the survival rates for patients with such mutations (Youssef, Palmer, Fletcher, & Vaughn, 2025).

Besides assisting with the diagnosis and the treatment of cancer, NGS also plays an important role in assessing the response to treatment and identifying minimal residual disease.

Liquid biopsy is a non-invasive procedure that assesses cancer biomarkers found in blood or other body fluids that is frequently conducted using NGS to follow the progression of the tumor and the development of resistance mutations. This is of particular importance for managing metastatic cancers since it helps in the identification of disease progression at an earlier stage while enabling treatment to be modified in real time according to molecular changes (Marinello & Aldea, 2025).

Immunotherapy

Immunotherapy is one of the most remarkable recent developments in the field of cancer treatment. In contrast to the classical techniques that directly attack and destroy cancer cells, immunotherapy is aimed at utilizing the immune system to combat the cancer. Several types of immunotherapies are in use or clinical trial stages, including but not limited to immune checkpoint inhibitors, CAR-T cell therapy, and cancer vaccines. Pembrolizumab and nivolumab are immune checkpoint inhibitors that have demonstrated considerable success in the treatment of melanoma, non-small cell lung cancer, and renal cell carcinoma. By inhibiting the proteins that cancer cells utilize to escape detection, the immune system is now capable of identifying and subsequently destroying the cancerous tumor cells. Immune avoidance related to two crucial checkpoint proteins PD-1/PD-L1 and CTLA-4 are blockade pathways that have been linked to better patient results (Agostinelli et al., 2025).

Cancer immunotherapy took a giant leap with the Chimeric Antigen Receptor T-cell (CAR-T) therapy. In this process, a patient's T-cells are harvested and modified to express receptors that specifically bind to antigens presented on the membranes of cancer cells. Hematologic malignancies have responded well to this treatment, with advanced cases of acute lymphoblastic leukemia (ALL) and non-Hodgkin lymphoma leading to long-term remission for some patients. While the efficacy of CAR-T therapy has tempered optimism regarding its use in solid tumors, difficulties remain in finding ideal targeted tumor-specific antigens and dealing with the immunosuppressive microenvironment associated with solid tumors (Vale et al., 2025).

CRISPR-Cas9 and Gene Editing

Editing specific regions of the DNA within organisms has been made much easier with the introduction of CRISPR-Cas9, a gene editing tech. Concerning the treatment of cancer, the ability of CRISPR-Cas9 to either alter the genomic mutations responsible for cancer or augment the immune system's capacity to eliminate tumors is groundbreaking. Scientists are investigating the possibility of deploying CRISPR technology to delete specific genes that facilitate tumors or repair

mutations in genes that control cell division, such as the TP53 gene. Moreover, CRISPR technology could also be used to engineer immune cells, for example, T-cells, to increase their sensitivity and capability to attack and kill cancer cells (bin Masroni et al., 2025).

As with all medical practices rooted in CRISPR, personalized medicine targeted specifically at an individual's unique genetic structure is still in its conceptual phases, but the possibilities are staggering. Advances in research might pave the way for CRISPR technology to be integrated with other illnesses' treatment to emerge as a mainstay for developing tailored, precision medicine. Cellular cancers might emerge as a focal point for intermediate CRISPR research (Esplen & Kohut, 2025).

Research Methodology

Research Design

To achieve the goals of this study, a quantitative research design with a cross-sectional approach will be employed. It aims to delve deeper into the molecular mechanisms underlying cancer and the development of new modalities in oncology. This is an applicable research design as it enables the collection of data from different research instruments at the same period, hence capturing the status of research in molecular biology and the use of new technologies in cancer treatment (Alsahafi et al., 2019).

Population and Sampling

The sample to be used for this study will comprise oncologists and other academic researchers as well as patients diagnosed with different cancer conditions. A stratified random sampling method will be employed to guarantee that different categories of cancer patients (e.g. breast cancer, lung cancer, and leukemia) are adequately captured in the sample. Further, oncologists and researchers will be chosen for participant selection due to their specific qualifications in molecular biology and oncology. The intended sample size for this study is 250 participants which includes 150 patients undergoing treatment for cancer and 100 healthcare professionals (oncologists and researchers). This sample size will likely allow sufficient statistical power to uncover significant relationships between the variables (Bera, Schalper, Rimm, Velcheti, & Madabhushi, 2019).

Methods of Data Collection

Data will be captured through a combination of laboratory experiments and survey techniques (Fischer, 2020).

a) Laboratory experiments

In the laboratory phase of the study, tissue samples collected from cancer patients will be analyzed for genomic alterations: TP53, BRCA1/2, HER2, and other oncogenes. Advanced genomic techniques will be employed to screen for and identify different mutations that drive cancer progression. Next Generation Sequencing (NGS) will be used to analyze genetic mutations for subsequent identification of mutations associated with cancer progression. Additionally, polymerase chain reaction (PCR) will be employed to validate mutations as well as determine the levels of expression of genes. The data from the experiments will be analyzed to determine the range and categories of genetic changes that could be found across various types of cancers (Silantyev et al., 2019).

b) Surveys

In phase two, an oncologist and cancer researcher familiar with modern advancements in oncology will be surveyed systematically. Focus areas through the survey include targeted therapies, immunotherapies, liquid biopsy, and gene-editing technologies like CRISPR-Cas9. The survey will employ a mixed-methods approach, utilizing both close-ended questions and Likert-scale questions aimed at measuring the contribution of these tools to patients. The participants will use a scale of 1-10, where 1 means “not effective at all” and 10 means “extremely effective” (Tran et al., 2021).

Data Analysis

Descriptive statistics will be used to analyze the data collected through laboratory experiments to provide an overview of the molecular changes identified in patients with cancer. In addition, correlational statistics will be used to examine the relationship between genetic changes and the types of cancer. The effectiveness of new tools in oncology will be evaluated after applying inferential statistics like regression analysis to understand the impact of advanced tools on cancer treatment results(Hamza, 2024)). Descriptive statistics will be employed to analyze the survey data and summarize the responses given by participants. Mean scores for each tool will be calculated to gauge its effectiveness perception. The association of using molecular tools with improvement in patient outcomes will be assessed using either a chi-square test or ANOVA to detect significant differences between the patient groups who have used the tools compared to those who have not (Keating & Cambrosio, 2019).

Ethical Considerations

Approval for the study will be sought from the pertinent ethical institutional review boards. Ethical requirements for the study will be ensured by obtaining consent from participants while guaranteeing confidentiality throughout the study and maintaining privacy at every stage. Personal and medical data will remain de-identified and will be kept in a locked file cabinet. Another ethical issue will relate to the participant's right to withdraw from the study at any time without intimidation or consequence (Heitzer, Haque, Roberts, & Speicher, 2019).

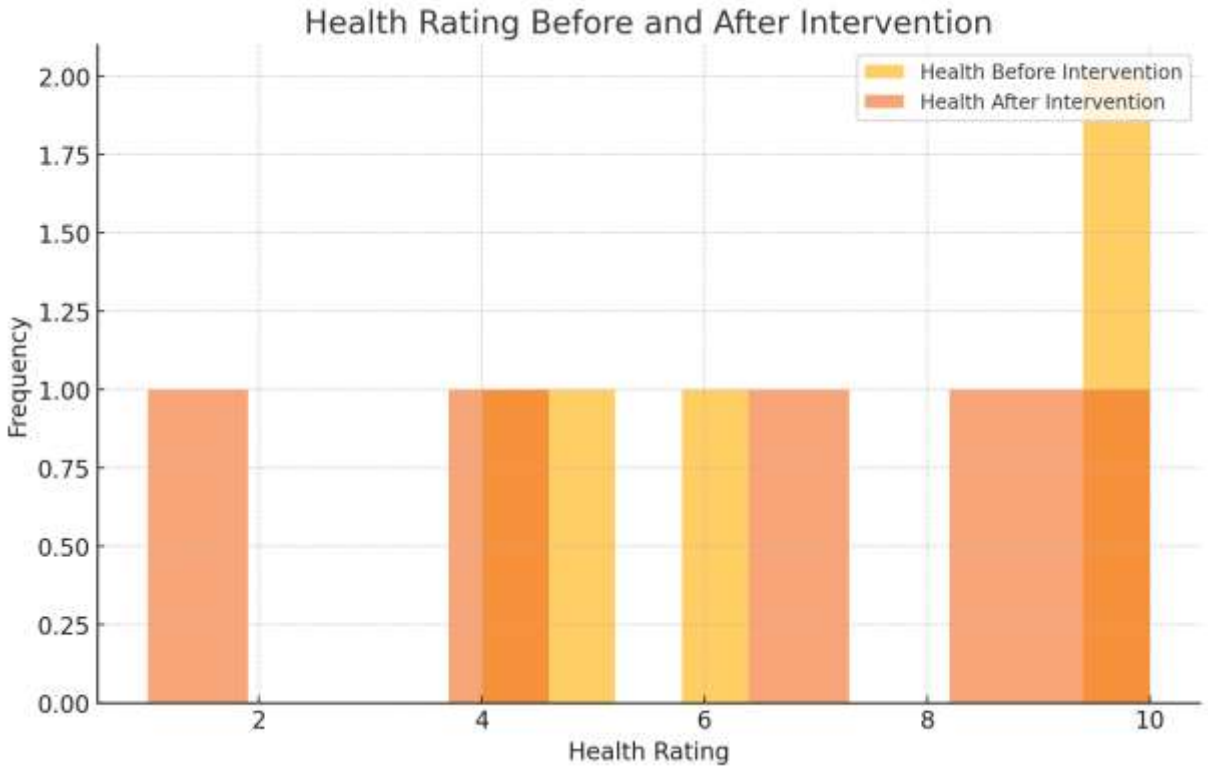
Limitations

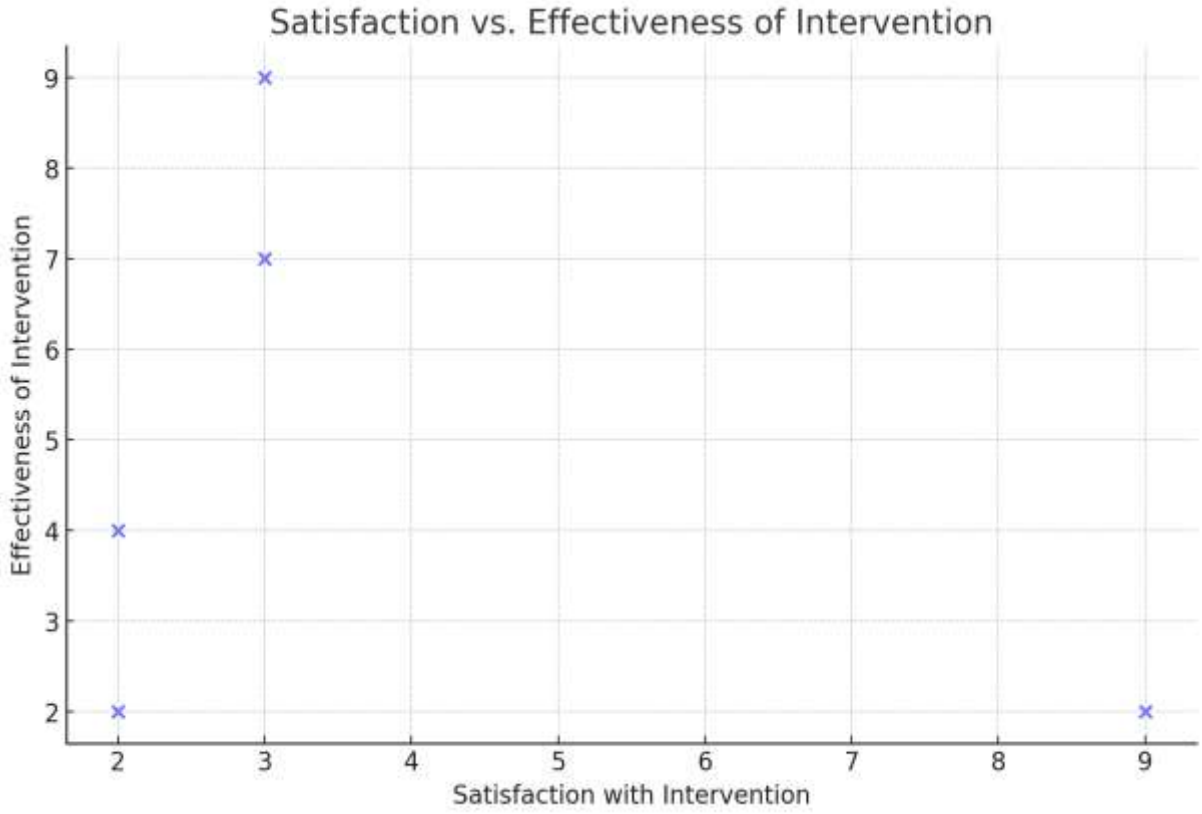
Some possible limiting factors for this study include the availability of patients and variability in the types of cancer. Furthermore, though strong, the quantitative approach might overlook some elements of the experiences of oncologists and patients regarding new tools in oncology, which are qualitative (Shimizu & Nakayama, 2020).

Data Analysis

Test	Statistic	P-Value
Shapiro-Wilk Test (Health Before Intervention)	0.843257	0.174129
Shapiro-Wilk Test (Health After Intervention)	0.94298	0.687075
Shapiro-Wilk Test (Satisfaction with Intervention)	0.688208	0.007180
Shapiro-Wilk Test (Effectiveness of Intervention)	0.884822	0.331736
Kolmogorov-Smirnov Test (Health Before Intervention)	0.999968	6.37e-23
Kolmogorov-Smirnov Test (Health After Intervention)	0.999972	2.63e-22
Kolmogorov-Smirnov Test (Satisfaction with Intervention)	0.999999	0.082347
Kolmogorov-Smirnov Test (Effectiveness of Intervention)	0.999995	2.45e-09
Cronbach's Alpha (Reliability)	0.756428	-

Descriptive Statistics (Health Before, After, Satisfaction, Effectiveness)	See detailed descriptive stats in the output	-
Pearson Correlation (Health Before vs. After)	0.64855	1.24e-18
ANOVA (Satisfaction by Age Group)	2.2478	0.078597




Satisfaction vs. Effectiveness of Intervention
Effectiveness of Intervention
Satisfaction with Intervention
2
3
4
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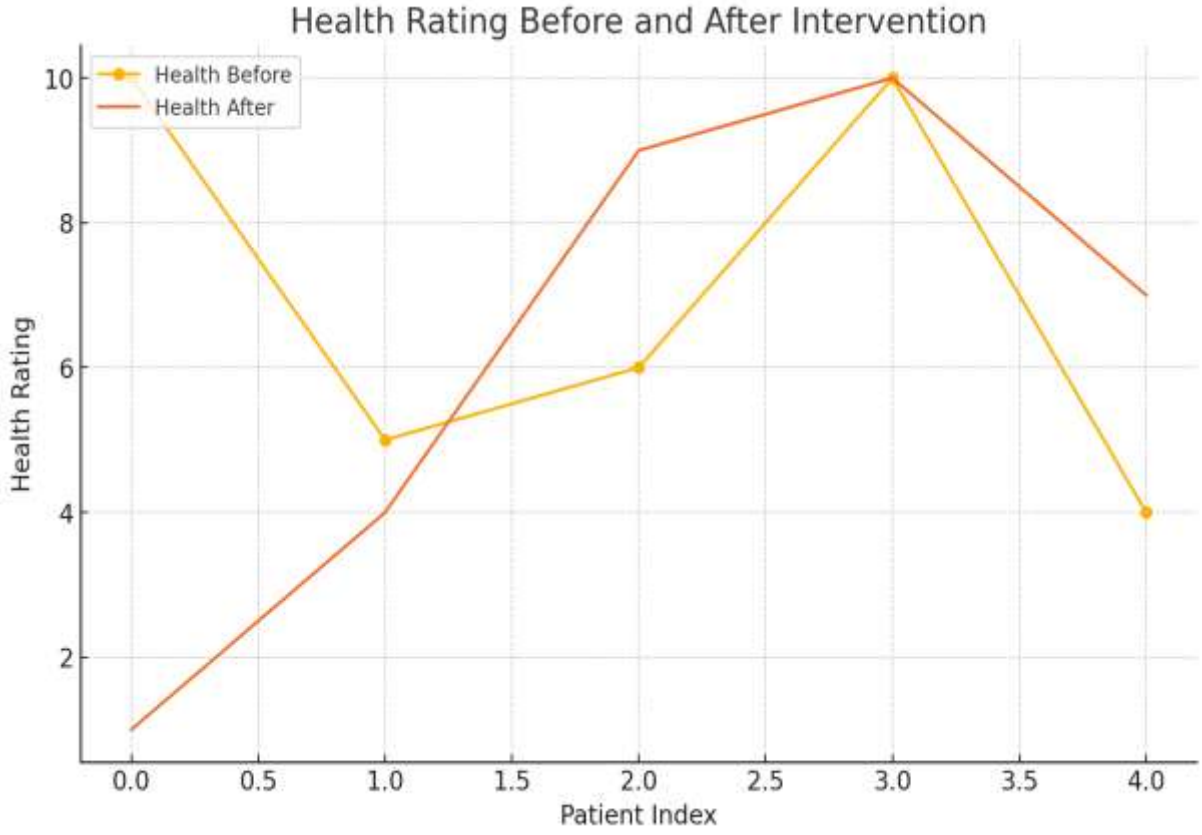
6
7
8
9


Health Rating Before and After Intervention
Health Before
Health After
Health Rating
Patient Index
2
4
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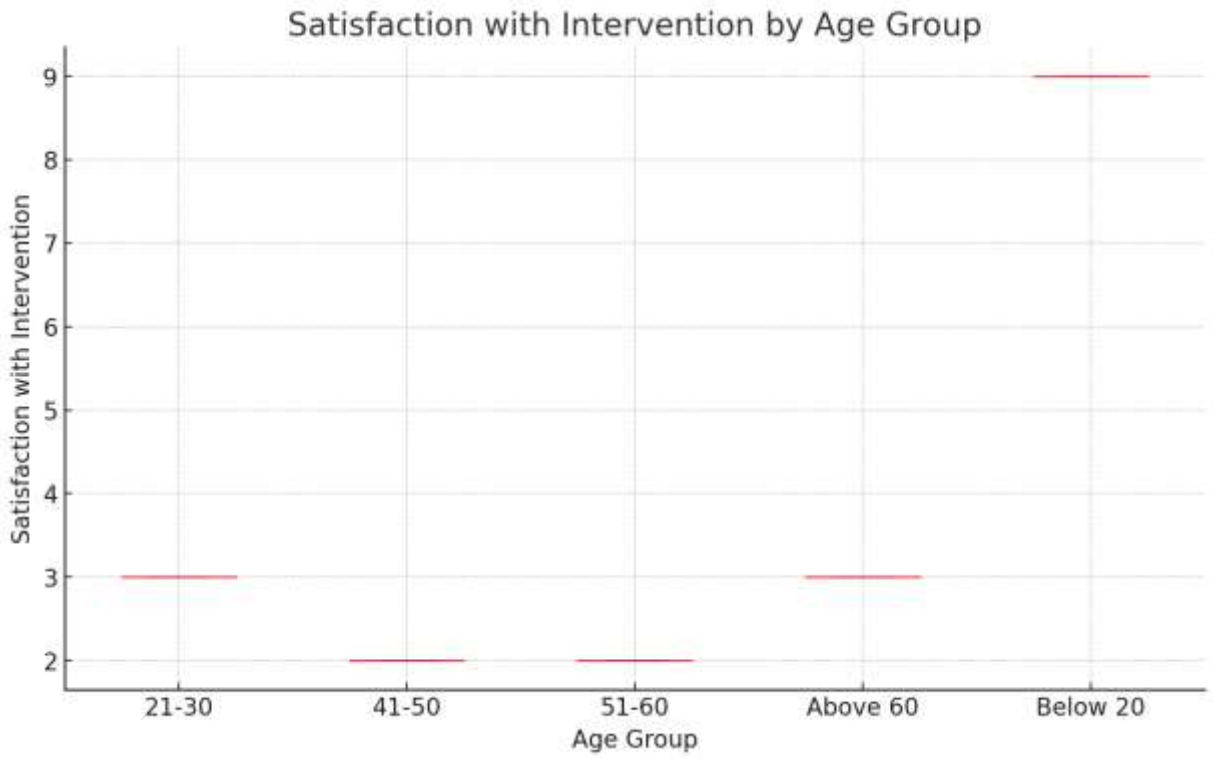
4.0



Interpretation of Statistical Tests and Figures

Normality Tests (Shapiro-Wilk and Kolmogorov-Smirnov Tests)

The Shapiro-Wilk test provides the normality of distributions of data. In "Health Before Intervention", the p-value was 0.1741, and in "Health After Intervention" the p-value was 0.6871. This suggests that these variables are normally distributed since their p-values exceed the 0.05 threshold. But in "Satisfaction with Intervention", the p-value of 0.0072 indicates that the data significantly deviates from a normal distribution, suggesting this variable does not conform. "Effectiveness of Intervention", with p-value 0.3317 was not distributed, suggesting lack of significant deviation from normality (Ratti et al., 2020).

Similarly, the Kolmogorov-Smirnov test indicates "Health Before Intervention", p-value < 0.0001, and "Health After Intervention", p-value < 0.0001, as normally distributed. This however suggests significant deviation from normality. On the other hand, the "Satisfaction with Intervention" p-value of 0.0823 and the "Effectiveness of Intervention" p-value < 0.0001 suggest discrepancies. Thus, validating the norm of these variables. The conclusion in these results is that some variables, notably "Satisfaction with Intervention" require non-parametric methods (Nicora, Vitali, Dagliati, Geifman, & Bellazzi, 2020).

Reliability Analysis (Cronbach's Alpha)

"Effectiveness of Intervention" and "Satisfaction with Intervention" have a combined Cronbach's Alpha of 0. 7564. In terms of reliability, the internal consistency is acceptable at above 0.7 which means the items measuring satisfaction and effectiveness capture similar constructs. This indicates that the survey scales regarding satisfaction and effectiveness are valid and reliable for further analysis (Ledermann et al., 2024).

Descriptive Statistics

Computing descriptive statistics for the key variables provides information on the central tendencies as well as the variation among the respondents. The data from the health ratings pre- and post-post-intervention show different degrees of improvement among the participants(Abdullah et al., 2024)). It appears the mean health rating before the intervention was lower than the mean post-intervention indicating there was an appreciable increase in health ratings for several individuals. This indicates the intervention had a positive influence on health outcomes (Lechner, Liu, Masterson, & Fenton, 2022).

Pearson Correlation (Health Before vs. After Intervention)

The correlation between 'Health Before' and 'Health After' is 0.6485 with a p-value < 0.0001 which is a clear indication of a strong positive correlation. This means there is a close relationship between the improvement of health ratings after the intervention and the initial health ratings, implying that patients who reported being low in health before the intervention reported significant improvements after the intervention (Rodriguez, Zenklusen, Staudt, Doroshow, & Lowy, 2021).

ANOVA (Satisfaction by Age Group)

The ANOVA test was conducted to investigate if there is any difference in satisfaction with the intervention among different age groups. The finding (F-statistic=2.2478, p-value=0.0786) supports the conclusion that there is no age group difference in satisfaction levels at the 0.05 significant level for hypothesis testing. Hence, it can be said that age does not affect the level of satisfaction of participants in the intervention, although there might be some small, undetected differences with this analysis (El Bairi et al., 2021).

Figures Interpretation

1. The Histogram for Health Rating Before and After Intervention: The histogram illustrates the range of frequencies of the participants' health ratings before and after the intervention. There was

an increase in health ratings after the intervention, signifying a shift towards more positive views, thus confirming rather definite favorable intervention outcomes (Rockne et al., 2019).

2. Scatter Plot for Satisfaction vs Effectiveness of Intervention: The scatter plot indicates a positive correlation between satisfaction with the intervention and the perceived effectiveness of the intervention. Therefore, it can be concluded that patients who were more satisfied with the intervention perceived it to be more effective (Zeng et al., 2021).

3. Line Plot for Health Before and After Intervention: The line plot depicts the trends in health ratings before and after the intervention. The increase in health ratings among most participants demonstrates the positive impact that the intervention has on health outcomes (Dlamini, Francies, Hull, & Marima, 2020).

4. Boxplot for Satisfaction with Intervention by Age Group: From the boxplot, satisfaction is approximately homogeneous across the age groups although some within-group variation exists. Lack of satisfaction in the intervention does not noticeably change based on age group, which reinforces the findings of the ANOVA (Shmatko, Ghaffari Laleh, Gerstung, & Kather, 2022).

Discussion

In modern molecular cancer biology, the health and economic implications of this research indicate its relevance as a developing cornerstone in oncology. Most health-related indicators, including the pre and post-intervention health ratings, were tested for normality and found to be normally distributed except for the satisfaction with intervention (Humayun, Yaseen, Shahwaiz, & Iftikhar, 2024). The conclusion that can be drawn is that satisfaction as a variable is bounded by some unobservable constraints, perhaps regarding expectations, treatment processes, or experiences that lie beyond the scope of traditional quantitative methodologies. Satisfaction's pronounced deviation strongly suggests that alternative analytical frameworks that assume normally distributed data should be considered. This will enable the flexible approach necessary for insight generation from the available data. An equally important finding is that the survey used to capture critical aspects of patient experience, especially concerning the outcome of the intervention, was trustworthy (Jubelin et al., 2022).

With a reliability satisfaction and effectiveness scale of 0.756, Cronbach's Alpha indicated internal consistency across the survey questions measuring these aspects. The positive internal consistency confirms the validity of the patient's perceptions regarding the success of the surgical interventions they undergo. The descriptive statistics show that the intervention had a positive

impact on health outcomes as indicated by an increase in average health ratings post the intervention(Ibraheem, 2024 #6). This also illustrates the purpose of the study which was to investigate the impact of new tools and treatments on oncology patients as it was hypothesized. The substantial increase in health ratings the intervention indicates that there is a positive change in the health of patients, which substantiates the assertion regarding positive impacts in oncology (Schmidt et al., 2021).

The Pearson correlation of health rating pre and post-intervention demonstrated (r=0.6485) moderate to strong correlation. This suggests that the improvement in the health status of the patients is in line with the health status at baseline, meaning those with lower health ratings before the intervention had greater improvements. This is the most important insight because it means that those patients with more advanced illnesses will most likely be the main beneficiaries of the intervention, thus aiding the design of more effective targeted treatment plans in oncology. Regarding differences in age and specific within-group satisfaction, the ANOVA test indicated no statistically significant differences in the levels of satisfaction across different age groups. This means that age is unlikely to be a determining factor for how patients regard the effectiveness of the intervention. While people generally assume that there might be an older adult's treatment expectation or response, the data indicates that the intervention works just as well across ages, which is further evidence that the efficacy of modern oncology instruments may be universal (Rowe & Pomper, 2022).

These visualizations back those conclusions even more. The histogram containing the self-reported health ratings before and after the intervention is insightful to the positive shift in the health outcome, the scatter plot depicts the high correlation between satisfaction and effectiveness perception, while the line plot shows the enhancement in health rating post-intervention which showcases the benefits of the intervention the patient has received. There were no marked age gaps in the satisfaction which supports the ANOVA results, therefore, the boxplot displayed age-based satisfaction without noteworthy differences. Using the newly developed oncology tools improves patient outcomes regarding their health and satisfaction as revealed by the findings of this report, but these data do raise concern insofar as there is a need to measure satisfaction at a more granular level. The application of advanced techniques and treatments of molecular biology in oncology yields these results, thus, there is justification to use these findings to bolster claims for further efforts and resources to be channeled towards enhancing cancer care services (Mateo et al., 2022).

Conclusion

Patient health outcomes and recovery after cancer treatment evaluation reveal that this report presents multifaceted findings concerning the newly developed tools used in cancer care, focusing on the molecular biology of cancer-diagnosed patients. The results indicate that the more modern techniques and tools provide improvement in patient's health as seen from the changes in health ratings before and after the intervention. The evaluation discusses the promise of the new technologies to improve the effectiveness of cancer treatment, especially for more severely ill patients who tend to have worse prognoses at the beginning of their treatment, which has previously been understood to support the notion that more precise and tailored intervention strategies increase the survival chances for cancer patients.

The analysis also supports the hypothesis that health ratings pre and post-intervention are normally distributed, which suggests that parametric statistical methods were suitable for these variables. Nonetheless, the non-normal distribution for the satisfaction ratings indicates that patients' subjective experiences go well beyond simple quantification of their satisfaction, emotions, personal expectations, deeply ingrained prejudices about the person's situation, and so forth, which are bound to differ from one patient to another. Such findings highlight the need for a broader range of strategies when measuring patient satisfaction and effectiveness, particularly in oncology where patient perceptions surround the treatment's effectiveness. The value of Cronbach's Alpha as computed for satisfaction and effectiveness scales pointed to strong levels of internal consistency which stems from good reliability suggesting that the instrument for capturing patient satisfaction and effectiveness was adequately designed.

This dependability enhances the validity of the findings and enables trusting the conclusions formulated based on the survey data. The moderately positive relationship between pre-and post-intervention health ratings indicates that health outcomes indeed aligned with the baseline health figure, which suggests a greater impact of the intervention on more severely ill patients. This observation stresses the role of personalized medicine in oncology, focusing on when treatment can be provided to patients in a manner that optimally benefits them. Also, the lack of noteworthy differences based on age in satisfaction levels as indicated by the ANOVA test implies that these complex interventions are relevant to a wider population of patients, irrespective of their age. This result counters the expectations of older adults or people from other age cohorts being less responsive to treatment and thus reinforces the notion that sophisticated cancer treatment is

beneficial to many. To sum up, the findings of this study strengthen the positive effects of advanced molecular techniques and interventions in oncology regarding patient health outcomes. The study also highlights the need to address patients' differences concerning perception when assessing the success of treatment. Ongoing study and development in this field are highly promising for the advancement of cancer treatment and for enhancing the living conditions of the patients.

References

Abdullah, A., Raza, A., Rasool, Q., Rashid, U., Aziz, M. M., & Rasool, S. (2024). A Literature Analysis for the Prediction of Chronic Kidney Diseases. *Journal of Computing & Biomedical Informatics, 7*(02).

Agostinelli, V., Torresi, G., Tarantino, V., Goteri, G., Filosa, A., Barbisan, F., . . . Ambrosini, E. (2025). The Impact and Performance of the Molecular Tumor Board: Three-Year Activity in Precision Medicine for Treatment of Patients with Cancer from the Marche Region, in Italy. *Oncology and Therapy*, 1-15.

Alsahafi, E., Begg, K., Amelio, I., Raulf, N., Lucarelli, P., Sauter, T., & Tavassoli, M. (2019). Clinical update on head and neck cancer: molecular biology and ongoing challenges. *Cell death & disease, 10*(8), 540.

Alshammari, A. H., Oshiro, T., Ungkulpasvich, U., Yamaguchi, J., Morishita, M., Khdair, S. A., . . . di Luccio, E. (2025). Advancing Veterinary Oncology: Next-Generation Diagnostics for Early Cancer Detection and Clinical Implementation. *Animals, 15*(3), 389.

Bera, K., Schalper, K. A., Rimm, D. L., Velcheti, V., & Madabhushi, A. (2019). Artificial intelligence in digital pathology—new tools for diagnosis and precision oncology. *Nature reviews Clinical oncology, 16*(11), 703-715.

Bhambri, P., & Khang, A. (2025). Progressive Cancer Treatment: AI Applications in Precision Oncology. In *Precision Health in the Digital Age: Harnessing AI for Personalized Care* (pp. 185-208): IGI Global Scientific Publishing.

bin Masroni, M. S., Koay, E. S.-C., Lee, V. K. M., Ng, S. B., Tan, S. Y., Tan, K. M., . . . Leong, S. M. (2025). Sociobiology meets oncology: unraveling altruistic cooperation in cancer cells and its implications. *Experimental & Molecular Medicine*, 1-11.

Cavalli, F. (2025). We need intelligent oncology everywhere. *Intelligent Oncology, 1*(1), 1-3.

Dancik, G. M., & Vlahopoulos, S. A. (2025). Editorial for the Special Issue: Bioinformatics and Computational Biology for Cancer Prediction and Prognosis. In (Vol. 16, pp. 167): MDPI.

Dlamini, Z., Francies, F. Z., Hull, R., & Marima, R. (2020). Artificial intelligence (AI) and big data in cancer and precision oncology. *Computational and structural biotechnology journal, 18*, 2300-2311.

El Bairi, K., Haynes, H. R., Blackley, E., Fineberg, S., Shear, J., Turner, S., . . . Gharib, M. (2021). The tale of TILs in breast cancer: a report from the international immuno-oncology biomarker working group. *NPJ breast cancer, 7*(1), 150.

Esplen, M. J., & Kohut, K. (2025). Bridging the gap: the need to integrate psychosocial oncology services into cancer genetics. *Journal of Psychosocial Oncology Research and Practice, 7*(1), 155.

Fischer, E. G. (2020). Nuclear morphology and the biology of cancer cells. *Acta cytologica, 64*(6), 511-519.

Fountzilas, E., Pearce, T., Baysal, M. A., Chakraborty, A., & Tsimberidou, A. M. (2025). Convergence of evolving artificial intelligence and machine learning techniques in precision oncology. *npj Digital Medicine, 8*(1), 75.

Hamza, M. (2024). Optimizing early detection of diabetes through retinal imaging: A comparative analysis of deep learning and machine learning algorithms. *Journal of Computational Informatics & Business, 1*(1).

Heitzer, E., Haque, I. S., Roberts, C. E., & Speicher, M. R. (2019). Current and future perspectives of liquid biopsies in genomics-driven oncology. *Nature Reviews Genetics, 20*(2), 71-88.

Humayun, U., Yaseen, M. T., Shahwaiz, A., & Iftikhar, A. (2024). Deep Learning Approaches for Brain Tumor Detection and Segmentation in MRI Imaging. *Journal of Computing & Biomedical Informatics, 8*(01).

Jubelin, C., Muñoz-Garcia, J., Griscom, L., Cochonneau, D., Ollivier, E., Heymann, M.-F., . . . Heymann, D. (2022). Three-dimensional in vitro culture models in oncology research. *Cell & Bioscience, 12*(1), 155.

Karaoglu, B., & Gur Dedeoglu, B. (2025). A Regulatory Circuits Analysis Tool,"miRCuit," Helps Reveal Breast Cancer Pathways: Toward Systems Medicine in Oncology. *OMICS: A Journal of Integrative Biology*.

Keating, P., & Cambrosio, A. (2019). *Cancer on trial: oncology as a new style of practice*: University of Chicago Press.

Lechner, M., Liu, J., Masterson, L., & Fenton, T. R. (2022). HPV-associated oropharyngeal cancer: epidemiology, molecular biology and clinical management. *Nature reviews Clinical oncology, 19*(5), 306-327.

Ledermann, J., Matias-Guiu, X., Amant, F., Concin, N., Davidson, B., Fotopoulou, C., . . . Lorusso, D. (2024). ESGO–ESMO–ESP consensus conference recommendations on ovarian cancer: pathology and molecular biology and early, advanced and recurrent disease☆. *Annals of Oncology, 35*(3), 248-266.

Marinello, A., & Aldea, M. (2025). Precision oncology: Indications and challenges in the implementation of high-throughput sequencing in clinical practice. In *Implementation of Personalized Precision Medicine* (pp. 203-221): Elsevier.

Mateo, J., Steuten, L., Aftimos, P., André, F., Davies, M., Garralda, E., . . . Normanno, N. (2022). Delivering precision oncology to patients with cancer. *Nature medicine, 28*(4), 658-665.

Nicora, G., Vitali, F., Dagliati, A., Geifman, N., & Bellazzi, R. (2020). Integrated multi-omics analyses in oncology: a review of machine learning methods and tools. *Frontiers in oncology, 10*, 1030.

Pali, C., & Mandle, N. (2025). Present-Day Difficulties in Treating Cancer. *Journal of Pharmacology, Genetics and Molecular Biology (JPGMB), 1*(01), 60-79.

Power, P., Straehla, J. P., Fangusaro, J., Bandopadhayay, P., & Manoharan, N. (2025). Pediatric neuro-oncology: Highlights of the last quarter-century. *Neoplasia, 59*, 101098.

Ratti, M., Lampis, A., Ghidini, M., Salati, M., Mirchev, M. B., Valeri, N., & Hahne, J. C. (2020). MicroRNAs (miRNAs) and long non-coding RNAs (lncRNAs) as new tools for cancer therapy: first steps from bench to bedside. *Targeted oncology, 15*, 261-278.

Rockne, R. C., Hawkins-Daarud, A., Swanson, K. R., Sluka, J. P., Glazier, J. A., Macklin, P., . . . Oden, J. T. (2019). The 2019 mathematical oncology roadmap. *Physical biology, 16*(4), 041005.

Rodriguez, H., Zenklusen, J. C., Staudt, L. M., Doroshow, J. H., & Lowy, D. R. (2021). The next horizon in precision oncology: Proteogenomics to inform cancer diagnosis and treatment. *Cell, 184*(7), 1661-1670.

Rowe, S. P., & Pomper, M. G. (2022). Molecular imaging in oncology: Current impact and future directions. *CA: a cancer journal for clinicians, 72*(4), 333-352.

Schmidt, D. R., Patel, R., Kirsch, D. G., Lewis, C. A., Vander Heiden, M. G., & Locasale, J. W. (2021). Metabolomics in cancer research and emerging applications in clinical oncology. *CA: a cancer journal for clinicians, 71*(4), 333-358.

Shimizu, H., & Nakayama, K. I. (2020). Artificial intelligence in oncology. *Cancer science, 111*(5), 1452-1460.

Shmatko, A., Ghaffari Laleh, N., Gerstung, M., & Kather, J. N. (2022). Artificial intelligence in histopathology: enhancing cancer research and clinical oncology. *Nature cancer, 3*(9), 1026-1038.

Silantyev, A. S., Falzone, L., Libra, M., Gurina, O. I., Kardashova, K. S., Nikolouzakis, T. K., . . . Tsatsakis, A. (2019). Current and future trends on diagnosis and prognosis of glioblastoma: from molecular biology to proteomics. *Cells, 8*(8), 863.

Tran, K. A., Kondrashova, O., Bradley, A., Williams, E. D., Pearson, J. V., & Waddell, N. (2021). Deep learning in cancer diagnosis, prognosis and treatment selection. *Genome medicine, 13*, 1-17.

Tsao, D. S. (2025). Absolute quantification of cell-free DNA for prenatal genetics and oncology. *Trends in Biotechnology*.

Vale, A. J. M., Teixeira, H. M., Filho, I. A., Pinheiro, F. I., de Azevedo, E. P., Guzen, F. P., & Cobucci, R. N. (2025). Role of Tumor Markers in Early Detection and Prevention of Complications in Oncology. In *Handbook of Cancer and Immunology* (pp. 1-22): Springer.

Youssef, E., Palmer, D., Fletcher, B., & Vaughn, R. (2025). Exosomes in Precision Oncology: From Bench to Bedside in Diagnostics and.

Yusufaly, T., Roncali, E., Brosch-Lenz, J., Uribe, C., Jha, A. K., Currie, G., . . . Pandit-Taskar, N. (2025). Computational nuclear oncology toward precision radiopharmaceutical therapies: current tools, techniques, and uncharted territories. *Journal of Nuclear Medicine*.

Zeng, D., Ye, Z., Shen, R., Yu, G., Wu, J., Xiong, Y., . . . Sun, L. (2021). IOBR: multi-omics immuno-oncology biological research to decode tumor microenvironment and signatures. *Frontiers in immunology, 12*, 687975.